

Supplementary Materials for **Inactivation of thermogenic UCP1 as a historical contingency in multiple placental mammal clades**

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The PDF file includes:

- fig. S1. Schematic maximum-likelihood tree of *ucp* sequences used in this study ($n = 400$).
- fig. S2. Exon alignments depicting deleterious mutations found in *UCP1* sequences of placental mammal taxa.
- fig. S3. Ribbon diagram of residues 13 to 304 of human UCP1 (UniProt accession number P25874) structurally modeled by SWISS-MODEL.
- fig. S4. Amino acid alignment of vertebrate sln.
- table S1. GenBank accession numbers of species used in this study.
- table S2. Likelihood ratio tests for *ucp1* CODEML models.
- table S3. Calculated *ucp1* inactivation dates (Ma) within the placental mammal lineage.
- table S4. Results of BiSSE models with and without constraints on the diversification rate for five trees from the work of Faurby and Svenning (56).
- table S5. BiSSE results for neutral character simulations.
- table S6. Deleterious mutations found in *ucp2* and *ucp3* sequences of placental mammal taxa.
- table S7. Specimen data and sources of tissue samples used for PCR amplification and DNA hybridization capture.
- table S8. Fossil constraints used in timetree analysis.

Other Supplementary Material for this manuscript includes the following:

(available at advances.sciencemag.org/cgi/content/full/3/7/e1602878/DC1)

- data file S1. Gene partitions, a maximum likelihood phylogram, and mcmcree (text file).

- data file S2. *ucp1* free ratio model (text file).
- data file S3. Fossil body mass, taxon diversity, and UCP1 diversification codings (Excel file).
- data file S4. *ucp2* free ratio model (Text file).
- data file S5. *ucp3* free ratio model (Text file).
- data file S6. *ucp1* coding sequence alignment (Fasta file).
- data file S7. *ucp2* coding sequence alignment (Fasta file).
- data file S8. *ucp3* coding sequence alignment (Fasta file).
- data file S9. Accession numbers for the 41 loci used to construct the 51-kb maximum likelihood species tree (Fasta file).
- data file S10. A 51-kb alignment (41 genes) for 140 vertebrate species (Text file).

