

Supplementary Information for

Multinational evaluation of genetic diversity indicators for the Kunming-Montreal Global Biodiversity Framework

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S1 Materials and methods

Standardized survey for data collection

A questionnaire comprising eight sections and approximately 50 questions/data field (depending on the number of extant populations and scenarios activated) was developed to facilitate the calculation of the genetic indicators for a given species (see sample questionnaire:

<https://aliciamstt.github.io/GeneticIndicators/#2-online-data-collection-form-using-kobotoolbox>). While

only four sections requested data that would directly lead to the calculation of each of the three indicators, the other four sections were used to gather additional information on the species and assessment country to allow for meaningful comparisons and interpretations of the results.

Participants were asked to familiarize themselves with all questions and data fields prior to data collection, with a detailed Kobo question manual created to help clarify any potential misunderstanding related to the questions posed (Manual available at

<https://aliciamstt.github.io/GeneticIndicators/Genetic%20Diversity%20Indicator%20Testing%20Kobo%20v4.0%20Manual.pdf>).

Table S1. Methodological approach and data sources used per country in compiling taxon data.

Country	Approach	Sources*
Australia**	Manual	RL, SL, SMP, W
Belgium	Manual + Expert	EI, ND, RL, SL, SMP, W
Colombia	Manual + Expert	EG, RL, ND, SL
France	Auto + Manual + Expert	AA, EI, RL, SMP, W
Japan	Auto + Manual	ND, RL
Mexico	Manual + Expert	EG, EI, RL, SL, SMP, W
South Africa	Manual + Expert	EI, RL, SL, SMP, W
Sweden	Manual + Expert	AA, EG, EI, RL, SL, SMP, W
USA**	Manual	RL, SL, SMP

*AA = additional analyses of existing data, EI = expert consultation - individual, EG = expert consultation - workshops, ND = national data set, RL = Red List (global, regional, and/or national), SL = scientific literature, SMP = species-specific management, action or recovery plan; W = websites

**only publicly available sources were used.

Table S2. Definitions of terms used for delimiting populations for the Populations Maintained (PM) indicator.

Term	Definition
Origin of population	
Historically natural populations	those populations where the native gene pool has been in that location for ‘some generations’ (e.g. before human influences). The genetic variation within these populations has developed through natural evolutionary processes and represents a unique, native gene pool within the species.
Introduced populations	populations that in the recent past (e.g. past hundreds of years) have never been known to occur at that particular location. Now they exist there, due to active translocation of individuals to that location.
Re-introduced populations	populations that went extinct in a location and have since been reintroduced, by humans or, more rarely, through natural processes. Depending on the source of the re-introduced individuals, the genetic composition of re-introduced populations may differ from the original genetic composition at that location
Supplemented (aka reinforced)	naturally occurring populations that have a native gene pool but have had new individuals introduced to support the population. Depending on the origin of the new individuals, e.g. from a breeding population or other population, the reinforced population may contain non-local genetic material.

Term	Definition
Methods to define populations	
Genetic clusters/clades	when a genetic (DNA-based) study has been performed which shows either (a) no gene flow between groups of individuals, and/or (b) a long period of time in which groups are separated (implying genetic divergence). In this case populations are normally delineated by identified genetic differences, e.g., mtDNA differences, population genetic clustering (STRUCTURE and similar), strong population division (FST), unique alleles, and other methods.
Geographic boundaries	when groups of individuals are separated by some uninhabited area which cannot easily be traversed (e.g. river, mountain, different habitat type, or other habitat types which can't be crossed by the species).
Ecological or Biogeographic proxies	differences in ecological conditions represent a proxy for potential local adaptations across a species' range. This may be especially useful for designating populations when groups of individuals occur in continuous fashion across multiple ecological zones, as there may be different local adaptations even in what seems a continuous distribution. In management this may be referred to as ecoregions, seed zones, proxies of genetic differentiation or similar terminology.
Traits (e.g., behavioral, morphological, physiological)	when groups of individuals have different traits that may represent adaptations or may prevent interbreeding (e.g., type of song in birds or whales,

Term	Definition
	adaptation to drier environments).
Management Units	when biologists at a management agency have identified boundaries in an otherwise continuous species range, recognizing that management (and adaptation) does need some delineation. Note that these defined units are often demographically distinct, but may sometimes just represent political or other boundaries.
Dispersal Buffers	when dispersal distances are available for a given species one can create buffer polygons around observation points (occurrence points). Polygons that overlap are fused together, and the resulting polygon, along with the points falling within its area, are considered a single population.

Sample national indicator calculation

Below is a dummy dataset of indicator values for several species within a given country, which will be used to calculate indicator values when a country has an unequal representation of species within various taxonomic groups (e.g., mammals, amphibians, birds, fish, angiosperms).

Table S3. Dummy dataset of indicator values for several species within a country.

Species	Taxonomic group	PM Indicator	Ne 500 Indicator
A	Amphibian	0.33	0.00
B	Amphibian	0.84	0.18
C	Amphibian	0.76	0.00
D	Reptile	1.00	1.00
E	Reptile	1.00	0.75
F	Fish	0.50	0.00
G	Fish	1.00	0.75
H	Fish	1.00	0.20
I	Fish	0.80	0.68
J	Mammal	1.00	0.30
K	Mammal	1.00	0.67
L	Mammal	0.78	0.63
M	Mammal	0.50	0.00
N	Mammal	1.00	1.00
O	Mammal	1.00	0.86
P	Mammal	0.40	0.90
Q	Bird	1.00	0.39
R	Bird	0.60	0.33
S	Angiosperm	0.76	0.00
T	Angiosperm	1.00	0.50
U	Angiosperm	1.00	0.25
V	Angiosperm	0.80	0.50

Step 1. Calculate average indicator values per taxonomic group (simple equation [Equation 1] in Hoban, da Silva, Mastretta-Yanes, et al., 2023)

Table S4. Dummy dataset of indicator values per taxonomic group.

Taxonomic Group	Number of species	PM Indicator	Ne 500 Indicator
Amphibian	3	0.64	0.06
Reptile	2	1.00	0.88
Fish	4	0.83	0.41
Mammal	7	0.81	0.62
Bird	2	0.80	0.36
Angiosperm	4	0.89	0.31

Step 2. Calculate a national value for each indicator giving equal weight to each taxonomic group (Equation 3 in Hoban, da Silva, Mastretta-Yanes, et al., 2023).

Amphibian + Reptile + Fish + Mammal + Bird + Angiosperm

6

$$\text{PM} = \frac{0.64 + 1.00 + 0.83 + 0.81 + 0.80 + 0.89}{6} = 0.83$$

6

$$\text{Ne 500} = \frac{0.06 + 0.88 + 0.41 + 0.81 + 0.62 + 0.36 + 0.31}{6} = 0.44$$

6

S2 Species selection, alternative assessment of data sources, and data availability

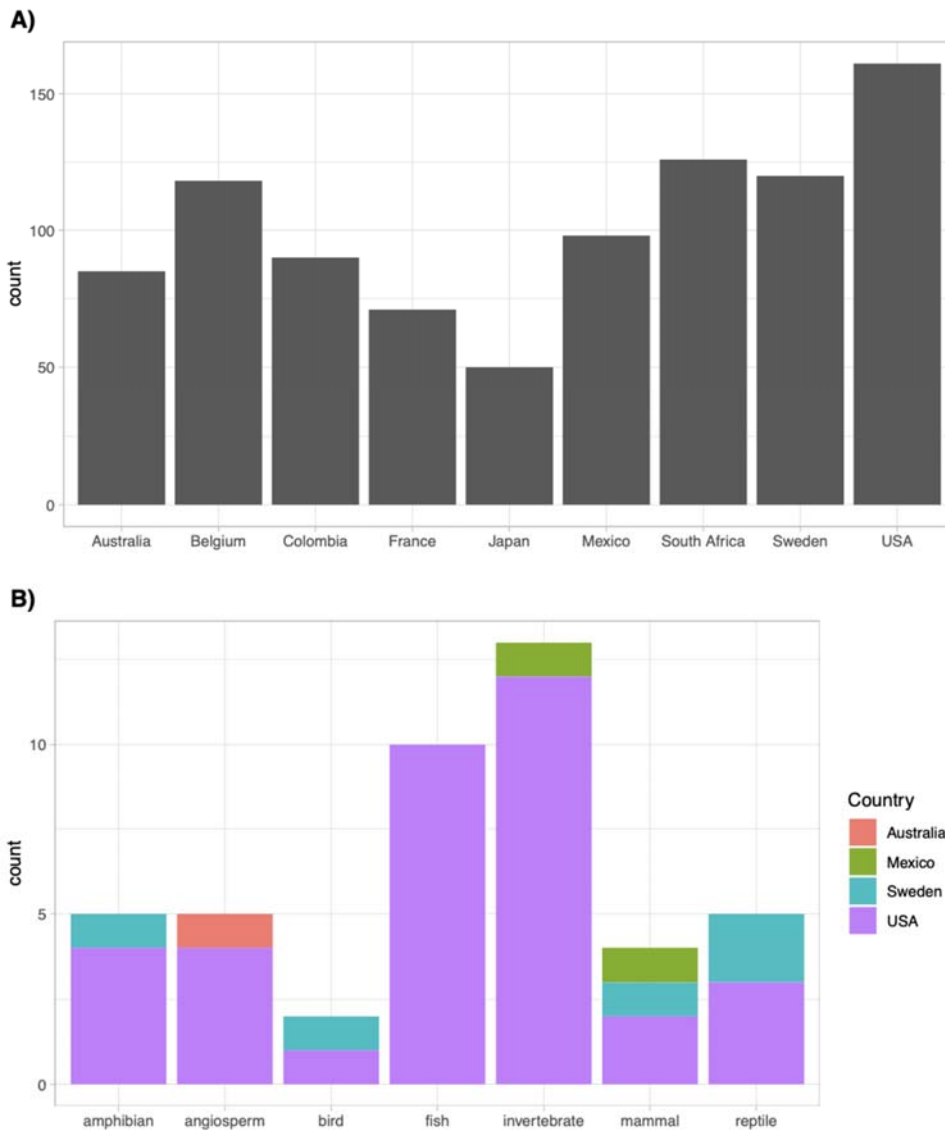


Figure S1. (A) Number of taxa assessed by country after alternative assessments of taxa within a single country were averaged (n=919) ; (B) Number and taxonomic representation of the species that were assessed more than once (n=44), identified by country. Alternative assessments per taxon ranged from 2-4 with a mode of 2.

