Supporting Information for 'Bird community responses to habitat creation in a long-term, large-scale natural experiment' accepted for publication in *Conservation Biology* published by Wiley-Blackwell. The published version of the article can be found at:

Appendix S1: Bird survey methodology (additional information)

All hand-drawn bird registrations from field maps were digitised into Geographic Information System (GIS) format using ArcMap *v*10.2. (ESRI, 2011). Records of individuals flying over the patch or observed outside of the patch boundary were excluded from analyses. Species were considered present (i.e. probably breeding) if territorial behaviour (song, alarm call, mating, nest building, active nest, male and female pair) was observed on at least one visit, or if the species was detected during two of the three surveys. Since survey effort and the criteria used to determine breeding status were less stringent than similar studies (e.g. > 3 visits with territory mapping), we validated results by comparing an observed *vs* expected species-area curve for a subset of woodland species ($n = 17$ species) that were also surveyed by Bellamy et al. (1996). We found no significant difference (Fig. S2), suggesting the methodology was robust.

Records of Nightingale *Luscinia megarhynchos* ($n = 1$ site), Lesser Whitethroat *Sylvia curruca* ($n = 3$ sites), and Marsh Tit *Poecile palustris* ($n = 5$ sites) were excluded due to their restricted geographical range and historic absence from the Scottish study area (Balmer et al. 2013). Nuthatch *Sitta europaea* ($n = 3$ sites) was excluded from functional group analysis because it was a rare breeding species in Scotland at the time of assessment by French and Picozzi (2002), who did not therefore assign it to any group. Grey Wagtail *Motacilla cinerea*, Cuckoo *Cuculus canorus*, Siskin *Spinus spinus*, Goldcrest *Regulus regulus*, Swallow *Hirundo rustica* and Mallard *Anas platyrhynchos* were also excluded from functional group analyses due to the low number of individuals and species in their respective groups.

Appendix S2: Description of meta model and hypothesised relationships

Our primary response variables of interest were total bird species richness and relative abundance, and within functional group species richness and relative abundance. Species richness was calculated as the total number of breeding species recorded in a patch, and relative abundance was calculated as the pooled, total number of adult birds recorded from all three visits.

Preliminary graphical analyses suggested that, as expected, relative abundance and species-richness were positively correlated. As such, we hypothesised that local and landscape characteristics indirectly influence species richness through their direct effects on abundance. This was based on the assumption that species are sampled in proportion to their availability (i.e. abundance) in the local species pool. Thus, if a patch can support more individuals then the probability that a species is sampled from the local species pool is higher.

Ecological continuity (patch age, calculated from the date of planting; see Watts et al. 2016) can influence colonisation rates either by increasing colonisation probability over time, or by allowing time-dependent resources (such as tree cavities for hole-nesting birds) to develop in a patch (Vesk et al. 2008). Since birds are generally highly mobile it is likely that colonisation can occur rapidly, but only where there are sufficient patch-level resources. For example, cavity nesting birds might rapidly reach a woodland but fail to breed (i.e. colonise) due to a lack of mature trees and associated tree holes. Other potentially limiting resources include, for example, a lack of invertebrate prey species associated with mature, veteran trees (Davies et al. 2008). Older woodlands are also likely to have greater within-patch heterogeneity and thus greater niche diversity, for example as a result of canopy gaps created by tree falls. We therefore expected ecological continuity to indirectly influence bird abundance and diversity through its direct effects on stand structure (an index of resource/niche availability). This was accounted for in the model by

including a direct path between patch age and tree DBH mean, which in turn was expected to directly influence stand heterogeneity (tree DBH standard deviation) and bird abundance.

Intensive grazing pressure in woodlands can reduce woodland bird abundance and diversity (Martin & McIntyre 2007), for example through changes in understory structure. We therefore hypothesised that livestock presence (an index of grazing pressure) would indirectly influence abundance by reducing woodland understory cover. Wild ungulates can also influence woodland bird communities through grazing pressure (Gill & Fuller 2007) but this was not assessed here since it is difficult to accurately quantify deer abundance/presence in such a large number of woodlands.

Evidence from similar studies suggests that there are positive log-linear and power-law relationships between patch size and bird species richness and abundance in woodland patches (Bellamy 2000; Dolman et al. 2007). Here, continuing with our hypothesis that abundance drives species richness through sampling effects, we included only a direct path between patch area (log transformed) and abundance in our a-priori model. An index of patch 'compactness' (see Table S1 for further details) was also included to account for potential edge effects (Dolman 2012). Larger patches were expected to be more compact, since several of the smaller patches were linear shelter belts, and we therefore also included a direct path between patch area and compactness.

