Skorupski J. 2021. **Characterisation of the complete mitochondrial genome of critically endangered Mustela lutreola (Carnivora: Mustelidae) and its phylogenetic and conservation implications** – Supplementary Materials

Table S1. Percent base composition and nucleotide skews for coding and non-coding regions found in the mtDNA of European mink.

Mitogenome section	A (%)	T (%)	G (%)	C (%)	A+T (%)	AT-skew	GC-skew
nad1	30.44	28.14	12.03	29.39	58.58	0.039	-0.419
nad2	37.62	26.10	8.83	27.45	63.72	0.181	-0.513
cox1	27.44	31.07	17.54	23.95	58.51	-0.062	-0.154
cox2	32.75	28.07	13.89	25.29	60.82	0.077	-0.291
atp8	40.69	29.90	6.86	22.55	70.59	0.153	-0.533
atp6	30.69	28.49	11.45	29.37	59.18	0.037	-0.439
cox3	27.17	28.32	15.69	28.83	55.48	-0.021	-0.295
nad3	33.14	28.24	12.39	26.22	61.38	0.080	-0.358
nad4l	27.61	33.00	12.79	26.60	60.61	-0.089	-0.350
nad4	32.73	27.07	11.68	28.52	59.80	0.095	-0.419
nad5	33.33	26.91	11.64	28.12	60.24	0.107	-0.414
nad6 [1]	21.47	42.18	26.74	9.60	63.65	-0.325	0.472
Cytb	29.12	27.81	13.07	30.00	56.93	0.023	-0.393
overall of protein-coding genes [2]	**31.00**	**28.83**	**13.44**	**26.73**	**59.83**	**0.036**	**-0.331**
1st in codon [3]	31.66	23.17	21.44	23.73	54.83	0.155	-0.051
2nd in codon [3]	19.55	41.96	12.32	26.17	61.51	-0.364	-0.360
3rd in codon [3]	41.93	21.31	6.52	30.24	63.24	0.326	-0.645
rrnS	37.54	23.36	17.52	21.58	60.90	0.233	-0.104
rrnL	36.41	24.89	17.31	21.39	61.30	0.188	-0.105
overall of rRNA genes	**36.84**	**24.31**	**17.39**	**21.46**	**61.15**	**0.205**	**-0.105**
$tRNA^{Phe}$	43.48	21.74	17.39	17.39	65.22	0.333	0.000
$tRNA^{Val}$	35.29	30.88	14.71	19.12	66.18	0.067	-0.130
$tRNA^{Leu(UUA)}$	30.67	26.67	18.67	24.00	57.33	0.070	-0.125
$tRNA^{Ile}$	37.68	31.88	15.94	14.49	69.57	0.083	0.048
$tRNA^{Gln}$ [1]	24.32	41.89	24.32	9.46	66.22	-0.265	0.440
$tRNA^{Met}$	26.09	27.54	18.84	27.54	53.62	-0.027	-0.188
$tRNA^{Trp}$	35.82	22.39	19.40	22.39	58.21	0.231	-0.071
$tRNA^{Ala}$ [1]	28.99	34.78	21.74	14.49	63.77	-0.091	0.200
$tRNA^{Asn}$ [1]	26.03	31.51	27.40	15.07	57.53	-0.095	0.290
$tRNA^{Cys}$ [1]	28.36	25.37	23.88	22.39	53.73	0.056	0.032
$tRNA^{Tyr}$ [1]	32.35	29.41	23.53	14.71	61.76	0.048	0.231
$tRNA^{Ser(UCA)}$ [1]	34.48	24.64	15.94	24.64	59.42	0.171	-0.214
$tRNA^{Asp}$	35.82	35.82	16.42	11.94	71.64	0.000	0.158
$tRNA^{Lys}$	37.31	26.87	16.42	19.40	64.18	0.163	-0.083
$tRNA^{Gly}$	34.78	30.43	14.49	20.29	65.22	0.067	-0.167
$tRNA^{Arg}$	42.65	35.29	8.82	13.24	77.94	0.094	-0.200
$tRNA^{His}$	43.48	34.78	8.70	13.04	78.26	0.111	-0.200

tRNA$^{Ser(AGC)}$	33.87	22.58	16.13	27.42	56.45	0.200	-0.259
tRNA$^{Leu(CUA)}$	41.43	27.14	17.14	14.29	68.57	0.208	0.091
tRNA^{Glu} [1]	30.43	37.68	18.84	13.04	68.12	-0.106	0.182
tRNA^{Thr}	32.35	33.82	14.71	19.12	66.18	-0.022	-0.130
tRNA^{Pro} [1]	34.85	18.18	15.15	31.82	53.03	0.314	-0.355
overall of tRNA genes	**34.06**	**29.70**	**17.72**	**18.52**	**63.76**	**0.068**	**-0.022**
control region	29.23	26.41	15.23	29.14	55.64	0.051	-0.314
O_L [1]	8.57	31.43	25.71	34.29	40.00	-0.571	-0.143
intergenic spacers	35.48	38.71	3.23	22.58	74.19	-0.043	-0.750
overall of non-coding regions	**28.76**	**26.90**	**15.22**	**29.12**	**55.66**	**0.033**	**-0.313**
overall of the mitogenome	**32.82**	**27.24**	**13.83**	**26.11**	**60.06**	**0.093**	**-0.308**

[1] L-strand, [2] excluding presumed polyadenylated incomplete termination codons [31], [3] including presumed polyadenylated incomplete termination codons [31]; genes and non-coding/regulatory regions are color-coded: light blue – tRNA genes, light green – rRNA genes, light yellow – protein-coding genes, light red – non-coding/regulatory regions (O_L – light strand replication origin).

Table S2. Tandem repeats detected in the mitochondrial genome of *Mustela lutreola*.

Position (bp)	Motif length (bp)	Repeats	Sequence (5′-3′)
681	2	3	TATATA
743	2	3	AAAAAA
808	2	3	ACACAC
873	2	3	AGAGAG
906	2	3	CACACA
935	2	3	ACACAC
1,076	2	3	ATATAT
1,571	2	3	AGAGAG
1,684	2	3	ACACAC
2,639	2	3	CCCCCC
3,243	2	3	CACACA
3,432	3	3	CATCATCAT
3,612	2	3	AAAAAA
3,684	2	3	CCCCCC
4,043	2	3	AAAAAA
4,309	2	3	AAAAAA
4,318	2	3	CCCCCC
4,357	2	4	ACACACAC
4,462	2	3	CACACA
4,721	2	3	AAAAAA
4,868	2	3	AAAAAA
5,189	2	3	AAAAAA
5,726	2	3	CCCCCC
5,919	3	3	CTTCTTCTT
6,012	2	3	GGGGGG
6,128	2	3	AAAAAA
6,211	2	3	ATATAT
6,238	2	3	ACACAC
6,389	2	3	GGGGGG
6,846	2	3	CACACA

