Phylogenetic and functional diversity in large carnivore assemblages

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Large terrestrial carnivores are important ecological components and prominent flagship species, but are often extinction prone due to a combination of biological traits and high levels of human persecution. This study combines phylogenetic and functional diversity evaluations of global and continental large carnivore assemblages to provide a framework for conservation prioritization both between and within assemblages. Species rich assemblages of large carnivores simultaneously had high phylogenetic and functional diversity, but species contributions to phylogenetic and functional diversity components were not positively correlated. The results further provides ecological justification for the largest carnivore species as focus for conservation action, and suggests that range contraction is a likely cause of diminishing carnivore ecosystem function. This study highlights that preserving species rich carnivore assemblages will capture both high phylogenetic and functional diversity, but that prioritizing species within assemblages will involve trade-offs between optimizing contemporary ecosystem function versus the evolutionary potential for future ecosystem performance.

Key words: Carnivora, predation, ecosystem function, conservation priorities, biodiversity

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1. Introduction

The expansion of human environmental footprint over the past 100 years has been accompanied by dramatic declines in components of the earth's biodiversity [1]. This biodiversity decline can have radical impacts on humanity by altering ecosystem properties and the subsequent goods and services provided [2, 3]. Uneven spatial distribution of diversity coupled with limited resources available for conservation has generated a large body of work identifying biodiversity conservation priorities [4]. However, many of these approaches rely on taxonomic richness as a proxy for diversity [5]. This is a potentially serious shortcoming, since the ecological significance of diversity is also influenced by the relative functional attributes of different organisms [6].

Both phylogenetic and functional diversity have been related to ecosystem function [7], and it is now generally accepted that ecosystem function may differ substantially between species assemblages with the same taxonomic richness [8, 9]. Unfortunately, there are still no unified metrics that includes all aspects of biodiversity [10], and the use of phylogenetic diversity as a proxy for functional diversity is not unequivocally supported [2, 11, 12]. Since it may not be possible to simultaneously optimize conservation of all aspects of biodiversity, it is important to recognize the value of each component. For instance, since one of the fundamental advantages of genetic variation is the potential to adapt to future conditions [13], we can regard phylogenetic diversity, which generally is closely related to genetic diversity, to describe the potential for future functional diversity and hence future ecosystem performance [14]. This would then stand in contrast to functional diversity, which primarily relates to present ecosystem function.

Large terrestrial carnivores are critically important for ecosystem dynamics [15], and have high cultural values and public appeal [16-18]. However, they are often extinction prone due to high levels of human persecution coupled with low population densities and slow growth rates [19]. Recent carnivore conservation efforts typically target protection of local populations, and although there have been suggestions for taxonomic and functional prioritizations both on regional [20] and global scales [21], simultaneous evaluations of phylogenetic and functional diversity between and within carnivore assemblages are lacking.

I used an adaptation of a carnivore super-tree [22, 23] combined with a dendrogram based measure of functional diversity [24] to quantify phylogenetic diversity, functional diversity, and functional redundancy across the global and continental assemblages of large carnivores, as well as to quantify relative species contributions to these diversity components. I included species which body mass average 10kg or more, hence both including large carnivores (as defined from energetic models [25]) and mesocarnivores [21] in the assessment.

2. Material and methods

I followed the conventional definition of the world as consisting of 7 continents, i.e. Africa, Asia, Europe, North America, South America, Australasia and Antarctica. I did not include data from Australasia and Antarctica since neither of these two continents has any indigenous species within contemporary Carnivora. North America was defined as containing Unites States of America, Cananda, Mexico and the Central

American countries, and I delineated Europe as continental Europe eastwards until the Black Sea. I included Russia in the Asian continent.

Species definitions as well as global and continental conservation status for each species were taken from the IUCN redlist [26]. The continental conservation statuses for European species were complemented by a mammal status survey for Europe since this provided a more refined regional assessment for this continent [27].

(a) Measurement of phylogenetic diversity and species contributions

I used a previously published complete carnivore composite super-tree [22], with the amendment that skunks and stink-badgers were regarded as a monophyletic Mephitidae rather than as part of Mustelidae [23,28]. I selected this hypothesis over more recent molecular ones [22,29-30] because it contained all species identified as large carnivores in this study and therefore provided a more complete evaluation of phylogenetic diversity for the analyses.

I calculated the evolutionary distinctiveness for each species as the sum of all branches along each species phylogenetic trajectory where each branch were weighted by the number of species sharing it [31], and the unique phylogenetic contribution of a species as the length of each species terminal branch (electronic supplementary materials, figure S1). I estimated the evolutionary distinctiveness of each assembly (ED) as the sum of the evolutionary distinctiveness of contributing species, and the unique phylogenetic contribution of each assembly (PC) as the sum of the phylogenetic contributions of species endemic to that assemblage. For ease of interpretation, continental values of ED and PC were scaled so that they represent the proportion of total phylogenetic diversity contained within Carnivora. To quantify the contribution of individual species to the evolutionary distinctiveness and phylogenetic contribution of assemblages, I scaled species contributions by the total evolutionary distinctiveness and phylogenetic contribution within each assemblage. Phylogenetic calculations were conducted using the Tuatara package for the phylogenetic software Mesquite (version 2.74) [31,32].

(b) Measurement of functional diversity, redundancy and functional species contributions

My aim was to measure the functional diversity with regard to predation processes. I therefore compiled data on a set of traits that all relate to predation effects in some way; diet, body size, hunting group size, and area use (Electronic supplementary materials, tables S1 and S2). Although these traits may not directly quantify all functional aspects of predation by large carnivores, the traits were selected because there is quantified trait data for all included species and they all relate to a wide range of predation related ecosystem effects. In addition, since hunting mode may indirectly influence the effects of predators in addition to direct predation effects [33], I also added a palaeomorphological classification of carnivore functional groups [21,34]. Although this classification is based on skeletal morphology, it is closely related to the hunting mode of the respective species [34] and may therefore provide information regarding predation effects caused by antipredatory responses of prey.

I quantified functional diversity and redundancy using dendrograms created from cluster analyses on continental trait matrices [24]. Such dendrograms can be

used as both an index of relative functional diversity and redundancy of species assemblages, as well as to measure individual contribution to functional diversity and redundancy [9,24]. Each continental trait matrix was converted into a distance matrix which was clustered into a corresponding dendrogram. I used Gower's distance method since I had data containing both numerical and categorical variables [35] and the UPGMA (Unweighted Pair-Group Method using Arithmetic averages) clustering method since this method generated the highest cophenetic correlation [36,37]. I followed the usual protocol of standardizing trait matrices so that each trait had a mean of 0 and a standard deviation of 1 before they were used to produce distance matrices. I used the Xtree function contributed by J. Schumacher (http://owenpetchey.staff.shef.ac.uk/Code/Code/calculatingfd_assets/Xtree.r) to transform the output from each cluster analyses into the appropriate species-branch matrices and branch-length vectors [38].

Analogous to calculations of evolutionary distinctiveness and phylogenetic contribution, I calculated the functional diversity contribution of each species as the sum of all contributed branches where each branch were weighted by the number of species sharing it, and unique functional contribution as the length of the terminal branch (Electronic supplementary materials, figure S1). I calculated contribution to functional redundancy as the sum of all branch fractions that was shared with other species (i.e. total branch length – functional diversity, Electronic supplementary materials, figure S1). I calculated the functional diversity of each assemblage FD as the sum of all species' functional diversity values (i.e. the sum of all branches [24]), functional redundancy FR as the sum of all species functional redundancy values (i.e. the sum of all species total branch lengths – their functional diversity values [9]), and functional contribution FC as the sum of the terminal branch length of endemic species (Electronic supplementary materials, figure S1).

