Supplementary Information

β-diversity calculation

Following (Chase *et al.*, 2011), we corrected our estimates of β-diversity using null models. We first calculated the pairwise dissimilarity between sites within each year of the dataset using a dissimilarity estimator that incorporates species abundances, while also accounting for unobserved species (Chao *et al.*, 2005).

We next created an expected distribution by generating randomized communities and calculating the dissimilarity of these communities. To do this, we defined the species pool within each year as the species and number of individuals present across all samples from that year. We then generated 9999 random communities by constraining either 1) the total number of individuals caught at each site or 2) the species richness at each site (for details on the community generation algorithms, see Section). For each of these communities, we calculated the pair-wise dissimilarity between sites. We then used these dissimilarities to calculate the expected β-diversity when communities are randomly assembled but constrained so that they have either the same 1) number of individuals or 2) species richness as the observed communities and with species drawn from a meta-community with the same species abundance distributions. In order to do this, we followed Chase *et al.* (2011). Specifically, we calculated the fraction of randomly assembled communities with dissimilarity values less than (and half of those equal to) that of the observed community. We used this fraction as a "corrected dissimilarity score" for our observed data. Corrected dissimilarity values near one indicate that our observed communities exhibit more species turnover between sites than expected under a random assembly process while values near 0.5 indicate that our observed communities exhibit levels of turnover

more in line with the null expectation. We calculated the corrected dissimilarities for each type of randomized community.

We also corrected dissimilarity values by calculating z-scores (subtracting the mean of the nulls from the observed dissimilarity and dividing by the standard deviation of the nulls (Trøjelsgaard *et al.*, 2015) to confirm that the method of calculating the corrected dissimilarity score did not qualitatively affect results.

We then generated principle coordinate axes (PCoA) based on the corrected pair-wise dissimilarities (Oksanen *et al.*, 2013; Anderson *et al.*, 2006, 2011; Anderson, 2006). We calculated dispersion for each site type by finding the centroid in PCoA space for that site type and then calculating the distances from sites of that type to that centroid. The centroid is the point that minimizes the sum of these distances. We calculated dispersion scores separately for each year in order to account for possible changes in the total species pool that can occur between years (e.g., Petanidou *et al.*, 2008). The dispersion values were then used in linear mixed-effect models to investigate the effect of different site types on β-diversity.

Though commonly used (e.g., Karp *et al.*, 2012), average pairwise dissimilarity may be misleading if spatial heterogeneity in community composition is due to nestedness and not species replacement (Baselga, 2012, 2013). However, in our case, because dissimilarity is due to species replacement, pair-wise measures of β-diversity are comparable to multi-site measures (Baselga, 2013).

Community randomization algorithms

Randomly assembled communities were generated by either constraining 1) the species richness at a site or 2) the number of individuals at a site so that they were the same as

those in the observed communities. In 1) we begin by randomizing a binary matrix while maintaining the same row sums (species richness at a site) and column sums (number of sites at which a species was observed) using the quasi-swap method in the R function commsimulator (Oksanen *et al.*, 2013). Next, we fill the matrix by drawing species with probabilities proportional to their relative abundances until the total number of individuals in the randomly assembled community is the same as that in the observed community (Vázquez *et al.*, 2007). To constrain the total number of individuals at a site but not the species richness at that site, we used a swap-algorithm (Gotelli & Graves, 1996).

