Online Resource 2

The management effectiveness of protected areas in Kenya

Kenneth Otieno Onditi [1,2,3,4#], Xueyou Li [1#], Wenyu Song [1,2], Quan Li [1], Simon Musila [3,4], James Mathenge [5], Esther Kioko [3,4], Xuelong Jiang [1,4]*

[1] State Key Laboratory of Genetic Resources and Evolution, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, China

[2] Kunming College of Life Sciences, University of Chinese Academy of Sciences, Kunming, China

[3] Department of Zoology, National Museums of Kenya, Nairobi, Kenya

[4] Sino-Africa Joint Research Centre, Chinese Academy of Sciences, Nairobi, Kenya

[5] Kenya Wildlife Service, Nairobi, Kenya
[#] contributed equally

[*] Correspondence; email: jiangxl@mail.kiz.ac.cn, telephone: +86 871 6512 5226

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ESM_1 Extended explanation of how various biodiversity indices were derived (*Section 2.4: Estimation of diversity indices*). Refer to the main manuscript for the bibliography of the citations.

Estimation of diversity indices

The species, phylogeny, traits, and metadata datasets were sorted to correspond using the functions *match.phylo.comm* and *match.phylo.data* in R package *picante* (Kembel *et al.* 2010) and the all.equal function in the *base* package (R Core Team 2020). The species richness [SR] per PA was estimated by summing the unique species in a PA using the *specnumber* function in the R package *vegan* (Oksanen *et al.* 2019). We also computed between-PA species dissimilarity distances using the *vegdist* function in vegan, then translated the distances to ultrametric dendrograms using the unweighted pair group method with arithmetic mean to visually demonstrate whether PAs were uniquely clustered based on governance and designation categories (Fig. 1). The phylogenetic diversity was estimated using Faith's phylogenetic diversity index [PD^{RIC}] (Faith 1992), mean pairwise distance [MPD], and mean nearest taxon distance [MNTD] (Webb *et al.* 2002; Webb and Donoghue 2005). The PD^{RIC} index quantifies the phylogenetic richness by summing the branch lengths of a phylogenetic tree connecting all species in a sampling unit (Faith 1992) while MPD and MNTD estimate the mean pairwise phylogenetic distance between all species [net relatedness] in a sampling unit and the pairwise phylogenetic distance between a species and its closest relative [nearest congener], respectively. Accordingly, MPD relays phylogenetic mechanisms at basal relationships while MNTD relays these dynamics at late evolutionary processes (Webb *et al.* 2002; Webb and Donoghue 2005). We further assessed the phylogenetic structure of PAs using the standardized effect sizes [SES] of MPD and MNTD, i.e., nearest relative [NRI] and nearest taxon [NTI], respectively. When compared to a null model community, the NRI and NTI indicate whether sampled communities are phylogenetically more related/clustered [positive values] or less related/over-dispersed [negative values] than expected by chance. We used null communities generated using 1000 iterations through 9999 randomizations based on the independent swap algorithm (Gotelli and Entsminger 2003), which shuffles species occurrences in communities while maintaining their occurrence frequency within the community (Kembel 2009), to generate null model communities. The algorithm was preferred because it combines good Type I error rates with power to detect niche-based assembly processes and is better-suited at detecting niche processes when multiple traits are involved in community assembly (Kembel 2009). The PD^{RIC} was derived using the *ses.pd* function of *picante* while MPD and NRI and MNTD and NTI were derived using the *ses.mpd* and *ses.mntd* functions in *picante*, respectively.

For functional diversity, we estimated the mean pairwise trait distance separating species in a PA [FD^{MPD}] and the mean nearest taxon distance [FD^{MNTD}] as indices of functional divergence using a Gower distance matrix of the functional traits (Webb *et al.* 2002; Webb *et al.* 2008). Like the phylogenetic diversity computations, we inferred the SES of FD^{MPD} and FD^{MNTD} [FD^{NRI} and FD^{NTI}, respectively] to estimate whether the distribution/regularity of functional traits within a PA was lesser or greater than expected when compared to a null-model community. The estimations were implemented using the same functions of the *picante* package – *ses.mpd* and *ses.mntd*. We similarly applied the independent swap algorithm with 1000 iterations through 9999 randomizations when generating null model communities for inferring FD^{NRI} and FD^{NTI}.

We further evaluated the functional richness in a PA using Villeger *et al.* (2008)'s functional richness [FD^{RIC}] index as implemented in the R package *FD* (Laliberté *et al.* 2014); the estimation is based on the trait space/volume occupied by a species within in a community (Cornwell *et al.* 2006; Villeger *et al.* 2008). A pairwise species trait matrix is generated using the Gower dissimilarity distance (Gower 1971), with the trait dimensionality then reduced using principal coordinates analysis [PCoA], and retaining only the first few axes capturing the highest variance in the input traits [we retained the first three PCoA axes which consistently retained >88% quality of the input trait space in all species groups].

The wholeness of species representation in various PA managements and designations relative to all the species found in PAs was assessed using completeness and uniqueness indices. The completeness index was derived as the log-transformed ratio of observed richness [SR]/dark diversity [i.e., Pärtel *et al.* (2013)]. The dark diversity represented the species absent from a particular PA but represented in others (Münzbergová and Herben 2004; Bello *et al.* 2016), and was derived using the *beals* function in R package *vegan*, which estimates the occurrence probability for a species presence in a community based on its joint occurrence with other species. We also derived PA level species uniqueness coefficients based on Pavoine and Ricotta (2019) using the *uniqueness* function in R package *adiv* (Pavoine and Goslee 2020). The complementarity between designation and governance PA categories based on dissimilarity of species composition was determined using Jaccard similarity coefficient.