To account for the relative amount of space that species occupies in the calculations of their functional contributions to each assemblage, I also calculated functional metrics scaled by the proportional geographic range size for each species. This was done by replacing the binary coding in the species-branch matrices with the proportional range size of each species. The proportional range sizes were based on species distribution polygons from IUCN [26]. Each set of species polygons was first projected according to the EASE-Grid equal area coordinate system [39] and then cropped to be contained within each continental border. Proportional range sizes were calculated as the ratio of the area of all species polygons for a given species within a continent divided by the total land area for that continent. Continental borders were obtained from political country borders available from Blue Marble Geographics (http://www.bluemarblegeo.com/products/worldmapdata.php?). Only species polygons classed as 1 (extant) and 2 (probably extant) where included in the analyses [26].

For ease of interpretation, I scaled FD, FC as well as the geographically scaled values to range between 1 and 0, where 1 was the FD for the global assemblage. With this scaling, the value of each assemblage thus reflects functional diversity in relation to the total functional diversity of large carnivores on earth [37]. I scaled FR to represent the proportion of redundancy for each assemblage in relation to the sum of all individual branch segments. This value therefore represents the proportion of the total ecosystem function within an assemblage that is overlapping among species. Although such overlapping functionality previously was regarded as superfluous, it is now generally regarded as a desirable component of ecosystems since it increases

resilience to environmental perturbations [9]. Within assemblages, I calculated the proportional contribution of species to the functional diversity and redundancy of each specific assemblage, and the proportion of functional diversity that was uniquely contributed by each species. Since the species contributions within assemblages are heavily influenced by species richness (i.e., species in a species poor assemblage will make larger individual contributions than species in a species rich assemblage), I have presented species contributions as the deviation from equal contribution of each species. Both phylogenetic and functional contributions for all species are given in the electronic supplementary materials (table S3).

(c) Statistical analyses

To evaluate if the phylogenetic or functional diversity of continental assemblages deviated from expectations based on random assemblages with the same corresponding species richness, I tested the observed values for each continental assemblage against predictions from distributions of ED, PC, FD and FR values calculated on 10,000 bootstrapped assemblages containing the same number of species as the empirical assemblages. The species for each bootstrapped assemblage were drawn from the global species pool without replacement. The functional (FC) and phylogentic (PC) contributions were calculated on a random number of selected species within each bootstrapped assemblage, to also enable randomization of the number of endemic species within assemblages.

I evaluated the relationships between functional and phylogenetic metrics in carnivore assemblages as well as relationships between species contributions to phylogenetic and functional diversity in respective assemblage using Spearman rank correlations. Since I repeated correlations on raw and geographically scaled functional metrics, as well as on global and continental assemblages, I adjusted the statistical significance of these multiple tests according to the false discovery rate method [40]. I similarly adjusted the significance from the bootstrap analyses to account for simultaneous evaluations across all continents for a single metric. All functional calculations as well as statistical analyses where conducted using the statistical software package R version 2.15.1 for Linux (http://www.r-project.org).

3. Results

(a) Assemblage comparisons

Large carnivores contain 18% of the phylogentic diversity within Carnivora, and uniquely contribute to 11% of this diversity. Scaled by species geographic range sizes, the global carnivore assemblage only retained 23% of its functional diversity (Table 1). Although the total functional redundancy within the global assemblage was high (73%), it was reduced by more than half after geographic scaling (30%). Asia and Africa contain the two most species rich assemblages, the highest number of endemic species, and the highest level of phylogenetic diversity and contribution as well as functional diversity and redundancy (Table 1). Europe had very low phylogenetic and functional contributions caused by its single endemic species (Iberian lynx, *Lynx pardinus*).

Species richness in continental assemblages was positively correlated to both evolutionary distinctiveness ($r_s = 1.00$, p = 0.02) and functional diversity ($r_s = 1.00$, $p_{adj} = 0.03$), but not to phylogenetic contribution ($r_s = 0.60$, p = 0.35) or any of the other functional metrics (FD_{scaled}: $r_s = 0.70$, $p_{adj} = 0.23$; FR: $r_s = 0.87$, $p_{adj} = 0.10$; FR_{scaled}: $r_s = 0.70$, $p_{adj} = 0.35$; FC: $r_s = -0.15$, $p_{adj} = 0.95$; FC_{scaled}: $r_s = 0.10$, $p_{adj} = 0.95$). Evolutionary distinctiveness was positively correlated to functional diversity ($r_s = 1.00$, $p_{adj} = 0.03$), but not to either geographically scaled functional diversity ($r_s = 0.70$, $p_{adj} = 0.23$) or to functional redundancy (FR: $r_s = 0.87$, $p_{adj} = 0.10$; FR_{scaled}: $r_s = 0.70$, $p_{adj} = 0.23$). Similarly, phylogenetic contribution was not correlated to functional contribution (FC: $r_s = 0.41$, $p_{adj} = 0.27$; FC_{scaled}: $r_s = -0.10$, $p_{adj} = 0.95$).

Neither evolutionary distinctiveness (Africa: z=1.57, $p_{adj}=0.23$; Asia: z=0.20, $p_{adj}=0.84$: Europe: z=-1.48, $p_{adj}=0.23$; North America: z=-2.19, $p_{adj}=0.14$, South America: z=-0.25, $p_{adj}=0.84$) nor phylogenetic contribution differed from expectations based on species richness in any of the continental assemblages (Africa: z=1.57, $p_{adj}=0.29$; Asia: z=0.45, $p_{adj}=0.70$: Europe: z=-0.77, $p_{adj}=0.70$; North America: z=-1.63, $p_{adj}=0.29$; South America: z=0.38, $p_{adj}=0.70$).

The African (z = -5.10, $p_{adj} < 0.001$) and Asian (z = -7.05, $p_{adj} < 0.001$) assemblages had lower functional diversity than expected from their species richness, and there was a trend for the European assemblage to have lower than expected functional diversity (z = -2.07, $p_{adj} = 0.06$). The functional diversity in North (z = -1.38, $p_{adj} = 0.21$) and South America (z = -1.12, $p_{adj} = 0.26$) did not differ from random expectations. The Asian assemblage had lower than expected (z = -2.50, $p_{adj} = 0.03$) and the South American assemblage had higher than expected (z = 2.51, $p_{adj} = 0.03$) functional contribution. The functional contribution did not differ from random expectations in either of the other continental assemblages (Africa: z = -1.03, $p_{adj} = 0.38$; Europe: z = -1.03, $p_{adj} = 0.38$; North America: z = 0.08, $p_{adj} = 0.94$), nor did functional redundancy (Africa: z = 1.86, $p_{adj} = 0.31$; Asia: z = -1.29, $p_{adj} = 0.49$: Europe: z = 0.70, $p_{adj} = 0.60$; North America: z = -0.379, $p_{adj} = 0.71$; South America: z = -1.02, $p_{adj} = 0.51$).

(b) Species contributions

Large species generally had large functional contributions. For instance, the lion (*Panthera leo*) provided unique function to the African assemblage and the gray wolf (*Canis lupus*) to the assemblages in Europe and North America (figure 1). The smaller bodied meso-carnivores typically clustered together exhibiting large functional overlap (figure 1).

