Discrepancies between the drivers of alpha and beta plant diversity in arable field margins

Figure S1. A bocage landscape in the northern part of the Zone Atelier Armorique, in Brittany (France). Source: ©Air Papillon.

Figure S2. Photographs illustrating the diversity of field margins sampled in this study. Source: ©A. Alignier, S. Boinot.

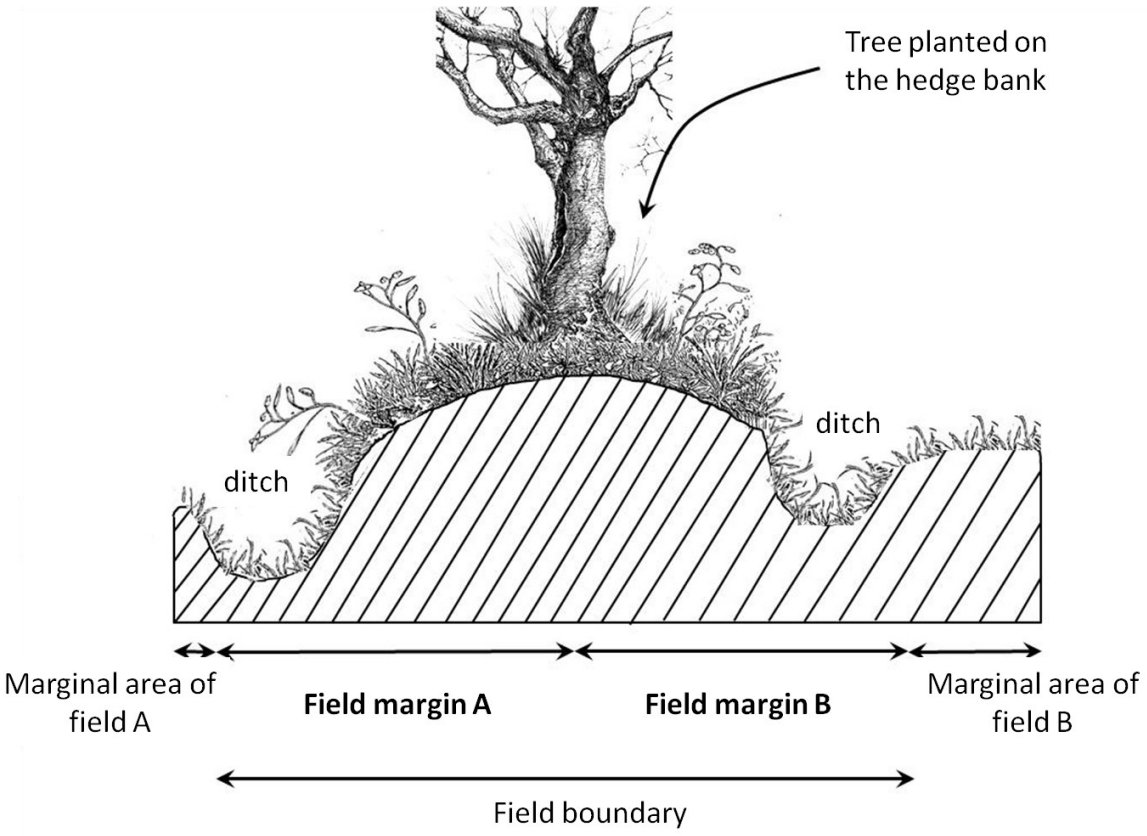

Figure S3. Spatial delineation of a field boundary and its margins. Note that the ditch, the bank, the tree and the shrub layers may be not present.