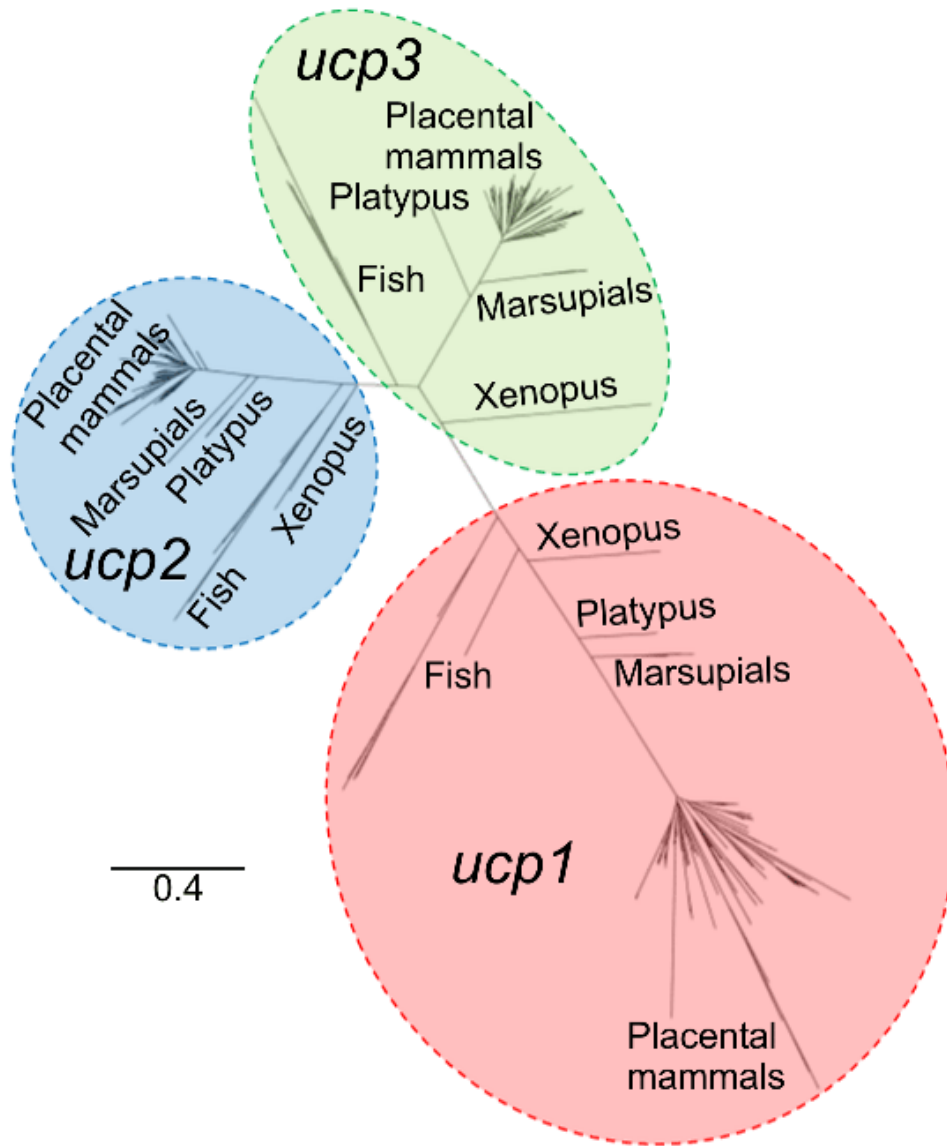


fig. S1. Schematic maximum-likelihood tree of *ucp* sequences used in this study ($n = 400$).
Branch lengths denote number of substitutions per site.

Exon 1

1 10 20 30 40 50
|...|...|...|...|...|...|...|...|...|...|...|
Homo sapiens ATGGGGGGCCTGA-CAGCCTCGGACGTACACCCGACCC---TGGGGGTCC
Bradypus variegatus ???
Choloepus hoffmanni ???
Mylonodon darwinii ???
Cyclopes didactylus ???
Dasybus novemcinctus ATGGGGCGCCAGGCTCCCGCGGGCTCACCCCGCGC-----
Procvavia capensis CTG--AGTTAAGA-CAACCTCAGAAATGCCGCTAC-----GCA
Elephas maximus ACGGTAGGCCAGA-CGACCGCAGACGTGCCCGGACCATGGTGGGGGTCA
Mammuthus primigenius ACGGTAGGCCAGA-CGACCGCAGACGTGCCCGGACCATGGTGGGGGTCA
Loxodonta africana ACCGTAGGCCAGA-CGACCGCAGACGTGCCCGGACCATGGTGGGGGTCA
Trichechus manatus ATGGTGGGCCAGA-CTACCTGGGATGTGCCCCGACCA---TGGGCGTCA
Dugong dugon ATGGTGGGCCAGA-CTACCTCGGATGTGCCCCGACCA---TGGGCGTCA
Hydrodamalis gigas ATGGTGGGCCAGA-CTACCTCGGATGTGCCCCGACCA---TGGGCGTCA
Sus scrofa CTGTCAGGA-TGA-CAGTTCCTGAAGTGCCCCGACCA---TAGCGGTCA
Sus verrucosus CTGTCAGGA-TGA-CAGTTCCTGAAGTGCCCTCGACCA---TAGCGGTCA
Sus cebifrons CTGTCAGGA-TGA-CAGTTCCTGAAGTGCCCTCGACCA---TAGCGGTCA
Physeter macrocephalus ATGGTGGGACTCG-CAGCCTCATACTGCCCCGACCA---TGGGCGTCA
Delphinapterus leucas -----
Lipotes vexillifer ATGGTGGGACTCG-CAGCCTCAGACGTGCCCCGACCA---TGGGCGTCA
Balaena mysticetus ATGGTGGCACTCA-CAGCCTCAGACGTGCCCCGACCA---TGGGCGTCA
Balaenoptera acutorostrata ATGCTGGGACTCA-CAGCCTCAGACGCGCCCCGACCG---TGGGCGTCA
Balaenoptera physalus ATGCTGGGACTCA-CAGCCTCAGACGCGCCCCGACCA---TGGGCGTCA
Balaenoptera bonaerensis ATGCTGGGACTCA-CAGCCTCAGACGCGCCCCGACCA---TGGGCGTCA
Equus asinus ATGGTGGGGCCCA-CAGCCTCGGACCCGCCCCGACCA---TGGGCGTCA
Equus quagga boehmi ATGGTGGGGCCCA-CAGCCTCGGACCGCCCCGACCA---TGGGCGTCA
Equus przewalskii ???
Equus caballus ATGGTGGGGCCCA-CAGCCTCGGACGTGCCCCGACCA---TGGGCGTCA
Manis pentadactyla -----