Within the global assemblage, there were significant negative correlations between species contributions to evolutionary distinctiveness and functional diversity (raw: $r_s = -0.32$, $p_{adj} = 0.04$, geographically scaled: $r_s = -0.33$, $p_{adj} = 0.04$; figure. 2a,b), and there was a trend for a negative correlation between unique species contributions to phylogenetic and functional diversity ($r_s = -0.31$, $p_{adj} = 0.09$; figure. 2e). However, there were no significant correlations between species contributions to evolutionary distinctiveness and functional redundancy (raw: $r_s = 0.23$, $p_{adj} = 0.27$, geographically scaled: $r_s = 0.16$, $p_{adj} = 0.32$, figure 2c,d) nor between unique contributions to phylogenetic and scaled functional diversity ($r_s = -0.20$, $p_{adj} = 0.21$, figure 2f). Within continental assemblages, there were no significant correlations between species contributions to evolutionary distinctiveness and either functional diversity (raw: $r_s = -0.04$, $p_{adj} = 0.76$, geographically scaled: $r_s = -0.05$, $p_{adj} = 0.76$,

figure 3a,b) or functional redundancy (raw: $r_s = 0.08$, $p_{adj} = 0.59$, geographically scaled: $r_s = 0.07$, $p_{adj} = 0.59$, figure 3c,d), nor between unique species contributions to phylogenetic and functional diversity (raw: $r_s = -0.13$, $p_{adj} = 0.40$, geographically scaled: $r_s = -0.11$, $p_{adj} = 0.40$, figure 3e,f).

(c) Relationships between raw and geographically scaled functional diversity

Among assemblages, there were no significant correlations between raw and geographically scaled functional diversity ($r_s = 0.70$, p = 0.23), functional redundancy ($r_s = 0.82$, p = 0.09) or functional contributions ($r_s = 0.67$, p = 0.22). However, within both the global ($r_s = 0.90$, $p_{adj} < 0.001$) and continental ($r_s = 0.73$, $p_{adj} < 0.001$) assemblages, there were positive correlations between species contributions to raw and geographically scaled functional diversity (figure 4a,b). Although there was a positive correlation between species contributions to raw and geographically scaled functional redundancy ($r_s = 0.61$, $p_{adj} < 0.001$) and a trend for a significant positive correlation between unique species contributions to raw and geographically functional diversity ($r_s = 0.33$, $p_{adj} = 0.06$) in the global assemblage, there were no significant correlations within continental assemblages (functional redundancy: $r_s = 0.22$, $p_{adj} = 0.326$, unique functional contribution: $r_s = 0.14$, $r_s = 0.12$, figure 4c-f).

4. Discussion

My results suggest that prioritizing species rich assemblages of large carnivores simultaneously will capture high phylogenetic and functional diversity, as well as functional redundancy and associated resilience [9]. This study thus confirms previous theoretical and empirical studies, which similarly have highlighted a positive relationship between species richness and functional diversity [9, 24, 41]. Dalerum et al. [21] suggested that one global conservation priority should be to protect and reconstruct as functionally complete assemblages as possible. Results from the present study accentuate this recommendation, since species rich assemblages of large carnivores also seem to harbor a large amount of phylogenetic history as well as high functional redundancy. Such redundancy has been closely linked to ecological resilience and may hence aid in buffering ecosystems from the ecological effects of environmental perturbations [42].

Previous studies on bat and avian assemblages have shown lower functional diversity within local assemblages than expected by chance [41, 43]. This study does not uniformly support these results on a continental scale for large carnivores. Petchey et al. [41] suggested that environmental filtering, i.e. local environmental conditions promoting species with similar adaptations to these conditions to co-exist, could potentially cause the lower than expected local functional diversity, and highlighted that their patterns likely occurred within regional scales. Three continental assemblages of large carnivores, including the two most species rich ones (Asia and Africa), showed lower functional diversity than expected by chance, whereas the assemblages in North and South America did not deviate from random expectations. These results indicate that regional processes do not necessarily cause large carnivore species to be more similar than expected by chance, and also suggest that different processes may have shaped the community structure of large carnivores across the

different continents. One possible explanation for the contradictory results among continents could be that the heavy species depletions in North and South America since the Late Pleistocene [21] have diluted their species pool so that species on average have become less similar compared to continents with more intact assemblages, i.e. the species that have gone extinct have been more similar to extant species than expected by chance. Such non-random extinction patterns could for instance have occurred if extinct species were ecologically similar but less competitive than their extant counterparts. There appears to be little deviation from random expectations with regards to phylogenetic diversity distributed across continents, as well as the functional redundancy contained within each continental assemblage.

Although it seems possible to reconcile simultaneous optimization of phylogenetic and functional diversity when prioritizing between carnivore assemblages, the same does not appear to hold for prioritizations between species within assemblages. The analyses do not support that individual species of large carnivores simultaneously provide high contributions to phylogenetic and functional components of diversity. Contrarily, globally there appears to be a direct cost of prioritizing one diversity component over another, indicated by the negative correlation between contributions to phylogenetic and functional diversity. For instance, the two species that provided the largest contribution to evolutionary distinctiveness to the global assemblage, the giant panda (Ailuropoda melanoleuca) and the aardwolf (Proteles cristata) both had low contributions to functional diversity. Similarly, the lion had by far the highest contribution to functional diversity in the global assemblage, but was ranked as a low contributor to both evolutionary distinctiveness and unique phylogenetic contribution. Therefore, conservation decisions prioritizing large carnivore species may face an ecological future discount problem analogous to economic cost-benefit analyses, where contemporary functional benefits have to be weighted against evolutionary potential for maintaining future ecosystem function [44].

Several large species, such as the lion, the grey wolf and the tiger (*Panther tigris*) either had large unique contributions to functional diversity, or clustered together into groups with large contributions. Some of these species are among the most recognized and utilized conservation flagship species in the world [17]. The results from this study provide ecological justification for this attention, and highlight that a conservation focus on large apex predators may have large contemporary ecological benefits. Unfortunately, many of these species are also exceptionally conflict prone, as they are often accused of causing real or perceived financial losses and other types of suffering for local human societies. Management and conservation of these types of species is therefore politically complex [45], a complexity that is accentuated by their possession of biological traits which often lead to elevated local, regional or global extinction risks [19].

The substantial declines in functional diversity and redundancy of assemblages after scaling species contributions by geographic range sizes suggest that habitat alteration and loss is reducing the ecosystem services provided by higher trophic levels [46]. Weak correlations between raw and geographically scaled functional diversity, redundancy and contributions of assemblages further points to a large influence of range contraction on large carnivore ecosystem function across continental scales. Similarly, weak correlations between geographically scaled metrics and species richness and phylogenetic diversity highlight that spatial distribution of

species may be critical for determining how well species richness and phylogenetic diversity capture carnivore ecosystem function across assemblages. However, geographic range sizes did not seem to alter relative species contributions to functional diversity within assemblages.

The results from studies like these are dependent on the reliability of the quantifications of phylogenetic and functional relationships. Although the phylogenetic tree used in this study is over a decade old [22], it is still the most complete phylogeny presented for the extant Carnivora. It was based on consensus information at the time of its publication, and must be regarded as a reliable hypothesis for the phylogenetic relationships among carnivore species. The number and the nature of traits selected to depict functional relationships, as well as the methods used to quantify them, are highly influential on functional diversity [9, 24, 47]. Although dendrogram based measures of functional diversity have been criticized [48], their similarity to phylogenetic analyses provides a congruent framework for simultaneous evaluations of phylogenetic and functional diversity. In addition, if used in a relative context, as has been done in this study, they provide an unbiased quantification of relative functional diversity among assemblages [8].

To conclude, this study suggests that prioritizing species rich assemblages of large carnivores will simultaneously capture high phylogenetic diversity, functional diversity, and functional redundancy. However, a lack of positive correlations between species contributions to phylogenetic and functional diversity components suggests that conservation prioritizations of large carnivore species may face trade-offs between selecting species that will optimize contemporary ecosystem function versus the evolutionary potential for future ecosystem performance. The results provide some ecological justification for large apex carnivores as a focus for conservation action, and moreover suggests that range contraction is a likely cause of diminishing carnivore ecosystem function.

