

Figure S1. Pedigree of the ten zoo-managed Pallas’s cats (*Otocolobus manul*) sampled in this study and their founding ancestors. The ten Pallas’s cats sampled in this study are labeled Oman11 through Oman20. Each shape includes the individual’s studbook number. The pedigree information was collected from the Association of Zoos and Aquariums’ North American Regional Pallas’s Cat Studbook [15].

Table S1. Description of 29 microsatellites used to genotype six wild and ten zoo-managed Pallas's cats (*Otocolobus manul*). These loci were previously used in an analysis of range-wide snow leopard (*Panthera uncia*) phylogeography diversity [31]. The amplified loci are the same as the domestic cat (*Felis catus*) loci from [33,34] but were redesigned but to match snow leopard sequence and amplify shorter amplicons to increase genotyping success in scat DNA (i.e., PUN1157 corresponds to FCA1157). The size ranges for *P. uncia* were collected from [31]. The wild Pallas's cat scats were collected in Shenza, Tibet Autonomous Region (n = 1) and the Western and Eastern Beauties of Mongolia (n = 2 and n = 3, respectively).

Designation	Total A _N	Total A _E	P _{ID}	Wild A _N	Wild A _E	Zoo A _N	Zoo A _E	Size Range (bp)	Size Range (bp)
								<i>O. manul</i>	<i>P. uncia</i>
PUN1157F	5	2.286	0.252	5	3.130	2	1.835	100 – 108	92 – 112
PUN843P	5	2.236	0.245	4	2.057	4	2.198	104 – 116	106 – 114
PUN935F	4	2.107	0.292	3	1.674	3	2.151	118 – 134	103 – 125
PUN894V	5	3.066	0.162	4	3.429	2	1.724	111 – 119	106 – 124
PUN124N	4	3.103	0.170	4	3.130	3	2.632	102 – 108	88 – 102
PUN272P	5	2.639	0.201	3	2.182	3	2.198	120 – 128	120 – 138
PUN82F	7	3.606	0.120	7	6.000	4	2.439	97 – 109	99 – 113
PUN1262N	6	3.606	0.114	5	3.600	3	2.410	116 – 130	118 – 128
PUN225P	4	2.926	0.185	3	2.667	3	2.198	170–178	166 – 182
PUN100F	8	4.531	0.079	5	4.500	6	3.846	84 – 102	88 – 98
PUN1283N	4	2.510	0.235	4	2.483	3	1.802	131 – 137	123 – 131
PUN668P	6	5.224	0.065	4	4.000	5	4.255	194 – 204	175 – 191
PUN80F	1	1.000	1.000	1	1.000	1	1.000	91	100 – 120
PUN1270N	7	3.710	0.107	6	4.000	5	2.410	137 – 163	122 – 144
PUN1030F	6	3.368	0.125	5	4.800	4	2.299	107 – 119	104 – 122
PUN9013D1V	6	4.339	0.091	4	2.667	3	2.817	89 – 99	86 – 98
PUN1275N	3	2.723	0.212	3	2.571	3	2.778	145 – 149	128 – 148
PUN1047F	6	4.655	0.079	5	4.500	4	2.941	111 – 121	112 – 118
PUN917V	2	1.133	0.786	1	1.000	2	1.220	160 – 162	156 – 162
PUN1289N	3	1.210	0.691	2	1.180	3	1.227	112 – 130	108 – 142
PUN347P	2	1.822	0.403	2	1.600	2	1.923	116 – 120	110 – 122
PUN1131F	9	6.649	0.041	4	2.769	7	5.263	103 – 123	92 – 124
PUN924V	5	2.695	0.191	3	2.880	4	2.041	143 – 159	124 – 144
PUN1293N	7	4.655	0.078	4	2.667	5	3.333	116 – 128	112 – 124
PUN44P	6	3.879	0.103	5	3.600	3	2.062	112 – 126	110 – 122
PUN1138F	5	3.282	0.134	3	2.571	4	1.695	108 – 118	106 – 116
PUN928V	6	4.197	0.091	5	4.500	5	3.077	108 – 118	106 – 116
PUN1307N	8	4.303	0.080	7	5.538	4	2.381	103 – 119	102 – 114
PUN664P	3	2.359	0.269	3	1.946	3	2.381	148 – 152	136 – 146