7,763	2	3	TCTCTC
7,838	2	3	TTTTTT
8,223	2	3	CACACA
8,631	2	3	ACACAC
8,778	2	3	ATATAT
9,207	2	3	TTTTTT
9,461	2	3	AGAGAG
9,681	3	3	ACTACTACT
9,897	2	3	TATATA
9,970	2	3	CTCTCT
10,450	2	3	AAAAAA
11,101	2	3	TATATA
11,726	2	3	AAAAAA
11,830	2	3	TATATA
12,222	3	3	GATGATGAT
12,273	2	3	TATATA
12,650	2	3	AAAAAA
13,431	2	3	AAAAAA
13,906	2	3	CCCCCC
13,939	2	3	AAAAAA
14,485	2	3	TATATA
14,628	2	3	ATATAT
14,954	2	3	ACACAC
15,455	2	3	CTCTCT
15,465	2	3	ATATAT
15,508	2	4	TTTTTTTTT
15,518	2	3	CCCCCC
15,568	2	3	TATATA
15,823	2	3	CACACA
15,860	2	3	TTTTTT
15,867	2	3	GGGGGG
16,008	2	3	ACACAC
16,030	10	16	GCACACGTACGCACACGTACGCACACGTACGCACACGT ACGCACACGTACGCACACGTACGCACACGTACGCACAC GTACGCACACGTACGCACACGTACGCACACGTACGCAC ACGTACGCACACGTACGCACACGTACGCACACGTACGC ACACGTAC
16,199	8	4	CACACGTACACACGTACACACGTACACACGTA
16,030	10	22.1	GCACACGTACGCACACGTACGCACACGTACGCACACGT ACGCACACGTACGCACACGTACGCACACGTACGCACAC GTACGCACACGTACGCACACGTACGCACACGTACGCAC ACGTACGCACACGTACGCACACGTACGCACACGTACGC ACACGTACACACGTACGCACACGTACACACGTACACAC GTACACACGTACGCACACGGTAC
16,284	2	3	CCCCCC
16,293	2	3	CCCCCC
16,371	2	3	ATATAT

Table S3. Inverted repeats in the mitochondrial genome of European mink.

Length of repeat (bp)	Length of spacer (bp)	Position (bp)	Sequence (5′-3′)[1]
6	1	394	GTTAAA–A–TTTAAC
6	17	402	TTAACA–AGGCTGTAAAAAGCCAC–TGTTAA
6	5	448	AAGTAA–CTTTA–TTACTT
6	10	532	ATAATT–ATCACAACAA–AATTAT
6	4	821	AGTTTT–TATG–AAAACT
8	7	821	AGTTTTTA–TGAAAAC–TAAAAACT
6	13	834	ACTAAA–AACTAAAGGTGGA–TTTAGT
6	6	841	ACTAAA–GGTGGA–TTTAGT
7	9	863	AATTAAG–AATAGAGAG–CTTAATT
9	6	1,527	TCTAAAAAG–GTACAG–CTTTTTAGA
6	4	1,701	TCTATT–TTAT–AATAGA
6	15	1,774	GTTAAC–GAATACCCACTGATA–GTTAAC
6	13	1,940	CCTCCA–GCATATCTAGTAT–TGGAGG
6	8	2,112	TTCCCG–TGAAGAGG–CGGGAA
7	11	2,254	CTCGGAG–AATAAAATAAC–CTCCGAG
6	9	2,322	TTGATC–CAATAATTT–GATCAA
6	17	2,376	CCTATT–TGAGAGTCCATATCAAC–AATAGG
8	17	2,541	TACTTCTC–CCAGTACGAAAGGACAA–GAGAAGTA
7	4	2,647	AACCCTA–GAAA–TAGGGTT
8	10	2,858	TTGTAGGA–CCCTACGGCC–TCCTACAA
6	1	3,139	CTACGG–G–CCGTAG
6	1	3,645	TATATG–A–CATATA
6	18	3,887	GGTTTA–TCCCCTTCCCGTACTAAT–TAAACC
6	16	3,941	TACTAT–TATCTCAGGGACTATC–ATAGTA
6	11	4,882	TATTAC–CCCCATTAATT–GTAATA
7	3	4,994	TAAGTGA–CAC–TCACTTA
11	13	5,171	CTTCTCCCGCC–GCGAAGGAAAAAA–GGCGGGAGAAG
6	18	5,201	AGAAGC–CCCGGCAGGGTTGAAGCT–GCTTCT
7	3	5,231	TTGAATT–TGC–AATTCAA
6	8	5,355	TGATTA–TTCTCCAC–TAATCA
6	7	6,072	ATCCTG–ATTCTCC–CAGGAT
6	12	6,204	GCCCAC–CATATATTTACT–GTGGGC
6	15	6,554	AAATGA–TGTATGAGCAAAAAT–TCATTT
6	13	6,720	TCATTA–ACGGCAGTCATAC–TAATGA
6	7	6,791	AGTTGA–ATTAACC–TCAACT
8	1	6,977	TGACTTTG–T–CAAAGTCA
6	13	7,103	ACTAAT–AATTGTATTTCTA–ATTAGT
6	0	7,424	ACTTCT–AGAAGT
6	16	7,460	AGAAAT–AACAATTCGTATACTA–ATTTCT
6	2	7,945	GAAAAT–CT–ATTTTC
6	0	8,273	CAGTAA–TTACTG
6	15	8,569	GCTTAC–GTCTTTACCCTACTA–GTAAGC
6	4	9,594	TGATCC–CTTA–GGATCA
7	6	9,861	ATTGTAA–CTCATA–TTACAAT
6	15	9,885	AAATGT–CCGTAGTATATATCA–ACATTT

6	14	9,996	TGTTAT–CCCTCTTCGTCATA–ATAACA
6	10	10,135	CACATA–CGGGACAGAT–TATGTG
6	7	10,188	TATTAT–CCCAACC–ATAATA
8	15	10,248	AATTAATA–CAACAGCTCACAGCA–TATTAATT
6	20	10,387	TGGCTT–CTTCCCCTGATGCTCATAGC–AAGCCA
7	19	10,758	ACTATGA–CTAGCATGCATAATAGCAT–TCATAGT
6	7	10,972	TTATGA–GGGATAA–TCATAA
6	12	11,108	GAGCAA–CAGCCCTAATAA–TTGCTC
9	2	11,201	TAATCCTCG–CA–CGAGGATTA
7	7	11,525	ACCCTAA–AATTATC–TTAGGGT
6	1	11,548	ATTTAC–T–GTAAAT
7	3	11,578	TTAGATT–GTG–AATCTAA
7	10	11,596	AATAAAA–GCTCAAACCT–TTTTATT
6	8	11,611	CTTTTT–ATTTACCG–AAAAAG
6	9	11,637	GCATGA–ACTGCTAAC–TCATGC
6	6	11,660	CCGTGT–ATAAAA–ACACGG
9	6	12,193	AGTAGGAAT–TATATC–ATTCCTACT
6	16	12,204	TATCAT–TCCTACTTATCGGATG–ATGATA
6	18	12,899	GGAATA–CCCTTCTTAACGGGATTT–TATTCC
6	12	13,073	ATTATT–ACAATCAACGAG–AATAAT
6	10	13,191	AGATAA–CTATGCCTTA–TTATCT
6	11	13,410	TTCTAG–ATATAATTTGA–CTAGAA
8	4	14,021	AGGGTTTT–GAAG–AAAACCCT
6	12	14,024	GTTTTG–AAGAAAACCCTA–CAAAAC
6	18	14,069	GAATAA–ATACAATGTATGTCATCA–TTATTC
7	10	14,279	GAATCTG–CCTAATTATT–CAGATTC
6	7	14,875	CTAATA–CTAACAC–TATTAG
6	5	14,879	TACTAA–CACTA–TTAGTA
6	12	15,027	ATTAGG–AGGGGTACTAGC–CCTAAT
6	7	15,329	TTTGGT–CTTGTAA–ACCAAA
6	7	15,399	ATCAGC–ACCCAAA–GCTGAT
6	17	15,564	CATGTA–TATATTATGGTTGATTT–TACATG
6	16	15,877	ACTTGG–TATCACTCAGCTATGG–CCAAGT
6	4	16,035	CGTACG–CACA–CGTACG
6	4	16,045	CGTACG–CACA–CGTACG
6	4	16,055	CGTACG–CACA–CGTACG
6	4	16,065	CGTACG–CACA–CGTACG
6	4	16,075	CGTACG–CACA–CGTACG
6	4	16,085	CGTACG–CACA–CGTACG
6	4	16,095	CGTACG–CACA–CGTACG
6	4	16,105	CGTACG–CACA–CGTACG
6	4	16,115	CGTACG–CACA–CGTACG
6	4	16,125	CGTACG–CACA–CGTACG
6	4	16,135	CGTACG–CACA–CGTACG
6	4	16,145	CGTACG–CACA–CGTACG
6	4	16,155	CGTACG–CACA–CGTACG
6	4	16,165	CGTACG–CACA–CGTACG
6	12	16,175	CGTACG–CACACGTACACA–CGTACG
6	15	16,218	ACGTAC–ACACGTACGCACACG–GTACGT
6	7	16,226	ACGTAC–GCACACG–GTACGT