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	Year						
	2007	2008	2009	2010	2011	2012	2013
Control-1	0	0	3	4	0	4	5
Control-2	3	3	0	0	0	0	0
Control-3	3	3	3	0	2	4	5
Control-4	0	0	0	0	0	4	5
Control-5	3	3	3	0	2	4	5
Control-6	0	0	3	0	0	4	5
Control-7	0	0	0	0	0	0	5
Control-8	3	3	3	0	2	4	5
Control-9	3	3	3	0	2	4	5
Control-10	3	3	3	0	2	4	5
Control-11	0	0	3	0	0	4	5
Control-12	0	0	0	0	0	4	0
Control-13	3	3	3	0	2	0	0
Control-14	0	0	3	4	0	4	5
Control-15	0	0	0	0	0	0	5
Control-16	0	0	0	0	0	0	5
Control-17	0	0	0	0	0	4	0
Control-18	3	3	3	0	2	4	5
Control-19	0	0	0	0	0	4	5
Control-20	3	3	3	0	2	4	5
Control-21	3	3	3	0	2	4	5
Control-22	3	3	3	0	2	4	5
Control-23	0	0	0	0	0	4	5
Control-24	0	0	0	4	0	4	5

Table S1: The number of sampling rounds conducted at each control site in each year of the study.

	Year						
	2007	2008	2009	2010	2011	2012	2013
Hedgerow-1	0	0	0	0	0	4	5
Hedgerow-2	0	0	0	0	0	0	5
Hedgerow-3	0	0	0	0	0	4	5
Hedgerow-4	0	0	3	4	2	4	5
Hedgerow-5	0	0	0	0	0	4	5
Hedgerow-6	0	0	3	0	2	4	5
Hedgerow-7	0	0	0	0	0	4	5
Hedgerow-8	0	0	0	4	2	4	5
Hedgerow-9	0	0	0	0	0	4	5
Hedgerow-10	0	0	0	0	0	4	5
Hedgerow-11	0	0	3	4	2	4	5
Hedgerow-12	0	0	3	0	2	4	5
Hedgerow-13	0	0	0	0	0	4	0
Hedgerow-14	0	0	0	0	2	4	5
Hedgerow-15	0	0	3	0	2	4	5
Hedgerow-16	0	0	0	0	0	4	5
Hedgerow-17	0	0	3	0	2	4	5
Hedgerow-18	0	0	0	0	0	0	5
Hedgerow-19	0	0	3	0	2	4	5
Hedgerow-20	0	0	0	0	0	4	5
Hedgerow-21	0	0	0	0	2	4	5

Table S2: The number of sampling rounds conducted at each hedgerow site in each year of the study.

Only Hedgerows	Both Hedgerows & Controls	Only Controls
Andrena angustitarsata	Agapostemon texanus	Andrena nigrocaerulea
Andrena subaustralis	Andrena auricoma	Andrena subchalybea
Andrena w-scripta	Andrena candida	Ceratina timberlakei
Anthidium manicatum	Andrena cerasifolii	Colletes hyalinus
Ashmeadiella cactorum basalis	Andrena chlorogaster	Diadasia consociata
Bombus vandykei	Andrena cressonii infasciata	Diadasia diminuta
Calliopsis hesperia equina	Andrena knuthiana	Diadasia ochracea
Calliopsis scitula	Andrena piperi	Eucera actuosa
Coelioxys apacheiorum	Andrena scurra	Eucera frater albopilosa
Coelioxys gilensis	Anthidiellum notatum robertsoni	Hylaeus leptocephalus
Coelioxys novomexicana	Anthophora urbana	Lasioglossum (Evylaeus) diatretum
Dianthidium ulkei	Ashmeadiella aridula astragali	Lasioglossum mellipes
Heriades occidentalis	Ashmeadiella bucconis denticulata	Megachile brevis
Hylaeus calvus	Bombus californicus	Nomada sp. A
Hylaeus episcopalis	Bombus crotchii	Osmia nemoris
Lasioglossum (Evylaeus) granosum	Bombus melanopygus	
Lasioglossum (Evylaeus) nigrescens	Bombus vosnesenskii	
Megachile coquilletti	Ceratina acantha	
Megachile occidentalis	Ceratina arizonensis	
Melissodes communis alopex	Ceratina dallatorreana	
Osmia aglaia	Ceratina nanula	
Osmia coloradensis	Coelioxys octodentata	
Osmia granulosa	Diadasia enavata	
Osmia laeta	Halictus ligatus	
Osmia texana	Halictus tripartitus	
Peponapis pruinosa	Hoplitis producta gracilis	
Stelis laticincta	Hylaeus bisinuatus	
Stelis montana	Hylaeus conspicuus	
Triepeolus sp. A	Hylaeus mesillae	