Other patch-level metrics expected to be important included tree species richness and % dead wood cover, both of which can increase resource availability and niche diversity in a patch. Bird boxes were also common in many of the woodlands and we expected a positive relationship between their availability and the abundance of birds (within functional groups) that commonly nest in boxes.

At the landscape scale, we expected higher proportions of woodland in the landscape to act as a source for the focal patch, and thus expected a direct positive relationship between woodland

amount (either broadleaf woodland or any woodland depending on the functional group of interest) in the landscape and bird abundance. Landscape configuration (broadleaf woodland connectivity) was expected to be important for obligate woodland species, which are less likely to cross non-wooded habitats during dispersal.

Agricultural activity in the landscape can have a negative impact on bird communities (Donald et al. 2006). Here, we hypothesised that the % cover of agriculture in the landscape would indirectly affect woodland bird communities by reducing the amount of semi-natural habitat surrounding the woodland, and thus reducing potential foraging habitat. Lastly, we predicted that the % of urban land cover in the landscape would directly reduce bird abundance, perhaps by limiting colonisation or reducing foraging opportunities.

Table S1. Description and source of local and landscape metrics used in analyses. Summary statistics for all variables are given in Table S2.

Variable	Description	Source
Management	*Edge habitat, patch age and management practices inside patch boundary*	
Patch age (years)	Time since appearance on historic maps	Ordnance Survey maps
n bird boxes	Counted on final bird survey	Field survey 2015
Livestock presence/absence	Sheep, cattle or horses inside patch	Field survey 2015
Vegetation structure	*Metrics describing habitat structure and heterogeneity inside the patch*	
Tree species richness	*n* tree species	Field survey 2013/14
Tree DBH[b] mean	Mean for patch	Field survey 2013/14
Tree DBH SD[c]	SD of patch mean	Field survey 2013/14
Understory cover %	Mean for patch	Field survey 2013/14
Dead wood cover %	Mean for patch	Field survey 2013/14
Patch geometry	*2D patch size and shape*	
Patch area	ha	GIS NFI dataset
Shape index	Patch perimeter divided by perimeter of perfect circle with same area	GIS NFI dataset
Landscape	*Measures of landscape connectivity and matrix composition, each calculated at eight spatial scales[d]*	
Broadleaf woodland connectivity	Index (incidence function model)	GIS NFI dataset
Any woodland %	Percentage cover	GIS NFI dataset
BL %	Percentage cover	GIS NFI dataset
Urban areas %	Percentage cover	GIS LCM (2007) habitat codes 22 & 23
Arable / agriculturally improved grassland %	Percentage cover	GIS LCM (2007) habitat codes 3 & 4
Semi-natural land cover %	Percentage cover	GIS LCM (2007) habitat codes 5 – 14, 17 – 21

[a]Geographic Information System (GIS) data calculated using ArcMap *v*10.2 and National Forest Inventory (Forestry Commission, 2013) and Land Cover Map 2007 data (Morton et al. 2011).
[b]Diameter at breast height
[c]Standard deviation
[d]Metric calculated in nested buffers at 100 m, 250 m, 500 m, 1000 m, 1500 m, 2000 m, 2500 m and 3000 m surrounding each woodland patch.
[e]Index based on Incidence Function Model (Hanski 1994; Moilanen & Hanski 2001; Moilanen & Nieminen 2002). The sum contribution from all surrounding woodland patches of each category was calculated based on their size and distance from the target patch (i.e. each of our study sites), assuming that 5% of dispersers would potentially reach each of the previously defined buffer sizes (i.e. 100, 250, 500, 1000, 1500, 2000, 2500 and 3000 m). Thus the contribution from each surrounding patch declines along a negative exponential dispersal function to the target patch.

Table S2. Summary statistics for predictor variables used in analyses, showing subsets of management, vegetation structure, patch geometry and landscape variables.

