

Materials and Methods.

Part 1. Details of the study site

The study site was Norwood Farm, Somerset, UK (51.3128° N 2.3206° W). The farm was 125ha in size and we defined 10 ‘habitats’ for sampling purposes (table S1). Habitats were defined by their current vegetation characteristics and thus we treated different parts of the arable crop rotation as distinct from each other (e.g. cereal, ley and lucerne). Norwood Farm is a mixed-use farm, with approximately 50% of the cropped land being arable and 50% grass pasture or ley; livestock was mostly cattle and sheep. It has been managed organically since 1990 and had been part of the ‘Countryside Stewardship’ agri-environment scheme since 2003 and part of the Organic Entry Level Stewardship agri-environment scheme in 2005 (both administered by Defra for the UK Government). These schemes provided payment for specific environmental options such as sympathetic hedgerow management, protection of in-field trees, 1.5km of 6m field margin, one field of recreated species-rich meadow and several fields of sympathetically-managed grazed pasture and subsidy for the organic status of the farm. Additional field margins and relatively low-intensity arable farming were established through the farmer’s own volition. The length of mature and new hedges was 11.0 and 1.4 km, respectively. The average hedge size, weighted by hedge length, was 4.1 m high and 3.6 m wide for mature hedges and 1.9 m high and 1.3 m wide for new hedges (31). For each of the two years, habitats were mapped on a geographic information system (GIS) and their areas calculated; these changed between the two years due to changes in farm management (31) (table S1). In all cases, estimates of species abundance and interaction frequency were scaled-up by habitat area to provide quantitative networks for the whole farm.

Part 2. Constructing the interaction networks

The overriding aim of our approach was to express all the species and interactions on the farm field site in the same units, that of abundance on the farm. Field sampling occurred in each of 10 habitats on the farm. The sampling time for each network is shown in fig. S1.

Obtaining these estimates involved a range of different sampling approaches in the field. It also involved the aggregation of the data collected over multiple habitats and multiple sampling periods. Estimates were summed across habitats and either summed across sampling periods (for insects, and in so doing we assumed the lifespan of an individual was less than the monthly sampling period) or averaged across sampling periods (for vertebrates and plants, and in so doing we assumed individuals had a continual presence on the farm for the duration of the study). The construction of each of the networks, which are illustrated in Fig. 1 in the main text, is described below.

The interaction networks were constructed for Norwood Farm during 2007 and 2008 with field data of interaction strengths or, in the case of butterflies, birds and rodents, from field surveys of their abundance and novel approaches which we developed to estimate interaction strengths from the literature (see details below).

Quantifying vegetation

Vegetation was quantified at the whole farm extent as species-specific leaf area. This approach is fully described elsewhere (31), but for completeness is briefly described below. Leaf area was quantified differently for herbaceous and woody vegetation. Herbaceous vegetation was surveyed concurrently with the transects for leaf-miners and aphids. It was surveyed along a total of 327 transects (each 9×1m) in randomly chosen locations in each of the habitats (3-4 transects per habitat per month) and the ground cover and height of each species was quantified. At about the same time as the surveys the leaf area index of the vegetation in the transect (leaf area per unit area of ground) was recorded with an LI-COR LAI-2000 Plant Canopy Analyzer meter (LI-COR Biosciences, Lincoln, Nebraska) (32) and multiplied by the ground area of the transect. The total leaf area of the transect was then apportioned between the plants present in the transect and scaled-up to the total area of each habitat. Leaf area index of hedgerows and sub-storey vegetation in woodland was recorded with an LAI-2000 meter, multiplied by the area of ground and apportioned between the plants present, based on field surveys. All standing trees were identified and surveyed to record the height and radius of the canopy. Leaf area was calculated from previously quantified relationships with canopy height and radius (33). The species composition of the woodland canopy was determined by field surveys each 10 m interval in the woods. Literature-derived estimates of leaf area index (34) were multiplied by the area of woodland and apportioned by species, based on field surveys of the woodland composition. The value of leaf area used in the calculation of relative importance of each plant taxon was the maximum of the monthly estimates for the months of June, July and August 2007.

Quantifying floral units

Flowers were surveyed at the same time and along the same transects as the surveys for flower visitors. They were surveyed along a total of 361 transects in randomly chosen locations in each of the habitats (3-4 transects per habitat per month). Transects were 25×1m in 2007 and 50×1m in 2008 (the greater length of these transects in 2008 was due to the relatively low numbers of captures of insects in 2007, but the resulting density of captures was similar between years). Flowers were counted as 'floral units' (35). Heuristically, floral units are entities that flower-visiting insects will fly between, rather than walk between.

Quantifying seeds

This approach is fully described elsewhere (36), but for completeness is briefly described below. We quantified soil-surface seeds from soil suction samples (37) (obtained with a hand-held, Stihl BG 85 blower-vacuum; Stihl Incorporated, Virginia), following published methodology (38). We collected approximately 250 suction samples at the end of August and mid November 2007. We used GIS to obtain sampling points that were separated by >20m and randomly located within each of the different habitats and took an increasing number of samples in habitats with increasingly large area. At each sampling point, we placed the suction-sampling tube directly onto the soil in three adjacent locations for approximately 7 s intervals each, giving a total suction sample area of 306cm² over 20 s. All sampling was undertaken on dry days between 10:00h and 16:00h. Samples were dried in a 45 °C oven for 48 hours and weighed to obtain total dry mass. Graded test sieves were used to separate seeds from the soil and other matter, and species were identified by specialists (see acknowledgements). Only intact seeds were used in the analysis. Large samples were sub-sampled where necessary and multiplied up prior to analysis.

Network 1: Flower–flower visitor network

Flower visitors were surveyed along a total of 361 transects using established techniques (39). Transects were run in randomly chosen locations in each of the habitats (3-4 transects per habitat per month). Transects were 25×1m in 2007 and 50×1m in 2008 (the greater length in 2008 was due to the relatively low numbers of captures of insects in 2007, but the resulting density of captures was similar between years). We scaled up insect density by habitat area in order to give an estimate for the whole farm. These differences in transect length did not affect the abundances of insects in the network.

Transects were carried out during relatively warm, still and dry days during Mar-Sep 2007 and during May-Aug 2008. Transects were walked at a slow walking pace and flower visitors were captured with a sweep net, their host plant was recorded and each insect was retained for later identification. Estimates from transects were scaled up to provide a total per habitat, summed across habitats (to give farm-scale monthly totals), summed across months and averaged across the two years to give the final network.

Network 2: Flower–butterfly network

Butterflies were rarely seen visiting flowers on the pollinator transects but given their potential importance as bioindicators (9), we undertook twice-monthly butterfly transects (modified from (40)) around the farm during 2007 on sunny and relatively calm days. Total transect length was 7138 m and butterflies were counted 2 m either side of the transect line and up to 3 m in front of the observer. The transect covered 2% of the total area of the farm. Counts of each species of butterfly were assigned to habitats and then scaled up to provide an estimate of total abundance for the farm.

Nectar sources for each species of butterfly were obtained from our pollinator transects and from (41). For each habitat in each month, butterflies were assigned to nectar plants that they are recorded to visit, in proportion to the abundance of the flowers of each plant species. The interaction totals were summed across months and habitats to give the final network.

Network 3: Plant–Leaf-miner parasitoid network

Sampling for leaf miners in herbaceous and hedgerow vegetation was undertaken in 230 transects (each 9×1 m) according to standard methodology during 2007 (42). Transects were run in randomly chosen locations in each habitat (3-4 transects per habitat per month). Leaf

area was estimated for each plant species as described above. A thorough search of the vegetation in each transect was undertaken and leaves with leaf miners were returned to the laboratory for rearing parasitoids using established methods (43). Estimates from transects were scaled up to the estimated total per habitat, summed across habitats (to give farm-scale monthly totals) and summed across months. Additionally, in order to sample leaf miner parasitoids from trees, we undertook an approach similar to (44). In total, 157 branches, each with c. 200 leaves, were sampled from randomly selected standing trees in hedgerows (*Quercus robur* and *Fraxinus excelsior*) and trees in woodland (*Quercus robur*, *Fraxinus excelsior*, *Acer campestre* and *Ulmus* sp.). We calculated total leaf area by multiplying average leaf size by leaf count, and estimates of parasitoid numbers were scaled up to the leaf area of each species of tree and summed across months. The network of interactions from the vegetation transects and the tree samples were summed to give the total network.

Due to time constraints in 2007, it was not possible to identify the parasitoid host (e.g. based on leaf mine morphology (45)), before rearing parasitoids, so miners from different host plants were combined, as done when constructing some seed-feeding insect networks, e.g. (46, 47). Additional sampling in June 2008 confirmed that parasitoids were generalist on leaf-mining insects on each species of plant, but that leaf-miners were specialised on a plant taxon. We therefore assumed that our observed network of interactions between plants and leaf-miner parasitoids approximated the true network of interactions between leaf-miner hosts and their parasitoids.

Network 4: Plant–aphid–parasitoid network

Sampling for aphids and parasitized aphids was undertaken in 9x1m transects according to standard methodology (48). Logistically, we were unable to effectively sample for both aphids and leaf-miners simultaneously so we sampled aphids and their parasitoids in 2008. We sampled aphids and their parasitoids in 94 transects in randomly chosen locations in each habitat (3 or 4 transects per habitat per month). Along each transect, whenever an aphid colony was encountered the number of aphids was estimated and specimens from each colony were collected for later identification. All parasitized aphids (aphid ‘mummies’) were collected for rearing in the laboratory according to a standard protocol (48). Secondary parasitoids (which in our case were almost all pupal parasitoids) were assigned directly to the host aphid, in common with previous studies, because they are highly generalised (17). Numbers of aphids and their parasitoids were multiplied up to the area of each habitat, summed across habitat and summed across months to give the total network.

Network 5: Seed–Seed-feeding invertebrate–parasitoid network

This approach is fully described elsewhere (36), but for completeness is briefly described below. We collected seed heads from Carduoideae (a subfamily of Asteraceae), Fabaceae and hedgerow berries (*Rubus fruticosus*, *Prunus spinosa* and *Crataegus monogyna*) during transects for leaf-miners. We considered only these hosts based on pilot data on the hosts of seed-feeding invertebrates in British farmland habitats. For each species, up to 50 berries or seed-heads were collected from each transect from August – December 2007. Seeds and berries were placed in plastic pots and checked weekly for emergence of seed-feeding insects and parasitoids until 30 April 2008. A range of insects emerged, including primary seed-feeders, fungi-feeders, predators and parasitoids. From the literature, we determined which species were seed-feeders and which were likely to be parasitoids of the seed feeders. We defined parasitoids as generalist on all hosts or specialised on either Coleoptera or Diptera and assigned them to host species proportionally to the abundance of hosts reared (see ref.