A_N = number of alleles, A_E = effective number of alleles ($1/(\sum p^2)$), P_{ID} = probability of identity

Table S2. The nine multiplex panels of the 29 microsatellite primers used to genotype six wild and ten zoo-managed Pallas's cats (*Otocolobus manul*). These loci were previously used in an analysis of range-wide snow leopard (*Panthera uncia*) phylogeography diversity [31]. As specified by [31], each primer was designated by the prefix "PUN" and respective locus number used by [33,34]. All microsatellite primers were directly labeled with the fluorescent dyes VIC (V), FAM (F), NED (N), and PET (P). The wild Pallas's cat scats were collected in Shenza, Tibet Autonomous Region (n = 1) and the Western and Eastern Beauties of Mongolia (n = 2 and n = 3, respectively).

<i>Uncia</i> A	<i>Uncia</i> B	<i>Uncia</i> C	<i>Uncia</i> D	<i>Uncia</i> E	<i>Uncia</i> F	<i>Uncia</i> G	<i>Uncia</i> H	<i>Uncia</i> I
PUN1157F	PUN935F	PUN82F	PUN100F	PUN80F	PUN1030F	PUN1047F	PUN1131F	PUN1138F
PUN843P	PUN894V	PUN1262N	PUN1283N	PUN1270N	PUN9013D1V	PUN917V	PUN924V	PUN928V
	PUN124N	PUN225P	PUN668P		PUN1275N	PUN1289	PUN1293N	PUN1307N
	PUN272P					PUN347P	PUN44P	PUN664P

