

Does taxonomic diversity in indicator groups influence their effectiveness in identifying priority areas for species conservation?

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Abstract

The identification of priority areas for biodiversity conservation is a cornerstone of systematic conservation planning. However, biodiversity, or even the distribution of all species, cannot be directly quantified, due to the inherent complexity of natural systems. Species indicator groups may serve as important tools for the identification of priority areas for conservation. Yet, it is unclear which factors make certain indicator groups perform better than others. In this study, using data on the Danish distribution of 847 species of plants, vertebrates and insects, we assessed whether the taxonomic diversity in species indicator groups influence their effectiveness in the identification of priority areas for species conservation. We tested whether indicator groups comprising a higher taxonomic diversity (i.e. indicator groups consisting of species from many different taxonomic groups) perform better than indicator groups comprising a lower taxonomic diversity. The performance of the indicator groups was evaluated on target groups, which, in terms of species composition, were independent of the indicator groups. Overall, we found that using taxonomically diverse indicator groups did not consistently increase the coverage of target species than when using less taxonomically diverse indicator groups. However, indicator groups chosen solely from one taxon were outperformed by taxonomically diverse groups. Second, we found that taxonomic diversity of the indicator did not influence the taxonomic diversity of the covered target species (in terms of number of represented families, orders, etc.) Thus, taxonomic diversity *per se* only had a marginal influence on the performance of indicator groups. Distributional characteristics, such as the proportion of species with narrow range sizes, had a larger impact on indicator performance. Our results suggest that it might be of minor importance to consider taxonomic diversity when acquiring species data for future conservation projects using indicator groups.

Introduction

One of the cornerstones of systematic conservation planning is the identification of priority areas for biodiversity conservation (Margules & Pressey, 2000). Yet, while the concept of biodiversity covers a hierarchy from the molecular to the ecosystem level, we only have limited knowledge regarding any given level of this hierarchy. Accordingly, there is an urgent practical need for easily measurable biodiversity indicators that – when targeted in conservation planning – result in an effective protection of overall biodiversity.

Many studies have assessed the performance of various species indicator groups in identifying area networks for the conservation of biodiversity. Some studies have tested indicator groups defined by species attributes such as endemism, red list status resulting in groups composed of species from various taxa (e.g. Andelman & Fagan, 2000;

Williams, Burgess & Rahbek, 2000; Bonn, Rodrigues & Gaston, 2002; Lund, 2002; Tognelli, 2005), while other studies have tested indicator groups composed of species from a single taxon, for example, birds, mammals or butterflies (e.g. Prendergast *et al.*, 1993; Howard *et al.*, 1998; Moritz *et al.*, 2001; Lund & Rahbek, 2002; Moore *et al.*, 2003; Juutinen & Mönkkönen, 2004; Kati *et al.*, 2004; Warman *et al.*, 2004; Williams *et al.*, 2006). The approach of using a taxonomically well-studied and easily measurable taxon as indicator group is appealing, and could constitute a significant shortcut for conservation planning if these taxa can be used to effectively identify area networks representing significant areas of biodiversity. However, several studies have documented that it can be ineffective to use one taxon as an indicator for other taxa (e.g. Sætersdal, Line & Birks, 1993; Van Jaarsveld *et al.*, 1998; Juutinen & Mönkkönen, 2004; Schulze *et al.*, 2004; Chiarucci *et al.*,

2005). A potential explanation is that biodiversity hotspots for different taxa do not always coincide (e.g. Prendergast *et al.*, 1993; Dobson *et al.*, 1997; Howard *et al.*, 1998) and that cross-taxon congruence of species distributions can be low (e.g. Lund & Rahbek, 2002; Grenyer *et al.*, 2006). Therefore, one might expect that indicator groups consisting of species from many taxonomic groups (i.e. indicator groups with high taxonomic diversity) will perform better than indicator groups consisting of species from solely one taxon (i.e. low taxonomic diversity). Intuitively, it seems a better approach to, for example, use both distributional data for plants, birds and insects to guide conservation planning rather than just using one taxonomic group. However, few studies have systematically assessed the importance of taxonomic diversity in indicator groups for their importance in efficiently guiding reserve selection. Larsen, Bladt & Rahbek (2007) use data on birds and mammals to preliminarily explore whether indicator groups consisting of species from a higher number of different genera or families (e.g. 150 spp. from 80 families) performed better than indicator groups consisting of species from fewer different genera and families (e.g. 150 spp. from 26 families). They found that the number of different genera and families represented in the indicator group has little effect on the performance of the indicator group. In fact, increasing the number of genera and families in indicator groups resulted in slight decreases in indicator performance.

In this study, we specifically aim to assess the importance of taxonomic diversity in indicator groups for their performance in guiding area selection. This study expands on the previous work by analysing a taxonomically diverse dataset (e.g. amphibians, birds, bugs, butterflies, dragonflies, grasshoppers, hoverflies, moths, orchids and reptiles). We want to test whether indicator groups comprising a higher taxonomic diversity (i.e. indicator groups consisting of species from many different taxonomic groups) perform better than indicator groups comprising a lower taxonomic diversity. To test this, we compare the effectiveness of indicator groups with different taxonomic diversities. Specifically, we systematically change the taxonomic diversity of randomly chosen indicator groups at various taxonomic levels. In order to assess the performance of the indicator groups, we evaluate both the representation of species (all, threatened and range-restricted species) and taxonomic diversity (in terms of number of genera, families and orders represented among the captured species) by the selected reserve networks.

Methods

Data on species distributions and taxonomic diversity

We used the distribution (presence/absence) of 847 terrestrial species of amphibians, birds, bugs, butterflies, dragonflies, grasshoppers, hoverflies, moths, orchids and reptiles compiled for 10 km UTM quadrates (= 100 km², $n = 622$) in Denmark (see Table 1). Other versions of the dataset have been used in other studies of quantitative biodiversity

Table 1 Overview of the species dataset and the taxonomic sections used in the analysis

Division 1	Division 2	Families	Genera	Species
Plants	Orchids	1	18	41
Vertebrates	Reptiles and amphibians	10	10	19
	Birds	50	118	189
<i>Lepidoptera</i> spp.	Moths	10	105	156
	Butterflies	4	45	60
<i>Diptera</i> spp.	Hoverflies	3	77	252
Other invertebrates	Grasshoppers	4	15	26
	Dragonflies	9	21	41
	Bugs	8	51	63
5	9	99	460	847

The dataset includes species of amphibians/reptiles (Amphibia/Reptilia), birds (Aves), hoverflies (Diptera: Syrphidae), butterflies (Lepidoptera: Hesperioidea, Papilionoidea), moths (Lepidoptera: Helioloidea, Cossioidea, Zygaenoidea, Tineoidea, Yponomatoidea, Bombycoidea, Geometroidea, Sphingoidea, Notodontoidea, Noctuoidea), true bugs (Hemiptera: Pentatomidea, Coreoidea, Pyrrhocoridae), grasshoppers (Orthoptera), dragonflies (Odonata) and orchids (Orchidaceae). Vagrant, casual and exotic species were excluded from the dataset.

analysis in Denmark (Lund, 2002; Lund & Rahbek, 2002; Larsen *et al.*, 2008).

Selection and evaluation of indicator groups

We used the following procedure composed of four steps:

- (1) *Divide species into taxonomic sections*: We divided the species into taxonomic sections (e.g. genera or families) by which we could change the taxonomic diversity (e.g. the number of genera in the indicator group).
- (2) *Selection of indicator groups*: We constructed a large number ($n = 11\,500$, see below) of species indicator groups, for which we systematically changed the taxonomic diversity by altering the species composition. For example, we constructed indicator groups consisting of 50 species from 10, 20, 30, 40 or 50 different families, respectively.
- (3) *Selection of area networks*: Each indicator group was used to select a protected area network to maximize the representation of the species in the indicator group.
- (4) *Evaluation of reserve networks*: We evaluated the performance of each network by measuring the coverage of the species from a target group.

Below, we elaborate on the specific procedure for each of the four steps (a detailed outline of the procedure is given in Fig. 1).

Divide species into taxonomic sections

We divided the species into taxonomic sections in four different ways in order to test the influence of taxonomic diversity. We divided the species based on two strictly taxonomically defined nomenclature ranks (genera and families) and two pragmatically defined categories (referred to as Divisions 1 and 2), similar to those used in practice for

- (a) 1) Divide the species in the full dataset randomly into two pools, each consisting of 50 % of the species. One pool, the indicator pool, constitutes the set of species from where the indicator group is drawn. The other pool constitutes the independent target group.
- 2) Among the genera present in the indicator pool, select k genera randomly without replacement. Each genus is selected with a probability proportional to the number of indicator-pool-species (species present in the indicator pool) in the genus.
- 3) If the k genera selected in step 2 contain less than 50 indicator-pool-species, return to step 1. Otherwise, proceed to step 4.
- 4) For each of the k genera add one randomly chosen indicator-pool-species to the indicator group. Add the remaining indicator-pool-species from the k genera to a temporary species buffer.
- 5) Select $50-k$ randomly chosen species from the species buffer and add these to the indicator group. The indicator group now consists of 50 indicator-pool-species from k genera. Select an area network to maximise representation of the species in the indicator group.
- 6) Assess indicator performance of the network by measuring the representation of the species in the target group (consisting of 50 % of the species in the dataset).

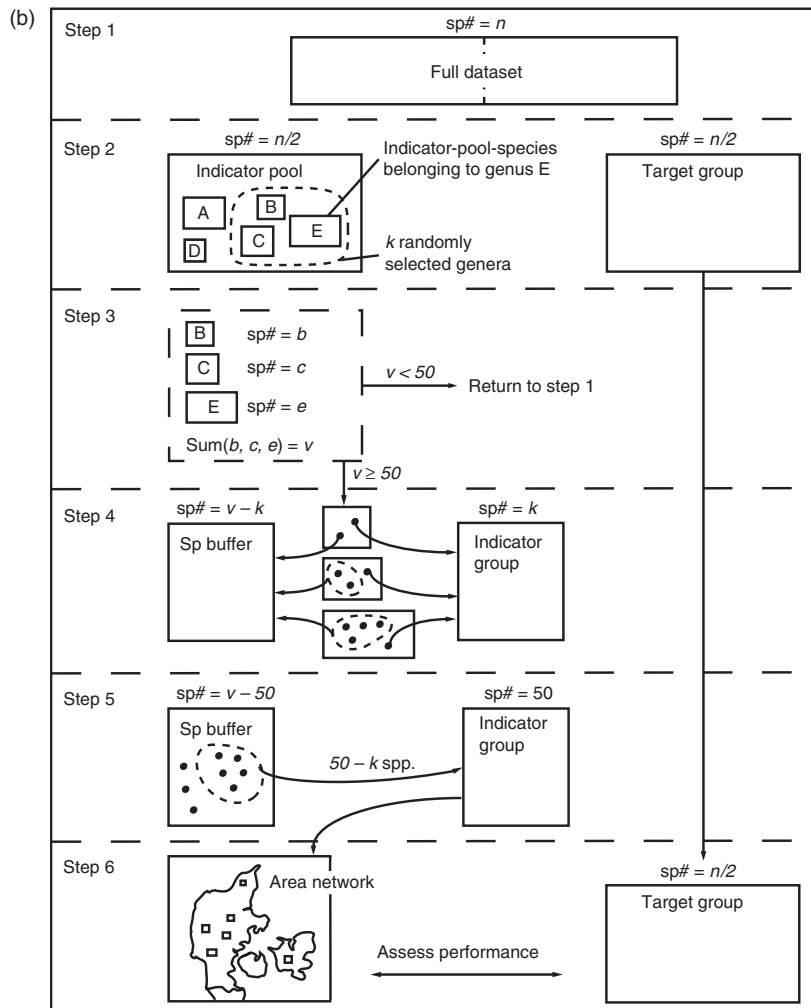


Figure 1 Description (a) and flow chart diagram (b) of the procedure used to select indicator groups with a specific number k of taxonomic sections (exemplified with genera) and to assess the indicator performance. Increasing k means increasing the taxonomic diversity of the indicator groups. The indicator groups contain 50 species. Area networks were selected to cover 5% (i.e. 31 sites, $\sim 3100 \text{ km}^2$) of the total area. The procedures were repeated 500 times for each of the major taxonomic categories (genera, families, Divisions 1 and 2) and for each value of k (see 'Methods' for complete outline of the experiments). For instance, we constructed 500 indicator groups with species from 30 genera, and for each of the 500 trials, we divided the species in the dataset into an indicator poll and a target group.

data monitoring and in related studies (see Table 1) (e.g. Sætersdal *et al.*, 1993; Howard *et al.*, 1998; Moore *et al.*, 2003). Division 1 included five taxonomic sections: plants, vertebrates, Lepidoptera spp., Diptera spp. and other invertebrates, while Division 2 included nine taxonomic sub-sections of Division 1 (see Table 1).