(46)). Interactions were summed across sampling periods and densities were multiplied by habitat area and summed across habitats to give the final network.

Vertebrate seed-feeders

We constructed vertebrate seed-feeder food webs from information on the recorded abundance of the animals in late summer (August) and autumn (November) 2007, their known diet (from the literature) and the abundance of soil-surface seeds on the farm (36). We selected to restrict our analysis in this study to late summer and autumn because these were the peak seasons for seed abundance and diversity. We constructed these differently for the rodents and the birds, as described below.

Network 6: Seed–seed-feeding rodent–ectoparasite network

For granivorous mammals we considered all rodents, except *Microtus agrestis* (because less than 10% of its food consists of seeds (49)) and *Mus musculus* and *Rattus norvegicus* (because both were almost entirely commensal and rarely recorded in our outdoor habitats). We obtained high-quality information on the habitat-specific abundances per species of rodent from spatially-explicit capture-recapture models of data from live-trapping (Pocock, unpubl. data) and used this in combination with habitat-specific estimates of seed abundance (described above). For each habitat and each rodent species, we considered all the species of seed which it is known to feed upon ((50) and refs therein) and apportioned the estimated abundance of seeds according to frequency-dependant foraging, taking account of the profitability of each species of seed (see below). To produce an overall food web, we summed across habitats and averaged across August and November, when seed abundance was highest.

We assumed that animals fed upon seeds according to a modified form of frequency dependent predation: $p_i = \theta_i \cdot a_i / \sum (\theta \cdot a)$, where a is the abundance of each species of seed and θ is the value of the seed independently of its availability (51), e.g. the seed preference (52), which we consider as $\theta = (\text{energy per seed}) / (\text{handling time per seed})$. Handling time per seed has not been empirically determined for rodents, but typically scales with seed size (53). We obtained handling times for two species of rodent (54, 55). Handling time was best modelled as a function of $\sqrt{(\text{seed mass})}$, including species as a fixed factor ($R^2_{\text{adj}}=0.61$; while for the models with untransformed seed mass and $\exp(\text{seed mass})$, $R^2_{\text{adj}}=0.46$ and 0.45 , respectively). Although we know that seed make up only one-third of the diet of bank voles during the winter (56), we assumed that each mammal species that we considered was dependant on seeds in their diet.

In addition, we sampled the ectoparasites on mammals that had been caught by brushing through their fur at first capture (57) and sampled ticks by a thorough search of the individual. From this we estimated the average number of each species of ectoparasite per individual, multiplied by the abundance of each species of rodent in each habitat and summed across habitats to give the final network.

Network 7: Seed–seed-feeding bird network

We considered the granivorous birds listed by ref. (58), plus *Corvus monedula* (jackdaw) and *Corvus corax* (rook), the latter two because the majority of their winter diet was seeds (59), but excluded *Phasianus colchicus* (pheasant; an abundant species on Norwood Farm, but one that primarily derived from captive stock released on a neighbouring farm) and *Pyrhula pyrrhula* (bullfinch; a scarce species on the farm that rarely forages on the ground, which is where our estimates of seed abundance were obtained). We obtained estimates of their

abundance across the whole farm based on field surveys in August and November 2007 using field perimeter counts followed by a transect through the field (modified from ref. (60)).

For birds we obtained information on the seeds that they eat from two sources: quantitative information on the families of seeds consumed from refs (58) and (59), and qualitative information on seeds known to be consumed (61). For the two species lacking fully quantified information on their diet, we assumed that *Emberiza citronella* (yellowhammer) ate cereals as recorded (58), but otherwise had the same diet as *Emberiza cirrus* (cirl bunting) and that *Streptopelia decaocto* (collared dove) had the same diet as *Columba palumbus* (wood pigeon; although see note on habitats below).

For plant species in families recorded by (58) as seed food sources for each species of bird, we estimated the total energy of seeds of each species recorded in suction samples. For plants in the families recorded as being present in the diet, but not quantified, we allocated them 0.5% of the total diet (a negligible amount). We apportioned plant species in each family according to their proportions recorded in each bird species' diet. After this, we apportioned species within each family according to their total energy content, as estimated from seed suction samples (see above). We apportioned seeds based on their total energy of seeds rather than any measure based on seed preference (energy per seed/handling time per seed) and frequency-dependant foraging (see mammals above) because of the unpredictable family-level differences in the handling times of seeds of different sizes (53).

Birds move widely over the landscape, and the habitats in which they were mostly observed (e.g. hedgerows) were often not the habitats in which they were feeding, so we applied our methods above to whole farm estimates of bird and seed abundance, with the exception of woodland and the 'rough ground' in the farmyard, which we treated separately. We summed across these habitats and then averaged across the data from August and November to give the final network.

Part 3. Robustness and its correlation

Considering our two models of robustness, R_S and R_Q : R_S is analogous to assessing effects on species richness, while R_Q is more analogous to assessing effects on species diversity; the quantitative information potentially making it more robust to sampling biases (62). These models assume that with the loss of a food source or host, animals are able to entirely switch to alternate hosts. These models also assume that we observed the entire possible host range. We accept that these are simplified models (63), and do not take account of features such as adaptive rewiring (21, 64) or correlation of apparent niche breadth with rarity (23). These models could be made more complex in an effort to make them more ‘realistic’ but the assumptions in the models become less clear. We chose relatively simple models with clear assumptions on the basis that models with “easily assailable but clearly articulated assumptions ought always to be preferable” (65) to more complex models. We therefore interpret ‘robustness’ as a relative index of vulnerability, rather than an assessment of true extinction rates.

We determined whether the varying robustnesses of the guilds were correlated to each other by calculating the pairwise Pearson’s regression coefficient (r) of robustness across the 20,000 scenarios of simulated plant loss. The implications of this are important and result in specific, testable hypotheses. If guilds positively covary ($r \rightarrow 1$), this suggests that sequences of plant taxon loss that are relatively benign for one animal group (i.e. the network has high robustness relative to other sequences of plant taxon loss) will be relatively benign to others. If the guilds are unrelated ($r \approx 0$) then sequences of plant taxon loss that are relatively benign for one animal group (i.e. having high robustness relative to other sequences of plant taxon loss) have no predictable association with how benign it is to other animal groups. The results are shown in Fig. 3E and F and Table S5.

These pairwise correlations are valuable but we also wanted an assessment of the overall correlations, so we used a network approach. Considering the network of correlations between the animal groups, we determined the connectivity of the whole network as the algebraic connectivity of the absolute correlation coefficients. Algebraic connectivity was defined as the second smallest eigenvalue (λ_2) of the graph Laplacian $L=D-A$, where A = the absolute correlation matrix between the $i=j$ guilds and where $A_{i=j}=0$ and D is the weighted degree matrix, where $D_{i,i}=\sum(j) A(i,j)$ and $D_{i \neq j}=0$ (66).

We compared the observed algebraic connectivity, λ_2 , of the pairwise correlations of sub-network robustness to 999 null models in which the correlations between the animal groups were randomised between the pairs of networks. If the observed algebraic connectivity was less than the null expectation, then this suggests that the overall network of correlations (and note that this ‘network of correlations’ is that shown in Fig. 3, and not the species’ interaction network shown in Fig. 1) is less well connected than would be expected by chance. This suggests an assortative or modular network (66) and so the positive effects of plant management or restoration for one taxon will not inevitably have benefits that ‘ripple’ through the network of networks to other groups. If the observed connectivity was greater than the null expectation then this would suggest that animal groups would respond more similarly to each other regarding their responses to the management of plants.

We found that for R_S : $\lambda_2 = 0.558$ and for R_Q : $\lambda_2 = 0.475$, and that this was significantly less than the null expectations (R_S : mean null $\lambda_2 = 1.030$; 95 percentiles: 0.731, 1.254; $P = 0.002$ with a two-tailed test; R_Q : mean null $\lambda_2 = 0.671$; 95 percentiles: 0.500, 0.802; $P = 0.008$). From Fig. 3E, it appears that the seed-feeding birds, seed-feeding rodents and rodent

ectoparasites networks are particularly distinct from invertebrate groups when considering R_S , while when considering R_Q there are relatively low pairwise correlations between most animal groups. When considering only the field-derived networks, the algebraic connectivity was no different to that under the null expectation (SOM Part 5) but, importantly, it was not more connected than would be expected under a random expectation.

The null model described above is the one we discussed in the main text, but an alternative null expectation could be where the robustness values from the simulations were randomised within the simulations (i.e. retaining the guild-level information on the spread of R , but removing the relationships in R between guilds). We consider it not surprising that our observed networks of correlations between animal groups had higher algebraic connectivity than expected (R_S : mean null $\lambda_2 = 0.035$; 95 percentiles: 0.024, 0.047; R_Q : mean null $\lambda_2 = 0.035$; 95 percentiles: 0.024, 0.047; $P > 0.999$ for both) because under this null expectation all pairwise correlations between the animal groups were close to zero. Considering this null expectation, however, an alternative perspective on this network of correlations would be that it is more connected than expected by chance, but we consider that this approach is not particularly informative when seeking to understand the relationships between animal groups based on correlations between their robustness to simulated extinctions of plant taxa.

Part 4. Relative importance of plants

Calculating relative importance

We calculated the importance of each species of plants, while taking account of abundance, based on the weighted sums of the contributions of each plant to the robustness of each guild of animals. This was done in a step-wise fashion as illustrated in Fig. 3 of the main paper and described in detail here.

1. The importance of each plant to the robustness of each animal group. This was assessed for each plant taxon j from the correlation (r_{ij}) of robustness of each animal group i (R_S, R_Q) with the order of the plant in the 20 000 extinction sequences. Our rationale is that the ‘importance’ of a plant cannot be directly assessed from the number of secondary extinctions caused by its loss (because if lost at the start of the sequence few secondary extinctions will result), but if a plant is ‘important’ then overall robustness will be lower if it was lost early in the sequence than if it was lost later. Correlation coefficients are not additive, so we used the square of the correlation coefficient (i.e. the coefficient of determination, $(r_{ij})^2$) to calculate the absolute importance of each plant.

