

Table S1. Summary of models predicting IUCN threat status in 16 orders of mammal. The IUCN category (an ordinal variable from 1 to 5) was the dependent variable. The predictors were log range size ('logRS'), log body mass ('logMass'), human encroachment and impacts ('Encroach' and 'HII', see text for definitions), and the interaction between log range size and log mass ('RS * Mass'). In the table coefficient values and their significance (* $p < 0.05$, ** $p < 0.05$, *** $p < 0.001$) are given. Maximum likelihood values of ϕ (measuring spatial effects), λ' (measuring phylogenetic dependence) and γ (variation independent of space and phylogeny) are also reported. R^2 values refer to models for the 5-level ordinal threat score. AUC is a threshold independent measure of the models' ability to predict species binary threat status (see methods). Sens/Spec gives the value of both sensitivity and specificity as it applies to the predicted threat probability threshold used to categorize species as threatened or non-threatened (the threshold was set as the value where sensitivity = specificity). For order species richness see Fig 2.

Order	Models for IUCN threat status					Spatial & phylogenetic			Model fit & predictions		
	logRS	logMass	Encroach	HII	RS * Mass	λ'	ϕ	γ	R ²	AUC	Sens/Spec
DIDELPHIMORPHIA	-0.75 ^{***}	0.14	1.10	-0.04	0.77 ^{***}	0.00	0.00	1.00	0.60	0.98	0.96
PERAMELEMORPHIA	-1.11 ^{***}	1.32 [*]	0.58	-0.20	1.30	0.00	0.00	1.00	0.81	0.92	0.82
DASYUROMORPHIA	-0.92 ^{***}	0.66 ^{***}	-1.05	0.01	0.13	0.10	0.62	0.28	0.50	0.84	0.78
DIPROTODONTIA	-1.08 ^{***}	0.22	1.91	0.02	0.17	0.00	0.00	1.00	0.46	0.87	0.77
CINGULATA	-1.16 [*]	0.98	0.88	-0.01	1.64	0.00	0.00	1.00	0.53	0.52	0.50
AFROSORICIDA	-1.30 ^{***}	0.91 ^{***}	1.26	0.07	-0.50	0.00	0.00	1.00	0.64	0.91	0.80
MACROSCELIDEA	-0.69 ^{**}	1.25 ^{***}	3.62	-0.07	-0.98 ^{***}	0.99	0.00	0.01	0.96	1.00	1.00
EULIPOTYPHLA	-0.99 ^{***}	0.31 ^{***}	0.57	0.02	-0.08	0.02	0.91	0.07	0.52	0.97	0.91
CHIROPTERA	-0.77 ^{***}	0.19 ^{**}	-1.14 [*]	0.05	-0.01	0.08	0.69	0.23	0.45	0.94	0.87
PERISSODACTYLA	-0.60	0.23	-0.60	0.08	2.57	0.00	0.00	1.00	0.24	-	0.32
CARNIVORA	-0.86 ^{***}	0.57 ^{***}	1.42	-0.04 ^{***}	-0.29 ^{**}	0.26	0.01	0.73	0.44	0.88	0.80
CETARTIODACTYLA	-0.96 ^{***}	0.34 [*]	1.69 [*]	-0.09 ^{***}	-0.16	0.08	0.81	0.11	0.40	0.86	0.78
PRIMATES	-1.08 ^{***}	0.95 ^{***}	0.74	0.02	-0.08	0.66	0.00	0.34	0.44	0.91	0.84
SCANDENTIA	-0.58 [*]	-0.01	-1.44	-0.03	-0.35	0.01	0.99	0.00	0.84	0.90	0.90
RODENTIA	-0.77 ^{***}	0.20 ^{***}	0.01	0.00		0.02	0.81	0.17	0.41	0.92	0.83
LAGOMORPHA	-0.78 ^{***}	0.13	0.07	0.00	0.18	0.00	0.00	1.00	0.53	0.93	0.85