Selection of indicator groups

All indicator groups contained 50 randomly selected species, drawn from a varying number of taxonomic sections to represent different levels of taxonomic diversity. We constructed indicator groups composed of species from either

20, 30, 40 or 50 different genera, 10, 20, 30, 40 or 50 different families, one to nine different sections from Division 2 or finally one to five different sections from Division 1 (see Table 1). For comparison, 50 randomly selected species on average contained 46 different genera, 28 different families, eight different sections from Division 2 and five different sections from Division 1. The specific procedure for selection of indicator groups of varying taxonomic diversity and for assessment of indicator performance is available in Fig. 1.

We used indicator groups of constant size (i.e. 50 species) in order to isolate the effect of taxonomic diversity. Thus, the number of species sampled is treated as a fixed cost regardless of the composition of taxonomic sections, and the number of sections involved.

We chose indicator groups of 50 species for pragmatic reasons. This allowed us to select indicator groups with very low taxonomic diversity (e.g. species from only one group from Division 1 or 2) and with high diversity (e.g. species from 50 genera or families). Larsen *et al.* (2007) performed similar analyses with three different indicator group sizes and found overall the same pattern in the results for all three scenarios. Hence, we do not expect that changing the indicator group size will change the pattern of the results in the present analysis.

Selection of area networks

Area networks were selected to cover 5% (i.e. 31 sites, ~3100 km²) of the total area. All reserve selection problems were solved to optimality using the software package ILOG CPLEX 10.0 (ILOG, 2006)

Evaluation of reserve networks

We followed the data division procedure by Larsen *et al.* (2007), in which indicator groups were selected from one half of the species dataset, while the remaining half of the species constituted the target groups (i.e. the species that should be represented in networks based on the indicator groups) (see Fig. 1). If the target groups were composed of all non-indicator species in the dataset (e.g. Manne & Williams, 2003; Moore *et al.*, 2003; Kati *et al.*, 2004), the composition of the target groups would directly depend on the species composition of the indicator groups. Consequently, it would be difficult to determine whether high indicator performance is due to beneficial properties of the indicator group or to properties of the target group (see Larsen *et al.*, 2007). By dividing the dataset, the species compositions of the target groups are independent of the species compositions in the indicator groups. As the target groups consist of randomly chosen species, they have a species composition (taxonomic as well as distributional) similar to the dataset as a whole, capable of representing the best possible approximation to overall biodiversity given the available data.

However, avoiding this source of discrepancy in the present analysis comes at the cost of reducing the size of the target groups. We could have chosen to use a larger proportion (e.g. 80%) of the species in the full dataset as target groups to increase the power of testing the indicator performance. However, this would leave us with smaller indicator pools (*sensu* Fig. 1), thereby reducing the possible span of taxonomic diversity of the indicator groups.

We evaluated the performance of the resulting networks in terms of their representation of all target species, threatened target species and range-restricted target species, respectively. Threatened species were defined as those falling under the 'Critically endangered' (CR), 'Endangered' (EN) and 'Vulnerable' (VU) of The Danish Red Data Book (B-FDC, 2004). For true bugs and moths, we used the categories 'Endangered' (E) and 'Vulnerable' (V) in The Danish Red Data Book 1997 (Stoltze & Pihl, 1998), as these two groups are not yet updated in the most recent data book. Range-restricted species were defined as the quartile of species with the smallest distribution in *each* of the taxonomic sections in Division 2. We thereby avoided getting disproportionately many range-restricted species from those sections (e.g. orchids) that in general are more range restricted than species from other sections (e.g. birds) (in accordance with the procedure used by Moore *et al.*, 2003; Larsen *et al.*, 2007). Because several species within a section may have the same range size, in practice, the percentage of species from each taxonomic group included in the range-restricted species varied slightly (between 21 and 29%). Some species are both threatened and range restricted, and hence the two species groups partially overlap. Still, we evaluated the representation of both groups due to their relevance in conservation. In addition, we evaluated the representation of taxonomic diversity within the species in the target groups by measuring the number of genera, families and orders represented by the covered target species.

As benchmarks of performance, we compared the performance of the indicator groups with the effectiveness of area networks

- (1) selected randomly (1000 repetitions, Manne & Williams, 2003), which gives an estimate of the expected effectiveness by selecting the given area (5% of the total area) without any information on species' distributions;
- (2) selected to maximize the representation of 50 randomly chosen species from the indicator pools (500 repetitions), which gives insight into whether the indicator groups perform better than could be expected by random selection of species among all taxa;
- (3) selected to maximize the representation of all target species ($n = 423$) (500 repetitions), which gives an estimate of the maximal representation that is possible within the given area. The target groups were obtained by making 500 random divisions of the dataset (i.e. step 1 in Fig. 1).

We carried out standard analyses of variance to determine the level of statistical significance of the differences in effectiveness between the different indicator groups.

Methods to select indicator groups and to evaluate indicator performance were implemented in Java using the Java 2 Platform (Enterprise Edition Technology, version 1.4, Sun Microsystems, Santa Clara, CA, USA).

Results

Coverage of target species

Overall, we found that increasing the level of taxonomic diversity among the species in indicator groups resulted in no or only marginal increases in the overall effectiveness in representing species (Fig. 2a, Tables S1 and S3–S5). In other words, indicator groups composed of species from many different genera, families, etc. (i.e. representing high taxonomic diversity) overall did not perform considerably better than indicator groups comprising a lower taxonomic diversity (i.e. indicator groups composed of species from a smaller number of genera, families, etc.). Although increasing the level of taxonomic diversity did not generally increase effectiveness, changing the taxonomic diversity of indicator groups did result in some statistical significant differences in effectiveness.

The performance increased to some extent when increasing diversity at the higher taxonomic levels (Divisions 1 and 2). When changing diversity at the genus level, there were only statistically significant differences in the effectiveness of indicator groups composed of species from 20 genera and groups composed of species from 40 genera (see Table S3). Increasing the number of families had no significant influence on the performance except from the indicator groups with the highest taxonomic diversity (species from 50 families) which had significantly lower performance than indicator groups with lower diversity at the family level (see Table S3). These differences in performance were also apparent when measuring effectiveness in terms of the number of covered threatened or range-restricted species (see Tables S4 and S5).

As expected, the highest performance in representing target species (all, threatened and range-restricted species) is reached when area networks are selected to maximize the representation of all 423 target species. None of the indicator groups of varying taxonomic diversity performed significantly better than the indicator groups composed of 50 randomly selected species. In contrast, all indicator groups with varying taxonomic diversity outperformed randomly selected area networks.

Taxonomic diversity of covered species

Similarly, we found that increasing the taxonomic diversity of indicator groups resulted in no or only minor increases in the effectiveness of representing taxonomic diversity of the covered target species. Thus, indicator groups comprising a higher taxonomic diversity did not perform considerably better in representing species from different genera, families and orders than indicator groups of lower taxonomic diversity.

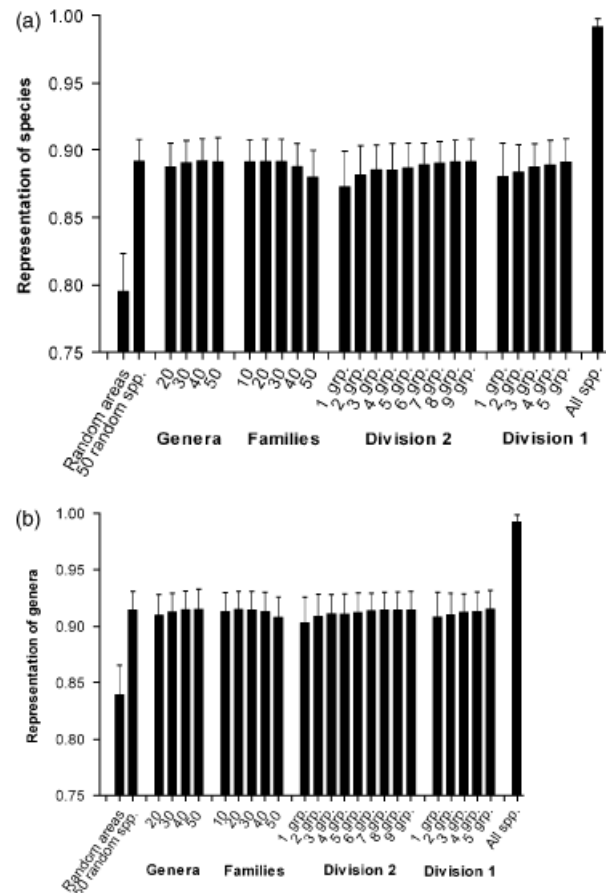


Figure 2 Representation of all target species (a) and target genera (b) by area networks selected to maximize species representation of randomly chosen indicator groups with changes in taxonomic diversity. The bars for each of the four taxonomic categories represent, from left to right, area networks based on indicator groups with increasing levels of taxonomic diversity. For comparison, results are shown for randomly selected area networks, networks selected to maximize the representation of 50 randomly chosen species and finally networks selected to maximize the representation of all target species. Error bars denote standard deviation.

As expected, reserve networks selected to maximize the representation of all target species had the highest coverage of genera, families and orders. In addition, groups of varying taxonomic diversity did not represent taxonomic diversity better than indicator groups composed of 50 randomly selected species. When measuring the number of genera and families represented by the covered target species, all indicator groups of varying taxonomic diversity performed significantly better than area networks selected at random. However, when measuring the number of orders represented by the covered target species, only indicator groups composed of species from nine sections from Division 2 performed better than random area selection.

Discussion

Our study shows that increasing the taxonomic diversity of randomly chosen indicator groups only has a marginal influence on the effectiveness in representing species or taxonomic diversity. The influence of varying the level of taxonomic diversity in indicator groups may be slightly positive or slightly negative, but overall the impact on indicator performance seems not to be considerable.

Although, it might intuitively seem as a better approach to target plants, birds and insect rather than targeting only plants, our results show that this is not necessarily the case (if the same number of species is used). Taxonomically distant species (e.g. a bird and an orchid) may live in the same habitat and thereby do not always contribute with more ecological or distributional variation than two closely related species.

However, our analysis suggests that indicator groups with particularly low diversity at the higher taxonomic levels tend to have the lowest performance. In particular, indicator groups with species from only one section from Division 2 (e.g. orchids, birds, moths, butterflies) had significantly lower performance in representing species (all, threatened and range-restricted species, $P < 0.05$) than all other groups of varying taxonomic diversity in our study.

These findings could have practical implications when acquiring data for future conservation projects. Our findings suggest that there might not be any benefit in acquiring distributional data for a large number of taxonomic sections, because species data from a few higher taxonomic sections are likely to be just as effective when used for protected area priority setting. Thus, it might be of minor importance to consider taxonomic diversity when selecting indicator groups for guiding reserve selection.

It might be more cost-efficient to acquire data from taxonomic groups that are well studied and easily sampled in the field, rather than collecting data for many groups where taxonomic expertise may be less readily available.

However, it should be noted that we only assess indicator groups of 50 species. Thus, using several taxonomic groups rather than one could indeed improve indicator performance, but that would probably be a result of an increased species number rather than an increased taxonomic diversity *per se*. Moreover, it should be emphasized that the present analysis assesses the influence of taxonomic diversity *per se*, rather than whether specific taxonomic groups or specific combinations of groups perform better than others. Moreover, it is left for future studies to repeat the analyses for other geographical regions and different spatial scales too.

Because taxonomic diversity *per se* only marginally influences effectiveness, other factors account for the observed variation in effectiveness among the indicator groups of varying taxonomic diversity (see SD in Fig. 2a and 2b). These other factors may include distributional characteristics such as narrow range size, which appear to influence the indicator performance (e.g. Manne & Williams, 2003; Larsen *et al.*, 2007). Larsen *et al.* (2007) found that increasing the proportion of range-restricted species or threatened species in

indicator groups resulted in an increased representation of species, in particular, an improved representation of other range-restricted species. In the present study, the analyses were repeated on the Danish dataset to assess whether range-restricted species could account for the differences in the indicator performance for the Danish dataset. We created randomly chosen indicator groups of 50 species with 0, 10, 20, 30, 40 and 50 species, being either range restricted or threatened. Despite differences in spatial scale (both extent and grain size) and biogeographic region between the sub-Saharan African dataset and the Danish dataset, the results supported the findings by Larsen *et al.* (2007), that increasing the proportion of range-restricted or threatened species increases the representation of species (about 1–2%), and in particular, the representation of other range-restricted species (between 5 and 23%) compared with randomly selected indicator groups (Tables S2, S10–S12).

This relationship between the indicator group performance and the proportion of range-restricted species in the indicator group may also explain why performance decreased at the family level (rather than increased as for the other taxonomic levels).

