

## ELECTRONIC SUPPLEMENTARY MATERIAL FOR:

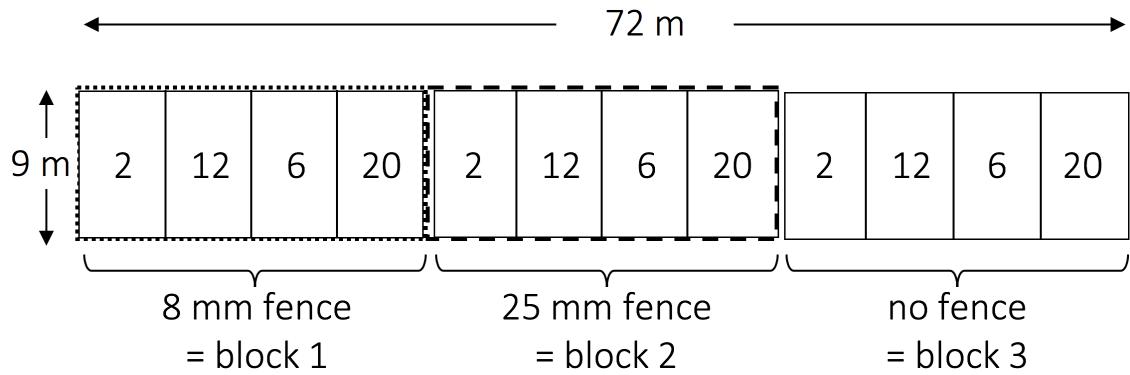
### **Understanding negative biodiversity-ecosystem relationship in semi-natural wildflower strips**

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#### **Appendix S1 - Experimental setup of the wildflower strips**

The Predator exclusion (PE) and predator and herbivore exclusion (PHE) were created with fences of mesh sizes of 25 mm and 8 mm respectively, were 1 m high and extended 0.2 m in the ground. The control plot was left unfenced. The design of the experimental wildflower strips, with the exclosure treatment and the sown species richness (SownS), is given in Fig. S1.1. In the PHE plots, we supplemented molluscicide mini-pellets containing 5% metaldehyde (Metarex®, De Sangosse) to control slug density. Treatment order was randomly designated to each field. For the substitutive design (each plant species added with the same proportion (Jolliffe 2000)) the seed density of the diversity mixtures was corrected to 1000 germinable seeds m<sup>-2</sup> according to germination rates predicted by the commercial seed provider (UFA Samen Lyssach, Switzerland). If predicted germination success of a species was not equal to 100%, the amount of seeds was adjusted, i.e., proportionally more seeds were added. As other projects in our study system were concerned with the fauna (Fabian et al. 2012, 2013, 2014, Bruggisser et al. 2012), and because several studies suggested that weeding might increase invasion of undesired species (Wardle 2001, Roscher et al. 2009), we kept weeding to a minimum, removing only agricultural harmful weeds (*Cirsium arvense* and *Rumex obtusifolius*). In each field we also established an area with the original wildflower mixture, yet this data was excluded from the current analysis.



**Fig. S1** Design of an experimental wildflower strip. Numbers within plots represent the sown species richness (SownS). The dashed and the dotted line represent the predator (PE) and the predator and herbivore (PHE) exclusion treatments, respectively

## Appendix S2 – Lists of plant species

**Table S2.1** List of sown plant species

Plant family	Plant species
Apiaceae	<i>Daucus carota</i> L. <i>Pastinaca sativa</i> L.
Asteraceae	<i>Achillea millefolium</i> L. <i>Anthemis tinctoria</i> L. <i>Centaurea cyanus</i> L. <i>Centaurea jacea</i> L. <i>Cichorium intybus</i> L. <i>Leucanthemum vulgare</i> LAM. <i>Tanacetum vulgare</i> L.
Boraginaceae	<i>Echium vulgare</i> L.
Caryophyllaceae	<i>Agrostemma githago</i> L. <i>Silene latifolia</i> POIR.
Hypericaceae	<i>Hypericum perforatum</i> L.
Caprifoliaceae	<i>Dipsacus fullonum</i> L.
Lamiaceae	<i>Origanum vulgare</i> L.
Malvaceae	<i>Malva moschata</i> L. <i>Malva sylvestris</i> L.
Papaveraceae	<i>Papaver rhoeas</i> L.
Scrophulariaceae	<i>Verbascum thapsus</i> L. <i>Verbascum lychnitis</i> L.

