Soliveres, S *et al.* 2016. Locally rare species influence grassland ecosystem multifunctionality. *Phil. Trans. R. Soc. B* **371** doi: 10.1098/rstb.2015.0269

Supplementary Material

INDEX

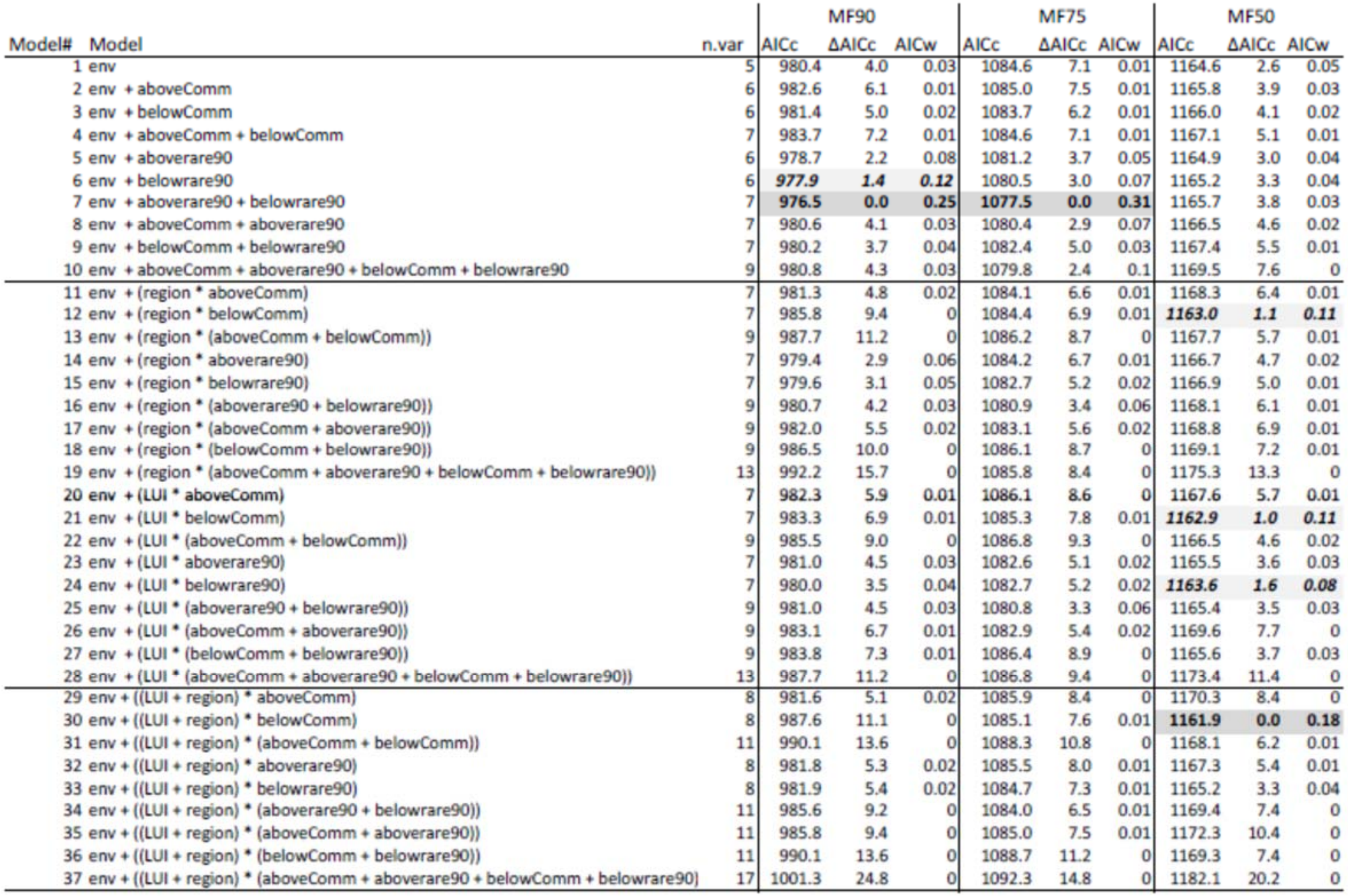
Table S1. Details of the sampling procedure for each trophic group. Note that for belowground groups the taxonomic unit was either operational taxonomic units (OTU: fungi and protists) or families (bacteria and belowground insect larvae). Abundance measures were: % cover (plants, bryophytes), number of individuals captured (arthropods) and relative proportion of sequence reads assigned to each family among all reads within each plot (protists, soil bacteria and mycorrhiza).

