

Dhendup et al. 2026. Pallas’s cats recorded in Bhutan after a decade. *Cat News* 85, 13–15. Supporting Online Material.

**Table T1. Recent records of the Pallas’s cat from the Himalayas and the trans-Himalayan region of India and Nepal.**

Country	Year	No. of locations	Evidence type	Place name with elevation	Area	Source
Bhutan	2012	2	Camera trap image	Marangbu (4,982 m) Boera (3,635 m)	Wangchuck Centennial National Park	WCNP 2016
		1	Camera trap image	Mentsiphu (4,122 m)	Jigme Dorji National Park	Thinley 2013
Nepal	2014	2	Camera trap image	Thorkya (4,200 m) Angumila Lapche (4,650 m)	Annapurna Conservation Area	Shrestha et al. 2014
	2014-15	6	Camera trap image	Tangtisa (3,988 m) Kyarken (4,340 m) Pripche (4,590 m)	Annapurna Conservation Area	Regmi et al. 2020
	2016	1		Scat DNA	Upper Dolpa (5,593 m)	
India	2007	1	Sighting/photograph	Tso Plateau (5,073 m)	Sikkim	Chanchani 2008
	2015	2	Sighting/photograph	Hanle (4,202 m)	Ladakh	Mahar et al. 2017
	2019	1	Camera trap image	Nelang Valley (4,800 m)	Gangotri National Park, Uttarakhand	Pal et al. 2019
	2022	1	Sighting/photograph	Hanle (4,300 m)	Ladakh	Maheshwari et al. 2023
	2024	3	Camera trap image	Hangrang Valley (3,900–4100 m) Staklung (4,160 m)	Himachal Pradesh	Sharma et al. 2024

**Table T2. Details of Pallas's cat records from the nationwide snow leopard survey 2022–23, and the Pallas's cat survey 2022–23 (\* = nearby location, CT = Camera traps, JDNP = Jigme Dorji National Park, WCNP = Wangchuck Centennial National Park).**

Area	Location coordinates	Elevation in metres	Dates of record	Evidence type
JDNP	27.799584, 89.330710	4'914	16/8/2022, 17/11/2022, 28/11/2022	CT
JDNP	27.798779, 89.330990	4'899	17.11.2022	CT
JDNP	27.792090, 89.335900	4'653	17.11.2022	CT
JDNP	27.801530, 89.330710	4'963	21.02.2023	CT
JDNP*	27.814300, 89.343320	4'484	6/11/2022, 3/12/2022, 4/12/2022	CT
JDNP	27.690505, 89.382545	4'800	NA	Scat DNA
JDNP	27.799610, 89.330630	4'930	Collected on 26/10/2022	Scat DNA
JDNP*	27.814300, 89.343320	4'484	Collected on 27/10/2022	Scat DNA
WCNP	27.944038, 90.637974	4'892	22.10.2022	CT

## Species ID Methods

### *DNA metabarcoding*

DNA metabarcoding of the scat samples was conducted to identify the origin of each scat and potential prey consumed. An approximately 100-bp fragment of the *MT-RNR1* locus was chosen as the DNA barcode due to its wide use for taxonomic identification of mammals and birds in scat (van der Heyde et al., 2021). PCR reactions contained 1 µL DNA template (extracted using the Qiagen QIAamp Fast DNA Stool Mini kit), 5 µL KAPA HIFI HotStart Ready Mix (2x), 0.5 µL of each primer (20 µM), and 3 µL PCR grade water. PCRs were run under the following conditions: denaturation at 95°C for 3 minutes, 40 cycles of 95°C for 30 seconds, 60°C for 30 seconds, and 72°C for 30 seconds, and a final extension step of 5 minutes at 72°C. Products were confirmed via gel electrophoresis. Amplicons were purified with Agencourt AMPure XP beads (Beckman Coulter Inc., Brea, CA, USA). An indexing PCR was used to incorporate unique barcodes to each sample via a Nextera XT index kit (Illumina, Inc., San Diego, CA, USA). PCR reactions contained 5 µL DNA template, 12.5 µL KAPA HIFI HotStart Ready Mix (2x), 2.5 µL of forward index primer, 2.5 µL of reverse index primer, and 2.5 µL PCR grade water. PCRs were run under the following conditions: denaturation at 95°C for 3 minutes, 10 cycles of 95°C for 30 seconds, 55°C for 30 seconds, and 72°C for 30 seconds, and a final extension step of 5 minutes at 72°C. Products were

purified with Agencourt AMPure XP beads and ran on a gel. Samples were pooled and diluted to 4 nM. The library was loaded and sequenced on an Illumina MiSeq with a paired-end run using a MiSeq Reagent Micro Kit V2 at the Janecka Genomics Laboratory.

After sequencing, FASTQ sequences were demultiplexed, adaptors were removed, and reads were imported into CLC Genomic Workbench v22 (Qiagen Bioinformatics, Redwood City, CA, USA) for a preliminary analysis. Raw reads were quality checked and trimmed with a quality score of 0.05. *De novo* assembly was conducted using the following parameters: mismatch cost of 2, insertion cost of 2, deletion cost of 3, minimum contig length of 90 bp, 90% length fraction, 94% similarity, and nonspecific matches were mapped randomly. Contigs with at least 500 reads were extracted and identified using NCBI's Basic Local Alignment Search Tool (BLAST; <https://blast.ncbi.nlm.nih.gov/Blast.cgi>). Contigs were assigned to a species with the greatest max identity in the GenBank database, but only if the max identity was at least 97%. In cases with multiple carnivore species identified, the carnivore with the largest read count was determined to be the host.