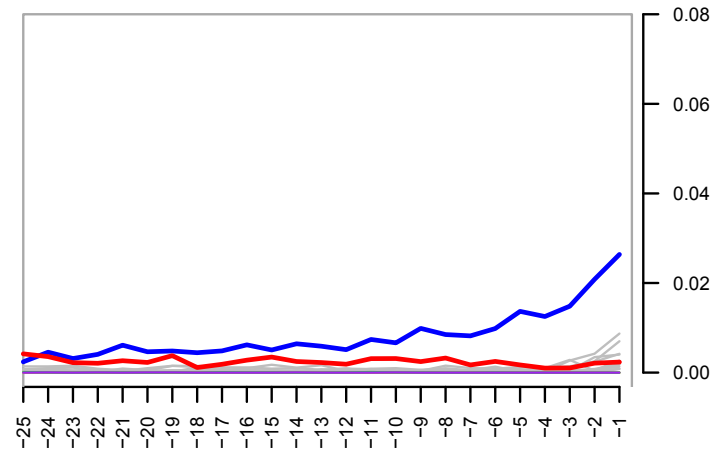
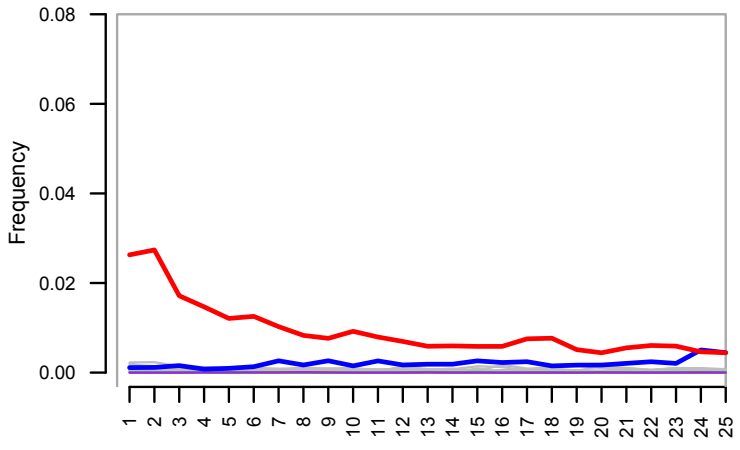