Variable	Scale	Mean	Median	SD	Min.	Max.	N obs. (factors)
Management							
Age (year)	Patch	68.28	50.00	47.26	10.00	160.00	-
n bird boxes	Patch	0.29	0.00	1.12	0.00	7.00	-
Livestock (yes)	Patch	-	-	-	-	-	21
Livestock (no)	Patch	-	-	-	-	-	80
Vegetation structure							
Tree species richness	Patch	4.45	4.00	2.29	1.00	13.00	-
Tree DBH mean	Patch	28.12	24.30	15.00	8.11	90.20	-
Tree DBH standard deviation	Patch	12.22	10.75	7.79	1.33	43.38	-
Understory cover %	Patch	1.98	1.20	2.01	0.00	8.00	-
Dead wood cover %	Patch	1.76	1.80	0.63	0.00	3.00	-
Patch geometry							
Area	Patch	3.37	1.87	5.04	0.50	31.89	-
Shape index	Patch	1.60	1.44	0.47	1.12	3.17	-
Landscape							
Any woodland %	100 m GIS buffer	0.05	0.00	0.09	0.00	0.52	-
Any woodland %	250 m GIS buffer	0.07	0.04	0.09	0.00	0.53	-
Any woodland %	500 m GIS buffer	0.10	0.06	0.09	0.00	0.47	-
Any woodland %	1000 m GIS buffer	0.13	0.11	0.10	0.00	0.43	-
Any woodland %	1500 m GIS buffer	0.13	0.12	0.09	0.00	0.42	-
Any woodland %	2000 m GIS buffer	0.13	0.13	0.09	0.01	0.37	-
Any woodland %	2500 m GIS buffer	0.13	0.13	0.09	0.01	0.37	-
Any woodland %	3000 m GIS buffer	0.13	0.12	0.08	0.01	0.35	-
Broadleaf woodland %	100 m GIS buffer	0.02	0.00	0.04	0.00	0.21	-
Broadleaf woodland %	250 m GIS buffer	0.03	0.02	0.04	0.00	0.21	-
Broadleaf woodland %	500 m GIS buffer	0.05	0.04	0.05	0.00	0.25	-
Broadleaf woodland %	1000 m GIS buffer	0.06	0.05	0.05	0.00	0.22	-
Broadleaf woodland %	1500 m GIS buffer	0.06	0.05	0.04	0.00	0.18	-
Broadleaf woodland %	2000 m GIS buffer	0.06	0.05	0.04	0.01	0.18	-
Broadleaf woodland %	2500 m GIS buffer	0.06	0.04	0.04	0.00	0.17	-

Variable	Scale	Mean	Median	SD	Min.	Max.	N obs. (factors)
Broadleaf woodland %	3000 m GIS buffer	0.05	0.04	0.04	0.00	0.17	-
Broadleaf woodland connectivity	100 m GIS buffer	8643.05	348.07	25904.61	0.00	190035.08	-
Broadleaf woodland connectivity	250 m GIS buffer	21717.34	6511.39	39893.08	0.00	222386.70	-
Broadleaf woodland connectivity	500 m GIS buffer	49557.79	26431.09	63434.33	0.00	321256.86	-
Broadleaf woodland connectivity	1000 m GIS buffer	120934.83	85210.94	120224.75	740.21	672950.41	-
Broadleaf woodland connectivity	1500 m GIS buffer	211126.08	168084.60	178144.69	6388.44	1039764.24	-
Broadleaf woodland connectivity	2000 m GIS buffer	319189.01	249295.42	238279.40	21565.77	1405338.56	-
Broadleaf woodland connectivity	2500 m GIS buffer	444288.34	350377.67	302396.37	49482.91	1791266.07	-
Broadleaf woodland connectivity	3000 m GIS buffer	586000.65	469856.74	370738.26	89612.11	2202040.28	-
Urban %	100 m GIS buffer	0.02	0.00	0.05	0.00	0.24	-
Urban %	250 m GIS buffer	0.02	0.00	0.05	0.00	0.30	-
Urban %	500 m GIS buffer	0.03	0.00	0.06	0.00	0.36	-
Urban %	1000 m GIS buffer	0.04	0.01	0.07	0.00	0.33	-
Urban %	1500 m GIS buffer	0.05	0.02	0.08	0.00	0.36	-
Urban %	2000 m GIS buffer	0.06	0.02	0.08	0.00	0.37	-
Urban %	2500 m GIS buffer	0.06	0.02	0.08	0.00	0.34	-
Urban %	3000 m GIS buffer	0.06	0.02	0.07	0.00	0.35	-
Arable/agriculturally improved grassland %	100 m GIS buffer	0.80	0.85	0.23	0.00	1.00	-
Arable/agriculturally improved grassland %	250 m GIS buffer	0.79	0.84	0.20	0.00	1.00	-
Arable/agriculturally improved grassland %	500 m GIS buffer	0.75	0.78	0.20	0.00	1.00	-
Arable/agriculturally improved grassland %	1000 m GIS buffer	0.69	0.75	0.20	0.07	0.99	-
Arable/agriculturally improved grassland %	1500 m GIS buffer	0.66	0.70	0.21	0.09	0.96	-
Arable/agriculturally improved grassland %	2000 m GIS buffer	0.63	0.65	0.23	0.03	0.95	-
Arable/agriculturally improved grassland %	2500 m GIS buffer	0.60	0.60	0.23	0.02	0.94	-
Arable/agriculturally improved grassland %	3000 m GIS buffer	0.58	0.60	0.25	0.03	0.93	-
Semi-natural land cover %	100 m GIS buffer	0.17	0.08	0.22	0.00	1.00	-
Semi-natural land cover %	250 m GIS buffer	0.17	0.12	0.19	0.00	1.00	-
Semi-natural land cover %	500 m GIS buffer	0.19	0.12	0.19	0.00	1.00	-
Semi-natural land cover %	1000 m GIS buffer	0.22	0.16	0.19	0.00	0.93	-
Semi-natural land cover %	1500 m GIS buffer	0.23	0.17	0.18	0.00	0.80	-
Semi-natural land cover %	2000 m GIS buffer	0.23	0.19	0.18	0.01	0.73	-
Semi-natural land cover %	2500 m GIS buffer	0.23	0.19	0.18	0.02	0.74	-

