

Supplementary Information

Screening for the ancient polar bear mitochondrial genome reveals low integration of mitochondrial pseudogenes (numts) in bears

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Supplementary Data 1

Maximum likelihood of individual *numt* fragment loci compared to mitochondrial orthologs of all bear species, dog and cat. Black numbers on branches indicate branch lengths and bootstrap values are given in red below branches.

Supplementary Data 2

Excel spreadsheet (XLSX format) with intersection analyses of *numt* loci with genomic deletions in the genomes of two polar bear individuals (POL01, POL02), a brown bear (BRO) and an American black bear (AMB). A “1” in the table indicates a overlap, and “0” indicates that no overlap between numt loci and the deletion loci was identified.

Supplementary Tables

Table S1. Specimens for phylogenetic analyses with corresponding Genbank ID

Description	Name	Genbank Id
Polar bear	<i>Ursus maritimus</i>	gi 514237234 dbj AP012597.1
Brown bear	<i>Ursus arctos</i>	gi 514237164 dbj AP012592.1
American black bear	<i>Ursus americanus</i>	gi 19343488 ref NC_003426.1
Asian black bear	<i>Ursus thibetanus</i>	gi 195182344 emb FM177759.1
Spectacled bear	<i>Tremarctos ornatus</i>	gi 195182420 emb FM177764.1
Sun bear	<i>Helarctos malayanus</i>	gi 195182435 emb FM177765.1
Sloth bear	<i>Melursus ursinus</i>	gi 195182405 emb FM177763.1
Panda	<i>Ailuropoda melanoleuca</i>	gi 195182374 emb FM177761.1
Dog	<i>Canis lupus familiaris</i>	gi 294774361 dbj AB499817.1
Domestic cat	<i>Felis catus</i>	gi 814936256 gb KP202275.1

Table S2: Genomic loci in the polar bear genome containing NuMts insertions. The loci are consecutively numbered, and the number of NuMt fragments per locus and the locus length is given.

LOCUS	SCAFFOLD	START	END	NO_FRAGMENTS	LENGTH
1	scaffold1	19176679	19177582	1	903
2	scaffold100	5568310	5570656	1	2346
3	scaffold126	3684606	3684896	1	290
4	scaffold159	746082	746875	1	793
5	scaffold18	12418188	12419257	1	1069
6	scaffold18	19909859	19919849	2	9990
7	scaffold299	350193	357102	3	6909
8	scaffold39	17871509	17875385	1	3876
9	scaffold449	24328	30629	3	6301
10	scaffold46	296529	307643	3	11114
11	scaffold55	2339127	2341674	2	2547
12	scaffold615	1384	4336	2	2952
13	scaffold73	4946867	4947069	1	202

Table S3: Regions between fragmented NuMts in the polar bear genome. For each NuMt loci that contain several NuMt fractions, the regions between NuMts fragments are labelled (a,b) and the distance between the fragments on the polar bear mtDNA and the distance between fragments on the nuclear genome is shown. Δ Distance is the differences between the distances on mtDNA and nuDNA and the presence of inserted transposable elements or short tandem repeats (STR) indicated.

LOCUS_NO	FRAG_GAP	Distance mtDNA	Distance nuDNA	Δ Distance	INSERT
6	a	6451	7761	1310	STR; L1 (frag)
7	a	724	927	203	SINE
7	b	1718	1625	-93	
9	a	720	937	217	SINEC1D_CF
9	b	3700	3406	-294	
10	a	2509	7137	4628	L1_Ame (frag)
10	b	7629	9371	1742	L1_Ame
11	a	102	554	452	STR
12	a	771	71	-700	