Trophic group	**Subgroup**	**Sampling method**	**Author**
Autotrophs	Plants, bryophytes	Measurement of % cover in a 4×4 m subplot, done in 2009	Boch, Heinze, Hölzel, Klaus, Kleinebecker, Müller, Prati, Socher, Fischer
Aboveground herbivores	Herbivorous insects	Sweep netting (Hemiptera: Heteroptera/Auchenorrhyncha, Hymenoptera, Neuroptera and Orthoptera). Transects of 150m with 60 double sweeps, done twice per plot in 2008-2010.	Lange, Paŝalić, Türke, Gossner, Weisser
Aboveground predators	Carnivorous insects	Sweep netting (Hemiptera: Heteroptera/Auchenorrhyncha, Hymenoptera, Neuroptera and Orthoptera). Transects of 150m with 60 double sweeps done twice per plot in 2008-2010.	Lange, Paŝalić, Türke, Gossner, Weisser
	Spiders	Sweep netting. Transects of 150m with 60 double sweeps, done twice per plot in 2008-2010.	Lange, Paŝalić, Türke, Gossner, Weisser
	Chilopoda	Kempson extraction from one soil core of 20 ×5 cm per plot, done in 2008	Birkhofer, Diekötter, Wolters
Detritivores	Annelids	Hand sorting from two soil cores of 20 ×10 cm per plot, done in 2008	Birkhofer, Diekötter, Wolters
	Diplopoda	Kempson extraction from one soil core of 20 ×5 cm per plot, done in 2008	Birkhofer, Diekötter, Wolters
	Detritivorous insects	Sweep netting (Hemiptera: Heteroptera/Auchenorrhyncha, Hymenoptera, Neuroptera and Orthoptera). Transects of 150m with 60 double sweeps, done twice per plot in 2008-2010.	Lange, Paŝalić, Türke, Gossner, Weisser
Microbial decomposers	Soil bacteria	cDNA amplicon sequencing of partial (V3) 16S rRNA gene transcripts, done in 2011	Baumgartner, Sikorski, Overmann
Bacterivores	Bacterivorous protists	18S rDNA gene PCR and amplicon sequencing (454) filtering for rhizarians, alveolates, stramenopiles and opisthokonts, done in 2011	Venter, Arndt
Symbionts	Arbuscular mycorrhizal fungi	Pyrotag sequencing of the NS31 - AM1 fragment of the 18S rDNA genes, done in 2011	Klemmer, Wubet, Buscot
Belowground herbivores	Insect larvae	Extracted from a heat/moisture gradient in one soil core of 20 x 5 cm per site, done in 2011 over a period of eight days.	Sonnemann, Wurst
Belowground predators	Insect larvae	Extracted from a heat/moisture gradient in one soil core of 20 x 5 cm per site, done in 2011 over a period of eight days.	Sonnemann, Wurst

Table S2. Details of the sampling procedure for each ecosystem function.

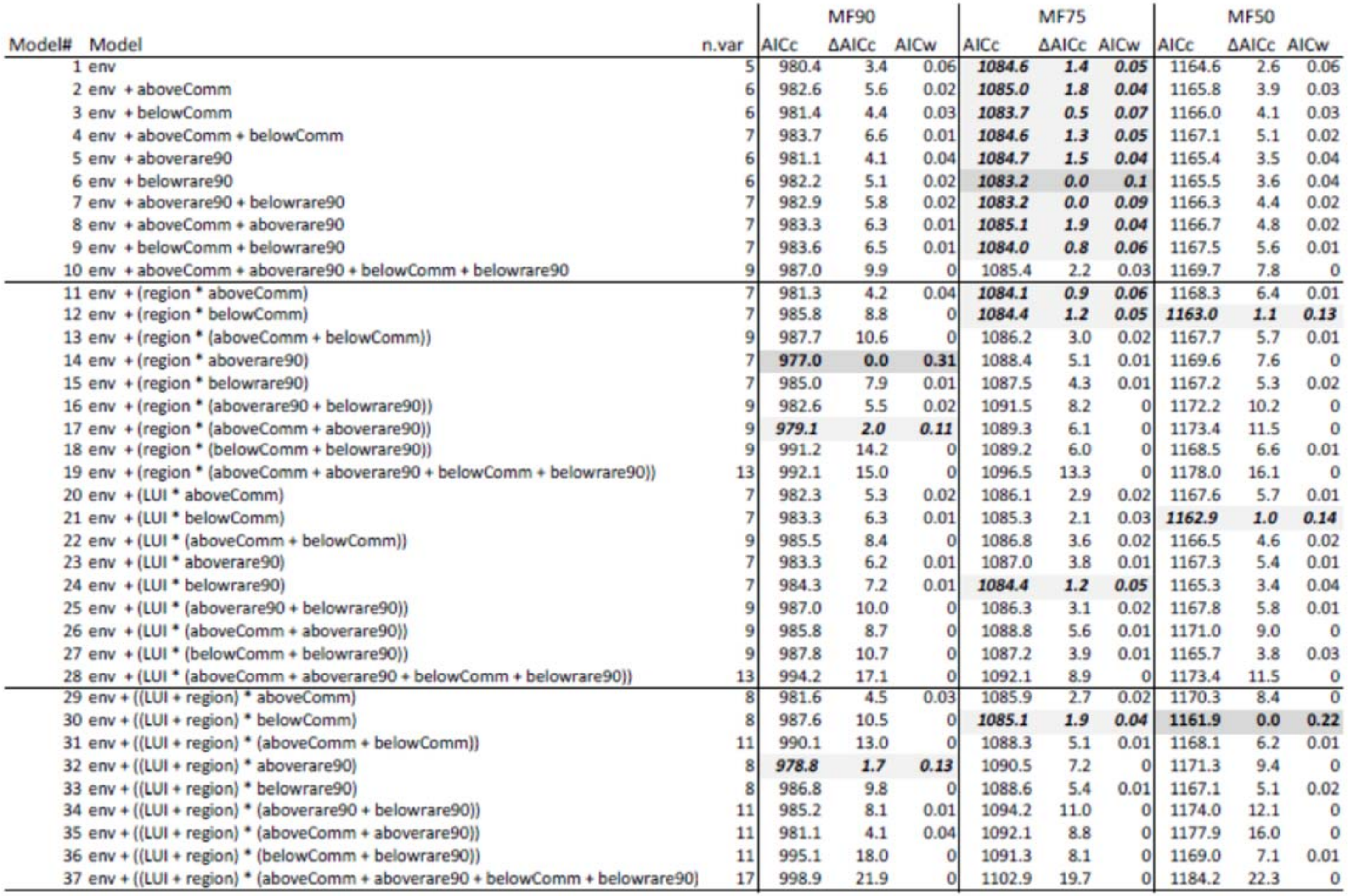
Function	Sampling method	Author
Aboveground plant biomass	Harvested in four 0.5 m × 0.5 m quadrats per plot, done in May-June in 2008-2012.	Schmitt, Prati, Fischer, Klaus, Kleinebecker, Hölzel
Belowground plant biomass	Measured in 14 soil cores (10 × 5 cm). Fine roots were sorted according to a diameter size class of < 2 mm and weighted after drying in the oven, done in May 2011	Solly, Schöning, Schrumpf
Root decomposition rate	Measured as the mass loss from root litter bags after 6 months, done in March 2012.	Solly, Schöning, Schrumpf
Potential nitrification	10 mM ammonium sulphate solution was added as substrate to 2.5g of soil composite samples (i.e. the same samples as for soil carbon; see below).	Stempfhuber, Schloter
Phosphorus uptake and retention	Proportion of P in plants and microbes (shoot P stock + microbial P stock) / (shoot P stock + microbial P stock + soil extractable P [$NaHCO_3$]).	Alt, Sorkau, Oelman, Wilcke
Arbuscular mycorrhizal fungal root colonization	Cultured in sterile soil in the field from April to October 2011 and then extracted with sodium hexametaphosphate (35 g l^{-1}). Hyphal length was quantified after staining with trypan blue.	Morris, Rillig
Stability of soil aggregates	A subsample of the same soil than above (AMF colonization) was passed through a 250 µm sieve under water to determine the percentage of water stable macroaggregates.	Morris, Rillig
Soil organic Carbon	Measured in 14 soil cores (40 × 5 cm). Calculated as the difference between total carbon (measured with a CN analyzer "Vario Max" [Elementar Analysensysteme GmbH, Hanau, Germany]) and inorganic carbon (determined after combustion of organic carbon in a muffle furnance; 450°C for 16 h), done in October 2011	Schöning, Solly, Schrumpf
Forage quality	Was calculated as a function of mean of scaled crude protein concentration and scaled relative forage value, done in May-June in 2008-2012.	Klaus, Kleinebecker, Hölzel
Resistance to plant pathogens	Calculated as the inverse of the total cover of foliar fungal pathogens. The cover of pathogens was measured in four 25 × 1 m transects per plot, were proportion of plants infected, and leaf area infected of these individuals was measured; done in October 2011,	Blaser, Prati, Fischer
Pest control	Number of trap nesting wasps known to feed on pest insects, done between April and October 2008.	Steckel, Westphal, Steffan-Dewenter
Pollinator abundance	Estimated as the total abundance of flower visitors, measured in one 200 × 3 m transect per plot, done in May 2008	Krauss, Klein, Weiner, Werner, Blüthgen
Bird diversity	Measured as the cumulative species richness estimated by audio-visual point-counts, done in May-June 2008-2010	Renner, Böhm, Tschapka
Flower cover	Measured as the number of inflorescences in four 50 × 3 m transects per plot. Flower area for each species was obtained from the literature.	Binkenstein, Schaefer