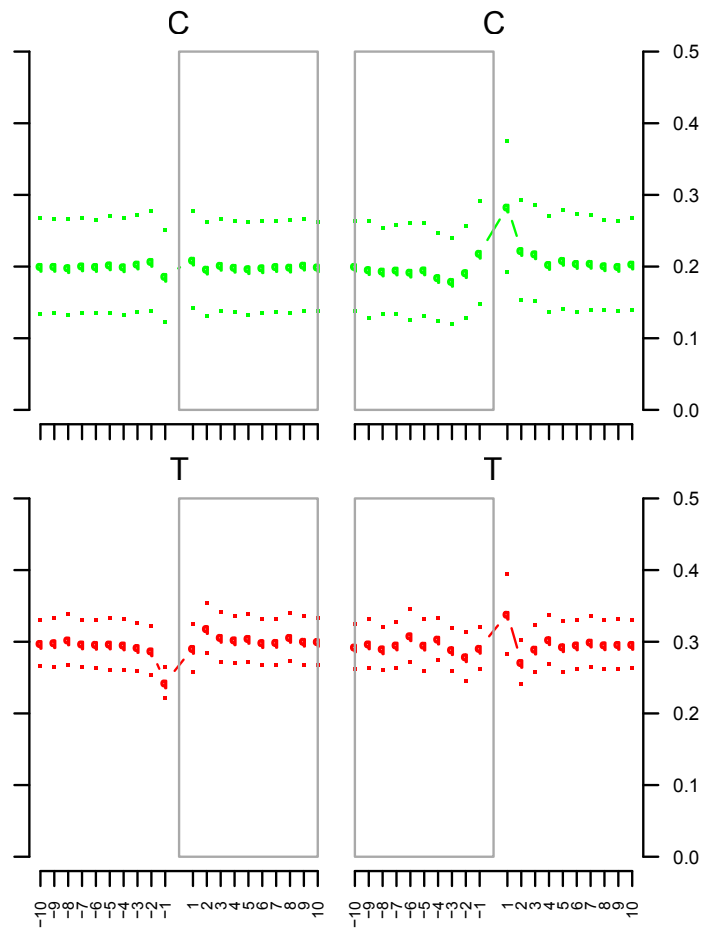
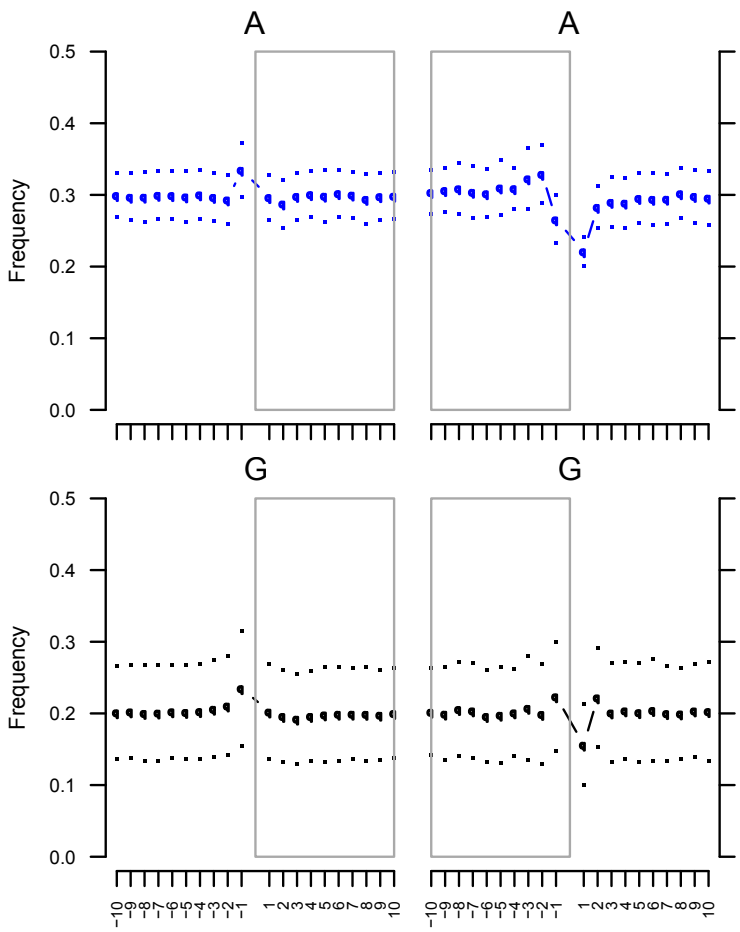
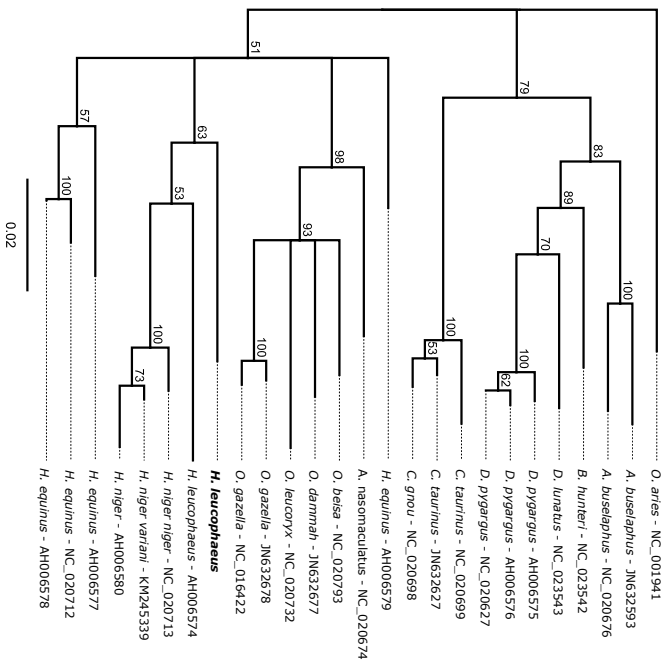