6	4	16,309	AAGTAT─ACAA─ATACTT
6	6	16,374	TATTAG─AAGTCA─CTAATA

[1] base motif – intervening sequence – repeated inverted sequence, complementary to a base motif

Table S4. Palindromic sequences found in the European mink mitogenome.

Position	Sequence (5'-3')	Length (bp)
287	TGTTAACA	8
288	GTTAAC	6
305	AAATTT	6
321	ACCGCGGT	8
322	CCGCGG	6
398	AAATTT	6
532	ATAATTAT	8
533	TAATTA	6
613	CCTCTAGAGG	10
614	CTCTAGAG	8
615	TCTAGA	6
636	ATCGAT	6
681	TATATA	6
732	TAATATTA	8
733	AATATT	6
944	AATATT	6
1,040	TTAATTAA	8
1,041	TAATTA	6
1,076	ATATAT	6
1,080	ATTAAT	6
1,201	CTATAG	6
1,289	AGCTAGCT	8
1,290	GCTAGC	6
1,291	CTAGCTAG	8
1,292	TAGCTA	6
1,314	AGATCT	6
1,318	CTTAAG	6
1,477	TTTAAA	6
1,479	TAAATTTA	8
1,480	AAATTT	6
1,511	TAAATTTA	8
1,512	AAATTT	6
1,515	TTTAAA	6
1,598	TAGGCCTA	8
1,599	AGGCCT	6
1,707	TTATAA	6

1,760	ATAAGCTTAT	10
1,761	TAAGCTTA	8
1,762	AAGCTT	6
1,766	TTATAA	6
1,774	GTTAAC	6
1,795	GTTAAC	6
1,827	AATATT	6
1,843	CAATTG	6
1,863	GCATGC	6
1,983	ACTAGT	6
1,993	CGGCCG	6
1,996	CCGCGG	6
2,061	TGGCCA	6
2,205	AGGCCT	6
2,317	ATTAAT	6
2,335	TTGATCAA	8
2,336	TGATCA	6
2,355	CCCTAGGG	8
2,356	CCTAGG	6
2,453	ATTAAT	6
2,533	ATTATAAT	8
2,534	TTATAA	6
2,537	TAATTA	6
2,747	TTATAA	6
2,750	TAATTA	6
2,885	CAATTG	6
3,044	GGATCC	6
3,096	ATCCGGAT	8
3,097	TCCGGA	6
3,284	TAGCTA	6
3,359	AACTAGTT	8
3,360	ACTAGT	6
3,511	ATTAAT	6
3,557	GAATTC	6
3,614	AAAATTTT	8
3,615	AAATTT	6
3,668	TTATAA	6
3,763	TTCTAGAA	8
3,764	TCTAGA	6
3,820	AAATTT	6
3,852	TAATTA	6
3,865	GGGCCC	6

3,907	TAATTA	6
3,964	TAGTACTA	8
3,965	AGTACT	6
4,063	CAATTG	6
4,080	AAATATTT	8
4,081	AATATT	6
4,276	CATTAATG	8
4,277	ATTAAT	6
4,365	TTATTAATAA	10
4,366	TATTAATA	8
4,367	ATTAAT	6
4,375	CTATAG	6
4,412	AGGCCT	6
4,533	ATTATAAT	8
4,534	TTATAA	6
4,732	TAATTA	6
4,738	CTGCAG	6
4,745	AATATT	6
4,892	ATTAAT	6
5,078	TTAATTAA	8
5,079	TAATTA	6
5,132	GTTAAC	6
5,237	TTGCAA	6
5,346	ATTAAT	6
5,350	ATCGAT	6
5,498	TTATAA	6
5,639	AAGCTT	6
5,721	GTATAC	6
5,895	TGATCA	6
5,905	TAATTA	6
5,949	GCCGGC	6
6,175	CAATTG	6
6,184	TCCTAGGA	8
6,185	CCTAGG	6
6,211	ATATAT	6
6,231	GACGTC	6
6,234	GTCGAC	6
6,301	TCAGCTGA	8
6,302	CAGCTG	6
6,340	GAGCTC	6
6,445	ATACGTAT	8
6,446	TACGTA	6

6,499	TTGCAA	6
6,703	CCATGG	6
6,748	TCATGA	6
6,760	AAGCTT	6
6,852	TTCGAA	6
6,867	TACGTA	6
7,043	AGGCCT	6
7,119	CTAATTAG	8
7,120	TAATTA	6
7,167	AAGCTT	6
7,182	AGTACT	6
7,186	CTATAG	6
7,240	TGATCA	6
7,267	GAATTC	6
7,424	ACTTCTAGAAGT	12
7,425	CTTCTAGAAG	10
7,426	TTCTAGAA	8
7,427	TCTAGA	6
7,474	GTATAC	6
7,505	CTCATGAG	8
7,506	TCATGA	6
7,523	CCTAGG	6
7,677	TTCGAA	6
7,802	TGATTAATCA	10
7,803	GATTAATC	8
7,804	ATTAAT	6
8,145	ATTAAT	6
8,241	CCTAGG	6
8,248	ATAGCTAT	8
8,249	TAGCTA	6
8,273	CAGTAATTACTG	12
8,274	AGTAATTACT	10
8,275	GTAATTAC	8
8,276	TAATTA	6
8,396	CCATGG	6
8,445	ATTAAT	6
8,491	AGTACT	6
8,507	TAATTA	6
8,567	AAGCTT	6
8,585	TACTAGTA	8
8,586	ACTAGT	6
8,677	GAGCTC	6

8,750	CCTAGG	6
8,778	ATATAT	6
9,035	CTCCGGAG	8
9,036	TCCGGA	6
9,054	TGGGCCCA	8
9,055	GGGCCC	6
9,122	CCTAGG	6
9,125	AGGCCT	6
9,321	TTCGAA	6
9,327	GCAGCTGC	8
9,328	CAGCTG	6
9,441	AACTAGTT	8
9,442	ACTAGT	6
9,479	TAATATTA	8
9,480	AATATT	6
9,578	CATATG	6
9,630	AAAATTTT	8
9,631	AAATTT	6
9,644	TAGCTA	6
9,822	TAATTA	6
9,897	TATATA	6
9,898	ATATAT	6
10,202	TAATATTA	8
10,203	AATATT	6
10,206	ATTAAT	6
10,249	ATTAAT	6
10,272	ATTAAT	6
10,274	TAATTA	6
10,371	ACTAGT	6
10,474	GTAATATTAC	10
10,475	TAATATTA	8
10,476	AATATT	6
10,493	TAATTA	6
10,496	TTATAA	6
10,565	TAATTA	6
10,690	GGTACC	6
10,704	ATTAAT	6
10,768	GCATGC	6
10,770	ATGCAT	6
10,882	CTTAAG	6
10,958	TTATAA	6
11,100	CTATATAG	8