Variable	Scale	Mean	Median	SD	Min.	Max.	N obs. (factors)
Semi-natural land cover %	3000 m GIS buffer	0.23	0.19	0.18	0.02	0.75	-

Table S3. Full piecewise structural equation model (SEM) for total species richness. The hypothesised beta sign shows the expected, a-priori relationship between pairs of variables as well missing paths that were considered likely to be causative. All significant and non-significant predictors are shown. Pairs of variables with correlated errors (i.e. those not considered causative but which had a significant correlation) are denoted ~~. For variables measured at multiple scales (see Tables S1 & S2), the 'best' scale was selected using AICc prior to constructing the SEM (see main text). Goodness of fit statistics for the model are given in Table S10.

Response	Predictor	Hypothesised Beta sign	Observed Beta	SE	P	R^2
Raw richness	Log(abundance)	+	3.482	0.463	< 0.001	0.72
	Log(tree DBH mean)	Missing path in a-priori model	1.091	0.305	0.001	
	Broadleaf conn. 250 m	Missing path in a-priori model	0.591	0.275	0.035	
	Log(area)	Missing path in a-priori model	1.017	0.486	0.039	
Understory cover	Livestock y/n	-	-0.329	0.119	0.007	0.07
Semi-nat. % 100 m	Arable / AG % 100 m	-	-0.748	0.070	< 0.001	0.54
	Broadleaf % 100 m	-	-0.147	0.070	0.038	
Shape index	Log(area)	+	0.282	0.096	0.004	0.08
Log(tree DBH mean)	Age	+	0.660	0.076	< 0.001	0.44
Log(abundance)	Log(area)	+	0.831	0.069	< 0.001	0.70
	Tree richness	+	0.131	0.060	0.031	
	Semi-nat. % 100 m	+	0.091	0.058	0.124	
	Understory cover	+	-0.082	0.063	0.197	
	Shape index	+	0.063	0.063	0.321	
	Broadleaf conn. 250 m	+	0.058	0.066	0.383	
	Broadleaf % 100 m	+	0.026	0.065	0.693	
	Log(tree DBH mean)	+	0.018	0.066	0.784	
~~ Tree richness	~~ Shape index	NA	0.247	NA	0.006	
~~ Understory cover	~~ Log(area)	NA	0.298	NA	0.001	
~~ Understory cover	~~ Northing	NA	-0.473	NA	1.000	
~~ Log(abundance)	~~ Northing	NA	0.330	NA	< 0.001	
~~ Log(tree DBH mean)	~~ Log(area)	NA	-0.278	NA	0.998	

Table S4. Full piecewise structural equation model (SEM) for the broadleaf trees/hedgerows functional group. The hypothesised beta sign shows the expected, a-priori relationship between pairs of variables as well missing paths that were considered likely to be causative. All significant and non-significant predictors are shown. Pairs of variables with correlated errors (i.e. those not considered causative but which had a significant correlation) are denoted ~~. For variables measured at multiple scales (see Tables S1 & S2), the 'best' scale was selected using AICc prior to constructing the SEM (see main text). Goodness of fit statistics for the model are given in Table S10.