Table S3. Model selection summary. Results for each multifunctionality scenario are shown with the best model highlighted in grey. Results for each multifunctionality scenario are shown with the best model highlighted in dark grey. Those models with ΔAICc < 2 (and therefore equally plausible than the best one) are shown in light grey. For each of the models performed, an identification number (model #), the number of variables (n.var), AICc, ΔAICc and AIC weight (AICw) are shown. Env = environmental variables (region+soil ph+soil depth+land-use intensity+ topographic wetness index).wetness index).



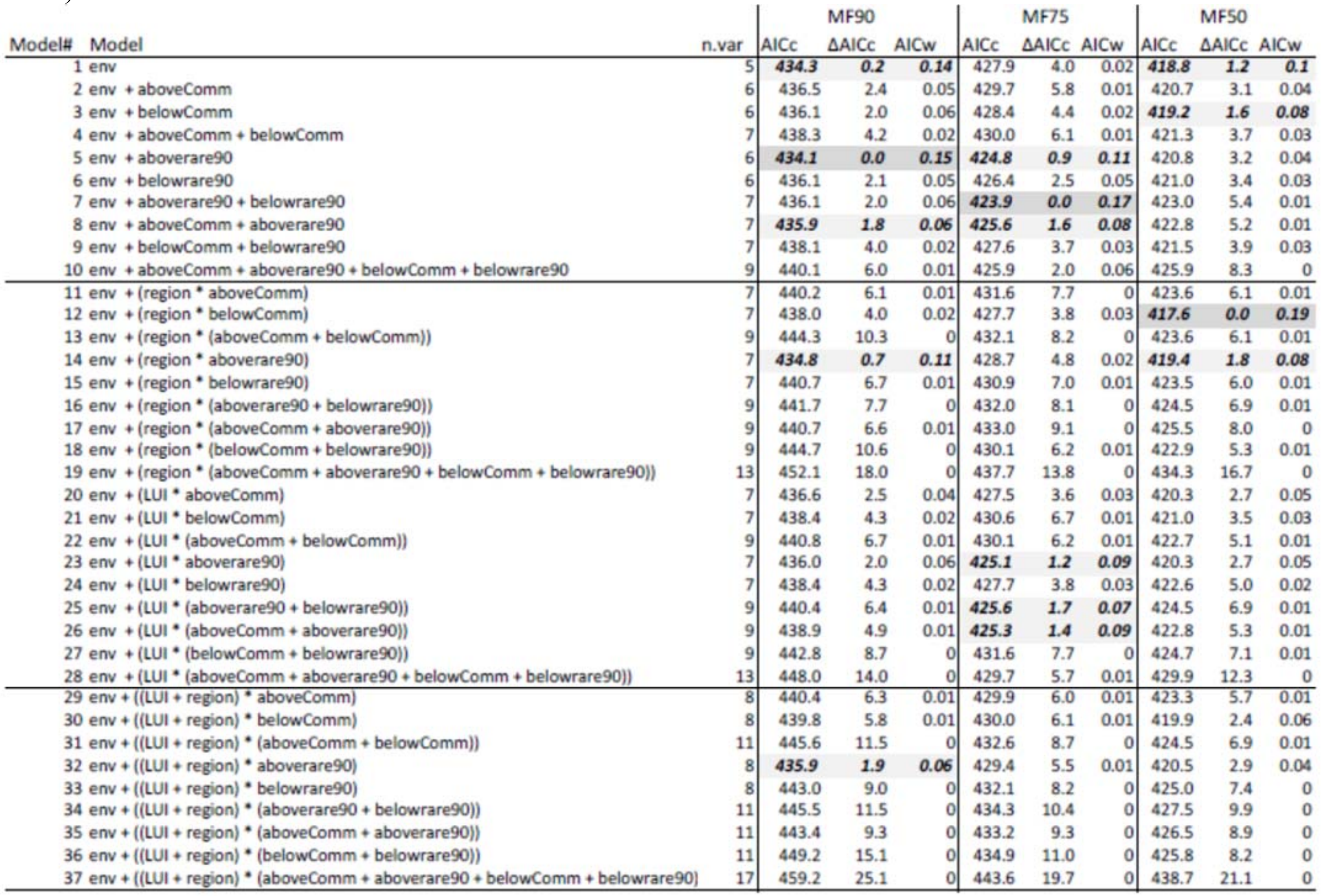
			MF90			MF75			MF50		
Model#	Model	n.var	AICc	ΔAICc	AICw	AICc	ΔAICc	AICw	AICc	ΔAICc	AICw
1	env	5	980.4	4.0	0.03	1084.6	7.1	0.01	1164.6	2.6	0.05
2	env + aboveComm	6	982.6	6.1	0.01	1085.0	7.5	0.01	1165.8	3.9	0.03
3	env + belowComm	6	981.4	5.0	0.02	1083.7	6.2	0.01	1166.0	4.1	0.02
4	env + aboveComm + belowComm	7	983.7	7.2	0.01	1084.6	7.1	0.01	1167.1	5.1	0.01
5	env + aboverare90	6	978.7	2.2	0.08	1081.2	3.7	0.05	1164.9	3.0	0.04
6	env + belowrare90	6	***977.9***	***1.4***	***0.12***	1080.5	3.0	0.07	1165.2	3.3	0.04
7	env + aboverare90 + belowrare90	7	**976.5**	**0.0**	**0.25**	**1077.5**	**0.0**	**0.31**	1165.7	3.8	0.03
8	env + aboveComm + aboverare90	7	980.6	4.1	0.03	1080.4	2.9	0.07	1166.5	4.6	0.02
9	env + belowComm + belowrare90	7	980.2	3.7	0.04	1082.4	5.0	0.03	1167.4	5.5	0.01
10	env + aboveComm + aboverare90 + belowComm + belowrare90	9	980.8	4.3	0.03	1079.8	2.4	0.1	1169.5	7.6	0
11	env + (region * aboveComm)	7	981.3	4.8	0.02	1084.1	6.6	0.01	1168.3	6.4	0.01
12	env + (region * belowComm)	7	985.8	9.4	0	1084.4	6.9	0.01	***1163.0***	***1.1***	***0.11***
13	env + (region * (aboveComm + belowComm))	9	987.7	11.2	0	1086.2	8.7	0	1167.7	5.7	0.01
14	env + (region * aboverare90)	7	979.4	2.9	0.06	1084.2	6.7	0.01	1166.7	4.7	0.02
15	env + (region * belowrare90)	7	979.6	3.1	0.05	1082.7	5.2	0.02	1166.9	5.0	0.01
16	env + (region * (aboverare90 + belowrare90))	9	980.7	4.2	0.03	1080.9	3.4	0.06	1168.1	6.1	0.01