11,101	TATATA	6
11,335	TCATGA	6
11,689	TTTAAA	6
11,754	TAATTA	6
11,830	TATATA	6
11,858	TACGTA	6
11,886	TCATGA	6
11,889	TGATCA	6
11,993	TTTAAA	6
12,047	TGATCA	6
12,058	AGAATTCT	8
12,059	GAATTC	6
12,098	AATCGATT	8
12,099	ATCGAT	6
12,110	AAGTACTT	8
12,111	AGTACT	6
12,260	CTGCAG	6
12,273	TATATA	6
12,592	CCTAGG	6
12,688	ATTAAT	6
12,775	CATATG	6
12,782	TCCGGA	6
12,842	TTTAAA	6
13,022	AGTACT	6
13,325	AACATGTT	8
13,326	ACATGT	6
13,411	TCTAGA	6
13,498	AGGCCT	6
13,664	CTATAG	6
13,767	TTTTAAAA	8
13,768	TTTAAA	6
13,868	TAGCTA	6
13,869	AGCTATAGCT	10
13,870	GCTATAGC	8
13,871	CTATAG	6
13,991	TAATTA	6
14,119	ACTAGT	6
14,162	CATTAATG	8
14,163	ATTAAT	6
14,288	TAATTA	6
14,380	GACGTC	6
14,485	TATATA	6

14,486	ATATAT	6
14,566	CCATGG	6
14,599	GTAATTAC	8
14,600	TAATTA	6
14,628	ATATAT	6
14,791	TCCGGA	6
14,794	GGAATTCC	8
14,795	GAATTC	6
14,853	CCTAGG	6
14,857	GGCGCC	6
14,891	TAGTACTA	8
14,892	AGTACT	6
15,111	AATATT	6
15,242	TCATGA	6
15,322	TAATTA	6
15,465	ATATAT	6
15,553	ATGCAT	6
15,568	TATATA	6
15,569	ATATAT	6
15,587	TACATGTA	8
15,588	ACATGT	6
15,631	CTCGAG	6
15,679	GGGCCC	6
15,819	TGATCA	6
15,896	TGGCCA	6
16,014	ATATAT	6
16,028	GTGCAC	6
16,035	CGTACG	6
16,045	CGTACG	6
16,055	CGTACG	6
16,065	CGTACG	6
16,075	CGTACG	6
16,085	CGTACG	6
16,095	CGTACG	6
16,105	CGTACG	6
16,115	CGTACG	6
16,125	CGTACG	6
16,135	CGTACG	6
16,145	CGTACG	6
16,155	CGTACG	6
16,165	CGTACG	6
16,175	CGTACG	6

16,193	CGTACG	6
16,227	CGTACG	6
16,240	TACGTA	6
16,243	GTATAC	6
16,311	GTATAC	6
16,323	TTATAA	6
16,371	ATATAT	6
16,399	CAATTG	6
16,424	TCTAGA	6
16,435	ATCTATAGAT	10
16,436	TCTATAGA	8
16,437	CTATAG	6
16,449	TTATAA	6

Table S5. Characteristics of the open reading frames (ORFs) identified in the *Mustela lutreola* mitogenome.

ORF	Strand	Frame	Start	Stop	Length (bp)	Length (aa) [1]
ORF1	+	2	143	259	117	38
ORF2	-	2	234	127	108	35
ORF3	-	1	382	197	186	61
ORF4	-	2	513	427	87	28
ORF5	-	1	637	536	102	33
ORF6	-	2	813	679	135	44
ORF7	+	3	888	977	90	29
ORF8	-	3	938	798	141	46
ORF9	-	2	1,077	967	111	36
ORF10	-	1	1,189	1,058	132	43
ORF11	+	2	1,418	1,513	96	31
ORF12	-	1	1,645	1,487	159	52
ORF13	+	1	1,732	1,824	93	30
ORF14	-	2	1,821	1,702	120	39
ORF15	-	1	2,218	2,087	132	43
ORF16	+	3	2,379	2,480	102	33
ORF17	-	1	2,434	2,357	78	25
ORF18	+	2	2,453	2,539	87	28
ORF19	+	1	2,476	2,574	99	32
ORF20	+	2	2,672	2,752	81	26
ORF21	-	2	2,727	2,650	78	25
ORF22	+	1	2,740	3,699	960	319
ORF23	+	3	3,537	3,701	165	54
ORF24	-	2	3,834	3,757	78	25
ORF25	+	3	3,882	4,952	1,071	356
ORF26	+	2	4,850	4,960	111	36
ORF27	+	3	5,166	5,303	138	45
ORF28	-	3	5,255	5,148	108	35
ORF29	+	3	5,304	6,884	1,581	526
ORF30	+	3	7,002	7,706	705	234

ORF31	+	2	7,778	7,981	204	67
ORF32	+	1	7,939	8,619	681	226
ORF33	+	3	8,547	9,446	900	299
ORF34	+	1	9,355	9,465	111	36
ORF35	+	1	9,469	9,828	360	119
ORF36	+	2	9,818	10,183	366	121
ORF37	+	1	10,171	11,700	1,530	509
ORF38	-	3	10,277	10,131	147	48
ORF39	+	2	11,654	13,576	1,923	640
ORF40	-	3	11,711	11,619	93	30
ORF41	-	2	11,913	11,647	267	88
ORF42	+	1	14,071	14,160	90	29
ORF43	-	3	14,096	13,560	537	178
ORF44	+	1	14,167	15,306	1,140	379
ORF45	-	3	14,222	14,109	114	37
ORF46	-	1	14,257	14,153	105	34
ORF47	-	3	15,362	15,258	105	34
ORF48	+	3	15,432	15,608	177	58
ORF49	+	1	15,484	15,609	126	41
ORF50	+	3	15,621	15,773	153	50
ORF51	+	1	15,685	15,810	126	41
ORF52	+	2	15,746	15,916	171	56
ORF53	+	3	15,810	15,971	162	53
ORF54	-	2	15,954	15,790	165	54
ORF55	-	1	16,372	15,941	432	143
ORF56	-	2	16,410	16,333	78	25

[1] length of putative protein-product; open reading frames coincide with identified protein-coding genes marked in gray.

