Supplementary Materials for

Parasite biodiversity faces extinction and redistribution in a changing climate

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Other Supplementary Material for this manuscript includes the following:
(available at advances.sciencemag.org/cgi/content/full/3/9/e1602422/DC1)

- table S11. Source data (Excel).
- table S12. Source data (Excel).
- table S13. Source data (Excel).

text S1. Primary, secondary, and compounded extinction rates.

Dobson *et al.* (*24*) provide the following values for mean host specificity (top) and parasite species richness (bottom):

table S1. Host specificity and parasite species richness.

	Chondrichthyes	Osteichthyes	Amphibia	Reptilia	Aves	Mammalia
Trematoda	2	6.35	5.4	1.77	2.97	2.01
	(51)	(5,831)	(1,170)	(3,773)	(9,862)	(3,714)
Cestoda	1.69	6.38	4.75	2.21	2.36	1.89
	(1,352)	(4,466)	(283)	(1,112)	(14,058)	(4,637)
Acanthocephala	—	14.95	6.74	12.5	8.35	4.32
		(1,226)	(140)	(212)	(779)	(301)
Nematoda	2.67	10.28	5.27	2.12	3.28	6.07
	(152)	(2,631)	(2,662)	(6,389)	(9,150)	(2,979)

Using a formula for coextinction rates, some simple math allows an updated estimation from different levels of host extinction risk, based on other estimates than IUCN data. Koh *et al.*'s (*101*) method for affiliate extinction probability from host risk E and specificity s estimates

$$\bar{A} = (0.35E - 0.43)E \ln s + E$$

Plugging in a 15-37% extinction risk for hosts (an extreme scenario) and the values for host specificity give a best case scenario:

table S2. Thomas best-case scenario coextinction rates.

	Chondrichthyes	Osteichthyes	Amphibia	Reptilia	Aves	Mammalia
Trematoda	11.08%	4.53%	5.45%	11.77%	8.84%	11.05%
Cestoda	12.03%	4.51%	6.18%	10.51%	10.14%	11.40%
Acanthocephala	—	0%	4.20%	0.70%	2.98%	6.71%
Nematoda	9.44%	1.81%	5.59%	10.75%	8.27%	4.79%

And a worst case scenario:

table S3. Thomas worst-case scenario coextinction rates.

	Chondrichthyes	Osteichthyes	Amphibia	Reptilia	Aves	Mammalia
Trematoda	29.29%	16.45%	18.25%	30.65%	24.90%	29.24%
Cestoda	31.17%	16.40%	19.68%	28.18%	27.45%	29.92%
Acanthocephala	—	6.93%	15.79%	8.92%	13.40%	20.73%
Nematoda	26.08%	11.09%	18.52%	28.65%	23.79%	16.95%

Weighting these each by the relative richness of different host groups gives the following final assessment:

table S4. Thomas total coextinction rates.

Clade	Richness	CI based on Thomas *et al.*
Trematoda	24,401	8.4% to 24.1%
Cestoda	25,908	9.5% to 26.1%
Acanthocephala	2,658	1.9% to 11.0%
Nematoda	23,963	7.5% to 22.3%

And a total: 76,930 species of helminths with a weighed estimate of 8.3% to 23.8% extinction rate. If specialist parasites are disproportionally hosted by low-risk species, this may explain some of the reason parasite extinction is less prevalent than predicted (*25*). But a more parsimonious explanation is that the low projected rate comes from the use of incomplete IUCN red list data that underestimates host vulnerability.

We focus in the above analysis on providing a less conservative estimate of how extinction rates might compound with host vulnerability, and maintaining a consistent estimate based on the Thomas *et al.* SAR for both hosts and parasites. However, we could just as easily implement the same analysis using the conservative meta-analysis based figure Urban recently published (*7*). Estimates based on the SAR suggest a 22% extinction rate and estimates based on expert opinion are similarly high. But Urban suggests an overall extinction baseline across plants and animals of approximately 7.9%. Using that metric, we can once again calculate by-group estimates, but we can refine it even further by using Urban's by-group estimates for amphibians (12.9%), reptiles (9.0%), mammals (8.6%), fish (7.6%, using the same value for chondrichthyes and osteichthyes) and birds (6.3%). We can even use the 95% credible interval, once again, to generate a best-case scenario table:

table S5. Urban best-case scenario coextinction rates.

	Chondrichthyes	Osteichthyes	Amphibia	Reptilia	Aves	Mammalia
Trematoda	2.41%	0.77%	2.61%	4.21%	2.47%	4.21%
Cestoda	2.65%	0.77%	3.03%	3.71%	2.90%	4.36%
Acanthocephala		0%	1.89%	0%	0.54%	2.37%
Nematoda	2.00%	0.09%	2.69%	3.80%	2.29%	1.54%

And, a worst-case scenario:

table S6. Urban worst-case scenario coextinction rates.

	Chondrichthyes	Osteichthyes	Amphibia	Reptilia	Aves	Mammalia
Trematoda	11.93%	4.98%	7.76%	10.71%	5.16%	9.59%
Cestoda	12.94%	4.95%	8.67%	9.55%	5.99%	9.90%
Acanthocephala		0%	6.17%	0.48%	1.41%	5.74%
Nematoda	10.19%	2.08%	7.93%	9.77%	4.80%	4.02%

And, aggregated by group:

table S7. Urban total coextinction rates.

Clade	Richness	CI based on Urban
Trematoda	24,401	2.61% to 6.79%
Cestoda	25,908	2.82% to 7.05%
Acanthocephala	2,658	0.31% to 1.35%
Nematoda	23,963	2.40% to 6.11%

These numbers may represent a more literature-based estimation of helminth co-extinction rates, but we present the Thomas *et al.* based numbers in the main text to maintain consistency of methods across hosts and parasites, and to present a true worst-case scenario for how severe the threats parasites face might become.

To determine how these different projections affect total extinction rate projections, we implement a combinatorics formula that assumes (with no prior knowledge) zero covariance between host and parasite extinction from climate change (or, more accurately, no covariance between primary and secondary extinctions)

$$P(extinction) = 100\% - \left(100\% - p_{direct\ extinction\ from\ climate\ change}\right) * \left(100\% - p_{coextinction}\right)$$

Giving us the estimates presented in the main text with dispersal:

table S8. Cumulative extinctions with dispersal.

	Primary Extinction	Secondary (Urban)	1° + 2° (Urban)	Secondary (Thomas)	1° + 2° (Thomas)
Trematoda	0.11% to 1.2%	2.61% to 6.79%	**2.72% to 7.91%**	8.4% to 24.1%	**8.50% to 25.0%**
Cestoda	0.07% to 0.07%	2.82% to 7.05%	**2.89% to 7.12%**	9.5% to 26.1%	**9.56% to 26.15%**
Acanthocephala	0.21% to 0.60%	0.31% to 1.35%	**0.52% to 1.94%**	1.9% to 11.0%	**2.11% to 11.53%**
Nematoda	1.3% to 3.3%	2.40% to 6.11%	**3.67% to 9.21%**	7.5% to 22.3%	**8.70% to 24.86%**

And without dispersal:

table S9. Cumulative extinctions with dispersal.