2. The absolute importance of each plant. The absolute importance of each plant taxon j was calculated as the sum of the coefficients of determination for each animal group. These sums could be weighted, either due to *a priori* consideration of the importance of the groups (e.g. according to the value of their ecosystem service provision) or to take account of the uniqueness of the groups. We used uniqueness (i.e. functional uniqueness (67)) in this analysis because we considered some groups that could have been functionally similar (e.g. butterflies and other flower-visitors, or primary and secondary aphid parasitoids) and treating each group independently could have resulted in biasing the importance of plant taxa towards the groups that were most similar to each other. Specifically, we calculated the Euclidian distance between the absolute importance values for the plants across each pair of animal groups (d_{ij}). The uniqueness of each animal group i , with respect to the importance of plants to the taxa in that animal group was calculated as the sum of the differences for each group j , d_{ij} (according to the detail in (67)). We found that there was relatively little variation in the uniqueness of each animal group (table S3), although when combining other types of network this might be an important consideration.

3. The relative importance of each plant taking abundance into account. We \log_{10} -transformed the abundance and importance of plant taxa to approximate to normality. Plotting these data showed a clear distinction between plant taxa where importance increased with abundance and plant taxa that had low importance, irrespective of their abundance. We used a two-component mixture regression model to distinguish these two relationships (fitted with the package ‘mixtools’ (68) in R 2.12.2 (69)). We then considered the relative importance (RI) to be the residual of the point from the regression line (i.e. the line with the steepest slope).

We found that a few very scarce plants (estimated leaf area was $<100\text{m}^2$) showed particularly high relative importance. We cannot be confident that this was not an artefact, so we excluded these from further consideration (they are shown in Fig. 4G but not in Fig. 4A). We used leaf area as a measure of abundance because it was relevant and estimated for every species of plant taxon on the farm independently from the food web analysis (31), whereas seed abundance or floral unit (sensu ref. (35)) abundance was not available for all species. Full results are given in Table S6.

Relative importance of plants and their relationship to plant traits

We found a high level of agreement between the relative importance values derived from R_S and R_Q (intra-class correlation between the two measures = 0.744), however for particular species the rankings varied. The relative importance of plant taxa in this study is, for completeness, presented in table S6. Observation of the relative importance of plant taxa according to plant traits (Fig S3) shows that plant taxa with high relative importance tended to be found in hedgerow bases and field margins, were members of the Apiaceae and Asteraceae and were non-woody perennials, although these patterns are clearer with RI calculated with R_S than with R_Q .

Considering different weightings of animal groups

We considered weighting the animal groups according to their functional uniqueness based on the importance of plant taxa, as explained above. There are innumerable different ways of weighting the animal groups but we considered four additional ways as examples to illustrate how importance of plant taxa changes according to the weighting. We considered: (i) weighting all animal groups equally, (ii) excluding the literature-derived networks, (iii) considering only flower visitors, aphid parasitoids and leaf-miner parasitoids because all could be regarded as ‘ecosystem service providers’ and (iv) considering only flower-visitors, butterflies and seed-feeding birds because all of these could be regarded as ‘bioindicators’. We emphasise that these are all simply illustrations and that, depending on the questions, arguments could be made and evidence presented for weighting the animal groups differently. We found that, although some individual plant taxa changed substantially in their relative importance, the overall pattern was similar to weighting all groups by their functional uniqueness (Fig. S5). Therefore, with some specific exceptions, plants found to be disproportionately important (considering their abundance) were important no matter how the animal groups were weighted.

Part 5. Robustness of our conclusions to our assumptions

Part 5.1. Considering the exclusion of literature-derived networks

The construction of some of our networks required including information from the literature. These networks represented an approximation of the taxon's realized niche, and so would be expected to be more generalized than the networks derived from observations. We therefore repeated our analyses in order to assess whether our general results were robust to the exclusion of literature-derived networks; specifically assessing the relationship of robustness with network metrics, the correlated robustness, and plant importance. We therefore considered six of the 11 bipartite networks that relied solely on information obtained from the field (these were the networks comprising: flower-visitors, plant-aphids, aphid-primary parasitoids, aphid-secondary parasitoids and invertebrate seed-feeders). We excluded the bird and rodent seed-feeder, butterfly-flower visitor and seed-feeding insect parasitoid networks because they included information from the literature in their construction. The rodent-ectoparasite network was entirely estimated from field-derived data, but was linked to the plants through the rodent seed-feeder network and so was also excluded.

Our reported estimates of the relationship between robustness and H_2' and e^{H_2} , calculated with package 'bipartite' (70) in R 2.12.2 (64), were robust to the exclusion of networks with literature-derived interactions, as well as being robust to the type of network metric (whether they were derived from binary or quantitative networks) and to the simultaneous inclusion of both (table S4). Overall, there was no relationship of robustness with interaction diversity (e^{H_2}). There was a negative relationship of robustness with niche differentiation (H_2'); this relationship with R_S when excluding literature-derived networks was not significant, but the regression slope was so similar across all analyses (table S4) that we have confidence that this is a genuine relationship.

Considering the algebraic connectivity of the correlations between the robustness of animal to the simulated extinction of plants, we found that the algebraic connectivity of the 'network' of correlations was higher when excluding than when including the literature-derived networks (R_S : observed $\lambda_2 = 1.017$; R_Q : observed $\lambda_2 = 0.605$). When including the literature-derived networks we found that algebraic connectivity was lower than the null expectation. This was not the case when excluding the literature-derived networks: the algebraic connectivity was not significantly different to the null expectation (R_S : mean null $\lambda_2 = 1.042$; 95 percentiles: 0.772, 1.264; $P = 0.406$; R_Q : mean null $\lambda_2 = 0.589$; 95 percentiles: 0.472, 0.681; $P = 0.597$). This was higher because some of the animal groups that were excluded tended to have weak correlations with other groups (Fig. 3). Importantly, though, the 'networks' of correlations were not more connected than would be expected under a random expectation.

Considering the importance of plant taxa within the network, the exclusion of literature-derived networks had little overall effect on the relative importance of plants, although a few specific taxa with moderate relative importance exhibited substantial decreases in relative importance (with relative importance based on R_S : Fig. S4B).

Part 5.2. Considering variations in sampling efficiency in the field-based networks

We would expect that, due to the nature of field-based work, there would be variation in the sampling efficiency of the networks that were constructed from field-based observations. We

assessed whether this was the case from the estimated proportion of the total species (and interactions) that were observed. We followed the protocol of (71) and used the Chao 2 (72) estimator to estimate the proportion of the total species (in the higher trophic level) and interactions that were observed. We found that, depending on the animal group, between 52 and 99% of species and between 30 and 92% of interactions were estimated to have been observed (table S3). We note, however, that the Chao 2 estimator may suffer biases when applied to flower-visitor networks (discussed in (71)) and biases could be further compounded when considering different types of network, as we have here.

Given that there appear to be differences in sampling efficiency, we were faced with how to take these differences into account when assessing the robustness of our results to this variation. We used rarefaction to sample reduce our networks to the same degree of sampling efficiency, which was the estimated sampling efficiency of the flower-visitor network. We selected this network because it was speciose and was based on many samples from the field but, based on the estimates of sampling efficiency, it was the most poorly sampled network. (The aphid-secondary aphid parasitoid network was estimated to have a smaller proportion of the total interactions observed, but it was based on relatively few samples.) We therefore adopted sample-based rarefaction (73) and, for each network, we removed samples one-by-one until the desired level of sampling efficiency for species or interactions (whichever came first) was reached (Table S7).

We then compared the results from the rarefaction to take account of variation in sampling efficiency with the results for the full dataset. We used intra-class correlation to compare the median values of robustness (logit-transformed because some values were close to one) and the relative importance of plants, and we compared the dissimilarity of the groups (where dissimilarity is the square-root of one minus the correlation) between the robustness of animal groups with a Mantel test (Table S7). We undertook this rarefaction 18 times and found that in all cases the results were similar to those reported for the full dataset. We therefore conclude that there was no evidence that variation in sampling efficiency affected our overall conclusions. We note that the effect of sampling on measures of network structure is a continuing area of research (62, 71 and references therein) and that this analysis is a contribution to its development. Given the complexity of our network in combining different types of network aggregated across habitats and over time, we are therefore cautious about the conclusions that we derived from these analyses.

These simulations were carried out using the computational facilities of the Advanced Computing Research Centre, University of Bristol – <http://www.bris.ac.uk/acrc/>.

Network	Resource	Consumer	Second trophic level	Interaction type	Source of quantitative data	Previous examples of species' interaction networks in the literature
1	Flower	Flower visitor	-	Mutualistic	Field sampling of interactions	(18, 21, 39, 74-76)
2	Flower	Butterfly	-	Mutualistic	Field sampling of abundances, literature for presence of interactions, assumed proportional foraging for quantifying interactions	None specific to butterflies
3	Leaf and shoot	Aphid	Primary and secondary parasitoid *	Trophic	Field sampling of interactions	(17, 48, 77)
4	Leaf	Leaf-miner †	Leaf-miner parasitoid	Trophic	Field sampling of interactions	(42, 43, 78)
5	Seed	Insect seed-feeder	Seed-feeder parasitoid	Trophic	Field sampling of interactions	(46, 47)
6a	Seed	Rodent	-	Trophic §	Field sampling for abundances, literature for presence of interactions, assumed foraging proportional to seed preferences for quantifying interactions	(79) considered large mammal seed dispersal
6b	-	Rodent	Ectoparasite	Parasitic	Field sampling of interactions	(57)
7	Seed	Granivorous bird	-	Trophic §	Field sampling for abundances, literature for presence and quantification of interactions	(79) and (80) considered seed dispersal by birds

Table S1. Description of the species' interaction networks.

* The host of secondary aphid parasitoids could not be determined by laboratory rearing, so in the network they were linked directly to the aphid host, which is described and justified in SOM Part 2.

† Leaf-miners were not quantified directly, but their presence was inferred as described and justified in SOM Part 2.

§ The vertebrate-seed feeder networks that we considered were of trophic interactions. However, birds and mammals can be important dispersers of some seeds, so a subset of the trophic interactions would have been mutualistic.