**Table S2.2** List of external colonizer plant species recorded in the experimental plots

Plant family	Plant species
Amaranthaceae	<i>Amaranthus retroflexus</i> L. <i>Chenopodium album</i> L. <i>Chenopodium polyspermum</i> L. <i>Chenopodium sp.</i>
Apiaceae	<i>Aethusa cynapium</i> L.
Asteraceae	<i>Chamomilla recutita</i> (L.) RAUSCHERT <i>Cirsium arvense</i> (L.) SCOP. <i>Conyza canadensis</i> (L.) CRONQUIST <i>Crepis biennis</i> L. <i>Filaginella uliginosa</i> (L.) OPIZ <i>Galinsoga ciliata</i> (RAF.) S.F.BLAKE <i>Lactuca serriola</i> L. <i>Senecio vulgaris</i> L. <i>Sonchus arvensis</i> L. <i>Sonchus asper</i> (L.) Hill <i>Sonchus oleraceus</i> L. <i>Taraxacum officinale</i>
Boraginaceae	<i>Myosotis arvensis</i> (L.) HILL
Brassicaceae	<i>Brassica napus</i> L. <i>Capsella bursa-pastoris</i> (L.) MEDIK. <i>Sinapis alba</i> L.
Campanulaceae	<i>Campanula patula</i> L.
Caryophyllaceae	<i>Cerastium sp.</i> <i>Sagina apetala</i> Ard. <i>Stellaria media</i> (L.) VILL.
Convolvulaceae	<i>Convolvulus arvensis</i> L.
Equisetaceae	<i>Equisetum arvense</i> L.
Euphorbiaceae	<i>Euphorbia helioscopia</i> L. <i>Euphorbia stricta</i> L. <i>Mercurialis annua</i> L.
Fabaceae	<i>Lotus corniculatus</i> L. <i>Medicago lupulina</i> L. <i>Medicago sativa</i> L. <i>Melilotus albus</i> MEDIK. <i>Onobrychis viciifolia</i> SCOP. <i>Trifolium pratense</i> L. <i>Trifolium repens</i> L. <i>Vicia hirsuta</i> (L.) GRAY
Geraniaceae	<i>Geranium rotundifolium</i> L.
Juglandaceae	<i>Juglans regia</i> L.
Juncaceae	<i>Juncus bufonius</i> L. <i>Juncus sp.</i>
Lamiaceae	<i>Glechoma hederacea</i> L. <i>Lamium amplexicaule</i> L. <i>Lamium purpureum</i> L. <i>Mentha arvensis</i> L. <i>Prunella vulgaris</i> L.

Plant family	Plant species
Onagraceae	<i>Epilobium</i> sp. <i>Oenothera biennis</i> L.
Orobanchaceae	<i>Orobanche</i> sp.
Oxalidaceae	<i>Oxalis stricta</i> L.
Plantaginaceae	<i>Chaenorhinum minus</i> (L.) LANGE <i>Kickxia elatine</i> (L.) DUMORT. <i>Kickxia spuria</i> (L.) DUMORT. <i>Linaria vulgaris</i> MILL. <i>Plantago lanceolata</i> L. <i>Plantago major</i> L. <i>Veronica persica</i> Poir. <i>Veronica serpyllifolia</i> L.
Poaceae	<i>Agrostis stolonifera</i> L. <i>Apera spica-venti</i> (L.) P.BEAUV. <i>Arrhenatherum elatius</i> (L.) P.BEAUV. ex J.PRESL & C.PRESL <i>Dactylis glomerata</i> L. <i>Digitaria sanguinalis</i> (L.) SCOP. <i>Echinochloa crus-galli</i> (L.) P.BEAUV. <i>Elymus repens</i> (L.) GOULD <i>Festuca</i> sp. <i>Holcus lanatus</i> L. <i>Lolium perenne</i> L. <i>Phleum pratense</i> agg. <i>Poa annua</i> L. Poaceae (undetermined) <i>Setaria pumila</i> (POIR.) SCHULT. <i>Triticum</i> sp.
Polygonaceae	<i>Fallopia convolvulus</i> (L.) A.LÖWE <i>Polygonum aviculare</i> L. <i>Polygonum mite</i> (= <i>Persicaria laxiflora</i> ) <i>Polygonum</i> sp. <i>Rumex obtusifolius</i> L.
Primulaceae	<i>Anagallis arvensis</i> L.
Ranuculaceae	<i>Ranunculus repens</i> L.
Rosaceae	<i>Potentilla reptans</i> L. <i>Rubus</i> sp.
Rubiaceae	<i>Galium album</i> MILL. <i>Galium aparine</i> L.
Salicaceae	<i>Salix alba</i> L. <i>Salix caprea</i> L.
Sapindaceae	<i>Acer pseudoplatanus</i>
Scrophulariaceae	<i>Scrophularia nodosa</i> L.
Solanaceae	<i>Solanum nigrum</i> L.
Urticaceae	<i>Urtica dioica</i> L.
Verbenaceae	<i>Verbena officinalis</i> L.
Violaceae	<i>Viola arvensis</i> MURRAY