17	env + (region * (aboveComm + aboverare90))	9	982.0	5.5	0.02	1083.1	5.6	0.02	1168.8	6.9	0.01
18	env + (region * (belowComm + belowrare90))	9	986.5	10.0	0	1086.1	8.7	0	1169.1	7.2	0.01
19	env + (region * (aboveComm + aboverare90 + belowComm + belowrare90))	13	992.2	15.7	0	1085.8	8.4	0	1175.3	13.3	0
20	env + (LUI * aboveComm)	7	982.3	5.9	0.01	1086.1	8.6	0	1167.6	5.7	0.01
21	env + (LUI * belowComm)	7	983.3	6.9	0.01	1085.3	7.8	0.01	***1162.9***	***1.0***	***0.11***
22	env + (LUI * (aboveComm + belowComm))	9	985.5	9.0	0	1086.8	9.3	0	1166.5	4.6	0.02
23	env + (LUI * aboverare90)	7	981.0	4.5	0.03	1082.6	5.1	0.02	1165.5	3.6	0.03
24	env + (LUI * belowrare90)	7	980.0	3.5	0.04	1082.7	5.2	0.02	***1163.6***	***1.6***	***0.08***
25	env + (LUI * (aboverare90 + belowrare90))	9	981.0	4.5	0.03	1080.8	3.3	0.06	1165.4	3.5	0.03
26	env + (LUI * (aboveComm + aboverare90))	9	983.1	6.7	0.01	1082.9	5.4	0.02	1169.6	7.7	0
27	env + (LUI * (belowComm + belowrare90))	9	983.8	7.3	0.01	1086.4	8.9	0	1165.6	3.7	0.03
28	env + (LUI * (aboveComm + aboverare90 + belowComm + belowrare90))	13	987.7	11.2	0	1086.8	9.4	0	1173.4	11.4	0
29	env + ((LUI + region) * aboveComm)	8	981.6	5.1	0.02	1085.9	8.4	0	1170.3	8.4	0
30	env + ((LUI + region) * belowComm)	8	987.6	11.1	0	1085.1	7.6	0.01	**1161.9**	**0.0**	**0.18**
31	env + ((LUI + region) * (aboveComm + belowComm))	11	990.1	13.6	0	1088.3	10.8	0	1168.1	6.2	0.01
32	env + ((LUI + region) * aboverare90)	8	981.8	5.3	0.02	1085.5	8.0	0.01	1167.3	5.4	0.01
33	env + ((LUI + region) * belowrare90)	8	981.9	5.4	0.02	1084.7	7.3	0.01	1165.2	3.3	0.04
34	env + ((LUI + region) * (aboverare90 + belowrare90))	11	985.6	9.2	0	1084.0	6.5	0.01	1169.4	7.4	0
35	env + ((LUI + region) * (aboveComm + aboverare90))	11	985.8	9.4	0	1085.0	7.5	0.01	1172.3	10.4	0
36	env + ((LUI + region) * (belowComm + belowrare90))	11	990.1	13.6	0	1088.7	11.2	0	1169.3	7.4	0
37	env + ((LUI + region) * (aboveComm + aboverare90 + belowComm + belowrare90)	17	1001.3	24.8	0	1092.3	14.8	0	1182.1	20.2	0