ESM_2 Comparison of diversity indices between designation categories in the full dataset with unequal number of PAs per category and in a randomly-sampled dataset with equal number of protected areas per category.

a) All cases

Designation type		SR	MPD	FD^{MPD}	NRI	NTI	FD^{NRI}	FD^{NTI}
Community Conservancy	Mean	127	166.3	0.2073	0.0220	0.1576	-0.3263	-0.0149
	SD	5	1.0	0.0020	0.2739	0.4885	0.1394	0.2752
Community Nature Reserve	Mean	100	164.8	0.2138	0.3552	0.0088	-0.6249	0.0544
	SD	17	1.8	0.0064	0.3110	0.3138	0.3279	0.3245
Forest Reserve	Mean	116	166.0	0.2016	0.0805	-0.0021	0.2232	0.0227
	SD	18	1.0	0.0064	0.2017	0.3664	0.4461	0.2912
National Park	Mean	113	165.6	0.2061	0.1497	0.1040	-0.0410	0.2294
	SD	29	1.8	0.0093	0.3224	0.4919	0.5113	0.2803
National Reserve	Mean	104	165.2	0.2095	0.1989	0.0499	-0.3242	0.1844
	SD	22	2.0	0.0091	0.3365	0.3939	0.6224	0.3376
Others	Mean	110	166.1	0.2033	-0.0131	-0.1239	0.0269	0.0614
	SD	21	1.3	0.0051	0.3242	0.4654	0.3691	0.2372
Private Reserve	Mean	117	165.9	0.2048	0.1255	-0.0530	-0.0994	-0.0314
	SD	11	0.9	0.0040	0.2382	0.4143	0.3203	0.1572
	SS	13012	61.4	0.0052	2.9559	1.6545	27.1934	1.6613
	MS	2169	10.2	0.00	0.49	0.28	4.53	0.28
	F	6	6.7	20.56	7.77	1.76	23.91	3.39
	Sig.	0.00	0.00	0.00	0.00	0.11	0.00	0.00

Community Conservancy, N = 22; Community Nature Reserve, N = 27; Forest Reserve, N = 234; National Park, N = 23; National Reserve, N = 30; Others, N = 48; Private Reserve, N = 16;
SS = Sum of Squares; MS = mean square; F = F statistics, Sig. = p-value

b) Randomly-sampled cases

| Designation type		SR	MPD	FD^{MPD}	NRI	NTI	FD^{NRI}	FD^{NTI}
Community Conservancy	Mean	127	166.5	0.2072	-0.0138	0.184	-0.321	-0.0342
	SD	4	0.9	0.0021	0.2521	0.5049	0.1452	0.2798
Community Nature Reserve	Mean	100	164.7	0.214	0.3607	-0.0101	-0.6292	0.0497
	SD	18	1.8	0.0064	0.312	0.312	0.3337	0.3403
Forest Reserve	Mean	115	166.2	0.2036	0.0038	0.0086	0.0736	0.0955
	SD	21	0.7	0.0069	0.1826	0.4652	0.4705	0.2897
National Park	Mean	121	165.9	0.2043	0.0954	0.0667	-0.0029	0.2034
	SD	22	1.3	0.0077	0.2898	0.5053	0.5341	0.2901
National Reserve	Mean	101	165.4	0.2092	0.1671	0.0714	-0.2988	0.2418
	SD	20	2.0	0.0102	0.3381	0.4006	0.6947	0.3279
Others	Mean	114	166.2	0.2018	-0.0308	-0.1259	0.1423	0.0604
	SD	21	0.9	0.0047	0.2849	0.488	0.3897	0.2099
Private Reserve	Mean	117	165.9	0.2048	0.1255	-0.053	-0.0994	-0.0314
	SD	11	0.9	0.004	0.2382	0.4143	0.3203	0.1572
	SS	12039	46.6	0.00	2.25	1.17	8.78	1.31
	MS	2006	7.8	0.00	0.37	0.19	1.46	0.22
	F	6	4.7	7.83	4.90	0.97	7.33	2.78
	Sig.	0.00	0.00	0.00	0.00	0.45	0.00	0.01

SS: Sum of Squares; MS: mean square; Community Conservancy, N =20; Community Nature Reserve, N =20; Forest Reserve, N =20; National Park, N =20; National Reserve, N =20; Others, N =20; Private Reserve, N =16;

ESM_3 Tests of statistical significances of variances in diversity indices shown in Table 2 explained by various PA categorisations. The values show the type III sum of squares analysis of variance of significances of differences in count of species composition [AS], averaged species richness [SR], averages of diversity indices less correlated with SR: phylogenetic mean pairwise distance [MPD], functional mean pairwise distance [FD^{MPD}], phylogenetic nearest relative distance [NRI], phylogenetic nearest taxon distance [NTI], functional nearest relative distance [FD^{NRI}], and functional nearest taxon distance [FD^{NTI}]. Significant p values in in bold.