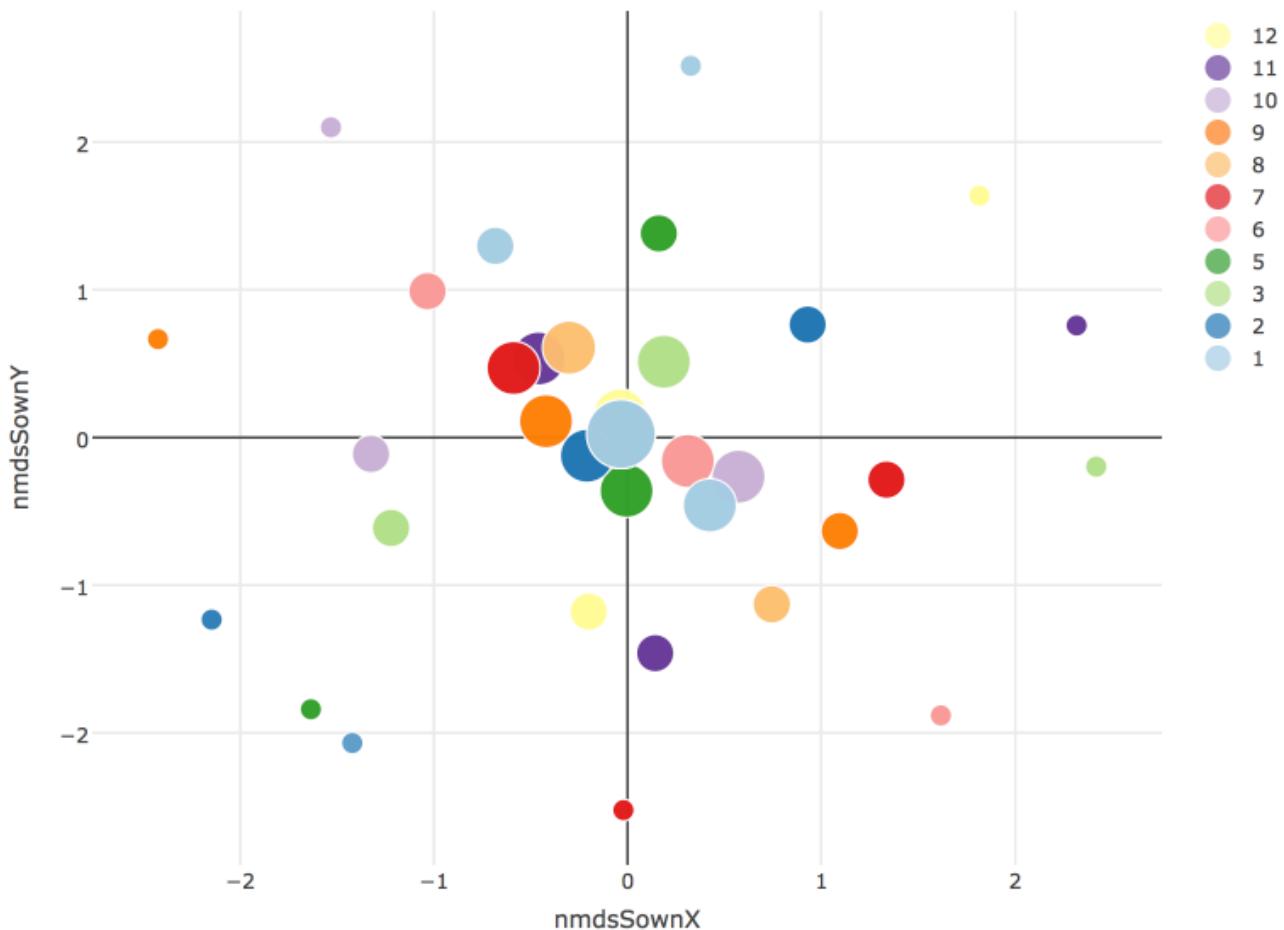
### **Appendix S3 - Above-ground biomass estimations using leaf area index (LAI)**

Biomass was predicted from the leaf area index (LAI): 27 measures per plot were taken using a LAI-2000 Plant Canopy Analyser from Li-COR Biosciences (Lincoln, Nebraska).