	Primary Extinction	Secondary (Urban)	1° + 2° (Urban)	Secondary (Thomas)	1° + 2° (Thomas)
Trematoda	3.8% to 6.0%	2.61% to 6.79%	**6.31% to 12.38%**	8.4% to 24.1%	**11.88% to 28.65%**
Cestoda	3.6% to 4.0%	2.82% to 7.05%	**6.32% to 10.77%**	9.5% to 26.1%	**12.76% to 29.06%**
Acanthocephala	3.8% to 4.9%	0.31% to 1.35%	**4.10% to 6.18%**	1.9% to 11.0%	**5.63% to 15.36%**
Nematoda	5.4% to 9.3%	2.40% to 6.11%	**7.67% to 14.84%**	7.5% to 22.3%	**12.50% to 29.53%**

We note one particular difference of interest to researchers – by incorporating the covariance between different host group extinction rates and their specificity, the gap between acanthocephalans and other more threatened helminths emerges very clearly.

Future work relating coextinction to parasite primary extinction rates will require an approach that links host and parasite distributions and accounts for the missing covariance. While a few odd winners in any group will have the pre-existing niche breadth to benefit from climate change, theory predicts that the majority of species should suffer at least partial range loss – both hosts and parasites included – and at its most extreme this means that vulnerability should compound across parasites and obligate hosts. In our study, fragmented host information and the heavy bias towards agricultural and human-infectious species makes such an approach

impractical or uninformative; however, we outline a targeted approach for subsequent studies that focus on smaller specialist clades. Key to that approach is simulating the simultaneous shift of hosts and parasites and searching for potential discrepancies between their ranges, an approach notably used by Pickles *et al.* (*32*). Host information is readily available for mammals and many reptiles and amphibians from the IUCN (*102*), and for birds by BirdLife International range maps (*103*). Projecting the joint shift of hosts and parasites can be used to calculate a host-constrained projection of parasite future ranges, which accounts for potential independence in shifting habitat suitability.

This approach also allows another, more conceptual approach to exploring parasite vulnerability; in this approach, the Thomas *et al.* method can be implemented for hosts alone (following an identical procedure for projecting range shifts) and converted into parasite vulnerability using Koh *et al.* (2004)'s method for affiliate extinction probability from host risk E and specificity s (which can be calculated from host-parasite association network data). This host-as-proxy regional estimation can then be compared against a reimplementation of the Thomas *et al.* method using parasite areal changes (with or without host ranges as constraints, corresponding to total and intrinsic vulnerability to extinction). We term the relative fraction of vulnerability driven by hosts (the Koh-converted extinction risk divided by the constrained parasite-based extinction risk) the *compounded risk factor* and suggest that future analyses using our global parasite database could explore how much greater than 1.0 those values are for parasites with different levels of specificity in different ecosystems. For highly specialized species with a single host, the extinction rates should have a rough 1:1 correspondence; however, generalist and parasitic species with several free-living stages should be more severely affected by their intrinsic vulnerability to extinction and have a smaller proportional compounded risk factor.

text S2. Canonical and MaxEnt approaches to the SAR.

In the canonical Arrhenius species area relationship (SAR)

$$S = cA^z$$

a slope z of 0.25 provides a convenient solution to extinction rate estimation in the Thomas *et al.* method. Despite the substantial criticism the method has faced, especially in a seminal series of papers by Harte and Kitzes (*41*, *94*, *104*), the canonical SAR is still valid under a very specific set of circumstances. Harte and Kitzes suggest that for an island SAR in particular, the slope can be predicted as 0.25 if "(i) total abundance in the new area A is proportional to area, (ii), individuals found in A are chosen by a random draw of all individuals in A_0, and (iii) the number of individuals of each species in A_0 follows a canonical lognormal abundance distribution" (*104*). Moreover, they draw a parallel to predicting extinction from climate change, recommending the nested SAR is more applicable to loss of native range (shrinking suitable habitat of an entire region) while the island SAR may be more applicable to ranges shifting into novel habitat.

There is, in the Harte & Kitzes method (the Maximum Entropy Theory of Ecology, or METE), a method for deriving a nested SAR that accurately predicts its curvature towards $z = 0$ at continental scales. They define a probability of survival P (compared to the original probability of survival P_0) that, in the original canonical SAR, is

$$P = P_0 \left(\frac{A}{A_0}\right)^z$$

The METE formulation of P accounts for initial abundance n_0 and suggests species face certain extinction when the ratio of abundance n and n_0 drops below a threshold r_c (i.e., the pseudo-extinction threshold or minimum viable population). For a single species

$$P\left(\frac{n}{n_0} \le r_c\right) = 1 - \frac{\left[\frac{n_0\beta}{1 + n_0\beta}\right]^{r_c n_0} - \left[\frac{n_0\beta}{1 + n_0\beta}\right]^{n_0}}{(1 + n_0\beta)\ln(1 + \frac{1}{n_0\beta})}$$

where they substitute β for A/A_0. This approach allows direct calculation of an extinction area relationship by evaluating each species' fate (or, by making top-level assumptions about abundance distributions in the community) (*41*). We observe that analyses with uncertainty about abundance distributions and viable population sizes could easily be implemented in a Bayesian framework, with basic priors assumed for the demographic free parameters.

To do that, or to use the METE approach in general, requires assumptions about the population trajectory and aggregation of parasites, the distribution of their abundances within a community (log-normal or not), and the critical population size below which extinction is certain. For endoparasite helminths, critical population sizes might be easily solved through conventional epidemiological methods (*105*). The host density threshold is a frequently used metric in epidemiology, and basic assumptions about parasite aggregation within a single infected individual might make relating the HDT to r_c readily possible. But the data to inform such assumptions is absent at broad scales in parasite ecology; only a couple or a few species in our study have such data.

In summary, implementing the SAR to predict extinction for parasites is unprecedented, and so poses a number of problems. The applicability of the SAR with a slope of 0.25 or higher to parasites is assumed (given its applicability to their hosts), and is supported for use in our study by the limited literature applying SARs to parasites (*105*). We make the explicit choice to adhere to the Thomas *et al.* implementation of the SAR approach with $z = 0.25$ to avoid further entangling our estimates in unsubstantiated assumptions about parasite demography, or about how parasite aggregation among hosts (which can follow a negative binomial distribution, and in the context of climate change, will be non-independent from host area and abundance declines) would affect the validity of the METE. The derivation and empirical validity of the METE has already been the subject of one book and numerous articles, and exploring its applicability to parasites could require similar multi-year efforts, using data that is by-and-large missing from

current parasitology databases. Harte and Kitzes suggest three major tasks to refine their methods:

>*"1. Develop better projection methods for the number of species shared among sets of disjointed habitat patches.*
>
>*2. Enrich understanding of the shapes and slopes of SARs at large spatial scales.*
>
>*3. Enrich understanding of secondary species losses due to trophic web-induced and other interaction-induced cascades."* (*104*)

and we concur that these are critical tasks before the SAR and extinction area relationship for parasites can be better refined beyond the Thomas *et al.* methodology.

text S3. A more restrictive analysis based on 50+ point-per-species models.