Xeromelecta californica	Hylaeus rudbeckiae	
Xylocopa tabaniformis orpifex	Lasioglossum (Dialictus) brunneiiventre	
Xylocopa varipuncta	Lasioglossum (Dialictus) diversopunctatum	
	Lasioglossum (Dialictus) impavidum	
	Lasioglossum (Dialictus) incompletum	
	Lasioglossum (Dialictus) megastictum	
	Lasioglossum (Dialictus) punctatoventre	
	Lasioglossum (Dialictus) tegulare group	
	Lasioglossum (Evylaeus) kincaidii	
	Lasioglossum sisymbrii	
	Lasioglossum titusi	
	Megachile angelarum	
	Megachile apicalis	
	Megachile fidelis	
	Megachile frugalis	
	Megachile gentilis	
	Megachile lippiae	
	Megachile montivaga	
	Megachile onobrychidis	
	Megachile parallela	
	Megachile rotundata	
	Melissodes agilis	
	Melissodes lupina	
	Melissodes robustior	
	Melissodes stearnsi	
	Melissodes tepida timberlakei	
	Nomada sp. 3	
	Osmia atrocyanea	
	Osmia gaudiosa	

	Osmia lignaria propinqua	
	Osmia regulina	
	Sphecodes sp. B	
	Svastra obliqua expurgata	
	Triepeolus concavus	
	Triepeolus heterurus	
	Triepeolus melanarius	
	Triepeolus subnitens	
	Triepeolus timberlakei	

Table S3: Bee species found at hedgerows and controls.

Year	F-statistic	p-value
2009	$1.44_{2,18}$	0.18
2010	$0.18_{1,4}$	1.00
2011	$0.99_{2,17}$	0.48
2012	$1.71_{2,35}$	0.17
2013	$1.08_{2,37}$	0.40