The family level is the only taxonomic category for which it is possible to substantially increase the taxonomic diversity, as compared with the diversity represented by 50 randomly selected species (see 'Methods'). Even if families, and other taxonomic sections, are selected with probabilities proportional to the number of species present in the families, the species in indicator groups with a particularly high diversity of families (40 or 50 families) will largely be selected among species from species-poor families. Species from species-poor families tend to have much wider ranges. For example, species in families with less than five species are on average present in 271 UTM cells ($SD = 240$, $n = 93$), whereas species in families with five or more species on average are present in 164 UTM cells ($SD = 186$, $n = 754$). Accordingly, the species in the indicator groups with a diversity of 40 and 50 families have considerably larger mean range sizes than the other groups. Widespread species are poor indicators (Andelman & Fagan, 2000; Williams *et al.*, 2000; Moritz *et al.*, 2001; Larsen *et al.*, 2007) and the relatively high proportion of widespread species may explain the observed decrease in effectiveness at the family level for the highest diversity level.

Interestingly, none of the indicator groups of varying taxonomic diversity have a significantly higher performance than random sets of species, neither when measuring the number of species covered (all, threatened or range-restricted species), nor the taxonomic diversity of the covered species (number of genera, families and orders). However, the variance in performance within the set of 500 randomly selected indicator groups is high, as was the case with the indicator groups of varying taxonomic diversity. Therefore, it cannot be concluded that any set of species performs well as indicators. Available datasets can be biased towards species with specific distributional or ecological traits, which may influence the indicator performance. For example, datasets with a large proportion of wide-range species must

be expected to have a poorer indicator performance than unbiased random sets of species such as those used in the present analysis. Nevertheless, this study confirms the results of previous studies (Bonn *et al.*, 2002; Gaston & Rodrigues, 2003; Manne & Williams, 2003; Larsen *et al.*, 2007) that reserve networks selected to represent randomly selected indicator groups perform considerably better in representing target species (all, threatened and range-restricted species) than areas selected at random. Therefore, when choosing a benchmark for performance, it clearly makes a difference if random area networks (e.g. Lund & Rahbek, 2002; Lawler *et al.*, 2003; Moore *et al.*, 2003; Warman *et al.*, 2004) or networks selected to maximize the representation of random sets of species (Bonn *et al.*, 2002; Gaston & Rodrigues, 2003; Manne & Williams, 2003; Larsen *et al.*, 2007) are used, because indicator groups may be deemed to be effective when compared with random area networks, while considered ineffective when compared with networks selected to represent species groups.

This study also reveals that higher taxonomic groups are well represented, irrespective of the area selection approach. For instance, it is shown that random area selection is just as effective in covering species from a diversity of orders as networks selected to represent 50 randomly chosen species. This is because the cumulative range sizes of species in higher taxonomic groups usually increase with increasing level in the taxonomic hierarchy (e.g. Larsen & Rahbek, 2005). Thus, even randomly distributed sets of areas are likely to cover a large number of the higher taxonomic groups by chance. We also see that wide-ranged (common-quartile) species (Tables S1 and S6) are almost always represented even by random area networks due to their large range sizes. In the present analysis, all networks selected to represent indicator groups of varying taxonomic diversity have a coverage of wide-ranged species that is just as effective as networks selected to maximize the representation of all 423 target species (i.e. the estimate of the maximal representation that is possible within the given area).

Some caveats apply to this study. First, we use a simple measure of representation of species (or genera, families, etc.) to evaluate performance. Thus, this study does not consider, for example, the persistence of species, genetic diversity or ecosystem processes which are the ultimate goals of nature conservation (Margules & Pressey, 2000). Unfortunately, there is still a general lack of data about the distribution of these different measures of biodiversity, and we lack information about the distribution of processes that threaten their persistence. Thus, it remains one of the biggest challenges in systematic conservation planning to improve our ability to consider more complex goals of biodiversity representation, even more so biodiversity persistence. Using alternative conservation targets can potentially lead to other conclusions concerning the importance of taxonomic diversity in indicator performance than those found in the present analysis.

Second, the present study and the study carried out by Larsen *et al.* (2007) analyse the importance of taxonomic diversity defined as the number of taxonomic sections either

from certain taxonomic nomenclature ranks or from pragmatically defined categories. This definition of diversity is influenced by the ways these taxonomic divisions are interpreted within different taxonomic categories. For example, in the present dataset, 189 birds are divided into 50 families, whereas 252 hoverflies are divided into three families. We select the taxonomic sections (e.g. families) for the indicator groups with probabilities proportional to the number of species within each section to reduce the tendency of species-poor taxonomic sections to dominate the indicator groups. Still, as discussed above, our definition of taxonomic diversity and the selection procedure applied may influence the results of the analyses by biasing higher taxon diversity or the distributional characteristics (e.g. range size compositions) of the indicator groups. It appears that any definition of taxonomic diversity and any selection procedure either lead to some bias of the composition of the indicator and/or target groups, or, if using fully randomly selected indicator groups, reduce the taxonomic span that is likely to occur in the indicator groups.

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Supporting Information

Additional Supporting Information may be found in the online version of this article:

Table S1. Representation of target species and taxonomic diversity in per cent, standard deviation in parentheses.

Wide range species refer to the quartile of species with largest range sizes from each taxonomic section from Division 2. Area selection criteria are: random area selection, networks selected to maximise representation of 50 randomly chosen species, all target species, 50 randomly selected species from 20–50 genera, 10–50 families, 1–9 sections from Division 2 and finally 1–5 sections from Division 1.

Table S2. Representation of target species in per cent, standard deviation in parentheses. *Range-restricted* species refer to rare quartile species. *Narrow-ranged* species refer to species that occur in less than 6 sites. We included both ways of defining species with narrow range sizes in accordance with the analyses performed by Larsen *et al.*, In Press). Area selection criteria are: networks selected to maximise representation of 50 randomly selected species, 50 randomly chosen species of which 0–50 are either threatened or range-restricted, and finally 50 randomly selected species of which 0–40 are narrow-ranged. The dataset included 107 narrow-ranged species, but since the number of narrow-ranged species varied in the indicator pools by chance we avoided selection of indicator groups composed of 50 narrow-ranged species.

Table S3. Tukey HSD test of differences in performance measured as representation of all target species (see Table S1). Significant differences ($P < 0.05$) are marked with *.

Table S4. Tukey HSD test of differences in performance measured as representation of threatened target species (see Table S1). Significant differences ($P < 0.05$) are marked with *.

Table S5. Tukey HSD test of differences in performance measured as representation of range-restricted target

species (see Table S1). Significant differences ($P < 0.05$) are marked with *.

Table S6. Tukey HSD test of differences in performance measured as representation of wide ranged target species (see Table S1). Significant differences ($P < 0.05$) are marked with *.

Table S7. Tukey HSD test of differences in performance measured as representation of target genera (see Table S1). Significant differences ($P < 0.05$) are marked with *.

Table S8. Tukey HSD test of differences in performance measured as representation of target families (see Table S1). Significant differences ($P < 0.05$) are marked with *.

Table S9. Tukey HSD test of differences in performance measured as representation of target orders (see Table S1). Significant differences ($P < 0.05$) are marked with *.

Table S10. Tukey HSD test of differences in performance measured as representation of all target species (see Table S2). Significant differences ($P < 0.05$) are marked with *.

Table S11. Tukey HSD test of differences in performance measured as representation of range-restricted target species (see Table S2). Significant differences ($P < 0.05$) are marked with *.

Table S12. Tukey HSD test of differences in performance measured as representation of narrow-ranged target species (see Table S2). Significant differences ($P < 0.05$) are marked with *.

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Supplementary Table 1

Representation of target species and taxonomic diversity in per cent, standard deviation in parentheses. Wide range species refer to the quartile of species with largest range sizes from each taxonomic section from Division 2. Area selection criteria are: random area selection, networks selected to maximise representation of 50 randomly chosen species, all target species, 50 randomly selected species from 20-50 genera, 10-50 families, 1-9 sections from Division 2 and finally 1-5 sections from Division 1.

	All spp.	Threatened spp.	range-restricted spp.	Wide range spp.	Genera	Families	Orders
Random areas	79,62 (2,74)	40,57 (6,57)	33,17 (6,86)	99,98 (0,12)	84,07 (2,54)	91,90 (2,52)	96,17 (3,32)
50 random spp.	89,16 (1,63)	62,83 (6,00)	61,28 (5,27)	100,00 (0,00)	91,46 (1,60)	93,55 (2,38)	96,81 (2,97)
All target spp.	99,14 (0,59)	96,46 (2,63)	96,68 (2,23)	100,00 (0,00)	99,24 (0,64)	99,29 (0,96)	99,51 (1,41)
20 genera	88,72 (1,81)	61,41 (6,37)	59,66 (5,82)	100,00 (0,00)	90,99 (1,85)	93,41 (2,38)	96,56 (3,23)
30 genera	89,05 (1,63)	62,56 (5,92)	60,81 (5,36)	100,00 (0,00)	91,30 (1,66)	93,47 (2,34)	96,45 (3,28)
40 genera	89,21 (1,62)	63,49 (5,54)	61,39 (5,28)	100,00 (0,00)	91,48 (1,63)	93,54 (2,20)	96,62 (3,20)
50 genera	89,12 (1,83)	63,33 (6,42)	61,09 (5,97)	100,00 (0,00)	91,51 (1,80)	93,52 (2,30)	96,56 (3,22)
10 families	89,11 (1,65)	62,70 (6,09)	61,12 (5,26)	100,00 (0,00)	91,32 (1,68)	93,58 (2,32)	96,75 (3,23)
20 families	89,15 (1,65)	63,14 (5,94)	61,07 (5,45)	100,00 (0,00)	91,50 (1,66)	93,55 (2,25)	96,66 (3,17)
30 families	89,13 (1,66)	63,24 (6,07)	61,17 (5,27)	100,00 (0,00)	91,45 (1,65)	93,42 (2,30)	96,69 (3,11)
40 families	88,74 (1,75)	62,35 (6,29)	59,97 (5,64)	100,00 (0,04)	91,31 (1,72)	93,64 (2,27)	96,53 (3,09)
50 families	87,98 (1,98)	60,43 (6,56)	57,64 (6,11)	100,00 (0,04)	90,81 (1,77)	93,63 (2,25)	96,50 (3,08)
1 section, Div. 2	87,25 (2,63)	58,05 (6,96)	55,99 (7,86)	100,00 (0,04)	90,33 (2,23)	93,42 (2,32)	96,62 (3,13)
2 section, Div. 2	88,14 (2,21)	61,42 (6,77)	58,19 (6,86)	100,00 (0,04)	90,89 (1,98)	93,70 (2,37)	96,80 (3,28)
3 section, Div. 2	88,52 (1,87)	62,13 (6,29)	59,34 (5,91)	100,00 (0,00)	91,13 (1,70)	93,56 (2,24)	96,45 (3,16)
4 section, Div. 2	88,51 (1,99)	62,16 (6,09)	59,29 (6,22)	100,00 (0,04)	91,10 (1,77)	93,50 (2,13)	96,81 (3,21)
5 section, Div. 2	88,67 (1,86)	62,23 (6,25)	59,62 (5,94)	100,00 (0,00)	91,23 (1,74)	93,45 (2,33)	96,63 (3,19)
6 section, Div. 2	88,89 (1,64)	62,65 (5,62)	60,26 (5,30)	100,00 (0,00)	91,37 (1,58)	93,60 (2,17)	96,55 (3,17)
7 section, Div. 2	89,02 (1,62)	62,85 (5,96)	60,73 (5,32)	100,00 (0,00)	91,44 (1,57)	93,61 (2,19)	96,68 (3,31)
8 section, Div. 2	89,11 (1,64)	63,18 (5,91)	61,14 (5,35)	100,00 (0,00)	91,44 (1,60)	93,54 (2,38)	96,64 (3,13)
9 section, Div. 2	89,13 (1,68)	63,05 (6,16)	61,11 (5,50)	100,00 (0,04)	91,46 (1,64)	93,49 (2,32)	96,85 (3,12)
1 section, Div. 1	88,03 (2,50)	60,52 (7,26)	58,18 (7,50)	100,00 (0,04)	90,84 (2,19)	93,70 (2,19)	96,81 (3,14)
2 section, Div. 1	88,37 (2,02)	61,70 (6,56)	58,95 (6,42)	100,00 (0,00)	91,03 (1,89)	93,36 (2,32)	96,62 (3,26)
3 section, Div. 1	88,73 (1,75)	62,57 (5,96)	60,03 (5,64)	100,00 (0,00)	91,25 (1,64)	93,45 (2,29)	96,51 (3,27)
4 section, Div. 1	88,86 (1,85)	62,65 (6,22)	60,07 (5,91)	100,00 (0,04)	91,31 (1,72)	93,66 (2,32)	96,54 (3,26)
5 section, Div. 1	89,10 (1,72)	62,73 (6,04)	60,96 (5,40)	100,00 (0,00)	91,53 (1,66)	93,45 (2,34)	96,39 (3,32)

Supplementary Table 2

Representation of target species in per cent, standard deviation in parentheses.

Range-restricted species refer to rare quartile species. *Narrow-ranged* species refer to species that occur in less than 6 sites. We included both ways of defining species with narrow range sizes in accordance with the analyses performed by Larsen et al., In Press).