Sample size is an important limiting factor in all ecological niche modeling (ENM), and detailed attention to the role sample size plays in model accuracy is a key part of due diligence for researchers building and applying ENMs. In our analyses in the main text, we present results for species that have a minimum of 20 unique occurrences. However, in other work, 50 or more occurrences is a more stringent threshold that some might use. Here, we present the key analyses from our main text, re-analyzed for the subset of species with 50 unique occurrences. That reduces the sample size from 457 species down to 196; at the clade scale, the effects of that reduction are most apparent.

In the restrictive analysis (versus the 20 point analysis in the main text), climate scenarios have essentially the same effect on habitat loss, with an average native range loss of 21.4% (vs. 20.2%) in the optimistic RCP 2.6 scenario, and of 41.2% (vs. 37.4%) in the pessimistic RCP 8.5 scenario. Across scenarios, species lose an average of 31.5% (vs. 29%) of total habitat without dispersal. Of 196 species, 36 lost more than 50% of their range, and one lost more than 80% of its range. Even allowing for dispersal, 106 of 196 (versus 202 of 457) species lost range by 2070, and 14 species lost more than half of their global suitable range; despite those losses, species gained an average of 0.3% suitable habitat (vs. 16.2%; the only noticeable difference from the main analysis); four species doubled the extent of their range, and none tripled. Strictly-wildlife parasites experienced an average of 10% more range gain (vs. 17%) than zoonoses. That effect still originates in endoparasite vs. ectoparasite differences, with endoparasites gaining 31% (vs. 36%) more range than ectoparasites with dispersal (p < 0.001), and losing 12% less native range (vs. 10%; p < 0001). Clade differences are still significant (one-way ANOVA: F = 8.287, p < 0.001 vs. F = 15.441, p < 0.001).

Recreating Table 1 for this analysis yields roughly comparable results (next page). The most significant difference between these analyses comes for mites and lice, which experience substantially less gain, and for which the sign of average habitat loss is flipped from positive to negative (and the upper bounds of potential habitat gain are substantially reduced). This is likely due to the reduction of sample size to 2 species each for both clades, on which grounds, we note

table S10. 50+ points subanalysis-based habitat loss rates.

CLADE	N_{SPECIES}	HABITAT LOSS (MEAN)	HABITAT LOSS RANGE (5TH-95TH PERCENTILE)	% COMMITTED TO EXTINCTION
0% DISPERSAL				
ACANTHOCEPHALA	5	**-19.8%**	(-52.3%, 0.0%)	5.2% / 5.4% / 6.2%
ASTIGMATA (*)	2	**-37.0%**	(-44.1%, -0.3%)	9.2% / 10.9% / 11.0%
CESTODA	8	**-20.4%**	(-29.6%, -10.3%,)	6.1% / 5.6% / 5.7%
IXODIDA	98	**-34.5%**	(-55.3%, -2.6%)	8.5% / 10.0% / 10.7%
NEMATODA	37	**-24.2%**	(-55.5%, -5.1%)	5.5% / 6.7% / 7.3%
PHTHIRAPTERA (*)	2	**-57.9%**	(-62.1%, -53.7%)	19.9% / 19.4% / 19.5%
SIPHONAPTERA	30	**-37.1%**	(-51.7%, -16.7%)	9.4% / 10.9% / 11.3%
TREMATODA	14	**-23.8%**	(-63.4%, -2.2%)	6.0% / 6.8% / 8.8%
100% DISPERSAL				
ACANTHOCEPHALA	5	**+38.2%**	(-17.0%, +78.2%)	0.7% / 1.5% / 1.7%
ASTIGMATA (*)	2	**-32.3%**	(-43.1%, -21.5%)	6.8% / 9.3% / 9.6%
CESTODA	8	**+30.6%**	(-2.0%, +70.8%)	0.2% / 0.2% / 0.2%
IXODIDA	98	**-12.6%**	(-53.3%, +47.6%)	4.9% / 6.0% / 6.6%
NEMATODA	37	**+13.6%**	(-37.1%, +47.0%)	0.7% / 1.5% / 1.8%
PHTHIRAPTERA (*)	2	**-0.53%**	(-60.1%, -45.9%)	17.9% / 17.2% / 17.4%
SIPHONAPTERA	30	**-0.03%**	(-41.2%, +43.1%)	1.6% / 3.5% / 3.8%
TREMATODA	14	**+43.3%**	(-24.9%, +138.4%)	0.2% / 1.2% / 1.7%

that the results marked with an asterisk should likely be entirely disregarded (especially as the extinction estimators are unlikely to be at all meaningful). More generally, restricting sample size even further produces a minor increase in habitat loss, and therefore extinction rates; overall, the patterns of extinction risk are comparable, with 7.2-9.8% of species committed to extinction without dispersal (vs. 5.7%-9.2%), and 2.3%-4.6% with dispersal (vs. 1.7%-4.0%). For our "IUCN classification" analysis, with dispersal, none would be critically endangered (vs. 0.7%), 7.1% (vs. 6.3%) of species would be endangered, 26.5% (vs. 18.8%) vulnerable, and 66.3% (vs. 74%) least concern; without dispersal, 0.5% (vs. 1.8%) would be critically endangered, 17.8% (vs. 17.1%) endangered, 42.8% (vs. 49.5%) vulnerable, and 38.8% (vs. 31.7%) least concern, continuing to reflect an overall subtle increase in risk associated with the restricted sample size.

For poorer-sampled clades (Astigmata and Phthiraptera, and to a lesser extent, Acanthocephala and Cestoda), reducing the sample size is likely to have substantially reduced the validity of the analyses we present in the main text. More generally, it may be the case that models with more occurrence data better capture the equilibrium realized niche of the species, and therefore find less "novel habitat" for species to expand into. Alternatively, it may be that other subtle biases in data collection (such as spatial autocorrelation between sample sites) have produced more detailed data for species with overall more restricted niches or ranges. Speculation as to the mechanisms of the pattern is likely to be unsuccessful given the combination of data sources assembled in the study, each contributing their own intrinsic pattern of sampling bias. However, the more restricted analysis only further confirms that every group in our study is likely to have a handful of species experiencing devastating range loss, leading to significant extinction risk.