Response	Predictor	Hypothesised Beta sign	Observed Beta	SE	P	R^2
Log(richness)	Log(abundance)	+	1.066	0.040	< 0.001	0.92
	Log(area)	Missing path in a-priori model	-0.154	0.040	< 0.001	
Understory cover	Livestock y/n	-	-0.329	0.119	0.007	0.07
Log(tree DBH mean)	Age	+	0.660	0.076	< 0.001	0.44
Shape index	Log(area)	+	0.282	0.096	0.004	0.08
Semi-nat. % 3000 m	Arable / AG % 3000 m	-	-0.710	0.071	< 0.001	0.50
Log(abundance)	Log(area)	+	0.645	0.081	< 0.001	0.61
	Livestock y/n	Missing path in a-priori model	-0.315	0.100	0.002	
	Broadleaf % 1000 m	+	-0.238	0.097	0.016	
	Broadleaf conn. 3000 m	+	0.160	0.095	0.097	
	Understory cover	+	0.087	0.073	0.240	
	Semi-nat. % 3000 m	+	0.088	0.077	0.254	
	Log(tree DBH mean)	+	0.081	0.077	0.295	
	Shape index	+	0.036	0.074	0.624	
	Tree richness	+	0.012	0.072	0.871	
~~ Log(tree DBH mean)	~~ Livestock y/n	NA	0.129	NA	0.099	
~~ Log(tree DBH mean)	~~ Log(area)	NA	-0.278	NA	0.998	
~~ Semi-nat. % 3000 m	~~ Livestock y/n	NA	0.285	NA	0.002	
~~ Semi-nat. % 3000 m	~~ Broadleaf conn. 3000 m	NA	-0.248	NA	0.994	
~~ Log(area)	~~ Arable / AG % 3000 m	NA	0.436	NA	< 0.001	
~~ Log(area)	~~ Northing	NA	-0.651	NA	1.000	
~~ Understory cover	~~ Arable / AG % 3000 m	NA	0.347	NA	< 0.001	
~~ Understory cover	~~ Log(area)	NA	0.298	NA	0.001	
~~ Tree richness	~~ Northing	NA	0.157	NA	0.059	
~~ Tree richness	~~ Arable / AG % 3000 m	NA	-0.155	NA	0.939	
~~ Shape index	~~ Tree richness	NA	0.267	NA	0.004	

Table S5. Full piecewise structural equation model (SEM) for the open/mixed and general wood/scrub functional group. The hypothesised beta sign shows the expected, a-priori relationship between pairs of variables as well missing paths that were considered likely to be causative. All significant and non-significant predictors are shown. Pairs of variables with correlated errors (i.e. those not considered causative but which had a significant correlation) are denoted ~~. For variables measured at multiple scales (see Tables S1 & S2), the 'best' scale was selected using AICc prior to constructing the SEM (see main text). Goodness of fit statistics for the model are given in Table S10.

Response	Predictor	Hypothesised Beta	Observed Beta	SE	P	R^2
Log(richness)	Log(abundance)	+	0.998	0.093	< 0.001	0.70
	Log(area)	Missing path in a-priori model	-0.306	0.091	0.001	
	Any woodland % 500 m	Missing path in a-priori model	0.176	0.057	0.003	
Understory cover	Livestock y/n	-	-0.329	0.119	0.007	0.07
Semi-nat. % 100 m	Arable / AG % 250 m	-	-0.702	0.084	< 0.001	0.44
	Any woodland % 500 m	Missing path in a-priori model	-0.093	0.084	0.270	
Log(tree DBH mean)	Age	+	0.660	0.076	< 0.001	0.44
Log(abundance)	Log(area)	+	0.820	0.076	< 0.001	0.68
	Livestock y/n	-	-0.173	0.082	0.039	
	Any woodland % 500 m	+	0.125	0.064	0.053	
	Tree richness	+	0.091	0.062	0.145	
	Understory cover	+	-0.086	0.066	0.195	
	Semi-nat. % 100 m	+	0.070	0.064	0.276	
	Cumulative woody debris	+	0.057	0.063	0.371	
	N bird box	+	-0.041	0.064	0.524	
	Log(tree DBH mean)	-	0.042	0.071	0.551	
~~ Abundance	~~ Northing	NA	0.455	NA	< 0.001	
~~ Log(area)	~~ N bird box	NA	0.263	NA	0.004	
~~ Log(area)	~~ Any woodland % 500 m	NA	0.071	NA	0.239	
~~ Log(area)	~~ Cumulative woody debris	NA	-0.281	NA	0.998	
~~ Log(area)	~~ Northing	NA	-0.651	NA	1.000	
~~ Understory cover	~~ Log(area)	NA	0.298	NA	0.001	
~~ Understory cover	~~ Northing	NA	-0.473	NA	1.000	
~~ Log(tree DBH mean)	~~ Livestock y/n	NA	0.129	NA	0.099	
~~ Log(tree DBH mean)	~~ Log(area)	NA	-0.278	NA	0.998	