Table S4: The test statistics for the permutation anovas comparing pollinator community composition between mature hedgerows, maturing hedgerows and unrestored controls within each year. The community composition did not vary significantly between site statuses in any year.
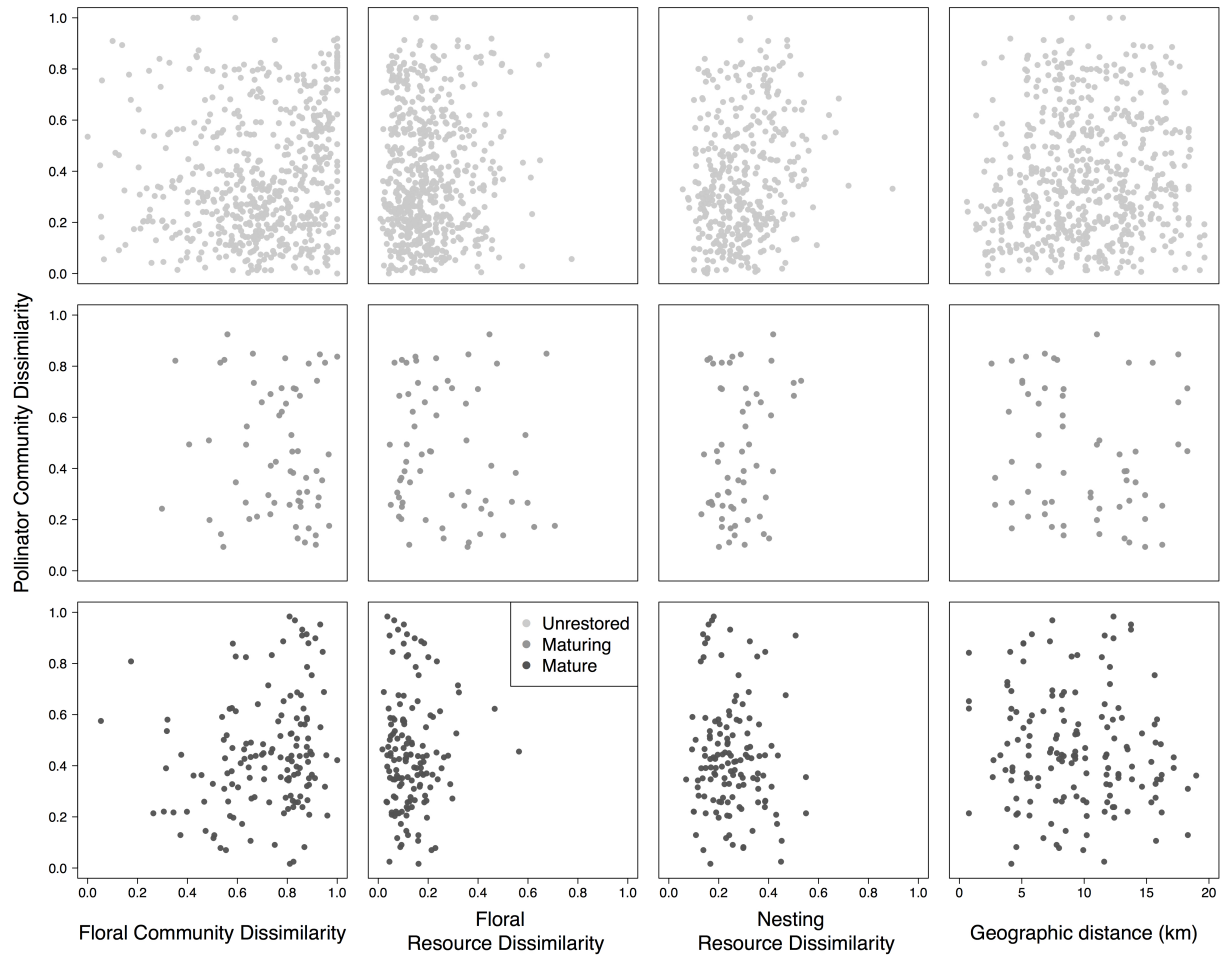
Figure S1: The dissimilarity of pollinator communities as a function of the dissimilarity of the floral communities, floral resources, nesting resources, and geographic distance at each site type across all years of the study. Pollinator community dissimilarity is not correlated with any of the variables investigated.
