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Supplementary information

The results of biodiversity–ecosystem functioning experiments are realistic

In the format provided by the
authors and unedited

1   **Supplementary Information** for Jochum et al. 2020 Nature Ecology and Evolution paper entitled

2   "The results of biodiversity-ecosystem functioning experiments are realistic"

3   **Supplementary Methods**

4   **1. Details of ecosystem function measurement in the Jena Experiment and BioDIV**

5   **Jena and BioDIV plant aboveground biomass** In Jena, aboveground plant biomass was harvested bi-

6   annually (late May and late August), just prior to mowing. Here, we used only the first harvest, which

7   represents peak standing biomass in most years, from years 2006–2015. All vegetation was clipped at 3

8   cm above ground in up to four rectangles of 0.2 m × 0.5 m per plot with the location of these rectangles

9   being randomly assigned each year. For BioDIV, aboveground peak plant biomass was harvested

10   annually in August by clipping 0.1 m × 6 m strips (see above) each year from 2006–2015. For both

11   studies, harvested target-species biomass was sorted into individual species, dried to constant weight at

12   70 °C for at least 48 h and weighed. Target plant community biomass was then calculated as the sum of

13   the biomass of the individual sown species $(g\ m^{-2})$.

14   **Jena and BioDIV aboveground plant biomass C:N ratio** In Jena, the combined target species

15   material from the spring biomass harvest (May) was shredded (Analysenmühle, Kinematica, Littau,

16   Switzerland). A subsample of the shredded material was milled to fine powder in a ball-mill (mixer mill

17   MM2000 Retsch, Haan, Germany) and 5–10 mg was used for CN analysis with an elemental analyzer.

18   C and N content were calculated as percentage elemental concentration of dry material and C:N ratios

19   as the ratio between those percentages for years 2007-2012.

20   In BioDIV, two strips of 0.1 m × 6 m were clipped, typically in late July or early August with

21   clip strip locations rotated each year. Unsorted biomass was air-dried at 40 °C. Dried biomass samples

22   were ground (standard Thomas Wiley mill) and the resulting sample homogenized. A sub-sample was

23 re-ground in a Wiley Mini-Mill, stored in glass scintillation vials and re-dried prior to lab analysis.

24 Percent C and N content in dry matter were determined using an elemental analyzer (NA1500, Carlo-

25 Erba Instruments or ECS 4010, COSTECH Analytical Technologies Inc., Valencia, CA, USA) at

26 University of Minnesota or at the Ecosystems Analysis Lab, University of Nebraska, Lincoln. Ratios of

27 dry mass elemental content were then calculated from these results for year 2006.

28 **BioDIVsoil organic C** Soil C samples were taken at all BioDIV plots during summer 2006 at 0–20 cm

29 depth on nine sites per plot [1]. Samples were sieved to remove roots, combined for each plot, mixed and

30 ground. Subsequently, soil samples were dried at 40 °C for 5 days. For each plot, two soil samples were

31 analysed for total C by combustion and gas chromatography (Costech Analytical ECS 4010 instrument,

32 Costech Analytical Technologies Inc., Valencia, CA). Because of the acidic sandy soil at the BioDIV

33 experiment, soil organic C can be considered a close approximation of total C here. We used the

34 average of the two measurements of C in % total carbon of dry weight.

35 **Jena soil organic C** Soil organic C in the Jena "main" experiment was determined in 2008, 2011 and

36 2014. Using a split-tube sampler (4.8 cm diameter), three soil cores per plot were taken to a depth of 30

37 cm [2]. Soil cores were segmented into 5 cm depth sections and pooled per depth sections and plot. Soil

38 was then dried, sieved and milled. Subsequently, total C was determined by combustion with an

39 elemental analyzer at 1,150 °C (Elementaranalysator vario Max CN, Elementar Analysensysteme

40 GmbH, Hanau, Germany). Because of the calcareous bedrock, Jena soil contains high proportions of

41 inorganic carbon (e.g., in 2014, the proportion of inorganic Cwas on average 39 % and ranged from 18

42 % to 73 %). To account for this, inorganic C concentration was measured after oxidative removal of

43 organic C for 16 h at 450 °C in a muffle furnace. Finally, organic C concentration was calculated as the

44   difference between total and inorganic C for each 5-cm-layer [2] and we averaged over the two

45   uppermost layers to get organic C content for 0–10 cm depth. Subsequently, we averaged over the three

46   samples to get soil organic C content per plot in g kg^{-1} soil for each year.

47   **Jena and BioDIV root biomass** In Jena, standing root biomass was sampled down to 40 cm depth in

48   all plots in June 2011 and 2014. On each plot, three cores of 3.5 cm diameter were taken and

49   immediately stored at 4 °C until further handling. The total sample was washed to determine root

50   biomass. Bulk samples were carefully washed by hand over a sieve of 0.5 mm mesh size. Remaining

51   soil particles and stones were removed with tweezers. Roots were dried at 60–70 °C and weighed

52   subsequently [3]. Unit: g m^{-2}

53   In BioDIV, root biomass was sampled in 2010 after aboveground biomass clipping by collecting

54   three 5 cm diameter × 30 cm depth cores per clipped strip [1]. Roots were washed free of soil, sorted

55   from other organic material, dried and weighed. Unit: g m^{-2}

56   **Jena herbivory rate** In Jena, invertebrate herbivory rates were assessed as proportional damage for

57   every plant species × plot-combination. Herbivory rates of individual plant species were used to

58   calculate community herbivory rates based on four different types of invertebrate herbivory: chewing,

59   rasping, sap sucking and leaf mining. Samples of the Jena biomass harvest were used after sorting to

60   species. For a maximum of 20 randomly chosen leaves per plant species, damage area was estimated in

61   mm^2 as total value of the four damage types and total leaf area of every leaf was measured with an area

62   meter (LI-3000C Area Meter equipped with a LI3050C transparent belt conveyor accessory, LI-COR

63   Biosciences, Lincoln, USA). For details on the methods used see [4]. Here, we used percentage herbivory

64   of the target species community from the late harvest, as this was available for three years from 2010–

65 2012. Unit: % damage

66 **Jena soil microbial biomass C** Soil sampling and measurement of basal and substrate-induced

67 microbial respiration with an oxygen-consumption apparatus was done on each plot in September 2010

68 [5]. Oxygen consumption of soil microorganisms in a fresh-soil equivalent to 3.5 g dry weight was

69 measured at 22 °C. Substrate-induced respiration was determined by adding D-glucose to saturate

70 catabolic enzymes of microorganisms according to preliminary studies (4 mg g^{-1} dry soil solved in 400

71 µl deionized water; [6,7]). Maximum initial respiratory response (µl O_2 g^{-1} dry soil h^{-1}) was calculated as

72 mean of the lowest three oxygen consumption values within the first 10 h after glucose addition.

73 Microbial biomass C (µg C g^{-1} dry soil) was calculated as 38 × maximum initial respiratory response as

74 suggested by preliminary studies [8]. Previous work has shown that the 2010 microbial biomass data are

75 representative for long-term plant diversity effects [7].

76 **Jena phosphatase activity** Nine soil cores (diam. 2 cm, 0–5 cm depth) were combined to one

77 composite sample per plot to assess phosphatase activity in 2013 [9]. Because of the alkaline pH of the

78 soil, we measured alkaline phosphomonoesterase activity (phosphatase activity) according to the assay

79 by [10]. For each soil sample, one replicate and one blank value were included. One gram of field moist

80 soil was mixed with toluene, modified universal buffer (MUB) and p-nitrophenylphosphate (pNP), and

81 incubated at 37 °C for 1 hour. Subsequently, we added $CaCl_2$ and NaOH. To blanks, pNP was added

82 after incubation. The solution was filtered through P-free filters (MN 619 G ¼, Macherey-Nagel GmbH

83 & Co. KG, Düren, Germany). Directly after filtration, pNP concentrations [µg ml^{-1}] were measured at

84 400 nm with a spectrophotometer (PU 8675 VIS spectrophotometer, Philips GmbH, Hamburg,

85 Germany). The soil moisture was determined gravimetrically, i.e. by weighing before and after drying

86 at 105 °C to convert phosphatase activities to dry matter (μg pNP g^{-1} h^{-1}).

87 **Jena pollinator abundance** In 2010 and 2012, hymenopterans were sampled by suction sampling

88 using a modified commercial vacuum cleaner (Kärcher A2500, Kärcher GmbH, Winnenden, Germany).

89 In each year, within each plot, two random subplots of 0.75 m x 0.75 m were chosen, covered with a

90 gauze-coated cage of the same size, and arthropods within cages were sampled. The sampling was

91 carried out between 9 a.m. and 4 p.m. within two 4-day sampling periods. The overall abundance of

92 hymenopterans across the two samples per plot was used as a proxy of pollinator abundance and thus

93 potential for pollination on each plot in the respective year. Unit: number of individuals

94 **2. Processing TRY and other plant-trait data to generate species-level values**

95 For each of the geographical species subsets, TRY trait data were processed separately following a

96 standardized protocol: i) Removal of duplicate observations (e.g. duplicate entries of leaf mass from the

97 same individual). ii) Removal of non-open data and removal of data obtained from outside the

98 respective target continents. iii) Calculation of outliers for each trait-species combination (trait mean

99 +/- 1.96 SD as outlier definition). iv) Removal of observations with TRY ErrorRisk > 4. v) Averaging

100 over trait-species values per TRY dataset. vi) Removal of TRY datasets with more than 5% of values

101 identified as outliers. vii) Averaging over trait-species mean values of the remaining datasets. For the

102 US species, TRY data was combined with additional trait data collected in naturally occurring

103 polycultures at Cedar Creek (personal communication with J.A. Catford [11] now available on TRY as

104 dataset 354, P.B. Reich, J. Cavender-Bares). These Cedar Creek trait averages per dataset were

105 included into the averaging process at step v). Finally, trait values of synonyms and accepted species

106 names were averaged and assigned to the accepted plant-species names where necessary.

Supplementary Information on sensitivity analyses I.

To test how robust our results are to key methodological decisions in our analysis, we performed a number of sensitivity analyses. Specifically, we tested how methodological decisions regarding the PCA analysis of comparing plant-community properties affected the number and identity of experimental plots selected as realistic. These methodological choices include the selection of community properties entering the PCA, the method of calculating multidimensional overlap, and a set of other methodological details such as, for example, the number of PCA axes used for calculating multidimensional overlap or the choice of real-world datasets (see below). If not noted otherwise, we used the 12 vif-selected community properties and the convex-hull volume method to calculate intersections (main analysis) for both the German and US comparison. The different analyses are described below. Please refer to Supplementary Tables S2 and S3 below for a comparison of selected realistic plots for the main analysis and the sensitivity analyses presented here.

We assessed the impact of using different subsets of community properties in the PCAs by re-running our analysis with the following subsets: i) all 21 community properties available ("All21"), ii) the 12 vif-selected community properties ("Full12", main analysis), iii) four subsets defined by excluding one class of community properties (taxonomic, phylogenetic, functional diversity, or CWM functional traits; called "Allbuttax", "Allbutphyl", "Allbutfun", and "AllbutCWM"), and iv) all 21 properties except the 5 properties showing the biggest differences between experimental and real-world datasets in the two regions ("remove5", sensitivity A), respectively. Supplementary Table 1 below summarizes which community properties are used in which analysis.

To test what impact the methodology used for calculating multidimensional overlap had on our findings, we combined the above-described community-property subsets with three overlap calculation methods: i) three-dimensional convex hull volumes (main analysis), ii) three-dimensional

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130 hypervolumes, and iii) two-dimensional 95% confidence interval ellipses (see main text methods for

131 details).

132 Performing all possible combinations of subsets and methods would lead to an unmanageable number

133 of results and, given the relative robustness of our results to most methodological decisions, seems

134 unnecessary. Hence, we present results for a selection of combinations. For two community-property

135 subsets, namely the All21 and the Full12 subsets, all three overlap calculation methods were run. For

136 the remaining subsets, only the convex hull volume method was used. The resulting overlap (realistic

137 plots) is presented for all these combinations in Supplementary Tables S2 and S3. Alternative versions

138 of Fig. 1 (PCA and overlap calculation) are shown in Supplementary Fig. 1 for all above-described

139 combinations. Alternative versions of Fig. 2 (BEF) relationships are shown in Supplementary Fig. 3 for

140 all combinations of the All21 and Full12 subsets and the three overlap calculation methods and

141 additionally for the species-abundance based NMDS, for the USA dataset.

142 Below, we provide additional details for these analyses and succinctly summarize their results.

143 **Full12:** Here, we used the same community property subset as in the main analysis (see Supplementary

144 Table 1), but tested two additional overlap calculation methods. For the Jena Experiment, this resulted

145 in 24 and 21 plots to be chosen as realistic (instead of 23) with 91 and 87 % of overlap with the main

146 analysis realistic subset for the "hyper" and "ellipse" method, respectively (Supplementary Table 2 and

147 Supplementary Fig. 1). For BioDIV, 109 and 133 plots were deemed realistic, with 87 and 96 %

148 overlap with the main analysis realistic subset, for the "hyper" and "ellipse" methods, respectively

149 (Supplementary Table 3 and Supplementary Fig. 1). For the BEF relationships (Supplementary Fig. 3),

150 these changes resulted in a slight increase of the number of relationships that changed significantly

151 after subsetting (confidence intervals not containing each other's slope estimate) from the

152 unconstrained to the constrained dataset (3 and 4 BEF relationships compared to 2 in the main analysis

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153   for "hyper" and "ellipse", respectively).

154   **All 21:** Here, instead of removing community properties based on the vif-based selection of

155   multicollinear variables, all 21 community properties entered the PCA's. For the Jena Experiment, this

156   resulted in 33, 32, and 34 of 82 (40, 39, and 41 %) plots to be selected as realistic which included 91,

157   96, and 96 % of the plots selected as realistic in the main analysis for the "chull", "hyper", and

158   "ellipse" methods, respectively. For BioDIV, 121, 104, and 136 of 159 (76, 65, and 86 %) were selected

159   as realistic, containing 95, 85, and 91 % of the main analysis realistic plots for the "chull", "hyper", and

160   "ellipse" methods, respectively. For the BEF relationships, these slight changes translated into 2, 1 and

161   1 BEF relationships changing significantly between the unconstrained and the constrained dataset

162   (compared to 2 changes in the main analysis) for the "chull", "hyper", and "ellipse" methods,

163   respectively (see Supplementary Fig. 3 for details). Given this very strong similarity to the main

164   analysis, we conclude that using all 21 community properties would not change our conclusions. Thus,

165   we stick to choosing community properties based on the vif selection to reduce multicollinearity among

166   variables entering the PCA.

167   **Allbuttax:** Here, we used all community properties except for the taxonomic diversity properties (see

168   Supplementary Table 1). For the Jena Experiment, 44 instead of 23 of 82 plots were deemed realistic,

169   including all plots chosen as realistic in the main analysis. For BioDIV, 122 instead of 121 of 159 plots

170   were deemed realistic, including 94 % of the ones chosen as realistic in the main analysis.

171   **Allbutphyl:** Here, we used all community properties except for the phylogenetic diversity properties

172   (see Supplementary Table 1). For the Jena Experiment, 41 instead of 23 of 82 plots were deemed

173   realistic, including all plots chosen as realistic in the main analysis. For BioDIV, 125 instead of 121 of

174   159 plots were deemed realistic, including 96 % of the ones chosen as realistic in the main analysis.

175   **Allbutfun:** Here, we used all community properties except for the functional diversity properties (see

176   Supplementary Table 1). For the Jena Experiment, 30 instead of 23 of 82 plots were deemed realistic,

177   including 96% of the plots chosen as realistic in the main analysis. For BioDIV, 124 instead of 121 of

178   159 plots were deemed realistic, including 96 % of the ones chosen as realistic in the main analysis.

179   **AllbutCWM:** Here, we used all community properties except for the CWM functional traits (see

180   Supplementary Table 1). For the Jena Experiment, 19 instead of 23 of 82 plots were deemed realistic,

181   including 83 % of the plots chosen as realistic in the main analysis. For BioDIV, 126 instead of 121 of

182   159 plots were deemed realistic, including 90 % of the ones chosen as realistic in the main analysis.

183   Below, we describe the additional sensitivity analyses (A-F) for which results are shown in

184   Supplementary Table 1, but not in Supplementary Fig. 1 and Fig. 3.

185   **A: Remove only 5 community properties:** Here, we removed community properties based on the

186   proportion of biodiversity experiment communities falling within the real-world range of those

187   properties (see Supplementary Tables S4 and S5). As the similarity of biodiversity experiment and real-

188   world communities regarding these properties differed between the German and US dataset, we

189   removed different variables for these two data sets. For each dataset, we removed the 5 community

190   properties with the lowest proportion of biodiversity experiment communities falling within the real-

191   world range for these properties. For the German PCA, we removed SEve, S, PD, FRic, and MNTD.

192 For the US PCA; we removed LDMC, FEve, SLA, leaf N, and FRic. For the Jena Experiment, this

193 resulted in 49 of 82 (60 %) plots to be selected as realistic with all of the main analysis realistic plots

194 included in this subset. For BioDIV, 112 of 159 (70 %) were selected as realistic, containing 83 % of

195 the main analysis realistic plots. Given this very strong overlap with the main analysis, we conclude

196 that using this subset of community properties would not change our conclusions. Thus, we stick to

197 choosing community properties based on the vif selection to reduce multicollinearity among variables

198 entering the PCA.

199 **B: Change number of axes in PCA used for convex hull intersection:** In the main analysis, we used

200 the first three PCA axes for 3-dimensional convex hull and hypervolumes to determine the intersection

201 between biodiversity experiment and real-world communities in multidimensional space (see Extended

202 Data Fig. 6 for an overview of the variance explained by all PCA axes). Here, we changed this number

203 of axes to the number of axes explaining above-average variance. All axes explaining more than 1/12

204 (above average) of the total variance were included. For the German dataset, these were the first five

205 axes, explaining a summed total of 73 % of the total variance (compared to the first three axes

206 explaining 53 %). When using these five axes, 19 instead of 23 (of 82, 23 %) Jena Experiment plots

207 were selected as realistic (Supplementary Table 2 and 3), containing 83 % of the plots selected as

208 realistic in the main analysis. For the US dataset, it was the first four axes, together explaining 64 % of

209 the total variance (compared to the first three axes explaining 55 %). Due to an R "geometry" error in

210 the convex hull calculation when using four axes in the US dataset (most likely some PCA points too

211 close to each other), the intersection could not be calculated. This was probably caused by a few

212 communities being too similar (nearly coincident points) in these four axes. The error did not occur at

213 three axes and is more likely to occur at 4-D and more according to the package documentation. Given

10

214   the broadly comparable number and identity of realistic plots between the 2-D ellipse, 3-D convex hull

215   and 3-D hypervolume intersection calculation (see Supplementary Table 3), we assume that adding the

216   fourth dimension (explaining 9 % of the total variance) to the convex hull is unlikely to heavily

217   influence the selection of realistic plots for BioDIV. Overall, although changing the number of axes

218   changed the number and identity of selected realistic plots, there is still a strong overlap of realistic

219   plots selected by this sensitivity analysis and the main analysis, so we conclude that, qualitatively, our

220   results would not change.