Habitat	Description	Area in 2007 (ha)	Area in 2008 (ha)
Wood	Three small woods that had been present for more than 100 years.	3.0	3.0
Cereal	Each type of cereal (winter wheat, winter triticale, spring barley, winter oats, spring oats, and cereal left fallow over summer) was sampled separately. These were part of the organic crop rotation.	33.0	59.8
Lucerne	A legume that was harvested for silage. This was part of the organic crop rotation.	5.7	0
Grass margin	Uncultivated margins up to 10m wide, introduced voluntarily and mostly removed in 2008 due to a change of farm ownership.	5.5	0.2
Permanent pasture	Grass that had been established for at least 10 years and used for grazing, hay and silage production.	22.2	22.2
Ley pasture	A grass and clover mix that had been established for less than 4 but more than 2 years as part of the organic crop rotation.	48.2	14.3
New ley	A grass and clover mix that had been established for less than 1 year as part of the organic crop rotation.	0	18.1
Mature hedge	Hedge present more than 100 years (recorded on the 1890 Ordnance Survey map); average 5.4 m high. Area includes the hedge base extending 0.5m from the dripline of the hedge.	3.7	3.7
New hedge	Hedge planted within the previous 10 years; average 2.5 m high. Area includes the hedge base extending 0.5m from the dripline of the hedge.	0.4	0.4
Rough ground	Land with no specific use which was dominated by ruderal vegetation. Part of the rough ground was developed in 2008 leading to it being excluded from sampling.	2.0	1.2
Excluded	Including access roads, farm buildings and the concrete farm yard.	1.3	2.1
Total		125.0	125.0

476 **Table S1. Description of the habitats on the farm field site.**

Animal group	Mean R_S (90 percentiles)	Mean R_Q (90 percentiles)	A	P	I	N	S	%O	H_2'	e^{H_2}	U
Flower visitors	0.59 (0.46,0.73)	0.80 (0.69,0.89)	241	47	501	4×10^5	1251	52/38	0.62	4.84	1.07/1.05
Butterflies	0.80 (0.64,0.92)	0.89 (0.71,0.98)	16	26	74*	6×10^3	256*	-	0.57	2.23	0.97/0.72
Leaf-miner parasitoids	0.61 (0.46,0.75)	0.73 (0.57,0.90)	96	35	219	8×10^6	1666	73/56	0.65	3.82	1.03/1.19
Aphids	0.55 (0.45,0.65)	0.63 (0.41,0.86)	28	30	39	4×10^8	1207	99/92	1.00	1.84	0.93/0.81
Primary aphid parasitoids	0.75 (0.57,0.88)	0.87 (0.67,0.97)	11	12	21	8×10^5	86	92/60	0.39	2.83	1.01/1.17
Secondary aphid parasitoids	0.89 (0.71,0.99)	0.94 (0.78,1.00)	7	13	24	1×10^6	192	88/30	0.36	3.82	0.84/0.76
Seed-feeding birds	0.98 (0.95,1.00)	0.99 (0.96,1.00)	12	66	439	6×10^2	-*	-	0.45	3.47	0.99/0.98
Seed-feeding rodents	0.96 (0.88,1.00)	0.98 (0.92,1.00)	4	32	68	2×10^3	-*	-	0.07	1.90	0.81/0.78
Rodent ectoparasites	0.99 (0.93,1.00)	0.99 (0.93,1.00)	8	29	18	1×10^3	-*	-	0.02	2.51	0.75/0.68
Seed-feeding insects	0.51 (0.24,0.78)	0.51 (0.09,0.92)	19	6	20	2×10^6	51	68/65	1.00	1.55	1.40/1.35
Seed-feeding insect parasitoids	0.58 (0.28,0.83)	0.50 (0.07,0.93)	17	4	17	6×10^5	84	-	1.00	1.28	1.20/1.50

Table S3. Summary statistics of the individual animal groups in the seven quantified networks.

R_S and R_Q (robustness of the animal groups to the extinction of plants; as described in the text) was determined from 20 000 simulations of the sequential random removal of plant species;

A is the number of animal species;

P is the number of plant species that they are linked to either directly or indirectly (depending on the animal group);

I is the number of interactions;

N is the estimated annual total number of individual animals (see SOM Part 2 for full details);

S is the number of individual samples obtained in order to construct the networks;

%O is the percent of species/interactions observed relative to the total estimated, which is a measure of sampling efficiency (see SOM Part 5 for full details);

H_2' and e^{H_2} are measures of niche differentiation and interaction diversity, respectively (as described in the Main Text);

U is the functional uniqueness of the animal group compared to the expectation that all have equal uniqueness, based on the relative importance of plants, from R_S and R_Q , respectively (see Supplementary Methods Part 4 for full details).

* indicates that interactions were not directly observed in the field but were estimated as describe in the Supplementary Methods (Part 2).

500

Robustness measure	Networks with literature-derived interactions used (n=11) or not used (n=6)	Binary or quantitative networks used	H_2'			e^{H_2}		
			β	t	P	β	t	P
R_S	Used	Binary	-0.903	-2.316	0.046			
R_S	Used	Quant.	-0.491	-2.370	0.042			
R_Q	Used	Quant.	-0.545	-6.131	<0.001			
R_S	Used	Binary				0.018	0.231	0.823
R_S	Used	Quant.				0.012	0.146	0.887
R_Q	Used	Quant.				0.099	1.769	0.111
R_S	Used	Binary	-0.543	-2.381	0.044	-0.048	-0.660	0.528
R_S	Used	Quant.	-0.507	-6.040	<0.001	-0.030	-1.129	0.292
R_Q	Used	Quant.	-0.476	-6.579	<0.001	0.027	1.150	0.283
R_S	Not used	Binary	-0.569	-1.200	0.296			
R_S	Not used	Quant.	-0.486	-1.115	0.115			
R_Q	Not used	Quant.	-0.548	-6.037	0.004			
R_S	Not used	Binary				-0.007	-0.105	0.921
R_S	Not used	Quant.				0.014	0.181	0.865
R_Q	Not used	Quant.				0.076	1.419	0.229
R_S	Not used	Binary	-0.727	-1.280	0.290	-0.043	-0.649	0.562
R_S	Not used	Quant.	-0.637	-2.885	0.114	-0.064	-0.973	0.403
R_Q	Not used	Quant.	-0.518	-4.313	0.023	0.013	0.461	0.676

501

502 **Table S4. Relationship of mean robustness with measures of network generalization**
503 **(H_2') and complexity (e^{H_2}).** The number of networks was eleven and six depending on
504 whether networks with literature-derived interactions were present or not.

505

	flower visitors	butterflies	aphids	aphid parasitoids (primary)	aphid parasitoids (secondary)	leaf-miner parasitoids	seed-feeding insects	seed-feeder parasitoids	seed-feeding birds	seed-feeding rodents	rodent ectoparasites
Correlations based on R_S											
Flower visitors	1	0.37	0.31	0.32	0.01	0.39	0.18	0.23	0.06	-0.02	-0.03
Butterflies	0.37	1	0.41	0.14	0.01	0.23	0.59	0.75	0.08	0	0
Aphids	0.31	0.41	1	0.44	0.26	0.57	0.36	0.44	0.12	0.13	0.08
Aphid parasitoids (primary)	0.32	0.14	0.44	1	0.75	0.39	0.23	0.16	0.13	0.02	0.03
Aphid parasitoids (secondary)	0.01	0.01	0.26	0.75	1	0.23	0.06	0.04	0.09	0.04	0.03
Leaf-miner parasitoids	0.39	0.23	0.57	0.39	0.23	1	0.07	0.18	0.17	0.13	0.07
Seed-feeding insects	0.18	0.59	0.36	0.23	0.06	0.07	1	0.88	0.09	-0.01	0.02
Seed-feeder parasitoids	0.23	0.75	0.44	0.16	0.04	0.18	0.88	1	0.07	-0.04	0
Seed-feeding birds	0.06	0.08	0.12	0.13	0.09	0.17	0.09	0.07	1	0.17	0.28
Seed-feeding rodents	-0.02	0	0.13	0.02	0.04	0.13	-0.01	-0.04	0.17	1	0.68
Rodent ectoparasites	-0.03	0	0.08	0.03	0.03	0.07	0.02	0	0.28	0.68	1
Correlations based on R_Q											
Flower visitors	1	0.55	0.17	0.11	0.11	0.21	0.25	0.25	0.11	-0.04	-0.02
Butterflies	0.55	1	0.28	0.05	0.04	0.14	0.1	0.09	0.13	-0.04	-0.04
Aphids	0.17	0.28	1	0.17	0.28	0.15	0.04	0.03	0.02	-0.01	-0.01
Aphid parasitoids (primary)	0.11	0.05	0.17	1	0.66	0.13	0.1	0.1	0.07	0.04	0.05
Aphid parasitoids (secondary)	0.11	0.04	0.28	0.66	1	0.07	0.18	0.18	0.06	0.02	0.03
Leaf-miner parasitoids	0.21	0.14	0.15	0.13	0.07	1	0.03	0.03	0.12	0.08	0.06
Seed-feeding insects	0.25	0.1	0.04	0.1	0.18	0.03	1	1	0.04	0.02	0.04
Seed-feeder parasitoids	0.25	0.09	0.03	0.1	0.18	0.03	1	1	0.03	0.02	0.04
Seed-feeding birds	0.11	0.13	0.02	0.07	0.06	0.12	0.04	0.03	1	0.25	0.29
Seed-feeding rodents	-0.04	-0.04	-0.01	0.04	0.02	0.08	0.02	0.02	0.25	1	0.92
Rodent ectoparasites	-0.02	-0.04	-0.01	0.05	0.03	0.06	0.04	0.04	0.29	0.92	1

507

508 **Table S5. The network of correlations between the robustness of animal groups to the**
509 **simulated extinction of plant taxa.** These are the correlations between the robustness of
510 each animal group to the simulated sequential extinction of plant taxa, from which Figs 3E
511 and F were constructed.

Table S6. The values of the relative importance of plant taxa in the Norwood Farm network. Relative importance (RI) is the impact of the loss of the plant taxon on secondary extinctions in 13 species interaction networks (i.e. when considering the effect on robustness without or with taking account of species abundance; R_S and R_O , respectively), accounting for the abundance of the plant taxon, and is calculated as described above. All species are shown here, although only those with leaf area > 100m² are presented in Fig. 3A in the main text. Species are ordered according to the RI based on R_S . Abundance, i.e. leaf area, was estimated from field measurements (31). Main habitats are: W = woody plants, H = hedgerows and field margins, G = grass fields (including grass sp. and clover sp.), A = arable fields (excluding crops), C = crops (including lucerne). Life forms are: ann = annuals, per = non-woody perennials, w = woody perennials.

