1	Molecular dietary analysis of two sympatric felids in the Mountains of Southwest
2	China biodiversity hotspot and conservation implications
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Comparison of the PCR amplification of seven DNA extractions of Asiatic golden cat 11 faecal samples with 12SV5 primers without (on the left) and with (on the right) the 12 blocking oligonulceotide PrioB. PCR products were cloned into a sequencing vector 13 14 and five independent clones were sequenced for each PCR. Each horizontal bar represents the sequencing results of a faecal DNA sample, and the different colours 15 represent the proportions of clones containing the sequences of the predator or prey 16 items in the sample. 17





22 Sequence alignment of the PrioB blocking oligonucleotide with sequences of the

- 23 leopard cat and Asiatic golden cat and representative vertebrate species commonly
- 24 occurring in the study area (pika: *Ochotona curzoniae*; rodents: *Niviventer*
- 25 confucianus, Apodemus draco and Rhizomys sinensis; shrew: Episoriculus macrurus;
- 26 primate: *Rhinopithecus roxellana*; ungulates: *Sus scrofa*, *Budorcas taxicolor* and
- 27 Elaphodus cephalophus; birds: Garrulax ocellatus and Tragopan temminckii). Dots (.)
- indicate identical nucleotides as PrioB; dashes (–) indicate gaps in the sequence
- 29 compared to PrioB.
- 30

Species	Accession no.	Sequences (5'-3')
PrioB		CTATGCTTAGCCCTAAACTTAGATAGTTAATTTTAACAAAACTATC
Prionailurus bengalensis	JN392459.1	
Catopuma temminckii	KR132594.1	CA
Ochotona curzoniae	KM225729.1	CACCACAT
Niviventer confucianus	KJ152220.1	
Apodemus draco	HQ333255.1	T
Rhizomys sinensis	AF326254.1	GCAGACTCT
Episoriculus macrurus	GU981048.1	CCAGAATC.
Rhinopithecus roxellana	JQ821835.1	T
Sus scrofa	KM275217.1	CCACA.AT
Budorcas taxicolor	FJ006534.1	G-CAAAG.TT
Elaphodus cephalophus	AY184436.1	CTAC.AAT-CA.ATT
Garrulax ocellatus	AF484898.1	C.GTC.TGC.CG-A.CCGG.GC
Tragopan temminckii	FJ752427.1	C

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34 The equations for calculating dietary parameters.

Dietary specialisation was estimated by the standardised Levins' measure of 35 niche breadth $(B_A)^1$ at the taxon level: 36 $B = \frac{1}{\sum p_i^2}$ 37 (1)Standardised as: $B_A = \frac{B-1}{n-1}$ (2) 38 where *B* is Levins' measure of niche breadth², p_i is the percent frequency of 39 occurrence of the *i*th food resource (i.e. $%TX_i$) and *n* is the total number of resources 40 in the diet. 41 Dietary diversity was also measured by Shannon's diversity index (H) at the 42 taxon level: 43 $H = -\sum p_i Ln(p_i)$ 44 (3) Evenness of diet was estimated with Peilou's *J* at the taxon level: 45 $J = \frac{H}{\ln(n)}$ (4) 46

We used Pianka's measure of niche overlap³ to estimate dietary overlap between
spring (March–May) and autumn (September–November) for the LPC diet at the
taxon level:

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$$O_{jk} = \frac{\sum_{i}^{n} p_{ij} p_{ik}}{\sqrt{\sum_{i}^{n} p_{ij}^{2} \sum_{i}^{n} p_{ik}^{2}}}$$
(5)

where
$$O_{jk}$$
 is Pianka's measure of niche overlap between species *j* and *k*, p_{ij} is the
proportion of the *i*th resource of the total resources used by species *j* (i.e. %TX_{ij}), p_{ik}
is the proportion of the *i*th resource of the total resources used by species *k* (i.e. %TX_{ik})
and *n* is the total number of resource states (i.e. total number of prey taxa). We used

- the software EcoSim version 7.72 (http://www.garyentsminger.com/ecosim/) to test
- whether niche overlap was greater than expected by chance by generating 10,000
- 57 simulated matrices of a randomised diet composition.
- 58
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60 **References**

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- Altitudinal variations in diet composition by the prey orders identified in the leopard
- cat diet in northern Sichuan, China. < 1,500 m: n = 15; 1,500–2,000 m: n = 32;
- 73 2,000–2,500 m: n = 31; > 2,500 m: n = 13. Diet composition is presented as a percent
- 74 frequency of occurrence (%FC).