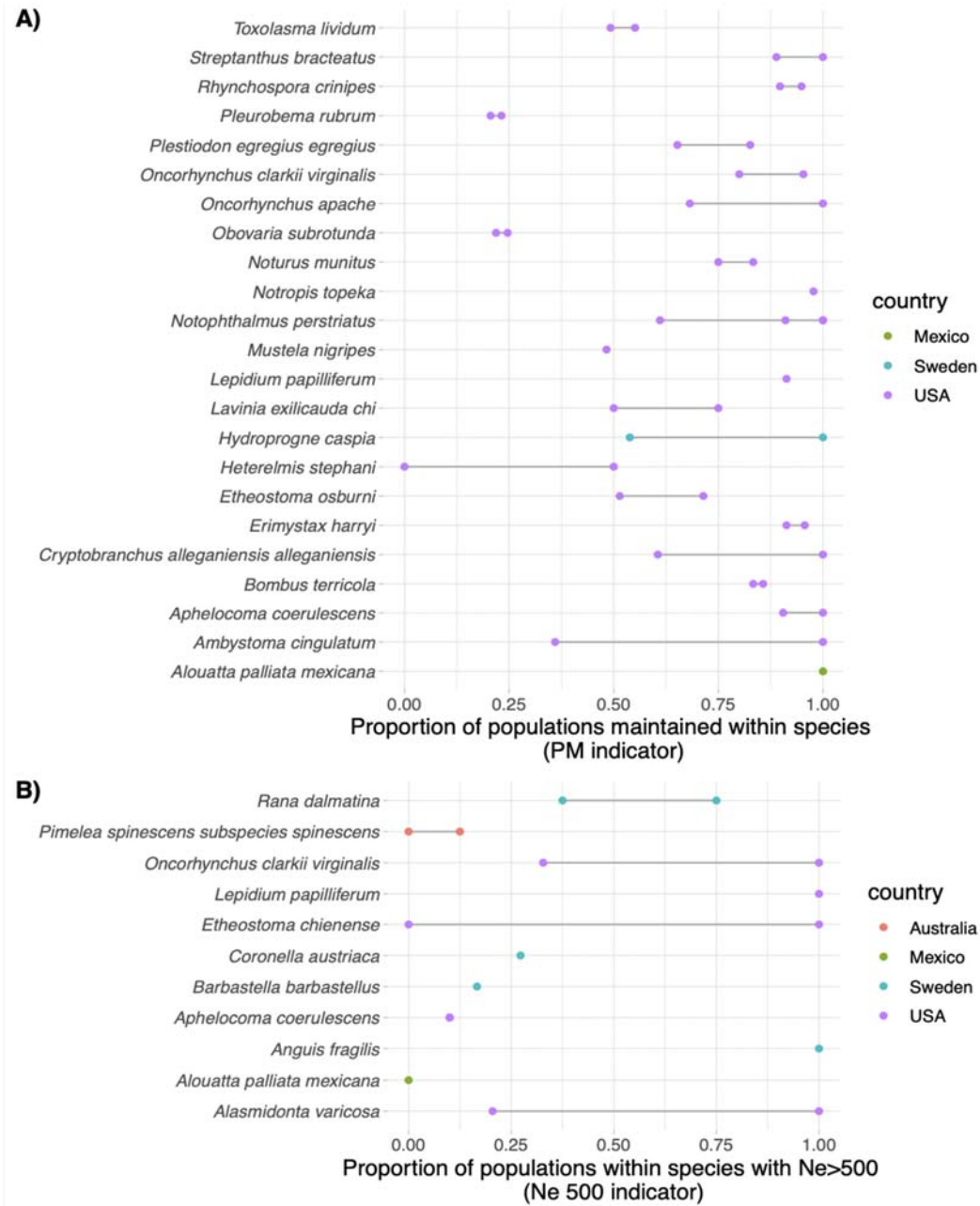


Figure S2. Changes in indicator values for taxa with alternative assessments. (A) Changes in the value of PM indicator for the taxa with alternative assessments. For taxa with only a single point (i.e., no change), the alternative assessment was unable to define the number of populations, therefore this indicator could not be calculated. (B) Changes in the Ne 500 indicator for the taxa with multiple assessments. If a single point appears, it is due to the inability to calculate the number of populations in the alternative assessment (i.e., number of extinct populations is unknown).

Table S5. Sample sizes and associated percentages of the number of assessments, taxa and populations reported in this study.

Level of assessment	Entire data set (alternative assessments reported separately)		Subset of the dataset (alternative assessments averaged)*	
	Number of Assessments (966)	Percent (out of 966)	Number of Taxa (919)	Percent (out of 919)
<i>Data on at least one of the two indicators</i>	802	83	765	83
<i>Data on PM indicator</i>	550	57	518	54
<i>No data on PM indicator</i>	416	43	401	43
<i>Data on Ne 500 indicator (for at least 1 pop)</i>	613	63	568	61
Population	Total Populations Assessed (5625)	Percent (out of 5625)	Total Populations (5271)	Percent (out of 5271)
<i>Ne calculated from Point Census data</i>	1266	22	1185	22
<i>Ne calculated from Range Census data</i>	2974	53	2862	54
<i>Ne calculated from No data</i>	349	6	222	4
<i>No size data available</i>	1063	19	1002	19

Bold values are reported in the study main text.

* Values between assessments and taxa differ, because data may have been provided in only one of the alternative assessments

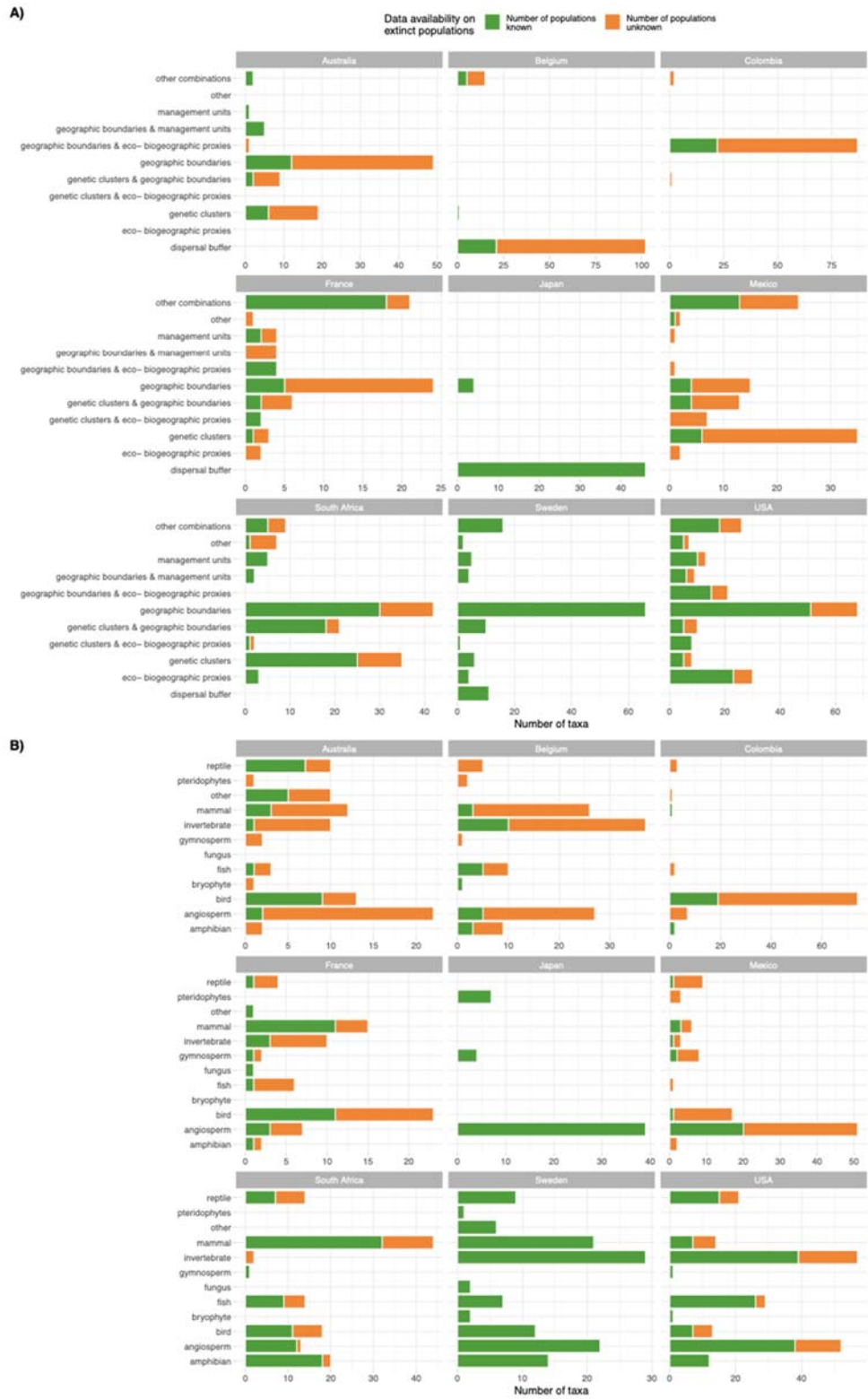


Figure S3. Availability of data on the number of extinct populations across countries and (A) method used to define populations or (B) taxonomic group.