Area selection criteria are: networks selected to maximise representation of 50 randomly selected species, 50 randomly chosen species of which 0-50 are either threatened or range-restricted, and finally 50 randomly selected species of which 0-40 are narrow-ranged. The dataset included 107 narrow-ranged species, but since the number of narrow-ranged species varied in the indicator pools by chance we avoided selection of indicator groups composed of 50 narrow-ranged species.

	All spp.	Range-restricted spp.	Narrow-ranged spp.
50 random spp.	89,16 (1,63)	61,28 (5,27)	42,00 (7,87)
0 range-restricted	89,13 (1,70)	61,02 (5,87)	41,96 (8,23)
10 range-restricted	89,09 (1,67)	61,11 (5,40)	42,30 (8,32)
20 range-restricted	89,42 (1,58)	61,75 (5,32)	42,80 (7,72)
30 range-restricted	90,02 (1,47)	63,84 (4,83)	45,89 (7,34)
40 range-restricted	90,19 (1,42)	64,43 (4,69)	45,95 (7,15)
50 range-restricted	90,57 (1,42)	65,42 (4,71)	47,35 (7,38)
0 narrow-ranged	88,87 (1,72)	60,33 (5,67)	39,83 (8,47)
10 narrow-ranged	89,29 (1,67)	61,46 (5,47)	43,10 (7,80)
20 narrow-ranged	89,81 (1,50)	63,07(5,06)	46,24 (6,96)
30 narrow-ranged	90,40 (1,35)	64,78 (4,36)	48,68 (6,60)
40 narrow-ranged	90,96 (1,31)	66,94 (4,38)	51,68 (6,35)
0 threatened	89,02 (1,69)	61,04 (5,47)	41,05 (8,47)
10 threatened	89,22 (1,67)	61,12 (5,43)	42,65 (8,03)
20 threatened	89,20 (1,68)	61,06 (5,53)	43,16 (7,80)
30 threatened	89,53 (1,55)	61,97 (5,18)	44,52 (7,42)
40 threatened	89,64 (1,55)	62,31 (5,12)	45,01 (7,17)
50 threatened	90,19 (1,44)	64,14 (4,74)	47,13 (6,79)

Supplementary table 3 (all target species)

(c)

	{1}	{2}	{3}	{4}	{5}	{6}	{7}	{8}	{9}	{10}	{11}
Random areas {1}		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
50 random spp. {2}	*0,000		*0,000	*0,000	*0,000	*0,000	*0,000	*0,010	0,888	1,000	1,000
All target spp. {3}	*0,000	*0,000		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
1 section Div.2 {4}	*0,000	*0,000	*0,000		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
2 section Div.2 {5}	*0,000	*0,000	*0,000	*0,000		0,249	0,324	*0,004	*0,000	*0,000	*0,000
3 section Div.2 {6}	*0,000	*0,000	*0,000	*0,000	0,249		1,000	1,000	0,264	*0,008	*0,000
4 section Div.2 {7}	*0,000	*0,000	*0,000	*0,000	0,324	1,000		1,000	0,199	*0,005	*0,000
5 section Div.2 {8}	*0,000	*0,010	*0,000	*0,000	*0,004	1,000	1,000		0,980	0,350	0,051
6 section Div.2 {9}	*0,000	0,888	*0,000	*0,000	*0,000	0,264	0,199	0,980		1,000	0,991
7 section Div.2 {10}	*0,000	1,000	*0,000	*0,000	*0,000	*0,008	*0,005	0,350	1,000		1,000
8 section Div.2 {11}	*0,000	1,000	*0,000	*0,000	*0,000	*0,000	*0,000	0,051	0,991	1,000	
9 section Div.2 {12}	*0,000	1,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,025	0,965	1,000	1,000

(d)

	{1}	{2}	{3}	{4}	{5}	{6}	{7}
Random areas {1}			*0,000	*0,000	*0,000	*0,000	*0,000
50 random spp. {2}	*0,000			*0,000	*0,000	*0,000	0,066 0,728
All target spp. {3}	*0,000	*0,000			*0,000	*0,000	*0,000
1 section Div.1 {4}	*0,000	*0,000	*0,000			0,420	*0,000 *0,000
2 section Div.1 {5}	*0,000	*0,000	*0,000	0,420			0,371 *0,013
3 section Div.1 {6}	*0,000	0,066	*0,000	*0,000	0,371		1,000
4 section Div.1 {7}	*0,000	0,728	*0,000	*0,000	*0,013	1,000	
5 section Div.1 {8}	*0,000	1,000	*0,000	*0,000	*0,000	0,291	0,973

Supplementary table 4 (threatened target species)

(c)

	{1}	{2}	{3}	{4}	{5}	{6}	{7}	{8}	{9}	{10}	{11}
Random areas {1}		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
50 random spp. {2}	*0,000		*0,000	*0,000	0,064	0,991	0,995	0,999	1,000	1,000	1,000
All target spp. {3}	*0,000	*0,000		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
1 section Div.2 {4}	*0,000	*0,000	*0,000		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
2 section Div.2 {5}	*0,000	0,064	*0,000	*0,000		0,987	0,979	0,946	0,234	0,052	*0,002
3 section Div.2 {6}	*0,000	0,991	*0,000	*0,000	0,987		1,000	1,000	1,000	0,986	0,569
4 section Div.2 {7}	*0,000	0,995	*0,000	*0,000	0,979	1,000		1,000	1,000	0,991	0,628
5 section Div.2 {8}	*0,000	0,999	*0,000	*0,000	0,946	1,000	1,000		1,000	0,998	0,756
6 section Div.2 {9}	*0,000	1,000	*0,000	*0,000	0,234	1,000	1,000	1,000		1,000	1,000
7 section Div.2 {10}	*0,000	1,000	*0,000	*0,000	0,052	0,986	0,991	0,998	1,000		1,000
8 section Div.2 {11}	*0,000	1,000	*0,000	*0,000	*0,002	0,569	0,628	0,756	1,000	1,000	
9 section Div.2 {12}	*0,000	1,000	*0,000	*0,000	*0,008	0,824	0,864	0,934	1,000	1,000	1,000

(d)

	{1}	{2}	{3}	{4}	{5}	{6}	{7}
Random areas {1}		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
50 random spp. {2}	*0,000		*0,000	*0,000	0,402	1,000	1,000
All target spp. {3}	*0,000	*0,000		*0,000	*0,000	*0,000	*0,000
1 section Div.1 {4}	*0,000	*0,000	*0,000		0,296	*0,000	*0,000
2 section Div.1 {5}	*0,000	0,402	*0,000	0,296		0,883	0,762
3 section Div.1 {6}	*0,000	1,000	*0,000	*0,000	0,883		1,000
4 section Div.1 {7}	*0,000	1,000	*0,000	*0,000	0,762	1,000	
5 section Div.1 {8}	*0,000	1,000	*0,000	*0,000	0,611	1,000	1,000

Supplementary table 5 (range-restricted target species)

(c)

	{1}	{2}	{3}	{4}	{5}	{6}	{7}	{8}	{9}	{10}	{11}
Random areas {1}		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
50 random spp. {2}	*0,000		*0,000	*0,000	*0,000	*0,000	*0,000	*0,002	0,534	1,000	1,000
All target spp. {3}	*0,000	*0,000		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
1 section Div.2 {4}	*0,000	*0,000	*0,000		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
2 section Div.2 {5}	*0,000	*0,000	*0,000	*0,000		0,268	0,351	*0,029	*0,000	*0,000	*0,000
3 section Div.2 {6}	*0,000	*0,000	*0,000	*0,000	0,268		1,000	1,000	0,737	*0,041	*0,000
4 section Div.2 {7}	*0,000	*0,000	*0,000	*0,000	0,351	1,000		1,000	0,641	*0,026	*0,000
5 section Div.2 {8}	*0,000	*0,002	*0,000	*0,000	*0,029	1,000	1,000		0,994	0,330	*0,011
6 section Div.2 {9}	*0,000	0,534	*0,000	*0,000	*0,000	0,737	0,641	0,994		1,000	0,807
7 section Div.2 {10}	*0,000	1,000	*0,000	*0,000	*0,000	*0,041	*0,026	0,330	1,000		1,000
8 section Div.2 {11}	*0,000	1,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,011	0,807	1,000	
9 section Div.2 {12}	*0,000	1,000	*0,000	*0,000	*0,000	*0,001	*0,000	*0,016	0,859	1,000	1,000

(d)

	{1}	{2}	{3}	{4}	{5}	{6}	{7}
Random areas {1}		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
50 random spp. {2}	*0,000		*0,000	*0,000	*0,000	0,138	0,181
All target spp. {3}	*0,000	*0,000		*0,000	*0,000	*0,000	*0,000
1 section Div.1 {4}	*0,000	*0,000	*0,000		0,938	*0,000	*0,000
2 section Div.1 {5}	*0,000	*0,000	*0,000	0,938		0,400	0,328
3 section Div.1 {6}	*0,000	0,138	*0,000	*0,000	0,400		1,000
4 section Div.1 {7}	*0,000	0,181	*0,000	*0,000	0,328	1,000	
5 section Div.1 {8}	*0,000	1,000	*0,000	*0,000	*0,000	0,716	0,786

Supplementary Table 7 Target genera

Tukey HSD test of differences in performance measured as representation of target genera (see supplementary table 1). Significant differences ($p < 0,05$) are marked with *.

(a)

	{1}	{2}	{3}	{4}	{5}	{6}
Random areas {1}		*0,000	*0,000	*0,000	*0,000	*0,000
50 random spp. {2}	*0,000		*0,000	*0,009	0,999	1,000
All target spp. {3}	*0,000	*0,000		*0,000	*0,000	*0,000
20 genera {4}	*0,000	*0,009	*0,000		0,581	*0,005
30 genera {5}	*0,000	0,999	*0,000	0,581		0,998
40 genera {6}	*0,000	1,000	*0,000	*0,005	0,998	
50 genera {7}	*0,000	1,000	*0,000	*0,001	0,980	1,000

(b)

	{1}	{2}	{3}	{4}	{5}	{6}	{7}
Random areas {1}		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
50 random spp. {2}	*0,000		*0,000	1,000	1,000	1,000	1,000
All target spp. {3}	*0,000	*0,000		*0,000	*0,000	*0,000	*0,000
10 families {4}	*0,000	1,000	*0,000		0,998	1,000	1,000
20 families {5}	*0,000	1,000	*0,000	0,998		1,000	0,998
30 families {6}	*0,000	1,000	*0,000	1,000	1,000		1,000
40 families {7}	*0,000	1,000	*0,000	1,000	0,998	1,000	
50 families {8}	*0,000	*0,000	*0,000	*0,002	*0,000	*0,000	*0,003

Supplementary table 7 (target genera)

(c)

	{1}	{2}	{3}	{4}	{5}	{6}	{7}	{8}	{9}	{10}	{11}
Random areas {1}		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
50 random spp. {2}	*0,000		*0,000	*0,000	*0,000	0,392	0,189	0,948	1,000	1,000	1,000
All target spp. {3}	*0,000	*0,000		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
1 section Div.2 {4}	*0,000	*0,000	*0,000		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
2 section Div.2 {5}	*0,000	*0,000	*0,000	*0,000		0,923	0,989	0,336	*0,007	*0,000	*0,000
3 section Div.2 {6}	*0,000	0,392	*0,000	*0,000	0,923		1,000	1,000	0,943	0,531	0,551
4 section Div.2 {7}	*0,000	0,189	*0,000	*0,000	0,989	1,000		1,000	0,789	0,287	0,304
5 section Div.2 {8}	*0,000	0,948	*0,000	*0,000	0,336	1,000	1,000		1,000	0,981	0,984
6 section Div.2 {9}	*0,000	1,000	*0,000	*0,000	*0,007	0,943	0,789	1,000		1,000	1,000
7 section Div.2 {10}	*0,000	1,000	*0,000	*0,000	*0,000	0,531	0,287	0,981	1,000		1,000
8 section Div.2 {11}	*0,000	1,000	*0,000	*0,000	*0,000	0,551	0,304	0,984	1,000	1,000	
9 section Div.2 {12}	*0,000	1,000	*0,000	*0,000	*0,000	0,450	0,227	0,965	1,000	1,000	1,000

(d)

	{1}	{2}	{3}	{4}	{5}	{6}	{7}
Random areas {1}		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
50 random spp. {2}	*0,000		*0,000	*0,000	*0,035	0,983	1,000
All target spp. {3}	*0,000	*0,000		*0,000	*0,000	*0,000	*0,000
1 section Div.1 {4}	*0,000	*0,000	*0,000		0,995	0,061	*0,008
2 section Div.1 {5}	*0,000	*0,035	*0,000	0,995		0,977	0,743
3 section Div.1 {6}	*0,000	0,983	*0,000	0,061	0,977		1,000
4 section Div.1 {7}	*0,000	1,000	*0,000	*0,008	0,743	1,000	
5 section Div.1 {8}	*0,000	1,000	*0,000	*0,000	*0,004	0,766	0,981

Supplementary Table 8 Target families

Tukey HSD test of differences in performance measured as representation of target families (see supplementary table 1). Significant differences ($p < 0,05$) are marked with *.