As a final precaution, we compared accuracy metrics for models under and above 50 points, to examine whether models might be failing using the 20-or-more criterion. A very small effect is detectable in the AUC (mean under 50: 0.945; mean over 50; 0.948; $t = -3.235$, $df = 8221.5$, $p = 0.00122$, 95% CI = (-0.0051,-0.0013)), but AUC is also a comparatively unreliable metric of model performance, and the overall effect is minimal as both groups appear to perform extremely well on average. (Moreover, the lowest AUC recorded in the entire study is 0.728, which is still within the range of well-performing, published models, and certainly gives no indication of objective model failure.) An opposite effect is detectable for the true skill statistic (means 0.815 vs. 0.797; $t = 6.6715$; $df = 08053.5$; $p < 0.0001$; 95% CI = (0.0127, 0.0232)), for which models under 50 points appear to perform slightly better, but again, with minimal effect. Based on both of these simple tests, we find no strong evidence to suggest models with between 20 and 50 points perform noticeably poorly and might introduce non-trivial error into our main results (again, noting that 20 or more points is a common threshold in the literature; see also van Proosdij *et al.* [2016] *Ecography* 39:542-552).

Given that extinction estimates for at least two clades (Astigmata and Phthiraptera) would become invalid with a more restricted analysis, and others would likely have been noticeably weakened, we elected to present results drawn from all 457 species in the main text. Our study highlights the challenges of data availability in parasitology research; the fact that two clades'

extinction rates would be essentially unmeasurable with a more restrictive sample size rule only highlights those challenges. However, we note that researchers interested in using the results of the more restricted analysis can find them here, and can also obtain individual sample sizes and accuracy metrics for every species and model in the supplemental datasets.
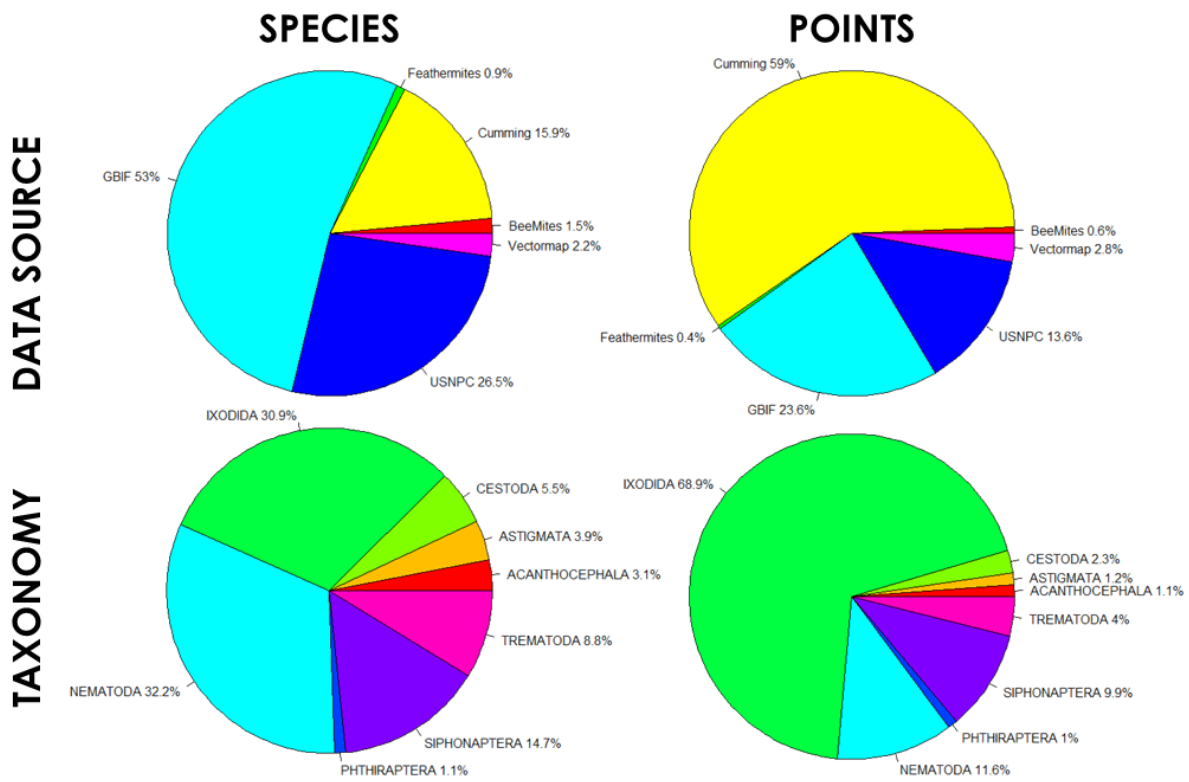
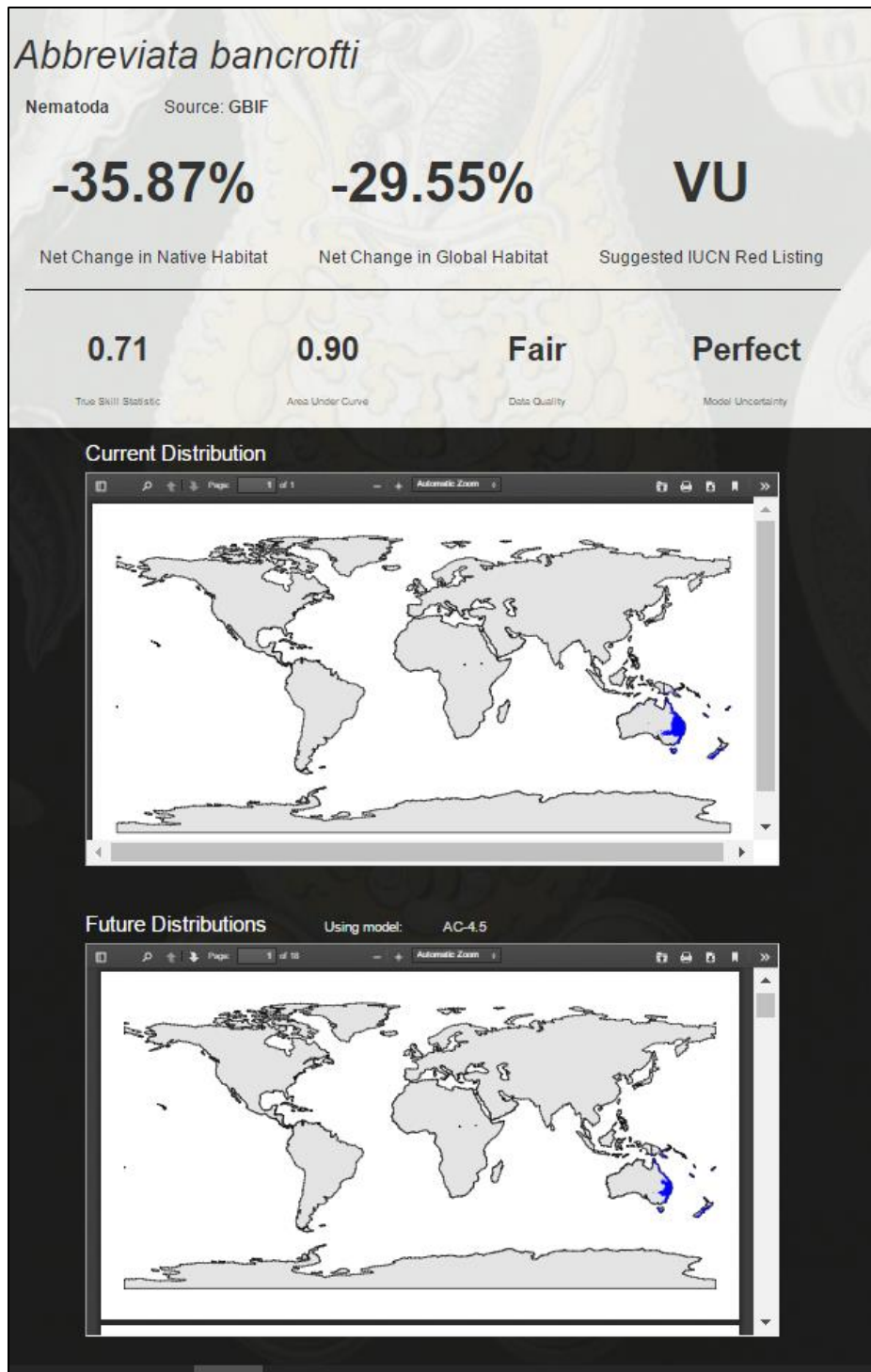**fig. S1. Final data set breakdown by source and clade.** Values are taken from the final 457 species dataset available in table S2.