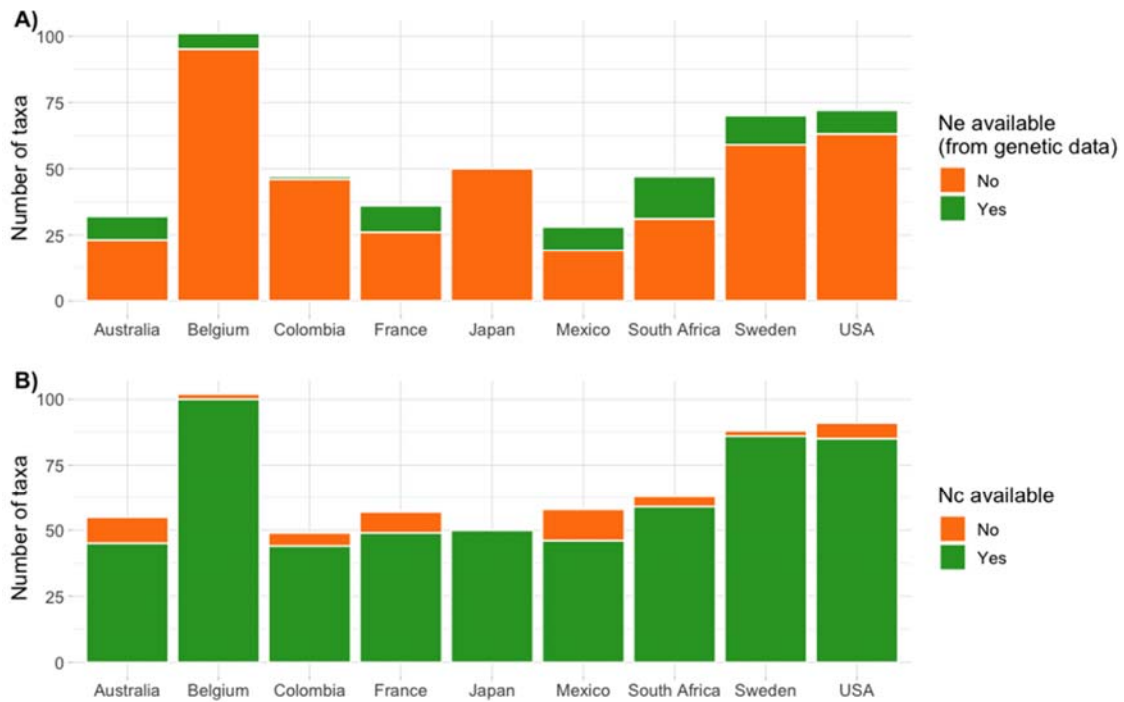


Figure S4. Barplots illustrating the availability and type of population size data for each of the nine participating countries. The extent of each bar represents the total number of taxa assessed for a given country. (A) Total number of taxa with effective population size (N_e) data; (B) total number of taxa with census data (N_c).



Figure S5. Availability of N_e or N_c population size data across taxonomic groups and countries.

Charts show the number of taxa within a given taxonomic group possessing population size data for at least one population. Data was considered available if effective population size (N_e) or census population size (N_c) data was present for at least one population of a taxa (green bars), but we also recorded if data was available for the taxa as a whole (“species or subspecies level”; blue bars). Taxa without any N_e or N_c data were classified as having “Insufficient data” (grey bars). The number of taxa are shown including the records of taxa that were assessed more than once.

S3 Defining populations

Correlations between the number of populations identified, range size and the methods used to define them

First, we tested whether the different methods used to define populations reported in this study were associated with varying numbers of populations obtained. For this analysis, we also controlled for range type, as we expect species with wider ranges to plausibly have more populations than species with narrower ranges. We found that species that were wide-ranging had significantly more populations than species with narrow ranges, when controlling for the method used to determine the number of populations (Table S6).

Considering “geographic boundaries” as our reference method for defining populations, we also observed that most methods were associated with a statistically significant lower number of populations identified, even when controlling for species range (Table S6). Substantially fewer populations were obtained using genetic methods (including genetic methods in combination with other methods) to identify the number of populations, after controlling for species range (Table S6). Our parameter estimates for the differences among methods, and effect of species range, were extremely precise, indicating that these differences show high reliability. Visual examination of the distribution of data across the various methods and two levels of species range (narrow vs wide ranging; Fig. S6), showed that data were present in all levels of the dataset (i.e., for all methods, and across both narrow and wide-ranging species). The fitted means of the model are consistent with the values obtained from the raw data (noting that the model controls for country-level variation, which is not incorporated into raw data means; Fig. S6; Table S6).

Table S6. Does the number of maintained populations vary with method and range?

GLMER: N_extant_pops ~ Method + Range + (1|Country), family = "Poisson". N = 903

Parameter	Est.	SE	Z	p		Fitted Mean
<i>Intercept (reference category for</i>						
<i>Method: geographic_boundaries +</i>	1.941	0.323	6.02	< 0.001	***	6.97
<i>Narrow range)</i>						
<i>Method: dispersal_buffer</i>	-1.161	0.051	-22.70	< 0.001	***	2.18
<i>Method: eco_biogeo_proxies</i>	0.060	0.034	1.75	0.080	.	7.40
<i>Method: genetic_clusters</i>	-1.415	0.064	-22.19	< 0.001	***	1.69
<i>Method: genetic_clusters &</i>	-1.292	0.094	-13.72	< 0.001	***	1.91
<i>eco_biogeo_proxies</i>						
<i>Method: genetic_clusters &</i>	0.159	0.090	-22.06	< 0.001	***	8.17
<i>geographic_boundaries</i>						
<i>Method: geographic_boundaries &</i>	-0.013	0.090	-22.06	0.757		6.88
<i>eco_biogeo_proxies</i>						
<i>Method: geographic_boundaries &</i>	-0.007	0.090	-22.06	0.894		6.92
<i>management_units</i>						
<i>Method: management_units</i>	-0.662	0.056	-11.91	< 0.001	***	3.59
<i>Method: other</i>	-1.172	0.112	-10.50	< 0.001	***	2.16
<i>Method: other_combinations</i>	-0.645	0.036	-18.03	< 0.001	***	3.65
<i>Range: wide-ranging</i>	0.983	0.020	48.00	< 0.001	***	18.61

Because method was so important for determining the number of populations, we also tested whether this effect remained after removing “wide-ranging” species from the model. The objective here was to test whether method alone would also produce varying numbers of populations, for example if species range is unknown. We found that the effect of method on number of populations identified remained strong, although the predicted values for number of populations varied compared to the model containing species range, indicating that species range is an important consideration when interpreting the effect of method on number of populations (Table S7).

Table S7. Does the number of maintained populations vary with the method used?GLMER: $N_{\text{extant_pops}} \sim \text{Method} + (1|\text{Country})$, family = "Poisson". N = 903

Parameter	Est.	SE	Z	p	Fitted	
					Mean	
<i>Intercept (reference category for Method geographic_boundaries)</i>	2.246	0.343	6.55	< 0.001	***	9.45
<i>Method: dispersal_buffer</i>	-0.871	0.053	-16.44	< 0.001	***	3.96
<i>Method: eco_biogeo_proxies</i>	0.304	0.034	8.92	< 0.002	***	12.81
<i>Method: genetic_clusters</i>	-1.118	0.063	-17.62	< 0.001	***	3.09
<i>Method: genetic_clusters & eco_biogeo_proxies</i>	-0.924	0.094	-9.84	< 0.001	***	3.75
<i>Method: genetic_clusters & geographic_boundaries</i>	0.346	0.035	9.79	< 0.001	***	13.36
<i>Method: geographic_boundaries & eco_biogeo_proxies</i>	0.275	0.041	6.79	< 0.002	***	12.45
<i>Method: geographic_boundaries & management_units</i>	0.067	0.051	1.30	0.192		10.11
<i>Method: management_units</i>	-0.243	0.055	-4.42	< 0.001	***	7.41
<i>Method: other</i>	-1.044	0.112	-9.35	< 0.001	***	3.33
<i>Method: other_combinations</i>	-0.387	0.035	-10.91	< 0.001	***	6.42

Extending from this result, we also tested whether species range alone is an important predictor of the number of extant populations, as species range is determined by the geographic spread of the species, but not necessarily fragmentation (i.e., a single, large population, or a number of fragmented populations over a wide area, could both be considered as “wide-ranging”). Unsurprisingly, we found that species range was a very reliable, statistically significant predictor of the number of populations identified for a species, with the estimated number of populations for wide-ranging species nearly three times the number of populations identified for narrow-range species in our dataset (after controlling for country-level variation in the mean number of populations identified across all the species assessed by each country team; Table S8).

Table S8. Does the number of maintained populations vary with range?

GLMER: N_extant_pops ~ Range + (1|Country), family = "Poisson". N = 903

Parameter	Est.	SE	Z	p		Fitted Mean
<i>Intercept (reference category = Narrow range)</i>	1.582	0.280	5.66	< 0.001	***	4.86
<i>Range: wide-ranging</i>	0.846	1.552	42.69	< 0.001	***	11.33

PM indicator (proportion of maintained populations within a species)

Our next goal was to determine whether the approach for delineating populations study design (i.e., clustering method) and/or species-level variables (number of populations, range) appropriately were associated with the measurement of the genetic indicators. When considering population delineation method alone, we found a statistically significant effect of genetic clustering methods on the proportion of maintained populations, whereby species for which populations were identified via genetic methods had higher values of the PM indicator, compared to species where geographic methods were used to identify populations (Table S9).

Table S9. Does the PM indicator vary with method?

GLMM: PM indicator ~ Method + (1|Country), family = "ordbeta". N = 548

Parameter	Est.	SE	Z	p	
<i>Intercept (reference category for Method:</i>					
<i>geographic_boundaries)</i>	0.582	0.227	2.56	0.010	*
<i>Method: dispersal_buffer</i>	0.258	0.248	1.04	0.298	
<i>Method: eco_biogeo_proxies</i>	0.128	0.220	0.58	0.559	
<i>Method: genetic_clusters</i>	0.510	0.260	1.96	0.050	*
<i>Method: genetic_clusters & eco_biogeo_proxies</i>	0.453	0.441	1.03	0.304	
<i>Method: genetic_clusters & geographic_boundaries</i>	-0.028	0.218	-0.13	0.899	
<i>Method: geographic_boundaries & eco_biogeo_proxies</i>	-0.076	0.235	-0.32	0.748	
<i>Method: geographic_boundaries & management_units</i>	0.349	0.338	1.03	0.302	
<i>Method: management_units</i>	-0.163	0.249	-0.65	0.513	
<i>Method: other</i>	0.078	0.513	0.15	0.879	
<i>Method: other_combinations</i>	0.441	0.169	2.62	0.009	**

Given the preceding relationships detected between method, number of populations, and species' range, we investigated associations between these variables and our indicator values in more detail, to aid in understanding the underlying mechanisms that were driving the association between method (especially genetic clusters) and the PM indicator. That is, we hypothesized that the relationship between method and the PM indicator may be an indirect result of the association between method and number of populations and species range.