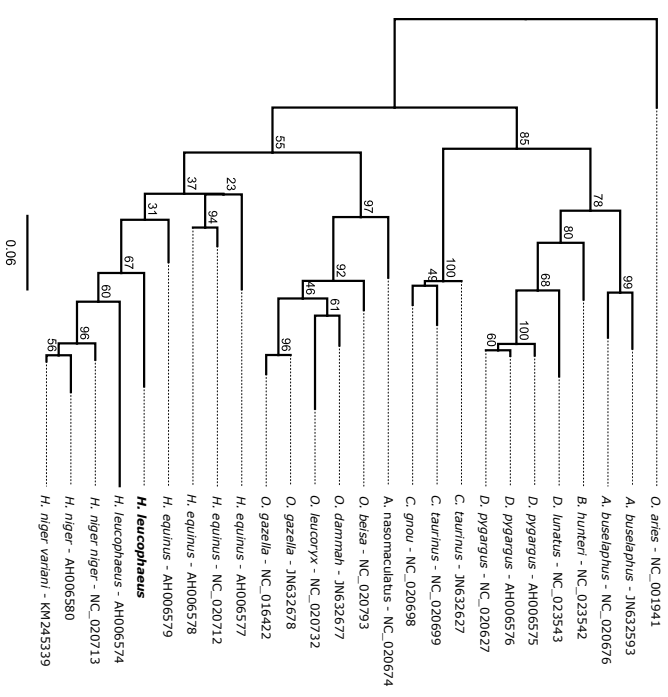
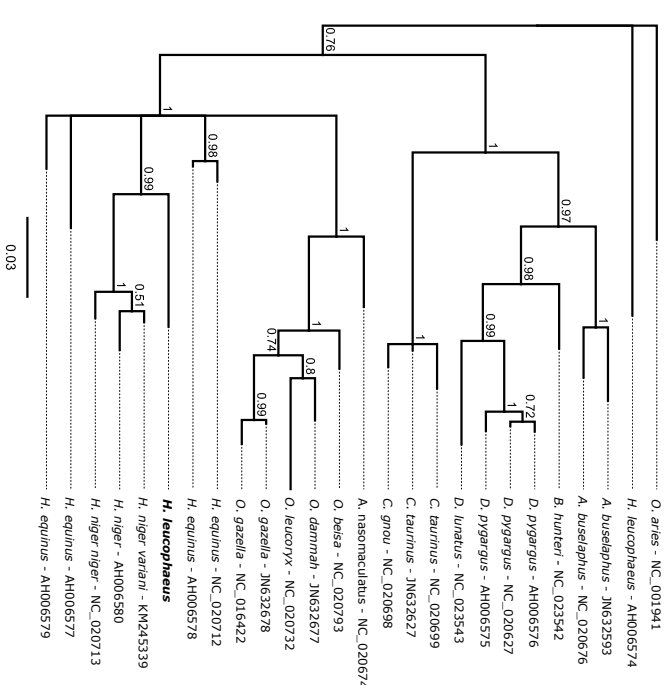