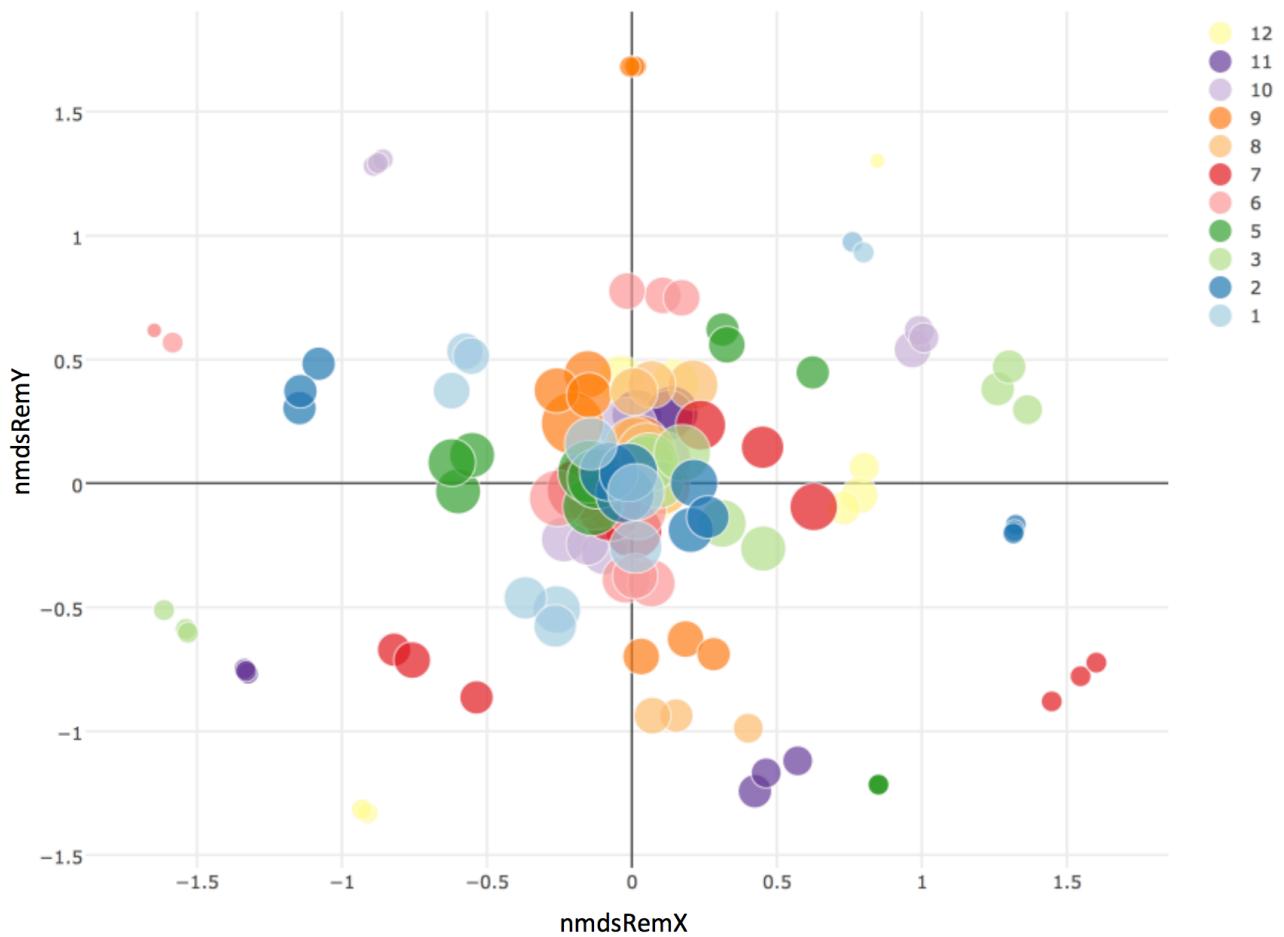
Additionally, we determined above-ground biomass in eight plots by cutting the above-ground biomass in five randomly selected 30 cm x 30 cm squares. As the Plant Canopy analyser cannot distinguish between leaf litter and senescent plant material, we did not sort the clipped samples into fresh biomass and dead biomass, instead we comprised all the plant material within the squares. Doing so we make sure to take into account plant material that was produced before the sampling event (Jenkins 2015). The plant material was bagged in paper bags and dried at 60°C until constant weight. To represent plot biomass, we calculated the average of the five samples.