First, we added the number of populations to our model testing the relationship between method and the PM indicator and found that number of populations did not have a qualitative effect on the results (i.e., number of populations was not a statistically significant predictor of the PM indicator when controlling for method; Table S10).

Table S10. Does the method still impact the PM indicator if we control for the number of maintained populations?

GLMM: PM indicator ~ Method + Npops + (1|Country), family = "ordbeta". N = 548

Parameter	Est.	SE	Z	p	
<i>Intercept (reference category for Method: geographic_boundaries)</i>	0.570	0.227	2.51	0.012	*
<i>Method: dispersal_buffer</i>	0.262	0.247	1.06	0.288	
<i>Method: eco_biogeo_proxies</i>	0.106	0.220	0.48	0.629	
<i>Method: genetic_clusters</i>	0.513	0.259	1.98	0.048	*
<i>Method: genetic_clusters & eco_biogeo_proxies</i>	0.466	0.441	1.06	0.290	
<i>Method: genetic_clusters & geographic_boundaries</i>	-0.054	0.219	-0.24	0.807	
<i>Method: geographic_boundaries & eco_biogeo_proxies</i>	-0.091	0.236	-0.39	0.700	
<i>Method: geographic_boundaries & management_units</i>	0.365	0.337	1.08	0.279	
<i>Method: management_units</i>	-0.155	0.249	-0.62	0.534	
<i>Method: other</i>	0.090	0.512	0.18	0.860	
<i>Method: other_combinations</i>	0.439	0.168	2.62	0.009	**
<i>Number of extant populations</i>	0.001	0.001	0.97	0.332	

Number of populations alone also did not show a statistically significant relationship with the PM indicator in our dataset (i.e., when not controlling for method; Table S11).

Table S11. Does the number of maintained populations alone affect the PM indicator?

GLMM: PM indicator ~ Npops + (1|Country), family = "ordbeta". N = 548

Parameter	Est.	SE	Z	p
<i>Intercept</i>	0.706	0.206	3.43	0.001 ***
<i>Number of extant populations</i>	0.001	0.001	0.72	0.472

However, there were statistically significant interactions on the PM indicator between the number of populations and some of the methods used (Table S12). Accordingly, the relationship between method and the PM indicator depends on the number of populations identified for several methods (or equivalently, the importance of the number of populations for the PM indicator depends on which method is used).

Table S12. Does the effect of the method on the PM indicator depend on the number of maintained populations?

GLMM: PM indicator ~ Method + Npops + Method*Npops + (1|Country), family = "ordbeta". N = 548

Parameter	Est.	SE	Z	p	
<i>Intercept (reference category for Method: geographic_boundaries)</i>	0.485	0.223	2.18	0.030	*
<i>Method: dispersal_buffer</i>	0.246	0.249	0.99	0.324	
<i>Method: eco_biogeo_proxies</i>	0.075	0.246	0.31	0.761	
<i>Method: genetic_clusters</i>	0.548	0.384	1.43	0.154	
<i>Method: genetic_clusters & eco_biogeo_proxies</i>	1.678	0.680	2.47	0.014	*
<i>Method: genetic_clusters & geographic_boundaries</i>	0.154	0.233	0.66	0.510	
<i>Method: geographic_boundaries & eco_biogeo_proxies</i>	0.108	0.258	0.42	0.676	
<i>Method: geographic_boundaries & management_units</i>	0.107	0.428	0.25	0.802	
<i>Method: management_units</i>	0.361	0.335	1.08	0.281	
<i>Method: other</i>	-1.502	0.970	-1.55	0.122	
<i>Method: other_combinations</i>	0.303	0.192	1.57	0.116	
<i>Number of extant populations</i>	0.004	0.002	1.98	0.047	*
<i>Method: dispersal_buffer * number of extant populations</i>	0.005	0.007	0.61	0.544	
<i>Method: eco_biogeo_proxies * number of extant populations</i>	-0.002	0.003	-0.51	0.611	
<i>Method: genetic_clusters * number of extant populations</i>	0.007	0.062	0.11	0.912	
<i>Method: genetic_clusters & eco_biogeo_proxies * number of extant populations</i>	-0.090	0.033	-2.72	0.007	**

Parameter	Est.	SE	Z	p	
<i>Method: genetic_clusters &</i>					
<i>geographic_boundaries * number of extant populations</i>	-0.006	0.003	-2.25	0.025	*
<hr/>					
<i>Method: geographic_boundaries &</i>					
<i>eco_biogeo_proxies * number of extant populations</i>	-0.007	0.003	-2.10	0.035	*
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<i>Method: geographic_boundaries &</i>					
<i>management_units * number of extant populations</i>	0.047	0.053	0.89	0.375	
<hr/>					
<i>Method: management_units * number of extant populations</i>					
<i>extant populations</i>	-0.032	0.015	-2.14	0.033	*
<hr/>					
<i>Method: other * number of extant populations</i>					
<i>populations</i>	0.466	0.286	1.63	0.103	
<hr/>					
<i>Method: other_combinations * number of extant populations</i>					
<i>extant populations</i>	0.007	0.005	1.25	0.211	

Incidentally, because the method used to define a population appears to be important for these relationships, we conducted an additional analysis, in which we simplified our dataset to only those species for which a single method was used to determine population clusters, and repeated the model presented above (evaluating a possible interaction between method and number of populations on the PM indicator). In this reduced analysis, we observed limited evidence of relationships among methods and number of populations on the PM indicator (Table S13).

Table S13. Does the effect of "a single" method on the PM indicator depend on the number of maintained populations?

GLMM: PM indicator ~ Method(single) + Npops + Method*Npops + (1|Country), family = "ordbeta". N = 351

Parameter	Est.	SE	Z	p	
<i>Intercept (reference category for Method: geographic_boundaries)</i>	0.450	0.225	2.00	0.135	*
<i>Number of extant populations</i>	0.003	0.002	1.50	0.478	
<i>Method: dispersal_buffer</i>	0.206	0.291	0.71	0.985	
<i>Method: eco_biogeo_proxies</i>	-0.005	0.250	-0.02	0.050	
<i>Method: genetic_clusters</i>	0.756	0.386	1.96	0.221	
<i>Method: management_units</i>	0.417	0.341	1.22	0.481	
<i>Method: dispersal_buffer * number of extant populations</i>	0.005	0.008	0.70	0.750	
<i>Method: eco_biogeo_proxies * number of extant populations</i>	-0.001	0.003	-0.32	0.915	
<i>Method: genetic_clusters * number of extant populations</i>	-0.007	0.063	-0.11	0.025	
<i>Method: management_units * number of extant populations</i>	-0.036	0.016	-2.24	< 0.001	*

Because we found a relationship between method and number of populations on the PM indicator, and a relationship between species range and number of populations, we further tested whether the effect of method on the PM indicator is moderated by species range. In a model including both method and species range, only range was a statistically significant predictor of the PM indicator (i.e. that when controlling for species range, method is no longer a statistically significant predictor of the PM indicator) (Table S14). This result suggests that species range may be more important than method when estimating the PM indicator.

We were unable to test for an interaction between method and species range (i.e., to determine whether species range was only associated with the PM indicator for some methods) because the

model did not converge correctly (perhaps due to limited data for some combinations of method/range).

Table S14. Does the method still impact the PM indicator if we control for species range?

GLMM: PM indicator ~ Method + Range + (1|Country), family = "ordbeta". N = 504

Parameter	Est.	SE	Z	p	
<i>Intercept (reference category for Method: geographic_boundaries + Narrow range)</i>	0.608	0.230	2.64	0.008	**
<i>Method: dispersal_buffer</i>	0.087	0.256	0.34	0.735	
<i>Method: eco_biogeo_proxies</i>	-0.108	0.243	-0.44	0.658	
<i>Method: genetic_clusters</i>	0.245	0.266	0.92	0.357	
<i>Method: genetic_clusters & eco_biogeo_proxies</i>	0.174	0.525	0.33	0.740	
<i>Method: genetic_clusters & geographic_boundaries</i>	-0.171	0.220	-0.78	0.437	
<i>Method: geographic_boundaries & eco_biogeo_proxies</i>	-0.294	0.251	-1.17	0.240	
<i>Method: geographic_boundaries & management_units</i>	0.253	0.337	0.75	0.453	
<i>Method: management_units</i>	-0.405	0.298	-1.36	0.174	
<i>Method: other</i>	-0.120	0.514	-0.23	0.816	
<i>Method: other_combinations</i>	0.259	0.177	1.47	0.143	
<i>Range: wide-ranging</i>	0.376	0.118	3.19	0.001	**

Ne 500 indicator (proportion of populations within a species with Ne > 500)

Our analysis of the Ne 500 indicator followed a parallel structure to our analysis of the PM indicator. First, we tested whether the method used was associated with variation in the Ne 500 indicator. Similar to the result for the PM indicator (Table S9), we found statistically significant variation in the Ne 500 indicator by method, where the predominant relationship was with three methods that included genetic clustering to define populations (Table S15). These three methods were all associated with

higher values of the Ne 500 indicator than cases where geographic boundaries were used to define populations (Table S15).

Table S15. Does the Ne 500 indicator vary with method?