Table S6. Characteristics of variable sites identified in the European mink mitogenome. 1

Position (bp) [1]	Mitogenome section	Specimen / SNVs [2] / haplotype																							Type of variable [3]	Codon	Amino acid
		MW197425	MW197426	MW148603	MT304869	MW197423	MW197424	AB119070	AF207714	AF207713	AF207712	AF068544	EU548044	EU548051	EU548039	EU548036	EU548043	EU548045	EU548041	JX982495	JX982502	JX982498	JX982501	JX982499	JX982500			
162	*rrnS*	G	G	G	G	G	C	G	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	trs		
422		C	C	C	C	C	C	T	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	trn		
1,299	*rrnL*	A	A	A	T	T	A	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	trs		
2,061		T	T	T	T	T	C	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	trn		
2,195		T	T	T	C	C	T	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	trn		
2,958	*nad1*	C	C	C	C	C	T	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	trn	GTC→GTT [4]	Val→Val
3,024		C	C	C	C	C	A	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	trs	CCC→CCA [4]	Pro→Pro
4,238	*nad2*	T	T	T	T	T	C	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	trn	CCT→CCC [4]	Pro→Pro
4,569		T	T	T	C	C	T	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	trn	TTT→TTC	Phe→Phe
4,901		A	A	A	G	G	G	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	trn	GTA→GTG [4]	Val→Val
5,459	*cox1*	A	A	A	G	G	A	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	trn	GAA→GAG [4]	Glu→Glu
5,708		G	G	G	A	A	G	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	trn	GGG→GGA [4]	Gly→Gly

5,774		G	G	G	G	G	A	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	trn	CTG→CTA [4]	Leu→Leu
6,110		T	T	T	C	C	C	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	trn	GTT→GTC [4]	Val→Val
6,309		T	T	T	C	C	C	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	trn	TTA→CTA	Leu→Leu
7,406	*cox2*	A	A	A	G	G	G	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	trn	CTA→CTG [4]	Leu→Leu
8,253	*atp6*	T	T	T	T	T	C	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	trn	GCT→GCC [4]	Ala→Ala
8,571		T	T	T	C	C	T	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	trn	GCT→GCC [4]	Ala→Ala
9,142	*cox3*	T	T	T	T	T	C	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	trn	GTC→GCC	Val→Ala [5]
9,289		G	G	G	G	G	A	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	trn	AGC→AAC	Ser→Asn [5]
10,284		A	A	A	G	G	G	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	trn	CTA→CTG [4]	Leu→Leu
10,857	*nad4*	G	G	G	A	A	A	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	trn	GGG→GGA [4]	Gly→Gly
11,166		C	C	C	T	T	T	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	trn	GCC→GCT [4]	Ala→Ala
12,331	*nad5*	T	T	T	T	T	C	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	trn	AAT→AAC [4]	Asn→Asn
13,114		C	C	C	T	T	T	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	trn	TCC→TCT [4]	Ser→Ser

13,141		C	C	C	T	T	T	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	trn	ATC→ATT [4]	Ile→Ile
13,205		T	T	T	C	C	C	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	trn	TAT→TAC [4]	Tyr→Tyr
13,462		C	C	C	C	C	T	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	trn	TTC→TTT [4]	Phe→Phe
13,887	*nad6*	T	T	T	T	T	C	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	trn	GGA→GGG [4]	Gly→Gly
14,218		C	C	C	C	C	C	?	T	C	C	C	?	?	?	?	?	?	?	?	?	?	?	?	trn	CTC→TTC	Leu→Phe [5]
14,233		G	G	G	G	G	G	?	G	A	G	G	?	?	?	?	?	?	?	?	?	?	?	?	trn	GCC→ACC	Ala→Thr [5]
14,406		A	A	A	A	A	A	?	A	A	G	A	?	?	?	?	?	?	?	?	?	?	?	?	trn	CGA→CGG [4]	Arg→Arg
14,571	*Cytb*	G	G	G	G	G	A	?	G	G	G	G	?	?	?	?	?	?	?	?	?	?	?	?	trn	TGG→TGA [4]	Trp→Trp
14,784		T	T	T	C	C	T	?	T	T	T	T	?	?	?	?	?	?	?	?	?	?	?	?	trn	AAT→AAC [4]	Asn→Asn
15,147		G	G	G	G	G	A	?	G	G	G	G	?	?	?	?	?	?	?	?	?	?	?	?	trn	CTG→CTA [4]	Leu→Leu
15,204		G	G	G	A	A	A	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	trn	CCG→CCA [4]	Pro→Pro
15,272		T	T	T	T	T	T	?	?	?	?	?	C	T	T	T	C	T	T	?	?	?	?	?	?	trn	ATC→ACC	Ile→Thr [5]
15,396	*tRNA^{Pro}*	G	G	G	G	G	G	?	?	?	?	?	G	T	G	G	G	G	G	?	?	?	?	?	?	trn		
15,463	control	T	T	T	T	T	T	?	?	?	?	?	T	C	T	T	T	T	T	?	?	?	?	?	?	trn		
15,470	region	T	T	T	T	T	T	?	?	?	?	?	T	C	T	T	T	T	T	?	?	?	?	?	?	trn		

15,474		A	A	A	A	A	A	?	?	?	?	?	A	A	G	A	A	A	A	A	A	A	A	A	A	trn
15,488		G	G	G	A	A	G	?	?	?	?	?	G	G	A	G	G	G	G	G	G	G	A	A	G	trn
15,489		C	C	C	C	C	C	?	?	?	?	?	C	C	C	C	C	C	C	G	C	C	C	C	C	trs
15,513		-	-	T	T	T	T	?	?	?	?	?	-	-	T	T	-	T	T	-	-	-	-	T	-	indel
15,514		T	T	T	T	T	T	?	?	?	?	?	-	-	-	-	-	T	T	-	-	-	-	-	-	indel
15,515		T	T	T	T	T	T	?	?	?	?	?	T	T	C	T	T	T	T	T	T	T	C	T	T	trn
15,518		C	C	C	C	C	C	?	?	?	?	?	C	C	C	C	C	C	C	C	T	C	C	C	C	trn
15,523		C	C	C	C	C	C	?	?	?	?	?	T	T	C	C	T	C	C	C	C	C	C	C	C	trn
15,579		G	G	G	G	G	A	?	?	?	?	?	G	G	G	G	G	G	G	G	G	G	G	G	G	trn
15,580		G	G	G	G	G	G	?	?	?	?	?	G	G	G	G	G	G	G	G	G	A	G	G	G	trn
15,585		T	T	T	T	T	T	?	?	?	?	?	T	T	T	C	T	T	T	T	T	T	T	T	T	trn
15,594		T	T	T	T	T	T	?	?	?	?	?	T	T	T	T	T	T	T	T	T	T	A	T	T	trs
15,599		C	C	C	C	C	T	?	?	?	?	?	C	C	C	C	C	C	C	C	C	C	T	C	C	trn
15,601		C	C	C	T	T	C	?	?	?	?	?	C	C	T	T	C	C	C	C	T	C	T	T	T	trn
15,604		C	C	C	C	C	C	?	?	?	?	?	C	C	C	C	G	C	C	C	C	C	C	C	C	trs
15,610		C	C	C	C	C	C	?	?	?	?	?	C	T	C	C	C	C	C	C	T	C	C	C	C	trn
15,616		G	G	G	G	G	G	?	?	?	?	?	G	G	G	G	G	G	G	G	G	G	A	G	G	trn
15,688		A	A	A	A	A	A	?	?	?	?	?	A	A	A	A	A	G	A	A	A	A	A	A	A	trn
15,701		C	C	C	C	C	T	?	?	?	?	?	T	C	C	C	T	T	T	C	C	T	C	C	C	trn
15,720		T	T	T	T	T	T	?	?	?	?	?	T	T	T	T	T	T	T	G	T	T	T	T	T	trn
15,749		T	T	T	T	T	T	?	?	?	?	?	T	T	T	T	T	T	T	T	C	T	T	T	T	trn
15,753		T	T	T	T	T	T	?	?	?	?	?	T	T	T	T	T	T	C	T	T	T	T	T	T	trn
15,901		A	A	A	A	A	A	?	?	?	?	?	A	A	A	A	A	A	A	T	A	A	A	A	A	trs
15,928		T	T	T	T	T	T	?	?	?	?	?	T	T	T	T	T	T	T	T	T	T	T	C	T	trn