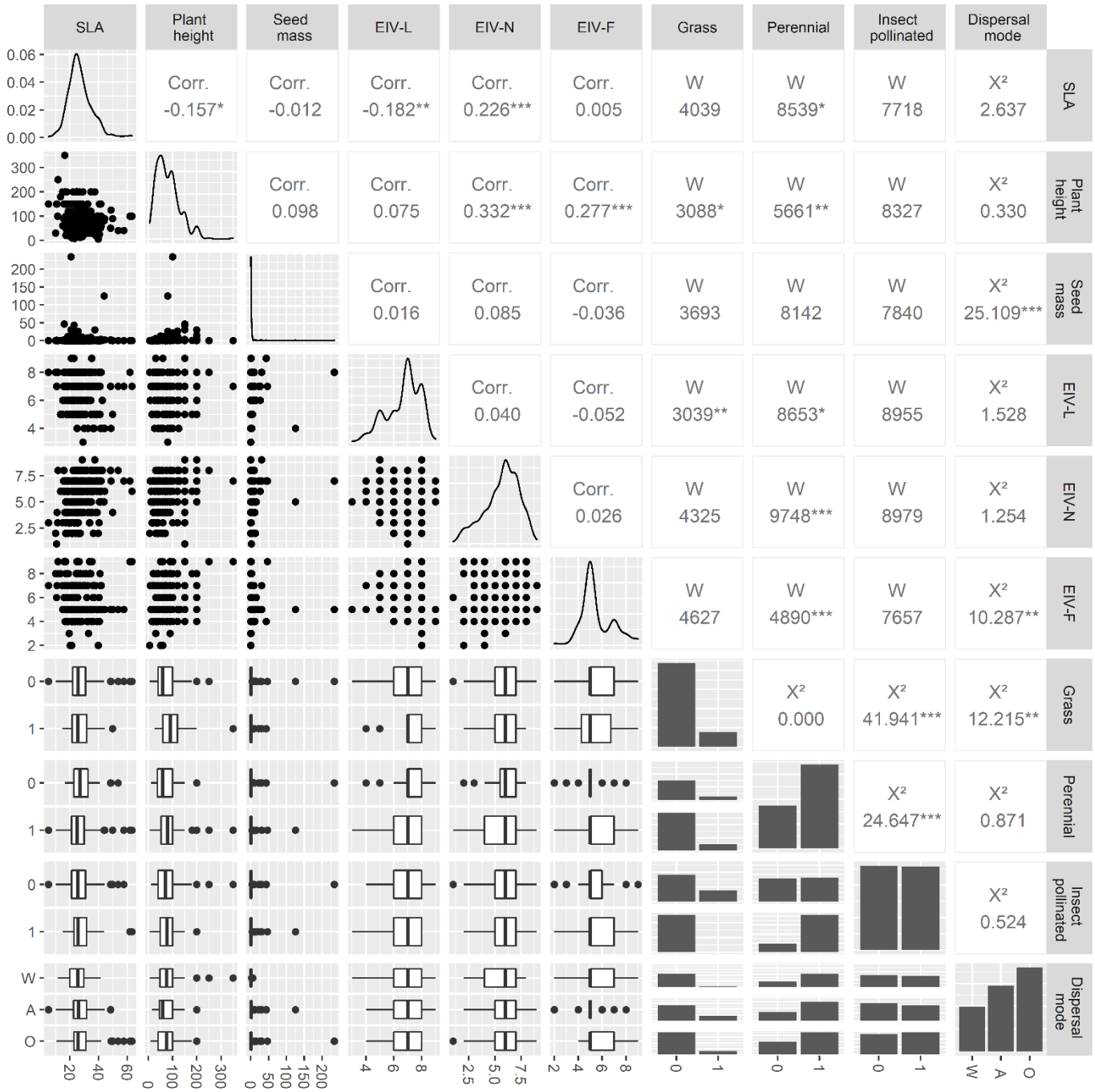

Figure S4. Generalized pairs plot for the trait dataset (scatterplots for quantitative-quantitative pairs, boxplots for quantitative-categorical pairs, and mosaic plots for categorical-categorical pairs). Corr. = Pearson correlations, W = Wilcoxon statistics, X² = chi-squared statistics (*P < 0.05, **P < 0.01, ***P < 0.001). EIV = Ellenberg Indicator Value (L for light, N for nutrients, F for soil moisture). Dispersal mode: W = wind-dispersed, A = animal-dispersed, O = other mode.