	Index	Type III SS	MS	F	p	R^2_{adj}
Governance	AS	NA	NA	NA	0.920	0.004
	SR	6698	1674	4.529	**0.001**	0.034
	MPD	42.99	10.75	6.848	**0.000**	0.056
	FD^{MPD}	0.003	0.001	17.91	**0.000**	0.145
	NRI	2.516	0.629	9.774	**0.000**	0.081
	NTI	1.334	0.334	2.128	0.077	0.011
	FD^{NRI}	18.52	4.631	22.03	**0.000**	0.174
	FD^{NTI}	0.279	0.070	0.818	0.514	-0.002
Designation	AS	NA	NA	NA	0.380	0.016
	SR	13012	2169	6.115	**0.000**	0.071
	MPD	61.40	10.23	6.697	**0.000**	0.079
	FD^{MPD}	0.005	0.001	20.556	**0.000**	0.227
	NRI	2.956	0.493	7.766	**0.000**	0.092
	NTI	1.655	0.276	1.764	0.105	0.011
	FD^{NRI}	27.19	4.532	23.91	**0.000**	0.256
	FD^{NTI}	1.661	0.277	3.386	**0.003**	0.035
GOV_TY	AS	NA	NA	NA	0.970	0.000
	SR	477.5	477.5	1.251	0.264	0.001
	MPD	0.631	0.631	0.380	0.538	0.538
	FD^{MPD}	0.002	0.002	40.74	**0.000**	0.091
	NRI	0.018	0.018	0.259	0.611	-0.002
	NTI	0.404	0.404	2.564	0.110	0.004
	FD^{NRI}	14.72	14.72	67.39	**0.000**	0.143
	FD^{NTI}	0.093	0.093	1.093	0.296	0.000
GOV_TYM	AS	NA	NA	NA	0.830	0.001
	SR	2547	1274	3.374	**0.035**	0.012
	MPD	18.14	9.070	5.593	**0.004**	0.023
	FD^{MPD}	0.003	0.002	34.26	**0.000**	0.143
	NRI	0.230	0.115	1.653	0.193	0.003
	NTI	0.746	0.373	2.374	0.094	0.007
	FD^{NRI}	20.63	10.31	50.51	**0.000**	0.199
	FD^{NTI}	1.173	0.586	7.135	**0.001**	0.030
IUCN	AS	NA	NA	NA	0.100	0.016
	SR	4151	1384	3.697	**0.012**	0.020
	MPD	13.55	4.515	2.758	**0.042**	0.013
	FD^{MPD}	0.001	0.000	9.031	**0.000**	0.057
	NRI	0.284	0.095	1.359	0.255	0.003
	NTI	0.930	0.310	1.976	0.117	0.007
	FD^{NRI}	6.080	2.027	8.395	**0.000**	0.053
	FD^{NTI}	1.623	0.541	6.656	**0.000**	0.041

SS = sum of squares, MS = mean squares (estimated variances), F = F statistics, R^2_{adj} = adjusted r squared