Plant name	Common name	RI based on R_S	Rank	RI based on R_O	Rank	Abundance (leaf area in m ²)	Main habitat	Plant family	Life form
<i>Cirsium vulgare</i>	Spear Thistle	1.1	1	-0.09	23	54676	H	Asteraceae	per
<i>Anthriscus sylvestris</i>	Cow Parsley	1.02	2	-0.17	28	528	H	Apiaceae	per
<i>Trifolium pratense/repens</i>	Clover sp.	0.91	3	0.99	2	1316522	G	Fabaceae	per
<i>Cirsium arvense</i>	Creeping Thistle	0.9	4	0.76	4	230284	H	Asteraceae	per
<i>Ranunculus repens</i>	Creeping Buttercup	0.81	5	0.53	6	287845	G	Ranunculaceae	per
<i>Acer pseudoplatanus</i>	Sycamore	0.71	6	0.48	7	61	W	Aceraceae	w
<i>Heracleum sphondylium</i>	Hogweed	0.59	7	0.07	16	8950	H	Apiaceae	per
<i>Urtica dioica</i>	Stinging Nettle	0.41	8	-0.77	68	62762	H	Urticaceae	per
Poaceae	Grass sp.	0.38	9	-0.28	38	3412994	G	Poaceae	per
<i>Rubus fruticosus</i>	Bramble	0.35	10	-0.04	18	83586	H	Rosaceae	per
<i>Cardamine flexuosa</i>	Wavy Bittercress	0.33	11	0.33	8	50	A	Brassicaceae	ann
<i>Quercus robur</i>	Oak	0.32	12	1.05	1	75148	W	Fagaceae	w
<i>Lamium galeobdolon</i>	Yellow Archangel	0.31	13	-0.62	58	2123	WU	Lamiaceae	per
<i>Veronica hederifolia</i>	Ivy-leaved Speedwell	0.29	14	0.1	13	50	A	Plantaginaceae	ann
<i>Brassica napus</i>	Oil seed rape	0.26	15	0.21	11	50	H	Brassicaceae	ann
<i>Matricaria recutita</i>	Scented Mayweed	0.22	16	0.32	9	113135	A	Asteraceae	ann
<i>Hyacinthoides non-scripta</i>	Bluebell	0.21	17	0.28	10	105	WU	Liliaceae	per
<i>Matricaria discoidea</i>	Pineappleweed	0.21	18	0.98	3	54	H	Asteraceae	ann
<i>Torilis japonica</i>	Upright Hedge-parsley	0.19	19	-0.5	53	1334	H	Apiaceae	per
<i>Stachys sylvatica</i>	Hedge Woundwort	0.19	20	-0.33	42	4780	H	Lamiaceae	per
<i>Chenopodium</i> sp.	Goosefoot sp.	0.17	21	-0.29	39	3669	A	Chenopodiaceae	ann
<i>Allium ursinum</i>	Ramsons (Wild Garlic)	0.16	22	0.12	12	129	WU	Liliaceae	per
<i>Clematis vitalba</i>	Traveller's Joy	0.14	23	0.09	14	414	H	Ranunculaceae	per
<i>Alliaria petiolata</i>	Garlic Mustard	0.1	24	-0.08	20	262	H	Brassicaceae	ann
<i>Veronica chamaedrys</i>	Germander Speedwell	0.08	25	-0.19	30	269	WU	Plantaginaceae	per
<i>Rosa</i> sp.	Rose sp.	0.07	26	-0.6	56	8436	H	Rosaceae	w
<i>Sambucus nigra</i>	Elder	0.03	27	-0.31	40	3092	W	Adoxaceae	w
<i>Lamium album</i>	White Dead-nettle	0.02	28	-0.08	19	184	H	Lamiaceae	per

<i>Picris echinoides</i>	Bristly Oxtongue	0.02	29	0.08	15	60	H	Asteraceae	ann
<i>Senecio vulgaris</i>	Groundsel	0.01	30	-0.15	27	115	A	Asteraceae	ann
<i>Vicia sativa</i>	Common Vetch	0.01	31	-0.79	70	3583	H	Fabaceae	per
<i>Arctium minus</i>	Lesser Burdock	-0.01	32	-0.24	33	777	H	Asteraceae	per
<i>Avena sativa</i>	Oat (winter sown)	-0.02	33	-0.14	26	571045	C	Poaceae	ann
× <i>Triticosecale</i>	Triticale	-0.02	34	-0.12	25	520607	C	Poaceae	ann
<i>Ajuga reptans</i>	Bugle	-0.03	35	-0.08	22	356	WU	Lamiaceae	per
<i>Sonchus asper/oleraceus</i>	Sow-thistle sp.	-0.04	36	-0.88	78	56869	H	Asteraceae	ann
<i>Galium odoratum</i>	Woodruff	-0.04	37	-0.27	36	1774	WU	Rubiaceae	per
<i>Cardamine pratensis</i>	Cuckooflower	-0.05	38	-0.08	21	175	WU	Brassicaceae	per
<i>Geum urbanum</i>	Herb Bennett	-0.06	39	-0.18	29	1287	WU	Rosaceae	per
<i>Scrophularia auriculata</i>	Water Figwort	-0.06	40	-0.01	17	50	H	Scrophulariaceae	per
<i>Cornus sanguinea</i>	Dogwood	-0.1	41	-0.2	31	685	W	Rosaceae	w
<i>Taraxacum officinale</i>	Dandelion	-0.12	42	-1.09	92	63969	G	Asteraceae	per
<i>Crataegus monogyna</i>	Hawthorn	-0.14	43	-0.64	59	46935	W	Rosaceae	w
<i>Fallopia convolvulus</i>	Black Bindweed	-0.14	44	-0.31	41	2887	A	Polygoniaceae	ann
<i>Triticum aestivum</i>	Wheat (winter sown)	-0.14	45	-0.27	35	1330055	C	Poaceae	ann
<i>Lapsana communis</i>	Nipplewort	-0.14	46	-0.38	45	3114	H	Brassicaceae	ann
<i>Lamium purpureum</i>	Red Dead-nettle	-0.16	47	-0.4	47	7353	A	Lamiaceae	ann
<i>Ranunculus acris</i>	Meadow Buttercup	-0.16	48	-0.49	52	1193	H	Ranunculaceae	per
<i>Senecio jacobaea</i>	Common Ragwort	-0.17	49	-0.88	77	11484	H	Asteraceae	per
<i>Trifolium dubium</i>	Lesser Trefoil	-0.17	50	-0.67	61	4215	H	Fabaceae	ann
<i>Sherardia arvensis</i>	Field Madder	-0.18	51	-0.36	44	1164	A	Rubiaceae	ann
<i>Euonymus europaeus</i>	Spindle	-0.18	52	-0.71	66	9055	W	Celastraceae	w
<i>Polygonum</i> sp.	Knotgrass sp.	-0.18	53	-0.68	63	23269	H	Polygoniaceae	ann
<i>Sinapis arvensis</i>	Charlock	-0.19	54	-0.28	37	25262	A	Brassicaceae	ann
<i>Chaerophyllum temulum</i>	Rough Chervil	-0.21	55	-0.27	34	768	H	Apiaceae	per
<i>Veronica arvensis</i>	Wall Speedwell	-0.21	56	-0.91	88	8775	A	Plantaginaceae	ann
<i>Sonchus arvensis</i>	Corn Sowthistle	-0.22	57	-0.55	54	4083	A	Asteraceae	ann
<i>Leontodon autumnalis</i>	Autumn hawkbit	-0.23	58	0.69	5	3525	G	Asteraceae	per
<i>Vicia sepium</i>	Bush Vetch	-0.24	59	-0.36	43	620	H	Fabaceae	per
<i>Stellaria graminea</i>	Lesser Stitchwort	-0.25	60	-0.38	46	2966	H	Caryophyllaceae	per
<i>Euphorbia helioscopia</i>	Sun Spurge	-0.27	61	-0.41	48	628	A	Euphorbiaceae	ann
<i>Rumex</i> sp.	Dock sp.	-0.28	62	-1.01	90	206905	H	Polygoniaceae	per
<i>Prunus spinosa</i>	Blackthorn	-0.3	63	-0.88	80	79837	W	Rosaceae	per
<i>Silene dioica</i>	Red Campion	-0.32	64	-0.43	49	1844	WU	Caryophyllaceae	per
<i>Dipsacus fullonum</i>	Teasel	-0.32	65	-0.46	51	2299	H	Dipsacaceae	per
<i>Persicaria</i> sp.	Persicaria sp.	-0.32	66	-0.87	75	36081	A	Polygoniaceae	ann
<i>Viburnum lanatum</i>	Wayfaring Tree	-0.34	67	-0.56	55	4358	W	Rosaceae	w