We calibrated the clipped biomass and the LAI values by performing a regression analysis, which resulted in a Pearson product-moment correlation of 0.89. The linear relationship was used to predict plant biomass per plot in  $\text{g} \cdot \text{m}^{-2}$  from the average LAI values.

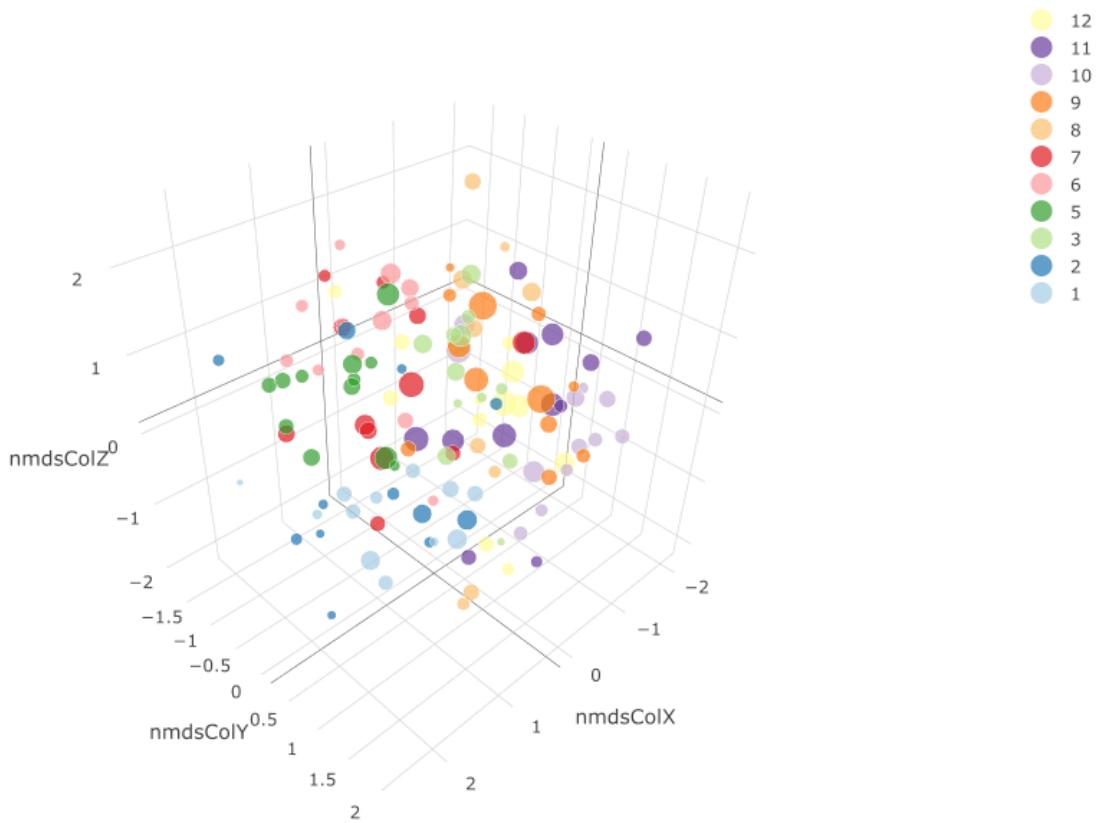
## Appendix S4 - Additional figures



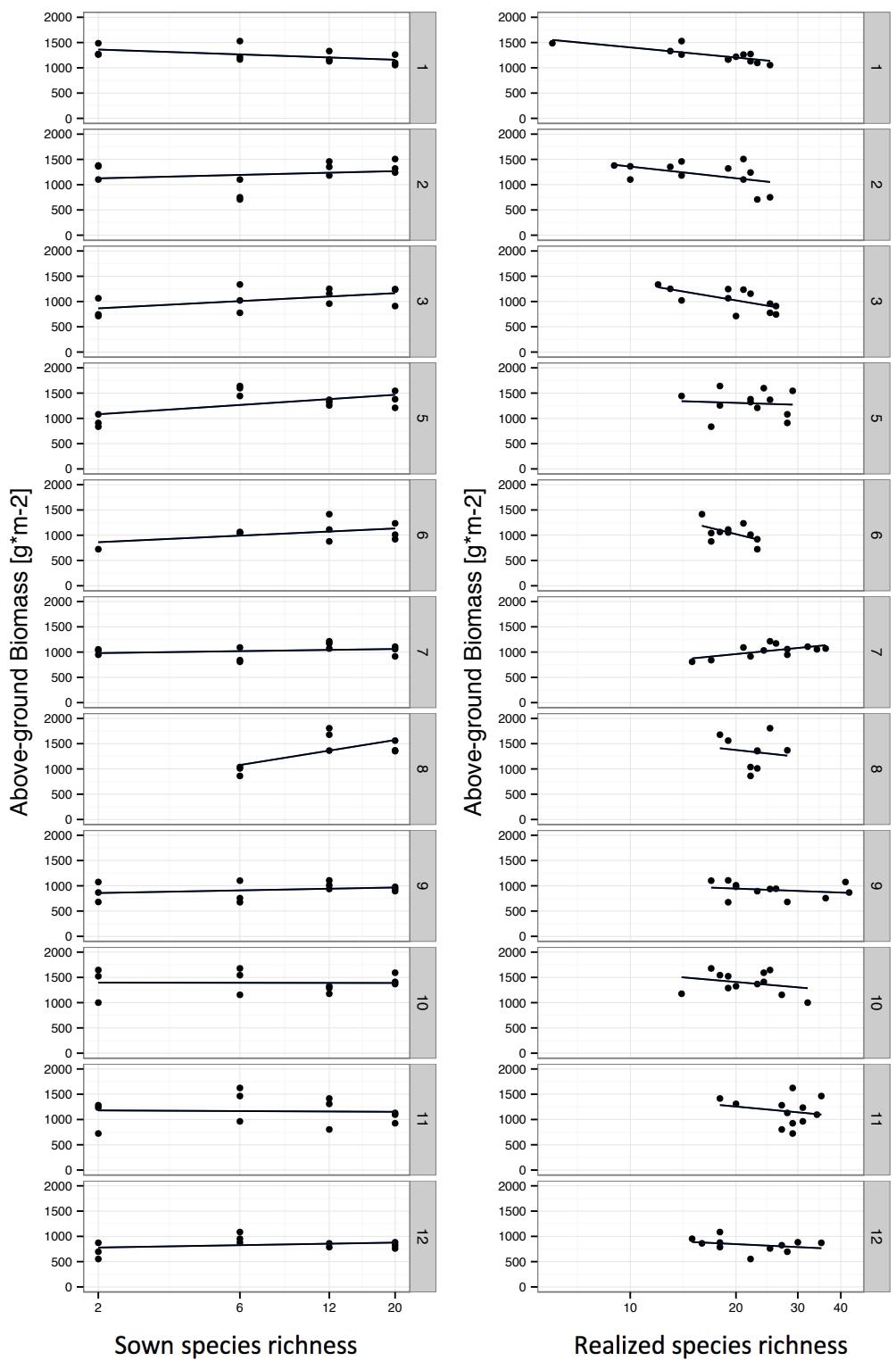
**Fig. S4.1** NMDS ordination showing Sørensen dissimilarity among plots based on the sown plant assemblages. The colour schemes refer to different fields and the size of the symbol displays the number of species. Symbols located close together in the two-dimensional graph plots with similar composition. Note, that the three plots with the same diversity level within each field have the exact same NMDS scores. The distribution of the plots reflects the experimental design of the experiment, with constrained selection of the species so that they occur in similar frequencies at the same diversity level. In this way, the sown compositions appear evenly placed on concentric ellipses



**Fig. S4.2** NMDS ordination showing Bray-Curtis dissimilarity based on plant species abundance among plots for remaining plant species composition. The colour schemes refer to different fields and the size of the symbol displays above-ground biomass



**Fig. S4.3** NMDS ordination showing Bray Curtis dissimilarity based on