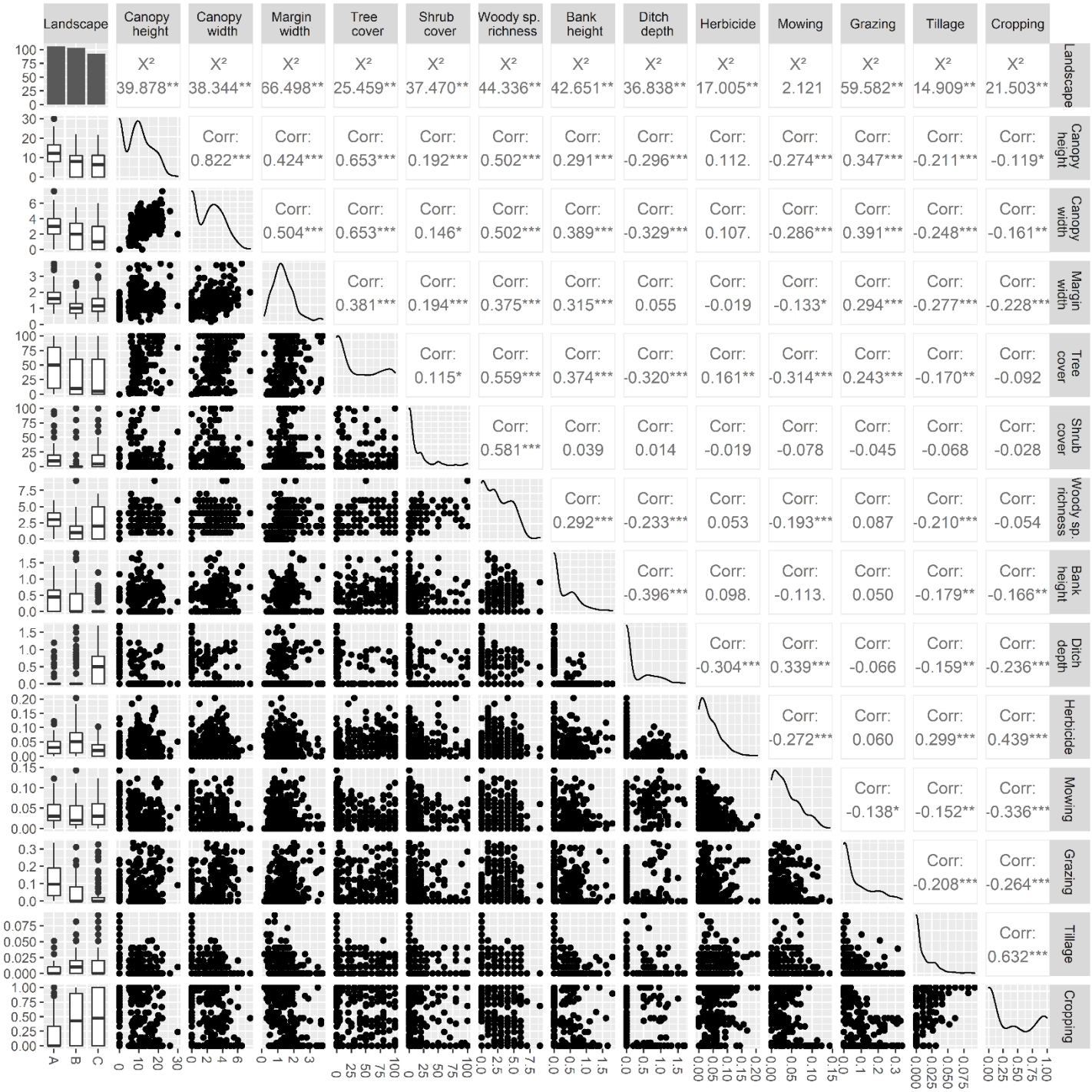

Figure S5. Scatterplots and Pearson correlations for explanatory variables (*P < 0.05, **P < 0.01, ***P < 0.001).