Supplementary Figure 1 – Misincorporation plot for collapsed mapped reads of Hleuco4 to the *Hippotragus niger* mitochondrial genome, generated with mapDamage 2.0. Top plots show the base frequency outside and in the read, delimited by the open grey box. The bottom plots are the position specific substitutions from the 5'' (left) and the 3'' end (right). Guanine to adenine and cytosine to thymine are reported in blue and red, respectively, with all other possible misincorporations represented in grey.



Supplementary Figure 2 – Cytochrome B phylogenetic tree of 25 individuals from 14 species of antelopes, calculated using Neighbor-Joining (A), Maximum Likelihood (B), and Bayesian inference (C). Branch labels indicate bootstrap support (A and B) or posterior probabilities (C). See text for details.

A**B****C**

Supplementary table 1 - Ka/Ks ratio between the mitochondrial genome of *Hippotragus leucophaeus* and other species of Hippotraginae and Alcelaphinae with publicly available mitochondrial genomes, calculated in DNAsp v5.0.

<i>Hippotragus leucophaeus</i> vs.	Ka/Ks ratio
Subfamily / species	
Hippotraginae	
<i>Addax nasomaculatus</i>	0.058
<i>Hippotragus niger</i>	0.053
<i>H. n. variani</i>	0.051
<i>H. equinus</i>	0.045
<i>Oryx beisa</i>	0.040
<i>O. dammah</i>	0.058
<i>O. gazella</i>	0.050
<i>O. leucoryx</i>	0.040
Alcelaphinae	
<i>Alcelaphus buselaphus</i>	0.040
<i>Connochaetes gnou</i>	0.038
<i>C. taurinus</i>	0.038
<i>Damaliscus pygargus</i>	0.040

Supplementary Table 2 - Synapomorphies supporting *H. leucophaeus* grouping with *H. niger* (including *H. n. variani*). Gene, position in relation to the mitochondrial sequence of *H. niger* (NC_020713), and type of substitution in relation to other Hippotraginae and Alcelaphinae (ancestral -> derived).

Gene	Position	Substitution
16S	1523	T -> C
16S	1647	T -> C
16S	1808	A -> G
16S	1811	A -> C
16S	1839	T -> C
16S	1844	C -> T
ND1	2794	C -> T
ND1	2851	G -> C
ND1	3502	A -> T
tRNA-Ile	3741	T -> C
tRNA-Gln	3781	C -> A
ND2	3916	T -> C
ND2	4391	C -> A
ND2	4483	T -> C
ND2	4790	T -> C
tRNA-Ala	5039	A -> G
COX1	6208	A -> C
COX1	6259	C -> T
COX1	6409	T -> C
COX1	6475	T -> C
COX1	6515	C -> T
ATP8	7906	C -> A
ATP6	8182	A -> G
ATP6	8422	T -> C
ATP6	8533	C -> T
COX3	8616	C -> G
COX3	8922	C -> T
COX3	9013	C -> T
COX3	9312	C -> T
tRNA-Gly	9403	T -> C
ND3	9766	C -> T
ND4L	10000	A -> G
ND4L	10157	C -> T
ND4	10230	C -> A
ND4	10323	A -> G
ND4	10359	A -> G
ND4	10389	A -> G
ND4	10452	C -> T
ND4	10745	T -> C
ND4	10924	G -> A
ND4	11085	C -> T
ND4	11090	T -> C
ND4	11099	C -> T
ND4	11136	A -> G
ND4	11322	A -> G

ND4	11499	C->A
tRNA-Ser	11642	C->T
tRNA-Leu	11685	A->C
ND5	12393	A->T
ND5	12612	C->T
ND5	13062	T->C
ND5	13063	A->T
ND5	13125	C->T
ND6	13775	C->T
ND6	13815	T->C
ND6	13910	T->C
ND6	13979	C->T
CYTB	14348	C->T
CYTB	14381	C->T
CYTB	14475	G->A
CYTB	15116	T->C
CYTB	15255	A->T
tRNA-Pro	15375	C->A

Supplementary Table 3 - Number of sequencing reads generated in this study from a DNA sample of *H. leucophaeus* and that mapped to the nuclear genome of *Ovis aries* and *Bos taurus*, for each chromosome.

Chromosome	<i>Ovis aries</i>	<i>Bos taurus</i>
1	101,262	33,603
2	91,567	30,394
3	78,104	25,960
4	44,288	26,255
5	38,396	24,402
6	42,850	24,117
7	36,671	22,599
8	34,974	23,875
9	35,618	22,791
10	30,880	22,490
11	17,881	21,431
12	27,321	17,358
13	27,552	16,206
14	18,790	18,229
15	27,552	15,731
16	25,235	15,671
17	24,525	13,902
18	22,550	11,446
19	19,921	10,463
20	16,260	14,151
21	14,217	13,430
22	16,613	11,678
23	21,956	9,625
24	11,543	12,442
25	14,099	6,727
26	14,920	9,751
27	NA	8,478
28	NA	8,301
29	NA	7,930
X	28,248	17,168
Total	883,793	516,604