221   **C: Use all available non-experiment plots as real world rather than just the most**

222   **methodologically comparable:** In the main analysis, we used only a subset of the available real-world

223   datasets to identify realistic biodiversity experiment plots in the intersection calculations. This decision

224   was made because the vegetation survey methodology of some real-world datasets differed quite

225   substantially from the methodology in the biodiversity experiments (transects, subplots, very different

226   vegetation survey area). Here, we tested the impact of using all available real-world datasets (see

227   Figure 1 a and e) in the intersection calculation on the selection of realistic experimental plots. For the

228   Jena Experiment, this resulted in 42 of 82 (52 %) plots to be selected as realistic with all of the main

229   analysis realistic plots included in this subset. For BioDIV, 122 of 159 (77 %) were selected as realistic,

230   containing all of the main analysis realistic plots. Looking at Figure 1 a and e, these numbers could

231   have been expected given that, in the German PCA, for example the Jena invasion communities are

232   shifted towards the real-world communities relative to the Jena Experiment main communities. In the

233   US comparison, however, most the additional real-world communities (Old field succession

234   chronosequence and Oak savannah communities) do not extend further towards the real-world

235   communities than the Fertilization 1 and 2 communities already used in the main analysis. Given this

236   very strong overlap with the main analysis, we conclude that using all real-world data sets available

237   would not change our conclusions. Thus, we stick to only using the most comparable datasets in our

238   main analysis.

239   **D: Change overlap criterion, i.e. explore number of years in intersection for each plot:** In the main

240   analysis, we selected biodiversity experiment plots as realistic if their plant communities fell in the

241   PCA-based intersection of experiment and real-world data in at least one year. Here, we show for how

242   many years which of the "realistic" plots had plant communities falling within the intersection.

243   For the Jena Experiment, 6 of 23 realistic plots were included in all years, all but three plots were at

244   least included in more than one year. For BioDIV, 74 of 122 realistic plots were included in all years,

245   and another 21 plots were included in all but one year. All other plots were included in fewer years.

246   This indicates that, for BioDIV, changing the criteria for being defined realistic (e.g. having at least 50

247   % of the annual communities in the intersection) would not change the conclusions a lot. In Jena,

248   however, choosing e.g. 50 % of annual communities as a threshold would lead to only very few plots

249   being selected as realistic. The vast majority of main-analysis realistic plots are not only included in

250   only a single year. Consequently, even the most realistic Jena Experiment plots are only real-world

251   comparable in a subset of all years considered here. However, these are the most real-world comparable

252   subset of the Jena Experiment plots. Our aim was to remove the most unrealistic plots from each

253   experiment and then compare BEf relationships. While it is interesting to see how the two biodiversity

254   experiments differ in their relation to the real-world communities, comparing BEF relationships is only

255   really possible if there are enough plots for each BEF model to fit a relatively reliable model. We

256   conclude that choosing a different threshold here would reduce the number of realistic plots, but mainly

257   impact our analysis by not providing enough data points to fit the Jena BEF relationships for the subset

258   of realistic plots only.

259   **E: Calculate realistic plots using species-abundance NMDS instead of community-property**

260   **PCA's:** In the main analysis, selection of realistic experimental plots is always based on the

261   community-property PCA's. Here, we test how the selection of realistic plots changes when using the

262   first three axes of a species-abundance based NMDS (function "metaMDS" in R package "vegan" [12]).

263   As visualized in the NMDS biplots of Supplementary Figure 2, the plant community composition of

264   biodiversity experiments and real-world systems differs far more in the German than in the US

265   comparison. In the US comparison, there is a good overlap in plant community NMDS space, resulting

266   in 53 of the 159 plots (33 %) to be selected as realistic, containing 43 % of plots selected as realistic

267   based on the community property PCA. In the US comparison, the biodiversity experiment and real-

268   world plots are all situated in a relatively small area, thus we expect some similarity in species

269   composition even though the management of these sites differs. Constraining data to only those 53

270   plots led to two of the four US BEF relationships changing significantly from the unconstrained to the

271   constrained dataset, but in both cases, the slopes of the realistic subsets were higher (see

272   Supplementary Fig. 3), thus suggesting that experiments might underestimate BEF relationships for

273   certain functions and thus strengthening our conclusion that experimental findings are generally robust.

274   In the German comparison, the Jena Experiment community NMDS space contains the real-world

275   plots, but, interestingly, very few Jena Experiment plots actually fall within the real-world NMDS

276   space (see Supplementary Figure 2). As such, only 2 of the Jena Experiment plots (2 %) would be

277   selected as realistic based on this methodology. This indeed is a very low percentage of realistic sites,

278   but this is not unexpected. The German real-world plots are spread out across three geographically

279   distant regions across Germany with a strong gradient of land-use intensity and the Jena Experiment

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280   was established in a single old field site with (obviously and intentionally) narrow environmental

281   gradients and plant species being selected from a deliberately regional species pool fitting for the given

282   environmental and geographical context. Consequently, we never expected the plant communities

283   themselves to be very similar in their composition. This is exactly the reason why our analysis is based

284   on comparing the properties of these plant communities irrespective of the identity of species involved.

285   **F: Only Germany: Use only real-world plots with management similar to Jena Experiment:** In the

286   main analysis, we compare plant communities from biodiversity experiments to those of real-world

287   plots covering a broad gradient of land-use intensities, especially in the German dataset (Biodiversity

288   Exploratories). In addition to visualizing the different land-use intensity and its components (mowing,

289   grazing, fertilization) in an alternative version of Figure 1 (Supplementary Figure 5), we tested the

290   impact of using only Biodiversity Exploratories plots with land use roughly comparable to the Jena-

291   Experiment for the German comparison. The Jena Experiment plots are mown twice a year and neither

292   fertilized nor grazed. Specifically, we removed all Biodiversity Exploratories plots that are grazed or

293   fertilized and those that are never mown, leaving only the mown (but neither grazed nor fertilized)

294   plots in the analysis. This procedure resulted in only 10 Exploratories plots left in the dataset (9 plots

295   from the North-East region Schorfheide-Chorin and one plot from the South-West region Schwäbische

296   Alb). Expectedly, this resulted in only a very small subset of the Jena Experiment plots being selected

297   as realistic, namely 10 of 82 plots (12 %), containing 43 % of the originally selected realistic plots. The

298   aim of our study was to compare the biodiversity experiments to real-world grasslands in the same

299   countries. These real-world grasslands are managed differently than the biodiversity experiments. Still,

300   we find experimental plots with plant communities comparable in their properties to those of the real-

301   world plots. While it would be interesting to compare the Jena Experiment to real-world plots

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302   undergoing similar land use, this is not feasible with our dataset and we thus stick to using all real

303   world datasets sampled in a relatively comparable manner to the biodiversity experiments.

304   Please note that, for the US data, when leaving all 21 or keeping 16 (removing the five most different)

305   community properties in the PCA, results of the intersection calculation should be taken with caution

306   due to a slight onset of horseshoe-like patterns in the PCA. We take this as another reason to stick to

307   our vif-based selection of community properties to enter the PCA for the main analysis.

308 **Supplementary Table 1.** Community properties used in the different main and sensitivity subsets.
309 Column "Class" specifies which class of community properties a given property belongs to (taxonomic,
310 phylogenetic, and functional diversity, and CWM functional traits). "Full 12 vif" is the vif-selected
311 subset used in the main analysis. The other subsets are used in sensitivity analyses.

Class		All 21	Full 12 vif	All but tax	All but phyl	All but fun	All but CWM	GER remove 5	USA remove 5
fun	FRic	1	1	1	0	1	0	0
fun	FEve	1	1	1	0	1	1	0
fun	FDiv	0	1	1	0	1	1	1
fun	FDis	0	1	1	0	1	1	1
fun	RaoQ	0	1	1	0	1	1	1
CWM	leaf_area	0	1	1	1	0	1	1
CWM	SLA	1	1	1	1	0	1	0
CWM	leaf_drymass	1	1	1	1	0	1	1
CWM	LDMC	1	1	1	1	0	1	0
CWM	leaf_N	1	1	1	1	0	1	0
CWM	leaf_P	1	1	1	1	0	1	1
CWM	height	1	1	1	1	0	1	1
CWM	seedmass	1	1	1	1	0	1	1
tax	S	0	0	1	1	1	0	1
tax	H	0	0	1	1	1	1	1
tax	D1	0	0	1	1	1	1	1
tax	D2	1	0	1	1	1	1	1
tax	SEve	1	0	1	1	1	0	1
phyl	PD	0	1	0	1	1	0	1
phyl	MPD	0	1	0	1	1	1	1
phyl	MNTD	1	1	0	1	1	0	1

312 **Supplementary Figure 1.** Alternative versions of Fig. 1 based on alternative intersection scenarios
313 (community- property subsets and overlap calculation methods). a & b: PCA and factor loadings; c &
314 d: 3D convex hull volume, e & f: 3D hypervolume, g & h: 2D ellipse. 12 different versions: For subsets
315 Full12 (vif selected) and All21, three methods are shown. For subsets excluding one of the community-
316 property classes (Allbuttax = all properties except taxonomic div. properties), only the convex hull
317 method is presented. All scenario's shown for both geographical datasets. See Supplementary Table 1
318 for community properties included per subset and Supplementary Fig. 3 and Supplementary Tables 2
319 and 3 for overlap for species-abundance based NMDS.
320 German Full12 (three methods):
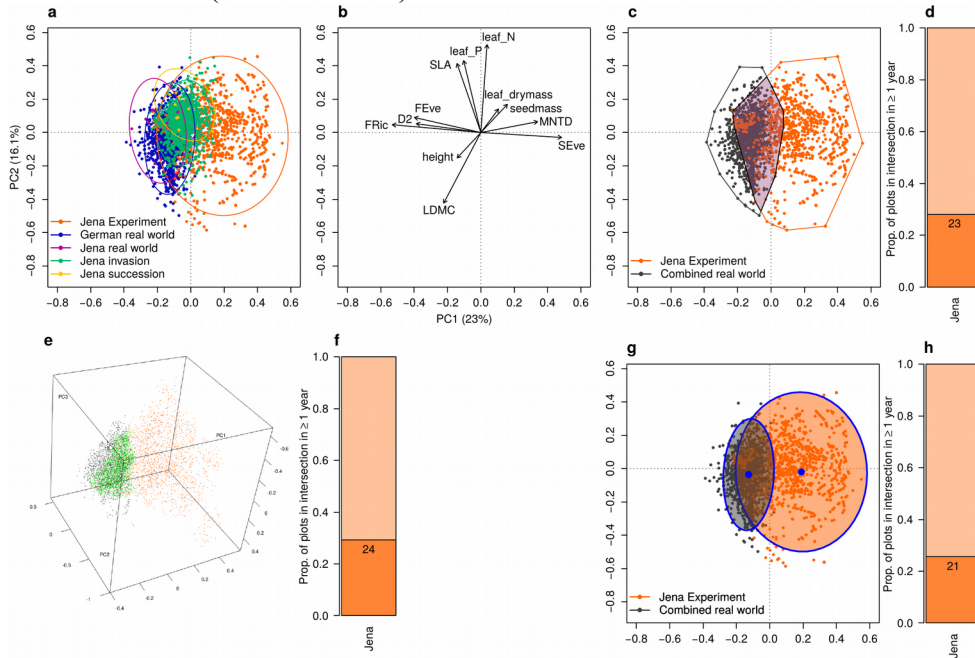
321 German All21 (three methods):

17
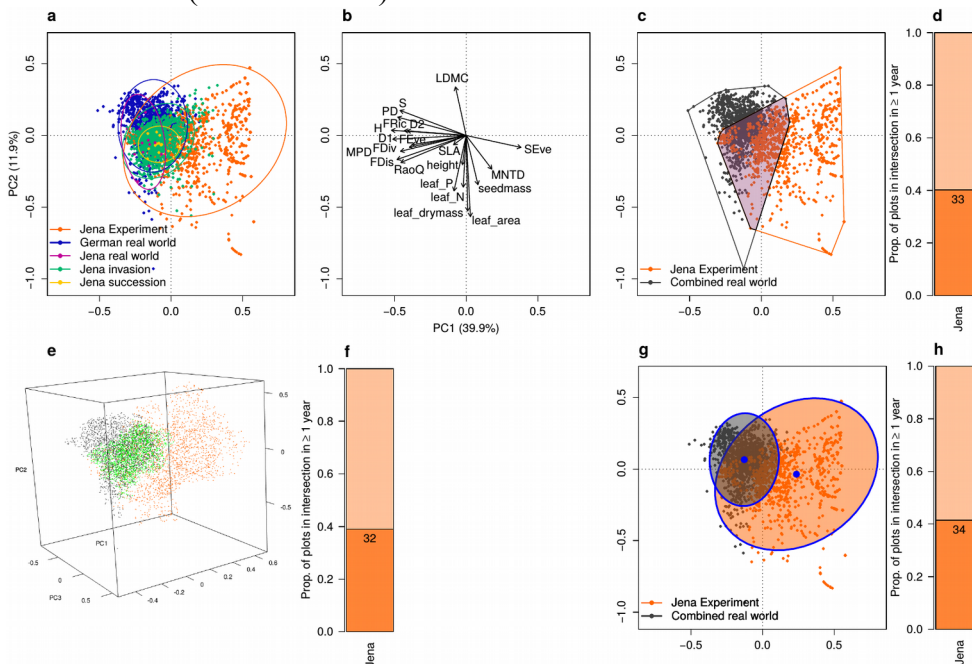
322   German Allbuttax (only chull):
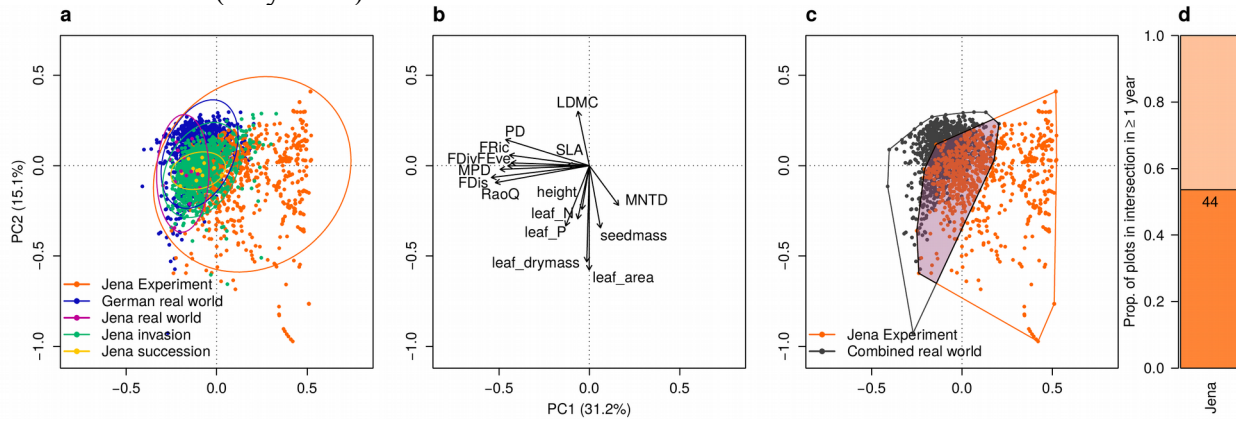
323   German Allbutphyl (only chull):