abundance plant species abundance among plots for colonizer plant species composition. The colour scheme refers to the 11 experimental fields and the size of the symbol displays above-ground biomass. We observe that plots from the same field tend to be clustered. We performed a Canonical Correspondence analysis on the same data, using field identity as explanatory variable, and found a highly significant effect of the latter (permutation test,  $p < 0.0001$ , analysis performed with functions `cca` and `anova.cca` from the `vegan` package; Oksanen et al. 2015)



**Fig. S4.4** Relationships of sown species richness (SownS) and realized species richness (S) and above-ground biomass within the different fields

## Appendix S5 - Results of the initial *a priori* piecewise structural equation model

**Table S5** This model gives all *a priori* relationships tested (see Table 3 and Fig. 7 for the final model).

Biomass of the remaining sown species (RemB) and of colonizer species (ColB) are the response variables of interest. Variables: ColPD = phylogenetic diversity of colonizers; RemPD = phylogenetic diversity of remaining sown species; SownS = sown species richness; RemS = richness of remaining sown species; nmdsColX, -Y, and -Z = 1<sup>st</sup>, 2<sup>nd</sup>, and 3<sup>rd</sup> axes for composition of colonizers; nmdsRemX, -Y = 1<sup>st</sup> and 2<sup>nd</sup> axes for composition of remaining sown species