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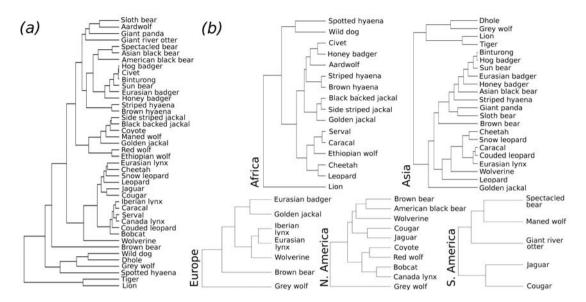


Figure 1. Functional relationships between species in the global (*a*) and the continental (*b*) assemblages of large carnivores (>10kg). The functional dendrograms were constructed from a data matrix of 10 traits related to predation effects.

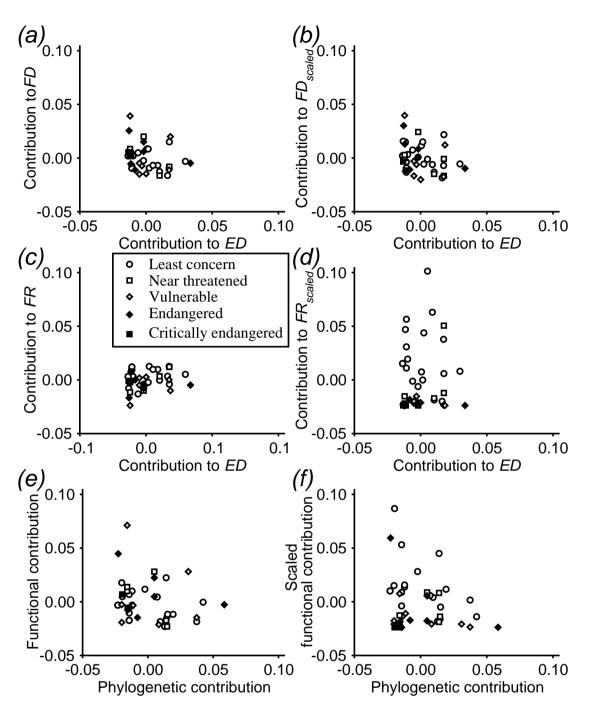


Figure 2. Relationships between contributions of large carnivore species (>10kg) to phylogenetic distinctiveness and functional diversity (raw *a*; geographically scaled *b*), phylogenetic distinctiveness and functional redundancy (raw c; geographically scaled *d*), and unique contributions to phylogenetic and functional diversity (raw *e*; geographically scaled *f*) within the global assemblage. Data represent residual contributions of each species after the value corresponding to equal contribution from all species has been removed. Each species has been is coded by their global IUCN status.

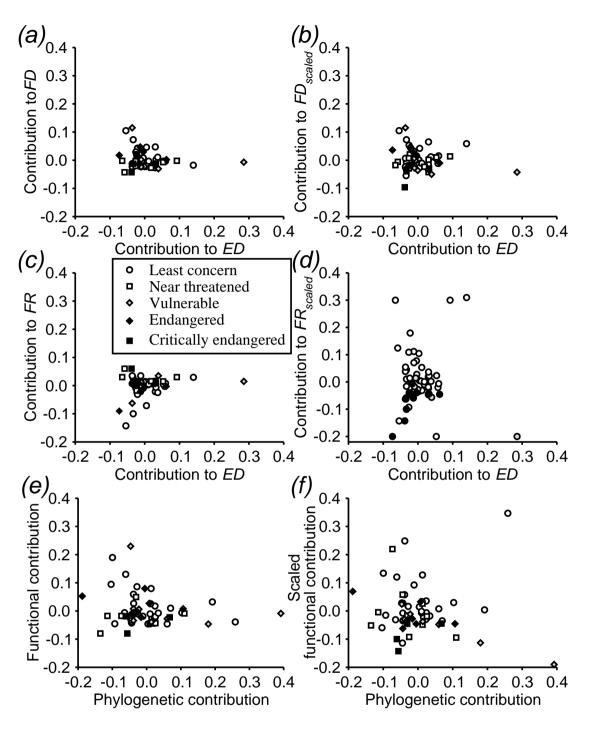


Figure 3. Relationships between contributions of large carnivore species (>10kg) to phylogenetic distinctiveness and functional diversity (raw a; geographically scaled b), phylogenetic distinctiveness and functional redundancy (raw c; geographically scaled d), and unique contributions to phylogenetic and functional diversity (raw e; geographically scaled f) within the continental assemblages. Data represent residual contributions of each species after the value corresponding to equal contribution from all species has been removed. Each species has been is coded by their global IUCN status.

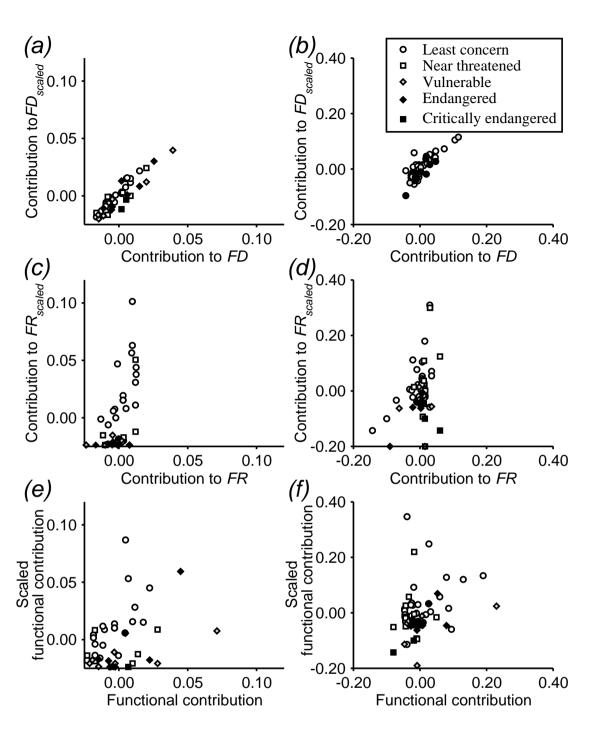


Figure 4. Relationships between the contribution of large carnivore species (>10kg) to raw and geographically scaled functional diversity within the global (a) and continental assemblages (b), to raw and geographically scaled functional redundancy in the global (c) and continental (d) assemblages, and between raw and geographically scaled unique functional contributions to the global (e) and continental (f) assemblages. Data represent residual contributions of each species after the value corresponding to equal contribution from all species within a given assemblage had been removed. Each species has been coded by their continental IUCN status.

Table 1. Evolutionary distinctiveness ED, phylogenetic contribution PC, functional diversity FD, functional redundancy FR and functional contribution FC of assemblages of large carnivores (>10kg). Functional indices are presented both for data not taking geographic distribution of species into account as well as metrics scaled by proportional continental range sizes for each species.