324   German Allbutfun (only chull):

18

325 German AllbutCWM (only chull):

326 US Full12 (three methods):

327   US All21 (three methods):

328   US Allbuttax (only chull):

329   US Allbutphyl (only chull):

330   US Allbutfun (only chull):

331   US AllbutCWM (only chull):

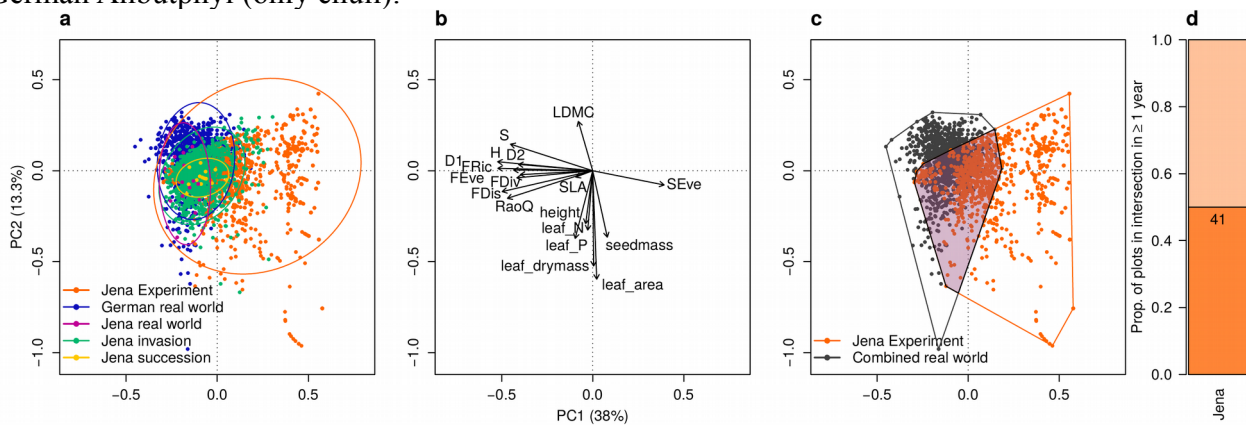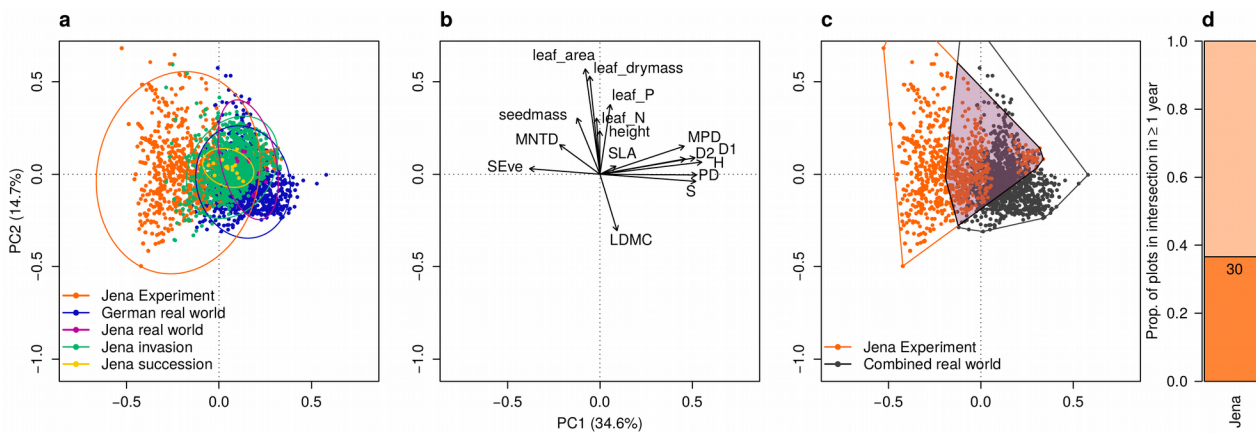| plot	sown_div	num_fg	Full12_chull	Full12_hyper	Full12_ellipse	All21_chull	All21_hyper	All21_ellipse	Allbuttax_chull	Allbutphyl_chull	Allbutfun_chull	AllbutCWM_chull	A_remove5	B_moreaxes	C_allreal	D_count	E_NMDS	F_LUIrem
B1A22	60	4	1	1	1	1	1	1	1	1	1	1	1	1	1	13	0	1
B2A03	60	4	1	1	1	1	1	1	1	1	1	1	1	1	1	13	0	1
B3A14	60	4	1	1	1	1	1	1	1	1	1	1	1	1	1	13	0	1
B4A01	60	4	1	1	1	1	1	1	1	1	1	1	1	1	1	13	0	1
B1A01	16	4	1	1	1	1	1	1	1	1	1	1	1	1	1	3	0	0
B1A06	16	2	1	1	1	1	1	1	1	1	1	1	1	1	1	6	0	0
B1A11	16	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	0	0
B1A20	16	3	1	0	0	1	1	1	1	1	1	1	1	0	1	1	0	0
B2A10	16	2	1	1	1	1	1	1	1	1	1	1	1	1	1	13	0	1
B2A18	16	4	1	1	1	1	1	1	1	1	1	1	1	1	1	8	0	1
B2A22	16	3	1	1	1	1	1	1	1	1	1	1	1	1	1	7	0	0
B3A09	16	1	1	1	1	1	1	1	1	1	1	1	1	1	1	11	1	1
B3A16	16	2	1	0	0	1	1	1	1	1	1	1	1	0	1	1	0	0
B3A22	16	4	1	1	1	1	1	1	1	1	1	1	1	1	1	6	0	0
B3A24	16	3	1	1	1	1	1	1	1	1	1	1	1	0	1	12	0	0
B4A02	16	3	1	1	1	1	1	1	1	1	1	1	1	1	1	6	0	0
B4A18	16	4	1	1	1	1	1	1	1	1	1	1	1	1	1	2	0	0
B4A20	16	2	1	1	1	1	1	1	1	1	1	1	1	0	1	4	0	1
B1A02	8	2	1	1	1	1	1	1	1	1	1	1	1	1	1	3	0	1
B1A03	8	3	0	1	0	1	1	1	1	1	1	0	1	0	1	0	0	0
B1A12	8	1	0	0	0	0	0	0	1	1	0	0	1	0	1	0	0	0
B1A14	8	4	0	1	0	1	1	1	1	1	1	0	1	0	1	0	0	0
B2A12	8	1	0	0	0	1	1	1	1	1	1	0	1	0	1	0	0	0
B2A14	8	4	0	0	0	1	1	1	1	1	1	0	1	0	1	0	0	0

B2A17	8	2	0	0	0	0	0	1	1	1	0	0	1	0	1	0	0	0
B2A21	8	3	0	0	0	1	1	1	1	1	1	0	1	0	1	0	0	0
B3A04	8	1	1	1	1	1	1	1	1	1	1	0	1	1	1	13	1	1
B3A05	8	3	1	1	1	1	1	1	1	1	1	0	1	1	1	3	0	0
B3A07	8	4	0	0	0	1	0	0	1	1	1	0	1	0	1	0	0	0
B3A20	8	2	0	0	0	0	0	0	1	1	0	0	1	0	1	0	0	0
B4A06	8	1	0	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0
B4A08	8	2	0	1	0	1	1	1	1	1	1	0	1	0	1	0	0	0
B4A10	8	3	0	0	0	1	1	1	1	1	1	0	1	0	1	0	0	0
B4A16	8	4	1	1	0	0	1	1	1	1	1	0	1	1	1	3	0	0
B1A04	4	4	0	0	0	0	0	0	1	1	0	0	1	0	0	0	0	0
B1A13	4	1	0	0	0	0	0	0	1	0	0	0	1	0	1	0	0	0
B1A19	4	3	0	0	1	1	0	1	1	1	0	0	1	0	1	0	0	0
B1A21	4	2	0	0	0	1	1	0	1	1	0	0	1	0	1	0	0	0
B2A01	4	4	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
B2A06	4	2	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0
B2A09	4	1	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0
B2A16	4	3	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
B3A03	4	3	0	0	0	1	0	1	1	1	0	0	1	0	1	0	0	0
B3A11	4	2	0	0	0	1	1	1	1	1	0	0	1	0	1	0	0	0
B3A13	4	1	1	1	1	0	0	0	1	1	0	0	1	1	1	1	0	0
B3A23	4	4	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0
B4A04	4	4	0	0	0	0	0	0	1	1	0	0	1	0	1	0	0	0
B4A07	4	2	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0
B4A11	4	3	0	0	0	0	0	0	1	1	0	0	1	0	0	0	0	0
B4A22	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B1A05	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B1A07	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B1A16	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B1A17	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B2A02	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B2A08	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B2A19	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B2A20	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B3A02	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B3A08	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B3A19	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B3A21	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B4A14	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B4A15	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B4A17	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

B4A21	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B1A08	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B1A09	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B1A15	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B1A18	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B2A04	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B2A05	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B2A13	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B2A15	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B3A01	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B3A06	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B3A12	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B3A17	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B4A03	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B4A09	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B4A12	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
B4A13	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sum			23	24	21	33	32	34	44	41	30	19	49	19	42	23	2	10
percent_tot			0.28	0.29	0.26	0.4	0.39	0.41	0.54	0.5	0.37	0.23	0.6	0.23	0.51	0.28	0.02	0.12
more			same	yes	no	yes	yes	yes	yes	yes	yes	no	yes	no	yes	same	no	no
percent_12vif				0.91	0.87	0.91	0.96	0.96	1	1	0.96	0.83	1	0.83	1	1	0.09	0.43

Supplementary Table 3. BioDIV plots included in the different sensitivity overlap scenarios vs. all experimental plots. BioDIV plots with their sown diversity (sown_div), number of functional groups (num_fg) and their selection as realistic plots (1) based on various sensitivity analyses described in Supplementary Information on sensitivity analyses I and Supplementary Table 1. The selection of "realistic" plots is compared to the main analysis (Full12_chull). Note that column D shows the number of years with communities falling inside the intersection of 3-D convex hull volumes (19 = all years). The last four rows show the number of chosen realistic plots (sum), the percentage of total BioDIV plots (159) chosen as realistic (percent_tot), if there are more plots selected as realistic than in the main analysis (yes, same, or no), and the proportion of realistic plots chosen in the main analysis (Full12_chull) also selected in each sensitivity analysis (percent_12vif). Plots are sorted by sown diversity levels.

plot	sown_div	num_fg	Full12_chull	Full12_hyper	Full12_ellipse	AlI21_chull	AlI21_hyper	AlI21_ellipse	Allbuttax_chull	Allbutphyl_chull	Allbutfun_chull	AllbutCWM_chull	A_remove5	C_allreal	D_count	E_NMDS
9	16	5	1	1	1	1	1	1	1	1	1	1	1	1	19	1
27	16	5	1	1	1	1	1	1	1	1	1	1	1	1	19	1
30	16	5	1	1	1	1	1	1	1	1	1	1	1	1	19	1
34	16	5	1	1	1	1	1	1	1	1	1	1	1	1	19	1
35	16	5	1	1	1	1	1	1	1	1	1	1	1	1	19	0
46	16	5	1	1	1	1	1	1	1	1	1	1	1	1	19	1
68	16	5	1	1	1	1	1	1	1	1	1	1	1	1	19	1
82	16	5	1	1	1	1	1	1	1	1	1	1	1	1	19	1
89	16	5	1	1	1	1	1	1	1	1	1	1	1	1	19	1
107	16	5	1	1	1	1	1	1	1	1	1	1	1	1	19	1
108	16	5	1	1	1	1	1	1	1	1	1	1	1	1	19	1
136	16	5	1	1	1	1	1	1	1	1	1	1	1	1	19	0
156	16	5	1	1	1	1	1	1	1	1	1	1	1	1	19	0
160	16	5	1	1	1	1	1	1	1	1	1	1	1	1	19	0
164	16	5	1	1	1	1	1	1	1	1	1	1	1	1	19	1
169	16	5	1	1	1	1	1	1	1	1	1	1	1	1	19	1
174	16	5	1	1	1	1	1	1	1	1	1	1	1	1	19	0
186	16	5	1	1	1	1	1	1	1	1	1	1	1	1	19	1
202	16	4	1	1	1	1	1	1	1	1	1	1	1	1	19	1
220	16	5	1	1	1	1	1	1	1	1	1	1	1	1	19	1
227	16	5	1	1	1	1	1	1	1	1	1	1	1	1	19	1
235	16	5	1	1	1	1	1	1	1	1	1	1	1	1	19	1
239	16	5	1	1	1	1	1	1	1	1	1	1	1	1	19	1
242	16	5	1	1	1	1	1	1	1	1	1	1	1	1	18	1

253	16	5	1	1	1	1	1	1	1	1	1	1	1	1	19	1
257	16	5	1	1	1	1	1	1	1	1	1	1	1	1	19	1
273	16	5	1	1	1	1	1	1	1	1	1	1	1	1	19	1
299	16	5	1	1	1	1	1	1	1	1	1	1	1	1	19	1
301	16	5	1	1	1	1	1	1	1	1	1	1	1	1	19	1
318	16	5	1	1	1	1	1	1	1	1	1	1	1	1	19	1
328	16	5	1	1	1	1	1	1	1	1	1	1	1	1	19	1
329	16	5	1	1	1	1	1	1	1	1	1	1	1	1	19	1
331	16	5	1	1	1	1	1	1	1	1	1	1	1	1	19	0
336	16	5	1	1	1	1	1	1	1	1	1	1	1	1	19	0
339	16	5	1	1	1	1	1	1	1	1	1	1	1	1	18	1
12	8	4	1	1	1	1	1	1	1	1	1	1	1	1	19	1
15	8	4	1	1	1	1	1	1	1	1	1	1	1	1	19	1
22	8	4	1	1	1	1	1	1	1	1	1	1	1	1	18	0
50	8	4	1	1	1	1	1	1	1	1	1	1	1	1	19	1
57	8	4	1	1	1	1	1	1	1	1	1	1	1	1	19	1
67	8	5	1	1	1	1	0	1	1	1	1	1	1	1	18	0
74	8	5	1	1	1	1	1	1	1	1	1	1	1	1	15	0
81	8	4	1	1	1	1	1	1	1	1	1	1	1	1	19	1
98	8	5	1	1	1	1	1	1	1	1	1	1	1	1	19	1
104	8	5	1	1	1	1	1	1	1	1	1	1	1	1	19	0
111	8	4	1	1	1	1	1	1	1	1	1	1	1	1	19	1
115	8	4	1	1	1	1	1	1	1	1	1	1	1	1	11	1
118	8	5	1	1	1	1	1	1	1	1	1	1	1	1	17	0
130	8	5	1	1	1	1	1	1	1	1	1	1	1	1	19	0
146	8	5	1	1	1	1	1	1	1	1	1	1	1	1	19	1
170	8	4	1	1	1	1	1	1	1	1	1	1	1	1	18	0
177	8	5	1	1	1	1	1	1	1	1	1	1	1	1	19	0
178	8	3	1	1	1	1	1	1	1	1	1	1	1	1	19	0
206	8	4	1	1	1	1	1	1	1	1	1	1	1	1	19	1
208	8	4	1	1	1	1	1	1	1	1	1	1	1	1	19	1
210	8	4	1	1	1	1	1	1	1	1	1	1	1	1	19	1
213	8	5	1	1	1	1	1	1	1	1	1	1	1	1	19	1
232	8	5	1	1	1	1	1	1	1	1	1	1	1	1	18	0
266	8	5	1	1	1	1	1	1	1	1	1	1	1	1	19	0
283	8	3	1	1	1	1	1	1	1	1	1	1	1	1	19	0
292	8	3	1	1	1	1	1	1	1	1	1	1	1	1	19	1
293	8	4	1	1	1	1	1	1	1	1	1	1	1	1	19	0
303	8	3	1	1	1	1	1	1	1	1	1	1	1	1	18	1

307	8	4	1	1	1	1	1	1	1	1	1	1	1	1	18	0
313	8	4	1	1	1	1	1	1	1	1	1	1	1	1	18	0
3	4	2	1	1	1	1	1	1	1	1	1	1	1	1	18	0
24	4	3	1	1	1	1	1	1	1	1	1	1	1	1	18	0
26	4	3	0	0	1	0	0	1	0	0	0	1	0	0	0	0
28	4	2	1	1	1	1	1	1	0	1	1	0	0	1	19	0
33	4	4	1	0	1	1	0	1	1	1	1	1	1	1	3	0
44	4	3	1	0	1	1	0	0	1	1	1	1	0	1	19	0
45	4	4	1	0	1	1	0	1	1	1	1	1	1	1	1	0
53	4	4	1	0	1	1	1	1	1	1	1	1	1	1	19	1
58	4	3	1	0	1	1	1	1	1	1	1	1	1	1	8	1
62	4	3	1	1	1	1	1	1	1	1	1	1	1	1	11	0
70	4	3	1	1	1	1	1	1	1	1	1	1	1	1	19	0
93	4	2	1	0	0	1	0	0	1	1	1	1	0	1	2	0
110	4	3	1	0	1	1	0	1	1	1	1	1	1	1	18	0
133	4	3	1	1	1	1	1	1	1	1	1	1	1	1	19	0
138	4	2	1	1	1	1	1	1	1	1	1	1	1	1	19	0
139	4	2	1	1	1	1	1	1	1	1	1	1	1	1	18	0
149	4	4	0	0	0	1	0	1	1	1	1	1	1	0	0	0
176	4	3	1	1	1	1	1	1	1	1	1	1	1	1	19	1
190	4	3	1	1	1	1	1	1	1	1	1	1	1	1	19	0
199	4	3	1	1	1	1	1	1	1	1	1	1	1	1	14	0
201	4	3	0	0	0	1	0	1	1	1	1	1	1	0	0	0
223	4	3	1	1	1	1	1	1	1	1	1	1	1	1	15	1
225	4	4	1	1	1	1	1	1	1	1	1	1	1	1	3	0
229	4	3	1	1	1	1	1	1	1	1	1	1	1	1	18	1
233	4	4	1	1	1	1	1	1	1	1	1	1	1	1	19	1
286	4	3	1	1	1	1	1	1	1	1	1	1	1	1	19	1
287	4	3	1	1	1	1	1	1	1	1	1	1	1	1	19	0
302	4	3	1	1	1	1	1	1	1	1	1	1	1	1	13	0
325	4	4	1	1	1	1	1	1	1	1	1	1	1	1	15	0
6	2	1	1	1	1	1	1	1	1	1	1	1	1	1	17	0
14	2	1	1	1	1	1	1	1	1	1	1	1	1	1	15	0
32	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
48	2	2	1	1	0	1	1	1	1	1	1	1	1	1	9	0
56	2	2	1	1	1	1	1	1	1	1	1	1	1	1	16	0
73	2	2	1	1	1	1	1	1	1	1	1	1	0	1	12	0
75	2	2	1	0	1	1	0	0	1	1	1	1	0	1	19	0
117	2	2	0	0	0	0	0	0	0	0	0	1	0	0	0	0

125	2	2	0	0	1	0	0	1	0	0	0	0	0	0	0	0
127	2	2	1	1	1	1	1	1	0	1	1	0	0	1	12	0
157	2	1	0	0	1	0	0	1	0	1	1	1	1	0	0	0
165	2	2	0	0	1	0	0	1	0	0	0	1	1	0	0	1
168	2	2	0	0	1	0	0	1	1	1	0	1	1	0	0	0
171	2	2	1	1	1	1	0	1	1	1	1	1	1	1	4	0
175	2	2	0	0	0	1	0	0	1	1	1	1	1	0	0	0
189	2	2	0	0	1	0	0	1	0	0	0	0	0	0	0	0
193	2	2	0	0	0	0	0	0	1	1	1	1	1	0	0	0
197	2	2	1	0	1	1	0	0	1	1	1	1	0	1	18	0
211	2	2	1	1	1	1	1	1	1	1	1	1	0	1	18	0
224	2	2	0	0	0	1	0	1	1	1	1	1	1	0	0	0
234	2	2	0	0	0	0	0	0	0	0	0	1	0	0	0	0
236	2	2	1	0	1	1	0	0	1	1	1	1	1	1	8	0
259	2	2	1	1	1	1	1	1	1	1	1	1	1	1	19	0
278	2	2	0	0	1	0	0	1	0	0	0	1	0	0	0	0
300	2	2	1	0	1	0	0	0	1	1	1	1	0	1	9	0
304	2	1	0	0	1	1	0	1	1	1	1	1	1	0	0	0
311	2	2	1	0	1	1	0	1	1	1	1	1	1	1	18	0
322	2	2	0	0	1	0	0	1	0	0	0	0	0	0	0	0
324	2	1	1	1	1	1	1	1	1	1	1	1	1	1	18	1
330	2	2	1	1	1	1	1	1	1	1	1	1	1	1	3	0
334	2	2	0	0	1	0	0	1	0	0	0	1	0	0	0	0
335	2	2	1	0	0	1	0	1	1	1	1	1	1	1	1	0
342	2	2	1	1	1	1	1	1	1	1	1	1	1	1	15	0
2	1	1	1	1	1	1	1	1	0	1	1	0	0	1	19	0
5	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
11	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
16	1	1	1	0	0	0	0	0	0	0	0	0	0	1	18	0
20	1	1	1	1	1	0	0	0	1	0	0	0	0	1	18	0
29	1	1	1	1	1	1	1	1	0	1	1	0	0	1	19	0
31	1	1	0	0	1	0	0	1	0	0	0	0	0	0	0	0
69	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
83	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
87	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0
92	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0
94	1	1	1	1	1	1	1	1	0	1	1	0	0	1	19	0
109	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
129	1	1	0	1	1	0	0	1	0	0	0	0	0	0	0	0