15,973	C	C	C	C	C	C	?	?	?	?	?	C	C	C	C	C	C	C	C	C	C	C	C	T	trn
16,170	G	G	G	G	G	A	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	trn
16,174	-	A	A	A	A	-	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	indel
16,175	-	C	C	C	C	-	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	indel
16,189+1	-	-	-	G	G	G	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	indel
16,189+2	-	-	-	C	C	C	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	indel
16,198	A	A	G	G	G	G	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	trn
16,208	A	A	A	G	G	A	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	trn
16,212	G	G	G	A	A	G	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	trn
16,213	T	T	T	C	C	T	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	trn
16,214+1	-	-	-	T	T	-	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	indel
16,214+2	-	-	-	A	A	-	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	indel
16,214+3	-	-	-	C	C	C	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	indel
16,214+4	-	-	-	G	G	G	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	indel
16,223+1	-	-	-	G	G	-	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	indel
16,223+2	-	-	-	C	C	-	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	indel
16,232	G	G	G	G	G	A	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	trn

[1] the numbering given is relative to the reference sequence, [2] single nucleotide variant, [3] trs – transversion, trn – transition, indel – insertion-deletion variation, [4] single nucleotide variability in the codon's wobble position, [5] nonsynonymous (missense) substitution; a dash indicates a deletion; ? – no data; single nucleotide variants identified by alignment with the mtDNA sequences of *M. lutreola* deposited in the GenBank (Accession No.: AB026105, EF689084, EF689085, EF987742, EU548039, EU548040, EU548041, EU548045, EU548046, EU548035, EU548036, EU548037, EU548038, EU548047, EU548048, EU548049, EU548050, EU548042, EU548043, EU548044, EU548051, AB051263, AF068544, AF207712, AF207713, AF207714, AY750628, AB119070, AB601576, JX982499, JX982495, JX982496, JX982497, JX982498, JX982500, JX982501, JX982502, AF207721, AF207724, AF207725, AF207720, AF207722, AF207723) marked in gray.

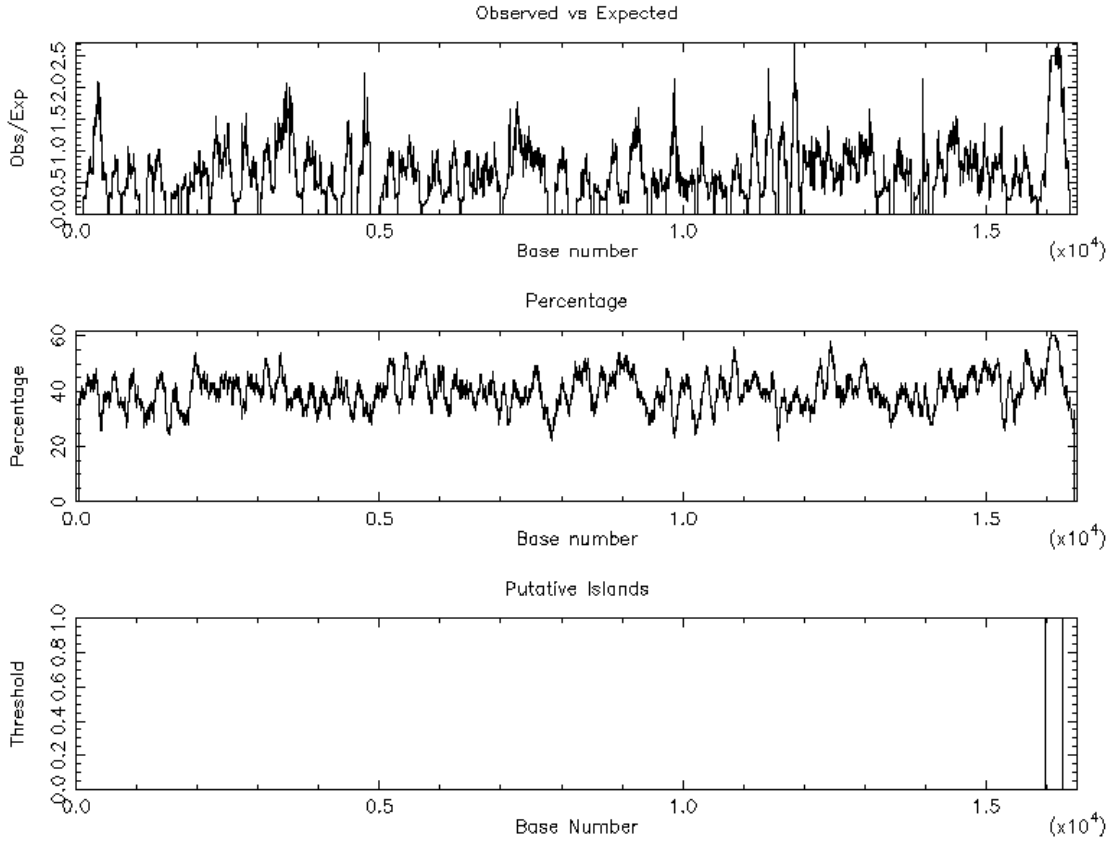

Figure S1. Graphical analysis of the European mink mitogenome sequence for the presence and distribution of CpG dinucleotides (upper graph – distribution of observed/expected ratios of CpG dinucleotides, middle graph – distribution of C+G nucleotides, lower graph – identification of putative CpG island).

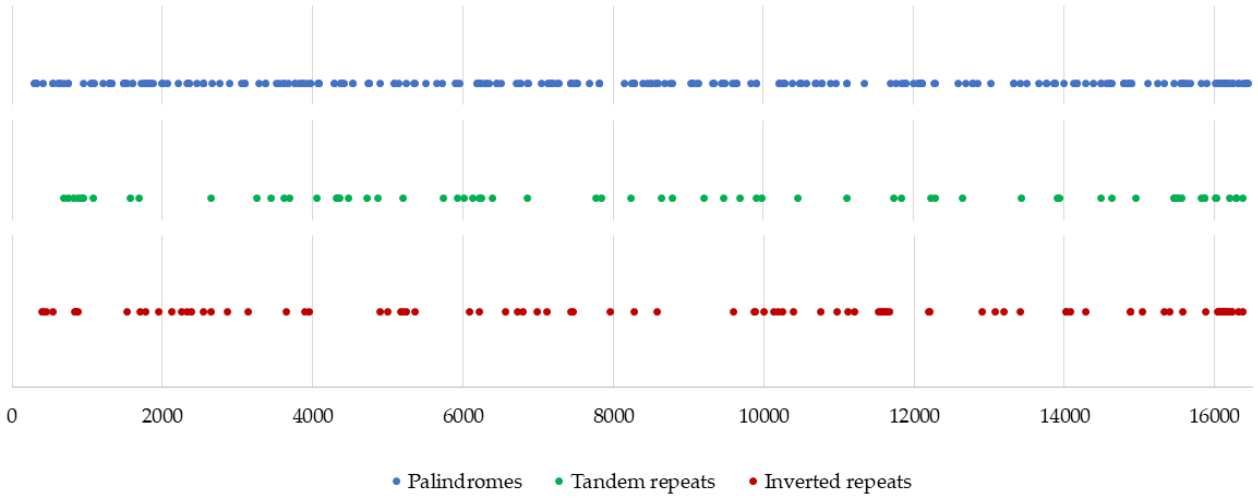

Figure S2. Distribution of repetitive and palindromic sequences in the European mink mitochondrial genome.