Table S2 Summary of models for predicting log body mass in mammals based on phylogenetic and spatial information. In the first set of analyses ϕ and λ were estimated individually, in the second set of analysis they were co-estimated to yield estimates of λ' , ϕ and γ . The superscripts denote likelihood ratio tests of whether the λ and ϕ statistics are different from 0 (first value) or 1 (second value). ns = not significant; * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$). R is a measure of the predictive ability of the phylogenetic model using the randomization method described in the text. 'N' gives total number of species in taxon, 'N missing' the number of species without body mass

	λ	ϕ	λ'	ϕ	γ	R	N	N missing
AFROSORICIDA	0.89 ^{***.ns}	0.00 ^{ns.***}	0.89	0.00	0.11	0.66	36	4
CARNIVORA	0.97 ^{***.***}	0.00 ^{ns.***}	0.97	0.00	0.03	0.85	226	19
CETARTIODACTYLA	0.99 ^{***.*}	0.05 ^{ns.***}	0.94	0.04	0.02	0.79	200	18
CHIROPTERA	0.90 ^{***.***}	0.05 ^{ns.***}	0.86	0.00	0.15	0.89	885	209
CINGULATA	0.62 ^{ns.ns}	0.00 ^{ns.***}	0.48	0.34	0.18	0.71	20	0
DASYUROMORPHIA	1.00 ^{***.ns}	0.32 ^{**.*}	0.67	0.34	0.00	0.83	60	5
DIDELPHIMORPHIA	1.00 ^{***.ns}	0.00 ^{ns.***}	1.00	0.00	0.00	0.85	61	1
DIPROTODONTIA	0.98 ^{***.*}	0.25 ^{**.*}	0.74	0.12	0.15	0.86	108	2
EULIPOTYPHILA	0.92 ^{***.ns}	0.00 ^{ns.***}	0.92	0.00	0.08	0.84	345	98
LAGOMORPHA	0.92 ^{***.*}	0.04 ^{ns.***}	0.88	0.02	0.10	0.89	79	21
MACROSCELIDEA	1.00 ^{***.ns}	0.00 ^{ns.***}	1.00	0.00	0.00	0.76	15	1
PERISSODACTYLA	0.99 ^{***.ns}	0.00 ^{ns.***}	0.99	0.00	0.01	0.71	16	1
PERAMELEMORPHIA	0.00 ^{ns.***}	0.00 ^{ns.***}	0.00	0.00	1.00	0.00	18	2
PRIMATES	1.00 ^{***.ns}	0.00 ^{ns.***}	1.00	0.00	0.00	0.96	228	10
RODENTIA	0.98 ^{***.*}	0.18 ^{ns.***}	0.81	0.06	0.13	0.91	1870	329
SCANDENTIA	0.85 ^{ns.ns}	0.00 ^{ns.ns}	0.84	0.00	0.16	0.73	19	3

Supplementary Figures

Fig S1. Predicted Order level threat probabilities for assessed species on the original 5-point ordinal scale of IUCN threat categories. This scale ranges from “Least Concern”, 1, to “Critically Endangered”, 5. For final analyses levels 3-5 were collapsed into one (“threatened”). Results for Perissodactyla not shown as this Order contained no data-deficient species

Figure S2. Explanatory and discriminative power of the fitted models of threat status for assessed species (based on linear models assuming multinomial errors, see Methods). The outputs of these models are the probabilities of being within each of the 5 IUCN states. From these we calculated the probability that each species was threatened (states 3-5) or not (states 1-2), to generate probabilities comparable with those in Figs 1 and 2. For other details see Fig 1.

Figure S3. Prediction of threats for individual mammal orders for assessed species (based on linear models assuming multinomial errors, see Methods). For details, see Fig 2 and S2.

Figure S4. Explanatory and discriminative power of the fitted models of threat status for assessed species (based on a 50% threat probability threshold set at IUCN ordinal threat level 2 rather than 2.5; see Methods). For other details see Fig 1.