GLMM: Ne 500 indicator ~ Method + (1|Country), family = "ordbeta". N = 583

Parameter	Est.	SE	Z	p	
<i>Intercept (reference category for Method: geographic_boundaries)</i>	-0.875	0.180	-4.85	< 0.001	***
<i>Method: dispersal_buffer</i>	0.323	0.301	1.07	0.284	
<i>Method: eco_biogeo_proxies</i>	-0.138	0.333	-0.42	0.678	
<i>Method: genetic_clusters</i>	0.605	0.242	2.50	0.012	*
<i>Method: genetic_clusters & eco_biogeo_proxies</i>	1.054	0.440	2.40	0.017	*
<i>Method: genetic_clusters & geographic_boundaries</i>	0.534	0.246	2.17	0.030	*
<i>Method: geographic_boundaries & eco_biogeo_proxies</i>	-0.103	0.339	-0.30	0.762	
<i>Method: geographic_boundaries & management_units</i>	0.626	0.332	1.89	0.059	.
<i>Method: management_units</i>	-0.050	0.416	-0.12	0.904	
<i>Method: other</i>	1.036	0.621	1.67	0.095	.
<i>Method: other_combinations</i>	0.366	0.203	1.81	0.071	.

As for the PM indicator, we next investigated whether the relationships between methods and the indicator were moderated by the role of number of populations and species range. We found that the Ne 500 indicator still showed variation with method when controlling for the number of populations that a species has (Table S16).

Table S16. Does the method still influence the Ne 500 indicator if we control for the number of populations?

GLMM: Ne 500 indicator ~ Method + Npops + (1|Country), family = "ordbeta". N = 583

Parameter	Est.	SE	Z	p	
<i>Intercept (reference category for Method: geographic_boundaries)</i>	-0.750	0.172	-4.37	< 0.001	***
<i>Method: dispersal_buffer</i>	0.204	0.282	0.72	0.469	
<i>Method: eco_biogeo_proxies</i>	-0.116	0.325	-0.36	0.721	
<i>Method: genetic_clusters</i>	0.529	0.238	2.22	0.026	*
<i>Method: genetic_clusters & eco_biogeo_proxies</i>	1.002	0.427	2.35	0.019	*
<i>Method: genetic_clusters & geographic_boundaries</i>	0.482	0.241	2.00	0.046	*
<i>Method: geographic_boundaries & eco_biogeo_proxies</i>	-0.132	0.325	-0.41	0.685	
<i>Method: geographic_boundaries & management_units</i>	0.613	0.324	1.89	0.059	.
<i>Method: management_units</i>	-0.069	0.404	-0.17	0.864	
<i>Method: other</i>	0.942	0.613	1.54	0.125	
<i>Method: other_combinations</i>	0.366	0.196	1.87	0.062	.
<i>Number of extant populations</i>	-0.005	0.002	-2.69	0.007	**

We also observed that number of populations alone (i.e., without controlling for method) was a statistically significant predictor of the Ne 500 indicator, whereby the indicator value was slightly lower for species with fewer populations in our dataset (Table S17).

Table S17. Does the number of maintained populations alone affect the Ne 500 indicator?

GLMM: Indicator1 ~ Npops + (1|Country), family = "ordbeta". N = 583

Parameter	Est.	SE	Z	p	
<i>Intercept</i>	-0.508	0.121	-4.18	< 0.001	***
<i>Number of extant populations</i>	-0.005	0.002	-2.84	0.005	**

For genetic clusters, the relationship between the method and the indicator was moderated by the number of populations (interaction term in the model), but for the most part, for the Ne 500 indicator, associations with method did not appear to depend on the number of populations (most interaction terms were not statistically significant, while main effects remained so) (Table S18).

As for the PM indicator, we also tested these relationships using a simplified dataset that targeted species that were classified using only a single method, and found that, for the Ne 500 indicator, the results were qualitatively similar to our main analysis (Table S18 & S19).

Table S18. Does the effect of the method on the Ne 500 indicator depend on the number of maintained populations?

GLMM: Ne 500 indicator ~ Method + Npops + Method*Npops + (1|Country), family = "ordbeta". N = 583

Parameter	Est.	SE	Z	p	
<i>Intercept (reference category for</i>					***
<i>Method: geographic_boundaries)</i>	-0.844	0.185	-4.58	< 0.001	
<i>Method: dispersal_buffer</i>	0.335	0.282	1.19	0.234	
<i>Method: eco_biogeo_proxies</i>	0.174	0.416	0.42	0.675	
<i>Method: genetic_clusters</i>	1.219	0.370	3.29	0.001	***
<i>Method: genetic_clusters &</i>					
<i>eco_biogeo_proxies</i>	1.036	0.629	1.65	0.100	
<i>Method: genetic_clusters &</i>					*
<i>geographic_boundaries</i>	0.680	0.306	2.22	0.026	
<i>Method: geographic_boundaries &</i>					
<i>eco_biogeo_proxies</i>	0.666	0.493	1.35	0.177	
<i>Method: geographic_boundaries &</i>					*
<i>management_units</i>	0.976	0.413	2.36	0.018	
<i>Method: management_units</i>	0.393	0.608	0.65	0.518	
<i>Method: other</i>	-0.831	1.567	-0.53	0.596	
<i>Method: other_combinations</i>	0.452	0.206	2.19	0.028	*
<i>Number of extant populations</i>	-0.002	0.003	-0.69	0.490	
<i>Method: dispersal_buffer * number of</i>					
<i>extant populations</i>	-0.004	0.004	-0.86	0.392	
<i>Method: eco_biogeo_proxies * number</i>					
<i>of extant populations</i>	-0.016	0.015	-1.13	0.260	
<i>Method: genetic_clusters * number of</i>					**
<i>extant populations</i>	-0.163	0.074	-2.20	0.028	
<i>Method: genetic_clusters &</i>					
<i>eco_biogeo_proxies * number of</i>					
<i>extant populations</i>	0.011	0.084	0.13	0.900	

Parameter	Est.	SE	Z	p
<i>Method: genetic_clusters &</i>				
<i>geographic_boundaries * number of extant populations</i>	-0.016	0.023	-0.69	0.489
<hr/>				
<i>Method: geographic_boundaries &</i>				
<i>eco_biogeo_proxies * number of extant populations</i>	-0.113	0.059	-1.93	0.054
<hr/>				
<i>Method: geographic_boundaries &</i>				
<i>management_units * number of extant populations</i>	-0.030	0.029	-1.03	0.302
<hr/>				
<i>Method: management_units * number of extant populations</i>				
	-0.055	0.068	-0.81	0.416
<hr/>				
<i>Method: other * number of extant populations</i>				
	0.723	0.785	0.92	0.357
<hr/>				
<i>Method: other_combinations * number of extant populations</i>				
	-0.004	0.004	-0.91	0.362

Table S19. Does the effect of "a single" method on indicator1 depend on the number of maintained pops?

GLMM: Ne 500 indicator ~ Method(single) + Npops + Method*Npops + (1|Country), family = "ordbeta". N = 384

Parameter	Est.	SE	Z	p	
<i>Intercept (reference category for Method: geographic_boundaries)</i>	-0.804	0.207	-3.90	< 0.001	***
<i>Number of extant populations</i>	0.000	0.003	-0.18	0.855	
<i>Method: dispersal_buffer</i>	0.199	0.399	0.50	0.619	
<i>Method: eco_biogeo_proxies</i>	0.177	0.436	0.41	0.684	
<i>Method: genetic_clusters</i>	1.136	0.386	2.95	0.003	**
<i>Method: management_units</i>	0.350	0.611	0.57	0.566	
<i>Method: dispersal_buffer * number of extant populations</i>	-0.004	0.004	-0.80	0.424	
<i>Method: eco_biogeo_proxies * number of extant populations</i>	-0.015	0.015	-1.01	0.314	
<i>Method: genetic_clusters * number of extant populations</i>	-0.151	0.078	-1.93	0.054	.
<i>Method: management_units * number of extant populations</i>	-0.050	0.066	-0.75	0.452	

We also tested whether associations between method, number of populations and the Ne 500 indicator could be explained by species range and found that species range is a plausible predictor of the Ne 500 indicator (Table S20). Unlike for the PM indicator, a model for the Ne 500 indicator that contained method and species range retained a statistically significant relationship between method "genetic clusters" and the indicator, whereby using genetic clusters to define populations was associated with higher values of the Ne 500 indicator than when geographic boundaries were used, even when controlling for species range (Table S20). As for the PM indicator, we were unable to test interactions between method and species range, as the model failed to converge, likely due to unbalanced data across the levels of interactions.

Table S20. Is there still an effect of method on the Ne 500 indicator if we control for species range?

GLMM: Ne 500 indicator ~ Method + Range + (1|Country), family = "ordbeta". N =544

Parameter	Est.	SE	Z	p	
<i>Intercept (reference category for Method: geographic_boundaries + Narrow range)</i>	-1.097	0.197	-5.57	< 0.001	***
<i>Method: dispersal_buffer</i>	0.120	0.288	0.42	0.678	
<i>Method: eco_biogeo_proxies</i>	-0.335	0.381	-0.88	0.379	
<i>Method: genetic_clusters</i>	0.709	0.261	2.72	0.007	**
<i>Method: genetic_clusters & eco_biogeo_proxies</i>	0.815	0.455	1.79	0.073	.
<i>Method: genetic_clusters & geographic_boundaries</i>	0.396	0.254	1.56	0.119	
<i>Method: geographic_boundaries & eco_biogeo_proxies</i>	-0.183	0.364	-0.50	0.614	
<i>Method: geographic_boundaries & management_units</i>	0.476	0.341	1.40	0.163	
<i>Method: management_units</i>	-0.118	0.436	-0.27	0.787	
<i>Method: other</i>	1.039	0.618	1.68	0.093	.
<i>Method: other_combinations</i>	0.219	0.212	1.03	0.302	
<i>Range: wide ranging</i>	0.567	0.139	4.08	< 0.001	***