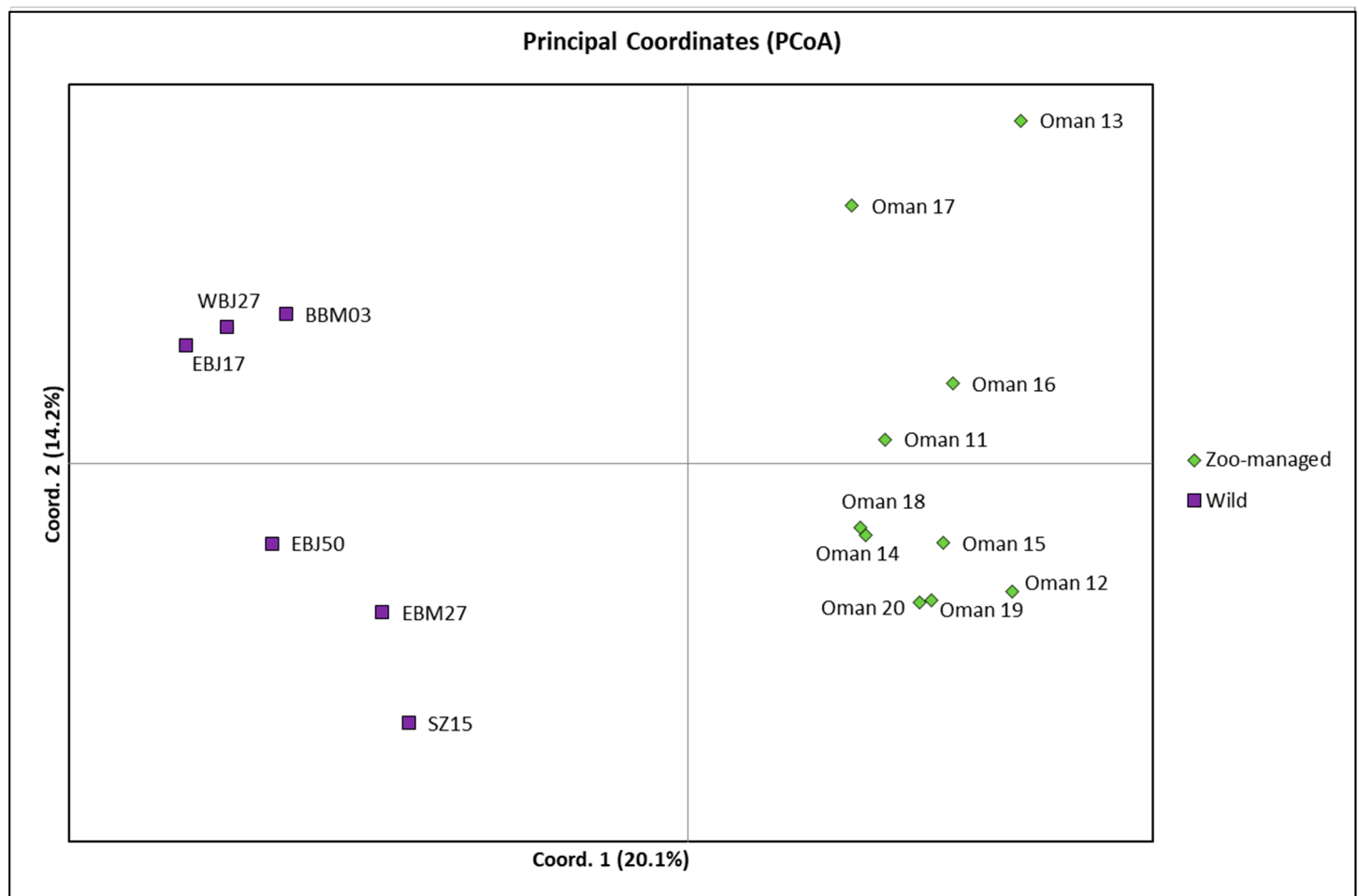


Figure S2. Principal coordinate analysis of six wild and ten zoo-managed Pallas's cats (*Otocolobus manul*) genotyped at 29 microsatellite loci. The associated pairwise F_{ST} value between the zoo-managed (green diamonds) and wild individuals (purple squares) was $F_{ST} = 0.143$ ($P = 0.001$). The wild Pallas's cat scats were collected in Shenza, Tibet Autonomous Region ($n = 1$) and the Western and Eastern Beauties of Mongolia ($n = 2$ and $n = 3$, respectively).

Haplotype 1

Definition:

TTAGCCCTAAACTTAGATAGTTAACTTAACAAAACCTATCCGCCAGAGAACTACTA-
GCCACAGCTTAAAACTCAAAGGACTTGGCGGTGCTT

Haplotype ID:

Oman11, Oman14, Oman17

SZ15, WBJ27, BBM03, EBJ17, EBM27, EBJ50

MH48879.1, KR132585.1

Haplotype 2

Definition:

TTAGCCCTAAACTTAGATAGTTAACTTAACAAAACCTATCCGCCAGAGAACTACTA-
GCCACAGCTTAAAACTCAAAGGACTTGGCGGTGCTT

Haplotype ID:

Oman13, Oman15

Haplotype 3

Definition:

TTAGCCCTAAACTTAGATAGTTAGCTTAACAAAACCTATCCGCCAGAGAACTACTA-
GCCACAGCTTAAAACTCAAAGGACTTGGCGGTGCTT

Haplotype ID:

Oman12, Oman16, Oman18, Oman19, Oman20

KX098454.1, KX098455.1, MH978908.1, NC_028323.1

Figure S3. Three observed mitochondrial 12S ribosomal RNA (MT-RNR1) haplotypes in 22 Pallas's cats (*Otocolobus manul*). The 91 bp sequences were amplified using primers 12SV5F/12SV5R [44]. The two segregating sites are highlighted. Pallas's cat sequences were collected from six cats collected during noninvasive surveys in Shenza, Tibet Autonomous Region (SZ15; n = 1) and the Western and Eastern Beauties of Mongolia (n = 2; WBJ27; BBM03 and n = 3; EBJ17; EBM27; EBJ50, respectively), ten zoo-managed Pallas's cats (Oman11 to Oman20), and six sequences available through GenBank (KX098454.1, KX098455.1, MH978908.1, NC_028323.1, MH48879.1, KR132585.1).