fig. S2. Example presentation of species distribution and conservation status on PEARL.
Real results are shown for *Abbreviata bancrofti* (Nematoda), a representative species in our study and the first available on the website alphabetically.
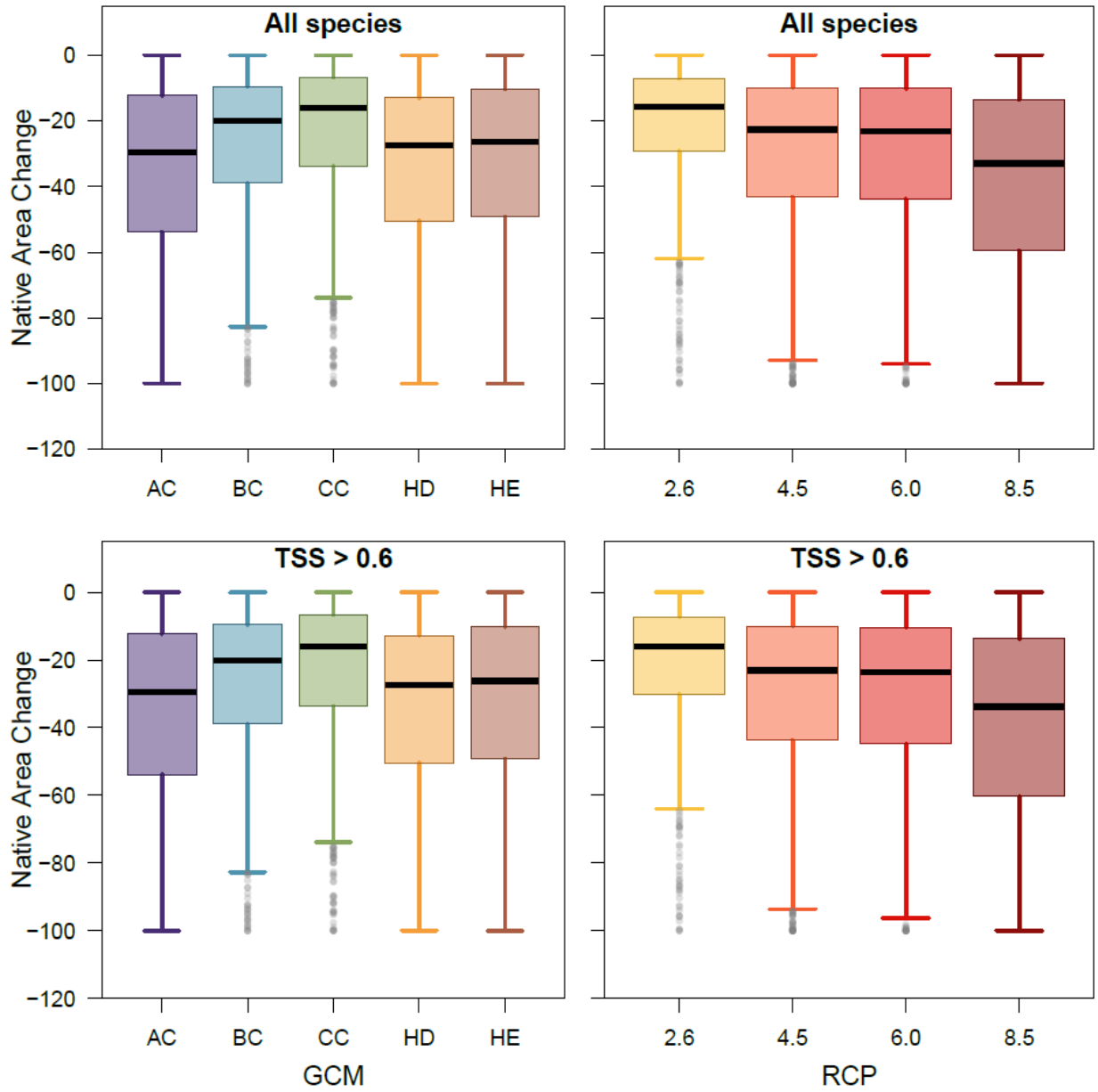
fig. S3. Loss of native habitat broken down by RCP and GCM. Results are broken down into all models and the subset of models that "perform well" (with a true skill statistic over 0.6).
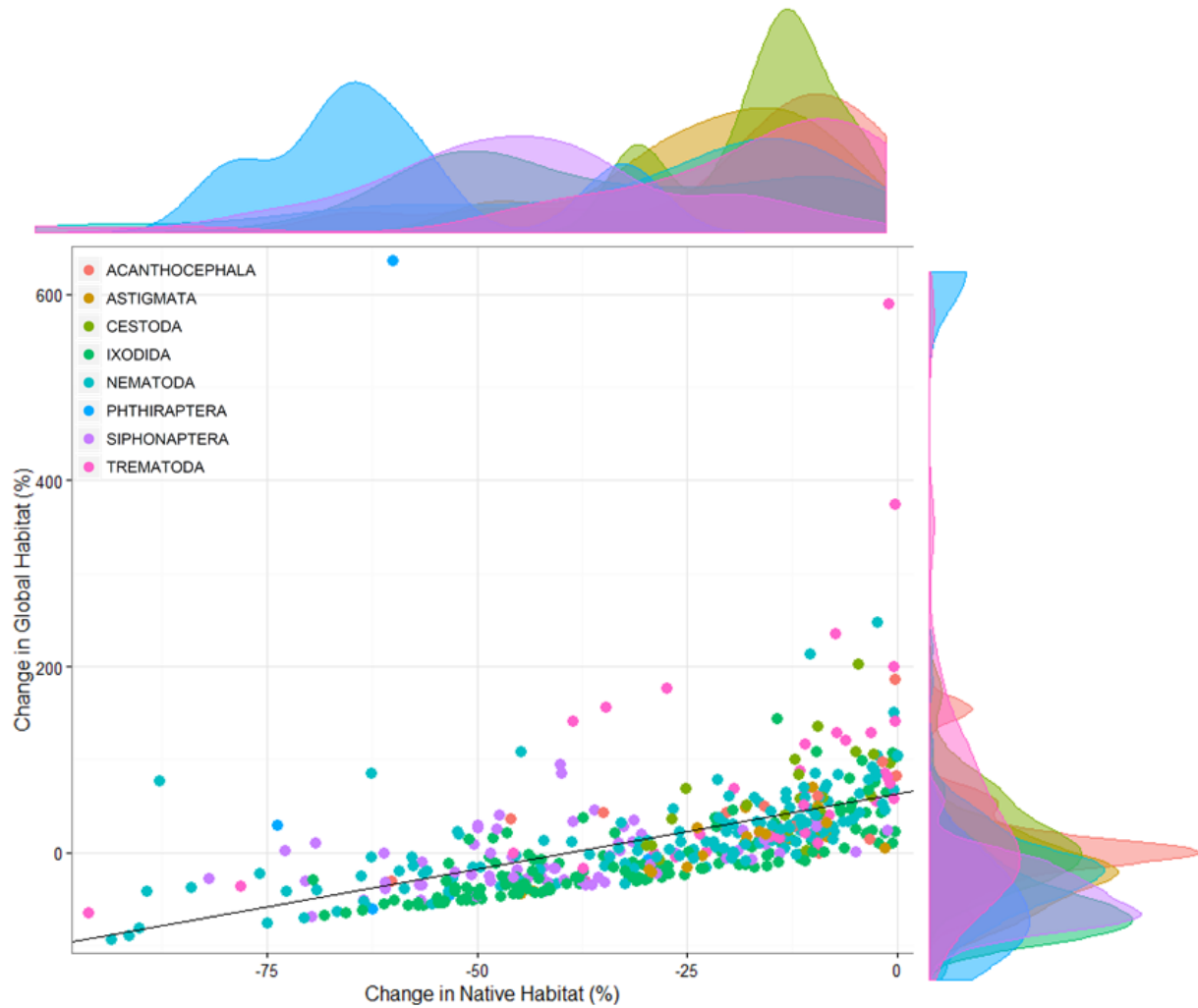