(a)

	{1}	{2}	{3}	{4}	{5}	{6}
Random areas {1}		*0,000	*0,000	*0,000	*0,000	*0,000
50 random spp. {2}	*0,000		*0,000	1,000	1,000	1,000
All target spp. {3}	*0,000	*0,000		*0,000	*0,000	*0,000
20 genera {4}	*0,000	1,000	*0,000		1,000	1,000
30 genera {5}	*0,000	1,000	*0,000	1,000		1,000
40 genera {6}	*0,000	1,000	*0,000	1,000	1,000	
50 genera {7}	*0,000	1,000	*0,000	1,000	1,000	1,000

(b)

	{1}	{2}	{3}	{4}	{5}	{6}	{7}
Random areas {1}		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
50 random spp. {2}	*0,000		*0,000	1,000	1,000	1,000	1,000
All target spp. {3}	*0,000	*0,000		*0,000	*0,000	*0,000	*0,000
10 families {4}	*0,000	1,000	*0,000		1,000	1,000	1,000
20 families {5}	*0,000	1,000	*0,000	1,000		1,000	1,000
30 families {6}	*0,000	1,000	*0,000	1,000	1,000		0,999
40 families {7}	*0,000	1,000	*0,000	1,000	1,000	0,999	
50 families {8}	*0,000	1,000	*0,000	1,000	1,000	0,999	1,000

Supplementary table 8 (target families)

(c)

	{1}	{2}	{3}	{4}	{5}	{6}	{7}	{8}	{9}	{10}	{11}
Random areas {1}		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
50 random spp. {2}	*0,000		*0,000	1,000	1,000	1,000	1,000	1,000	1,000	1,000	1,000
All target spp. {3}	*0,000	*0,000		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
1 section Div.2 {4}	*0,000	1,000	*0,000		0,975	1,000	1,000	1,000	1,000	1,000	1,000
2 section Div.2 {5}	*0,000	1,000	*0,000	0,975		1,000	1,000	0,994	1,000	1,000	1,000
3 section Div.2 {6}	*0,000	1,000	*0,000	1,000	1,000		1,000	1,000	1,000	1,000	1,000
4 section Div.2 {7}	*0,000	1,000	*0,000	1,000	1,000	1,000		1,000	1,000	1,000	1,000
5 section Div.2 {8}	*0,000	1,000	*0,000	1,000	0,994	1,000	1,000		1,000	1,000	1,000
6 section Div.2 {9}	*0,000	1,000	*0,000	1,000	1,000	1,000	1,000	1,000		1,000	1,000
7 section Div.2 {10}	*0,000	1,000	*0,000	1,000	1,000	1,000	1,000	1,000	1,000		1,000
8 section Div.2 {11}	*0,000	1,000	*0,000	1,000	1,000	1,000	1,000	1,000	1,000	1,000	
9 section Div.2 {12}	*0,000	1,000	*0,000	1,000	1,000	1,000	1,000	1,000	1,000	1,000	1,000

(d)

	{1}	{2}	{3}	{4}	{5}	{6}	{7}
Random areas {1}		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
50 random spp. {2}	*0,000		*0,000	1,000	1,000	1,000	1,000
All target spp. {3}	*0,000	*0,000		*0,000	*0,000	*0,000	*0,000
1 section Div.1 {4}	*0,000	1,000	*0,000		0,821	0,995	1,000
2 section Div.1 {5}	*0,000	1,000	*0,000	0,821		1,000	0,948
3 section Div.1 {6}	*0,000	1,000	*0,000	0,995	1,000		1,000
4 section Div.1 {7}	*0,000	1,000	*0,000	1,000	0,948	1,000	
5 section Div.1 {8}	*0,000	1,000	*0,000	0,993	1,000	1,000	1,000

Supplementary Table 9 Target orders

Tukey HSD test of differences in performance measured as representation of target orders (see supplementary table 1). Significant differences ($p < 0,05$) are marked with *.

(a)

	{1}	{2}	{3}	{4}	{5}	{6}
Random areas {1}		0,052	*0,000	0,890	0,998	0,641
50 random spp. {2}	0,052		*0,000	1,000	0,990	1,000
All target spp. {3}	*0,000	*0,000		*0,000	*0,000	*0,000
20 genera {4}	0,890	1,000	*0,000		1,000	1,000
30 genera {5}	0,998	0,990	*0,000	1,000		1,000
40 genera {6}	0,641	1,000	*0,000	1,000	1,000	
50 genera {7}	0,893	1,000	*0,000	1,000	1,000	1,000

(b)

	{1}	{2}	{3}	{4}	{5}	{6}	{7}
Random areas {1}		0,052	*0,000	0,134	0,480	0,340	0,949
50 random spp. {2}	0,052		*0,000	1,000	1,000	1,000	1,000
All target spp. {3}	*0,000	*0,000		*0,000	*0,000	*0,000	*0,000
10 families {4}	0,134	1,000	*0,000		1,000	1,000	1,000
20 families {5}	0,480	1,000	*0,000	1,000		1,000	1,000
30 families {6}	0,340	1,000	*0,000	1,000	1,000		1,000
40 families {7}	0,949	1,000	*0,000	1,000	1,000	1,000	
50 families {8}	0,984	0,999	*0,000	1,000	1,000	1,000	1,000

Supplementary table 9 (target orders)

(c)

	{1}	{2}	{3}	{4}	{5}	{6}	{7}	{8}	{9}	{10}	{11}
Random areas {1}		0,052	*0,000	0,670	0,060	0,998	0,053	0,614	0,912	0,358	0,568
50 random spp. {2}	0,052		*0,000	1,000	1,000	0,991	1,000	1,000	1,000	1,000	1,000
All target spp. {3}	*0,000	*0,000		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
1 section Div.2 {4}	0,670	1,000	*0,000		1,000	1,000	1,000	1,000	1,000	1,000	1,000
2 section Div.2 {5}	0,060	1,000	*0,000	1,000		0,993	1,000	1,000	1,000	1,000	1,000
3 section Div.2 {6}	0,998	0,991	*0,000	1,000	0,993		0,991	1,000	1,000	1,000	1,000
4 section Div.2 {7}	0,053	1,000	*0,000	1,000	1,000	0,991		1,000	1,000	1,000	1,000
5 section Div.2 {8}	0,614	1,000	*0,000	1,000	1,000	1,000	1,000		1,000	1,000	1,000
6 section Div.2 {9}	0,912	1,000	*0,000	1,000	1,000	1,000	1,000	1,000		1,000	1,000
7 section Div.2 {10}	0,358	1,000	*0,000	1,000	1,000	1,000	1,000	1,000	1,000		1,000
8 section Div.2 {11}	0,568	1,000	*0,000	1,000	1,000	1,000	1,000	1,000	1,000	1,000	
9 section Div.2 {12}	*0,024	1,000	*0,000	1,000	1,000	0,968	1,000	1,000	0,999	1,000	1,000

(d)

	{1}	{2}	{3}	{4}	{5}	{6}	{7}
Random areas {1}		0,052	*0,000	0,052	0,655	0,975	0,926
50 random spp. {2}	0,052		*0,000	1,000	1,000	0,999	1,000
All target spp. {3}	*0,000	*0,000		*0,000	*0,000	*0,000	*0,000
1 section Div.1 {4}	0,052	1,000	*0,000		1,000	0,999	1,000
2 section Div.1 {5}	0,655	1,000	*0,000	1,000		1,000	1,000
3 section Div.1 {6}	0,975	0,999	*0,000	0,999	1,000		1,000
4 section Div.1 {7}	0,926	1,000	*0,000	1,000	1,000	1,000	
5 section Div.1 {8}	1,000	0,936	*0,000	0,935	1,000	1,000	1,000

1 **Supplementary Table 12** Narrow-ranged target species

2 Tukey HSD test of differences in performance measured as representation of narrow-
 3 ranged target species (see supplementary table 2). Significant differences ($p < 0,05$) are
 4 marked with *.
 5

6 (a)

	{1}	{2}	{3}	{4}	{5}	{6}
50 random spp. {1}		1,000	1,000	0,994	*0,000	*0,000
0 range-restricted {2}	1,000		1,000	0,989	*0,000	*0,000
10 range-restricted {3}	1,000	1,000		1,000	*0,000	*0,000
20 range-restricted {4}	0,994	0,989	1,000		*0,000	*0,000
30 range-restricted {5}	*0,000	*0,000	*0,000	*0,000		1,000
40 range-restricted {6}	*0,000	*0,000	*0,000	*0,000	1,000	
50 range-restricted {7}	*0,000	*0,000	*0,000	*0,000	0,283	0,371

7

8 (b)

	{1}	{2}	{3}	{4}	{5}
50 random spp. {1}		*0,002	0,833	*0,000	*0,000
0 narrow-ranged {2}	*0,002		*0,000	*0,000	*0,000
10 narrow-ranged {3}	0,833	*0,000		*0,000	*0,000
20 narrow-ranged {4}	*0,000	*0,000	*0,000		*0,000
30 narrow-ranged {5}	*0,000	*0,000	*0,000	*0,000	
40 narrow-ranged {6}	*0,000	*0,000	*0,000	*0,000	*0,000

9

10 (c)

	{1}	{2}	{3}	{4}	{5}	{6}
50 random spp. {1}		0,961	1,000	0,751	*0,000	*0,000
0 threatened {2}	0,961		0,140	*0,003	*0,000	*0,000
10 threatened {3}	1,000	0,140		1,000	*0,024	*0,000
20 threatened {4}	0,751	*0,003	1,000		0,433	*0,026
30 threatened {5}	*0,000	*0,000	*0,024	0,433		1,000
40 threatened {6}	*0,000	*0,000	*0,000	*0,026	1,000	
50 threatened {7}	*0,000	*0,000	*0,000	*0,000	*0,000	*0,003

11

12

13

1 **Appendix 1**

2 **Supplementary table captions:**

3 Supplementary table 1

4 Representation of target species and taxonomic diversity in per cent, standard deviation in
5 parentheses. Wide range species refer to the quartile of species with largest range sizes
6 from each taxonomic section from Division 2. Area selection criteria are: random area
7 selection, networks selected to maximise representation of 50 randomly chosen species,
8 all target species, 50 randomly selected species from 20-50 genera, 10-50 families, 1-9
9 sections from Division 2 and finally 1-5 sections from Division 1.

10

11 Supplementary table 2

12 Representation of target species in per cent, standard deviation in parentheses.

13 *Range-restricted* species refer to rare quartile species. *Narrow-ranged* species refer to
14 species that occur in less than 6 sites. We included both ways of defining species with
15 narrow range sizes in accordance with the analyses performed by Larsen et al., In Press).

16 Area selection criteria are: networks selected to maximise representation of 50 randomly
17 selected species, 50 randomly chosen species of which 0-50 are either threatened or
18 range-restricted, and finally 50 randomly selected species of which 0-40 are narrow-
19 ranged. The dataset included 107 narrow-ranged species, but since the number of narrow-
20 ranged species varied in the indicator pools by chance we avoided selection of indicator
21 groups composed of 50 narrow-ranged species.

22

1 Supplementary table 3.

2 Tukey HSD test of differences in performance measured as representation of all target
3 species (see supplementary table 1). Significant differences ($p < 0,05$) are marked with *.

4

5 Supplementary table 4.

6 Tukey HSD test of differences in performance measured as representation of threatened
7 target species (see supplementary table 1). Significant differences ($p < 0,05$) are marked
8 with *.

9

10 Supplementary table 5.

11 Tukey HSD test of differences in performance measured as representation of range-
12 restricted target species (see supplementary table 1). Significant differences ($p < 0,05$) are
13 marked with *.

14

15 Supplementary table 6.

16 Tukey HSD test of differences in performance measured as representation of wide ranged
17 target species (see supplementary table 1). Significant differences ($p < 0,05$) are marked
18 with *.

19

20 Supplementary table 7.

21 Tukey HSD test of differences in performance measured as representation of target
22 genera (see supplementary table 1). Significant differences ($p < 0,05$) are marked with *.

23

1 Supplementary table 8.

2 Tukey HSD test of differences in performance measured as representation of target
3 families (see supplementary table 1). Significant differences ($p < 0,05$) are marked with *.

4

5 Supplementary table 9.

6 Tukey HSD test of differences in performance measured as representation of target orders
7 (see supplementary table 1). Significant differences ($p < 0,05$) are marked with *.

8

9 Supplementary table 10.

10 Tukey HSD test of differences in performance measured as representation of all target
11 species (see supplementary table 2). Significant differences ($p < 0,05$) are marked with *.

12

13 Supplementary table 11.

14 Tukey HSD test of differences in performance measured as representation of range-
15 restricted target species (see supplementary table 2). Significant differences ($p < 0,05$) are
16 marked with *.