ID																
135	1	1	0	0	1	0	0	1	0	0	0	0	0	0	0	0
137	1	1	1	1	1	0	0	0	1	0	0	0	0	1	19	0
142	1	1	0	0	0	0	0	1	0	0	0	1	1	0	0	0
153	1	1	1	1	1	1	1	1	1	1	1	0	0	1	10	0
163	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0
167	1	1	0	1	1	0	0	1	0	0	0	0	0	0	0	0
230	1	1	1	0	1	0	0	0	1	0	0	0	0	1	18	0
237	1	1	1	1	1	1	1	1	1	1	1	1	1	1	19	1
256	1	1	1	1	1	1	1	1	1	1	1	0	0	1	11	0
265	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
267	1	1	0	1	1	0	0	1	0	0	0	0	0	0	0	0
268	1	1	0	0	0	0	0	1	0	0	0	1	1	0	0	0
280	1	1	0	0	1	0	0	1	0	0	0	0	0	0	0	0
282	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0
290	1	1	1	1	1	1	1	1	1	1	1	1	0	1	19	0
308	1	1	1	0	0	0	0	0	0	0	0	0	0	1	19	0
333	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
338	1	1	1	1	1	1	1	1	1	1	1	0	1	19	0	
sum			122	109	133	121	104	136	122	125	124	126	112	122	122	53
percent_tot			0.77	0.69	0.84	0.76	0.65	0.86	0.77	0.79	0.78	0.79	0.7	0.77	0.77	0.33
more			same	no	yes	no	no	yes	yes	yes	yes	yes	no	yes	same	no
percent_12vif				0.87	0.96	0.95	0.85	0.91	0.94	0.96	0.96	0.9	0.83	1	1	0.43

354 **Supplementary Table 4.** T-test results for differences between German experimental and real-world
355 plots. Welsh t-tests with unequal variances. Full set of 21 community properties averaged across all
356 years per plot for Jena Experiment (82 plots) and combined real-world data (German real world: 150
357 plots, Jena real world: 14 plots). T-statistic, degrees of freedom (df), experimental (Exp) data mean and
358 real world (RW) data mean are rounded to two, p-values to 5 decimal places. The last column gives the
359 proportion of Jena plots falling within the community property range of the real-world plots.

model	t_statistic	df	mean_Exp	mean_RW	p_value	in_rw_range
FRic	-19.04	192.57	2.74	12.84	0	0.24
FEve	-5.57	83.98	0.34	0.52	0	0.5
FDiv	-5.34	85.44	0.46	0.68	0	0.59
FDis	-8.5	88.07	1.18	1.95	0	0.56
RaoQ	-9.51	105.73	2.39	4.61	0	0.55
leaf_area	1	106.43	1820.3	1648.03	0.31776	0.82
SLA	-4.54	140.03	24.26	26.44	0.00001	0.94
leaf_drymass	2.12	93.49	61.03	48.28	0.03662	0.82
LDMC	-5.27	98.28	0.22	0.25	0	0.61
leaf_N	1.31	96.71	25.66	24.81	0.19315	0.74
leaf_P	-1.44	109.38	2.19	2.26	0.15242	0.93
height	-2.36	115.5	0.45	0.5	0.01988	0.76
seedmass	3.95	84.7	2.76	1.52	0.00016	0.72
S	-18.8	195.11	6.45	28.05	0	0.11
H	-14.22	99.02	0.97	2.3	0	0.43
D1	-10.9	84.47	0.46	0.83	0	0.51
D2	-10.17	133.06	3.23	7.42	0	0.51
SEve	16.35	86.69	0.65	0.27	0	0.05
PD	-20.34	163.66	720.24	1704.8	0	0.12
MPD	-8.5	101.21	105.59	188.92	0	0.66
MNTD	6.62	82.65	109.29	31.2	0	0.29

360 **Supplementary Table 5.** T-test results for differences between US experimental and real-world plots.
361 Welsh t-tests with unequal variances. Full set of 21 community properties averaged across all years per
362 plot for BioDIV (159 plots) and combined real-world data (Fertilization 1 & 2; 207 and 162 plots,
363 respectively). T-statistic, degrees of freedom (df), experimental (Exp) data mean and real world (RW)
364 data mean are rounded to two, p-values to 5 decimal places. The last column gives the proportion of
365 BioDIV plots falling within the community property range of the real-world plots.

model	t_statistic	df	mean_Exp	mean_RW	p_value	in_rw_range
FRic	-7.59	243.07	1.4	2.62	0	0.51
FEve	-2.73	176.06	0.29	0.35	0.00693	0.28
FDiv	-8.42	182.59	0.37	0.63	0	0.59
FDis	0.79	187.27	1.02	0.97	0.43191	0.59
RaoQ	3.46	182.45	2.22	1.61	0.00068	0.6
leaf_area	8.82	176.29	1429.56	724.02	0	0.77
SLA	-8.01	204.34	14.77	16.5	0	0.4
leaf_drymass	10	193.36	74.23	45.67	0	0.73
LDMC	-2.57	169.1	0.3	0.32	0.01105	0.22
leaf_N	-4.9	237.85	16.97	18.77	0	0.5
leaf_P	-6.68	248.46	1.55	1.71	0	0.94
height	3.37	193.75	0.77	0.7	0.0009	0.56
seedmass	5.21	169.51	3.88	2.18	0	0.82
S	-12.12	291.42	4.03	7.85	0	0.76
H	-4.21	222.01	0.72	0.96	0.00004	0.73
D1	-4.18	215.21	0.36	0.47	0.00004	0.7
D2	-1.83	226.06	2.23	2.46	0.06831	0.71
SEve	18.02	188.98	0.71	0.38	0	0.8
PD	-13.45	338.91	605.02	861.86	0	0.67
MPD	-0.3	239.47	92.55	94.68	0.76228	0.68
MNTD	4.71	169.23	97.1	50.95	0.00001	0.6
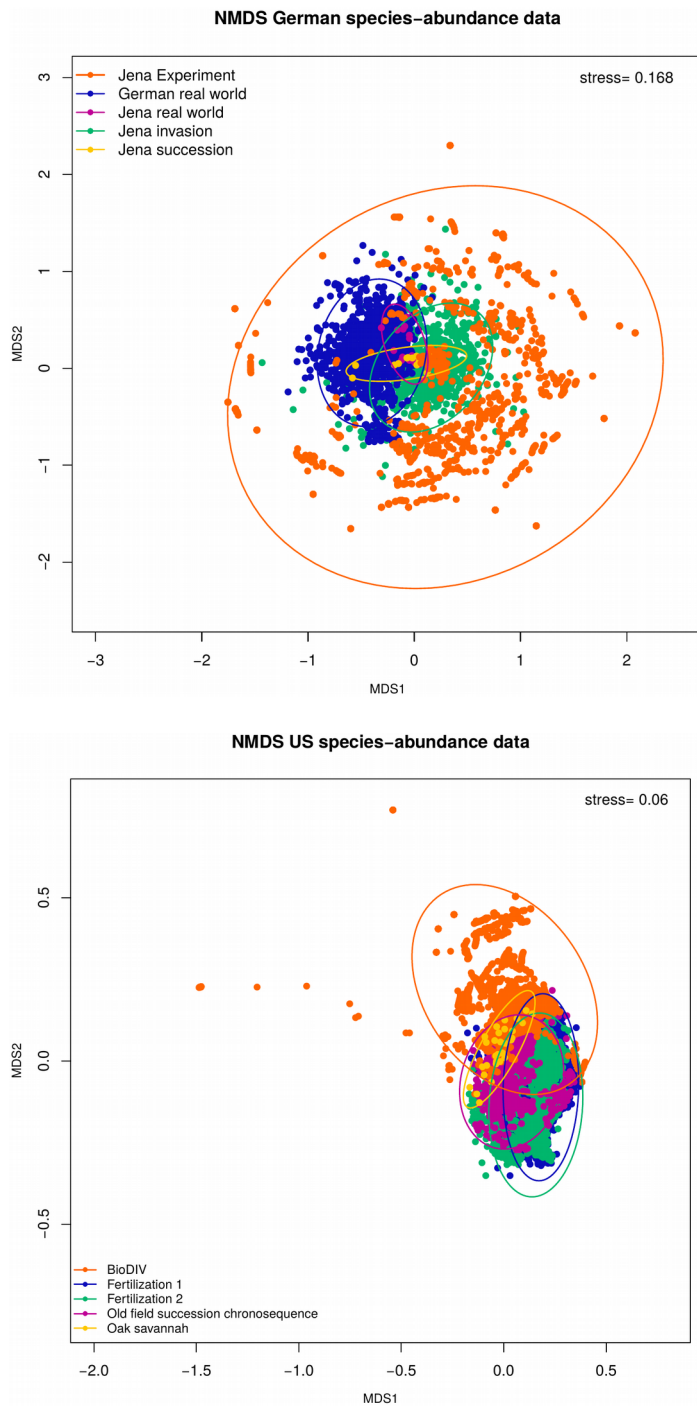
Supplementary Figure 2. NMDS biplots of species-abundance data for German and US dataset. First two axes of 3-dimensional NMDS for German (upper panel) and US (lower panel) species-abundance data as calculated with function "metaMDS" and plotted with function "biplot" in R package vegan [12]. Note that, for the US comparison, communities with 100 % relative abundance of *Elymus smithii* are not shown in this biplot since they show extreme values in the first axis.

Supplementary Table 6. T-test results for differences between realistic and unrealistic plots for the
372 Jena Experiment. Welsh t-tests with unequal variances. Realistic plots were calculated based on the 12
373 vif-selected community properties and the convex hull volume method. All properties were averaged
374 across all available years per plot (23 realistic and 59 unrealistic plots). T-statistic, degrees of freedom
375 (df), means of realistic (real) and unrealistic communities (unreal) are rounded to two, p-values to four
376 decimal places.

model	t_statistic	df	mean_real	mean_unreal	p_value
FRic	8.25	24.88	7.32	0.96	0
FEve	6.46	74.97	0.54	0.27	0
FDiv	7.82	66.62	0.75	0.34	0
FDis	9.61	77.96	1.98	0.87	0
RaoQ	9.22	55.01	4.49	1.58	0
leaf_area	0.13	75.23	1842.7	1811.57	0.8971
SLA	0.63	49.5	24.64	24.11	0.5334
leaf_drymass	-0.55	78.6	57.26	62.5	0.5845
LDMC	1.75	42.61	0.23	0.21	0.0865
leaf_N	0.3	78.09	25.88	25.58	0.7679
leaf_P	2.24	77.01	2.31	2.14	0.0281
height	1.87	61.58	0.5	0.42	0.0663
seedmass	-0.35	79.48	2.64	2.81	0.7303
S	5.66	22.7	15.18	3.05	0
H	9.17	34.51	1.92	0.6	0
D1	9.9	72.8	0.78	0.34	0
D2	5.06	22.72	6.65	1.9	0
SEve	-10.33	78.5	0.45	0.74	0
PD	5.7	25.31	1093.58	574.71	0
MPD	5.47	38.3	176.42	77.97	0
MNTD	-3.56	77.95	64.82	126.63	0.0006
sown diversity	4.77	22.34	21.74	3.46	0.0001
no funct groups	3.54	36.95	2.83	1.85	0.0011

Supplementary Table 7. T-test results for differences between realistic and unrealistic plots for
BioDIV. Welsh t-tests with unequal variances. Realistic plots were calculated based on the full set of
community properties and the convex hull volume method. All properties were averaged across all
available years per plot (122 realistic and 37 unrealistic plots). T-statistic, degrees of freedom (df),
means of realistic (real) and unrealistic communities (unreal) are rounded to two, p-values to four
decimal places.

model	t_statistic	df	mean_real	mean_unreal	p_value
FRic	10.7	121	1.82	0	0
FEve	14.65	121	0.38	0	0
FDiv	14.71	121	0.48	0	0
FDis	9.44	92.96	1.26	0.22	0
RaoQ	7.92	95.01	2.75	0.49	0
leaf_area	-0.11	44.52	1423.77	1448.65	0.9168
SLA	1.04	46.22	14.91	14.3	0.3043
leaf_drymass	-1.27	46.88	71.95	81.76	0.2119
LDMC	-0.66	44.55	0.3	0.31	0.5149
leaf_N	1.2	42.28	17.27	15.99	0.2366
leaf_P	1.42	46.02	1.57	1.48	0.1633
height	-1.81	40.78	0.75	0.87	0.0773
seedmass	0.15	41.7	3.92	3.76	0.8815
S	11.53	130.41	4.87	1.25	0
H	12.76	155.85	0.91	0.09	0
D1	12.7	145.19	0.45	0.06	0
D2	11.23	133.74	2.58	1.09	0
SEve	-10.43	102.79	0.64	0.92	0
PD	12.13	154.37	660.65	421.61	0
MPD	10.42	111.91	115.44	17.08	0
MNTD	1.95	55.87	107.8	61.82	0.056
sown diversity	11.51	137.13	7.81	1.65	0
no funct groups	10.95	122.28	3.49	1.54	0

Supplementary Figure 3. Alternative versions of Fig. 2 based on alternative intersection scenarios (community- property subsets and overlap calculation methodology). Panels a-h Jena Experiment, panels i-l BioDIV (see main text Fig. 2). 6 different versions: 3 methods (chull, hyper, ellipse) and 2 community property subsets (Full 12 vif selected and All 21 community properties; see Supplementary Table 1 for details on included community properties) plus one USA-only version based on overlap from species-abundance based NMDS with the chull method. Note that convex hull method with 12 vif-selected properties is main text Fig. 2.

Full 12 – hyper:

Full 12 – ellipse:

35
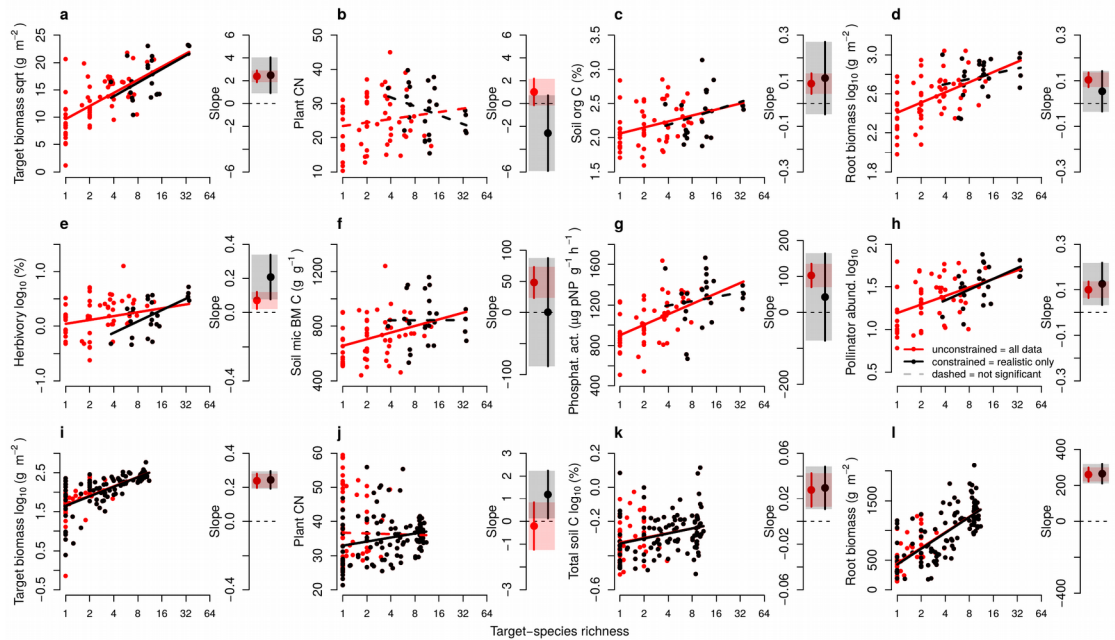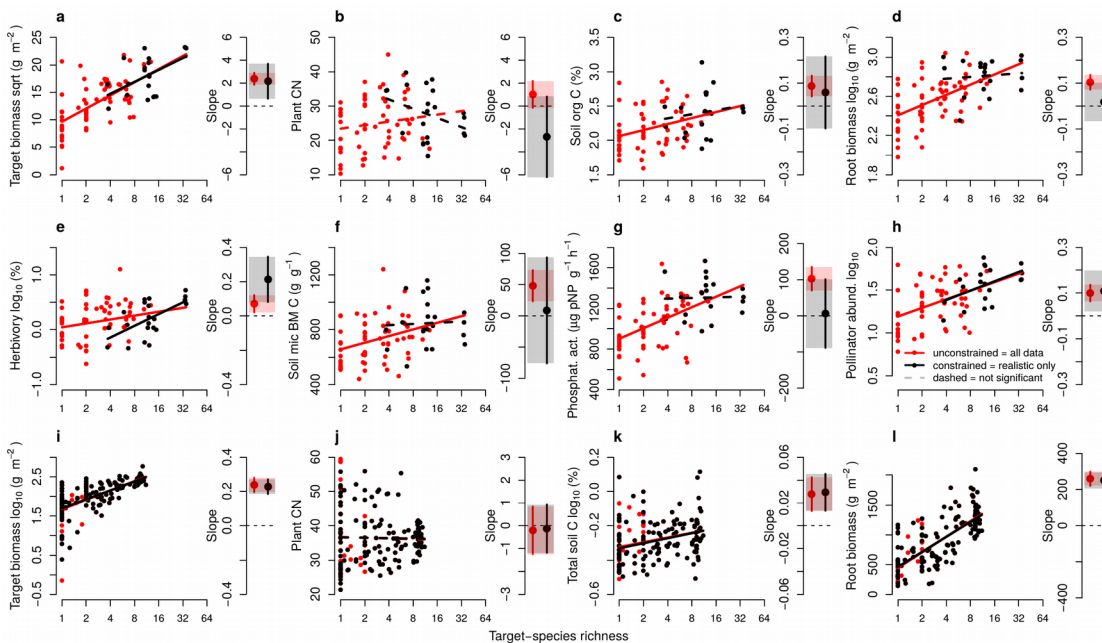
392   All 21 – chull:

393   All 21 – hyper:

36
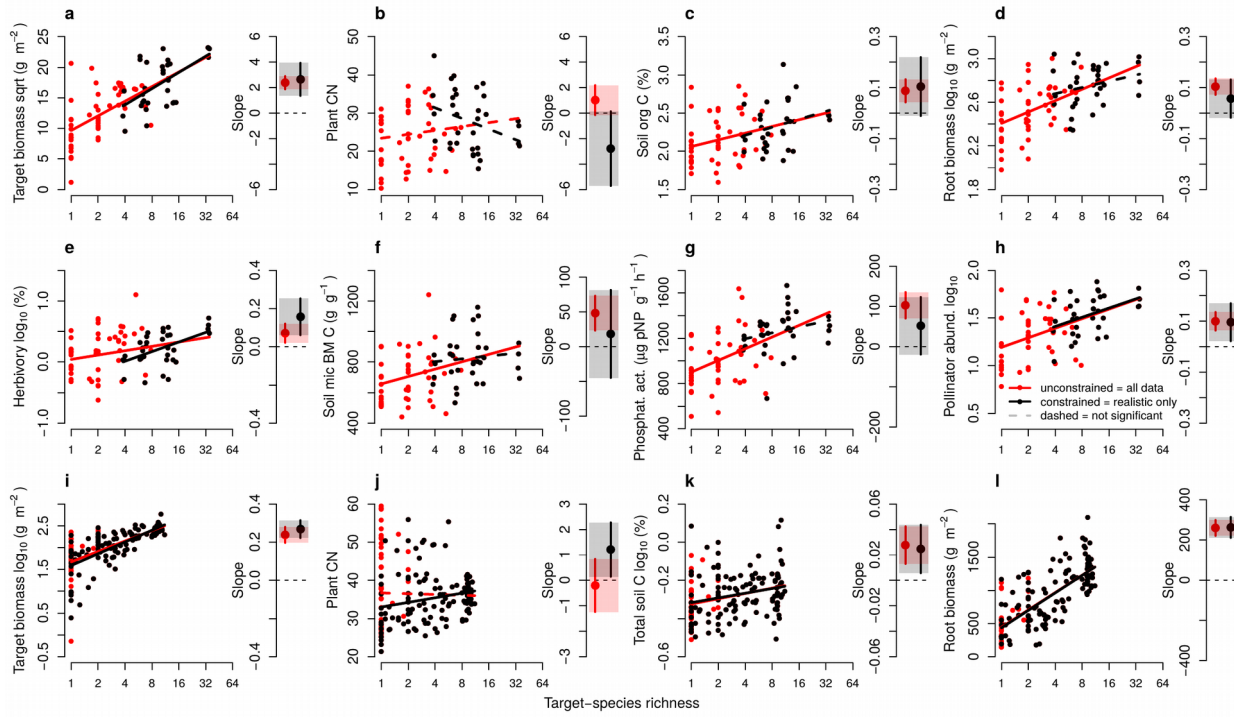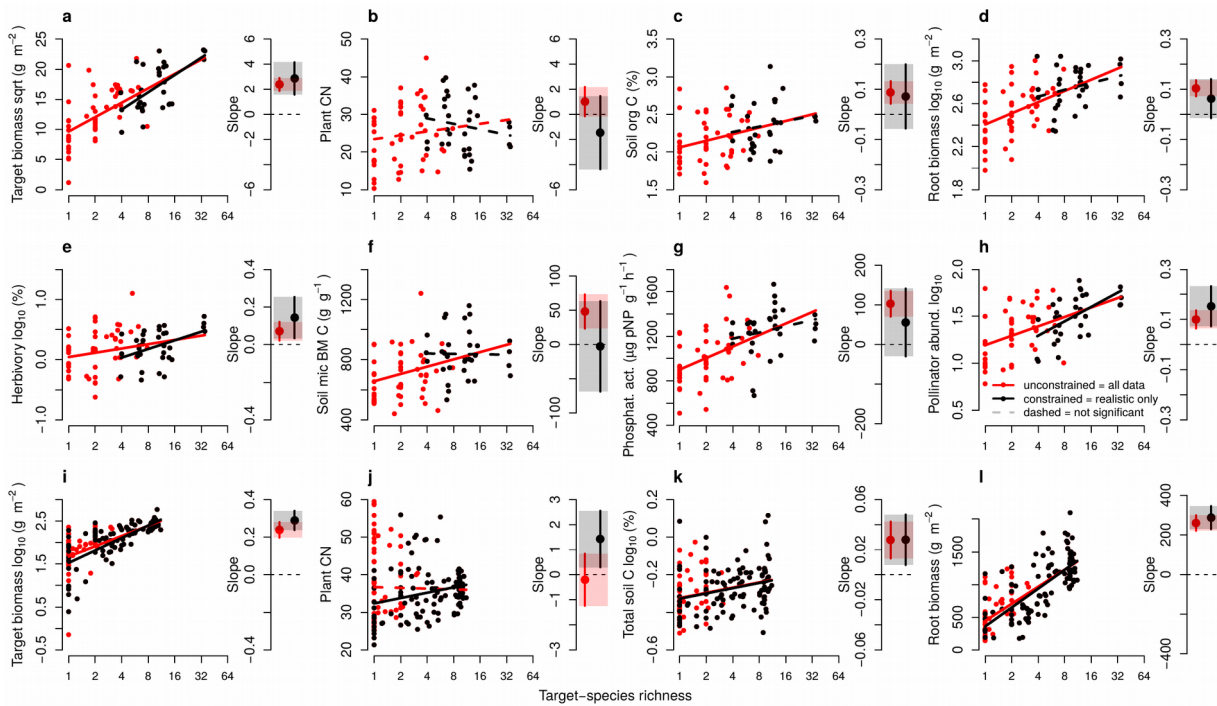
394   All 21 – ellipse:
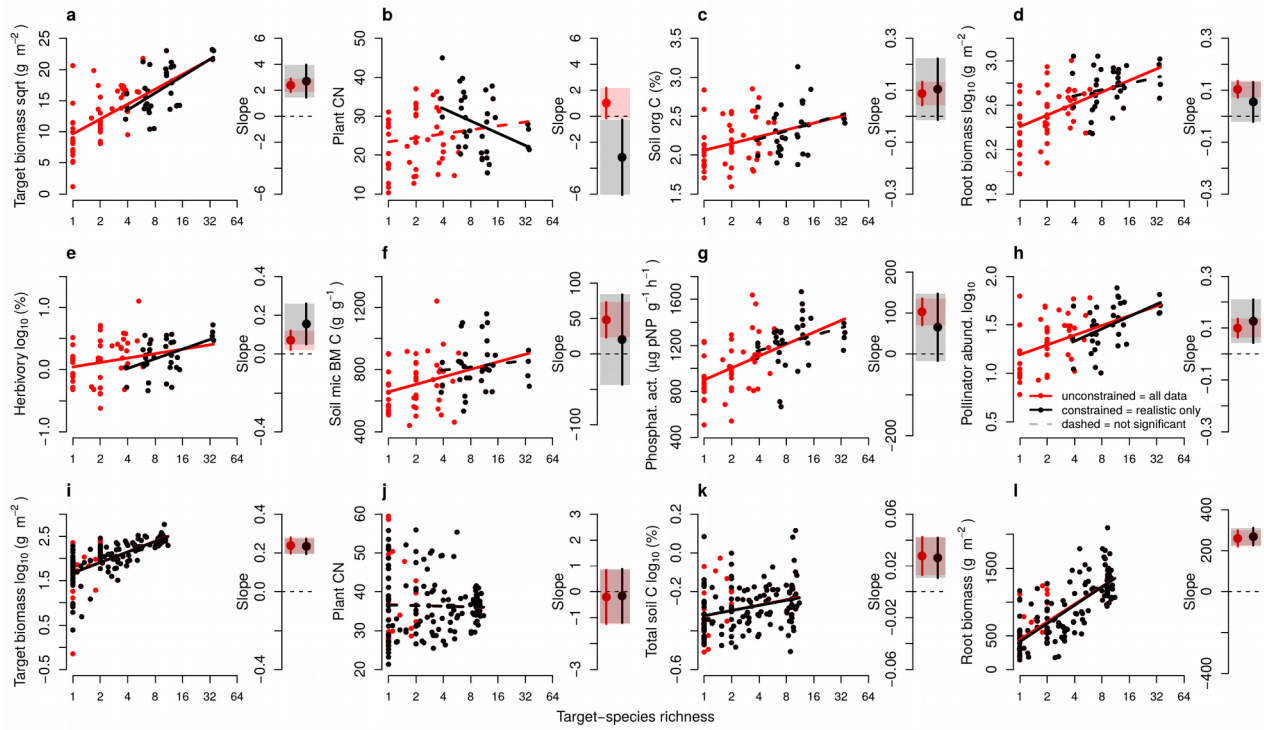
395   USA – NMDS – chull:
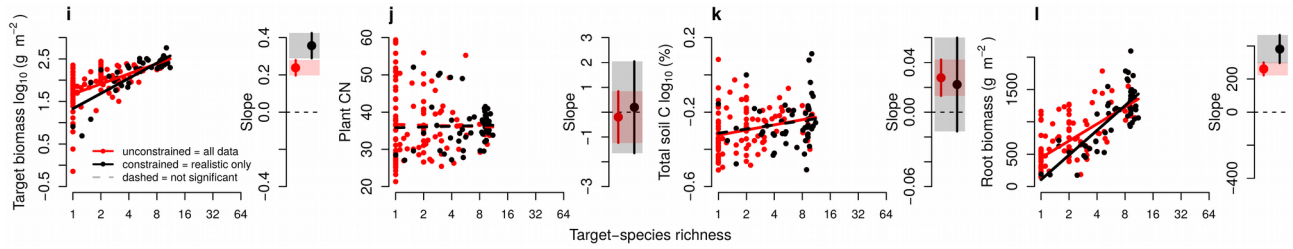
396 **Supplementary Table 8.** Constraining-related change in functioning at maximum species richness.
397 For each of the 12 BEF relationships from the Jena Experiment (J) and BioDIV presented in Fig. 2, the
398 table shows the constraining-related percentage change in the model-predicted function variable at
399 maximum species richness (the proportional difference in the un-transformed function value at the
400 right-hand tip of the black and red lines in Fig. 2). The average absolute percentage function change is
401 10.3% (SE: 4%).

function	% change in predicted functioning
J_biomass	-3.9
J_plantCN	-18.75
J_soilorgC	-0.46
J_rootbiomass	-20.24
J_herbivory	46.24
J_micBMC	-7.8
J_phosphatase	-8.17
J_pollinators	9.74
BioDIV_biomass	3.78
BioDIV_plantCN	3.59
BioDIV_soilC	0.39
BioDIV_rootbiomass	-0.05

Supplementary Information on sensitivity analyses II

We performed two very similar sensitivity analyses testing if changes in BEF relationships from being significant (all communities) to non-significant (realistic plots only) were likely caused by the related reduction in sample size or the reduced species richness gradient of the constrained Jena plots or if a randomly-selected reduced number of plots was still likely to result in a significant relationship. Therefore, for each of the four BEF relationships found to switch significance (Jena soil organic C (a-c), root biomass (d-f), soil microbial biomass C (g-i) and phosphatase activity (j-l)), we repeatedly (500 times), randomly selected 23 Jena plots and re-ran the model testing for the BEF relationship and saving the slope estimates and p-values (Supplementary Fig. S4a, fully random choice of plots). Supplementary Fig. 4 shows the distribution of these 500 random-selection slopes (boxplots in first column and orange lines in middle column) in comparison to the unconstrained (all plots, red lines) and constrained (PCA-selection based realistic plots only, black dashed lines) slopes from Fig. 2. Dotted black lines indicate zero slopes. The right column shows the frequency of positive significant, positive insignificant, negative insignificant and negative significant relationships obtained by the 500 random subsets of 23 plots with the black bar highlighting the PCA-based realistic result from Fig. 2.

In a second version of this analysis, we restricted the random choice of Jena plots to only draw from the 42 plots within the species richness range of the realistic plots in the main analysis (S equal to or larger than 3.7). Here, we repeated the random draw only 100 times. Otherwise, the analysis and figure are identical.

Supplementary Fig. 4 shows that black dashed lines and the results of the PCA-based realistic subset divert relatively strongly from the 500 random-selection results. Specifically, the PCA-based realistic subset resulted in strikingly shallower slopes than the random choices and non-significantly positive or even negative relationships while a big part of the random subsets resulted in significant positive or at least non-significantly positive relationships. As such, our PCA-based selection of realistic plots is highly non-random in comparison to the random-selection of plots, thus indicating that our methodology is successful in finding a subset of plots based on prior knowledge (realistic plots based on the multidimensional, multivariate comparison of communities) and does not simply create a random subset of plots. Furthermore, these results show that, for these four Jena soil processes, experiment-derived BEF relationships might not be as important or strong in real-world systems, at least as long as plant communities in those real-world systems deviate from those in experiments, e.g. in their species richness gradients. Future developments of real-world plant communities due to global change drivers and increasing anthropogenic pressure might change this conclusion by rendering less diverse communities realistic, thus aligning the species richness gradients of biodiversity experiments and related real-world systems and increasing the slope of the BEF relationships.

Interestingly, Supplementary Fig. 5 shows that, when restricting the species richness gradient of randomly drawn realistic plots to being comparable to the realistic plots chosen in the main analysis, the picture changes. The vast majority of random slopes is now not significant anymore, as can be seen from the barplots in the right-hand column. This shows that the change from significant to non-significant BEF relationships is not caused by the reduced sample size but primarily driven by the truncated species-richness gradient in more real-world comparable biodiversity experiment data subsets.
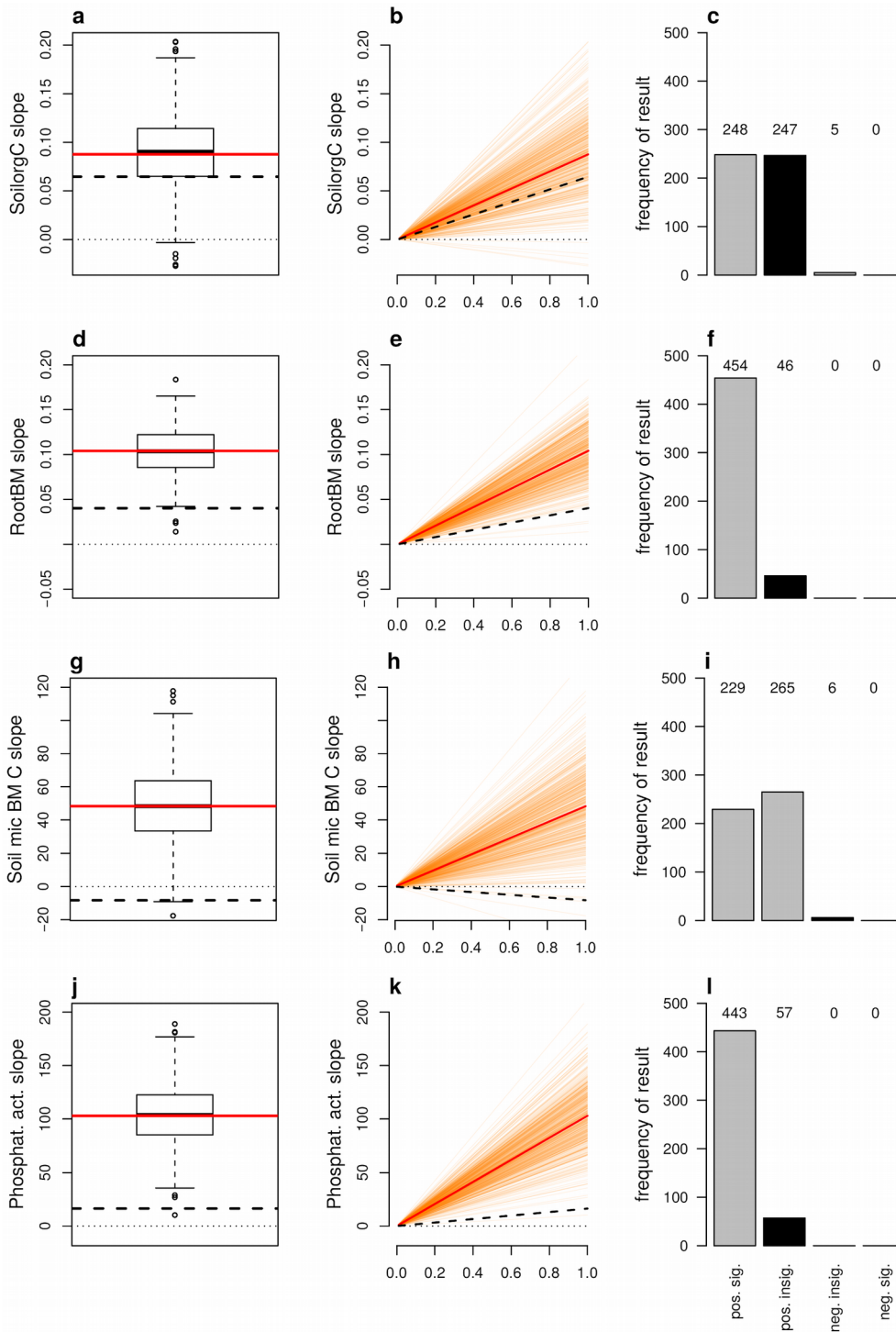
Supplementary Figure 4. Random selection sensitivity analysis for Fig. 2 relationships turning insignificant. 500 random draws of Jena plots and the respective BEF slopes for four selected functions.
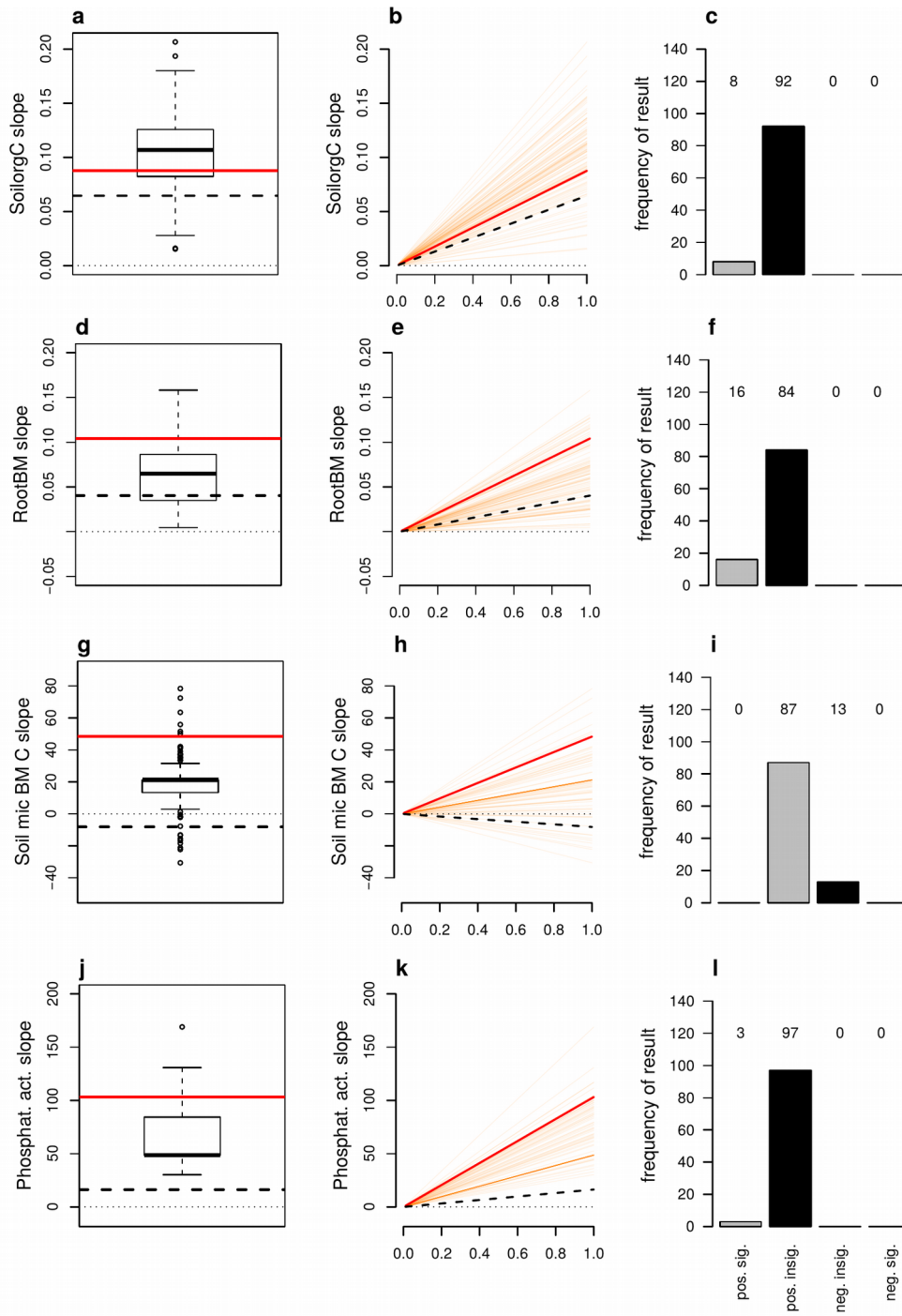
Supplementary Figure 5. Random selection sensitivity analysis for Fig. 2 relationships turning insignificant. 100 restricted random draws of Jena plots and the respective BEF slopes for four selected functions, random draws confined to the species richness gradient also covered by the realistic Jena plots in the main analysis (equal to or larger than 3.7 species).