ESM_4 The representation of species and species ranges in protected areas in Kenya. **a**) Bar plots of count of unique terrestrial mammal species in protected areas, PAs, in Kenya showing the number of PAs species are represented in by ordinal classification. **b**) the relative proportion of species ranges overlapping in PAs, contrasting representations in all PAs, SPAs, and PPAs.
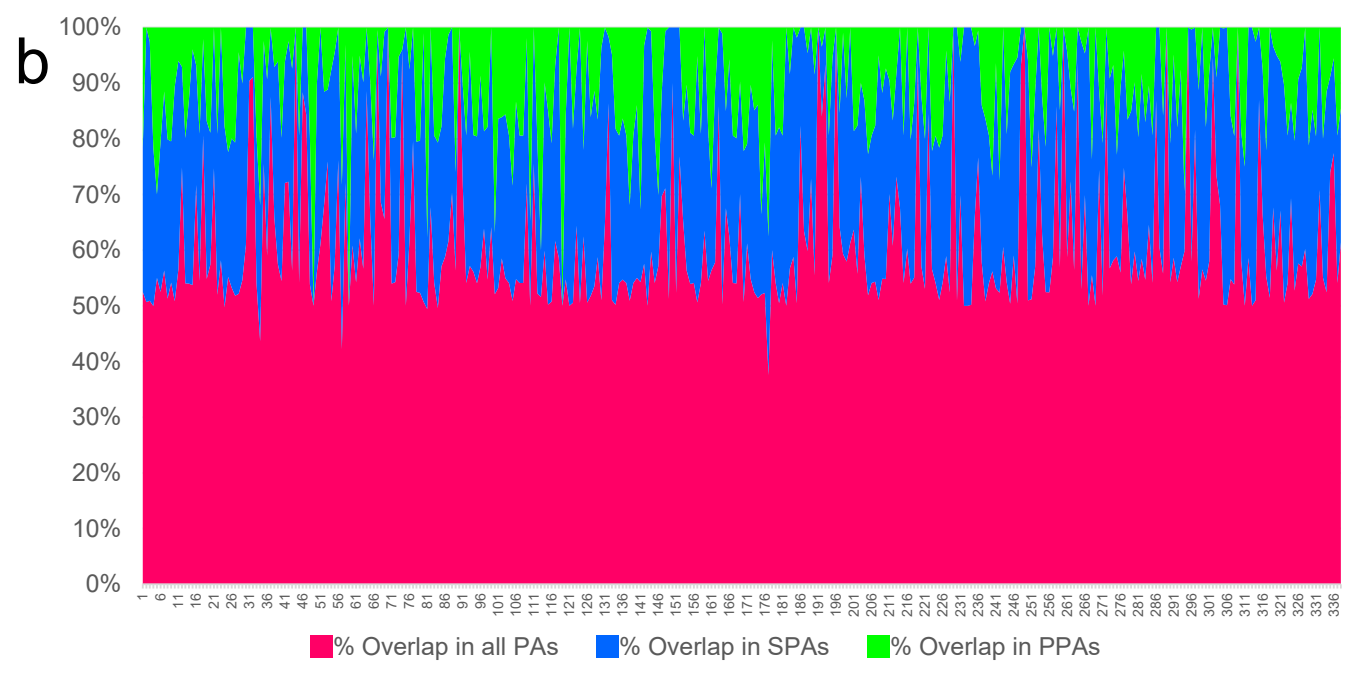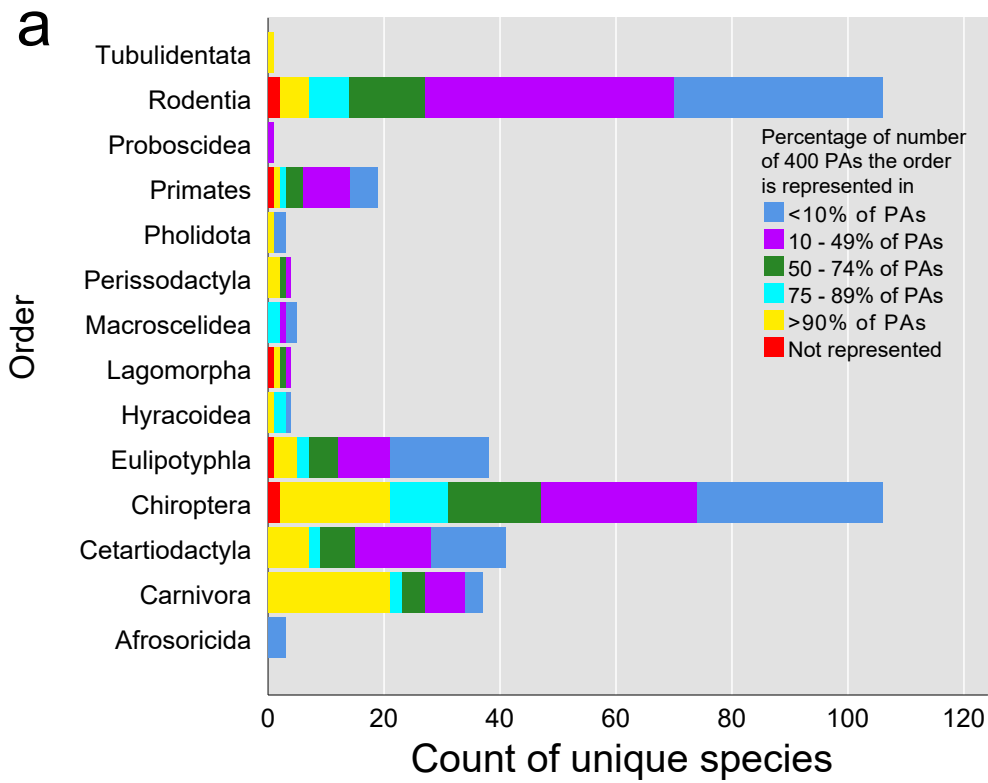
ESM_5 Bivariate correlations between diversity indices of terrestrial mammals in protected areas in Kenya based on Pearson's r. * indicate statistically significant (*p*<.05) associations
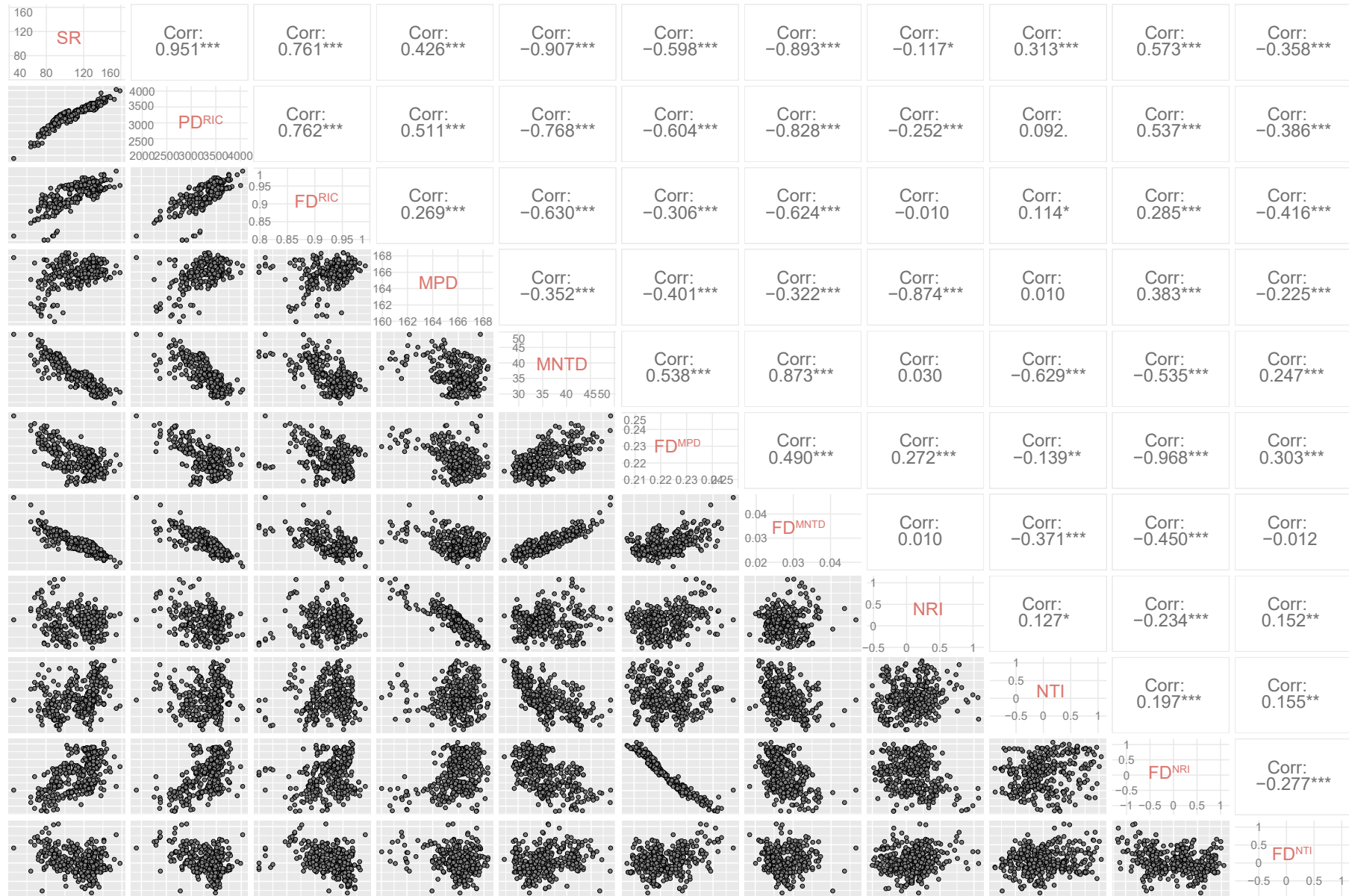
SR = species richness, PD^{RIC} = Faith's index of phylogenetic diversity, MPD = phylogenetic mean pairwise distance, MNTD = phylogenetic mean nearest taxon distance, NRI = nearest relative index [phylogenetic] NTI = nearest taxon index [phylogenetic], FD^{RIC} = Functional richness, FD^{MPD}= functional mean pairwise distance, FD^{MNTD} = functional mean nearest taxon distance, FD^{NRI}= functional nearest relative index FD^{NTI}= functional nearest taxon index