17

18 Supplementary table 12.

19 Tukey HSD test of differences in performance measured as representation of narrow-
20 ranged target species (see supplementary table 2). Significant differences ($p < 0,05$) are
21 marked with *.

22

1 Supplementary table 1

	All spp.	Threatened spp.	range-restricted spp.	Wide range spp.	Genera	Families	Orders
Random areas	79,62 (2,74)	40,57 (6,57)	33,17 (6,86)	99,98 (0,12)	84,07 (2,54)	91,90 (2,52)	96,17 (3,32)
50 random spp.	89,16 (1,63)	62,83 (6,00)	61,28 (5,27)	100,00 (0,00)	91,46 (1,60)	93,55 (2,38)	96,81 (2,97)
All target spp.	99,14 (0,59)	96,46 (2,63)	96,68 (2,23)	100,00 (0,00)	99,24 (0,64)	99,29 (0,96)	99,51 (1,41)
20 genera	88,72 (1,81)	61,41 (6,37)	59,66 (5,82)	100,00 (0,00)	90,99 (1,85)	93,41 (2,38)	96,56 (3,23)
30 genera	89,05 (1,63)	62,56 (5,92)	60,81 (5,36)	100,00 (0,00)	91,30 (1,66)	93,47 (2,34)	96,45 (3,28)
40 genera	89,21 (1,62)	63,49 (5,54)	61,39 (5,28)	100,00 (0,00)	91,48 (1,63)	93,54 (2,20)	96,62 (3,20)
50 genera	89,12 (1,83)	63,33 (6,42)	61,09 (5,97)	100,00 (0,00)	91,51 (1,80)	93,52 (2,30)	96,56 (3,22)
10 families	89,11 (1,65)	62,70 (6,09)	61,12 (5,26)	100,00 (0,00)	91,32 (1,68)	93,58 (2,32)	96,75 (3,23)
20 families	89,15 (1,65)	63,14 (5,94)	61,07 (5,45)	100,00 (0,00)	91,50 (1,66)	93,55 (2,25)	96,66 (3,17)
30 families	89,13 (1,66)	63,24 (6,07)	61,17 (5,27)	100,00 (0,00)	91,45 (1,65)	93,42 (2,30)	96,69 (3,11)
40 families	88,74 (1,75)	62,35 (6,29)	59,97 (5,64)	100,00 (0,04)	91,31 (1,72)	93,64 (2,27)	96,53 (3,09)
50 families	87,98 (1,98)	60,43 (6,56)	57,64 (6,11)	100,00 (0,04)	90,81 (1,77)	93,63 (2,25)	96,50 (3,08)
1 section, Div. 2	87,25 (2,63)	58,05 (6,96)	55,99 (7,86)	100,00 (0,04)	90,33 (2,23)	93,42 (2,32)	96,62 (3,13)
2 section, Div. 2	88,14 (2,21)	61,42 (6,77)	58,19 (6,86)	100,00 (0,04)	90,89 (1,98)	93,70 (2,37)	96,80 (3,28)
3 section, Div. 2	88,52 (1,87)	62,13 (6,29)	59,34 (5,91)	100,00 (0,00)	91,13 (1,70)	93,56 (2,24)	96,45 (3,16)
4 section, Div. 2	88,51 (1,99)	62,16 (6,09)	59,29 (6,22)	100,00 (0,04)	91,10 (1,77)	93,50 (2,13)	96,81 (3,21)
5 section, Div. 2	88,67 (1,86)	62,23 (6,25)	59,62 (5,94)	100,00 (0,00)	91,23 (1,74)	93,45 (2,33)	96,63 (3,19)
6 section, Div. 2	88,89 (1,64)	62,65 (5,62)	60,26 (5,30)	100,00 (0,00)	91,37 (1,58)	93,60 (2,17)	96,55 (3,17)
7 section, Div. 2	89,02 (1,62)	62,85 (5,96)	60,73 (5,32)	100,00 (0,00)	91,44 (1,57)	93,61 (2,19)	96,68 (3,31)
8 section, Div. 2	89,11 (1,64)	63,18 (5,91)	61,14 (5,35)	100,00 (0,00)	91,44 (1,60)	93,54 (2,38)	96,64 (3,13)
9 section, Div. 2	89,13 (1,68)	63,05 (6,16)	61,11 (5,50)	100,00 (0,04)	91,46 (1,64)	93,49 (2,32)	96,85 (3,12)
1 section, Div. 1	88,03 (2,50)	60,52 (7,26)	58,18 (7,50)	100,00 (0,04)	90,84 (2,19)	93,70 (2,19)	96,81 (3,14)
2 section, Div. 1	88,37 (2,02)	61,70 (6,56)	58,95 (6,42)	100,00 (0,00)	91,03 (1,89)	93,36 (2,32)	96,62 (3,26)
3 section, Div. 1	88,73 (1,75)	62,57 (5,96)	60,03 (5,64)	100,00 (0,00)	91,25 (1,64)	93,45 (2,29)	96,51 (3,27)
4 section, Div. 1	88,86 (1,85)	62,65 (6,22)	60,07 (5,91)	100,00 (0,04)	91,31 (1,72)	93,66 (2,32)	96,54 (3,26)
5 section, Div. 1	89,10 (1,72)	62,73 (6,04)	60,96 (5,40)	100,00 (0,00)	91,53 (1,66)	93,45 (2,34)	96,39 (3,32)

1 Supplementary table 2

	All spp.	Range-restricted spp.	Narrow-ranged spp.
50 random spp.	89,16 (1,63)	61,28 (5,27)	42,00 (7,87)
0 range-restricted	89,13 (1,70)	61,02 (5,87)	41,96 (8,23)
10 range-restricted	89,09 (1,67)	61,11 (5,40)	42,30 (8,32)
20 range-restricted	89,42 (1,58)	61,75 (5,32)	42,80 (7,72)
30 range-restricted	90,02 (1,47)	63,84 (4,83)	45,89 (7,34)
40 range-restricted	90,19 (1,42)	64,43 (4,69)	45,95 (7,15)
50 range-restricted	90,57 (1,42)	65,42 (4,71)	47,35 (7,38)
0 narrow-ranged	88,87 (1,72)	60,33 (5,67)	39,83 (8,47)
10 narrow-ranged	89,29 (1,67)	61,46 (5,47)	43,10 (7,80)
20 narrow-ranged	89,81 (1,50)	63,07(5,06)	46,24 (6,96)
30 narrow-ranged	90,40 (1,35)	64,78 (4,36)	48,68 (6,60)
40 narrow-ranged	90,96 (1,31)	66,94 (4,38)	51,68 (6,35)
0 threatened	89,02 (1,69)	61,04 (5,47)	41,05 (8,47)
10 threatened	89,22 (1,67)	61,12 (5,43)	42,65 (8,03)
20 threatened	89,20 (1,68)	61,06 (5,53)	43,16 (7,80)
30 threatened	89,53 (1,55)	61,97 (5,18)	44,52 (7,42)
40 threatened	89,64 (1,55)	62,31 (5,12)	45,01 (7,17)
50 threatened	90,19 (1,44)	64,14 (4,74)	47,13 (6,79)

2

1 Supplementary table 3 (all target species)

2 (a)

	{1}	{2}	{3}	{4}	{5}	{6}
Random areas {1}		*0,000	*0,000	*0,000	*0,000	*0,000
50 random spp. {2}	*0,000		*0,000	0,056	1,000	1,000
All target spp. {3}	*0,000	*0,000		*0,000	*0,000	*0,000
20 genera {4}	*0,000	0,056	*0,000		0,516	*0,015
30 genera {5}	*0,000	1,000	*0,000	0,516		1,000
40 genera {6}	*0,000	1,000	*0,000	*0,015	1,000	
50 genera {7}	*0,000	1,000	*0,000	0,171	1,000	1,000

3

4 (b)

	{1}	{2}	{3}	{4}	{5}	{6}	{7}
Random areas {1}		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
50 random spp. {2}	*0,000		*0,000	1,000	1,000	1,000	0,091
All target spp. {3}	*0,000	*0,000		*0,000	*0,000	*0,000	*0,000
10 families {4}	*0,000	1,000	*0,000		1,000	1,000	0,266
20 families {5}	*0,000	1,000	*0,000	1,000		1,000	0,134
30 families {6}	*0,000	1,000	*0,000	1,000	1,000		0,190
40 families {7}	*0,000	0,091	*0,000	0,266	0,134	0,190	
50 families {8}	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000

5

1 Supplementary table 3 (all target species)

2 (c)

	{1}	{2}	{3}	{4}	{5}	{6}	{7}	{8}	{9}	{10}	{11}
Random areas {1}		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
50 random spp. {2}	*0,000		*0,000	*0,000	*0,000	*0,000	*0,000	*0,010	0,888	1,000	1,000
All target spp. {3}	*0,000	*0,000		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
1 section Div.2 {4}	*0,000	*0,000	*0,000		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
2 section Div.2 {5}	*0,000	*0,000	*0,000	*0,000		0,249	0,324	*0,004	*0,000	*0,000	*0,000
3 section Div.2 {6}	*0,000	*0,000	*0,000	*0,000	0,249		1,000	1,000	0,264	*0,008	*0,000
4 section Div.2 {7}	*0,000	*0,000	*0,000	*0,000	0,324	1,000		1,000	0,199	*0,005	*0,000
5 section Div.2 {8}	*0,000	*0,010	*0,000	*0,000	*0,004	1,000	1,000		0,980	0,350	0,051
6 section Div.2 {9}	*0,000	0,888	*0,000	*0,000	*0,000	0,264	0,199	0,980		1,000	0,991
7 section Div.2 {10}	*0,000	1,000	*0,000	*0,000	*0,000	*0,008	*0,005	0,350	1,000		1,000
8 section Div.2 {11}	*0,000	1,000	*0,000	*0,000	*0,000	*0,000	*0,000	0,051	0,991	1,000	
9 section Div.2 {12}	*0,000	1,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,025	0,965	1,000	1,000

3

4 (d)

	{1}	{2}	{3}	{4}	{5}	{6}	{7}
Random areas {1}		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
50 random spp. {2}	*0,000		*0,000	*0,000	*0,000	0,066	0,728
All target spp. {3}	*0,000	*0,000		*0,000	*0,000	*0,000	*0,000
1 section Div.1 {4}	*0,000	*0,000	*0,000		0,420	*0,000	*0,000
2 section Div.1 {5}	*0,000	*0,000	*0,000	0,420		0,371	*0,013
3 section Div.1 {6}	*0,000	0,066	*0,000	*0,000	0,371		1,000
4 section Div.1 {7}	*0,000	0,728	*0,000	*0,000	*0,013	1,000	
5 section Div.1 {8}	*0,000	1,000	*0,000	*0,000	*0,000	0,291	0,973

5

1 Supplementary table 4 (threatened target species)

2 (a)

	{1}	{2}	{3}	{4}	{5}	{6}
Random areas {1}		*0,000	*0,000	*0,000	*0,000	*0,000
50 random spp. {2}	*0,000		*0,000	0,058	1,000	0,995
All target spp. {3}	*0,000	*0,000		*0,000	*0,000	*0,000
20 genera {4}	*0,000	0,058	*0,000		0,362	*0,000
30 genera {5}	*0,000	1,000	*0,000	0,362		0,791
40 genera {6}	*0,000	0,995	*0,000	*0,000	0,791	
50 genera {7}	*0,000	1,000	*0,000	*0,000	0,969	1,000

3

4 (b)

	{1}	{2}	{3}	{4}	{5}	{6}	{7}
Random areas {1}		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
50 random spp. {2}	*0,000		*0,000	1,000	1,000	1,000	1,000
All target spp. {3}	*0,000	*0,000		*0,000	*0,000	*0,000	*0,000
10 families {4}	*0,000	1,000	*0,000		1,000	1,000	1,000
20 families {5}	*0,000	1,000	*0,000	1,000		1,000	0,956
30 families {6}	*0,000	1,000	*0,000	1,000	1,000		0,860
40 families {7}	*0,000	1,000	*0,000	1,000	0,956	0,860	
50 families {8}	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000

5

1 Supplementary table 4 (threatened target species)

2 (c)

	{1}	{2}	{3}	{4}	{5}	{6}	{7}	{8}	{9}	{10}	{11}
Random areas {1}		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
50 random spp. {2}	*0,000		*0,000	*0,000	0,064	0,991	0,995	0,999	1,000	1,000	1,000
All target spp. {3}	*0,000	*0,000		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
1 section Div.2 {4}	*0,000	*0,000	*0,000		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
2 section Div.2 {5}	*0,000	0,064	*0,000	*0,000		0,987	0,979	0,946	0,234	0,052	*0,002
3 section Div.2 {6}	*0,000	0,991	*0,000	*0,000	0,987		1,000	1,000	1,000	0,986	0,569
4 section Div.2 {7}	*0,000	0,995	*0,000	*0,000	0,979	1,000		1,000	1,000	0,991	0,628
5 section Div.2 {8}	*0,000	0,999	*0,000	*0,000	0,946	1,000	1,000		1,000	0,998	0,756
6 section Div.2 {9}	*0,000	1,000	*0,000	*0,000	0,234	1,000	1,000	1,000		1,000	1,000
7 section Div.2 {10}	*0,000	1,000	*0,000	*0,000	0,052	0,986	0,991	0,998	1,000		1,000
8 section Div.2 {11}	*0,000	1,000	*0,000	*0,000	*0,002	0,569	0,628	0,756	1,000	1,000	
9 section Div.2 {12}	*0,000	1,000	*0,000	*0,000	*0,008	0,824	0,864	0,934	1,000	1,000	1,000