Response variable	Predictor variable	estimate	SE	p-value
log <sub>2</sub> (ColS)	RemB	-0.363	0.075	<0.001
	ColPD	0.264	0.065	<0.001
	log <sub>2</sub> (SownS)	-0.406	0.272	0.140
	log <sub>2</sub> (RemS)	0.065	0.276	0.812
	nmdsColX	0.053	0.074	0.475
	nmdsColY	0.002	0.073	0.974
	nmdsColZ	0.054	0.061	0.372
log <sub>2</sub> (RemS)	log <sub>2</sub> (SownS)	0.989	0.026	<0.001
	RemPD	-0.019	0.028	0.499
	nmdsRemX	-0.006	0.019	0.740
	nmdsRemY	0.048	0.019	0.012
RemB	log <sub>2</sub> (RemS)	0.424	0.098	<0.001
	RemPD	-0.03	0.103	0.772
	ColPD	-0.168	0.073	0.023
	nmdsRemX	0.173	0.068	0.012
	nmdsRemY	0.137	0.070	0.056
ColB	RemB	-0.694	0.082	<0.001
	nmdsColX	0.199	0.073	0.008
	RemPD	-0.123	0.081	0.132
	ColPD	0.093	0.07	0.190
	nmdsColY	0.066	0.073	0.368
	log <sub>2</sub> (ColS)	0.043	0.093	0.648
	log <sub>2</sub> (RemS)	-0.029	0.094	0.761
	nmdsColZ	0.015	0.061	0.809

## Appendix S6 - Details of model selection results

**Table S6** The table gives all models with a  $\Delta\text{AIC} \leq 6$ . Models with an orange background were not selected as they are more complex version of models with lower AIC. Variables: ColS = species richness of colonizers ( $\log_2$ -transformed); RemS = species richness of remaining sown species ( $\log_2$ -transformed); ColPD = phylogenetic diversity of colonizer species; RemPD = phylogenetic diversity of remaining sown species; nmdsColX, nmdsColY, and nmdsColZ = 1<sup>st</sup>, 2<sup>nd</sup>, and 3<sup>rd</sup> NMDS axes for the composition of colonizer species; nmdsRemX and nmdsRemY = 1<sup>st</sup> and 2<sup>nd</sup> NMDS axes for the composition of remaining sown species; SownS = sown species richness ( $\log_2$ -transformed); nmdsSownX and nmdsSownY = 1<sup>st</sup> and 2<sup>nd</sup> NMDS axes for sown composition. Note that the enclosure treatment was included in all models