450 **Supplementary Table 9.** Differences between range in function for unconstrained and constrained data
451 underlying the BEF relationships in Fig. 2. Values are presented for unconstrained (uncon) and
452 constrained (con) datasets of Jena (J) and BioDIV BEF relationships. Constraining was done using the
453 12 vif-selected community properties and the convex hull method. Ranges were calculated based
454 maximum and minimum function performance in unconstrained and constrained datasets. Range
455 changes were calculated as the proportion of unconstrained functioning still covered by constrained
456 functioning. Changes are caused by the removal of unrealistic plots which alters the distribution of
457 function values for a given species richness level, but also by the reduction of the species-richness
458 gradient that is caused by the removal of plots. The across-year species-richness gradient in Jena
459 changed from 1-35.2 species (unconstrained) to 3.7-35.2 species (constrained). The BioDIV species
460 richness gradient was 1-11.1 species and did not change from unconstrained to constrained datasets.

model_name	uncon_range	con_range	range_change
J_biomass	22	9.7	0.44
J_plantCN	34.59	24.33	0.7
J_soilorgC	1.54	1.26	0.82
J_rootbiomass	1.06	0.66	0.63
J_herbivory	1.72	1.05	0.61
J_micBMC	800.54	624.56	0.78
J_phosphatase	1159.23	956.63	0.83
J_pollinators	1.1	0.82	0.74
BioDIV_biomass	2.91	2.38	0.82
BioDIV_plantCN	38.04	34.59	0.91
BioDIV_soilC	0.62	0.62	1
BioDIV_rootbiomass	1952.87	1952.87	1
Jena_avg			0.69
BioDIV_avg			0.93
Overall_avg			0.77

461   **Supplementary Table 10.** Drivers of ecosystem functioning in all vs. realistic communities of
462   biodiversity experiments. In order to assess how the importance of function drivers changes, we
463   analysed relative importance of community properties in explaining functions for the complete set of
464   biodiversity experiment plots and realistic-only plots. As functions, we chose plant aboveground
465   biomass and soil organic carbon as they cover different types of functions (unlike e.g. plant
466   aboveground and root biomass) and are available for both experiments. For each of these functions
467   (response), in each of the two experiments (experiment), we compared the relative importance of 8
468   selected community properties (predictor), two taxonomic diversity metrics, two functional diversity
469   metrics, two phylogenetic diversity metrics and two community weighted mean functional traits (S,
470   SEve, FRic, FEve, PD, MNTD, seed mass, SLA). These pairs of community properties (from each of
471   the community property types (pred_type): tax, phyl, funct, CWM) were selected based on relatively
472   low correlation within the type of properties.
473   For each function, we set up a full model with the function variable as the response and the 8 selected
474   community properties as predictors (simple linear model, no interactions, just additive effects). All
475   variables were standardized to zero mean and unit variance before model runs to compare relative
476   importance. Subsequently, we used the function "dredge" in R package "MuMIn" to compute models
477   with all possible variable combinations and rank them by AICc. We then used the function
478   "importance" from the same R package to extract the summed akaike weight of all models that each
479   variable was present in as a predictor (weight_all). This procedure was repeated for the constrained
480   dataset to obtain predictor importance in the constrained (realistic plots only) datasets (weight_con;
481   based on the main-text analysis using convex hull volume and the vif-selected variable set for the
482   PCA's). Finally, for each of the eight predictors of both functions in both experiments, we calculated
483   the absolute difference in variable importance between the analyses with all plots and realistic plots
484   only (abs_change).

experiment	response	predictor	pred_type	weight_all	weight_con	abs_change
Jena	biomass	seedmass	CWM_trait	1	0.99	-0.01
Jena	biomass	SEve	taxonomic	0.9	0.91	0.01
Jena	biomass	S	taxonomic	0.9	0.99	0.09
Jena	biomass	FEve	functional	0.46	0.1	-0.36
Jena	biomass	PD	phylogenetic	0.32	0.79	0.47
Jena	biomass	MNTD	phylogenetic	0.28	0.17	-0.11
Jena	biomass	FRic	functional	0.25	0.3	0.05
Jena	biomass	SLA	CWM_trait	0.25	0.59	0.34
Jena	soilorgC	SEve	taxonomic	0.6	0.2	-0.4
Jena	soilorgC	FRic	functional	0.56	0.24	-0.32
Jena	soilorgC	PD	phylogenetic	0.33	0.2	-0.13
Jena	soilorgC	S	taxonomic	0.32	0.19	-0.13
Jena	soilorgC	FEve	functional	0.29	0.19	-0.1
Jena	soilorgC	seedmass	CWM_trait	0.29	0.46	0.17
Jena	soilorgC	MNTD	phylogenetic	0.27	0.26	-0.01

|						
Jena	soilorgC	SLA	CWM_trait	0.24	0.24	0
BioDIV	biomass	FRic	functional	0.99	0.99	0
BioDIV	biomass	MNTD	phylogenetic	0.88	0.75	-0.13
BioDIV	biomass	PD	phylogenetic	0.58	0.62	0.04
BioDIV	biomass	S	taxonomic	0.42	0.39	-0.03
BioDIV	biomass	seedmass	CWM_trait	0.32	0.28	-0.04
BioDIV	biomass	FEve	functional	0.31	0.28	-0.03
BioDIV	biomass	SEve	taxonomic	0.27	0.28	0.01
BioDIV	biomass	SLA	CWM_trait	0.26	0.3	0.04
BioDIV	soilC	SEve	taxonomic	0.79	0.88	0.09
BioDIV	soilC	seedmass	CWM_trait	0.73	0.25	-0.48
BioDIV	soilC	PD	phylogenetic	0.52	0.54	0.02
BioDIV	soilC	FEve	functional	0.43	0.37	-0.06
BioDIV	soilC	S	taxonomic	0.31	0.32	0.01
BioDIV	soilC	FRic	functional	0.29	0.29	0
BioDIV	soilC	SLA	CWM_trait	0.27	0.27	0
BioDIV	soilC	MNTD	phylogenetic	0.27	0.27	0

485 **Supplementary Table 11.** Correlation coefficients for CWM's versus functional, phylogenetic metrics
486 and evenness, German dataset. Pearson correlation coefficients for Jena Experiment (upper part) and
487 combined German real world community properties (lower part). Bold values are mean absolute
488 correlation coefficients for the columns, the overall mean is the absolute mean across all column
489 averages.

Jena	FEve	FDiv	FDis	RaoQ	SEve	MPD	MNTD
leaf_area	-0.02	-0.03	0.02	0.07	-0.01	0	0.12
SLA	0	-0.09	0.05	0.06	0.09	0.09	-0.02
leaf_drymass	0.05	0.11	0.1	0.08	-0.12	0.08	0.23
LDMC	0	0.03	0.02	0.06	-0.07	-0.08	-0.15
leaf_N	0.09	0.07	0.14	0.13	-0.09	0.05	-0.03
leaf_P	0.12	0.16	0.22	0.21	-0.16	0.18	0.02
height	0.04	0.05	0.04	0.1	-0.08	-0.08	-0.12
seedmass	-0.01	0.02	-0.02	0.03	0.01	-0.1	-0.13
avg_abs	**0.04**	**0.07**	**0.08**	**0.09**	**0.08**	**0.08**	**0.1**
overall mean	**0.08**						

German RW	FEve	FDiv	FDis	RaoQ	SEve	MPD	MNTD
leaf_area	-0.08	-0.09	0.34	0.47	0.19	0.04	0.12
SLA	-0.21	-0.21	0.07	0.07	0.14	-0.13	0.03
leaf_drymass	-0.03	0.12	0.52	0.57	0.25	0.36	0.18
LDMC	0.1	-0.09	-0.23	-0.2	-0.25	-0.5	-0.06
leaf_N	-0.15	-0.05	0.29	0.26	0.12	0.25	0.05
leaf_P	-0.19	-0.24	0.06	0.11	0.06	-0.16	0.03
height	-0.03	-0.22	-0.04	0.05	-0.07	-0.5	-0.07
seedmass	0.14	0.14	0.35	0.42	0.04	0.16	0.08
avg_abs	**0.12**	**0.15**	**0.24**	**0.27**	**0.14**	**0.26**	**0.08**
overall mean	**0.18**						

490 **Supplementary Table 12.** Correlation coefficients for CWM's versus functional, phylogenetic metrics
491 and evenness, US dataset. Pearson correlation coefficients for BioDIV (upper part) and combined US
492 real world community properties (lower part). Bold values are mean absolute correlation coefficients
493 for the columns, the overall mean is the absolute mean across all column averages.

BioDIV	FEve	FDiv	FDis	RaoQ	SEve	MPD	MNTD
leaf_area	0.13	0.2	0.4	0.47	-0.17	0.24	0.1
SLA	0.15	0.18	0.22	0.26	-0.19	0.15	-0.08
leaf_drymass	0.04	0.1	0.26	0.32	-0.1	0.12	0.07
LDMC	-0.11	-0.14	-0.3	-0.35	0.1	-0.25	-0.12
leaf_N	0.05	0.03	0.22	0.26	0.04	0.23	0.13
leaf_P	-0.02	-0.02	0.13	0.17	0.08	0.09	0.13
height	0.01	0.08	0.01	0.02	-0.15	-0.06	-0.07
seedmass	0.11	0.15	0.37	0.44	-0.13	0.27	0.14
avg_abs	**0.08**	**0.11**	**0.24**	**0.29**	**0.12**	**0.18**	**0.1**
overall mean	**0.16**						

USA RW	FEve	FDiv	FDis	RaoQ	SEve	MPD	MNTD
leaf_area	0.09	0.13	0.5	0.6	-0.07	0.38	0.12
SLA	0.06	0.08	0.15	0.14	-0.21	0.33	0.23
leaf_drymass	0.07	0.11	0.51	0.65	-0.04	0.32	0.1
LDMC	-0.11	-0.06	-0.27	-0.23	0.06	-0.33	-0.13
leaf_N	-0.18	-0.36	-0.29	-0.2	0.18	-0.2	0.13
leaf_P	0.13	-0.03	0.33	0.29	-0.01	0.48	0.38
height	-0.23	-0.18	-0.41	-0.28	0.08	-0.55	-0.24
seedmass	0.04	-0.03	0.29	0.36	0.01	0.29	0.29
avg_abs	**0.11**	**0.12**	**0.34**	**0.34**	**0.08**	**0.36**	**0.2**
overall mean	**0.22**						
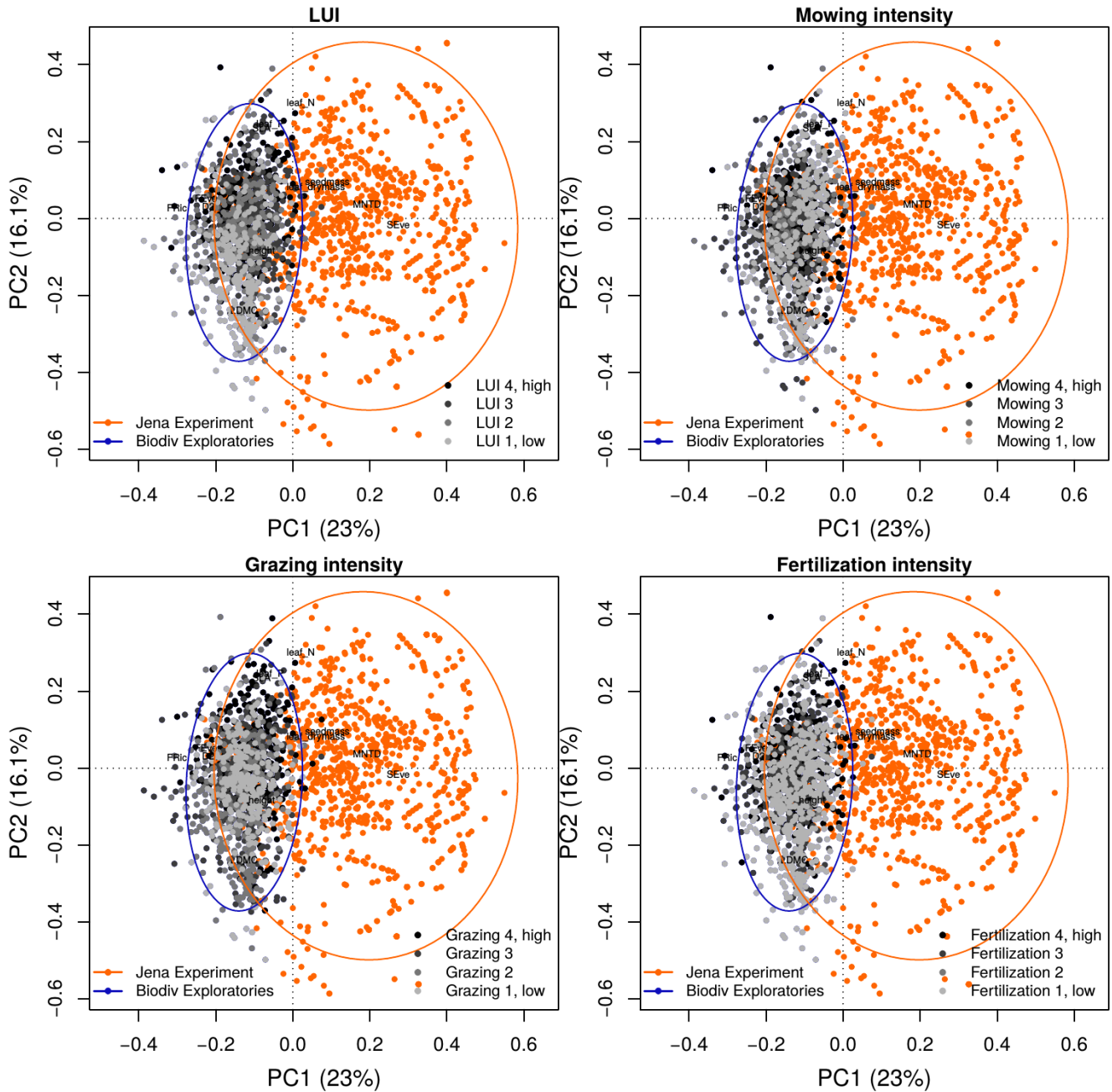
Supplementary Figure 6. Alternative versions of Fig. 1a showing Exploratories land-use intensity gradients. PCA biplot of Jena Experiment (orange dots and ellipse) and Biodiversity Exploratories communities (gray shaded dots, blue circle) showing land-use intensity (LUI), mowing, grazing and fertilization intensity of Exploratories plots. Land use intensity indices have been standardized across years 2008-2015 and across all three Exploratories regions [13]. Gray shades from light to dark depict increasing land-use intensity using categorical variables calculated based on the quantiles of the different land-use data.
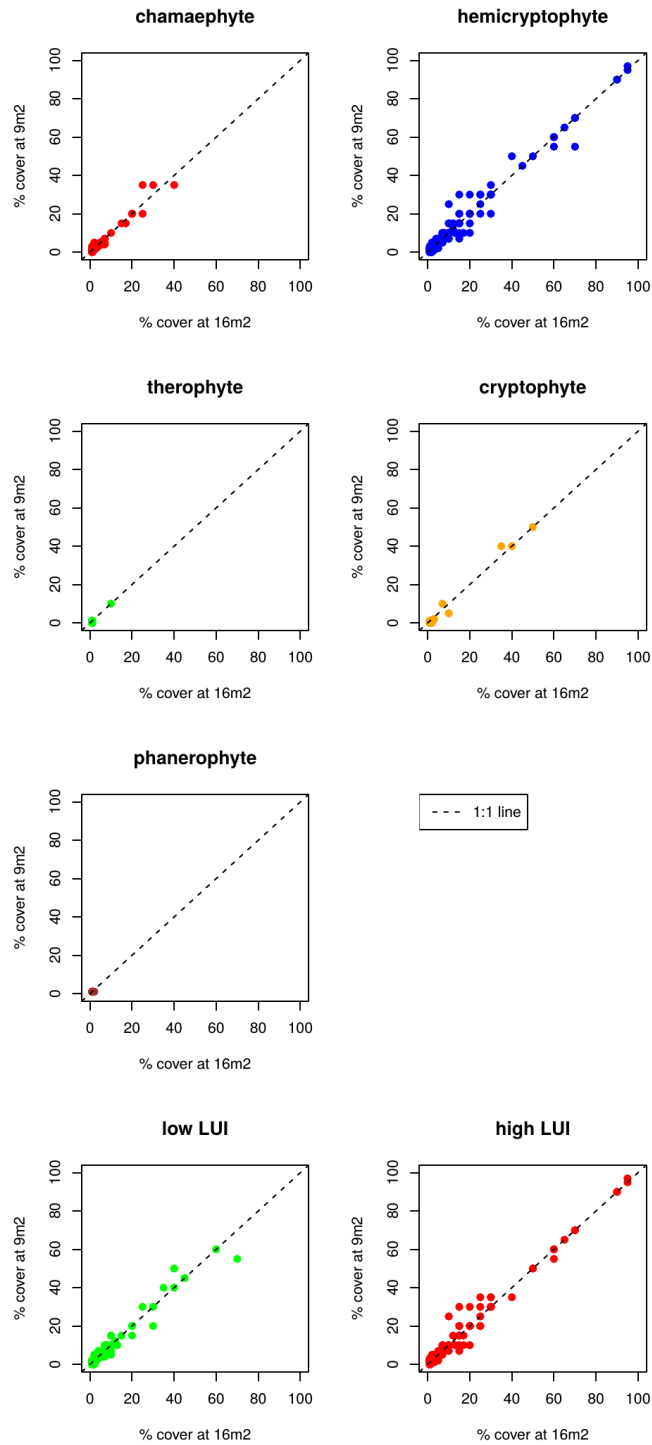
501 **Supplementary Figure 7.** Cover versus vegetation survey size scaling sensitivity check for
502 Biodiversity Exploratories (German real world). Here, 16 to 9 m², the latter being the vegetation survey
503 area of the Jena main and Jena real world plots. For this figure, species were sorted into lifeforms using
504 the R package "TR8" [14] and information from The Ecological Flora Database [15].
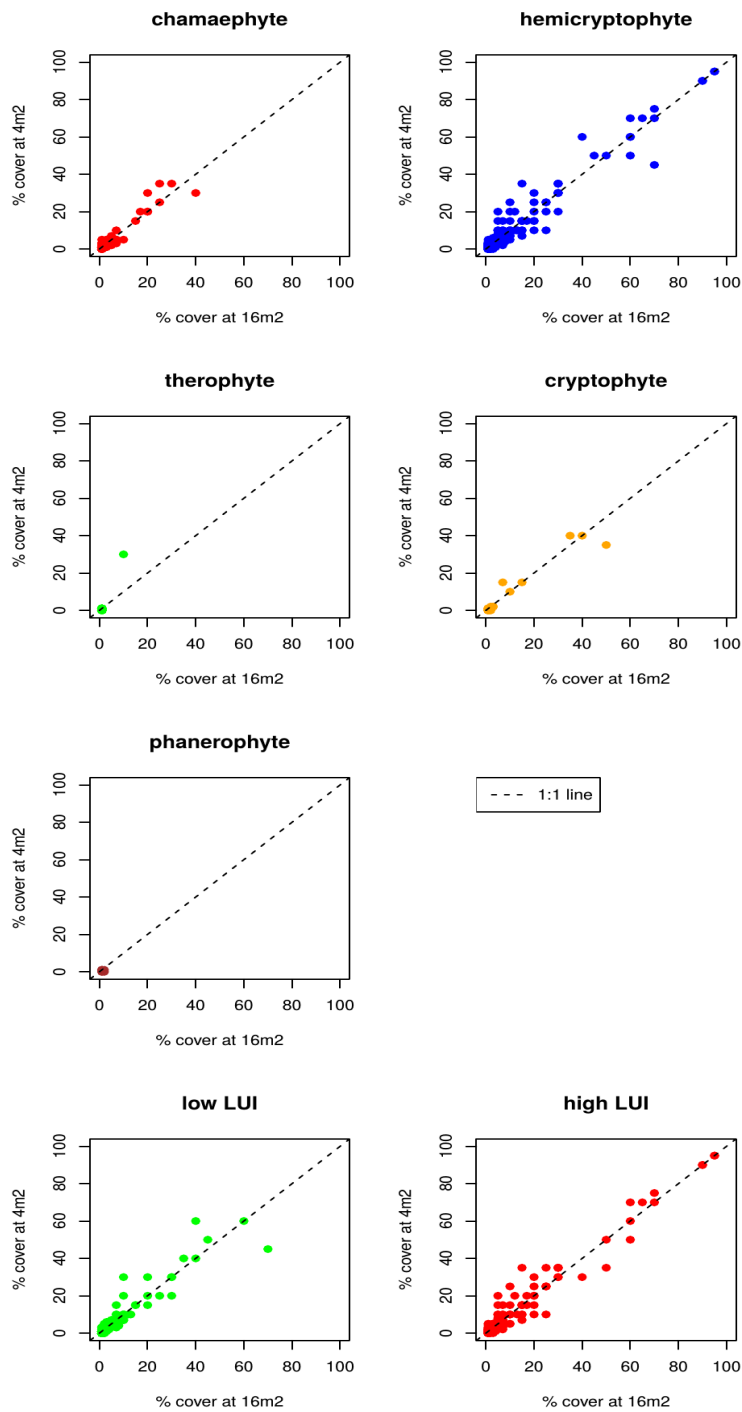
Supplementary Figure 8. Cover versus vegetation survey size scaling sensitivity check for
Biodiversity Exploratories (German real world). Here, 16 to 4 m², the latter resembling the vegetation
survey area of the Jena invasion plots. For this figure, species were sorted into lifeforms using the R
package "TR8" [14] and information from The Ecological Flora Database [15].