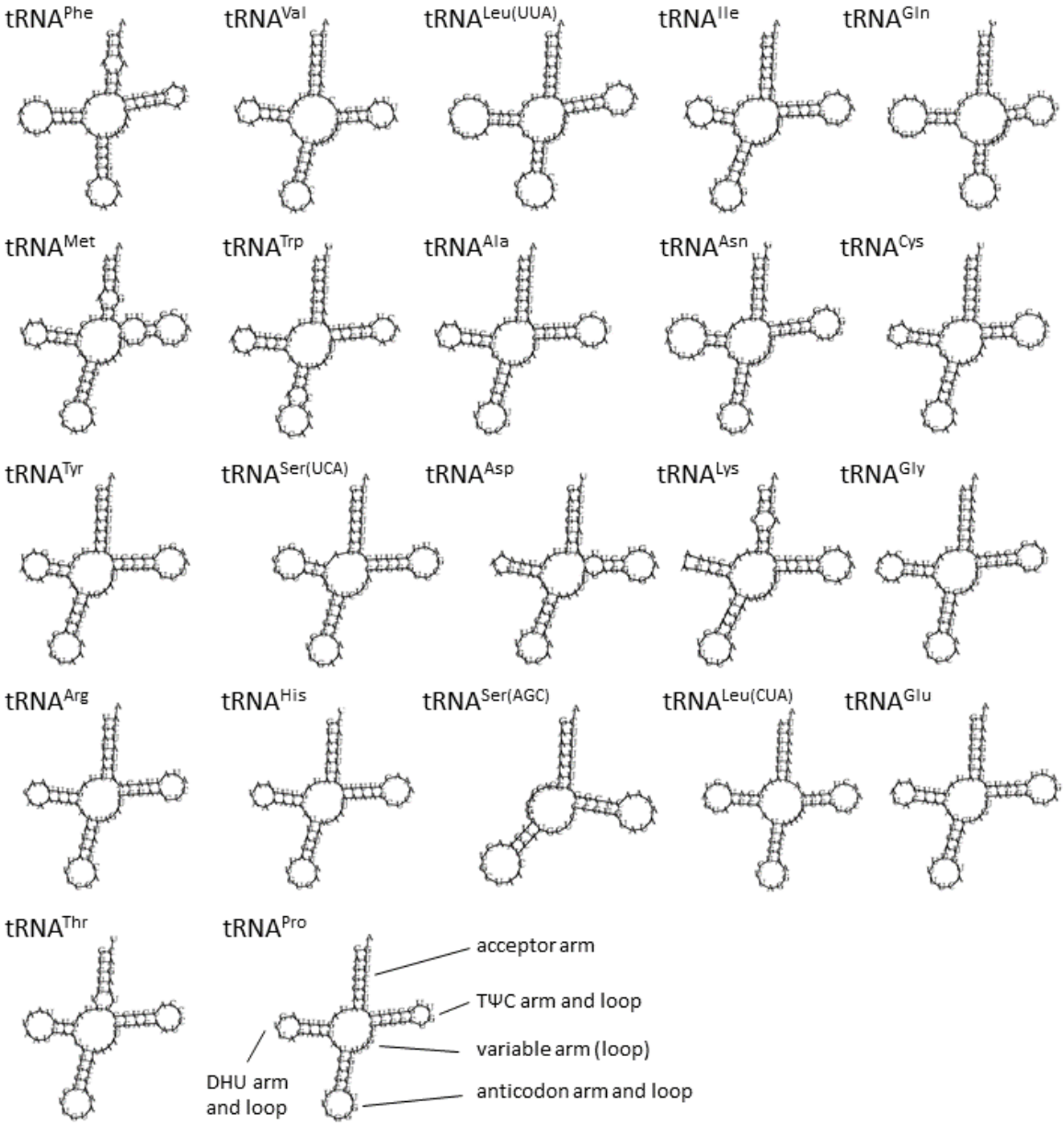

Figure S3. Predicted secondary structures of 22 mitochondrial tRNAs in European mink.

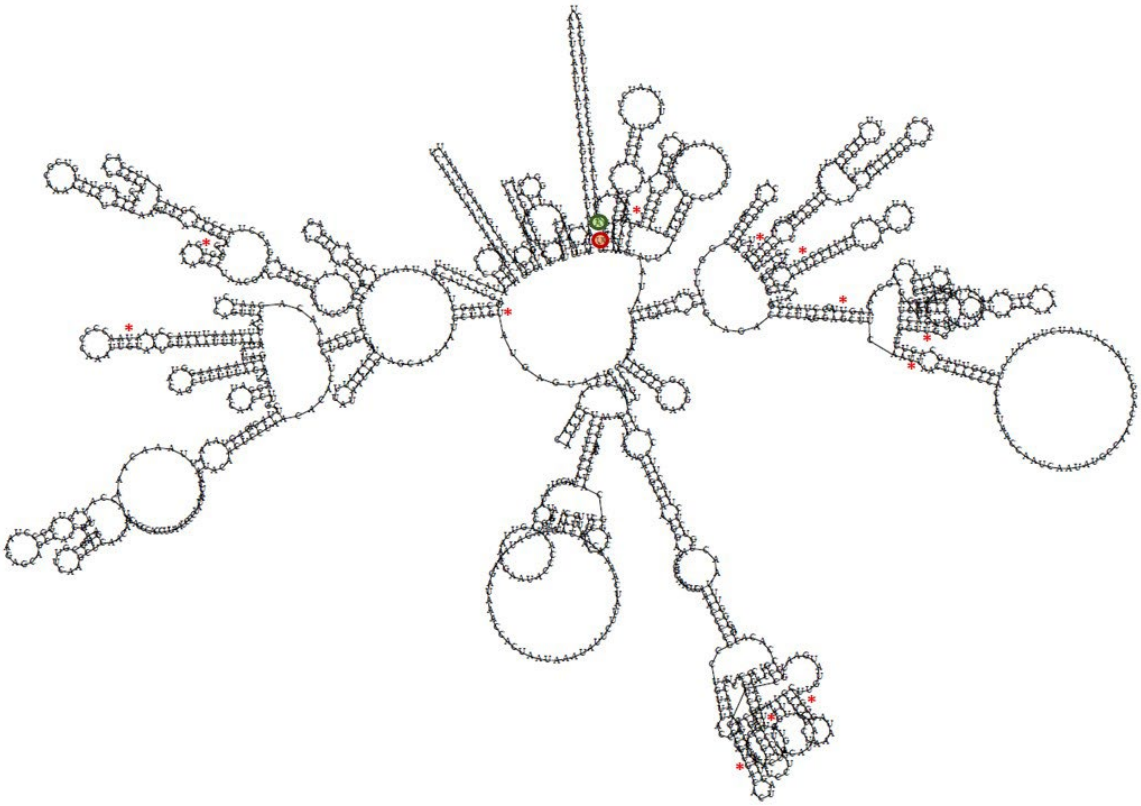

Figure S4. Predicted secondary structure of the mitochondrial ribosomal RNA of the large ribosomal subunit in *Mustela lutreola* (dashes indicate Watson-Crick base pairing; red asterisks indicate non-canonical G-U pairs; the 5′-end is marked with a green circle and the 3′-end with a red circle).