3

4 (d)

	{1}	{2}	{3}	{4}	{5}	{6}	{7}
Random areas {1}		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
50 random spp. {2}	*0,000		*0,000	*0,000	0,402	1,000	1,000
All target spp. {3}	*0,000	*0,000		*0,000	*0,000	*0,000	*0,000
1 section Div.1 {4}	*0,000	*0,000	*0,000		0,296	*0,000	*0,000
2 section Div.1 {5}	*0,000	0,402	*0,000	0,296		0,883	0,762
3 section Div.1 {6}	*0,000	1,000	*0,000	*0,000	0,883		1,000
4 section Div.1 {7}	*0,000	1,000	*0,000	*0,000	0,762	1,000	
5 section Div.1 {8}	*0,000	1,000	*0,000	*0,000	0,611	1,000	1,000

5

1 Supplementary table 5 (range-restricted target species)

2 (a)

	{1}	{2}	{3}	{4}	{5}	{6}
Random areas {1}		*0,000	*0,000	*0,000	*0,000	*0,000
50 random spp. {2}	*0,000		*0,000	*0,004	1,000	1,000
All target spp. {3}	*0,000	*0,000		*0,000	*0,000	*0,000
20 genera {4}	*0,000	*0,004	*0,000		0,260	*0,001
30 genera {5}	*0,000	1,000	*0,000	0,260		0,999
40 genera {6}	*0,000	1,000	*0,000	*0,001	0,999	
50 genera {7}	*0,000	1,000	*0,000	*0,027	1,000	1,000

3

4 (b)

	{1}	{2}	{3}	{4}	{5}	{6}	{7}
Random areas {1}		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
50 random spp. {2}	*0,000		*0,000	1,000	1,000	1,000	0,087
All target spp. {3}	*0,000	*0,000		*0,000	*0,000	*0,000	*0,000
10 families {4}	*0,000	1,000	*0,000		1,000	1,000	0,261
20 families {5}	*0,000	1,000	*0,000	1,000		1,000	0,361
30 families {6}	*0,000	1,000	*0,000	1,000	1,000		0,187
40 families {7}	*0,000	0,087	*0,000	0,261	0,361	0,187	
50 families {8}	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000

5

1 Supplementary table 5 (range-restricted target species)

2 (c)

	{1}	{2}	{3}	{4}	{5}	{6}	{7}	{8}	{9}	{10}	{11}
Random areas {1}		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
50 random spp. {2}	*0,000		*0,000	*0,000	*0,000	*0,000	*0,000	*0,002	0,534	1,000	1,000
All target spp. {3}	*0,000	*0,000		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
1 section Div.2 {4}	*0,000	*0,000	*0,000		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
2 section Div.2 {5}	*0,000	*0,000	*0,000	*0,000		0,268	0,351	*0,029	*0,000	*0,000	*0,000
3 section Div.2 {6}	*0,000	*0,000	*0,000	*0,000	0,268		1,000	1,000	0,737	*0,041	*0,000
4 section Div.2 {7}	*0,000	*0,000	*0,000	*0,000	0,351	1,000		1,000	0,641	*0,026	*0,000
5 section Div.2 {8}	*0,000	*0,002	*0,000	*0,000	*0,029	1,000	1,000		0,994	0,330	*0,011
6 section Div.2 {9}	*0,000	0,534	*0,000	*0,000	*0,000	0,737	0,641	0,994		1,000	0,807
7 section Div.2 {10}	*0,000	1,000	*0,000	*0,000	*0,000	*0,041	*0,026	0,330	1,000		1,000
8 section Div.2 {11}	*0,000	1,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,011	0,807	1,000	
9 section Div.2 {12}	*0,000	1,000	*0,000	*0,000	*0,000	*0,001	*0,000	*0,016	0,859	1,000	1,000

3

4 (d)

	{1}	{2}	{3}	{4}	{5}	{6}	{7}
Random areas {1}		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
50 random spp. {2}	*0,000		*0,000	*0,000	*0,000	0,138	0,181
All target spp. {3}	*0,000	*0,000		*0,000	*0,000	*0,000	*0,000
1 section Div.1 {4}	*0,000	*0,000	*0,000		0,938	*0,000	*0,000
2 section Div.1 {5}	*0,000	*0,000	*0,000	0,938		0,400	0,328
3 section Div.1 {6}	*0,000	0,138	*0,000	*0,000	0,400		1,000
4 section Div.1 {7}	*0,000	0,181	*0,000	*0,000	0,328	1,000	
5 section Div.1 {8}	*0,000	1,000	*0,000	*0,000	*0,000	0,716	0,786

5

1 Supplementary table 6 (wide range target species)

2 (a)

	{1}	{2}	{3}	{4}	{5}	{6}
Random areas {1}		*0,000	*0,000	*0,000	*0,000	*0,000
50 random spp. {2}	*0,000		1,000	1,000	1,000	1,000
All target spp. {3}	*0,000	1,000		1,000	1,000	1,000
20 genera {4}	*0,000	1,000	1,000		1,000	1,000
30 genera {5}	*0,000	1,000	1,000	1,000		1,000
40 genera {6}	*0,000	1,000	1,000	1,000	1,000	
50 genera {7}	*0,000	1,000	1,000	1,000	1,000	1,000

3

4 (b)

	{1}	{2}	{3}	{4}	{5}	{6}	{7}
Random areas {1}		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
50 random spp. {2}	*0,000		1,000	1,000	1,000	1,000	1,000
All target spp. {3}	*0,000	1,000		1,000	1,000	1,000	1,000
10 families {4}	*0,000	1,000	1,000		1,000	1,000	1,000
20 families {5}	*0,000	1,000	1,000	1,000		1,000	1,000
30 families {6}	*0,000	1,000	1,000	1,000	1,000		1,000
40 families {7}	*0,000	1,000	1,000	1,000	1,000	1,000	
50 families {8}	*0,000	1,000	1,000	1,000	1,000	1,000	1,000

5

1 Supplementary table 6 (wide range target species)

2 (c)

	{1}	{2}	{3}	{4}	{5}	{6}	{7}	{8}	{9}	{10}	{11}
Random areas {1}		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
50 random spp. {2}	*0,000		1,000	1,000	1,000	1,000	1,000	1,000	1,000	1,000	1,000
All target spp. {3}	*0,000	1,000		1,000	1,000	1,000	1,000	1,000	1,000	1,000	1,000
1 section Div.2 {4}	*0,000	1,000	1,000		1,000	1,000	1,000	1,000	1,000	1,000	1,000
2 section Div.2 {5}	*0,000	1,000	1,000	1,000		1,000	1,000	1,000	1,000	1,000	1,000
3 section Div.2 {6}	*0,000	1,000	1,000	1,000	1,000		1,000	1,000	1,000	1,000	1,000
4 section Div.2 {7}	*0,000	1,000	1,000	1,000	1,000	1,000		1,000	1,000	1,000	1,000
5 section Div.2 {8}	*0,000	1,000	1,000	1,000	1,000	1,000	1,000		1,000	1,000	1,000
6 section Div.2 {9}	*0,000	1,000	1,000	1,000	1,000	1,000	1,000	1,000		1,000	1,000
7 section Div.2 {10}	*0,000	1,000	1,000	1,000	1,000	1,000	1,000	1,000	1,000		1,000
8 section Div.2 {11}	*0,000	1,000	1,000	1,000	1,000	1,000	1,000	1,000	1,000	1,000	
9 section Div.2 {12}	*0,000	1,000	1,000	1,000	1,000	1,000	1,000	1,000	1,000	1,000	1,000

3

4 (d)

	{1}	{2}	{3}	{4}	{5}	{6}	{7}
Random areas {1}		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
50 random spp. {2}	*0,000		1,000	1,000	1,000	1,000	1,000
All target spp. {3}	*0,000	1,000		1,000	1,000	1,000	1,000
1 section Div.1 {4}	*0,000	1,000	1,000		1,000	1,000	1,000
2 section Div.1 {5}	*0,000	1,000	1,000	1,000		1,000	1,000
3 section Div.1 {6}	*0,000	1,000	1,000	1,000	1,000		1,000
4 section Div.1 {7}	*0,000	1,000	1,000	1,000	1,000	1,000	
5 section Div.1 {8}	*0,000	1,000	1,000	1,000	1,000	1,000	1,000

5

1 Supplementary table 7 (target genera)

2 (a)

	{1}	{2}	{3}	{4}	{5}	{6}
Random areas {1}		*0,000	*0,000	*0,000	*0,000	*0,000
50 random spp. {2}	*0,000		*0,000	*0,009	0,999	1,000
All target spp. {3}	*0,000	*0,000		*0,000	*0,000	*0,000
20 genera {4}	*0,000	*0,009	*0,000		0,581	*0,005
30 genera {5}	*0,000	0,999	*0,000	0,581		0,998
40 genera {6}	*0,000	1,000	*0,000	*0,005	0,998	
50 genera {7}	*0,000	1,000	*0,000	*0,001	0,980	1,000

3

4 (b)

	{1}	{2}	{3}	{4}	{5}	{6}	{7}
Random areas {1}		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
50 random spp. {2}	*0,000		*0,000	1,000	1,000	1,000	1,000
All target spp. {3}	*0,000	*0,000		*0,000	*0,000	*0,000	*0,000
10 families {4}	*0,000	1,000	*0,000		0,998	1,000	1,000
20 families {5}	*0,000	1,000	*0,000	0,998		1,000	0,998
30 families {6}	*0,000	1,000	*0,000	1,000	1,000		1,000
40 families {7}	*0,000	1,000	*0,000	1,000	0,998	1,000	
50 families {8}	*0,000	*0,000	*0,000	*0,002	*0,000	*0,000	*0,003

5

1 Supplementary table 7 (target genera)

2 (c)

	{1}	{2}	{3}	{4}	{5}	{6}	{7}	{8}	{9}	{10}	{11}
Random areas {1}		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
50 random spp. {2}	*0,000		*0,000	*0,000	*0,000	0,392	0,189	0,948	1,000	1,000	1,000
All target spp. {3}	*0,000	*0,000		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
1 section Div.2 {4}	*0,000	*0,000	*0,000		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
2 section Div.2 {5}	*0,000	*0,000	*0,000	*0,000		0,923	0,989	0,336	*0,007	*0,000	*0,000
3 section Div.2 {6}	*0,000	0,392	*0,000	*0,000	0,923		1,000	1,000	0,943	0,531	0,551
4 section Div.2 {7}	*0,000	0,189	*0,000	*0,000	0,989	1,000		1,000	0,789	0,287	0,304
5 section Div.2 {8}	*0,000	0,948	*0,000	*0,000	0,336	1,000	1,000		1,000	0,981	0,984
6 section Div.2 {9}	*0,000	1,000	*0,000	*0,000	*0,007	0,943	0,789	1,000		1,000	1,000
7 section Div.2 {10}	*0,000	1,000	*0,000	*0,000	*0,000	0,531	0,287	0,981	1,000		1,000
8 section Div.2 {11}	*0,000	1,000	*0,000	*0,000	*0,000	0,551	0,304	0,984	1,000	1,000	
9 section Div.2 {12}	*0,000	1,000	*0,000	*0,000	*0,000	0,450	0,227	0,965	1,000	1,000	1,000

3

4 (d)

	{1}	{2}	{3}	{4}	{5}	{6}	{7}
Random areas {1}		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
50 random spp. {2}	*0,000		*0,000	*0,000	*0,035	0,983	1,000
All target spp. {3}	*0,000	*0,000		*0,000	*0,000	*0,000	*0,000
1 section Div.1 {4}	*0,000	*0,000	*0,000		0,995	0,061	*0,008
2 section Div.1 {5}	*0,000	*0,035	*0,000	0,995		0,977	0,743
3 section Div.1 {6}	*0,000	0,983	*0,000	0,061	0,977		1,000
4 section Div.1 {7}	*0,000	1,000	*0,000	*0,008	0,743	1,000	
5 section Div.1 {8}	*0,000	1,000	*0,000	*0,000	*0,004	0,766	0,981

5

1 Supplementary table 8 (target families)

2 (a)