fig. S4. Trade-offs between biodiversity loss and emergence across parasite clades.
Discrepancies between current and future range size are projected as averages across all GCMs
and RCPs at the species level, with (y-axis) and without (x-axis) dispersal, and broken down by
our eight clades. Most clades are likely to be subject to moderate-to-extreme range loss; but the
species with projected extreme expansions are mostly helminth endoparasites (in particular,
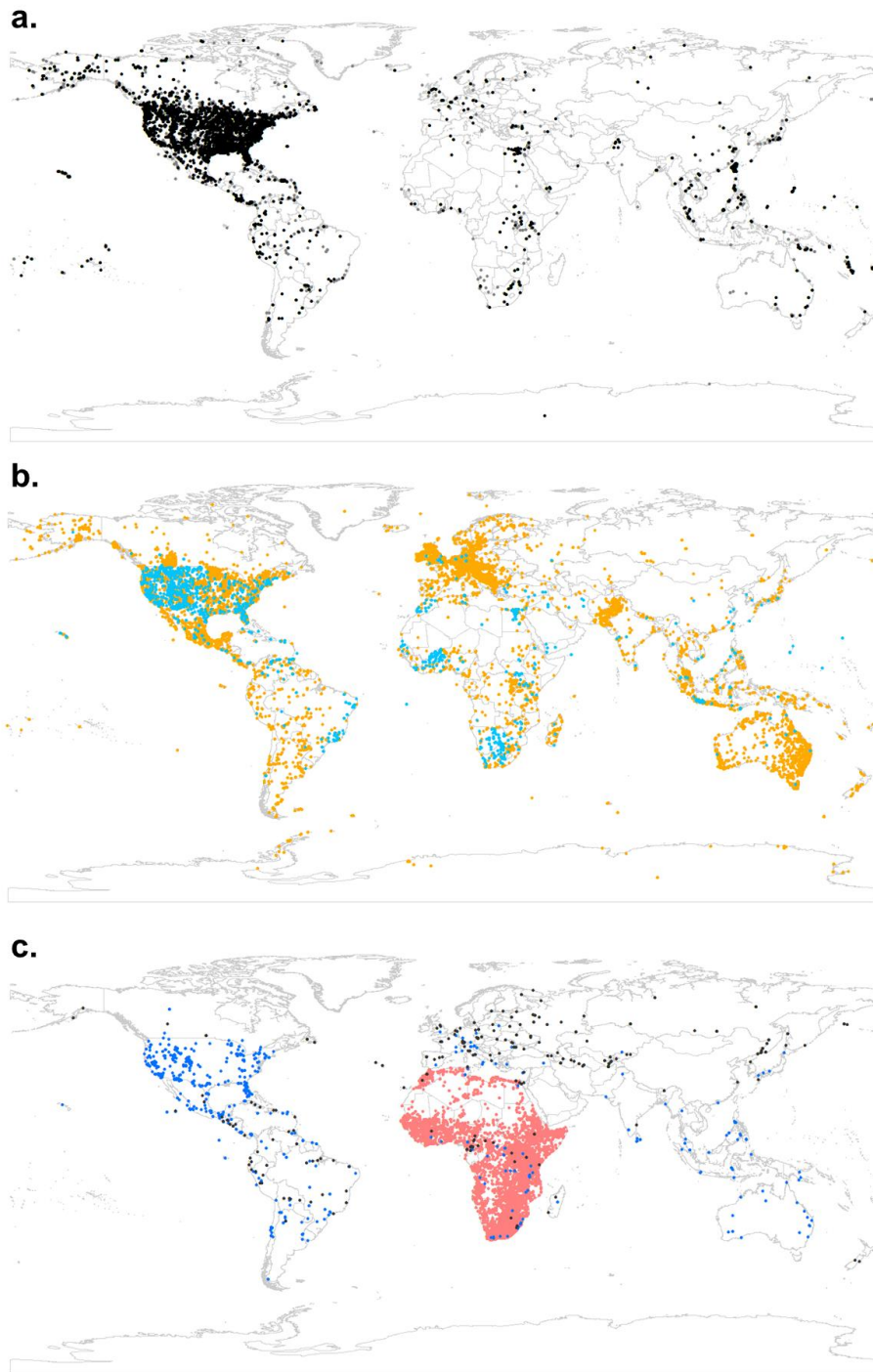nematodes and trematodes).