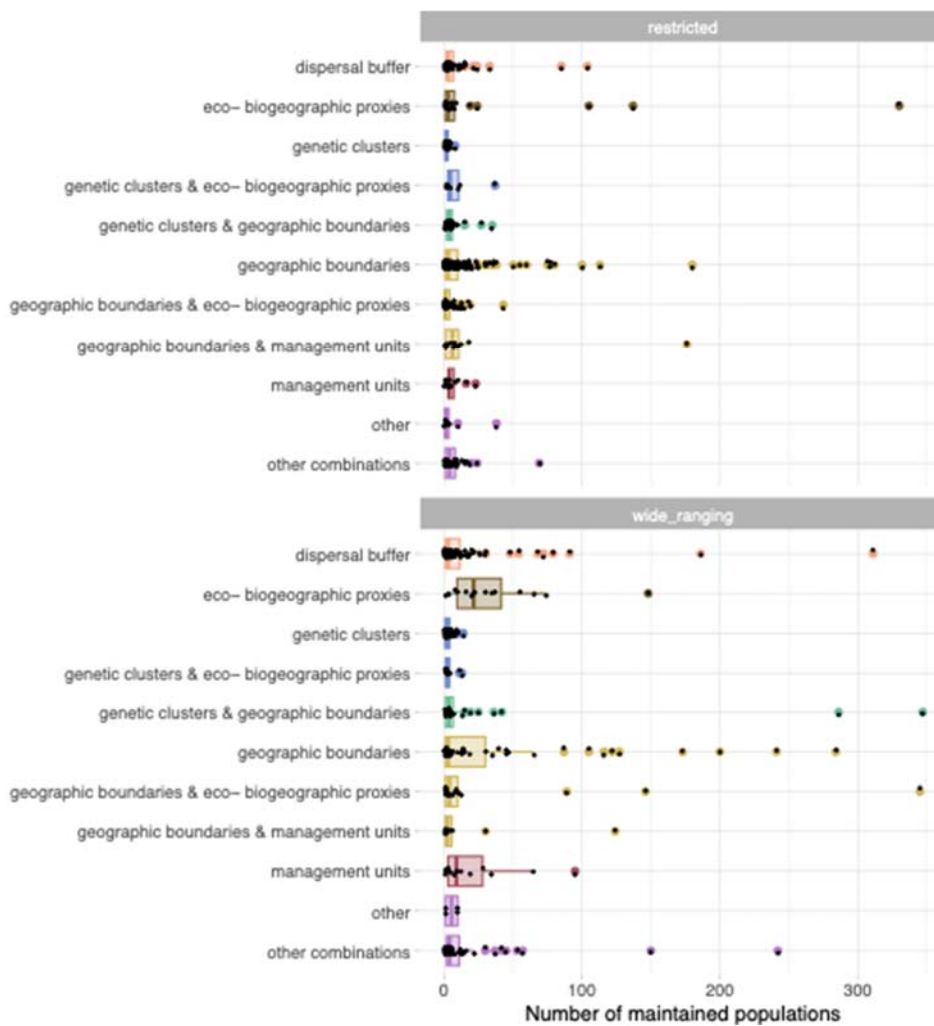


Figure S6. Aggregated results across the nine countries showing the number of extant maintained) populations per taxa assessed according to method used to define populations, separate by range type. Each dot represents the indicator value for a single assessment, and each colour is associated with a particular method (e.g., orange: dispersal buffer; brown: eco-biogeographic proxies; blue: genetic clusters; green: genetic cluster and geographic boundaries; yellow: geographic boundaries; red: management units; purple: other).

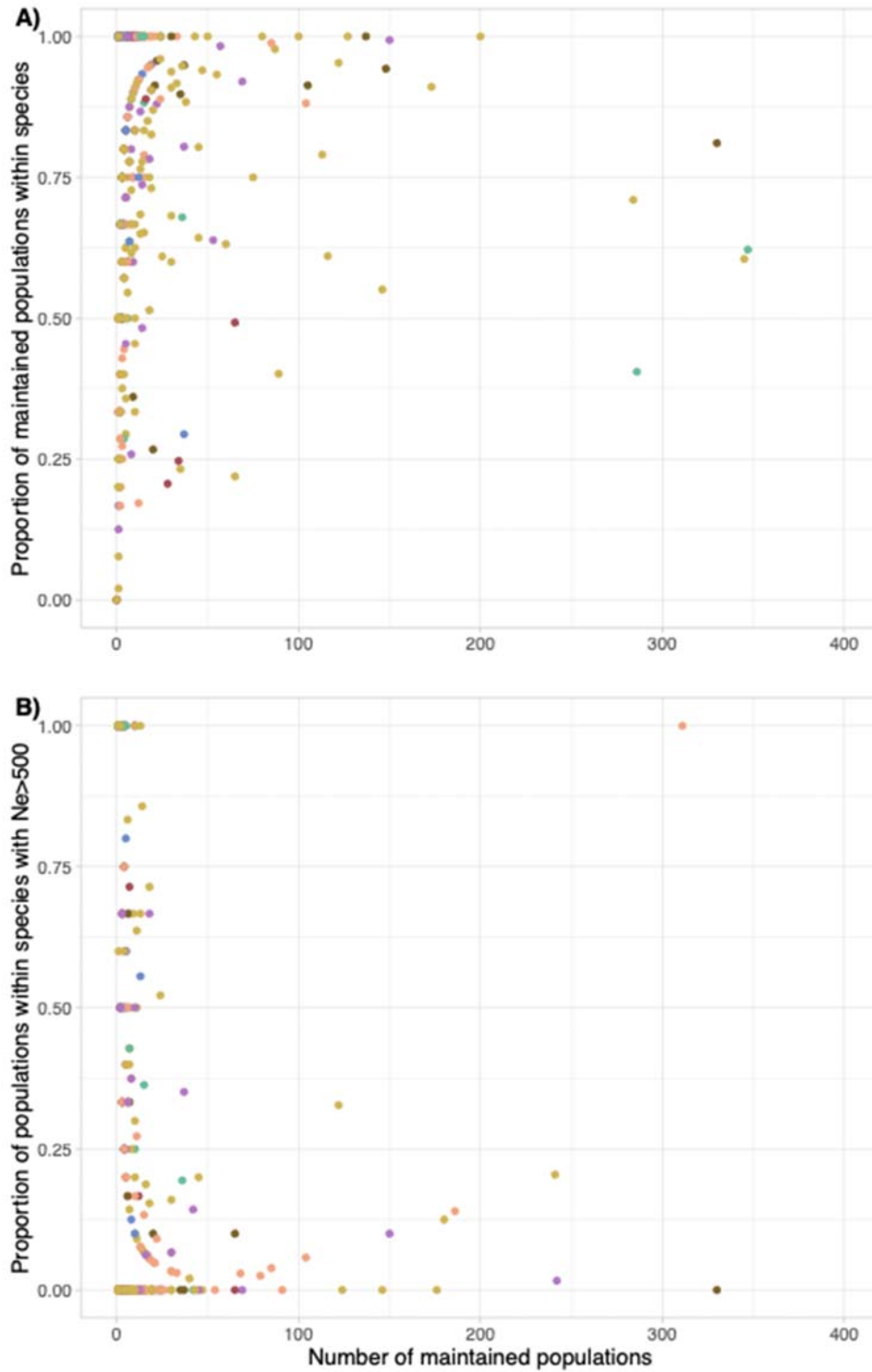


Figure S7. Relationship between indicator values and the number of extant (maintained) populations.

Points are coloured by method to define population, with colors as in Fig. S6 .

S4 Least Concern and Near Threatened taxa with low indicator values

Table S21. Taxa listed as Least Concern and Near Threatened by IUCN that have low Ne 500 indicator values (below or equal to 0.25). List was made based on the Ne 500 indicator (highlighted in bold); the PM indicator is also shown for reference.

Taxon	Taxonomic Group	Country	Ne 500 indicator	PM indicator
Least Concern				
<i>Alytes obstetricans</i>	Amphibian	Belgium	0.14	NA
<i>Bombina variegata</i>	Amphibian	Belgium	0	0.17
<i>Bufo calamita</i>	Amphibian	Belgium	0	NA
<i>Pelobates fuscus</i>	Amphibian	Belgium	0	0.5
<i>Pelophylax lessonae</i>	Amphibian	Belgium	0	NA
<i>Rana arvalis</i>	Amphibian	Belgium	0.14	NA
<i>Triturus cristatus</i>	Amphibian	Belgium	0.02	NA
<i>Calotriton asper</i>	Amphibian	France	0	NA
<i>Bombina bombina</i>	Amphibian	Sweden	0.25	1
<i>Bufotes viridis</i>	Amphibian	Sweden	0	0.87
<i>Epidalea calamita</i>	Amphibian	Sweden	0	0.92
<i>Pelobates fuscus</i>	Amphibian	Sweden	0	0.75
<i>Pelophylax lessonae</i>	Amphibian	Sweden	0	1
<i>Triturus cristatus</i>	Amphibian	Sweden	0.1	0.99

<i>Casuaris casuaris johnsonii</i>	Bird	Australia	0	NA
<i>Macronectes halli</i>	Bird	Australia	0	0.33
<i>Thalassarche melanophris</i>	Bird	Australia	0	0.94
<i>Anas georgica</i>	Bird	Colombia	0	NA
<i>Egretta rufescens</i>	Bird	Colombia	0	NA
<i>Falco naumanni</i>	Bird	France	0	NA
<i>Glareola pratincola</i>	Bird	France	0	NA
<i>Oenanthe hispanica</i>	Bird	France	0	NA