	Total	Endemic				Raw ^b			Scaled ^c			
_	species	species	<i>ED</i> (%) ^a	<i>PC</i> (%) ^a	FD^{d}	FR^{e}	FC^{f}	FD^{d}	FR^{e}	FC^{f}		
Global	43		17.6	11.2	1	0.73		0.23	0.30			
Africa	16	9	7.84	3.38	0.62	0.65	0.20	0.30	0.48	0.09		
Asia	22	10	9.37	2.97	0.70	0.60	0.15	0.24	0.14	0.05		
Europe	7	1	2.12	0.09	0.45	0.42	0.02	0.19	0.11	0		
N. America	10	5	2.81	0.54	0.58	0.42	0.16	0.28	0.22	0.11		
S. America	5	3	1.98	0.96	0.40	0.20	0.20	0.18	0.06	0.07		

- a) Represent % of total phylogenetic diversity within Carnivora
- b) Raw values refer to indices that had not been scaled by geographic range sizes
- c) Scaled values refers to indices that had been scaled by geographic range sizes of individual species
- d) Functional diversity FD was scaled by the global assemblage so that values represent the functional diversity relative to the total functional diversity of large carnivores on earth
- e) Functional redundancy FR was scaled so that values represent redundancy in relationship to the overall diversity in each assemblage
- f) Functional contribution FC was calculated as the unique functional contribution of endemic species within each continental assemblage, scaled by the total functional diversity contained within the global assemblage

Electronic Supplementary Information

Phylogenetic and functional diversity in large carnivore assemblages F. Dalerum

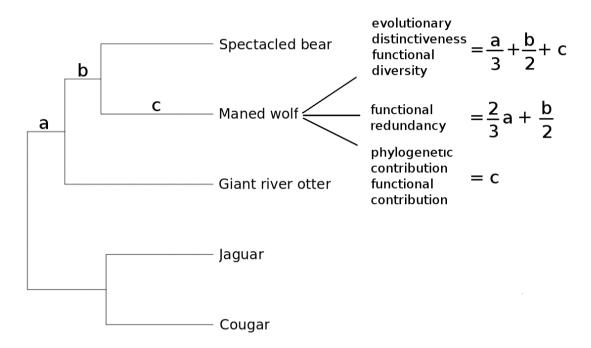


Figure S1: Visualization of calculations of evolutionary distinctiveness, phylogenetic contribution, functional diversity, functional redundancy and unique functional contribution. Although the example uses the functional dendrogram of the South American assemblage, an analogue approach was used on phylogenetic relationships to calculate evolutionary distinctiveness and phylogenetic contribution.

Table S1: Traits used to quantify functional diversity in large carnivore assemblages.

Trait	Explanation
Functional group ^a	Categorical classification of functional groups:
	Scavenger/Omnivore
	Bone-crushing
	Bone-cracking
	Stalk and ambush
	Pursuit
Home range size (km ²)	Average home range size recorded for the species (km ²)
Density (animals/100 km ²)	Average density recorded for the species (animals/100 km ²)
Diet	Categorical classification of main diet:
	Carnivore
	Insectivore
	Piscivore
	Herbivore
	Omnivore
Mean prey size (kg)	Average recorded prey size for the species (kg)
Max prey size (kg)	Maximum recorded prey size for the species (kg)
Min prey size (kg	Minimum recorded prey size for the species (kg)
Hunting group size	Average recorded hunting group size for the species
Body weight (kg)	Average body weight recorded for the species (kg)
Sexual dimorphism	Sexual dimorphism in body weight recorded for the species
Male:Female	(ratio of male to female)
Geographic range size ^b	Geographic range size (km ²) calculated from species presence polygons classed as 1 (extant) and 2 (probably
	extant) by the IUCN (2011).
Proportional range size ^b	Geographic range size divided by the total land area of
	respective continent (or for the global assembly the
	combined land area for the continents containing large
	carnivores).

a) Functional groups defined from Werdelin, L. in *Carnivore Behavior, Ecology and Evolution Volume 2*, J. L. Gittleman Ed. (Cornell Univ. Press, 1996), pp. 582-624.

b) Not included as a functional trait, but used to scale functional contributions within each assemblage.

Table S2: Functional traits for carnivore species > 10kg used to create functional diversity metrics.

Scientific name	Functional group*	Home range size	Density	Diet	Max prey size	Min prey size	Mean prey size	Hunting group size	Body weight	Sexual dimorph. M:F	Source
Canidae											
Canis adustus	P	10	100	Omn.	5	0.01	0.1	1	9	1.1	Atkinson et al. 2002 J Zool 257: 129-139
											Atkinson and Loveridge 2004. Pp 152-156 in Sillero-Zubiri et al. Canids: foxes, wolves, jackals and dogs Status survey and conservation action plan (IUCN/SSC Canid specialist group, Gland)
Canis aureus	P	1.5	200	Omn.	40	0.01	0.2	2.5	8	1.2	Loveridge and Macdonald 2002 J Zool 259: 143-153
											Jhala and Moehlman 2004. Pp 156-161 in Sillero-Zubiri et al. Canids: foxes, wolves, jackals and dogs Status survey and conservation action plan (IUCN/SSC Canid specialist group, Gland)
Canis	P	30	71	Omn.	50	0.1	5	3	12.8	1.2	Diniz-Fihlo and Torres 2002. Evol Ecol 16: 351-367
latrans Canis lupus	BCu	1000	1.7	Omn.	500	1	150	7	45	1.4	Mech 1974 Mamm Spec 37: 1-6
											Large Carnivore Initiative for Europe 2004. Status and trends for large carnivores in Europe (UNEP World Conservation Monitoring Centre, Cambridge) Mech and Boitani 2004. Pp 124-128 in Sillero-Zubiri et al. Canids: foxes, wolves, jackals and dogs Status survey and conservation action plan (IUCN/SSC Canid specialist group, Gland)
Canis mesomelas	P	8	40	Omn.	40	0.01	1	2	8.5	1.1	Loveridge and Nel 2004. Pp 161-166 in Sillero-Zubiri et al. Canids: foxes, wolves, jackals and dogs Status survey and conservation action plan (IUCN/SSC Canid specialist group,
Canis rufus	P	8	2.5	Carn.	50	0.1	10	3	26.4	1.2	Gland) Kelly et al. 2004. Pp 87-92 in Sillero-Zubiri et al. Canids: foxes, wolves, jackals and dogs Status survey and conservation action

											plan (IUCN/SSC Canid specialist group, Gland)
											Hinton et al., 2010 J Wildl Manage 74: 55-58
Canis simensis	P	10	15	Carn.	5	0.1	0.2	1	14.5	1.2	Sillero-Zubiri and Macdonald 1997. The Ethiopian wolf Status survey and conservation action plan (IUCN/SSC Canid Specialist group, Gland)
Chrysocyon brachyurus	P	50	4	Omn.	5	0.1	0.5	1	23.7	1	Marino and Sillero-Zubiri 2011. Canis simensis (IUCN 2012. IUCN Red List of Threatened Species. Version 2012.2. www.iucnredlist.org)
Cuon alpinus	BCu	50	10	Carn.	175	1	40	7	15	1.5	Diniz-Fihlo and Torres 2002. Evol Ecol 16: 351-367
Lyacon pictus	BCu	600	2	Carn.	250	3	50	10	25	1	Durbin et al. 2008. Cuon alpinus (IUCN 2012. IUCN Red List of Threatened Species. Version 2012.2. www.iucnredlist.org)
											Woodroffe et al. 1997 The African wild dog - status survey and conservation action plan (IUCN/SSC Canid specialist group, Gland) Creel and Creel 2002, The African wild dog: behavior, ecology, and conservation (Princeton University Press, Princeton) Sinclair et al 2003 Nature 425: 288-290
											Woodroffe et al. 2007. J Mamm 188: 181-193
											Woodroffe and Sillero-Zubiri 2012. <i>Lyacon pictus</i> (IUCN 2012. IUCN Red List of Threatened Species. Version 2012.2. www.iucnredlist.org)
Mustelidae											
Arctonyx collaris	SO	10	10	Omn.	10	0.001	0.1	1	11	1	Macdonald 2009. The Encyclopedia of mammals (Oxford University Press, Oxford)
Gulo gulo	SO	500	0.5	Carn.	100	0.1	10	1	13	1.4	Landa et al. 2000. Action plan for the conservation of wolverines (<i>Gulo gulo</i>) in Europe (Nature and environment, No. 115, Council of Europe Publishing, Strasbourg)
Meles meles	SO	5	50	Omn.	10	0.001	0.1	1	11	1.2	Macdonald 2009. The Encyclopedia of mammals (Oxford University Press, Oxford)
Mellivora capensis	SO	300	10	Omn.	1	0.01	0.1	2	9	1.3	Beggs et al 2003 J Zool 269: 301-316