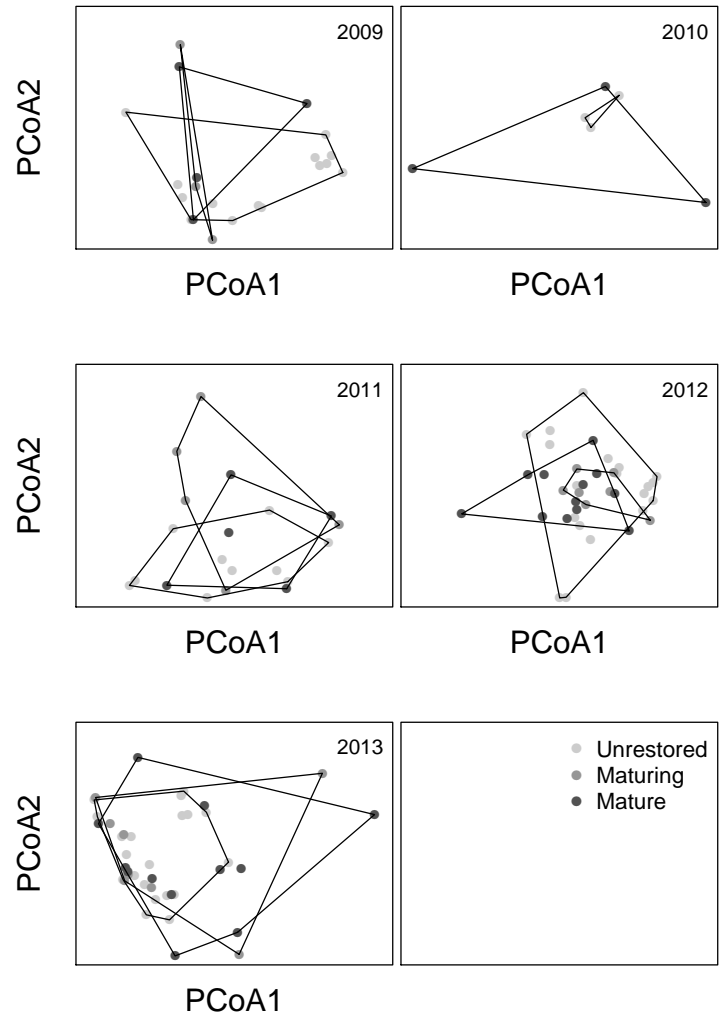
Figure S2: The dissimilarity of communities in multivariate space using a principal co-ordinate analysis. The axis represent the first two principal coordinate axes. There is substantial overlap in the community composition of the different site types.
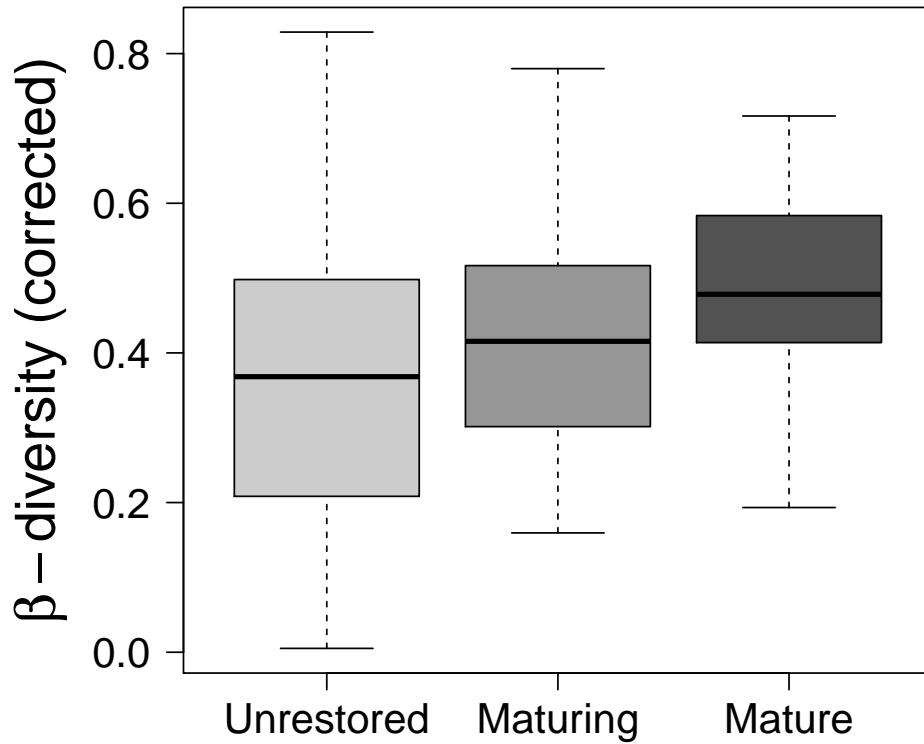
Figure S3: The β-diversity (corrected using random communities that have the same number of individual as observed communities) at unrestored