Table S6. Full piecewise structural equation model (SEM) for the tree/building nester functional group. The hypothesised beta sign shows the expected, a-priori relationship between pairs of variables as well missing paths that were considered likely to be causative. All significant and non-significant predictors are shown. Pairs of variables with correlated errors (i.e. those not considered causative but which had a significant correlation) are denoted ~~. For variables measured at multiple scales (see Tables S1 & S2), the 'best' scale was selected using AICc prior to constructing the SEM (see main text). Goodness of fit statistics for the model are given in Table S10.

Response	Predictor	Hypothesised Beta sign	Observed Beta	SE	P	R^2
Log(richness)	Log(abundance)	+	0.865	0.039	< 0.001	0.88
	Livestock y/n	Missing path in a-priori model	0.170	0.048	0.001	
Understory cover	Livestock y/n	-	-0.329	0.119	0.007	0.07
Semi-nat. % 1000 m	Arable / AG % 1500 m	-	-0.722	0.072	< 0.001	0.50
	Urban % 2000 m	Missing path in a-priori model	-0.178	0.072	0.016	
Log(tree DBH mean)	Age	+	0.660	0.076	< 0.001	0.44
Log(abundance)	Urban % 2000 m	+	0.300	0.083	0.001	0.39
	Livestock y/n	+	0.432	0.122	0.001	
	Log(area)	+	0.213	0.096	0.029	
	Semi-nat. % 1000 m	+	0.175	0.094	0.065	
	Understory cover	-	-0.148	0.090	0.104	
	Log(tree DBH mean)	-	0.119	0.094	0.207	
	Tree richness	+	0.004	0.084	0.958	
~~ Understory cover	~~ Arable / AG % 1500 m	NA	0.304	NA	0.001	
~~ Understory cover	~~ Log(area)	NA	0.298	NA	0.001	
~~ Understory cover	~~ Northing	NA	-0.473	NA	1.000	
~~ Livestock y/n	~~ Arable / AG % 1500 m	NA	-0.440	NA	1.000	
~~ Semi-nat. % 1000 m	~~ Livestock y/n	NA	0.226	NA	0.012	
~~ Semi-nat. % 1000 m	~~ Age	NA	-0.212	NA	0.983	
~~ Log(tree DBH mean)	~~ Log(area)	NA	-0.278	NA	0.998	

Table S7. Full piecewise structural equation model (SEM) for the farmland seed eater functional group. The hypothesised beta sign shows the expected, a-priori relationship between pairs of variables as well missing paths that were considered likely to be causative. All significant and non-significant predictors are shown. Pairs of variables with correlated errors (i.e. those not considered causative but which had a significant correlation) are denoted ~~. For variables measured at multiple scales (see Tables S1 & S2), the 'best' scale was selected using AICc prior to constructing the SEM (see main text). Goodness of fit statistics for the model are given in Table S10.

Response	Predictor/s	Hypothesised Beta sign	Observed Beta	SE	P	R^2
Log(richness)	Log(abundance)	+	0.730	0.072	< 0.001	0.53
	Age	Missing path in a-priori model	-0.265	0.093	0.006	
	Semi-nat. % 1500 m	Missing path in a-priori model	-0.184	0.073	0.013	
	Log(tree DBH mean)	Missing path in a-priori model	0.157	0.094	0.100	
Semi-nat. % 1500 m	Arable / AG % 2500 m	-	-0.668	0.075	< 0.001	0.45
Log(tree DBH mean)	Age	+	0.660	0.076	< 0.001	0.44
Log(abundance)	Log(area)	+	0.550	0.104	< 0.001	0.30
	Arable / AG % 2500 m	Missing path in a-priori model	-0.475	0.125	< 0.001	
	Urban % 100 m	+	-0.109	0.089	0.225	
	Log(tree DBH mean)	-	0.084	0.098	0.391	
	Semi-nat. % 1500 m	+	-0.031	0.117	0.790	
	Tree richness	-	-0.006	0.087	0.949	
~~ Log(tree DBH mean)	~~ Log(area)	NA	-0.278	NA	0.998	
~~ Abundance	~~ Northing	NA	0.489	NA	< 0.001	

Table S8. Full piecewise structural equation model (SEM) for the farmland seed eater functional group. The hypothesised beta sign shows the expected, a-priori relationship between pairs of variables as well missing paths that were considered likely to be causative. All significant and non-significant predictors are shown. Pairs of variables with correlated errors (i.e. those not considered causative but which had a significant correlation) are denoted ~~. For variables measured at multiple scales (see Tables S1 & S2), the 'best' scale was selected using AICc prior to constructing the SEM (see main text). Goodness of fit statistics for the model are given in Table S10.