Taxon	Taxonomic Group	Country	Ne 500 indicator	PM indicator
<i>Phylloscopus ibericus</i>	Bird	France	0	NA
<i>Pterocles alchata</i>	Bird	France	0	1
<i>Puffinus puffinus</i>	Bird	France	0	1
<i>Sterna dougallii</i>	Bird	France	0	1
<i>Promerops cafer</i>	Bird	South Africa	0	NA
<i>Anthus campestris</i>	Bird	Sweden	0	NA
<i>Circus pygargus</i>	Bird	Sweden	0	0.8
<i>Dendrocopos leucotos</i>	Bird	Sweden	0	0.08
<i>Emberiza calandra</i>	Bird	Sweden	0	0.67
<i>Emberiza hortulana</i>	Bird	Sweden	0	0.8
<i>Hydroprogne caspia</i>	Bird	Sweden	0	0.4
<i>Hydroprogne caspia</i>	Bird	Sweden	0	NA
<hr/>				
<i>Stiphodon semoni</i>	Fish	Australia	0	1
<i>Alosa fallax</i>	Fish	Belgium	0	1
<i>Cobitis taenia</i>	Fish	Belgium	0	0.67
<i>Lampetra fluviatilis</i>	Fish	Belgium	0	NA
<i>Misgurnus fossilis</i>	Fish	Belgium	0	NA
<i>Petromyzon marinus</i>	Fish	Belgium	0	NA
<i>Salmo salar</i>	Fish	Belgium	0	NA
<i>Salmo salar</i>	Fish	Sweden	0.19	1
<i>Siluris glanis</i>	Fish	Sweden	0	NA
<hr/>				
<i>Coenagrion hastulatum</i>	Invertebrate	Belgium	0	NA
<i>Coenagrion lunulatum</i>	Invertebrate	Belgium	0	1
<i>Ephippiger ephippiger</i>	Invertebrate	Belgium	0	1
<i>Erynnis tages</i>	Invertebrate	Belgium	0	0.2
<i>Euphydryas aurinia</i>	Invertebrate	Belgium	0	1

Taxon	Taxonomic Group	Country	Ne 500 indicator	PM indicator
<i>Hesperia comma</i>	Invertebrate	Belgium	0	0.29
<i>Leucorrhinia caudalis</i>	Invertebrate	Belgium	0	1
<i>Leucorrhinia pectoralis</i>	Invertebrate	Belgium	0	0.67
<i>Phengaris alcon</i>	Invertebrate	Belgium	0	0.54
<i>Pyrgus malvae</i>	Invertebrate	Belgium	0.17	1
<i>Satyrrium ilicis</i>	Invertebrate	Belgium	0.2	NA
<i>Somatochlora arctica</i>	Invertebrate	Belgium	0	0.5
<i>Stenobothrus stigmaticus</i>	Invertebrate	Belgium	0	0.41
<i>Leucorrhinia albifrons</i>	Invertebrate	France	0	NA
<i>Anthophora plagiata</i>	Invertebrate	Sweden	0	0.64
<i>Parnassius mnemosyne</i>	Invertebrate	Sweden	0	NA
<i>Stauroderus scalaris</i>	Invertebrate	Sweden	0.2	0.5
<i>Toxolasma lividum</i>	Invertebrate	United States	0	0.68
<i>Toxolasma lividum</i>	Invertebrate	United States	0	0.5
<hr style="border-top: 1px dashed black;"/>				
<i>Lynx lynx</i>	Mammal	Belgium	0	NA
<i>Myotis emarginatus</i>	Mammal	Belgium	0	0.27
<i>Myotis myotis</i>	Mammal	Belgium	0	0.25
<i>Nyctalus leisleri</i>	Mammal	Belgium	0	NA
<i>Capra ibex</i>	Mammal	France	0	NA
<i>Halichoerus grypus</i>	Mammal	France	0	0.5
<i>Lynx lynx carpathicus</i>	Mammal	France	0	NA
<i>Ursus arctos arctos</i>	Mammal	France	0	0.67
<i>Equus zebra zebra</i>	Mammal	South Africa	0	NA
<i>Hippotragus equinus equinus</i>	Mammal	South Africa	0	NA
<i>Hippotragus niger niger</i>	Mammal	South Africa	0	NA
<i>Nesotragus moschatus zuluensis</i>	Mammal	South Africa	0	NA

Taxon	Taxonomic Group	Country	Ne 500 indicator	PM indicator
<i>Ourebia ourebi ourebi</i>	Mammal	South Africa	0	NA
<i>Canis lupus</i>	Mammal	Sweden	0	0.6
<i>Gulo gulo</i>	Mammal	Sweden	0	0.6
<i>Phoca vitulina</i>	Mammal	Sweden	0.25	0.29
<i>Phocoena phocoena</i>	Mammal	Sweden	0	0.29
<i>Sorex isodon</i>	Mammal	Sweden	0	0.63
<i>Ursus arctos</i>	Mammal	Sweden	0	0.49
<i>Vulpes lagopus</i>	Mammal	Sweden	0	0.55

<i>Notechis scutatus</i>	Reptile	Australia	0	NA
<i>Coronella austriaca</i>	Reptile	Belgium	0.03	NA
<i>Lacerta agilis</i>	Reptile	Belgium	0	NA
<i>Natrix helvetica</i>	Reptile	Belgium	0.03	NA
<i>Vipera berus</i>	Reptile	Belgium	0.06	NA
<i>Ctenosaura acanthura</i>	Reptile	Mexico	0	1
<i>Ctenosaura pectinata</i>	Reptile	Mexico	0	1
<i>Lacerta agilis</i>	Reptile	Sweden	0	NA

<i>Carex diandra</i>	Angiosperm	Belgium	0	1
<i>Juncus capitatus</i>	Angiosperm	Belgium	0	1
<i>Luronium natans</i>	Angiosperm	Belgium	0.06	1
<i>Mentha pulegium</i>	Angiosperm	Belgium	0.03	1
<i>Orchis purpurea</i>	Angiosperm	Belgium	0.05	1
<i>Platanthera bifolia</i>	Angiosperm	Belgium	0.06	1
<i>Potamogeton coloratus</i>	Angiosperm	Belgium	0	1
<i>Schoenoplectus triqueter</i>	Angiosperm	Belgium	0	1
<i>Euterpe precatoria</i>	Angiosperm	Colombia	0	1
<i>obscured taxon species13</i>	Angiosperm	Japan	0	1

Taxon	Taxonomic Group	Country	Ne 500 indicator	PM indicator
<i>obscured taxon species21</i>	Angiosperm	Japan	0.06	1
<i>obscured taxon species29</i>	Angiosperm	Japan	0	1
<i>Salix bonplandiana</i>	Angiosperm	Mexico	0.8	NA
<i>Salix humboldtiana</i>	Angiosperm	Mexico	0.56	NA
<i>Eryngium maritimum</i>	Angiosperm	Sweden	0	NA
<i>Genista germanica</i>	Angiosperm	Sweden	0	NA
<i>Luronium natans</i>	Angiosperm	Sweden	0.25	NA
<i>Ranunculus hederaceus</i>	Angiosperm	Sweden	0	NA
<i>Ranunculus ophioglossifolius</i>	Angiosperm	Sweden	0	NA
<i>Podocarpus guatemalensis</i>	Gymnosperm	Mexico	0	NA
<i>Zamia obliqua</i>	Other	Colombia	0	0.88
Near Threatened				
<i>Procellaria cinerea</i>	Bird	Australia	0	0.33
<i>Hapalopsittaca amazonina</i>	Bird	Colombia	0	0.29
<i>Pyrilia Pyrilia</i>	Bird	Colombia	0	NA
<i>Alca torda</i>	Bird	France	0	NA
<i>Gypaetus barbatus</i>	Bird	France	0	1
<i>Tetrax tetrax tetrax</i>	Bird	France	0	NA
<i>Gypaetus barbatus</i>	Bird	South Africa	0	0.4
<i>Promerops gurneyi</i>	Bird	South Africa	0	0.38
<i>Limosa limosa</i>	Bird	Sweden	0	1
<i>Picoides borealis</i>	Bird	United States	0	1
<i>Vireo atricapilla</i>	Bird	United States	0.02	1
<i>Austroglanis gilli</i>	Fish	South Africa	0.19	NA
<i>Cucujus cinnaberinus</i>	Invertebrate	Belgium	0	1
<i>Elater ferrugineus</i>	Invertebrate	Belgium	0	NA

Taxon	Taxonomic Group	Country	Ne 500 indicator	PM indicator
<i>Lucanus cervus</i>	Invertebrate	Belgium	0.07	NA
<i>Melitta tricincta</i>	Invertebrate	Sweden	0.14	NA
<i>Phengaris arion</i>	Invertebrate	Sweden	0.13	NA
<i>Ornithorhynchus anatinus</i>	Mammal	Australia	0.6	NA
<i>Pseudomys shortridgei</i>	Mammal	Australia	0	0.89
<i>Barbastella barbastellus</i>	Mammal	Belgium	0	NA
<i>Castor fiber</i>	Mammal	Belgium	0	NA
<i>Lutra lutra</i>	Mammal	Belgium	0	NA
<i>Myotis bechsteinii</i>	Mammal	Belgium	0	0.78
<i>Myotis dasycneme</i>	Mammal	Belgium	0	1
<i>Myotis dasycneme</i>	Mammal	France	0	NA
<i>Caracal caracal</i>	Mammal	South Africa	0	NA
<i>CeratOtherium simum simum</i>	Mammal	South Africa	0	NA
<i>Barbastella barbastellus</i>	Mammal	Sweden	0.17	NA
<i>Myotis bechsteinii</i>	Mammal	Sweden	0	NA
<i>Pseudemys rubriventris</i>	Reptile	United States	0	NA
<i>Pseudemys rubriventris</i>	Reptile	United States	0	NA
<i>Eriophorum gracile</i>	Angiosperm	Belgium	0	0.5
<i>Liparis loeselii</i>	Angiosperm	Belgium	0	1
<i>Orchis morio</i>	Angiosperm	Belgium	0.2	1
<i>Potamogeton acutifolius</i>	Angiosperm	Belgium	0.08	1
<i>Baldellia ranunculoides</i>	Gymnosperm	Belgium	0.05	1
<i>Dioon edule</i>	Gymnosperm	Mexico	0	0.75
<i>Juniperus blancoi</i>	Gymnosperm	Mexico	0	1
<i>Leptogium rivulare</i>	Other	Sweden	0	1

Table S22. Taxa listed as Least Concern and Near Threatened by IUCN that have low PM indicator values (below or equal to 0.25). List was made based on the PM indicator (highlighted in bold); the Ne 500 indicator is also shown for reference.