fig. S5. Sources and distribution of occurrence data. (**a**). Data from the US National Parasite Collection (grey: not included in final dataset; black: included in the study based on minimum sample size, taxonomic cleaning, etc.). (**b**). Data from VectorMap (blue) and the Global Biodiversity Informatics Facility (orange). (**c**). Data from the Bee Mites database (blue), the Cumming tick database (red), and georeferenced data of the feather mite database (black).
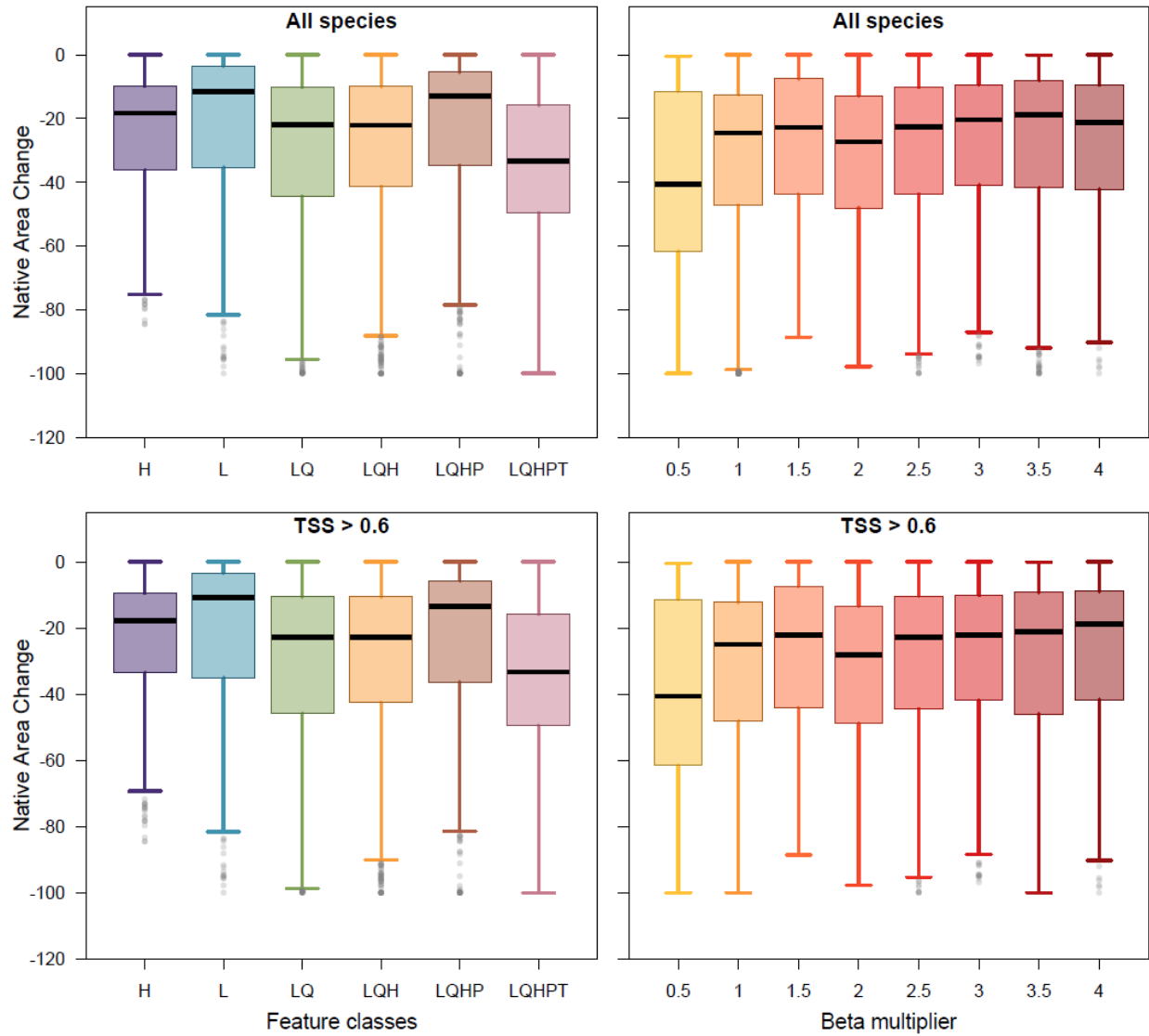
fig. S6. Loss of native habitat broken down by feature classes and regularization multiplier. Results are broken down into all models and the subset of models that "perform well" (with a true skill statistic over 0.6). Models are built from a combination of five feature classes: linear (L), quadratic (Q), hinge (H), product (P), and threshold (T).
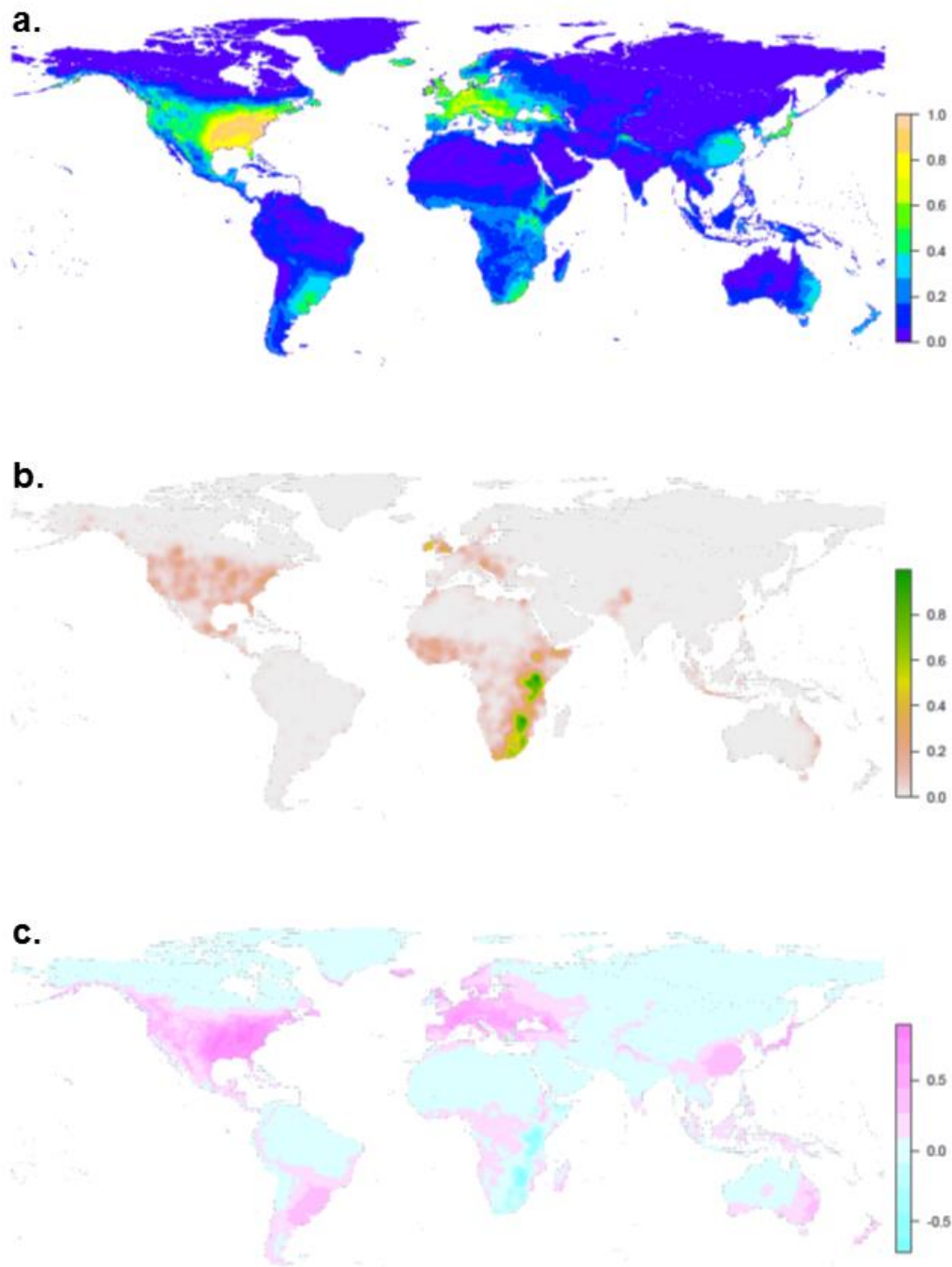
fig. S7. Visualizing spatial bias in species richness gradients. (**a** to **c**), From the distribution of points included in our global parasite database, we constructed a global compiled map of species richness (a) calculated by layering every species distribution model. But with biased sampling that map may reflect false patterns; so we also present the density of points smoothed with a Gaussian filter with σ = 1 (b), and subtract the latter from the former to show richness *relative to sampling intensity* (c).