Figure S5. Prediction of threats for individual mammal orders for assessed species (based on a 50% threat probability threshold set at IUCN ordinal threat level 2 rather than 2.5; see Methods). For other details see Fig 2.

Figure S1

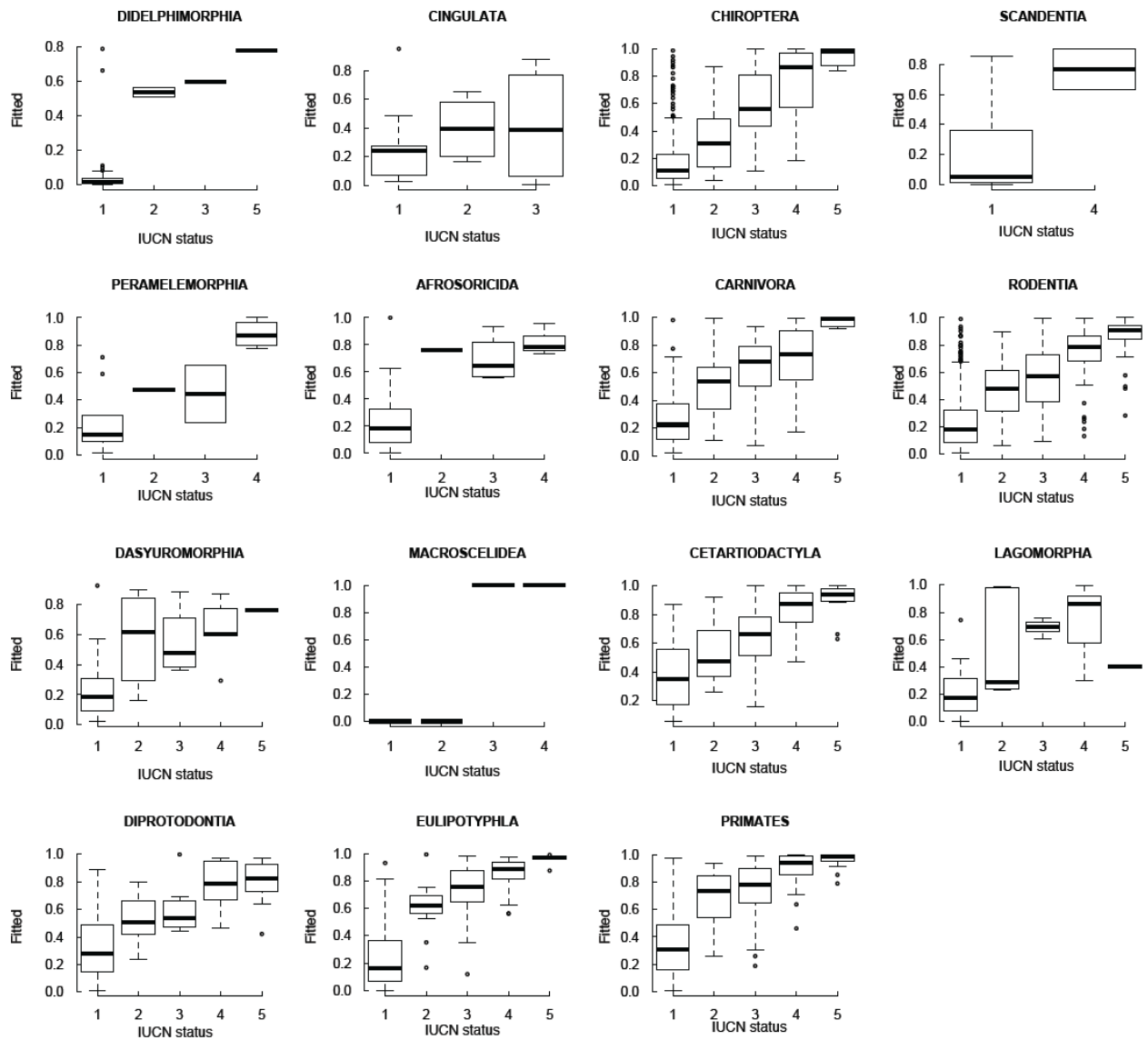


Figure S2

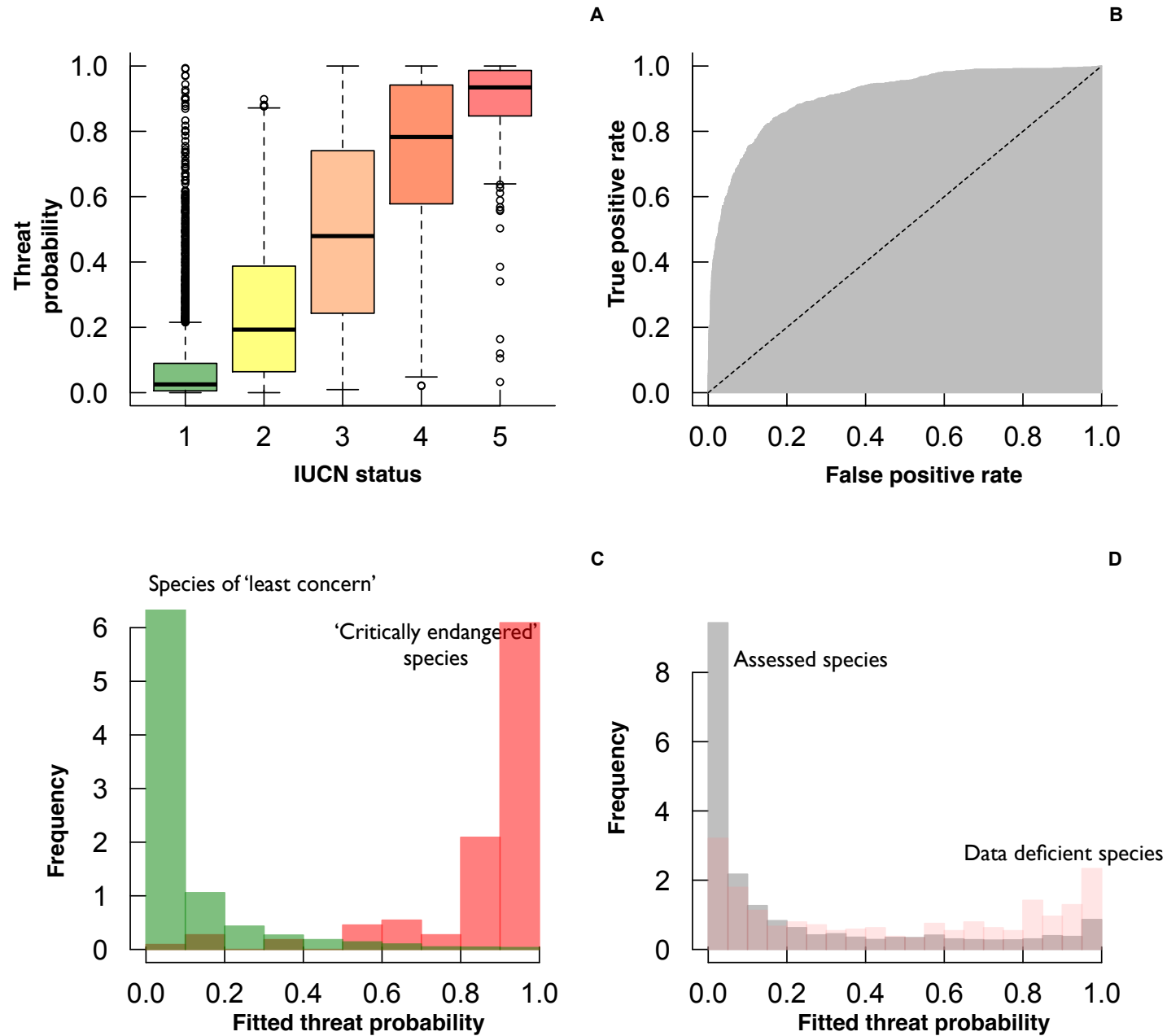


Figure S3