Model no	Intercept	ColS	RemS	ColPD	LeftPD	nmdsColX	nmdsColY	nmdsColZ	nmdsRemX	nmdsRemY	SownS	nmdsSownX	nmdsSownY	df	LogLik	AICc	DAIC	AIC weight
7958	-0.139	-0.241	NA	NA	-0.178	NA	NA	NA	0.228	0.032	0.176	-0.022	0.237	13	-151.04	303.71	0.00	0.098
7414	-0.092	-0.252	NA	NA	-0.243	0.220	0.049	-0.062	NA	NA	0.219	-0.161	0.160	14	-151.96	303.80	0.10	0.093
8166	-0.105	-0.227	NA	NA	NA	0.215	0.043	-0.058	0.262	0.094	0.058	0.009	0.181	15	-152.19	303.86	0.15	0.091
7942	-0.149	-0.250	NA	NA	NA	NA	NA	NA	0.287	0.097	0.040	0.021	0.205	12	-151.03	303.93	0.23	0.087
8182	-0.096	-0.218	NA	NA	-0.165	0.213	0.027	-0.060	0.209	0.034	0.180	-0.030	0.213	16	-152.38	304.05	0.34	0.082
7190	-0.136	-0.280	NA	NA	-0.265	NA	NA	NA	NA	NA	0.213	-0.162	0.180	11	-151.04	304.47	0.77	0.067
7422	-0.309	-0.285	NA	0.001	-0.252	0.243	0.040	-0.062	NA	NA	0.231	-0.151	0.163	15	-158.07	305.46	1.76	0.041
8190	-0.336	-0.254	NA	0.001	-0.178	0.239	0.016	-0.058	0.211	0.020	0.198	-0.025	0.225	17	-158.40	305.57	1.87	0.038
8174	-0.302	-0.256	NA	0.000	NA	0.237	0.035	-0.056	0.267	0.086	0.065	0.015	0.189	16	-158.39	305.72	2.02	0.036
7966	-0.232	-0.255	NA	0.000	-0.182	NA	NA	NA	0.228	0.027	0.182	-0.020	0.241	14	-157.53	306.07	2.36	0.030
7960	-0.132	-0.242	-0.100	NA	-0.185	NA	NA	NA	0.223	0.037	0.274	-0.024	0.236	14	-151.20	306.14	2.43	0.029
7416	-0.083	-0.252	-0.130	NA	-0.253	0.217	0.044	-0.065	NA	NA	0.348	-0.163	0.165	15	-152.09	306.22	2.51	0.028
7950	-0.201	-0.258	NA	0.000	NA	NA	NA	NA	0.288	0.096	0.042	0.023	0.207	13	-157.57	306.36	2.66	0.026
8168	-0.110	-0.226	0.077	NA	NA	0.217	0.046	-0.056	0.263	0.088	-0.013	0.009	0.182	16	-152.39	306.41	2.70	0.025
7944	-0.149	-0.250	0.006	NA	NA	NA	NA	NA	0.287	0.097	0.035	0.021	0.205	13	-151.25	306.41	2.71	0.025
7192	-0.121	-0.280	-0.221	NA	-0.280	NA	NA	NA	NA	NA	0.433	-0.167	0.187	12	-151.02	306.43	2.73	0.025
8184	-0.094	-0.219	-0.029	NA	-0.167	0.212	0.026	-0.060	0.208	0.036	0.208	-0.030	0.212	17	-152.58	306.71	3.00	0.022
7198	-0.208	-0.291	NA	0.000	-0.268	NA	NA	NA	NA	NA	0.217	-0.159	0.181	12	-157.55	306.81	3.11	0.021
8181	-0.086	NA	NA	NA	-0.179	0.225	0.024	-0.083	0.244	0.034	0.323	-0.015	0.222	15	-153.59	307.44	3.73	0.015
7398	-0.110	-0.279	NA	NA	NA	0.226	0.086	-0.053	NA	NA	0.037	-0.196	0.134	13	-153.45	307.45	3.74	0.015
8165	-0.095	NA	NA	NA	NA	0.228	0.042	-0.082	0.303	0.099	0.195	0.028	0.187	14	-153.59	307.68	3.98	0.013
7424	-0.318	-0.289	-0.180	0.001	-0.267	0.241	0.031	-0.065	NA	NA	0.411	-0.154	0.170	16	-158.13	307.77	4.07	0.013
7957	-0.132	NA	NA	NA	-0.194	NA	NA	NA	0.268	0.030	0.338	-0.004	0.249	12	-152.78	308.22	4.52	0.010
8192	-0.338	-0.256	-0.075	0.001	-0.184	0.238	0.013	-0.060	0.208	0.023	0.272	-0.026	0.225	18	-158.58	308.24	4.53	0.010
8176	-0.301	-0.255	0.049	0.000	NA	0.237	0.037	-0.055	0.267	0.083	0.019	0.015	0.190	17	-158.60	308.36	4.66	0.010
7968	-0.235	-0.258	-0.121	0.000	-0.191	NA	NA	NA	0.223	0.032	0.302	-0.023	0.240	15	-157.66	308.50	4.79	0.009
7200	-0.219	-0.296	-0.243	0.000	-0.285	NA	NA	NA	NA	NA	0.460	-0.163	0.189	13	-157.48	308.73	5.03	0.008
7952	-0.201	-0.258	-0.002	0.000	NA	NA	NA	NA	0.288	0.096	0.044	0.023	0.207	14	-157.78	308.89	5.19	0.007
7941	-0.143	NA	NA	NA	NA	NA	NA	NA	0.335	0.101	0.197	0.043	0.215	11	-152.98	308.91	5.21	0.007
7413	-0.078	NA	NA	NA	-0.275	0.237	0.050	-0.092	NA	NA	0.394	-0.165	0.156	13	-154.02	309.06	5.35	0.007
7174	-0.158	-0.311	NA	NA	NA	NA	NA	NA	NA	NA	0.005	-0.202	0.155	10	-153.04	309.13	5.42	0.007
7406	-0.272	-0.305	NA	0.000	NA	0.243	0.081	-0.052	NA	NA	0.041	-0.190	0.135	14.000	-159.747	309.497	5.791	0.005

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