Response	Predictor	Hypothesised Beta sign	Observed Beta	SE	P	R^2
Log(richness)	Log(abundance)	+	0.717	0.058	< 0.001	0.68
	Livestock y/n	Missing path in a-priori model	-0.214	0.074	0.005	
Understory cover	Livestock y/n	-	-0.329	0.119	0.007	0.07
Semi-nat. % 3000 m	Arable / AG % 3000 m	-	-0.737	0.072	< 0.001	0.52
	BL.1500	Missing path in a-priori model	-0.117	0.072	0.106	
Tree DBH SD	Age	+	0.647	0.076	< 0.001	0.44
	Tree richness	+	0.243	0.076	0.002	
Shape index	Log(area)	+	0.282	0.096	0.004	0.08
Log(abundance)	Log(area)	+	0.669	0.099	< 0.001	0.47
	Broadleaf conn. 2500 m	-	-0.238	0.086	0.007	
	Semi-nat. % 3000 m	+	-0.303	0.116	0.011	
	Tree richness	+	0.197	0.082	0.018	
	Arable / AG % 3000 m	-	-0.300	0.133	0.026	
	Understory cover	-	-0.029	0.089	0.745	
	Tree DBH SD	+	0.013	0.092	0.889	
~~ Semi-nat. % 3000 m	~~ Livestock y/n	NA	0.313	NA	0.001	
~~ Log(area)	~~ Arable / AG % 3000 m	NA	0.436	NA	< 0.001	
~~ Log(area)	~~ Northing	NA	-0.651	NA	1.000	
~~ Understory cover	~~ Arable / AG % 3000 m	NA	0.347	NA	< 0.001	
~~ Understory cover	~~ Log(area)	NA	0.298	NA	0.001	
~~ Understory cover	~~ Northing	NA	-0.473	NA	1.000	
~~ Shape index	~~ Tree richness	NA	0.267	NA	0.004	
~~ Abundance	~~ Northing	NA	0.069	NA	0.245	
~~ Tree DBH SD	~~ Log(area)	NA	-0.305	NA	0.999	

Table S9. Goodness of fit statistics for all piecewise structural equation models