509 **Supplementary Figure 9.** Phylogenetic backbone tree (one example of the 50 replicates).
510 Overall 664 species. 132 species (19.9%, pink dots) that were not present in the backbone phylogeny
511 used to build this tree were randomly inserted into their genera (see methods for details).
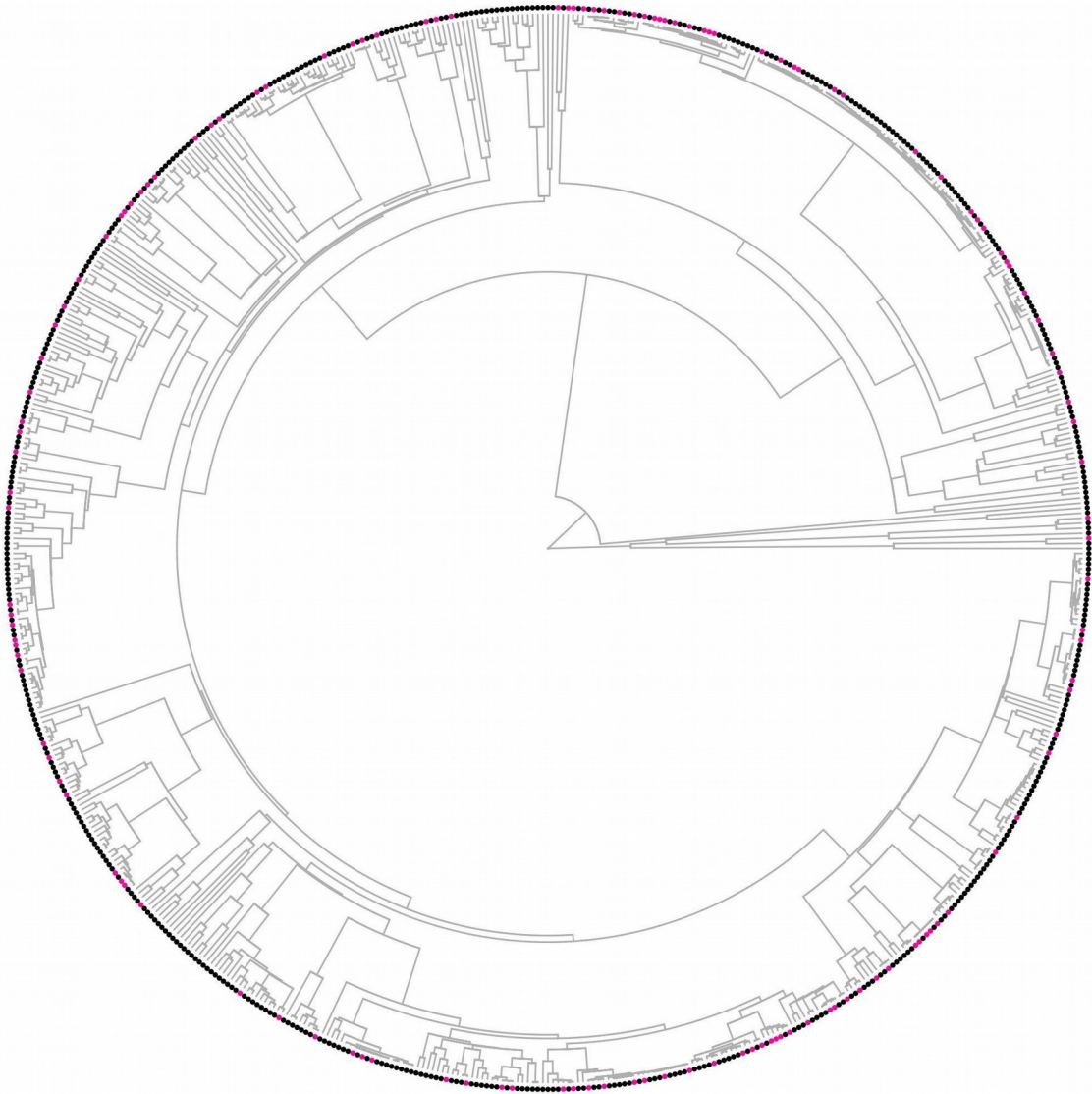
512 **Supplementary Table 13.** TRY references for plant species trait data from TRY [16] requests 2968 and
513 4106. Data sources are sorted by the region their trait data have been used for (Germany=GER or
514 USA). Note that, as mentioned in the main text, trait data for the USA dataset have been complemented
515 by data from Cedar Creek plant trait assessments by Jane Catford, Peter Reich and Jeannine Cavender-
516 Bares [11,17].

Region	TRY_Dataset	Reference
GER	Altitudinal Vicariants Spain	[89]
GER	ArtDeco Database	[92]
GER	BASECO: a floristic and ecological database of Mediterranean French flora	[100]
GER	BiolFlor Database	[110]
GER	BiolFlor Database	[28]
GER	BiolFlor Database	[29]
GER	BiolFlor Database	[30]
GER	BiolFlor Database	[31]
GER	BiolFlor Database	[18]
GER	BiolFlor Database	[23]
GER	BiolFlor Database	[24]
GER	BiolFlor Database	[25]
GER	BiolFlor Database	[26]
GER	BiolFlor Database	[27]
GER	BiolFlor Database	[37]
GER	BiolFlor Database	[38]
GER	BiolFlor Database	[39]
GER	BROT Plant Trait Database	[40]
GER	BROT Plant Trait Database	[41]
GER	Cedar Creek prairie plants (leaf, seed, dispersule, height, plant, root)	unpub.
GER	Climbing plants trait dataset	[90]
GER	Ecological Flora of the British Isles	[24]
GER	Functional traits explaining variation in plant life history strategies	[47]
GER	GLOPNET - Global Plant Trait Network Database	[91]
GER	GLOPNET - Global Plant Trait Network Database	[53]
GER	Grassland Plant Trait Database	[54]
GER	Grassland Plant Trait Database	[55]
GER	Harze Trait Intravar: SLA, LDMC and Plant Height for Calcareous Grassland Species in South Belgium	unpub.
GER	Herbs Water Relations on Soil Moisture Gradients	[56]
GER	Hydrophytes Traits Database	[93]
GER	Italian Alps Plant Traits Database	[94]
GER	Italian Alps Plant Traits Database	[95]

GER	KEW Seed Information Database (SID)	[58]
GER	KEW Seed Information Database (SID)	[59]
GER	Leaf Allometry Dataset	[96]
GER	Leaf Allometry Dataset	[97]
GER	Leaf and Whole Plant Traits Database	[98]
GER	Leaf and Whole Plant Traits Database	[99]
GER	Leaf and Whole Plant Traits Database	[101]
GER	Leaf and Whole Plant Traits Database	[102]
GER	Leaf and Whole Plant Traits Database	[103]
GER	Leaf and Whole Plant Traits Database	[104]
GER	Leaf and Whole Plant Traits Database	[105]
GER	Leaf and Whole Plant Traits Database	[106]
GER	Leaf and Whole Plant Traits Database	[107]
GER	Leaf and Whole Plant Traits Database	[108]
GER	Leaf and Whole Plant Traits Database	[109]
GER	Leaf and Whole Plant Traits Database	unpub.
GER	Leaf and Whole Plant Traits Database	[111]
GER	Leaf Area, Dry Mass and SLA Dataset	unpub.
GER	Leaf Economic Traits Across Varying Environmental Conditions	[61]
GER	Leaf N-Retention Database	[62]
GER	Leaf Physiology Database	[112]
GER	Leaf Physiology Database	unpub.
GER	Leaf Structure and Economic Spectrum	[66]
GER	Leaf Structure and Economic Spectrum	[67]
GER	Leaf Structure and Economic Spectrum	[68]
GER	Leaf Structure, Venation and Economic Spectrum	[69]
GER	Leaf Structure, Venation and Economic Spectrum	[70]
GER	Leaf Structure, Venation and Economic Spectrum	[60]
GER	Leaf Structure, Venation and Economic Spectrum	[71]
GER	Leaf traits from Baltic Island species	[113]
GER	Leaf Traits in Central Apennines Beech Forests	[114]
GER	Northern mixed-grass prairie species traits - Wyoming, USA	unpub.
GER	Nutrient Resorption Efficiency Database	[115]
GER	Nutrient Resorption Efficiency Database	[116]

GER	Photosynthesis Traits Worldwide	74
GER	PLANTATT - Attributes of British and Irish Plants	117
GER	Plant Coastal Dune Traits (France, Aquitaine)	unpub.
GER	Plant Traits of Acidic Grasslands in Central Spain	118
GER	Plant traits of grassland species	81
GER	Reich-Oleksyn Global Leaf N, P Database	51
GER	Reproductive Allocation	82
GER	Seed Information Database (SID) Seed Mass 2010	83
GER	Sheffield & Spain Woody Database	119
GER	Sheffield & Spain Woody Database	120
GER	Sheffield & Spain Woody Database	121
GER	Sheffield & Spain Woody Database	122
GER	Specific leaf area responses to environmental gradients through space and time	123
GER	The LEDA Traitbase	84
GER	The Netherlands Plant Traits Database	124
GER	The Netherlands Plant Traits Database	125
GER	The VISTA Plant Trait Database	85
GER	The VISTA Plant Trait Database	86
GER	The VISTA Plant Trait Database	87
GER	The VISTA Plant Trait Database	88
GER	The Xylem/Phloem Database	126
GER	The Xylem/Phloem Database	127
GER	Traits of the Hungarian flora	128
GER	UV-B Radiation Sensitivity of Hieracium Pilosella	129
GER	Wetland Dunes Database	130
GER	Wetland Dunes Database	131
GER	Wetland Dunes Database	unpub.
GER	Wetland Dunes Database	132
GER	Wetland Dunes Database	133
GER	Whole Plant Hydraulic Conductance	134
USA	ArtDeco Database	135
USA	BiolFlor Database	110
USA	BiolFlor Database	19
USA	BiolFlor Database	20
USA	BiolFlor Database	21

USA	BiolFlor Database	22
USA	BiolFlor Database	18
USA	BiolFlor Database	23
USA	BiolFlor Database	24
USA	BiolFlor Database	25
USA	BiolFlor Database	26
USA	BiolFlor Database	27
USA	BiolFlor Database	28
USA	BiolFlor Database	29
USA	BiolFlor Database	30
USA	BROT Plant Trait Database	31
USA	BROT Plant Trait Database	32
USA	California Coastal Grassland Database	33
USA	Cedar Creek Savanna SLA, C, N Database	17
USA	Cold Tolerance, Seed Size and Height of North American Forest Tree Species	unpub.
USA	ECOCRAFT	34
USA	ECOCRAFT	35
USA	ECOCRAFT	36
USA	Floridian Leaf Traits Database	37
USA	Functional traits explaining variation in plant life history strategies	38
USA	Functional Traits of Graminoids in Semi-Arid Steppes Database	39
USA	Functional Traits of Graminoids in Semi-Arid Steppes Database	40
USA	Global 15N Database	41
USA	Global A, N, P, SLA Database	42
USA	GLOPNET - Global Plant Trait Network Database	43
USA	GLOPNET - Global Plant Trait Network Database	44
USA	Grassland Plant Trait Database	45
USA	Grassland Plant Trait Database	46
USA	Herbs Water Relations on Soil Moisture Gradients	47
USA	Jasper Ridge leaf chemistry data	48
USA	KEW Seed Information Database (SID)	49
USA	KEW Seed Information Database (SID)	50
USA	Leaf Area, Dry Mass and SLA Dataset	unpub.
USA	Leaf economics spectrum and venation networks in Populus tremuloides	51
USA	Leaf Economic Traits Across Varying Environmental Conditions	52
USA	Leaf N-Retention Database	53
USA	Leaf Photosynthesis and Nitrogen at Oak Ridge Dataset	54
USA	Leaf Structure and Chemistry	55

USA	Leaf Structure and Chemistry	[56]
USA	Leaf Structure and Economics Spectrum	[57]
USA	Leaf Structure and Economics Spectrum	[58]
USA	Leaf Structure and Economics Spectrum	[59]
USA	Leaf Structure, Venation and Economic Spectrum	[60]
USA	Leaf Structure, Venation and Economic Spectrum	[61]
USA	Leaf Structure, Venation and Economic Spectrum	[51]
USA	Leaf Structure, Venation and Economic Spectrum	[62]
USA	Midwestern and Southern US Herbaceous Species Trait Database	unpub.
USA	New York Old Field Plant Traits Database	[63]
USA	Northern mixed-grass prairie species traits - Wyoming, USA	unpub.
USA	Old fields of Eastern US (Siefert Data)	[64]
USA	Photosynthesis and Leaf Characteristics Database	unpub.
USA	Photosynthesis Traits Worldwide	[65]
USA	Plant Traits for Pinus and Juniperus Forests in Arizona	[66]
USA	Plant Traits for Pinus and Juniperus Forests in Arizona	[67]
USA	Plant Traits of Canadian Forests	[68]
USA	Plant Traits of Canadian Forests	[78]
USA	Plant Traits of Canadian Forests	[79]
USA	Plant Traits of Canadian Forests	[80]
USA	Plant traits of grassland species	[81]
USA	Reich-Oleksyn Global Leaf N, P Database	[51]
USA	Reproductive Allocation	[82]
USA	Rocky Mountain Biological Laboratory WSR/gradient plant traits	unpub.
USA	Seed Information Database (SID) Seed Mass 2010	[83]
USA	The LEDA Traitbase	[84]
USA	The VISTA Plant Trait Database	[85]
USA	The VISTA Plant Trait Database	[86]
USA	The VISTA Plant Trait Database	[87]
USA	The VISTA Plant Trait Database	[88]
USA	Tundra Plant Traits Database	unpub.