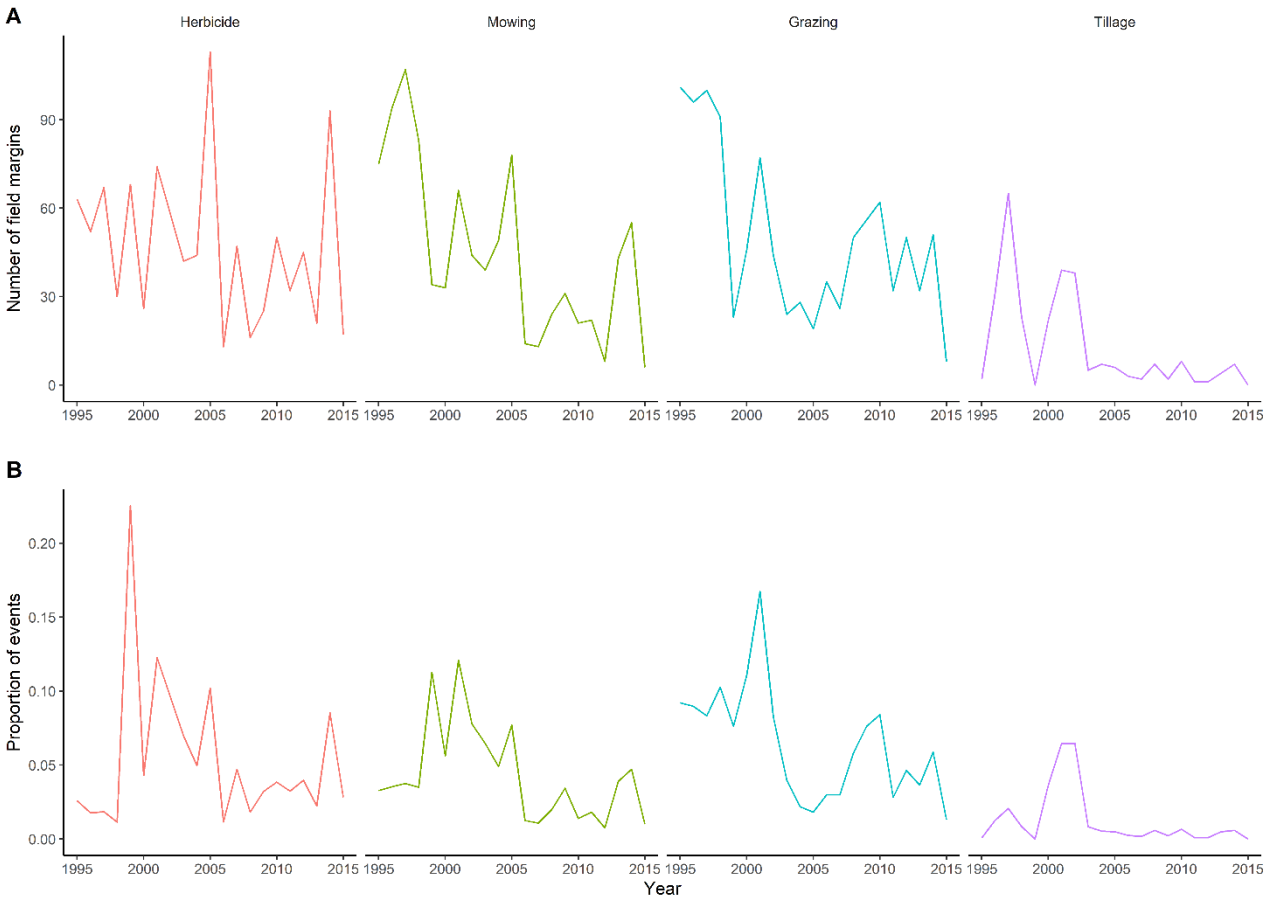

Figure S6. (A) Changes in the total number of field margins receiving at least one event for each management practice over the 20 years of observations. **(B)** Changes in the proportion of events across all field margins (total number of occurrences divided by the total number of observations) for each management practice over the 20 years of observations.

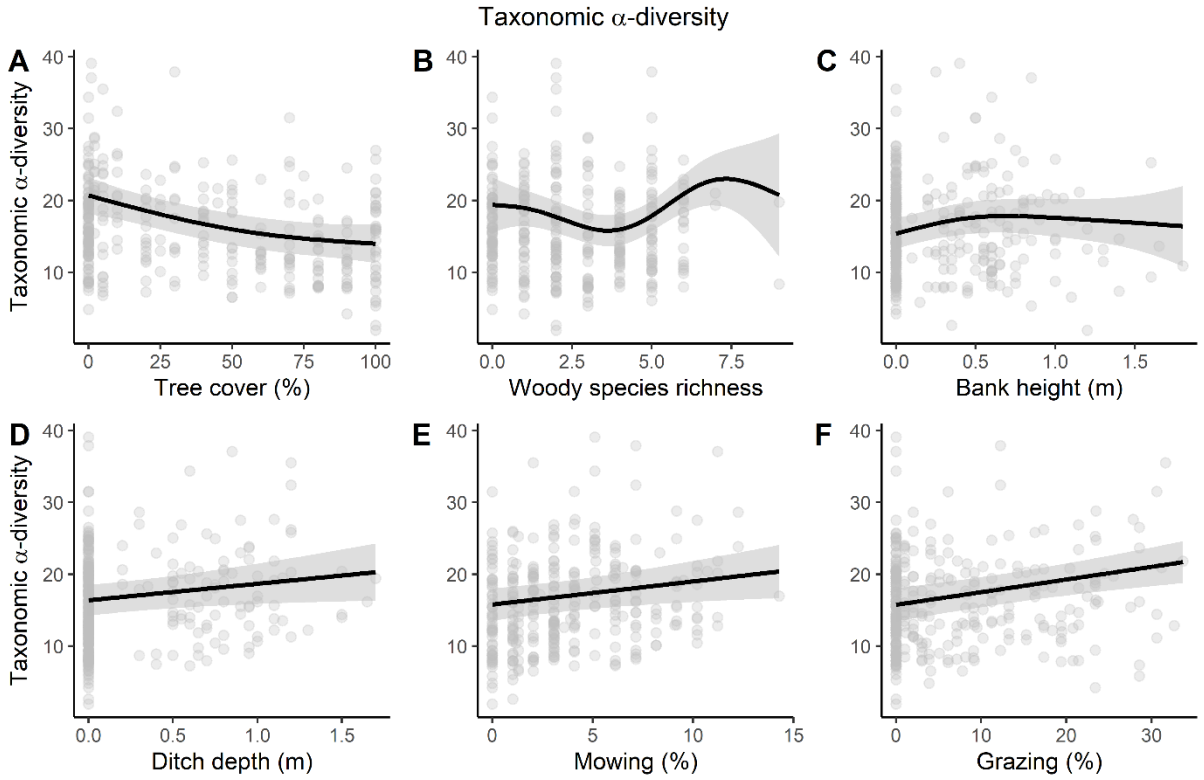

Figure S7. Field margin structure and long-term management both affected the taxonomic α-diversity of herbaceous plant communities, based on the results of generalized additive models. In particular, as with functional diversity, **(A)** taxonomic α-diversity decreased in an almost linear way with tree cover, whereas **(D)** ditch depth linearly increased taxonomic α-diversity. Further, **(E)** long-term grazing and **(F)** mowing intensity both linearly increased taxonomic α-diversity.