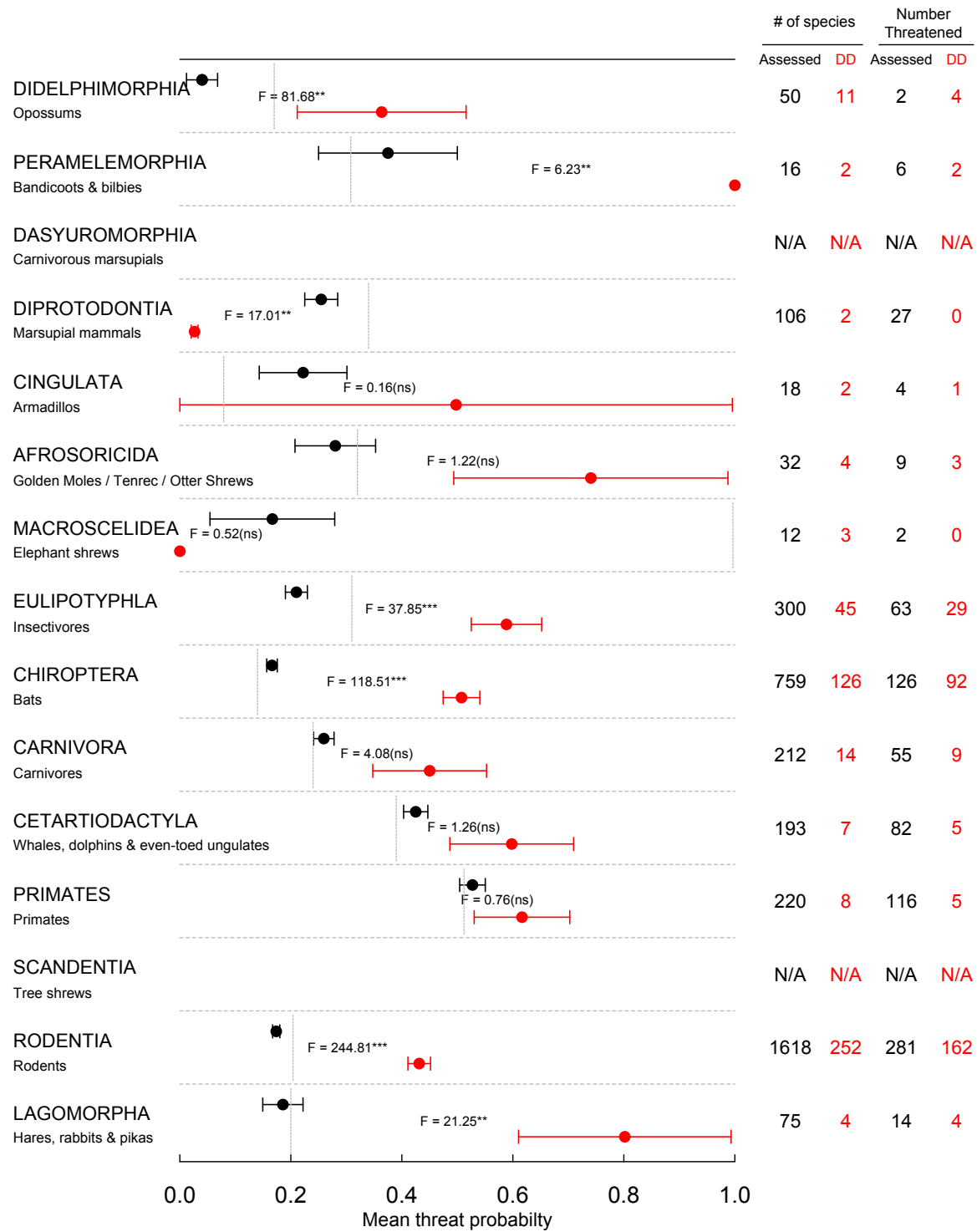


Figure S4

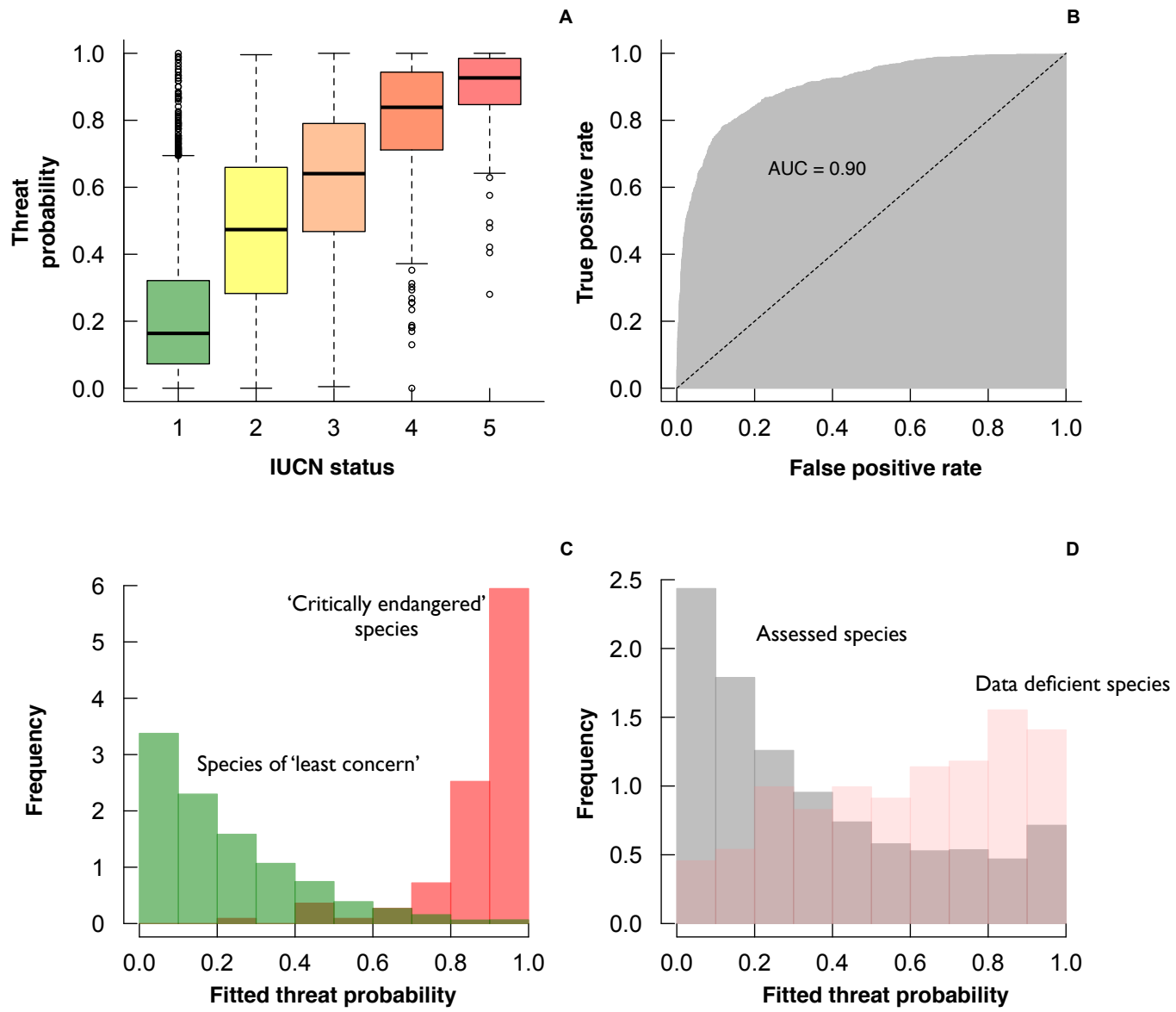


Figure S5