Table S4. Model selection summary for the analyses performed with the 50% least abundance species as rare species. Results for each multifunctionality scenario are shown with the best model highlighted in dark grey. Those models with ΔAICc < 2 (and therefore equally plausible than the best one) are shown in light grey. For each of the models performed, an identification number (model #), the number of variables (n.var), AICc, ΔAICc and AIC weight (AICw) are shown. Env = environmental variables (region+soil ph+soil depth+land-use intensity+ topographic wetness index).wetness index).



			MF90			MF75			MF50		
Model#	Model	n.var	AICc	ΔAICc	AICw	AICc	ΔAICc	AICw	AICc	ΔAICc	AICw
1	env	5	980.4	3.4	0.06	***1084.6***	***1.4***	***0.05***	1164.6	2.6	0.06
2	env + aboveComm	6	982.6	5.6	0.02	***1085.0***	***1.8***	***0.04***	1165.8	3.9	0.03
3	env + belowComm	6	981.4	4.4	0.03	***1083.7***	***0.5***	***0.07***	1166.0	4.1	0.03
4	env + aboveComm + belowComm	7	983.7	6.6	0.01	***1084.6***	***1.3***	***0.05***	1167.1	5.1	0.02
5	env + aboverare90	6	981.1	4.1	0.04	***1084.7***	***1.5***	***0.04***	1165.4	3.5	0.04
6	env + belowrare90	6	982.2	5.1	0.02	***1083.2***	***0.0***	***0.1***	1165.5	3.6	0.04
7	env + aboverare90 + belowrare90	7	982.9	5.8	0.02	***1083.2***	***0.0***	***0.09***	1166.3	4.4	0.02
8	env + aboveComm + aboverare90	7	983.3	6.3	0.01	***1085.1***	***1.9***	***0.04***	1166.7	4.8	0.02
9	env + belowComm + belowrare90	7	983.6	6.5	0.01	***1084.0***	***0.8***	***0.06***	1167.5	5.6	0.01
10	env + aboveComm + aboverare90 + belowComm + belowrare90	9	987.0	9.9	0	1085.4	2.2	0.03	1169.7	7.8	0
11	env + (region * aboveComm)	7	981.3	4.2	0.04	***1084.1***	***0.9***	***0.06***	1168.3	6.4	0.01
12	env + (region * belowComm)	7	985.8	8.8	0	***1084.4***	***1.2***	***0.05***	***1163.0***	***1.1***	***0.13***
13	env + (region * (aboveComm + belowComm))	9	987.7	10.6	0	1086.2	3.0	0.02	1167.7	5.7	0.01
14	env + (region * aboverare90)	7	**977.0**	**0.0**	**0.31**	1088.4	5.1	0.01	1169.6	7.6	0
15	env + (region * belowrare90)	7	985.0	7.9	0.01	1087.5	4.3	0.01	1167.2	5.3	0.02
16	env + (region * (aboverare90 + belowrare90))	9	982.6	5.5	0.02	1091.5	8.2	0	1172.2	10.2	0
17	env + (region * (aboveComm + aboverare90))	9	***979.1***	***2.0***	***0.11***	1089.3	6.1	0	1173.4	11.5	0
18	env + (region * (belowComm + belowrare90))	9	991.2	14.2	0	1089.2	6.0	0	1168.5	6.6	0.01
19	env + (region * (aboveComm + aboverare90 + belowComm + belowrare90))	13	992.1	15.0	0	1096.5	13.3	0	1178.0	16.1	0
20	env + (LUI * aboveComm)	7	982.3	5.3	0.02	1086.1	2.9	0.02	1167.6	5.7	0.01
21	env + (LUI * belowComm)	7	983.3	6.3	0.01	1085.3	2.1	0.03	***1162.9***	***1.0***	***0.14***
22	env + (LUI * (aboveComm + belowComm))	9	985.5	8.4	0	1086.8	3.6	0.02	1166.5	4.6	0.02
23	env + (LUI * aboverare90)	7	983.3	6.2	0.01	1087.0	3.8	0.01	1167.3	5.4	0.01
24	env + (LUI * belowrare90)	7	984.3	7.2	0.01	***1084.4***	***1.2***	***0.05***	1165.3	3.4	0.04
25	env + (LUI * (aboverare90 + belowrare90))	9	987.0	10.0	0	1086.3	3.1	0.02	1167.8	5.8	0.01
26	env + (LUI * (aboveComm + aboverare90))	9	985.8	8.7	0	1088.8	5.6	0.01	1171.0	9.0	0
27	env + (LUI * (belowComm + belowrare90))	9	987.8	10.7	0	1087.2	3.9	0.01	1165.7	3.8	0.03
28	env + (LUI * (aboveComm + aboverare90 + belowComm + belowrare90))	13	994.2	17.1	0	1092.1	8.9	0	1173.4	11.5	0
29	env + ((LUI + region) * aboveComm)	8	981.6	4.5	0.03	1085.9	2.7	0.02	1170.3	8.4	0
30	env + ((LUI + region) * belowComm)	8	987.6	10.5	0	***1085.1***	***1.9***	***0.04***	**1161.9**	**0.0**	**0.22**
31	env + ((LUI + region) * (aboveComm + belowComm))	11	990.1	13.0	0	1088.3	5.1	0.01	1168.1	6.2	0.01
32	env + ((LUI + region) * aboverare90)	8	***978.8***	***1.7***	***0.13***	1090.5	7.2	0	1171.3	9.4	0
33	env + ((LUI + region) * belowrare90)	8	986.8	9.8	0	1088.6	5.4	0.01	1167.1	5.1	0.02
34	env + ((LUI + region) * (aboverare90 + belowrare90))	11	985.2	8.1	0.01	1094.2	11.0	0	1174.0	12.1	0
35	env + ((LUI + region) * (aboveComm + aboverare90))	11	981.1	4.1	0.04	1092.1	8.8	0	1177.9	16.0	0
36	env + ((LUI + region) * (belowComm + belowrare90))	11	995.1	18.0	0	1091.3	8.1	0	1169.0	7.1	0.01
37	env + ((LUI + region) * (aboveComm + aboverare90 + belowComm + belowrare90)	17	998.9	21.9	0	1102.9	19.7	0	1184.2	22.3	0