ESM_6 The distribution of multidimensional diversity metrics of terrestrial mammals in protected areas in Kenya modeled using the centroid latitudes and longitudes of PAs as predictors and diversity indices as responses (**a**). The biogeographic regionalization of PAs based on species phylogenetic dissimilarity are shown in b, with the boxplots comparing mean species richness between the biogeographic regions
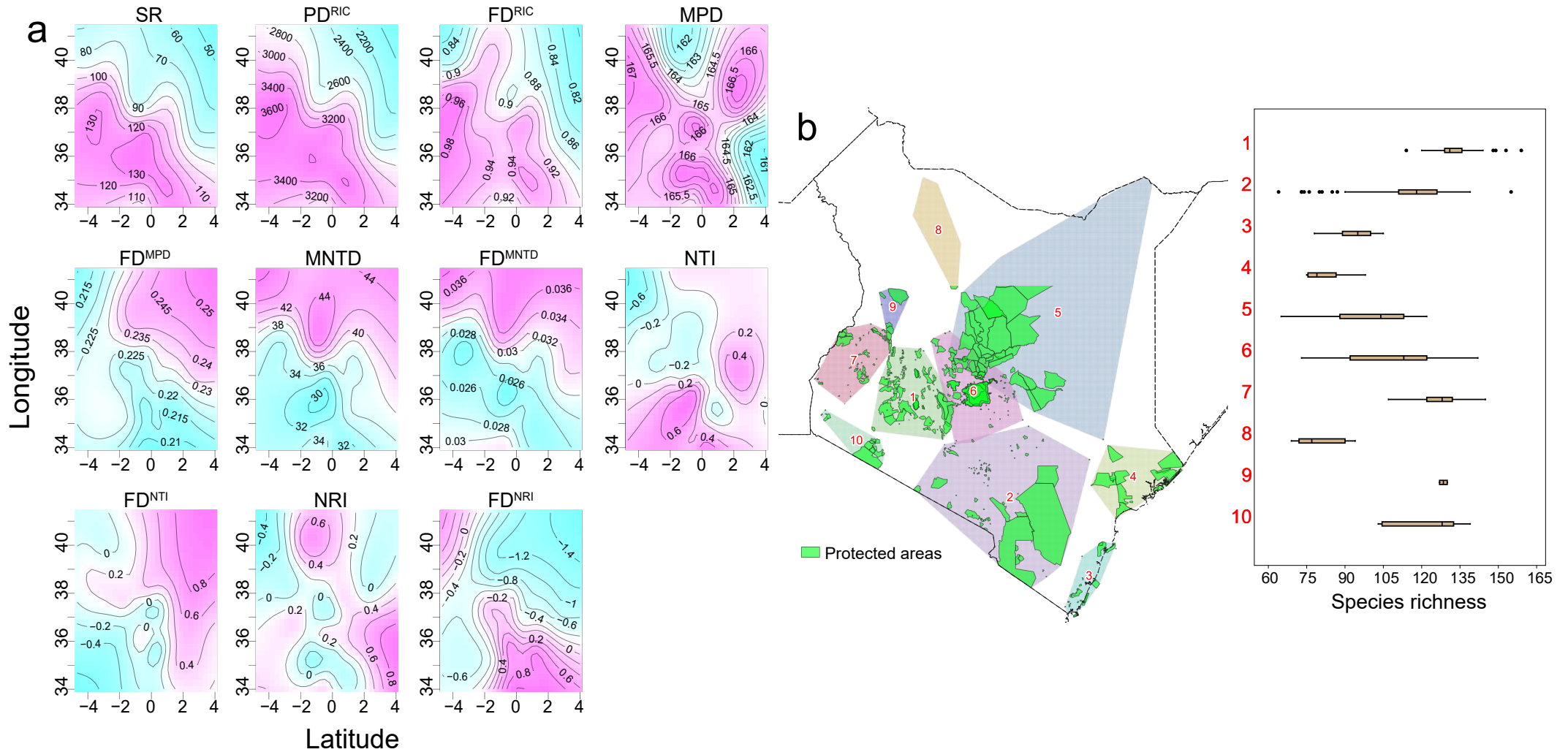
SR = species richness, PD^{RIC} = Phylogenetic richness, FD^{RIC} = Functional richness, MPD = phylogenetic mean pairwise distance, MNTD = phylogenetic mean nearest taxon distance, NRI = nearest relative index, NTI = nearest taxon index, FD^{MPD} = mean pairwise distance based on functional traits, FD^{MNTD}= mean nearest taxon distance based on functional, FD^{NRI} = nearest relative index of FD^{MPD}, FD^{NTI} = nearest taxon index of FD^{MNTD}]

ESM_7 Summary of relative proportion of species range overlaps in protected areas and Marxan results for the best-solution conservation priority areas.