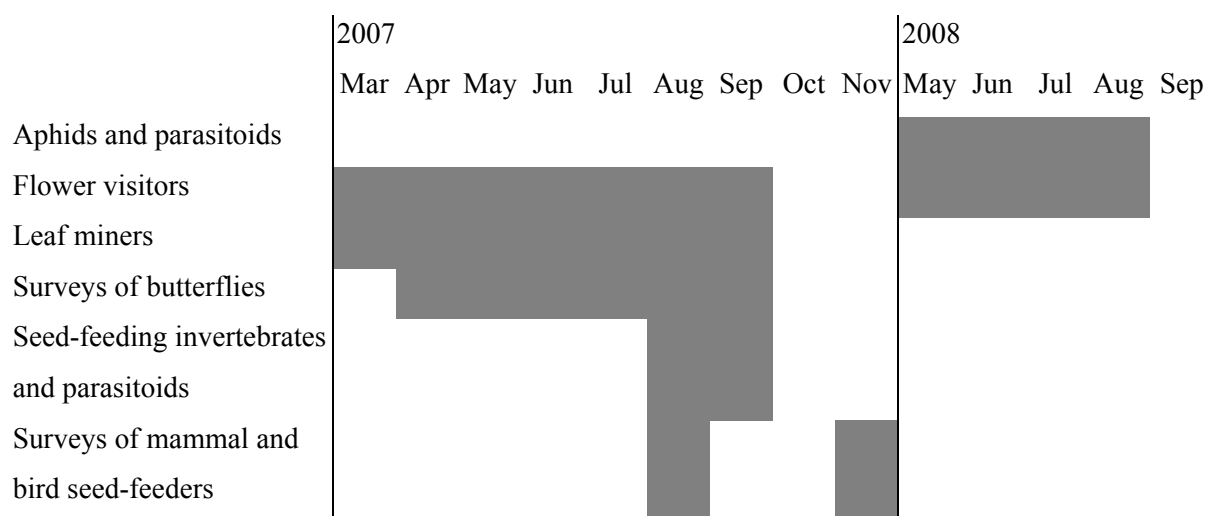
<i>Galium aparine</i>	Cleavers	-0.35	68	-1.12	94	20179	H	Rubiaceae	ann
<i>Ligustrum vulgare</i>	Wild Privet	-0.35	69	-0.67	62	1112	W	Oleaceae	w
<i>Capsella bursa-pastoris</i>	Shepherd's Purse	-0.38	70	-1.15	96	6221	A	Brassicaceae	ann
<i>Acer campestre</i>	Field Maple	-0.4	71	-0.85	71	39823	W	Aceraceae	w
<i>Corylus avellana</i>	Hazel	-0.4	72	-0.87	76	57409	W	Betulaceae	w
<i>Lonicera periclymenum</i>	Honeysuckle	-0.45	73	-0.77	67	2138	W	Caprifoliaceae	w
<i>Geranium dissectum</i>	Cut-leaved Crane's-bill	-0.46	74	-0.61	57	5257	A	Geraniaceae	ann
<i>Epilobium</i> sp.	Willowherb sp.	-0.51	75	-0.68	64	5545	H	Onagraceae	ann
<i>Viola arvensis</i>	Field Pansy	-0.53	76	-0.7	65	17615	A	Violaceae	ann
<i>Fraxinus excelsior</i>	Ash	-0.56	77	-1.06	91	89160	W	Oleaceae	w
<i>Hypochaeris/ Crepis</i> sp.	Hawkish Complex sp.	-0.57	78	-0.85	72	16256	G	Asteraceae	per
<i>Potentilla reptans</i>	Creeping Cinquefoil	-0.57	79	-0.66	60	4376	H	Rosaceae	per
<i>Mentha arvensis</i>	Corn Mint	-0.59	80	-0.89	82	6856	A	Lamiaceae	ann
<i>Stellaria media</i>	Common Chickweed	-0.59	81	-0.88	81	17118	A	Caryophyllaceae	ann
<i>Bellis perennis</i>	Daisy	-0.6	82	-0.9	84	4977	G	Asteraceae	per
<i>Lotus corniculatus</i>	Common Bird's-foot-trefoil	-0.64	83	-0.9	85	21877	H	Fabaceae	per
<i>Geranium robertianum</i>	Herb Robert	-0.64	84	-0.78	69	6810	WU	Geraniaceae	ann
<i>Ulmus</i> sp.	Elm sp.	-0.65	85	-0.91	87	18394	W	Ulmaceae	w
<i>Plantago</i> sp.	Plantain sp.	-0.67	86	-0.12	24	18667	G	Plantaginaceae	per
<i>Myosotis arvensis</i>	Field Forget-me-not	-0.69	87	-0.21	32	24410	A	Boraginaceae	ann
<i>Aphanes arvensis</i>	Parsley Piert	-0.76	88	-0.86	74	12380	A	Rosaceae	ann
<i>Spergula arvensis</i>	Corn Spurrey	-0.76	89	-0.89	83	11316	A	Caryophyllaceae	ann
<i>Medicago sativa</i> ssp. <i>sativa</i>	Lucerne	-0.76	90	-1.58	101	309495	C	Fabaceae	per
<i>Cerastium fontanum</i>	Common Mouse-ear	-0.77	91	-0.95	89	27991	A	Caryophyllaceae	ann
<i>Convolvulus/Calystegia</i>	Bindweed sp.	-0.8	92	-1.1	93	39207	H	Convolvulaceae	per
<i>Mercurialis perennis</i>	Dog's Mercury	-0.84	93	-0.91	86	50122	WU	Euphorbiaceae	per
<i>Vicia hirsute</i>	Hairy Tare	-0.84	94	-0.86	73	8498	A	Fabaceae	ann
<i>Glechoma hederacea</i>	Ground Ivy	-0.86	95	-0.88	79	12994	H	Lamiaceae	per
<i>Veronica persica</i>	Common Field Speedwell	-0.87	96	-1.18	97	69568	A	Plantaginaceae	ann
<i>Papaver</i> sp.	Poppy sp.	-0.95	97	-1.13	95	55155	A	Papaveraceae	ann
<i>Hordeum vulgare</i>	Barley (spring sown)	-0.99	98	-1.23	98	124392	C	Poaceae	ann
<i>Prunella vulgaris</i>	Selfheal	-1.04	99	-0.46	50	55434	G	Lamiaceae	per
<i>Avena sativa</i>	Oat (spring sown)	-1.06	100	-1.44	100	154255	C	Poaceae	ann
<i>Pulicaria dysenterica</i>	Common Fleabane	-1.13	101	-1.37	99	55273	G	Asteraceae	per

Variable	Statistical test	R_S		R_Q	
		Test statistic (mean \pm SD)	P (mean (maximum across simulations))	Test statistic (mean \pm SD)	P (mean, maximum across simulations)
Robustness of animal groups to simulated plant extinctions	Intra-class correlation on logit- transformed medians	0.791 \pm 0.116	<0.001 (<0.001)	0.831 \pm 0.102	<0.001 (<0.001)
Correlations between animal groups in their robustness to simulated plant extinctions	Mantel test on correlation- based dissimilarity between groups	0.884 \pm 0.070	0.003 (0.011)	0.870 \pm 0.097	0.005 (0.017)
Relative importance of plant taxa	Intra-class correlation	0.732 \pm 0.162	0.008 (0.151)	0.736 \pm 0.173	0.001 (0.020)

525

526 **Table S7. Comparisons of the reported results to the results taking account of sampling**
527 **efficiency for the animal groups sampled in the field.** These networks were reduced to a
528 standard level of estimated sampling efficiency (that of the flower visitors) by sample-based
529 rarefaction and the full analysis repeated. This process was undertaken 18 times, see SOM
530 Part 5 for full details. All these results were significantly similar to our reported results,
531 demonstrating that varying sampling efficiency in these networks had no substantial effect on
532 the overall conclusions.

533



534

535 **Figure S1. Times of field sampling to obtain estimates of species abundance and species**
 536 **interaction data.** Dark boxes show the times when sampling occurred.

537

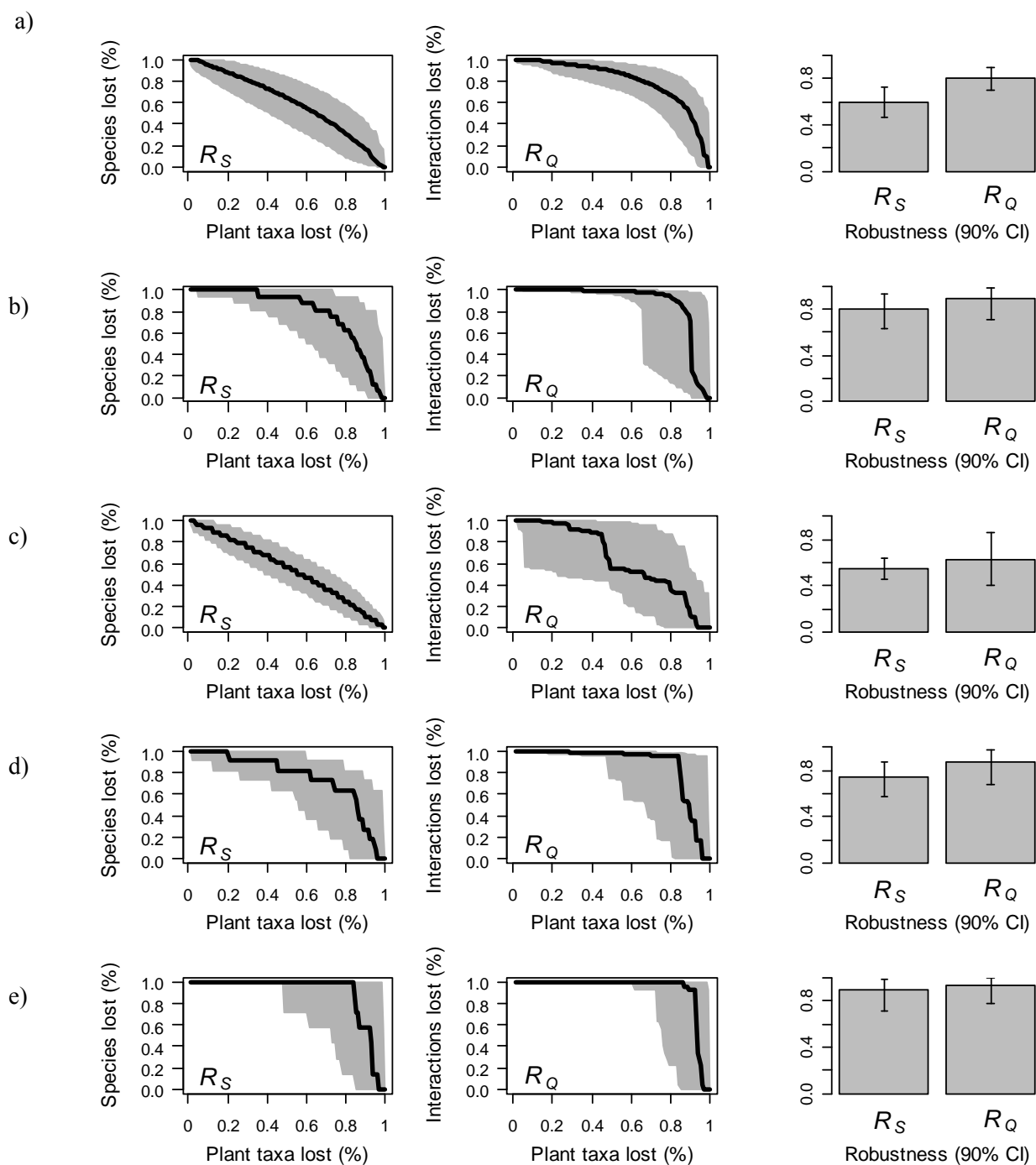
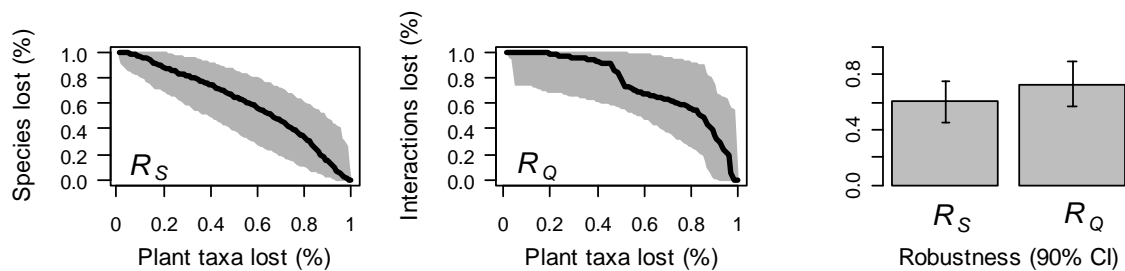
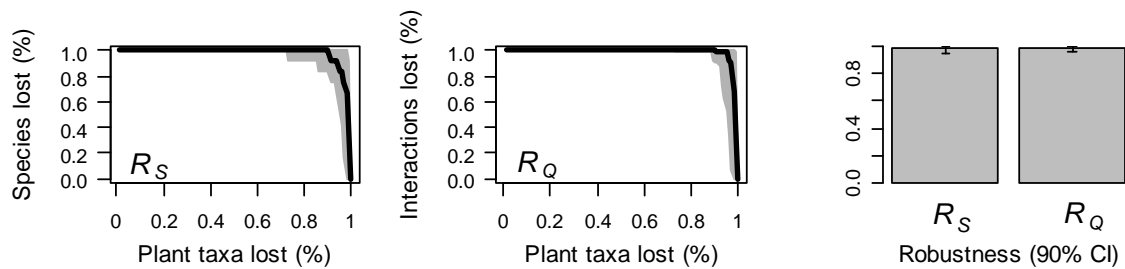