Table S5. Model selection summary for the analyses performed with abundance instead of species richness. Results for each multifunctionality scenario are shown with the best model highlighted in dark grey. Those models with ΔAICc < 2 (and therefore equally plausible than the best one) are shown in light grey. For each of the models performed, an identification number (model #), the number of variables (n.var), AICc, ΔAICc and AIC weight (AICw) are shown. Env = environmental variables (region+soil ph+soil depth+land-use intensity+ topographic wetness index).wetness index).



			MF90			MF75			MF50		
Model#	Model	n.var	AICc	ΔAICc	AICw	AICc	ΔAICc	AICw	AICc	ΔAICc	AICw
1	env	5	***434.3***	***0.2***	***0.14***	427.9	4.0	0.02	***418.8***	***1.2***	***0.1***
2	env + aboveComm	6	436.5	2.4	0.05	429.7	5.8	0.01	420.7	3.1	0.04
3	env + belowComm	6	436.1	2.0	0.06	428.4	4.4	0.02	***419.2***	***1.6***	***0.08***
4	env + aboveComm + belowComm	7	438.3	4.2	0.02	430.0	6.1	0.01	421.3	3.7	0.03
5	env + aboverare90	6	***434.1***	***0.0***	***0.15***	***424.8***	***0.9***	***0.11***	420.8	3.2	0.04
6	env + belowrare90	6	436.1	2.1	0.05	426.4	2.5	0.05	421.0	3.4	0.03
7	env + aboverare90 + belowrare90	7	436.1	2.0	0.06	***423.9***	***0.0***	***0.17***	423.0	5.4	0.01
8	env + aboveComm + aboverare90	7	***435.9***	***1.8***	***0.06***	***425.6***	***1.6***	***0.08***	422.8	5.2	0.01
9	env + belowComm + belowrare90	7	438.1	4.0	0.02	427.6	3.7	0.03	421.5	3.9	0.03
10	env + aboveComm + aboverare90 + belowComm + belowrare90	9	440.1	6.0	0.01	425.9	2.0	0.06	425.9	8.3	0
11	env + (region * aboveComm)	7	440.2	6.1	0.01	431.6	7.7	0	423.6	6.1	0.01
12	env + (region * belowComm)	7	438.0	4.0	0.02	427.7	3.8	0.03	***417.6***	***0.0***	***0.19***
13	env + (region * (aboveComm + belowComm))	9	444.3	10.3	0	432.1	8.2	0	423.6	6.1	0.01
14	env + (region * aboverare90)	7	***434.8***	***0.7***	***0.11***	428.7	4.8	0.02	***419.4***	***1.8***	***0.08***
15	env + (region * belowrare90)	7	440.7	6.7	0.01	430.9	7.0	0.01	423.5	6.0	0.01
16	env + (region * (aboverare90 + belowrare90))	9	441.7	7.7	0	432.0	8.1	0	424.5	6.9	0.01
17	env + (region * (aboveComm + aboverare90))	9	440.7	6.6	0.01	433.0	9.1	0	425.5	8.0	0
18	env + (region * (belowComm + belowrare90))	9	444.7	10.6	0	430.1	6.2	0.01	422.9	5.3	0.01
19	env + (region * (aboveComm + aboverare90 + belowComm + belowrare90))	13	452.1	18.0	0	437.7	13.8	0	434.3	16.7	0
20	env + (LUI * aboveComm)	7	436.6	2.5	0.04	427.5	3.6	0.03	420.3	2.7	0.05
21	env + (LUI * belowComm)	7	438.4	4.3	0.02	430.6	6.7	0.01	421.0	3.5	0.03
22	env + (LUI * (aboveComm + belowComm))	9	440.8	6.7	0.01	430.1	6.2	0.01	422.7	5.1	0.01
23	env + (LUI * aboverare90)	7	436.0	2.0	0.06	***425.1***	***1.2***	***0.09***	420.3	2.7	0.05
24	env + (LUI * belowrare90)	7	438.4	4.3	0.02	427.7	3.8	0.03	422.6	5.0	0.02
25	env + (LUI * (aboverare90 + belowrare90))	9	440.4	6.4	0.01	***425.6***	***1.7***	***0.07***	424.5	6.9	0.01
26	env + (LUI * (aboveComm + aboverare90))	9	438.9	4.9	0.01	***425.3***	***1.4***	***0.09***	422.8	5.3	0.01
27	env + (LUI * (belowComm + belowrare90))	9	442.8	8.7	0	431.6	7.7	0	424.7	7.1	0.01
28	env + (LUI * (aboveComm + aboverare90 + belowComm + belowrare90))	13	448.0	14.0	0	429.7	5.7	0.01	429.9	12.3	0
29	env + ((LUI + region) * aboveComm)	8	440.4	6.3	0.01	429.9	6.0	0.01	423.3	5.7	0.01
30	env + ((LUI + region) * belowComm)	8	439.8	5.8	0.01	430.0	6.1	0.01	419.9	2.4	0.06
31	env + ((LUI + region) * (aboveComm + belowComm))	11	445.6	11.5	0	432.6	8.7	0	424.5	6.9	0.01
32	env + ((LUI + region) * aboverare90)	8	***435.9***	***1.9***	***0.06***	429.4	5.5	0.01	420.5	2.9	0.04
33	env + ((LUI + region) * belowrare90)	8	443.0	9.0	0	432.1	8.2	0	425.0	7.4	0
34	env + ((LUI + region) * (aboverare90 + belowrare90))	11	445.5	11.5	0	434.3	10.4	0	427.5	9.9	0
35	env + ((LUI + region) * (aboveComm + aboverare90))	11	443.4	9.3	0	433.2	9.3	0	426.5	8.9	0
36	env + ((LUI + region) * (belowComm + belowrare90))	11	449.2	15.1	0	434.9	11.0	0	425.8	8.2	0
37	env + ((LUI + region) * (aboveComm + aboverare90 + belowComm + belowrare90)	17	459.2	25.1	0	443.6	19.7	0	438.7	21.1	0