517 **Supplementary Figure 10.** PCA of plant species and their traits for German and US comparison.
518 Each point represents the traits of a single species in the German or US dataset. For obvious outliers,
519 the ability of each species to score such extreme values was individually confirmed e.g. by checking
520 that certain species have unusually large leaf area or leaf nitrogen content. Note that since most of the
521 calculated community properties are relative-abundance weighted, these outliers have little impact on
522 the community properties of a given plant community.

523 Germany:
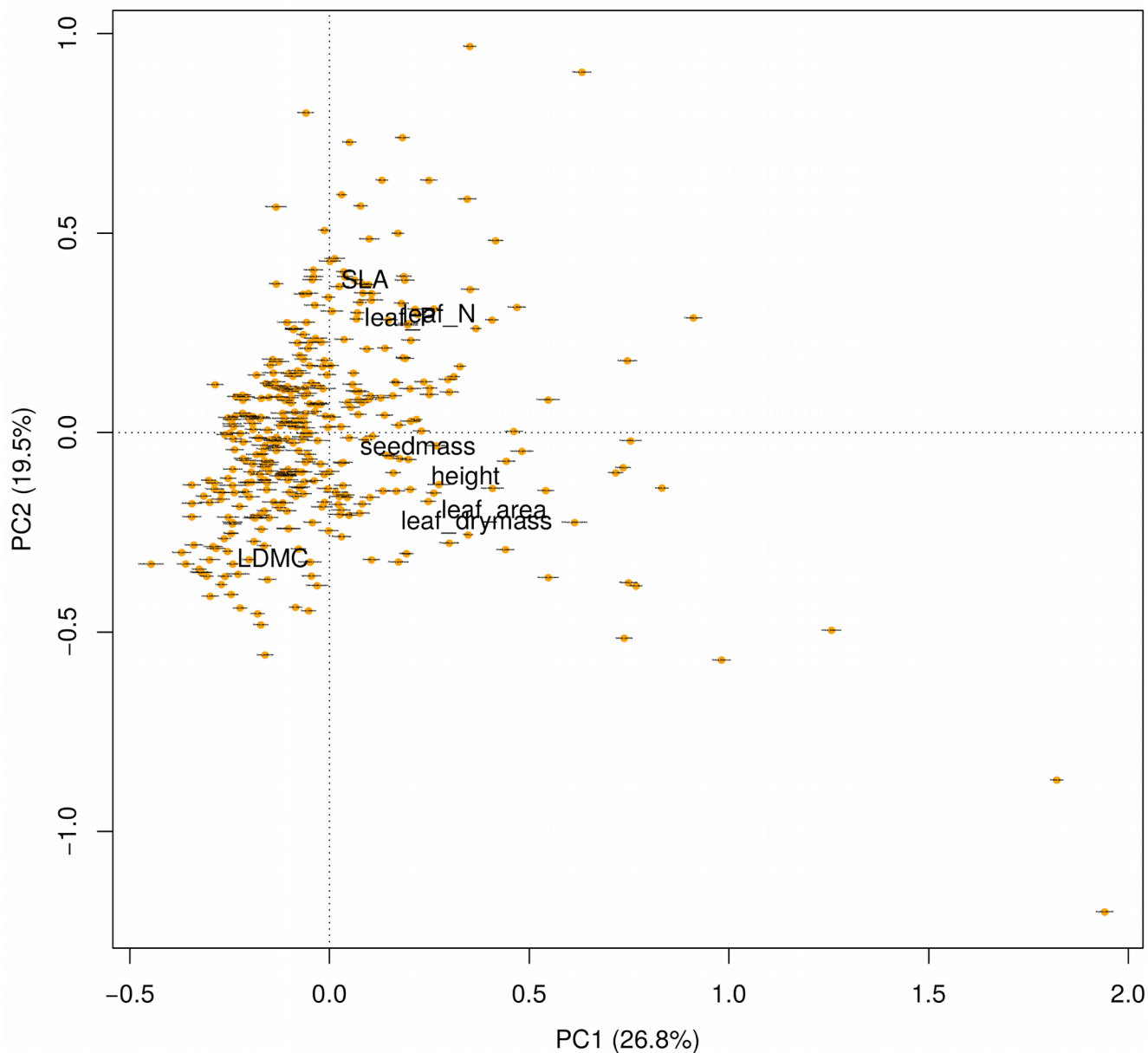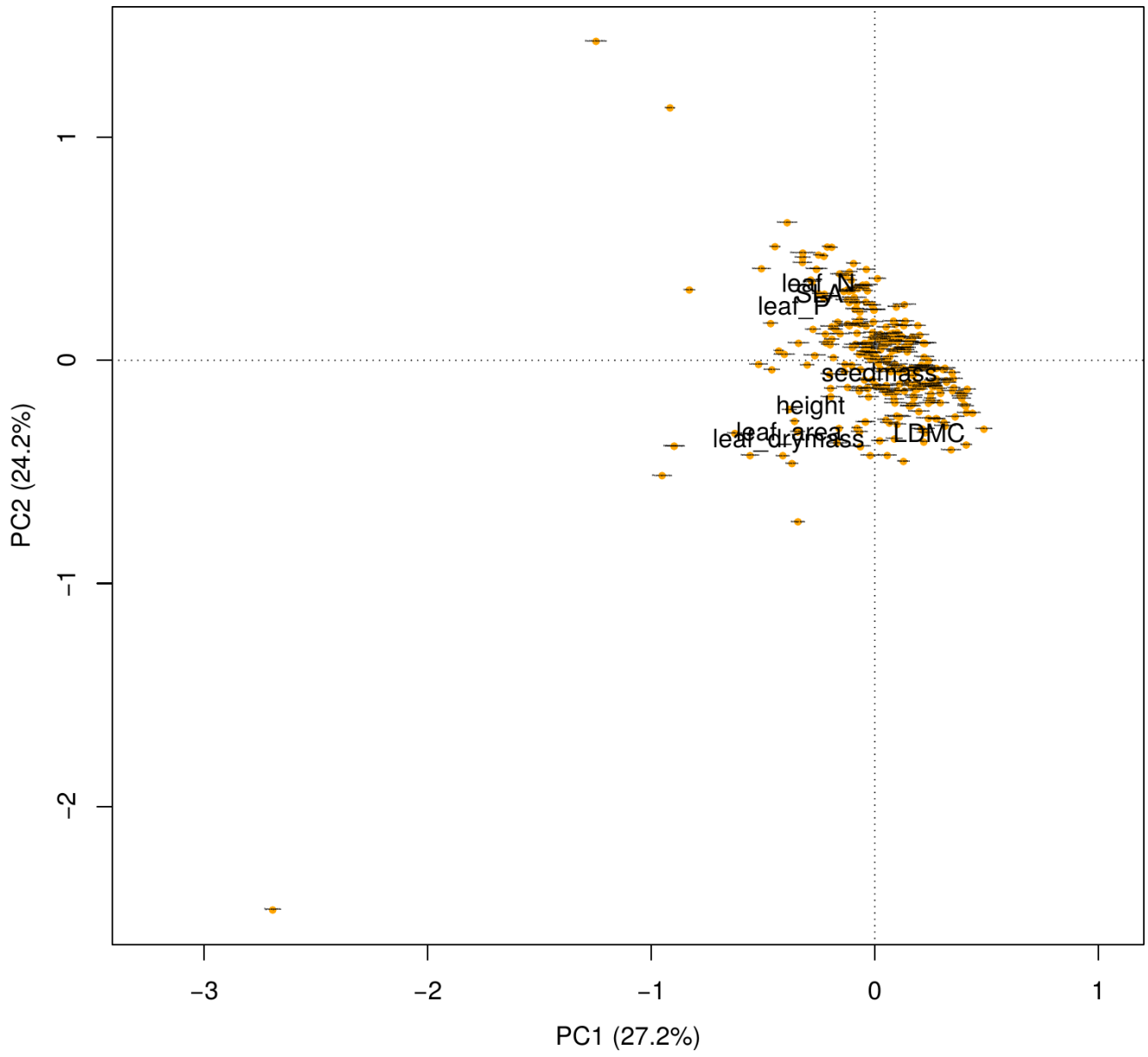
525 **Supplementary Table 14.** Percentage cover of species with trait information for the German and US
526 datasets. For each region (Germany = GER and USA = US) and each of the eight functional traits used
527 in the analysis, the table shows the percentage of total cover occupied by species with available,
528 unimputed trait information across all plots and all datasets of the respective region. As an example, the
529 first row shows that in the German dataset, 97.6 % of the total cover across all plots and all datasets
530 was occupied by species we had original (TRY or personal communication) trait data for. After genus-
531 based inference and imputation of trait data to fill all gaps, 2 % of species in the German dataset (8 of
532 373 species) and 8 % of species in the US dataset (23 of 291 species) had identical trait information
533 across all traits.

region	trait	summed cover %
GER	leaf_area	97.6
GER	SLA	89.7
GER	leaf_drymass	61.6
GER	LDMC	65.0
GER	leaf_N	85.2
GER	leaf_P	78.3
GER	height	99.9
GER	seedmass	99.0
US	leaf_area	99.0
US	SLA	98.4
US	leaf_drymass	99.5
US	LDMC	97.7
US	leaf_N	92.7
US	leaf_P	73.2
US	height	99.4
US	seedmass	99.4

534   **Supplementary Table 15.** Species with altered trait values to avoid Gower dissimilarity zeros.
535   Species are sorted by region (GER=Germany, US=USA) and by the percentage shift that their trait
536   values were subject to. In two cases in the US dataset, there were three same-genus species with
537   identical trait values and here two of them needed different shifts in order to obtain non-zero Gower
538   dissimilarity values.

GER, 0.001% shift up	US 0.001% shift up	US 0.002% shift up
Acinos arvensis	*Achillea sp*	*Antennaria sp*
Arabidopsis thaliana	*Agrostis sp*	*Tradescantia sp*
Chenopodium sp	*Allium stellatum*	
Clinopodium acinos	*Antennaria plantaginifolia*	
Echinochloa crus-galli	*Calamagrostis sp*	
Epilobium sp	*Echinacea serotina*	
Listera ovata	*Euphorbia geyeri*	
Mentha aquatica	*Galium sp*	
Sesleria albicans	*Gnaphalium sp*	
Orobanche caryophyllacea	*Melilotus sp*	
Rubus sp	*Parthenocissus inserta*	
Rumex thyrsiflorus	*Polygala sp*	
Poa angustifolia	*Polygonatum sp*	
Potentilla neumanniana	*Rhus sp*	
Veronica spicata	*Rumex sp*	
	Salix humilis	
	Solidago altissima	
	Stachys sp	
	Taraxacum sp	
	Tradescantia bracteata	

Supplementary Table 16. Correlation coefficients for 21 plant community properties for the German dataset. Pearson correlation coefficients and color code (see legend) for all 21 properties (upper diagram) and the subset of 12 community properties retained after stepwise removal due to variance inflation factors above 3 (lower diagram). Diagrams were created using the "corrplot" package [136] in R.
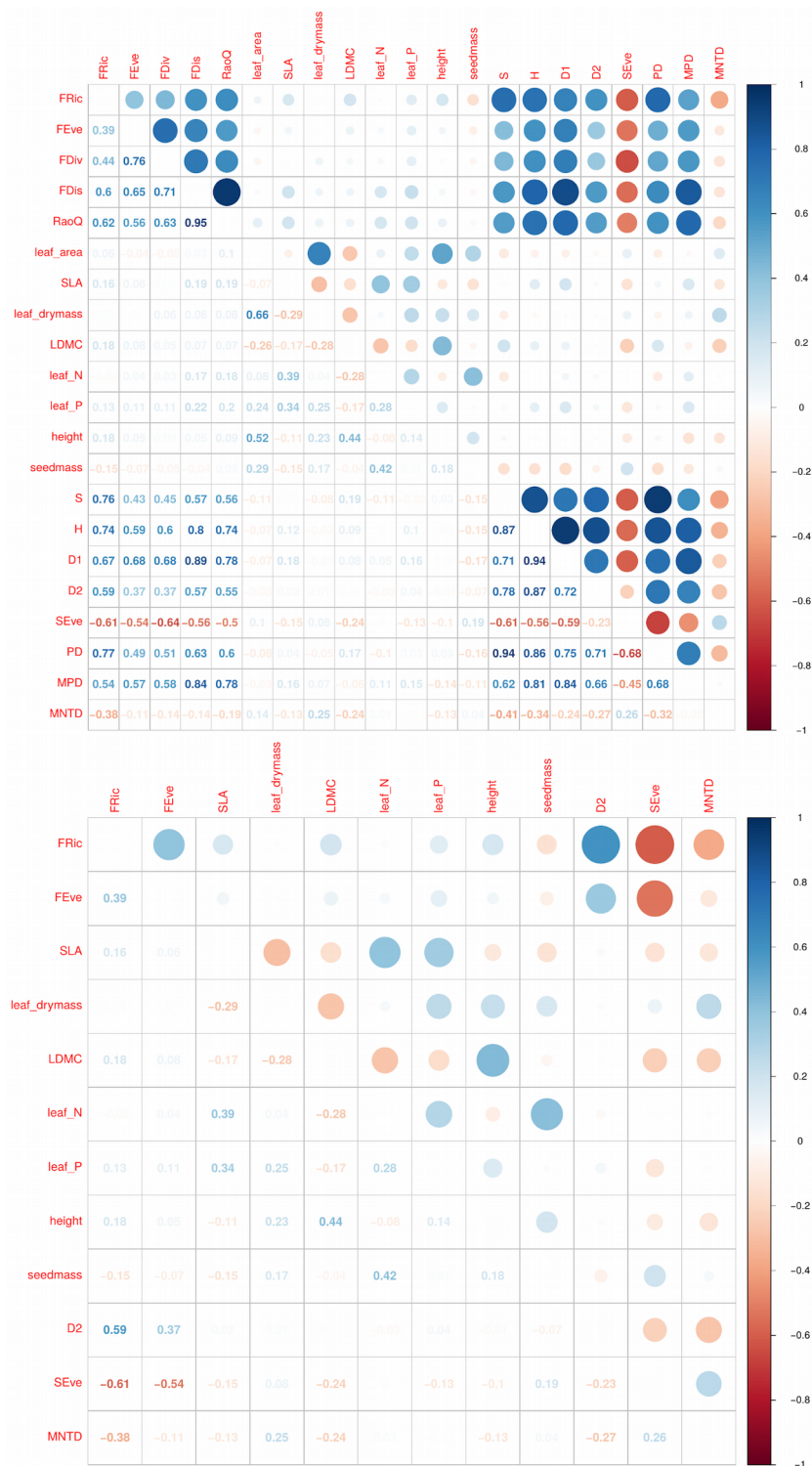
Supplementary Table 17. Correlation coefficients for 21 plant community properties for the US
dataset. Pearson correlation coefficients and color code (see legend) for all 21 properties (upper
diagram) and the subset of 12 community properties retained after stepwise removal due to variance
inflation factors above 3 (lower diagram). Diagrams were created using the "corrplot" package [136] in R.
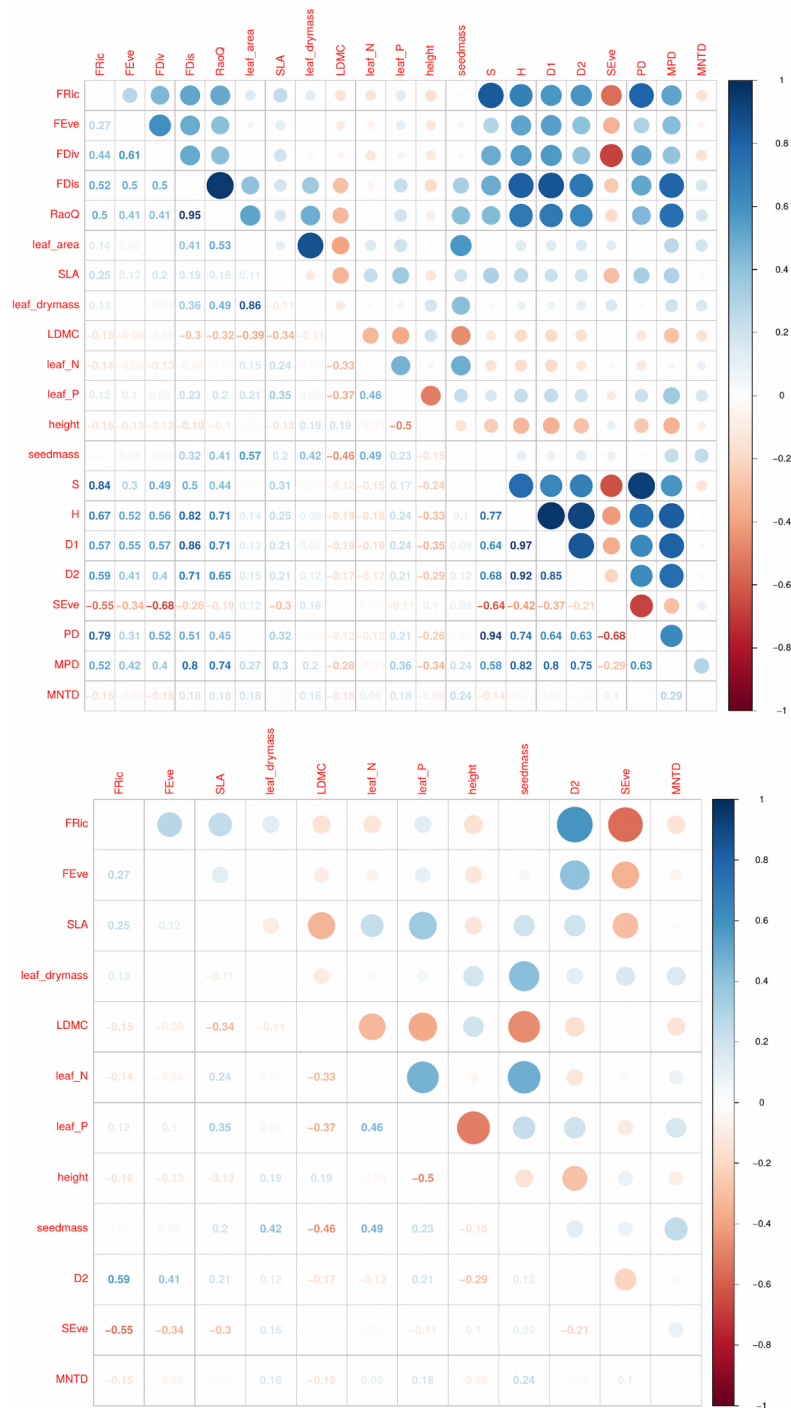
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