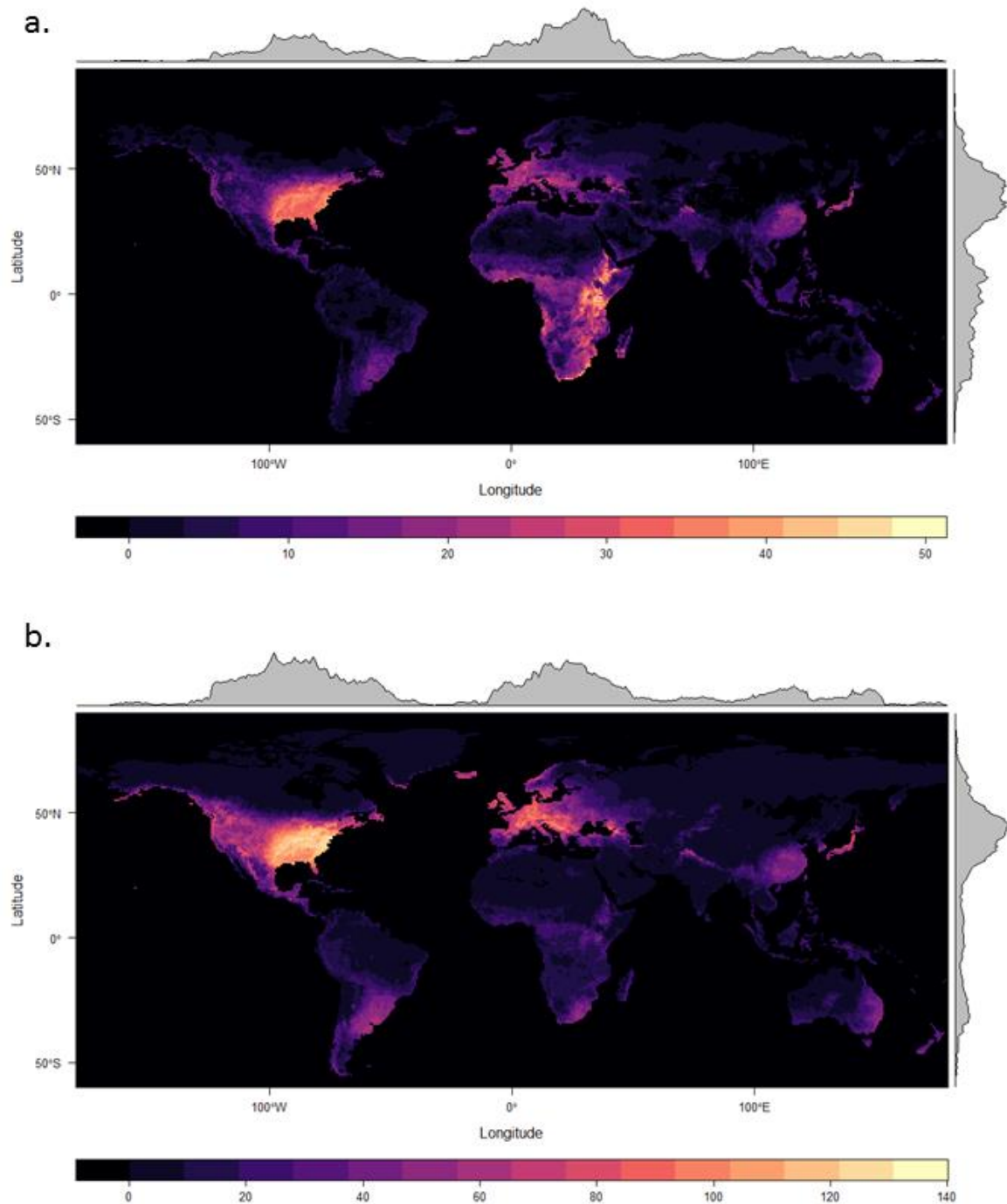**fig. S8. Parasite richness gradients by human health concern.** (**a**), Species richness gradients for species in our study with human health relevance (zoonotic endoparasites and ectoparasites with records of feeding on humans) compared to (**b**), richness gradients for strictly-wildlife or free-living species.