Table S6. Summary of the database used to test species-specific effects on multifunctionality. Number of species (n.species) and average abundance are given for each trophic group and category (common vs- rare species). Average positive (black) and negative (red) effects (measured as the standardized effect size) are shown (averages obtained only from those Standardized effect sizes > 2).

				Average.effects 50%		Average.effects 75%		Average.effects 90%	
		n.species	Average abundance	+	-	+	-	+	-
Autotrophs	common	25	6.59	3.15	-2.31	0.00	0.00	0.00	-2.05
	rare	25	1.64	2.37	0.00	2.34	0.00	3.06	0.00
Herbivores	common	25	19.96	2.19	0.00	2.62	-2.16	4.00	-2.20
	rare	25	2.61	3.12	0.00	0.00	-2.58	2.63	0.00
Microbe.decomposer	common	16	0.58	2.84	0.00	2.95	0.00	2.68	0.00
	rare	34	0.01	2.52	0.00	2.57	-2.07	2.22	-2.16
Predators	common	13	2.65	0.00	0.00	0.00	-2.30	0.00	0.00
	rare	7	1.30	2.19	0.00	2.01	0.00	0.00	0.00
Bacterivores	common	22	8.30	2.42	-2.05	2.25	-2.46	2.83	-2.21
	rare	28	1.54	0.00	0.00	2.22	0.00	0.00	0.00
Symbionts	common	23	13.66	0.00	-2.20	2.24	-2.34	2.10	-2.18
	rare	27	3.77	2.12	-2.72	3.17	-2.39	2.77	0.00

Table S7. Summary of the null-model approach applied to test the functional effects of individual species. The number of significant positive (black) and negative (red) effects are shown as the percentage of significant effects regarding the number of species tested (shown in parenthesis). The averaged results across the three multifunctionality scenarios is shown in grey.

	Trophic.group	50%	75%	90%	Average
% positive/negative effects	ALL (270)	7/5	6/4	5/3	6/4
	Autotrophs (50)	6/8	4/0	4/4	5/4
	Herbivores (50)	8/0	4/6	4/4	5/3
	Microbe.decomp (50)	14/0	8/2	10/2	11/1
	Predators (20)	5/0	5/10	0/0	3/3
	Bacterivores (50)	4/2	8/2	4/2	5/2
	Symbiont (50)	4/16	4/10	4/4	4/10

Table S8. Standardized estimated coefficients from the multiple regressions including the functional effect of each individual species (response variable), and its average abundance (Abundance) and response to land-use intensity (Resp. land-use) as predictors. Response to land-use intensity was measured as the standardized coefficient between the abundance of each species across every plot where it occurred and the land-use intensity index of the same plot). Coefficients were corrected by number of data points available to estimate the functional effect for each species. Main effects are reported for the model containing all functional groups together (All), in which the interactions of functional group by abundance and response to land-use were considered. Significant coefficients are highlighted in bold.

		50% Threshold	75% Threshold	90% Threshold
Autotrophs	Resp. land-use	0.20	-0.35	**-0.41**
	Abundance	0.12	0.07	0.23
	Height	0.18	0.01	0.04
	SLA	0.17	-0.08	-0.08
Herbivores	Resp. land-use	0.12	-0.21	**-0.43**
	Abundance	-0.16	0.03	0.11
	Body size	**-0.33**	-0.08	0.18
Predators	Resp. land-use	0.51	0.25	-0.14
	Abundance	0.27	-0.37	-0.27
	Body size	-0.21	-0.08	0.01
Microb.decomp	Resp. land-use	**0.40**	-0.09	**-0.33**
	Abundance	-0.13	0.06	-0.02
Bacterivores	Resp. land-use	-0.27	**-0.29**	**-0.32**
	Abundance	0.13	0.22	**0.30**
Symbionts	Resp. land-use	-0.22	**-0.28**	-0.14
	Abundance	-0.00	-0.10	-0.08
All	Resp. land-use	0.06	**-0.29**	**-0.46**
	Abundance	0.19	0.21	0.62