Pteronura	SO	12	15	Pisc.	10	0.1	1	5	26.5	1.2	Vanderhaar and Ten Hwang 2003. Mamm Spec 721: 1-8 Beggs et al 2005 J Zool 265: 23-35 Duplaix et al. 2008. <i>Pteronura brasiliensis</i> (IUCN 2012. IUCN
brasiliensis	2.5				- 0						Red List of Threatened Species. Version 2012.2. www.iucnredlist.org)
Ursidae											
Ailuropoda melanoleuca	SO	5	10	Herb.	0	0	0		95	1.2	Schaller et al. 1985. The Giant Pandas of Wolong (Univ. Chicago Press, Chicago)
Tremarctos ornatus	SO	100	5	Omn.	50	0.1	10	1	110	1.7	Peyton 1999. Pp 157-198 in Servheen and Peyton Bears status survey and conservation action plan (IUCN/SSC Bear specialist group, Gland) Diniz-Fihlo and Torres 2002. Evol Ecol 16: 351-367
											Rioz-Uzeda 2007. Ursus 18: 124-128
Ursus arctos	SO	400	5	Omn.	600	0.1	50	1	175	1.5	Pasitschnias-Arts 1993. Mamm Spec 439: 1-10
											Zedrosser et al. 2001. Ursus 12: 9-10
Ursus malayanus	SO	15	6	Omn.	1	0.001	0.01	1	55	1	Servheen 1999. Pp 219-224 in Servheen and Peyton Bears status survey and conservation action plan (IUCN/SSC Bear specialist group, Gland)
Ursus tibethanus	SO	100	1	Omn.	50	0.01	10	1	110	1.4	Grashelis and Steinmetz 2008. <i>Ursus thibetanus</i> (IUCN 2012. IUCN Red List of Threatened Species. Version 2012.2. www.iucnredlist.org) Hwang et al. 2010 Ursus 21: 81-96
Ursus ursinus	SO	12	27	Ins.	0.01	0.001	0.001	1	92.5	1.4	Garshelis et al. 1999. Pp 225-240 in Servheen and Peyton Bears status survey and conservation action plan (IUCN/SSC Bear specialist group, Gland) Garshelis et al. 2008. <i>Melursus ursinus</i> (IUCN 2012. IUCN Red List of Threatened Species. Version 2012.2. www.iucnredlist.org)
Usrus americanus	SO	175	20	Omn.	400	0.1	20	1	77.5	1.3	Lariviere 2001. Mamm Spec 647: 1-11 Diniz-Fihlo and Torres 2002. Evol Ecol 16: 351-367

Felidae											
Acinonyx jubatus	SA	300	0.5	Carn.	200	1	40	1	40	1.1	Krausman and Morales 2005. Mamm Spec 771: 1-6
Felis caracal	SA	10	10	Carn.	30	0.1	1	1	11.5	1.3	Durant et al. 2008. <i>Acinonyx jybatus</i> . (IUCN 2012. IUCN Red List of Threatened Species. Version 2012.2. www.iucnredlist.org) Nowell and Jackson 1996. Wild cats Status suvey and conservation action plan (IUCN/SSC Cat specialist group, Gland)
Felis concolor	SA	300	1	Carn.	400	0.1	40	1	46	1.5	Skinner and Chimimba 2005. Mammals of the southern African subregion (Cambridge Univ. Press, Cambridge) Nowell and Jackson 1996. Wild cats Status suvey and conservation action plan (IUCN/SSC Cat specialist group, Gland) Diniz-Fihlo and Torres 2002. Evol Ecol 16: 351-367
Felis serval	SA	12.5	40	Carn.	1	0.1	0.1	1	11	1.2	Caso et al. 2008. <i>Puma concolor</i> (IUCN 2012. IUCN Red List of Threatened Species. Version 2012.2. www.iucnredlist.org) Nowell and Jackson 1996. Wild cats Status suvey and conservation action plan (IUCN/SSC Cat specialist group, Gland)
Lynx canadensis	SA	30	20	Carn.	10	0.1	1.5	1	10	1.2	Skinner and Chimimba 2005. Mammals of the southern African subregion (Cambridge Univ. Press, Cambridge) Nowell and Jackson 1996. Wild cats Status suvey and conservation action plan (IUCN/SSC Cat specialist group, Gland) Diniz-Fihlo and Torres 2002. Evol Ecol 16: 351-367
Lynx lynx	SA	200	1	Carn.	100	0.1	20	1	20	1.2	Nowell and Jackson 1996. Wild cats Status suvey and conservation action plan (IUCN/SSC Cat specialist group, Gland) von Arx et al. 2001. Status and conservation of the Eurasian lynx (<i>Lynx lynx</i>) in Europe in 2001 (KORA Bericht No. 19, Muri)
Lynx pardinus	SA	15	16	Carn.	5	0.1	1.5	1	11	1.4	Nowell and Jackson 1996. Wild cats Status suvey and conservation action plan (IUCN/SSC Cat specialist group, Gland)
Lynx rufus	SA	100	60	Carn.	40	0.1	1	1	11	1.4	Nowell and Jackson 1996. Wild cats Status suvey and conservation action plan (IUCN/SSC Cat specialist group, Gland) Diniz-Fihlo and Torres 2002. Evol Ecol 16: 351-367
Neofelis nebulosa	SA	35	10	Carn.	80	1	10	1	15	1.3	Nowell and Jackson 1996. Wild cats Status suvey and conservation action plan (IUCN/SSC Cat specialist group, Gland) Sanderson et al. 2008. <i>Neofelis nebulosa</i> (IUCN 2012. IUCN Red List of Threatened Species. Version 2012.2. www.iucnredlist.org)

Pamthera tionis	SA	500	5	Carn.	800	20	150	1	135	1.6	Mazak 1981. Mamm Spec 152: 1-8
tigris Pantera leo	SA	1000	10	Carn.	500	5	150	3	150	1.5	Nowell and Jackson 1996. Wild cats Status suvey and conservation action plan (IUCN/SSC Cat specialist group, Gland) Nowell and Jackson 1996. Wild cats Status suvey and conservation action plan (IUCN/SSC Cat specialist group, Gland) IUCN 2012. Panthera leo (IUCN 2012. IUCN Red List of
Panthera onca	SA	50	3	Carn.	400	1	40	1	70	1.3	Threatened Species. Version 2012.2. www.iucnredlist.org) Nowell and Jackson 1996. Wild cats Status suvey and conservation action plan (IUCN/SSC Cat specialist group, Gland) Diniz-Fihlo and Torres 2002. Evol Ecol 16: 351-367
Panthera pardus	SA	1000	10	Carn.	1	100	20	1	60	1.3	Nowell and Jackson 1996. Wild cats Status suvey and conservation action plan (IUCN/SSC Cat specialist group, Gland)
Panthera uncia	SA	50	3	Carn.	150	5	30	1	45	1.2	Nowell and Jackson 1996. Wild cats Status suvey and conservation action plan (IUCN/SSC Cat specialist group, Gland)
Hyaenidae											
Crocuta crucuta	BCa	500	35	Carn.	500	0.1	40	15	55	0.85	Hofer 1998. Pp 29-38 in Mills and Hofer Hyaenas Status survey and conservation action plan (IUCN/SSC Hyaena specialist group, Gland) Cooper et al. 1999 Afr J Ecol 37: 149-160
Hyaena	BCa	300	2	Omn.	10	0.1	0.5	1	40	1	Mills 1982. Mamm Spec 194: 1-5
brunnea Hyaena hyaena	BCa	70	2	Omn.	50	0.1	10	1	30	1	Mills 1998. Pp 26-29 in Mills and Hofer Hyaenas Status survey and conservation action plan (IUCN/SSC Hyaena specialist group, Gland)
Proteles cristatus	SO	3	50	Ins.	0.01	0.001	0.001	1	10	1	Rieger 1981. Mamm Spec 150: 1-5