controls, maturing hedgerows and mature hedgerows. Corrected β-diversity is significantly higher in mature hedgerows than in unrestored controls (estimate $\pm$ standard error, 0.130 ± 0.044, p-value= 0.005). Boxplots represent medians (black horizontal line) first and third quartiles (box perimeter) and extremes (whiskers).
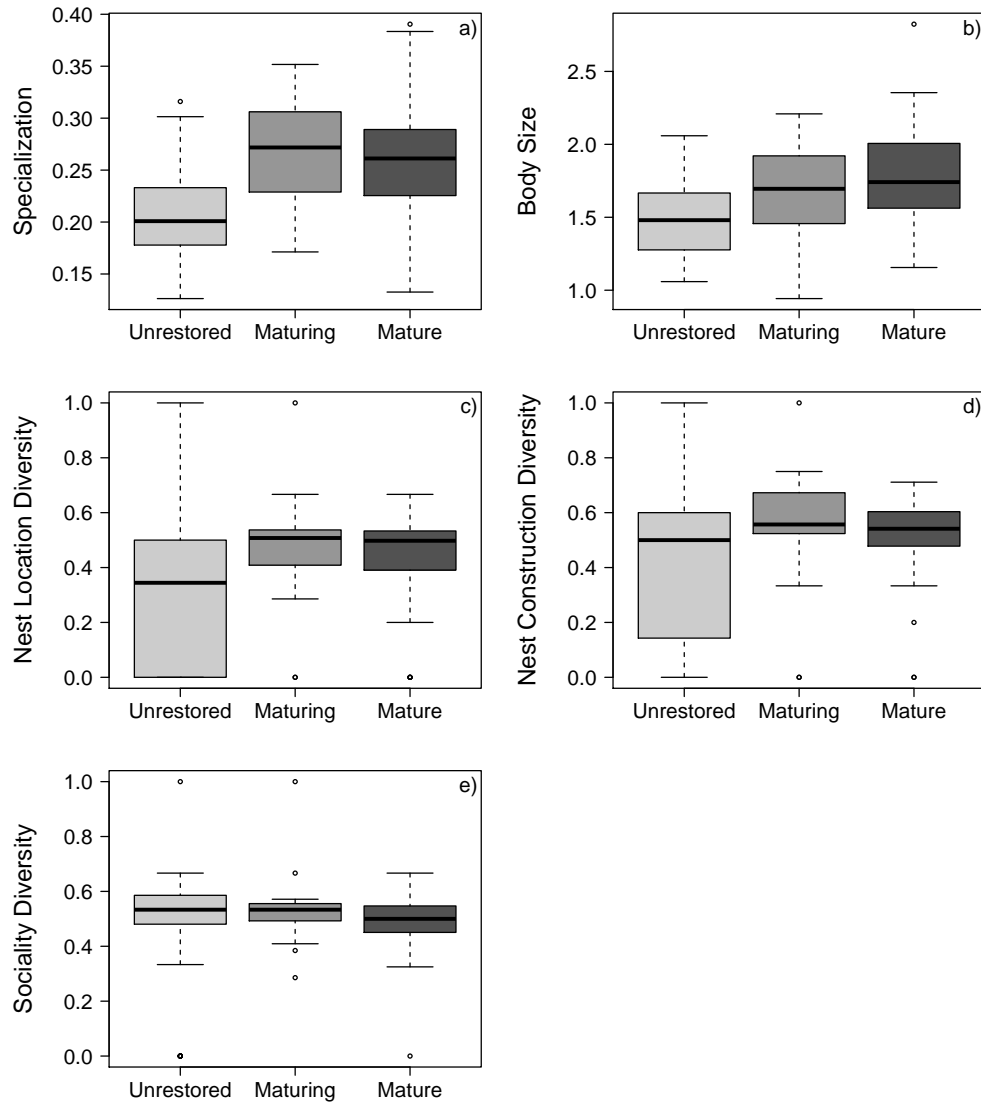
Figure S4: The mean trait value (a-b) and trait diversity (c-e) of pollinator communities at different site types. Mature and maturing hedgerows supported significantly higher trait values and diversity for all of the trait groups investigated expect sociality diversity.