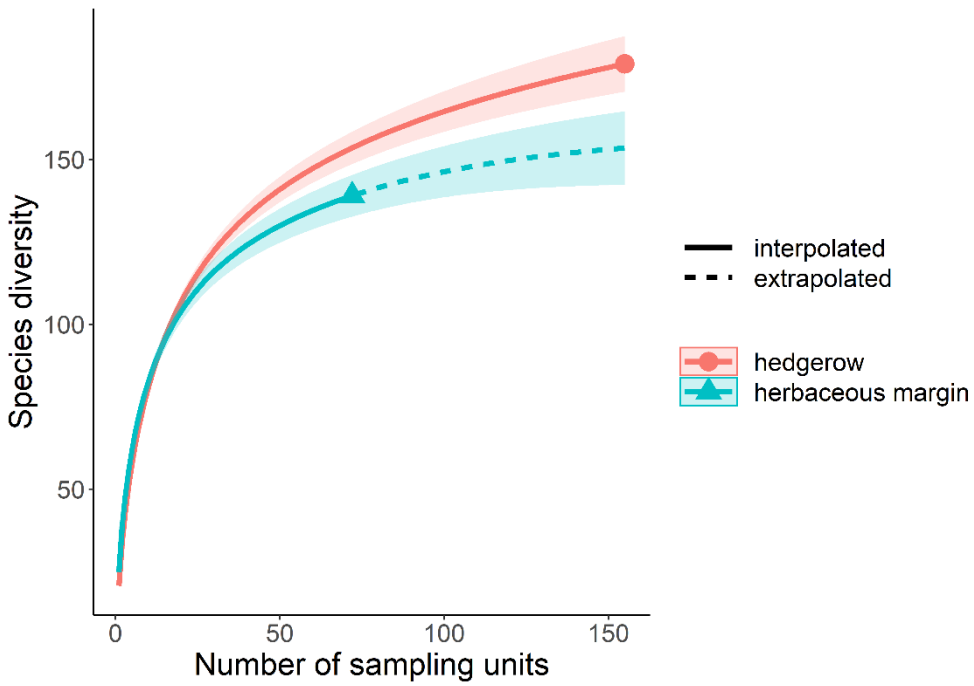

Figure S8. Species accumulation curves estimating species γ-diversity (at landscape scale) of hedgerows vs herbaceous field margins, using the R package iNext (Hsieh et al., 2016). Note that in our context, this approach has two limitations that GDM can overcome: **(1)** we cannot work with a continuous gradient and must use a threshold; we defined "herbaceous" field margins as those with tree cover = 0%, whereas we defined "hedgerows" as those with tree cover > 25%, and **(2)** we cannot include covariates, whereas GDM predicts effects on β-diversity by holding covariates constant.

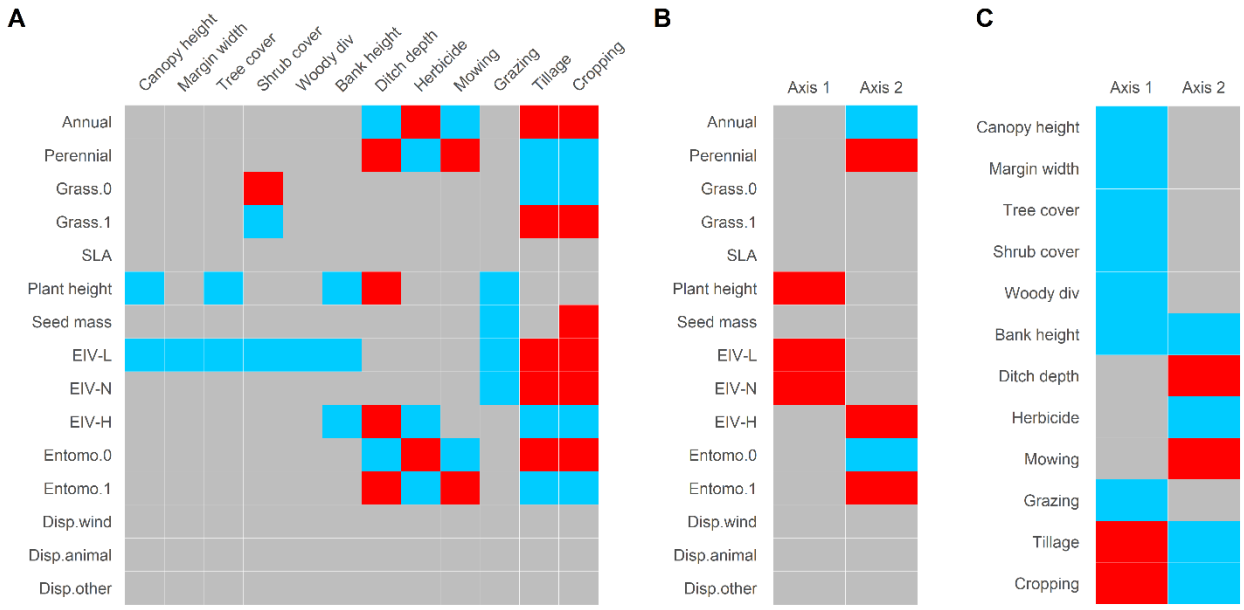

Figure S9. **(A)** Results of the fourth-corner analysis. **(B)** Results of the fourth-corner analysis testing the link between RLQ axes and traits and **(C)** environmental variables. Red cells correspond to positive significant relationships (p-value < 0.05) whereas blue cells correspond to negative significant relationships. Basic statistics for traits and environmental variables are given in Table S4.