Hofer 1998. Pp 21-26 in Mills and Hofer Hyaenas Status survey and conservation action plan (IUCN/SSC Hyaena specialist group, Gland)

Viverridae											
Civettictis	SO	10	10	Omn.	1	0.001	0.1	1	12	1	Ray 1995 Mamm Spec 488: 1-7
civetta Arctictis	SO	6	15	Omn.	1	0.01	0.1	1	12	1	Widmann et al. 2008. Arctictis binturong (IUCN 2012. IUCN Red
binturong											List of Threatened Species. Version 2012.2. www.iucnredlist.org)

Table S3: Species contributions to evolutionary distinctiveness (ED), phylogenetic contribution (PC), functional diversity (FD), functional redundancy (FR), and unique functional contribution (FC), as well as functional metrics scaled for proportional geographic range sizes. Data represent residual contributions of each species after the value corresponding to equal contribution from all species has been removed. The reported IUCN threat categories refer to regional assessments for respective continent.

			ic			Raw			Scaled	
	Caiantifia	IUCN	Endemic		 					
Assemblage	Scientific name	Ĕ	$\overset{ ext{H}}{ ext{H}}$ $ ext{ED}$	PC	FD	FR	FC	FD	FR	FC
GLOBAL	Canidae									
	Canis	LC	-0.011	-0.014	-0.010	0.012	-0.017	-0.009	0.031	-0.004
	adustus Canis	LC	-0.011	-0.014	-0.007	0.009	-0.010	-0.004	0.056	0.009
	aureus	LC	-0.011	-0.014	-0.007	0.009	-0.010	-0.004	0.030	0.009
	Canis latrans	LC	-0.011	-0.014	0.005	-0.001	0.007	0.015	0.047	0.053
	Canis lupus	LC	-0.013	-0.020	0.006	-0.008	0.005	0.016	-0.023	0.087
	Canis mesomelas	LC	-0.011	-0.014	-0.010	0.012	-0.017	-0.013	0.011	-0.014
	Canis rufus	CE	-0.013	-0.020	0.005	-0.001	0.007	-0.003	-0.024	-0.024
	Canis simensis	EN	-0.011	-0.014	-0.005	0.008	-0.006	-0.012	-0.024	-0.024
	Chrysocyon brachyurus	NT	-0.002	0.005	0.020	-0.010	0.028	0.024	-0.024	0.009
	Cuon alpinus	EN	-0.002	0.005	0.006	-0.008	0.005	0.001	-0.023	0.006
	Lyacon pictus	EN	-0.002	0.005	0.015	-0.004	0.022	0.008	-0.021	-0.018
	Mustelidae									
	Arctonyx collaris	NT	0.010	0.015	-0.016	0.003	-0.023	-0.015	-0.017	-0.014
	Gulo gulo	LC	-0.002	0.007	-0.002	-0.008	0.004	0.001	-0.006	0.006
	Meles meles	LC	0.010	0.015	-0.013	0.000	-0.014	-0.013	-0.019	-0.016
	Mellivora capensis	LC	0.005	0.019	-0.007	0.010	-0.012	-0.001	0.101	0.012
	Pteronura brasiliensis	EN	-0.013	-0.023	0.025	-0.017	0.045	0.030	-0.024	0.059
	Ursidae									
	Ailuropoda melanoleuca	EN	0.034	0.059	-0.005	-0.005	-0.003	-0.010	-0.024	-0.024
	Tremarctos ornatus	VU	0.018	0.031	0.020	-0.010	0.028	0.012	-0.024	-0.021
	Ursus americanus	LC	0.001	-0.002	0.008	-0.003	0.012	0.012	0.007	0.028
	Ursus arctos	LC	-0.006	-0.020	0.005	-0.013	0.018	0.007	-0.001	0.015
	Ursus malayanus	VU	-0.005	-0.020	-0.015	0.002	-0.019	-0.017	-0.020	-0.018
	Ursus tibethanus	VU	-0.003	-0.011	-0.007	-0.005	-0.003	-0.006	-0.015	-0.011
	Ursus ursinus	VU	-0.005	-0.020	-0.005	-0.005	-0.003	-0.003	-0.022	-0.021

	Felidae										
	Acinonyx jubatus	VU		0.017	0.037	-0.011	0.000	-0.015	-0.017	-0.024	-0.024
	Felis caracal	LC		0.002	0.009	-0.009	0.013	-0.018	-0.006	0.044	0.004
	Felis concolor	LC		0.002	-0.012	0.008	-0.002	0.010	0.015	0.000	0.016
	Felis serval	LC		0.017	0.037	-0.009	0.013	-0.018	-0.007	0.038	0.002
	Lynx canadensis	LC		-0.014	-0.023	0.002	0.003	-0.003	0.002	0.015	0.010
	Lynx lynx	LC		-0.014	-0.023	0.002	0.003	-0.003	0.002	0.015	0.010
	Lynx rufus	LC		-0.010	-0.012	0.002	0.003	-0.003	0.003	0.019	0.014
	Lynx pardinus	CE		-0.011	-0.016	0.002	0.008	-0.006	-0.012	-0.024	-0.024
	Neofelis nebulosa	VU		0.000	0.008	-0.015	0.003	-0.021	-0.020	-0.021	-0.021
	Panthera leo	VU		-0.012	-0.016	0.039	-0.024	0.071	0.040	-0.024	0.008
	Panthera onca	NT		-0.012	-0.016	0.008	-0.002	0.010	0.000	-0.022	-0.021
	Panthera pardus	NT		-0.012	-0.016	0.003	-0.012	0.014	0.003	-0.015	-0.013
	Panthera tigris	EN		-0.012	-0.016	0.002	-0.003	-0.007	0.013	-0.023	-0.019
	Panthera uncia	EN		-0.008	-0.008	-0.011	0.000	-0.015	-0.011	-0.018	-0.017
	Hyaenide										
	Crocuta crucutta	LC		0.018	0.014	0.015	-0.004	0.022	0.022	0.006	0.045
	Hyaena brunnea	NT		0.018	0.014	-0.008	0.012	-0.017	-0.017	-0.012	-0.019
	Hyaena hyaena	NT		0.018	0.014	-0.008	0.012	-0.017	-0.001	0.051	0.008
	Proteles cristata	LC		0.030	0.042	-0.003	0.005	0.000	-0.006	0.008	-0.014
	Viverridae										
	Arctictis binturong	LC		0.016	0.013	-0.016	0.003	-0.023	-0.018	-0.020	-0.018
	Civettictis civetta	LC		0.009	0.015	-0.007	0.010	-0.012	-0.006	0.063	-0.005
AFRICA	Canidae Canis	LC	Y	-0.033	-0.044	-0.022	0.012	-0.042	-0.022	0.010	-0.008
	adustus Canis	LC	N	-0.033	-0.044	-0.016	0.006	-0.021	-0.006	0.045	0.028
	aureus Canis mesomelas	LC	Y	-0.033	-0.044	-0.022	0.012	-0.042	-0.033	-0.016	-0.035
	Canis simensis	EN	Y	-0.035	-0.044	-0.010	0.002	-0.009	-0.030	-0.062	-0.062
	Lyacon pictus	EN	Y	-0.013	-0.005	0.047	-0.022	0.080	0.027	-0.059	-0.046
	Mustelidae Mellivora capensis	LC	N	0.003	0.024	-0.015	0.007	-0.025	0.001	0.104	0.036