Taxon	Taxonomic Group	Country	Ne500 indicator	PM indicator
Least Concern				
<i>Bombina variegata</i>	Amphibian	Belgium	0	0.17
<i>Genista germanica</i>	Angiosperm	Sweden	0	0.08
<i>Anthus campestris</i>	Bird	Sweden	0	0.2
<i>Charadrius alexandrinus</i>	Bird	Sweden	NA	0
<i>Coenagrion lunulatum</i>	Invertebrate	Belgium	0	0.25
<i>Gomphus vulgatissimus</i>	Invertebrate	Belgium	0.5	0.17
Near Threatened				
<i>Melitaea britomartis</i>	Invertebrate	Sweden	NA	0.2
<i>Pleurobema rubrum</i>	Invertebrate	United States	NA	0.21
<i>Pleurobema rubrum</i>	Invertebrate	United States	NA	0.23

Table S23. Comparison of Ne 500 indicator values using different Ne/Nc conversion ratios.

Taxonomic Group	Scientific name	No. Populations	Known Ne/Nc ratio	Indicator value based on Ne/Nc Ratio			
				Known	0.1	0.2	0.3
Angiosperm	<i>Lepanthes eltoensis</i>	1	0.14	0.00	0.00	1.00	1.00
Amphibian	<i>Pelophylax esculentrus</i>	1	0.08	1.00	1.00	1.00	1.00
Bird	<i>Centrocercus minimus</i>	7	0.20	0.00	0.00	0.00	0.14
Bird	<i>Falco naumanni</i>	3	0.39	0.00	0.00	0.00	0.00
Mammal	<i>Canis lupus</i>	1	0.25	0.00	0.00	0.00	0.00
Mammal	<i>Castor fiber</i>	1	0.25	1.00	1.00	1.00	1.00
Mammal	<i>Cervus elaphus elaphus</i>	1	0.23	1.00	1.00	1.00	1.00
Mammal	<i>Gulo gulo</i>	1	0.36	0.00	0.00	0.00	0.00
Mammal	<i>Lynx lynx carpathicus</i>	1	0.36	0.00	0.00	0.00	0.00
Mammal	<i>Syncerus caffer caffer</i>	3	0.26	0.33*	0.67*	0.67	0.67
Mammal	<i>Ursus arctos arctos</i>	1	0.35	0.00	0.00	0.00	0.00
Reptile	<i>Thamnophis sirtalis tetrataenia</i>	3	0.47	0.00	0.00	0.00	0.00

* Indicator values differ compared to when 0.1 ratio is used.

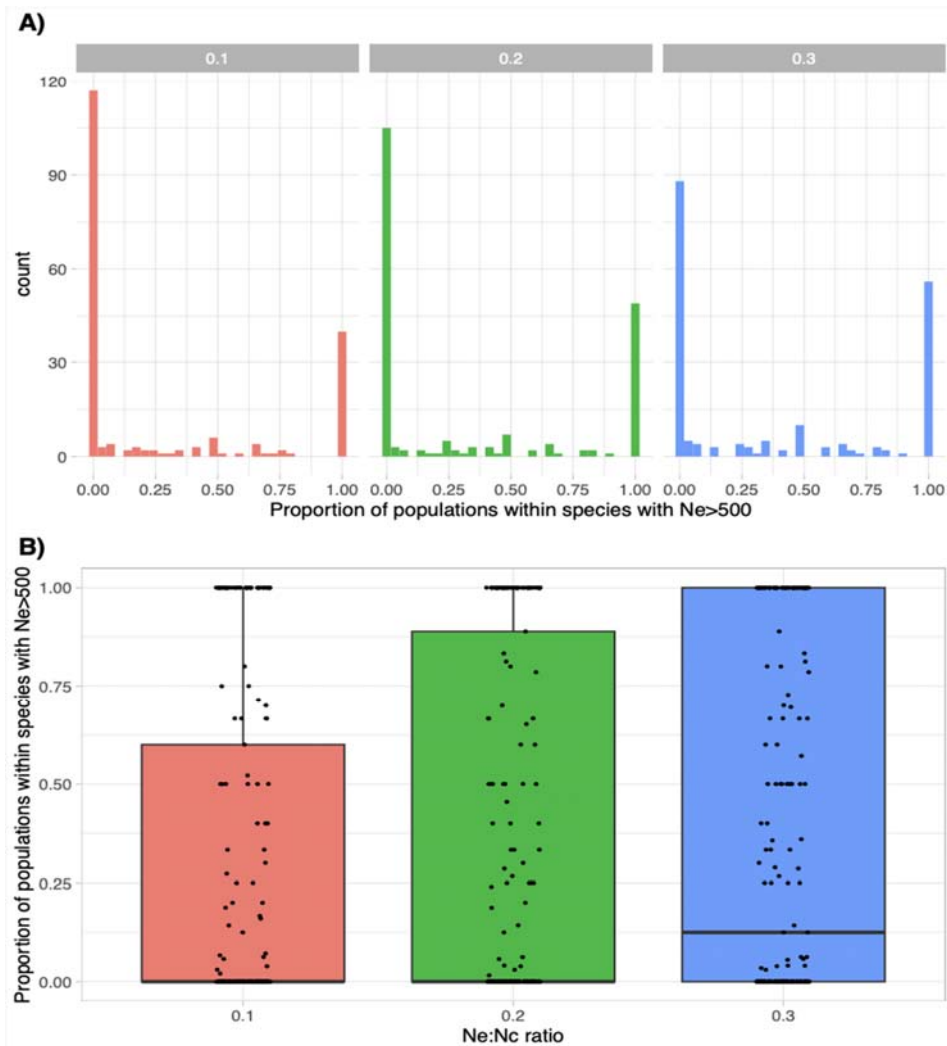


Figure S8. The distribution of values for the Ne 500 indicator with different Ne/Nc ratios applied for those assessments with either range or point estimate of Nc (n=197). The histogram and boxplot show that the indicator distribution shifts slightly to the right for ratios of 0.2 and 0.3 (the median Ne/Nc for some taxonomic groups), relative to the recommended ratio of 0.1. However, the overall shape of the distribution, with the majority of species having an indicator value of zero, and the low median value across species, does not change. The logistic mixed-effects model (glmmTMB) revealed a significant negative intercept (-0.6464, $p < 0.001$) and a positive effect for the 0.3 ratio (0.3553, $p = 0.0117$). The 0.2 showed a positive trend but was not statistically significant (0.2061, $p = 0.1545$).

S6 Quantifying national indicator values

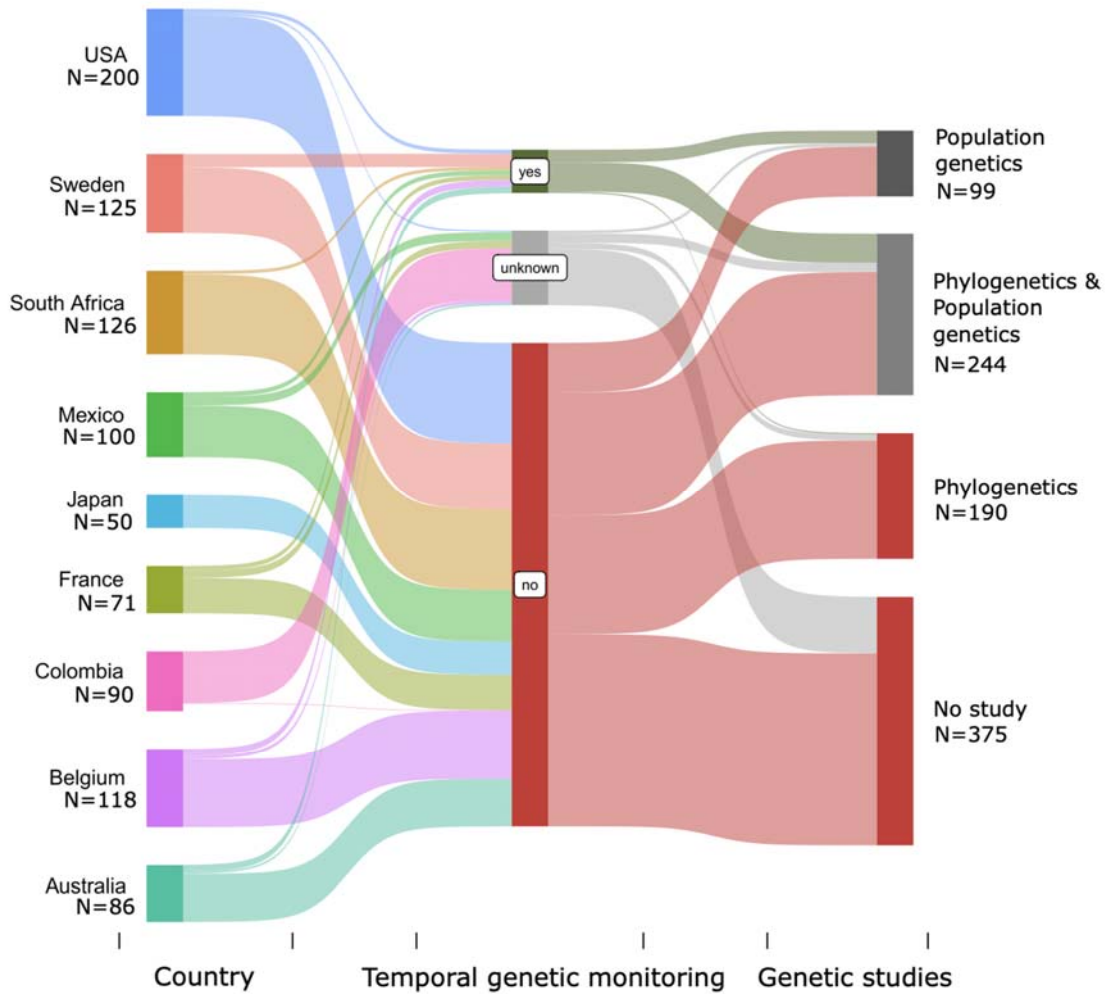


Figure S9. Data availability for the genetic monitoring indicator and genetic studies within countries. Each country is assigned a unique colour (left) and every species or subspecies (i.e., taxa) assessed is represented by a single (thin) line. The center shows whether temporal genetic monitoring is being performed in the species, each line (taxa) can be followed to the left to show its assessment country, and to the right to indicate if besides genetic monitoring, the taxon has genetic studies at the population (pop), phylogenetic (phylo) or both (phylo_pop) levels.