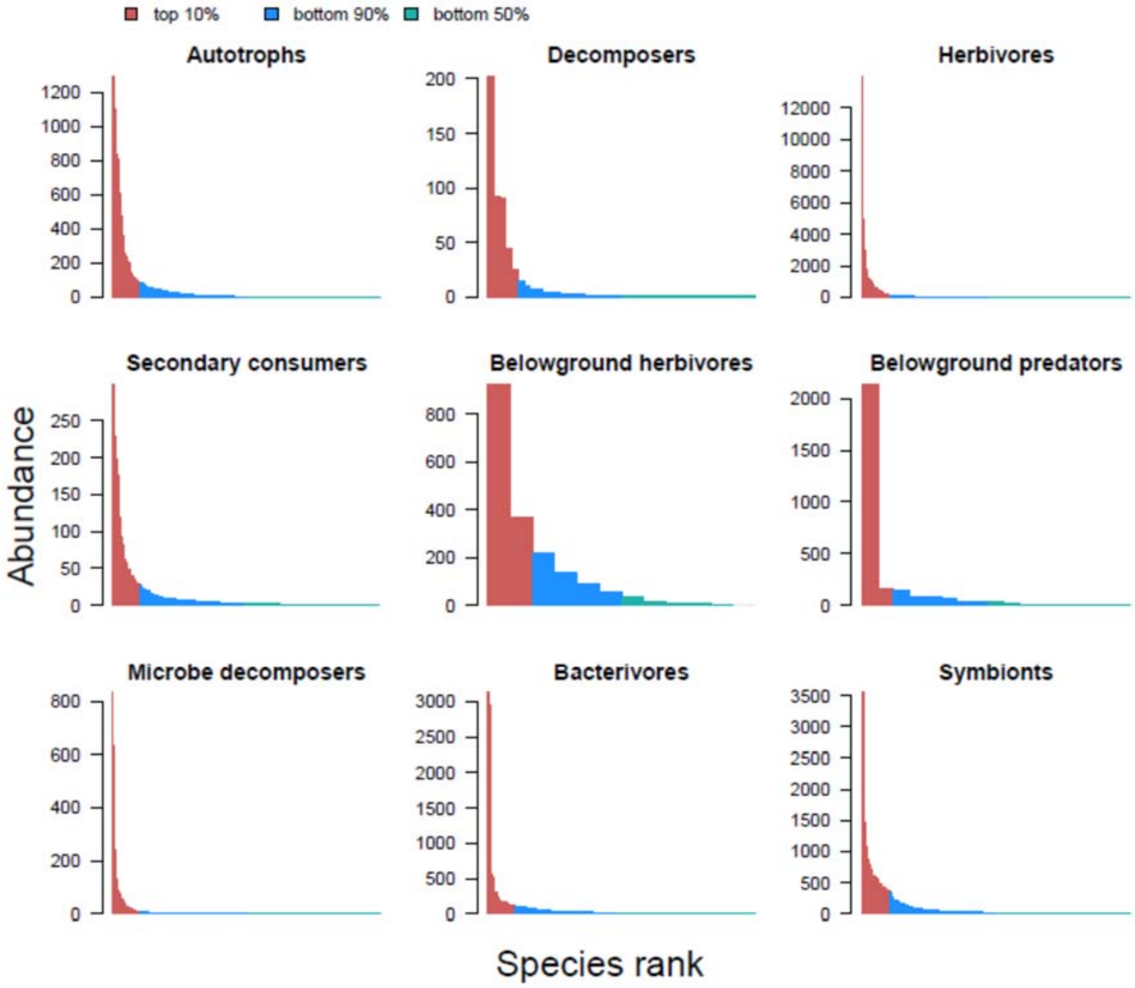


Figure S1. Abundance distribution of common and rare species within each trophic group. Different colors show those species considered common (the top 10%, in red), or rare (bottom 90% in blue and green, or bottom 50%, in green).

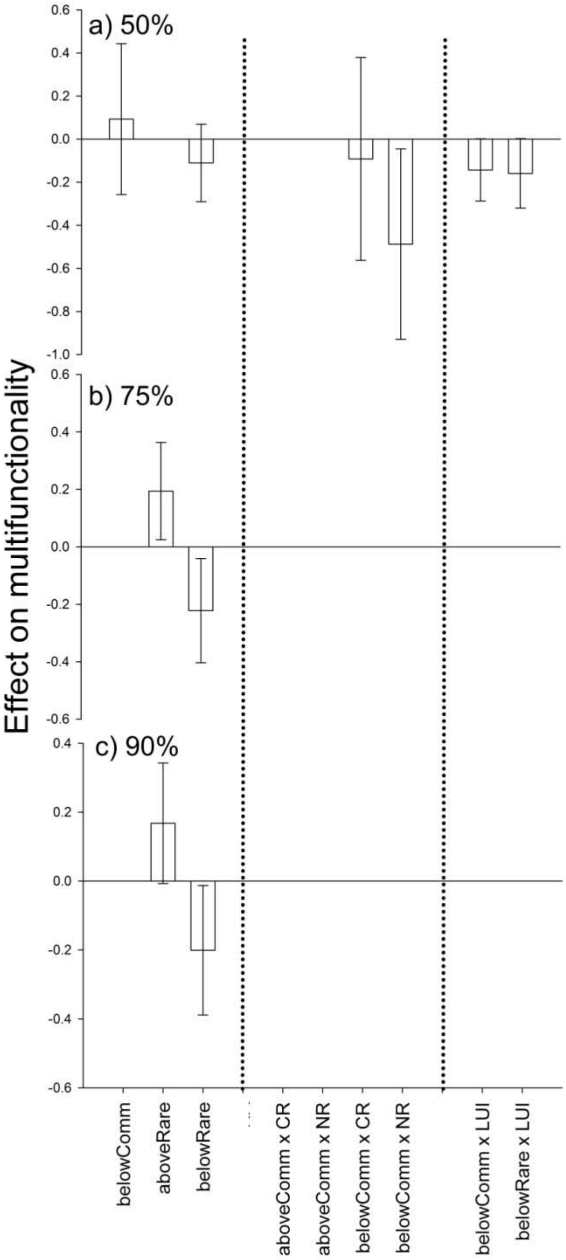


Figure S2. Standardized coefficients (with 95% confidence intervals) of the different terms related to biodiversity in our models obtained from model averaging using those models with ΔAICc < 2. These include interactions between multidiversity and region and LUI as drivers of multifunctionality. Regions are: Schwäbische Alb, Hainich-Dün (CR) and Schorfheide-Chorin (NR). Multidiversity of common species aboveground, and interactions between rare species multidiversity per region, and multidiversity of aboveground organisms per LUI were not included in any of the best models and therefore are not presented. If a given predictor was not included in the best models, the effect was considered to be 0.