	Felidae										
	Acinonyx jubatus	VU	N	0.030	0.060	-0.012	0.007	-0.028	-0.033	-0.045	-0.048
	Felis caracal	LC	N	-0.004	0.004	-0.022	0.013	-0.046	-0.012	0.028	0.015
	Pantera leo	VU	N	-0.036	-0.047	0.115	-0.063	0.230	0.115	-0.063	0.024
	Panthera pardus	LC	N	-0.036	-0.047	-0.012	0.007	-0.028	0.007	0.038	0.028
	Felis serval	LC	Y	0.030	0.060	-0.022	0.013	-0.046	-0.015	0.020	0.008
	Hyaenidae										
	Crocuta crucutta	LC	Y	0.030	0.013	0.047	-0.022	0.080	0.065	-0.023	0.128
	Hyaena brunnea	NT	Y	0.030	0.013	-0.018	0.012	-0.043	-0.042	-0.047	-0.049
	Hyaena hyaena	NT	N	0.030	0.013	-0.018	0.012	-0.043	0.002	0.037	0.026
	Proteles cristata	LC	Y	0.058	0.070	-0.004	-0.003	0.010	-0.011	-0.020	-0.035
	Viverridae										
	Civettictis civetta	LC	Y	0.011	0.015	-0.015	0.007	-0.025	-0.013	0.053	-0.010
ASIA	Canidae										
	Canis aureus	LC	N	-0.021	-0.028	0.043	-0.031	0.086	0.044	0.006	0.016
	Canis lupus	LC	N	-0.025	-0.038	0.029	-0.010	0.027	0.053	-0.040	0.249
	Cuon alpinus	EN	Y	-0.004	0.008	0.029	-0.010	0.027	0.016	-0.040	0.033
	Mustelidae										
	Arctonyx collaris	NT	Y	0.018	0.026	-0.027	0.016	-0.043	-0.023	0.001	-0.019
	Gulo gulo	LC	N	-0.004	0.012	0.008	-0.009	0.026	0.016	0.077	0.033
	Meles meles	LC	N	0.018	0.026	-0.017	0.007	-0.020	-0.019	-0.009	-0.025
	Mellivora capensis	LC	N	0.009	0.034	-0.011	0.003	-0.008	-0.010	0.003	-0.018
	Ursidae										
	Ailuropoda melanoleuca	EN	Y	0.062	0.107	0.002	-0.003	0.008	-0.010	-0.045	-0.045
	Ursus arctos	LC	N	-0.012	-0.038	0.026	-0.021	0.059	0.032	0.112	0.058
	Ursus malayanus	VU	Y	-0.010	-0.038	-0.024	0.012	-0.034	-0.028	-0.017	-0.029
	Ursus tibethanus	VU	Y	-0.007	-0.022	-0.004	-0.002	0.006	-0.001	0.014	-0.011
	Ursus ursinus	VU	Y	-0.010	-0.038	0.002	-0.003	0.008	0.007	-0.031	-0.037
	Felidae										
	Acinonyx jubatus	CE	N	0.032	0.068	-0.014	0.008	-0.023	-0.030	-0.044	-0.045
	Felis caracal	LC	N	0.004	0.016	-0.022	0.014	-0.039	-0.027	0.006	-0.022
	Lynx lynx	NT	N	-0.026	-0.044	-0.021	0.012	-0.033	0.008	0.109	0.058
	Neofelis nebulosa	VU	Y	-0.001	0.014	-0.022	0.014	-0.039	-0.036	-0.027	-0.037
	Panthera leo	CE	N	-0.023	-0.031	0.019	0.002	-0.004	-0.018	-0.045	-0.045

	Panthera pardus	NT	N	-0.023	-0.031	0.021	-0.018	0.049	0.021	0.014	-0.016
	Panthera tigris	EN	Y	-0.023	-0.030	0.019	0.002	-0.004	0.046	-0.040	-0.031
	Panthera uncia	EN	Y	-0.016	-0.016	-0.014	0.008	-0.023	-0.013	-0.006	-0.028
	Hyaenide Hyaena hyaena	LC	N	0.032	0.024	0.002	-0.006	0.018	0.005	0.023	-0.006
	Viverridae Arctictis binturong	LC	Y	0.030	0.022	-0.027	0.016	-0.043	-0.032	-0.019	-0.030
EUROPE	Canidae Canis aureus	LC	N	-0.034	-0.044	-0.018	0.029	-0.039	-0.055	-0.058	-0.114
	Canis lupus	LC	N	-0.054	-0.100	0.105	-0.143	0.190	0.105	-0.143	0.134
	Mustelidae Gulo gulo Meles meles	VU LC	N N	0.039 0.140	0.180 0.259	-0.030 -0.018	0.035 0.029	-0.046 -0.039	-0.050 0.059	-0.056 0.310	-0.113 0.347
	Ursidae Ursus arctos	LC	N	0.005	-0.103	0.046	-0.071	0.095	0.042	-0.034	-0.059
	Felidae Lynx lynx Lynx pardinus	NT CE	N Y	-0.058 -0.038	-0.135 -0.056	-0.043 -0.043	0.060 0.060	-0.080 -0.080	-0.006 -0.096	0.124 -0.143	-0.051 -0.143
NORTH AMERICA	Canidae										
	Canis latrans	LC	Y	-0.022	-0.011	-0.013	0.015	-0.019	0.015	0.179	0.092
	Canis lupus Canis rufus	LC CE	N Y	-0.033 -0.033	-0.061 -0.061	0.073 -0.013	-0.100 0.015	0.130 -0.019	0.073 -0.039	-0.100 -0.100	0.120 -0.100
	Mustelidae Gulo gulo	LC	N	0.038	0.192	0.011	-0.025	0.032	0.012	0.002	0.004
	Ursidae	T. C.	X 7	0.054	0.102	0.002	0.005	0.006	0.005	0.022	0.020
	Usrus americanus	LC	Y	0.054	0.103	-0.003	0.005	-0.006	0.005	0.023	0.030
	Ursus arctos	LC	N	0.012	-0.064	-0.003	0.005	-0.006	-0.011	-0.031	-0.031
	Felidae Felis concolor	LC	N	0.060	0.010	-0.003	0.008	-0.011	0.016	-0.006	-0.001
	Lynx canadensis	LC	Y	-0.036	-0.093	-0.023	0.035	-0.045	-0.023	0.054	-0.015
	Lynx rufus Panthera onca	LC NT	Y N	-0.012 -0.026	0.010 -0.025	-0.023 -0.003	0.035 0.008	-0.045 -0.011	-0.019 -0.029	0.071 -0.093	-0.006 -0.092

SOUTH
AMERICA

IERICA	Canidae Chrysocyon brachyurus	NT	Y	0.053	0.110	-0.007	0.015	-0.009	0.010	-0.200	-0.095
	Mustelidae Pteronura brasiliensis	EN	Y	-0.073	-0.188	0.018	-0.090	0.053	0.036	-0.200	0.069
	Ursidae Tremarctos ornatus	VU	Y	0.285	0.392	-0.007	0.015	-0.009	-0.043	-0.200	-0.190
	Felidae <i>Felis concolor</i>	NT	N	0.092	-0.073	-0.002	0.030	-0.018	0.014	0.300	0.220
	Panthera onca	NT	N	-0.065	-0.114	-0.002	0.030	-0.018	-0.018	0.300	-0.004