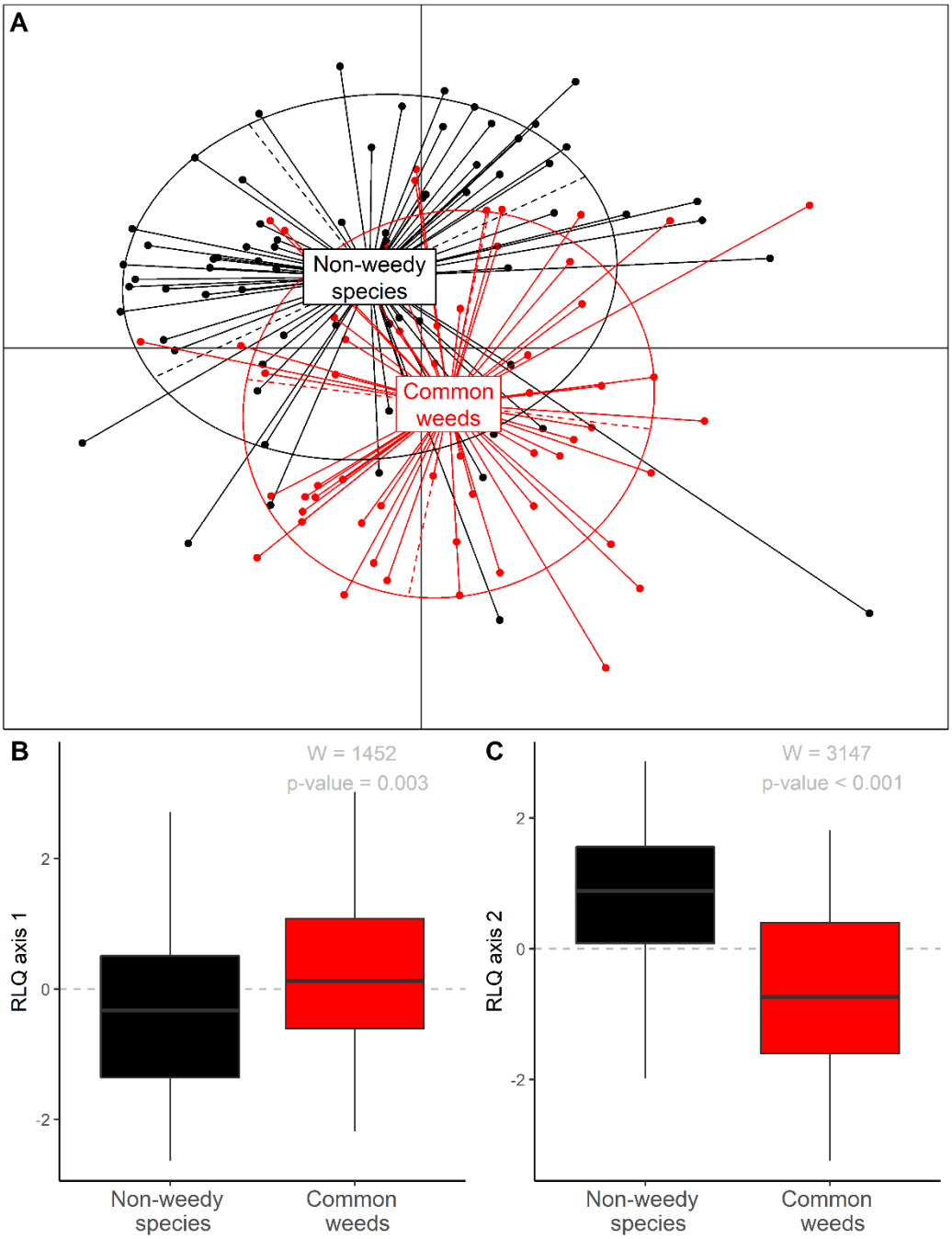

Figure S10. (A) Projection of non-weedy species vs common weeds on the first two RLQ axes. Centre of ellipses corresponds to the barycentre of point clouds formed by species of each group. Ellipse axes are principal axes of point clouds, whose length is equal to 1.5 times the standard deviation of species coordinates on these axes. **(B)** Distributions of non-weedy species vs common weeds on RLQ axis 1 and **(C)** RLQ axis 2. W = Wilcoxon test statistic.