	{1}	{2}	{3}	{4}	{5}	{6}
Random areas {1}		*0,000	*0,000	*0,000	*0,000	*0,000
50 random spp. {2}	*0,000		*0,000	1,000	1,000	1,000
All target spp. {3}	*0,000	*0,000		*0,000	*0,000	*0,000
20 genera {4}	*0,000	1,000	*0,000		1,000	1,000
30 genera {5}	*0,000	1,000	*0,000	1,000		1,000
40 genera {6}	*0,000	1,000	*0,000	1,000	1,000	
50 genera {7}	*0,000	1,000	*0,000	1,000	1,000	1,000

3

4 (b)

	{1}	{2}	{3}	{4}	{5}	{6}	{7}
Random areas {1}		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
50 random spp. {2}	*0,000		*0,000	1,000	1,000	1,000	1,000
All target spp. {3}	*0,000	*0,000		*0,000	*0,000	*0,000	*0,000
10 families {4}	*0,000	1,000	*0,000		1,000	1,000	1,000
20 families {5}	*0,000	1,000	*0,000	1,000		1,000	1,000
30 families {6}	*0,000	1,000	*0,000	1,000	1,000		0,999
40 families {7}	*0,000	1,000	*0,000	1,000	1,000	0,999	
50 families {8}	*0,000	1,000	*0,000	1,000	1,000	0,999	1,000

5

1 Supplementary table 8 (target families)

2 (c)

	{1}	{2}	{3}	{4}	{5}	{6}	{7}	{8}	{9}	{10}	{11}
Random areas {1}		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
50 random spp. {2}	*0,000		*0,000	1,000	1,000	1,000	1,000	1,000	1,000	1,000	1,000
All target spp. {3}	*0,000	*0,000		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
1 section Div.2 {4}	*0,000	1,000	*0,000		0,975	1,000	1,000	1,000	1,000	1,000	1,000
2 section Div.2 {5}	*0,000	1,000	*0,000	0,975		1,000	1,000	0,994	1,000	1,000	1,000
3 section Div.2 {6}	*0,000	1,000	*0,000	1,000	1,000		1,000	1,000	1,000	1,000	1,000
4 section Div.2 {7}	*0,000	1,000	*0,000	1,000	1,000	1,000		1,000	1,000	1,000	1,000
5 section Div.2 {8}	*0,000	1,000	*0,000	1,000	0,994	1,000	1,000		1,000	1,000	1,000
6 section Div.2 {9}	*0,000	1,000	*0,000	1,000	1,000	1,000	1,000	1,000		1,000	1,000
7 section Div.2 {10}	*0,000	1,000	*0,000	1,000	1,000	1,000	1,000	1,000	1,000		1,000
8 section Div.2 {11}	*0,000	1,000	*0,000	1,000	1,000	1,000	1,000	1,000	1,000	1,000	
9 section Div.2 {12}	*0,000	1,000	*0,000	1,000	1,000	1,000	1,000	1,000	1,000	1,000	1,000

3

4 (d)

	{1}	{2}	{3}	{4}	{5}	{6}	{7}
Random areas {1}		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
50 random spp. {2}	*0,000		*0,000	1,000	1,000	1,000	1,000
All target spp. {3}	*0,000	*0,000		*0,000	*0,000	*0,000	*0,000
1 section Div.1 {4}	*0,000	1,000	*0,000		0,821	0,995	1,000
2 section Div.1 {5}	*0,000	1,000	*0,000	0,821		1,000	0,948
3 section Div.1 {6}	*0,000	1,000	*0,000	0,995	1,000		1,000
4 section Div.1 {7}	*0,000	1,000	*0,000	1,000	0,948	1,000	
5 section Div.1 {8}	*0,000	1,000	*0,000	0,993	1,000	1,000	1,000

5

1 Supplementary table 9 (target orders)

2 (a)

	{1}	{2}	{3}	{4}	{5}	{6}
Random areas {1}		0,052	*0,000	0,890	0,998	0,641
50 random spp. {2}	0,052		*0,000	1,000	0,990	1,000
All target spp. {3}	*0,000	*0,000		*0,000	*0,000	*0,000
20 genera {4}	0,890	1,000	*0,000		1,000	1,000
30 genera {5}	0,998	0,990	*0,000	1,000		1,000
40 genera {6}	0,641	1,000	*0,000	1,000	1,000	
50 genera {7}	0,893	1,000	*0,000	1,000	1,000	1,000

3

4 (b)

	{1}	{2}	{3}	{4}	{5}	{6}	{7}
Random areas {1}		0,052	*0,000	0,134	0,480	0,340	0,949
50 random spp. {2}	0,052		*0,000	1,000	1,000	1,000	1,000
All target spp. {3}	*0,000	*0,000		*0,000	*0,000	*0,000	*0,000
10 families {4}	0,134	1,000	*0,000		1,000	1,000	1,000
20 families {5}	0,480	1,000	*0,000	1,000		1,000	1,000
30 families {6}	0,340	1,000	*0,000	1,000	1,000		1,000
40 families {7}	0,949	1,000	*0,000	1,000	1,000	1,000	
50 families {8}	0,984	0,999	*0,000	1,000	1,000	1,000	1,000

5

1 Supplementary table 9 (target orders)

2 (c)

	{1}	{2}	{3}	{4}	{5}	{6}	{7}	{8}	{9}	{10}	{11}
Random areas {1}		0,052	*0,000	0,670	0,060	0,998	0,053	0,614	0,912	0,358	0,568
50 random spp. {2}	0,052		*0,000	1,000	1,000	0,991	1,000	1,000	1,000	1,000	1,000
All target spp. {3}	*0,000	*0,000		*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000
1 section Div.2 {4}	0,670	1,000	*0,000		1,000	1,000	1,000	1,000	1,000	1,000	1,000
2 section Div.2 {5}	0,060	1,000	*0,000	1,000		0,993	1,000	1,000	1,000	1,000	1,000
3 section Div.2 {6}	0,998	0,991	*0,000	1,000	0,993		0,991	1,000	1,000	1,000	1,000
4 section Div.2 {7}	0,053	1,000	*0,000	1,000	1,000	0,991		1,000	1,000	1,000	1,000
5 section Div.2 {8}	0,614	1,000	*0,000	1,000	1,000	1,000	1,000		1,000	1,000	1,000
6 section Div.2 {9}	0,912	1,000	*0,000	1,000	1,000	1,000	1,000	1,000		1,000	1,000
7 section Div.2 {10}	0,358	1,000	*0,000	1,000	1,000	1,000	1,000	1,000	1,000		1,000
8 section Div.2 {11}	0,568	1,000	*0,000	1,000	1,000	1,000	1,000	1,000	1,000	1,000	
9 section Div.2 {12}	*0,024	1,000	*0,000	1,000	1,000	0,968	1,000	1,000	0,999	1,000	1,000

3

4 (d)

	{1}	{2}	{3}	{4}	{5}	{6}	{7}
Random areas {1}		0,052	*0,000	0,052	0,655	0,975	0,926
50 random spp. {2}	0,052		*0,000	1,000	1,000	0,999	1,000
All target spp. {3}	*0,000	*0,000		*0,000	*0,000	*0,000	*0,000
1 section Div.1 {4}	0,052	1,000	*0,000		1,000	0,999	1,000
2 section Div.1 {5}	0,655	1,000	*0,000	1,000		1,000	1,000
3 section Div.1 {6}	0,975	0,999	*0,000	0,999	1,000		1,000
4 section Div.1 {7}	0,926	1,000	*0,000	1,000	1,000	1,000	
5 section Div.1 {8}	1,000	0,936	*0,000	0,935	1,000	1,000	1,000

5

1 Supplementary table 10 (all target species)

2 (a)

	{1}	{2}	{3}	{4}	{5}	{6}
50 random spp. {1}		1,000	1,000	0,785	*0,000	*0,000
0 range-restricted {2}	1,000		1,000	0,597	*0,000	*0,000
10 range-restricted {3}	1,000	1,000		0,261	*0,000	*0,000
20 range-restricted {4}	0,785	0,597	0,261		*0,000	*0,000
30 range-restricted {5}	*0,000	*0,000	*0,000	*0,000		0,999
40 range-restricted {6}	*0,000	*0,000	*0,000	*0,000	0,999	
50 range-restricted {7}	*0,000	*0,000	*0,000	*0,000	*0,000	0,063

3

4 (b)

	{1}	{2}	{3}	{4}	{5}
50 random spp. {1}		0,508	1,000	*0,000	*0,000
0 narrow-ranged {2}	0,508		*0,022	*0,000	*0,000
10 narrow-ranged {3}	1,000	*0,022		*0,000	*0,000
20 narrow-ranged {4}	*0,000	*0,000	*0,000		*0,000
30 narrow-ranged {5}	*0,000	*0,000	*0,000	*0,000	
40 narrow-ranged {6}	*0,000	*0,000	*0,000	*0,000	*0,000

5

6 (c)

	{1}	{2}	{3}	{4}	{5}	{6}
50 random spp. {1}		1,000	1,000	1,000	0,111	*0,003
0 threatened {2}	1,000		0,987	0,995	*0,001	*0,000
10 threatened {3}	1,000	0,987		1,000	0,386	*0,022
20 threatened {4}	1,000	0,995	1,000		0,293	*0,013
30 threatened {5}	0,111	*0,001	0,386	0,293		1,000
40 threatened {6}	*0,003	*0,000	*0,022	*0,013	1,000	
50 threatened {7}	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000

7

1 Supplementary table 11 (range-restricted target species)

2 (a)

	{1}	{2}	{3}	{4}	{5}	{6}
50 random spp. {1}		1,000	1,000	1,000	*0,000	*0,000
0 range-restricted {2}	1,000		1,000	0,899	*0,000	*0,000
10 range-restricted {3}	1,000	1,000		0,976	*0,000	*0,000
20 range-restricted {4}	1,000	0,899	0,976		*0,000	*0,000
30 range-restricted {5}	*0,000	*0,000	*0,000	*0,000		0,991
40 range-restricted {6}	*0,000	*0,000	*0,000	*0,000	0,991	
50 range-restricted {7}	*0,000	*0,000	*0,000	*0,000	*0,001	0,369

3

4 (b)

	{1}	{2}	{3}	{4}	{5}
50 random spp. {1}		0,463	1,000	1,000	*0,000
0 narrow-ranged {2}	0,463		*0,033	0,137	*0,000
10 narrow-ranged {3}	1,000	0,137	1,000		*0,001
20 narrow-ranged {4}	*0,000	*0,000	*0,005	*0,001	
30 narrow-ranged {5}	*0,000	*0,000	*0,000	*0,000	*0,000
40 narrow-ranged {6}	*0,000	*0,000	*0,000	*0,000	*0,000

5

6 (c)

	{1}	{2}	{3}	{4}	{5}	{6}
50 random spp. {1}		1,000	1,000	1,000	0,942	0,273
0 threatened {2}	1,000		1,000	1,000	0,515	*0,038
10 threatened {3}	1,000	1,000		1,000	0,697	0,081
20 threatened {4}	1,000	1,000	1,000		0,550	*0,044
30 threatened {5}	0,942	0,515	0,697	0,550		1,000
40 threatened {6}	0,273	*0,038	0,081	*0,044	1,000	
50 threatened {7}	*0,000	*0,000	*0,000	*0,000	*0,000	*0,000

7

1 Supplementary table 12 (narrow-ranged target species)

2 (a)

	{1}	{2}	{3}	{4}	{5}	{6}
50 random spp. {1}		1,000	1,000	0,994	*0,000	*0,000
0 range-restricted {2}	1,000		1,000	0,989	*0,000	*0,000
10 range-restricted {3}	1,000	1,000		1,000	*0,000	*0,000
20 range-restricted {4}	0,994	0,989	1,000		*0,000	*0,000
30 range-restricted {5}	*0,000	*0,000	*0,000	*0,000		1,000
40 range-restricted {6}	*0,000	*0,000	*0,000	*0,000	1,000	
50 range-restricted {7}	*0,000	*0,000	*0,000	*0,000	0,283	0,371

3

4 (b)

	{1}	{2}	{3}	{4}	{5}
50 random spp. {1}		*0,002	0,833	*0,000	*0,000
0 narrow-ranged {2}	*0,002		*0,000	*0,000	*0,000
10 narrow-ranged {3}	0,833	*0,000		*0,000	*0,000
20 narrow-ranged {4}	*0,000	*0,000	*0,000		*0,000
30 narrow-ranged {5}	*0,000	*0,000	*0,000	*0,000	
40 narrow-ranged {6}	*0,000	*0,000	*0,000	*0,000	*0,000

5

6 (c)

	{1}	{2}	{3}	{4}	{5}	{6}
50 random spp. {1}		0,961	1,000	0,751	*0,000	*0,000
0 threatened {2}	0,961		0,140	*0,003	*0,000	*0,000
10 threatened {3}	1,000	0,140		1,000	*0,024	*0,000
20 threatened {4}	0,751	*0,003	1,000		0,433	*0,026
30 threatened {5}	*0,000	*0,000	*0,024	0,433		1,000
40 threatened {6}	*0,000	*0,000	*0,000	*0,026	1,000	
50 threatened {7}	*0,000	*0,000	*0,000	*0,000	*0,000	*0,003

7

8