Species	%Rep_in_PAs	%Rep_in_SPAs	1/3_RTarget	BSol_AllPAs	BSol_SPAs	Target_Met_?	MPM_AllPAs	MPM_[SPAs]
Acinonyx jubatus	17.19	8.48	11.54	11.66	11.64	yes	1.00	1.00
Alcelaphus buselaphus	20.85	13.81	4.39	5.48	6.60	yes	1.00	1.00
Aonyx capensis	18.09	8.74	13.00	13.09	13.01	yes	1.00	1.00
Bdeogale jacksoni	24.31	8.21	1.44	2.33	2.38	yes	1.00	1.00
Bdeogale omnivora	16.78	9.33	0.69	0.81	0.81	yes	1.00	1.00
Beatragus hunteri	19.09	12.49	0.30	0.31	0.30	yes	1.00	1.00
Cephalophus adersi	74.82	62.19	0.09	0.10	0.10	yes	1.00	1.00
Cephalophus silvicultor	48.97	5.20	0.17	0.18	0.19	yes	1.00	1.00
Ceratotherium simum	15.44	7.55	15.81	15.82	15.86	yes	1.00	1.00
Cercocebus galeritus	54.38	30.42	0.01	0.01	0.01	yes	0.98	1.00
Connochaetes taurinus	23.52	19.25	1.27	1.98	2.03	yes	1.00	1.00
Crocidura allex	24.06	7.52	0.05	0.05	0.06	yes	1.00	1.00
Crocuta crocuta	15.34	7.51	15.91	15.91	15.94	yes	1.00	1.00
Damaliscus lunatus	17.16	10.27	1.55	1.77	2.05	yes	1.00	1.00
Dendrohyrax validus	8.89	5.36	0.10	0.11	0.11	yes	1.00	1.00
Diceros bicornis	15.63	7.65	15.61	15.63	15.62	yes	1.00	1.00
Eidolon helvum	20.38	13.72	3.50	4.88	5.66	yes	1.00	1.00
Equus grevyi	32.92	6.95	2.15	3.33	3.62	yes	1.00	1.00
Equus quagga	23.29	13.31	8.37	8.56	9.22	yes	1.00	1.00
Giraffa camelopardalis	19.72	11.07	8.58	8.99	10.22	yes	1.00	1.00
Grammomys gigas	92.19	90.18	0.05	0.05	0.05	yes	1.00	1.00
Hippotragus equinus	71.89	71.89	0.01	0.01	0.01	yes	1.00	0.99
Hippotragus niger	8.29	5.50	0.09	0.11	0.11	yes	1.00	1.00
Hyaena hyaena	15.34	7.51	15.91	15.91	15.94	yes	1.00	1.00
Hydrictis maculicollis	16.16	3.61	7.80	8.08	8.81	yes	1.00	1.00
Hylochoerus meinertzhageni	21.04	5.60	2.14	3.32	3.62	yes	1.00	1.00
Kobus ellipsiprymnus	20.89	10.52	10.56	10.63	11.13	yes	1.00	1.00
Litocranius walleri	19.14	10.25	8.96	9.01	9.19	yes	1.00	1.00
Loxodonta africana	55.23	34.43	2.89	4.48	4.89	yes	1.00	1.00
Lycaon pictus	49.88	33.71	1.87	3.04	3.15	yes	1.00	1.00
Oryx beisa	17.41	9.32	10.27	10.40	11.01	yes	1.00	1.00
Otomops harrisoni	17.06	0.00	0.00	0.00	0.00	yes	1.00	1.00
Otomops martiensseni	19.82	19.10	0.00	0.00	0.00	yes	1.00	1.00
Otomys barbouri	91.85	91.85	0.00	0.00	0.00	yes	1.00	1.00
Panthera leo	39.76	25.68	3.67	5.42	6.07	yes	1.00	1.00
Panthera pardus	15.60	7.64	15.61	15.61	15.61	yes	1.00	1.00
Phataginus tricuspis	4.99	1.11	0.50	0.50	0.50	yes	1.00	1.00
Profelis aurata	100.00	100.00	0.00	0.00	0.00	yes	1.00	1.00
Redunca fulvorufula	15.89	4.91	6.98	7.28	8.29	yes	1.00	1.00
Rhinolophus deckenii	12.09	6.97	0.74	0.92	0.92	yes	1.00	1.00
Rhynchocyon chrysopygus	11.37	1.71	0.10	0.10	0.10	yes	1.00	1.00
Smutsia gigantea	2.96	2.28	0.05	0.05	0.05	yes	1.00	1.00
Smutsia temminckii	20.74	10.48	10.03	10.09	10.05	yes	1.00	1.00
Syncerus caffer	18.84	9.32	12.82	12.82	12.82	yes	1.00	1.00
Taphozous hildegardeae	4.70	2.00	0.50	0.51	0.51	yes	1.00	1.00
Tragelaphus eurycerus	84.39	55.67	0.14	0.15	0.17	yes	1.00	1.00
Tragelaphus imberbis	15.63	8.40	12.21	12.21	12.21	yes	1.00	1.00
Tragelaphus oryx	23.62	14.99	6.81	7.06	8.59	yes	1.00	1.00
Tragelaphus strepsiceros	15.27	6.91	7.88	7.88	7.88	yes	1.00	1.00