Figure S2 (continued on next page)..

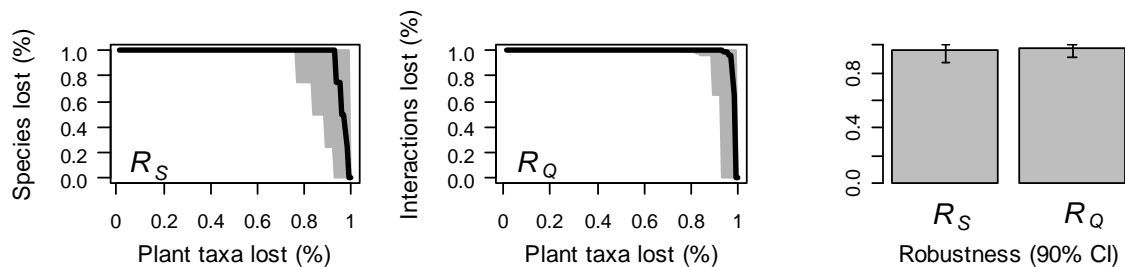
f)



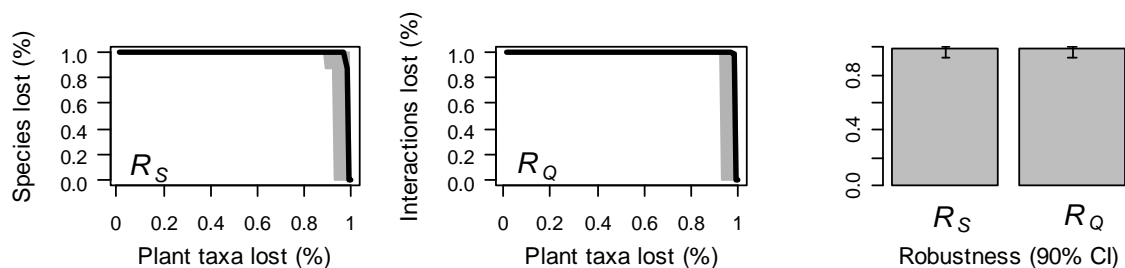
g)



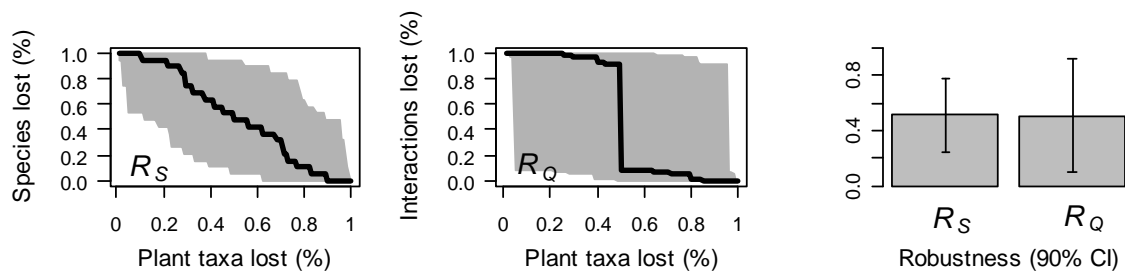
h)



i)



j)



k)

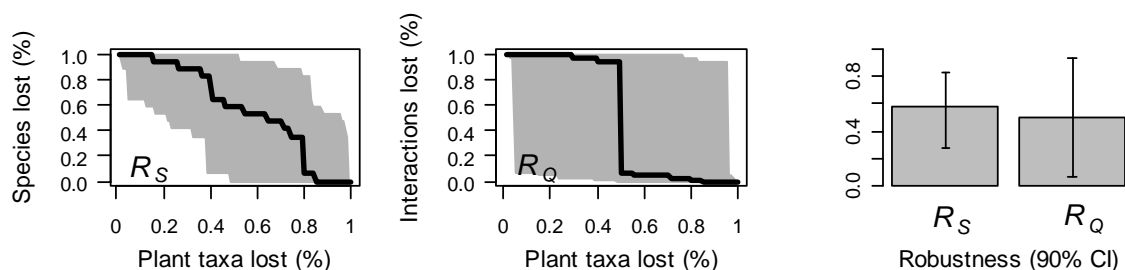
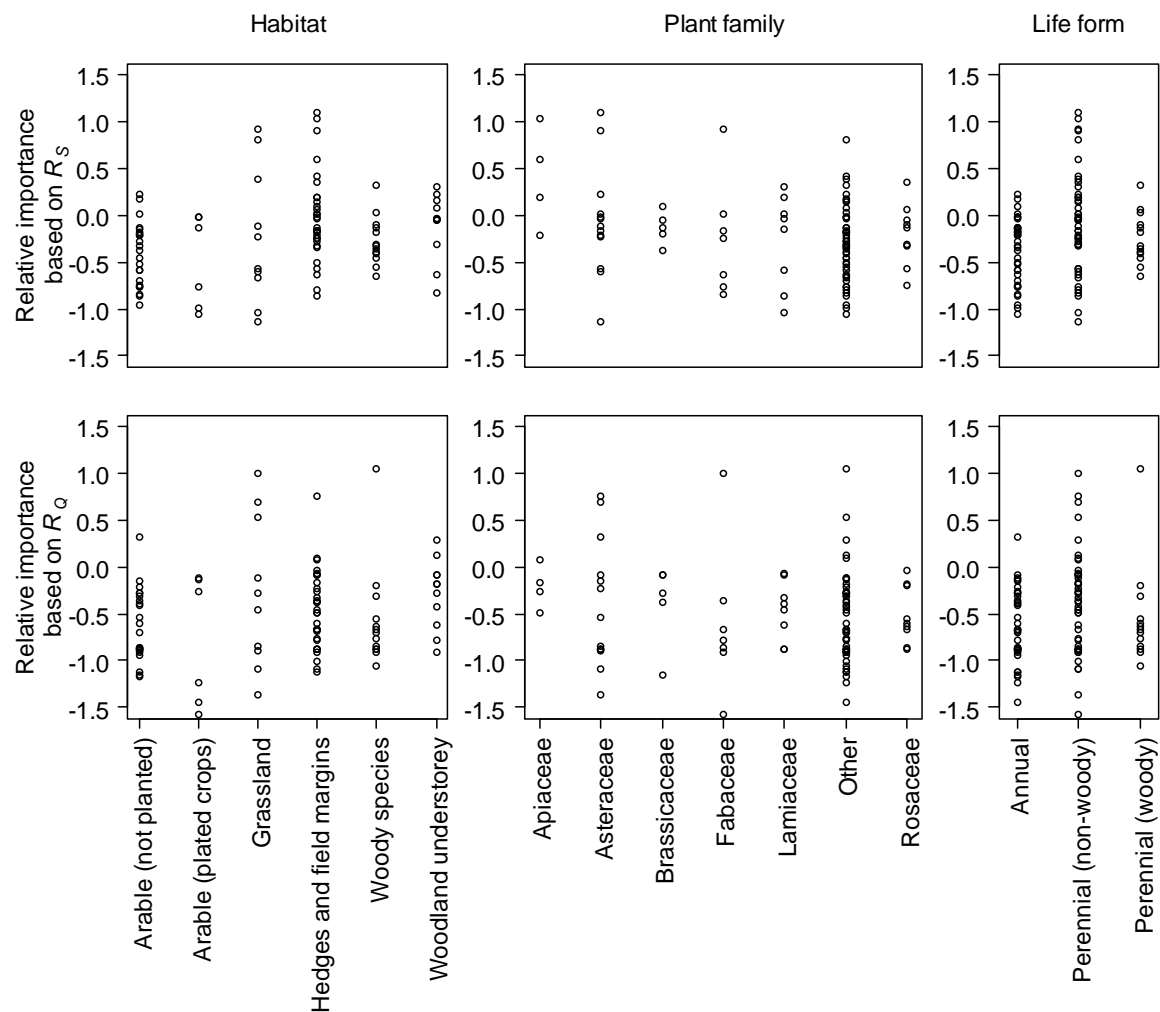


Figure S2 (continued on next page).

Figure S2 (above). Plots of predicted secondary extinctions in the face of plant taxon loss (see appendix 2) and bar graphs summarising these values. The dark lines indicate the median curve, the grey polygon represents the 95 percentiles. R , the assessment of robustness as used throughout the paper (see discussion in SOM Part 3), is the area underneath the curves in these graphs. The animal groups are: a) flower visitors, b) butterflies, c) aphids, d) primary aphid parasitoids, e) secondary aphid parasitoids, f) leaf miner parasitoids, g) bird seed-feeders, h) rodent seed-feeders, i) rodent ectoparasites, j) insect seed-feeders, k) parasitoids of insect seed-feeders.