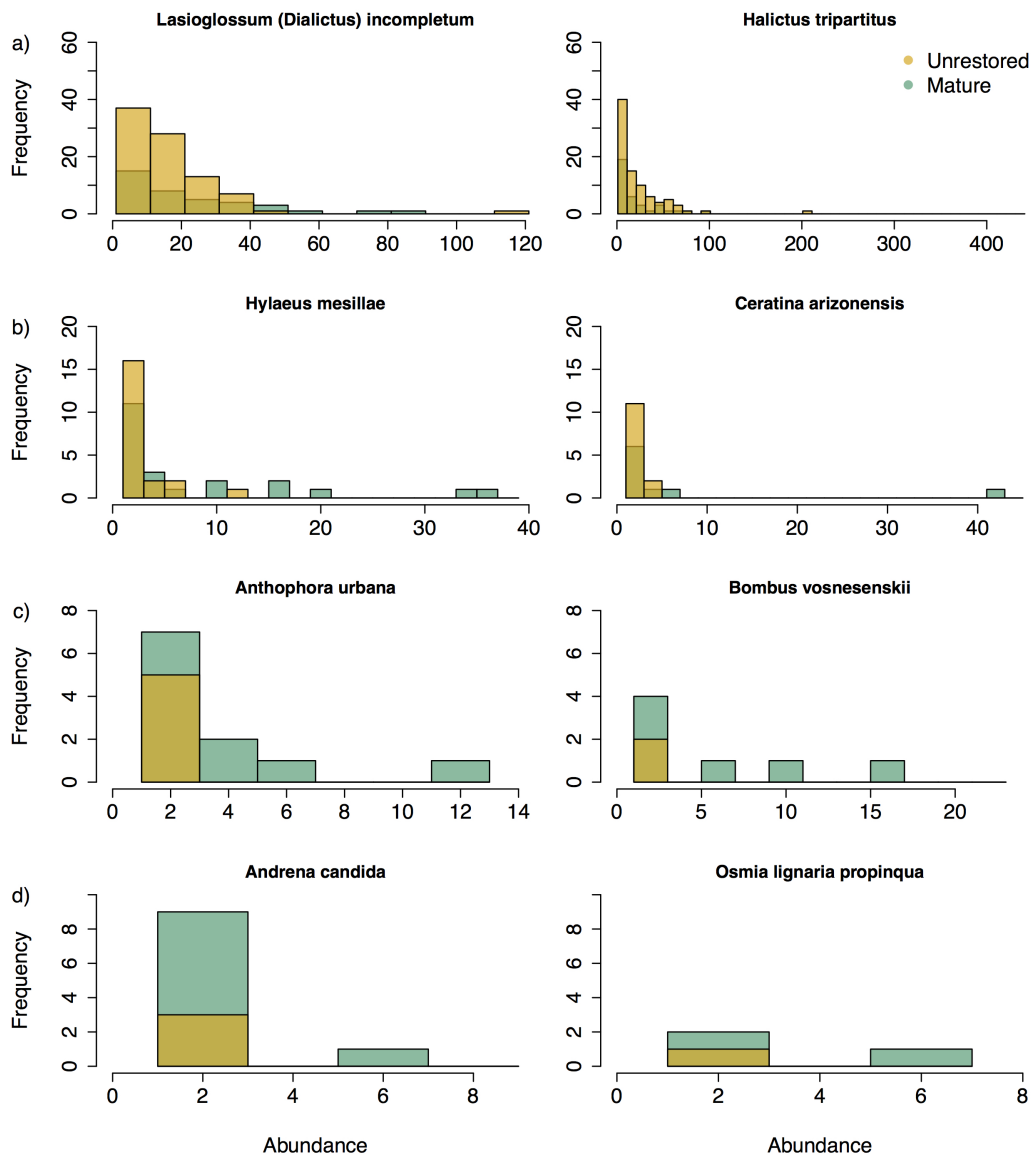
Figure S5: The frequency of observing specific abundances at a site across years of a sample of species found in both hedgerows and controls. The top panel, (a), are the two most abundant species (total abundance > 100 individuals), panel (b) are relatively common species (abundance between $20 - 50$ individuals), panel (c) are relatively infrequent (abundance between $10 - 20$ individuals), and panel (d) are very infrequent (< 10 individuals).