%Rep_in_PAs = % representation in all protected areas (PAs); %Rep_in_SPAs = % representation in government protected areas (SPAs); 1/3_RTarget = 1/3 species range; BSol_AllPAs = species range of the 1/3_RTarget represented in best solution conservation priority areas when all PAs are locked in; BSol_SPAs = species range of the 1/3_RTarget represented in best solution conservation priority areas when only SPAs are locked in; TargetMet? = whether the 1/3 range representation was met; MPM_AllPAs and MPM_[SPAs] = proportion of the /3_RTarget achieved
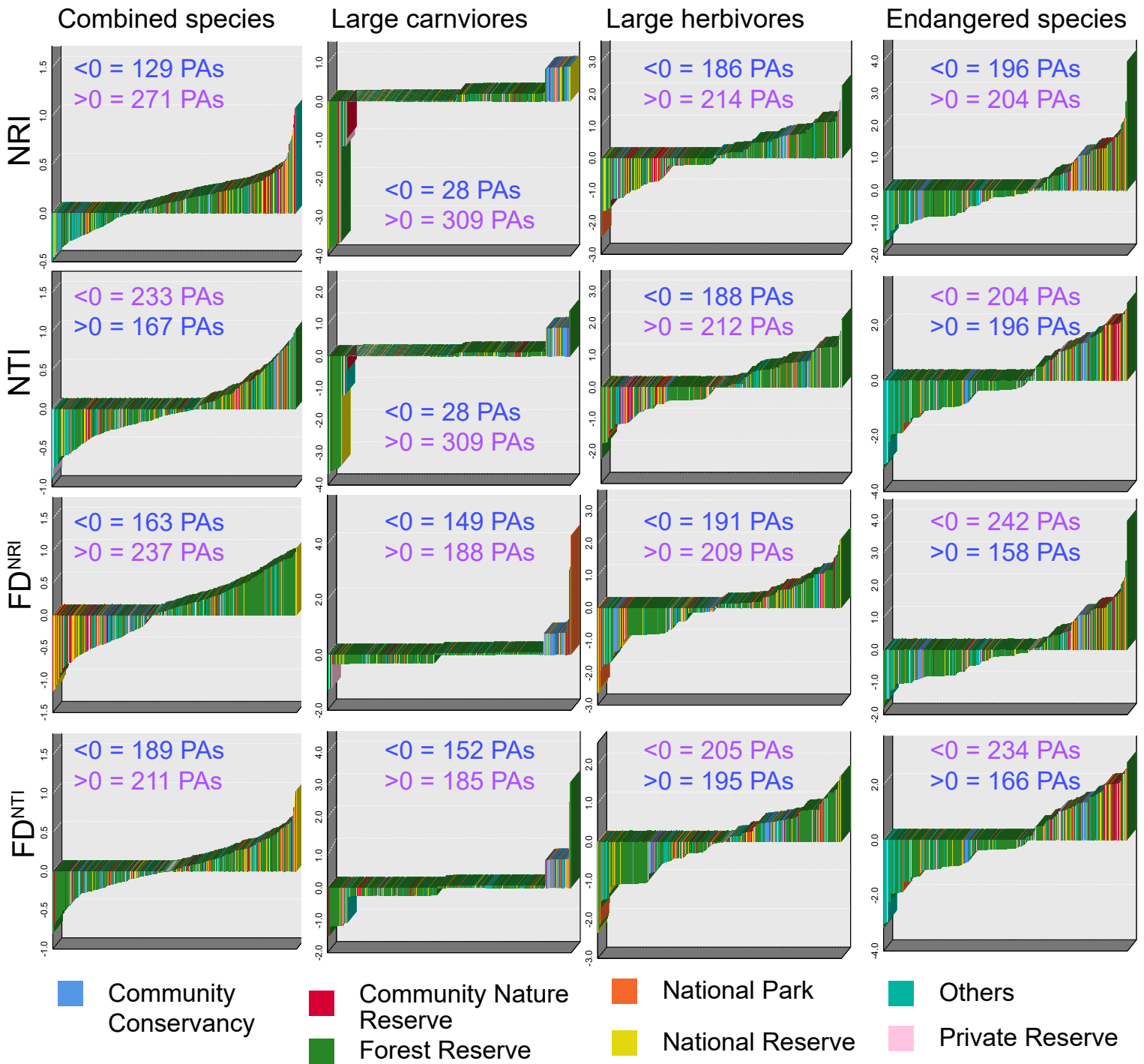
ESM_8 The association between species richness and PA status year and PA size, for **a)** focal species (as defined in the main text) and **b)** small mammals - Chiroptera and Rodentia orders. The scatter plots are partitioned by PA designation categories. Refer to Fig. 3 in the manuscript for the combined species pool plots.

ESM_9 Exploring the association between PA governance and designation categories on the diversity of terrestrial mammal in Kenya. The values represent the test for statistical significances of the variance in diversity indices explained by differences in PA governance and designation categorizations. Only metrics that are not highly correlated were included in the analysis [SR, FD^{MPD}, NRI, NTI, FD^{NRI}, FD^{NTI}, see **ESM_5** above for the bivariate correlation between indices]

	Species group	*chi*-square (*p*-values)	
		Governance	Designation
AS	Combined species	1.456 (0.92)	6.377 (0.38)
	Large Carnivores	3.73 (0.59)	4.788 (0.57)
	Large Herbivores	2.558 (0.77)	2.431 (0.88)
	Endangered	2.921 (0.71)	3.14 (0.79)
SR	Combined species	5.389 (0.37)	10.19 (0.07)
	Large Carnivores	5.589 (0.35)	9.23 (0.1)
	Large Herbivores	6.902 (0.23)	7.81 (0.17)
	Endangered	7.502 (0.19)	24.79 (**0**)
MPD	Combined species	0.036 (1)	0.05 (1)
	Large Carnivores	6.687 (0.25)	19.1 (**0**)
	Large Herbivores	9.32 (0.1)	19.27 (**0**)
	Endangered	0.254 (1)	2.516 (0.78)
FD^{MPD}	Combined species	0.001 (1)	0 (1)
	Large Carnivores	0.007 (1)	0.003 (1)
	Large Herbivores	0.021 (1)	0.049 (1)
	Endangered	0.015 (1)	0.014 (1)
NRI	Combined species	0.222 (1)	0.429 (0.99)
	Large Herbivores	0.702 (0.98)	0.7 (0.98)
	Endangered	0.035 (1)	0.178 (1)
NTI	Combined species	0.846 (0.97)	0.769 (0.98)
	Large Herbivores	0.683 (0.99)	0.67 (0.98)
	Endangered	0.017 (1)	0.06 (1)
FD^{NRI}	Combined species	0.371 (1)	0.053 (1)
	Large Herbivores	0.698 (0.98)	0.377 (1)
	Endangered	0.565 (0.99)	0.836 (0.97)
FD^{NTI}	Combined species	0.234 (1)	0.368 (1)
	Large Herbivores	0.287 (1)	0.136 (1)
	Endangered	1.343 (0.93)	0.883 (0.97)