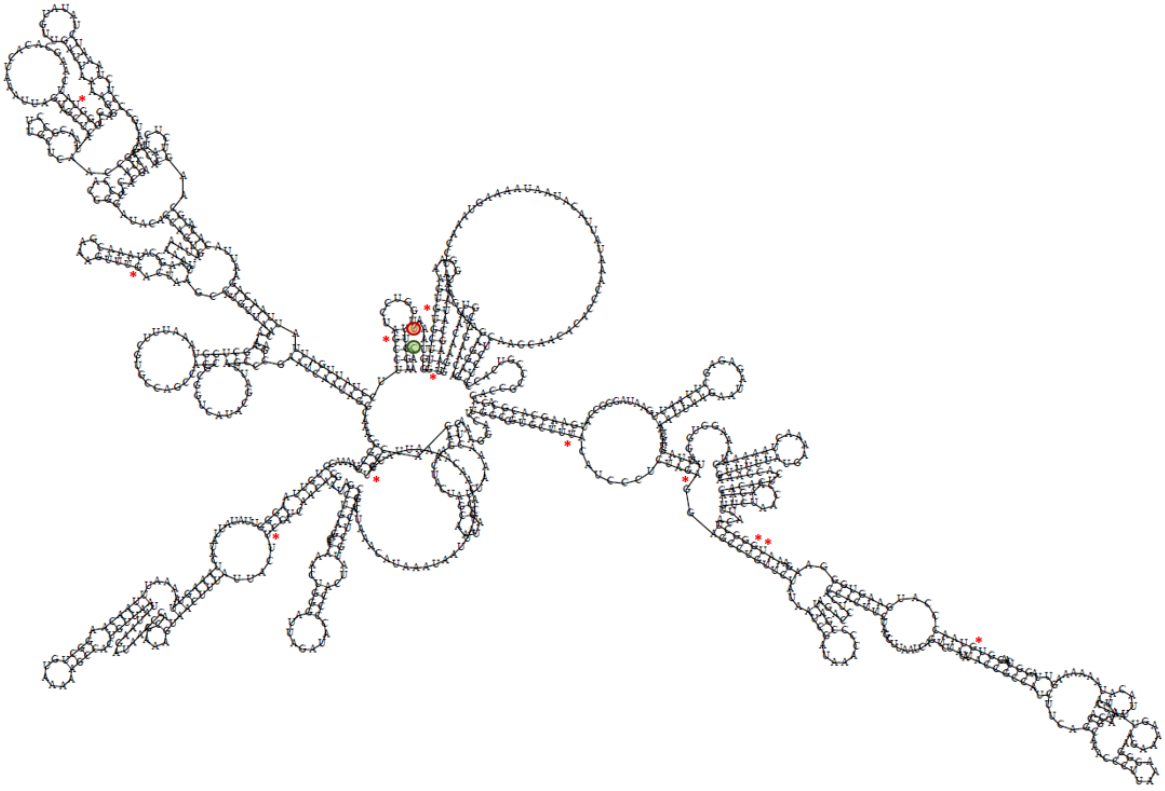

Figure S5. Predicted secondary structure of the mitochondrial ribosomal RNA of the small ribosomal subunit in *Mustela lutreola* (dashes indicate Watson-Crick base pairing; red asterisks indicate non-canonical G-U pairs; the 5′-end is marked with a green circle and the 3′-end with a red circle).

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    EU548041.1                              CTAATGTGCTTGCCCGGTATGTATTTCTTTTTT-
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    EU548045.1                              CTAATGTGCTTGCCCGGTATGTATTTCTTTTTT-
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    AF207725.1                              CTAATGTGCTTGCCCGGTATGTATTTCTTTTTT-
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    EU548046.1                              CTAATGTGCTTGCCCGGTATGTATTTCTTTTTT-
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    AF068544.1      ----------------------------------------------------------
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    JX982498.1
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    JX982497.1
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    JX982495.1
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    JX982496.1
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    JX982500.1
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    EU548049.1
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    EU548037.1
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    EU548038.1
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    EU548036.1
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    EU548035.1
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    AF207720.1
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    AB601576.1
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    EU548040.1
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    EU548039.1
ACTGGTTTGCCCCATGCATATAAGCATGTATATATTATGGTTGATTTTACATGTATCCAC   340
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ACTGGTTTGCCCCATGCATATAAGCATGTATATATTATGGTTGATTTTACATGTATCCAC   340
    EU548045.1
ACTGGTTTGCCCCATGCATATAAGCATGTATATATTATGGTTGATTTTACATGTATCCAC   340
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    EU548046.1
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    AF068544.1      ----------------------------------------------------
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    JX982498.1
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    JX982497.1
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    JX982495.1
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    JX982496.1
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    EU548044.1
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    EU548042.1
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    AF207723.1
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    EU548038.1
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    EU548036.1
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    EU548035.1
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    AF207720.1
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    AB601576.1
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    EU548039.1
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    AF207721.1
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    AF207724.1
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    EU548045.1
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    AF068544.1      ----------------------------------------------------------
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GTACACCTCTTCTCGCTCCGGGCCCATCAAATGTGGGGGTTCCTATCGTGAAACTATACC   249
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    JX982495.1
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    JX982496.1
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    JX982500.1
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    EU548049.1
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    EU548035.1
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    EU548040.1
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    EU548045.1
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    AF207725.1
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    EU548046.1
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TGGCATCTGGTTCTTACTTCAGGGCCATATCAATCCTCAACCCAATCCTACTAACCTCTC   309
    JX982498.1
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    JX982497.1
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    JX982495.1
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    JX982496.1
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    EU548044.1      TGGCATCTGGTTCTTACTTCAGGGCCATATCAATCCTCAACCC----------
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    EU548042.1      TGGCATCTGGTTCTTACTTCAGGGCCATATCAATCCTCAACCC----------
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    EU548043.1      TGGCATCTGGTTCTTACTTCAGGGCCATATCAATCCTCAACCC----------
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    EU548047.1      TGGCATCTGGTTCTTACTTCAGGGCCATATCAATCCTCAACCC----------
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    EU548049.1      TGGCATCTGGTTCTTACTTCAGGGCCATATCAATCCTCAACCC----------
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    EU548038.1      TGGCATCTGGTTCTTACTTCAGGGCCATATCAATCCTCAACCC----------
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    EU548036.1      TGGCATCTGGTTCTTACTTCAGGGCCATATCAATCCTCAACCC----------
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    EU548035.1      TGGCATCTGGTTCTTACTTCAGGGCCATATCAATCCTCAACCC----------
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    AF207724.1      TGGCAT-------------------------------------------------
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    JX982499.1
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    EU548041.1      TGGCATCTGGTTCTTACTTCAGGGCCATATCAACCCTCAACCC----------
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    EU548045.1      TGGCATCTGGTTCTTACTTCAGGGCCATATCAATCCTCAACCC----------
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    AF207725.1      TGGCAT-------------------------------------------------
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    EU548046.1      TGGCATCTGGTTCTTACTTCAGGGCCATATCAATCCTCAACCC----------
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    JX982497.1
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    AF207724.1      ----------------------------------------------------------
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    JX982499.1
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Figure S6. Multiple alignment for the 43 mtDNA sequences of *Mustela lutreola* deposited in the GenBank [23] aligned to the MW148603 reference sequence, reported in this paper.