609



610

611 **Figure S3. The relationship of relative importance (calculated with R_S and R_Q) to the**
612 **main habitats, families and life forms of the plant taxa. Plant taxa with estimated leaf area**
613 **on the farm $< 100\text{m}^2$ are not included.**

614

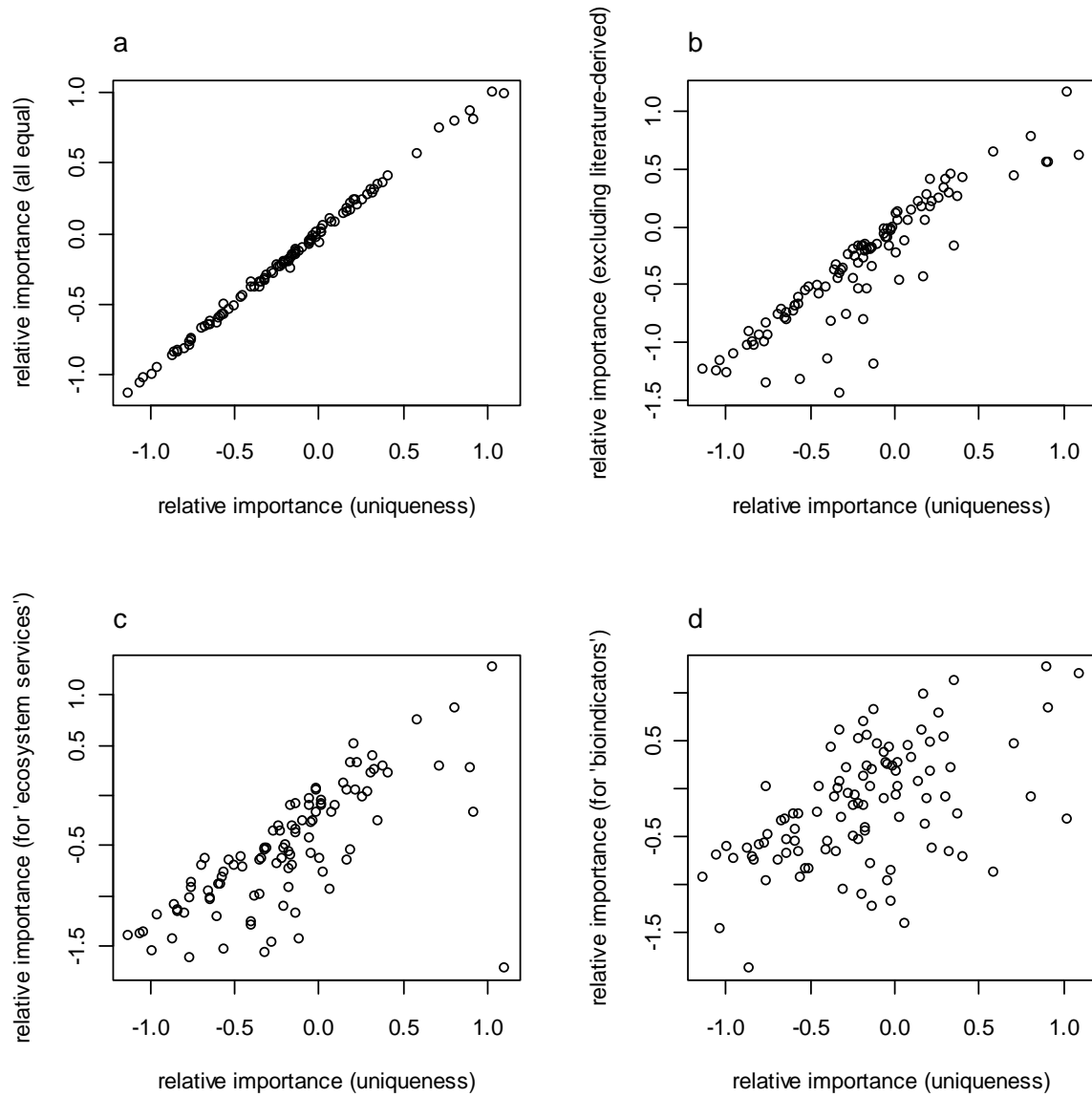


Figure S4. (Continued on next page.)

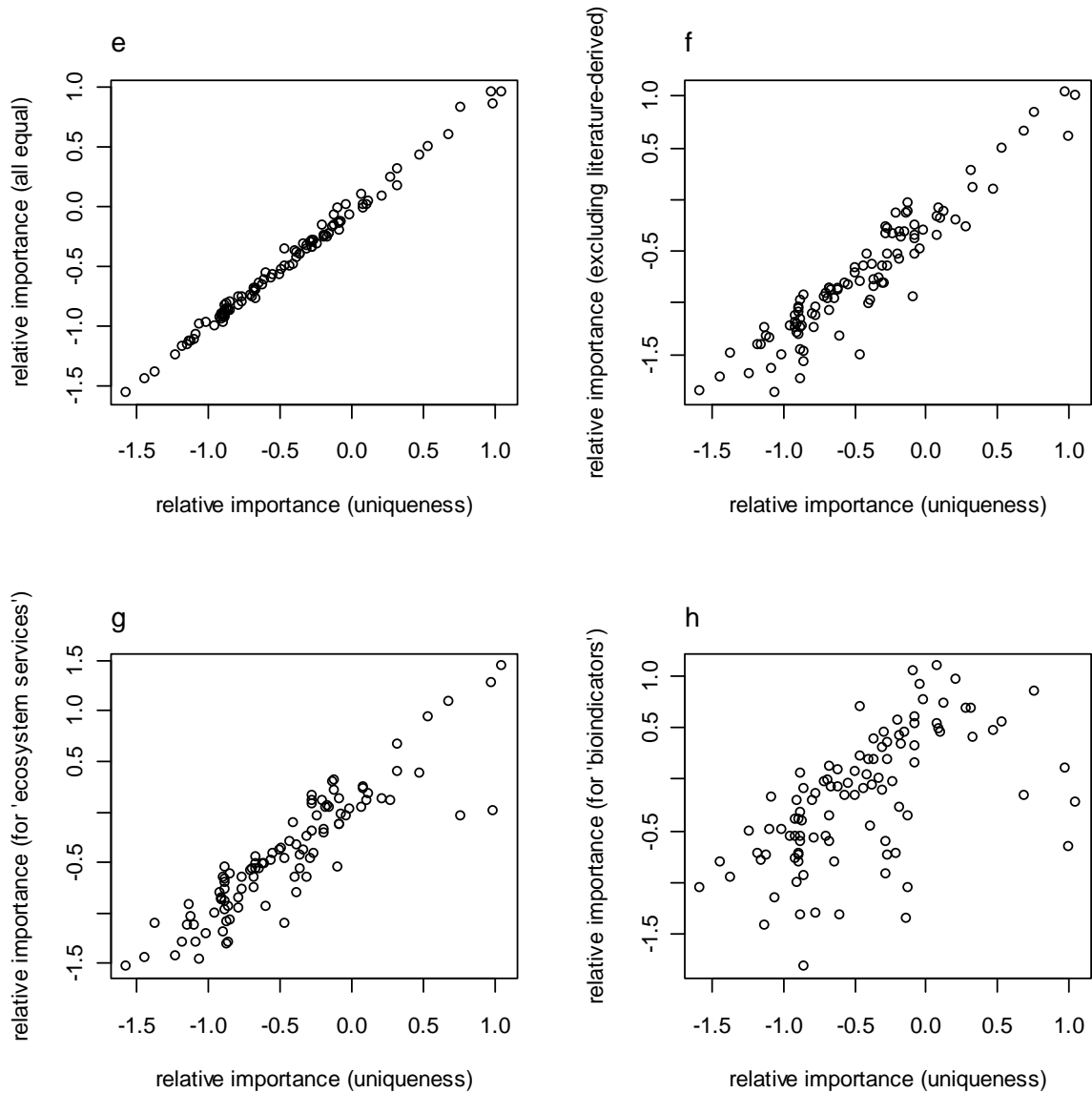


Figure S4. Comparison of the relative importance of plants calculated in this study with alternative ways of weighting the importance of plants to animal groups. The results show that although the relative importance of specific plant taxa may change considerably, the overall pattern is broadly similar despite substantial changes in the weighting, and whether considering relative importance based on R_S (A-D) or R_Q (E-H). The example alternatives that we considered were: (A, E) weighting all animal groups equally, (B, F) weighting all animal groups equally but excluding the literature-derived networks, (C, G) considering only potential ecosystem service providers (flower visiting insects, aphid parasitoids and leaf-miner parasitoids) weighted equally and (D, H) considering only groups regarded as ‘bioindicators’ (butterflies and seed-feeding birds).

629 **SOM text: Full acknowledgements**

630 We thank Cate Le Grice-Mack for granting access to the farm and supporting the project
631 from its inception. We thank Alistair Cooper for continuing to allow access in 2008.

632 We thank the following individuals for determining specimens and identifying samples:

- 633 • C. van Achterberg (parasitic Hymenoptera)
- 634 • H. Baur (parasitic Hymenoptera)
- 635 • G.R. Broad, Natural History Museum, London, UK (parasitic Hymenoptera)
- 636 • J. Deeming, National Museum Wales, Cardiff, UK (Diptera)
- 637 • M. Forshage (parasitic Hymenoptera)
- 638 • R. George, Bournemouth, UK (rodent fleas)
- 639 • H.C.J. Godfray, University of Oxford, UK (parasitic Hymenoptera)
- 640 • C. Hansson (parasitic Hymenoptera)
- 641 • G. Hopkins, The Ecology Consultancy, Norwich, UK (aphids)
- 642 • L. Jameson, Health Protection Agency, Porton Down, UK (rodent ticks)
- 643 • P. Jansta, (parasitic Hymenoptera)
- 644 • B. Levey, National Museum Wales, Cardiff, UK (Coleoptera)
- 645 • M. Pavett, National Museum Wales, Cardiff, UK (non-parasitic Hymenoptera)
- 646 • A. Polaszek, Natural History Museum, London, UK (parasitic Hymenoptera and
647 organising their distribution)
- 648 • T. West, Marshall Agroecology Ltd, Winscombe, UK (plant seeds)

649 We thank Jo Brooks for practical assistance throughout the project and for the other field and
650 laboratory assistants who worked on the project:

651 Sara Abo El Nour, Robin Arundel, Nick Boase, Nic Charlton, Kate Evans, Kiri Green, Rick
652 Hayes, Kate Henson, Francesca Jordan, Holly Kirk, James McCloud, Vanda Miravent,
653 Lauren Pascoe, Debs Scott, Karen Varnham.

654

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