Group	Fisher's C	Df	P	AICc	K	n
Raw richness	57.06	56	0.435	114.034	22	101
Tree/building nesters	40.96	44	0.603	101.298	23	101
Farmland seed eaters	34.98	26	0.112	85.48	20	101
Grassland and shrubs/trees	63.26	74	0.809	137.972	27	101
Broadleaf trees/hedgerows	71.53	70	0.427	146.242	27	101
Open/mixed and general wood/scrub	56.02	62	0.690	126.993	26	101
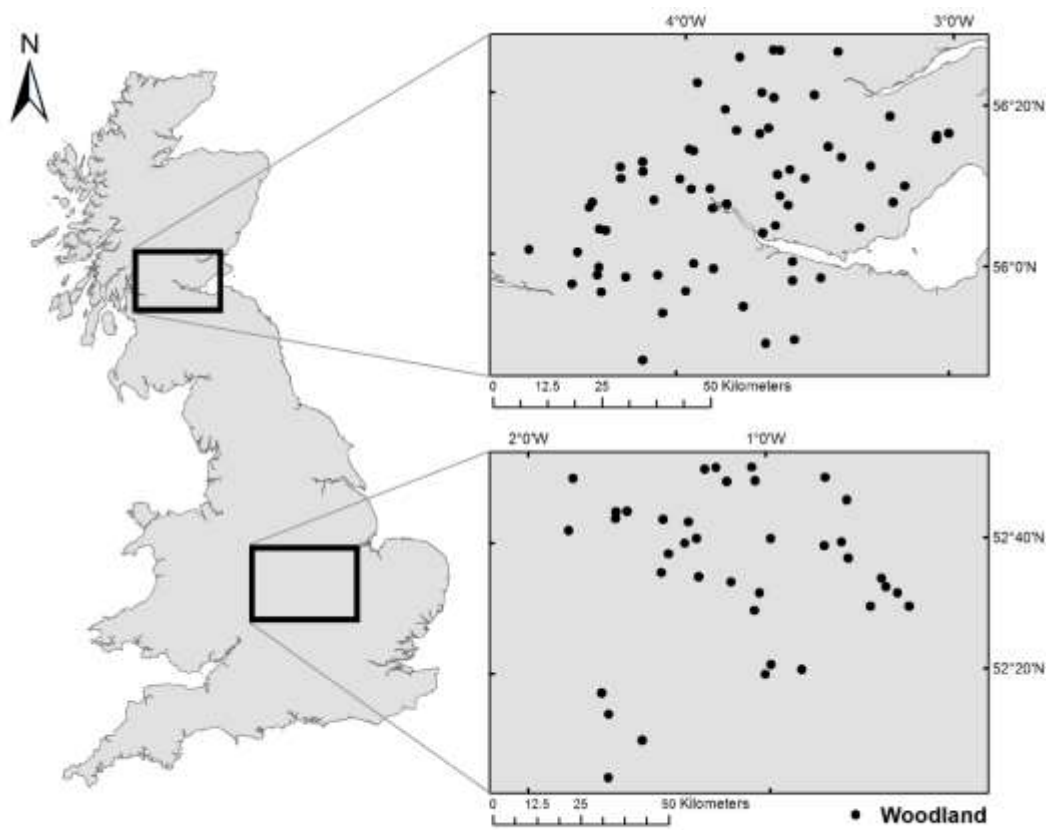
Figure S1. Map of Great Britain showing the two study areas in Scotland and England with approximate locations of the study woodlands.
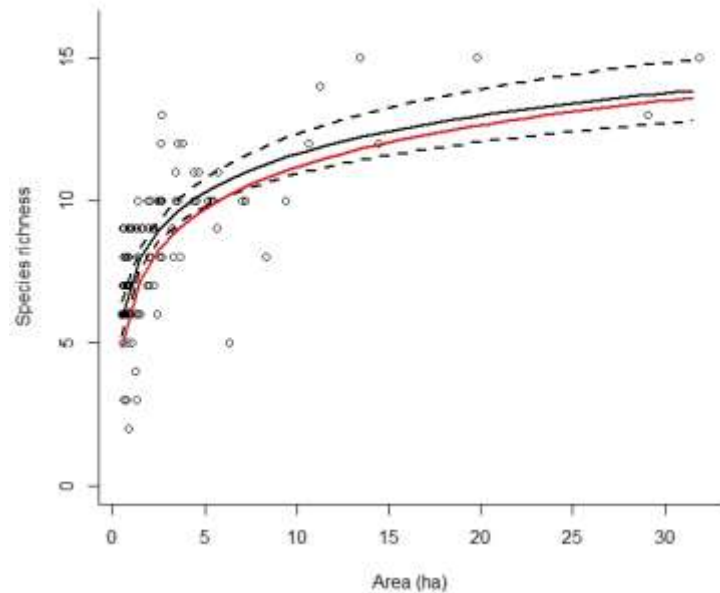
Figure S2. Observed species area curve (black line ±95% CI) from a linear regression model with raw species richness as the response and log(area) as a fixed effect, *vs* expected number of species (red line) based on formula given in Bellamy et al. (1996). Points show raw data from this study.

The following subset of species (*n* = 17) were used for direct comparison: Blackbird *Turdus merula,* Bullfinch *Pyrrhula Pyrrhula,* Blue tit *Cyanistes caeruleus,* Chaffinch *Fringilla coelebs,* Coal tit *Periparus ater,* Dunnock *Prunella modularis,* Green woodpecker *Picus viridis,* Goldcrest *Regulus regulus,* Great spotted woodpecker *Dendrocopos major,* Great tit *Parus major,* Jay *Garrulus glandrius,* Long-tailed tit *Aegithalos caudatus,* European nuthatch *Sitta europaea,* Robin *Erithacus rubecula,* Song thrush *Turdus philomelos,* Treecreeper *Certhia familiaris,* Wren *Troglodytes troglodytes*

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Formula S1

95 % confidence of the proportions shown in Figure 1 were calculated as:

$$\hat{p} \pm 1.96 \left(\sqrt{\frac{\hat{p}(1 - \hat{p})}{n}} \right)$$

Where n is the sample size and $\hat{p}$ is the sample proportion.