Table S1. Results of generalized additive model (GAM) for taxonomic α-diversity. Significant terms are in bold. A value of 1 for the effective degrees of freedom (edf) indicates a linear relationship. R^2_{adj} = 0.35. Deviance explained = 43.8%. Woody div = woody species richness, X = longitude, Y = latitude.

	edf	*F*-value	*P*-value
s(Canopy height)	2.624	2.334	0.072
s(Margin width)	1.000	0.171	0.680
s(Tree cover)	1.911	10.544	0.000 ***
s(Shrub cover)	1.000	0.116	0.734
s(Woody div)	3.765	3.977	0.003 **
s(Bank height)	2.156	3.212	0.037 *
s(Ditch depth)	1.000	4.420	0.036 *
s(Herbicide)	1.000	0.403	0.526
s(Mowing)	1.000	5.851	0.016 *
s(Grazing)	1.000	14.731	0.000 ***
s(Tillage)	1.000	0.009	0.923
s(Cropping)	1.813	1.237	0.267
s(x,y)	21.002	2.347	0.000 ***

Table S2. Results of generalized additive model (GAM) for functional α-diversity. Significant terms are in bold. A value of 1 for the effective degrees of freedom (edf) indicates a linear relationship. R^2_{adj} = 0.34. Deviance explained = 42.8%. Woody div = woody species richness, X = longitude, Y = latitude.

	edf	*F*-value	*P*-value
s(Canopy height)	2.181	1.473	0.215
s(Margin width)	1.000	1.575	0.211
s(Tree cover)	1.940	10.767	0.000 ***
s(Shrub cover)	1.305	0.816	0.558
s(Woody div)	3.780	5.610	0.001 ***
s(Bank height)	1.859	2.404	0.082
s(Ditch depth)	1.000	4.518	0.034 *
s(Herbicide)	1.000	0.045	0.832
s(Mowing)	1.000	5.905	0.016 *
s(Grazing)	1.000	19.966	0.000 ***
s(Tillage)	1.000	0.138	0.710
s(Cropping)	1.573	0.578	0.490
s(x,y)	21.46	2.023	0.003 **

Table S3. List of factors describing field margin structure and long-term management of herbaceous plant communities, as well as selected plant traits, with their abbreviations, units, basic statistics, and coordinates on the first two RLQ axes.

Variables	Code	Unit	Mean (Min; Max) or counts	RLQ axis 1	RLQ axis 2
Field margin structure					
Canopy height		m	8.77 (0.00; 30.00)	−0.217	−0.073
Margin width		m	1.36 (0.15; 3.80)	−0.169	0.021
Tree cover		%	37.3 (0.0; 100.0)	−0.211	−0.073
Shrub cover		%	15.2 (0.0; 100.0)	−0.079	0.028
Woody species richness	Woody div		2.46 (0.00; 9.00)	−0.156	−0.038
Bank height		m	0.29 (0.00; 1.80)	−0.184	−0.089
Ditch depth		m	0.25 (0.00; 1.70)	0.057	0.220
Long-term management					
Herbicide		%	4 (0; 20)	−0.003	−0.162
Mowing		%	4 (0; 14)	−0.008	0.133
Grazing		%	7 (0; 34)	−0.167	0.040
Tillage		%	1 (0; 9)	0.122	−0.121
Cropping		%	38 (0; 100)	0.188	−0.205
Functional traits					
Life form					
Annual			39	0.004	−0.453
Perennial			91	−0.001	0.115
Growth form					
Grass	Grass.1		20	0.189	−0.166
Other	Grass.0		110	−0.088	0.078
Specific leaf area	SLA	mm².mg-1	27.00 (4.90; 53.68)	−0.035	−0.078
Plant height		cm	85.5 (15.0; 200.0)	0.232	0.063
Seed mass		mg	3.26 (0.01; 125.32)	0.123	−0.045
Ellenberg light	EIV-L		6.46 (4.00; 9.00)	0.372	0.049
Ellenberg nutrients	EIV-N		5.87 (2.00; 9.00)	0.159	−0.100
Ellenberg soil moisture	EIV-F		5.45 (2.00; 8.00)	0.041	0.204
Pollination mode					
Entomogamous	Entomo.1		60	−0.095	0.228
Other	Entomo.0		70	0.061	−0.146
Seed dispersal strategy					
By wind	Disp.wind		29	0.201	0.145
By animals	Disp.animal		47	−0.051	−0.085
By other means	Disp.other		54	−0.014	0.053

Table S4. List of EPPO codes and scientific names.

EPPO codes	Scientific names
ACHMI	*Achillea millefolium*
AGRRE	*Elymus repens*
AGSST	*Agrostis stolonifera*
AGSTE	*Agrostis capillaris*
AIURE	*Ajuga reptans*
ANGAR	*Lysimachia arvensis*
ANKSY	*Angelica sylvestris*
AOXOD	*Anthoxanthum odoratum*
APHAR	*Aphanes arvensis*
ARBTH	*Arabidopsis thaliana*
ARREL	*Arrhenatherum elatius*
ATXPA	*Atriplex patula*
AVEFA	*Avena fatua*
BRCSI	*Brachypodium sylvaticum*
BROMO	*Bromus hordeaceus*
BROST	*Anisantha sterilis*
CAGSE	*Calystegia sepium*
CARHI	*Cardamine hirsuta*
CCTLA	*Cruciata laevipes*
CENNI	*Centaurea nigra*
CERFO	*Cerastium fontanum*
CHEAL	*Chenopodium album*
CHYLE	*Leucanthemum vulgare*
CIRAR	*Cirsium arvense*
CIRPA	*Cirsium palustre*
CIRVU	*Cirsium vulgare*
CJILU	*Circaea lutetiana*