ESM_10 The phylogenetic and functional structure of protected areas in Kenya based on terrestrial mammals. The bar plots show the distribution of phylogenetic [NRI] and functional [FD^{NRI}] nearest relative index and phylogenetic [NTI] and functional [FD^{NTI}] nearest taxon index shaded by the designation type. -(negative) values indicate overdispersion while +(positive) values indicate clustering. The results are partitioned by various species groups around the so-called focal species as explained in the main text. There are 400 bars each representing a single a protected area.

ESM_11 Multilevel comparison of diversity indices of terrestrial mammals in PAs in Kenya between governance and designation categories. Comparison was implemented for SR and the diversity indices not highly correlated with SR [see Online Resource 6 for the correlations between diversity indices]

PA category pairs	[SR, MPD, FD^{MPD}, NRI, NTI, FD^{NRI}, and FD^{NTI}]					[Turnover, Uniqueness, and Completeness]				
	SS	F	R2	p	padj	SS	F	R2	p	padj
Governance										
Government vs Indigenous peoples	4994.7	12.499	0.036	**0.002**	**0.02**	0.269	9.75	0.028	0.004	0.06
Government vs Nonprofit organizations	756.2	1.92	0.006	0.166	1	0.069	2.565	0.008	0.118	1
Government vs Individual or Community	488.2	1.246	0.004	0.245	1	0.078	2.894	0.009	0.088	1
Government vs Local communities	133.3	0.334	0.001	0.581	1	0.032	1.175	0.003	0.258	1
Indigenous people vs Nonprofit organizations	4550.1	19.363	0.326	**0.001**	**0.01**	0.278	15.524	0.28	**0.001**	**0.015**
Indigenous people vs Individual or Community	3985.9	18.27	0.314	**0.001**	**0.01**	0.246	14.876	0.271	**0.001**	**0.015**
Indigenous people vs Local communities	1902.1	6.269	0.111	**0.018**	0.18	0.123	5.525	0.1	**0.026**	0.39
Nonprofit organizations vs Individual or Community	15.6	0.163	0.005	0.732	1	0.008	1.198	0.038	0.28	1
Nonprofit organizations vs Local communities	867.1	3.729	0.085	0.067	0.67	0.053	3.282	0.076	0.075	1
Individual or Community vs Local communities	631.1	2.926	0.068	0.094	0.94	0.038	2.59	0.061	0.106	1
Designation										
Forest Reserve vs National Park	156.1	0.423	0.002	0.526	1	0.027	1.067	0.004	0.3	1
Forest Reserve vs National Reserve	3418.9	9.969	0.037	**0.002**	**0.042**	0.204	8.744	0.032	**0.005**	0.105
Forest Reserve vs Community Nature Reserve	5775	17.897	0.065	**0.001**	**0.021**	0.3	13.384	0.049	**0.001**	**0.021**
Forest Reserve vs Private Reserve	36.4	0.116	0	0.746	1	0.023	1.067	0.004	0.307	1
Forest Reserve vs Community Conservancy	2432.3	8.106	0.031	**0.005**	0.105	0.239	11.581	0.044	**0.002**	**0.042**
National Park vs National Reserve	968.4	1.522	0.029	0.2	1	0.058	1.29	0.025	0.273	1
National Park vs Community Nature Reserve	2013.5	3.692	0.071	0.07	1	0.14	3.44	0.067	0.06	1
National Park vs Private Reserve	169.4	0.31	0.008	0.555	1	0.053	1.327	0.035	0.28	1
National Park vs Community Conservancy	2108	4.818	0.101	**0.035**	0.735	0.217	6.720	0.135	**0.008**	0.168
National Reserve vs Community Nature Reserve	240.5	0.605	0.011	0.449	1	0.042	1.513	0.027	0.204	1
National Reserve vs Private Reserve	1723	4.771	0.098	**0.031**	0.651	0.153	6.372	0.126	**0.016**	0.336
National Reserve vs Community Conservancy	6316.5	21.764	0.303	**0.001**	**0.021**	0.489	25.31	0.336	**0.001**	**0.021**
Community Nature Reserve vs Private Reserve	2886.9	12.308	0.231	**0.001**	**0.021**	0.175	9.786	0.193	**0.006**	0.126
Community Nature Reserve vs Community Conservancy	8453	48.231	0.506	**0.001**	**0.021**	0.536	39.138	0.454	**0.001**	**0.021**
Private Reserve vs Community Conservancy	830	13.258	0.269	**0.002**	**0.042**	0.057	12.176	0.253	**0.002**	**0.042**

MPD = phylogenetic mean pairwise distance, FD^{MPD} = functional mean pairwise distance, NRI = phylogenetic nearest relative index, NTI = phylogenetic nearest taxon distance, FD^{NRI} = functional phylogenetic nearest relative index, and FD^{NTI} = functional phylogenetic nearest taxon distance