EPPO codes	Scientific names
CNQDE	*Conopodium majus*
CONAR	*Convolvulus arvensis*
CRXRE	*Carex remota*
CVPCA	*Crepis capillaris*
DACGL	*Dactylis glomerata*
DAUCA	*Daucus carota*
DECCA	*Deschampsia cespitosa*
DIKPU	*Digitalis purpurea*
EPHAM	*Euphorbia amygdaloides*
EPHHE	*Euphorbia helioscopia*
EPIAD	*Epilobium tetragonum*
EPIHI	*Epilobium hirsutum*
EPIMO	*Epilobium montanum*
EUPCA	*Eupatorium cannabinum*
FESAR	*Schedonorus arundinaceus*
FESRU	*Festuca rubra*
FRAVE	*Fragaria vesca*
FUMMU	*Fumaria muralis*
GAETE	*Galeopsis tetrahit*
GALAP	*Galium aparine*
GALMO	*Galium mollugo*
GALPA	*Galium palustre*
GERDI	*Geranium dissectum*
GERMO	*Geranium molle*
GERRO	*Geranium robertianum*
GEUUR	*Geum urbanum*
GLEHE	*Glechoma hederacea*
HERSP	*Heracleum sphondylium*
HOLLA	*Holcus lanatus*

EPPO codes	Scientific names
HOLMO	*Holcus mollis*
HYPHU	*Hypericum humifusum*
HYPPE	*Hypericum perforatum*
HYPPL	*Hypericum pulchrum*
IUNAF	*Juncus acutiflorus*
IUNBU	*Juncus bufonius*
IUNCG	*Juncus conglomeratus*
IUNEF	*Juncus effusus*
KICEL	*Kickxia elatine*
LAPCO	*Lapsana communis*
LINRP	*Linaria repens*
LOLMU	*Lolium multiflorum*
LOLPE	*Lolium perenne*
LOTCO	*Lotus corniculatus*
LOTUL	*Lotus pedunculatus*
LYTSA	*Lythrum salicaria*
MALMO	*Malva moschata*
MATIN	*Tripleurospermum inodorum*
MELAL	*Silene alba*
MENAQ	*Mentha aquatica*
MGJTR	*Moehringia trinervia*
MYOAR	*Myosotis arvensis*
OENCR	*Oenanthe crocata*
PGTMU	*Polygonatum multiflorum*
PIMMA	*Pimpinella major*
PLALA	*Plantago lanceolata*
PLAMA	*Plantago major*
POAAN	*Poa annua*
POATR	*Poa trivialis*

EPPO codes	Scientific names
POLAV	*Polygonum aviculare*
POLCO	*Fallopia convolvulus*
POLPE	*Persicaria maculosa*
PRIVU	*Primula vulgaris*
PRUVU	*Prunella vulgaris*
PTLRE	*Potentilla reptans*
PTLST	*Potentilla sterilis*
PULDY	*Pulicaria dysenterica*
RANAC	*Ranunculus acris*
RANRE	*Ranunculus repens*
RUMAA	*Rumex acetosella*
RUMAC	*Rumex acetosa*
RUMCR	*Rumex crispus*
RUMOB	*Rumex obtusifolius*
RUMSN	*Rumex sanguineus*
SCUNO	*Scrophularia nodosa*
SEDTE	*Hylotelephium telephium*
SENJA	*Jacobaea vulgaris*
SENVU	*Senecio vulgaris*
SOLDU	*Solanum dulcamara*
SONAR	*Sonchus arvensis*
SONAS	*Sonchus asper*
STAOF	*Betonica officinalis*
STAPA	*Stachys palustris*
STASI	*Stachys sylvatica*
STEGR	*Stellaria graminea*
STEHO	*Stellaria holostea*
STEMA	*Stellaria media*
STIVU	*Clinopodium vulgare*

EPPO codes	Scientific names
SYMOF	*Symphytum officinale*
TAROF	*Taraxacum officinale*
TEUSC	*Teucrium scorodonia*
TRFRE	*Trifolium repens*
TRZAX	*Triticum aestivum*
UMLRU	*Umbilicus rupestris*
URTDI	*Urtica dioica*
VERAR	*Veronica arvensis*
VERCH	*Veronica chamaedrys*
VERHE	*Veronica hederifolia*
VERPE	*Veronica persica*
VERSE	*Veronica serpyllifolia*
VICHI	*Ervilia hirsuta*
VICSA	*Vicia sativa*
VICTE	*Vicia tetrasperma*
VIORI	*Viola riviniana*

References

Hsieh, T.C., Ma, K.H., Chao, A., 2016. iNEXT: an R package for rarefaction and extrapolation of species diversity (H ill numbers). Methods in Ecology and Evolution 7, 1451–1456. doi:10.1111/2041-210X.12613.