51 60 70 80 90 100
|...|...|...|...|...|...|...|...|...|...|...|
Homo sapiens AGCTCTTCTCAGCTGGA---ATAGCGGGCTGCTTGGCGGACGTGATCACC
Bradypus variegatus ???
Choloepus hoffmanni ???
Mylonodon darwinii ???
Cyclopes didactylus ???
Dasybus novemcinctus -----GCGGAAACGAGGCGGC-----GGCAGGTGCACCCCGC
Procvavia capensis ACCTCTTCTCAGCTGGA---GTGGCGGCCTGCTTGGCCGGTGTGATCACC
Elephas maximus AGATCTTCTCAGCGGGA---GTGGCGGCCTGCTTGGCAGATGTAATTACC
Mammuthus primigenius AGATCTTCTCAGCGGGA---GTGGCGGCCTGCTTGGCAGATGTAATTACC
Loxodonta africana AGATCTTCTCAGCGGGA---GTGGCGGCCTGCTTGGCAGATGTAATTACC
Trichechus manatus AGATCGTCTCAGCTGGA---GTGTGGCCTGTTTGGCGGATGTGATCACC
Dugong dugon AGATTGTCTCAGCTGGA---GTGTGGCCTGTTTGGCGGATGTGATCACC
Hydrodamalis gigas AGATTGTCTCAGCTGGA---GTGTGGCCTGTTTGGCGGATGTGATCACC
Sus scrofa AGATCTTCTCAGCTGGA---GCAGCGGCCTGCGTGGCAGATGTGATCACC
Sus verrucosus AGATCTTCTCAGCTGGA---GCGGCGGCCTGCGTGGCAGATGTGATCACC
Sus cebifrons AGATCTTCTCAGCTGGA---GCGGCGGCCTGCGTGGCAGATGTGATCACC
Physeter macrocephalus AGATCTTCTCGGCTGGA---GTGGCGGCCTGCGTGGCGGATGTGATCACC
Delphinapterus leucas -----
Lipotes vexillifer AGATCTTCTCGGCTGGA---GTGGCGGCCAGCGTGGCGGATGTGATCACC
Balaena mysticetus CGATCTTCTCGGCTGGA---GTGGCGGCCGCGCTGGCGGATGTGATCACC
Balaenoptera acutorostrata CGATCTTCTCGGCTGGA---GTGGCGGCCGCGCTGGCGGATGTGATCACC
Balaenoptera physalus CGATCTTCTCGGCTGGA---GTGGCGGCCGCGCTGGCGGATGTGATCACC
Balaenoptera bonaerensis CGATCTTCTCGGCTGGA---GTGGCGGCCGCGCTGGCGGATGTGATCACC
Equus asinus AGATCTTCTCGGCTGGA---GTGGCGGCCTGCGTGGCGGACGTGATCGCC
Equus quagga boehmi AGATCTTCTCGGCTGGA---GTGGCGGCCTGCGTGGCGGACGTGATCGCC

Equus przewalskii ???CCTGCGTGGCGGACGTGATCGCC
Equus caballus AGATCTTCTCGGCTGGA--GTGGCGGCCTGCGTGGCGGACGTGATCGCC
Manis pentadactyla -----

	101	110	120	130

<i>Homo sapiens</i>	TTCCCGC	--TGGACACGGCCAAAGTCCGGCTCCAGgt		
<i>Bradypus variegatus</i>	????????	????????	????????	????????
<i>Choloepus hoffmanni</i>	????????	????????	????????	????????
<i>Mylonodon darwini</i>	????????	????????	????????	????????
<i>Cyclopes didactylus</i>	????????	????????	????????	????????
<i>Dasyurus novemcinctus</i>	CTCCTCCGC	TGGG	GCCGCCAGCCTGGGGCTGCAGct	
<i>Procavia capensis</i>	TTCCAC	--TGGACACTGCCCAAGTTCGGGTACAGgc		
<i>Elephas maximus</i>	TTCCCGC	--TGATCGCGGCCAAAGTTCGGCTGCAGat		
<i>Mammuthus primigenius</i>	TTCCCGC	--TGGTCGCGGCCAAAGTTCGGCTGCAGat		
<i>Loxodonta africana</i>	TTCCCGC	--TGGTCGCGGCCAAAGTTCGGCTGCAGat		
<i>Trichechus manatus</i>	TTCCAC	--TGGACACGGCCAAGGTTTCGGCTACAGgt		
<i>Dugong dugon</i>	TTCCAC	--TGGACACGGCCAAGGTTTCGGCTACAGgt		
<i>Hydrodamalis gigas</i>	TTCCAC	--TGGACACGGCCAAGGTTTCGGCTACAGgt		
<i>Sus scrofa</i>	TTGCAC	TTGGACACCGCCAAAGTCCGGCTACAGgt		
<i>Sus verrucosus</i>	TTGCAC	TTGGACACCGCCAAAGTCCGGCTACAGgt		
<i>Sus cebifrons</i>	TTGCAC	TTGGACACCGCCAAAGTCCGGCTACAGgt		
<i>Physeter macrocephalus</i>	TTCCCGC	--TGGACACGGCCAAGTCCGGCTACAGgg		
<i>Delphinapterus leucas</i>	-----			
<i>Lipotes vexillifer</i>	TTCCCGC	--TGGACACGGCCAAGTCCGGCTACAGgg		
<i>Balaena mysticetus</i>	TTCCCGC	--TGGACACGGCCAAGTCCGGCTACAGgt		
<i>Balaenoptera acutorostrata</i>	TTCCCGC	--TGGACACGGCCATAGTCCGGCTACAGgt		
<i>Balaenoptera physalus</i>	TTCCCGC	--TGGACACGGCCAAGTCCGGCTACAGgt		
<i>Balaenoptera bonaerensis</i>	TTCCCGC	--TGGACACGGCCATAGTCCGGCTACAGgt		
<i>Equus asinus</i>	TTCCCGC	--TGGACACGGCCAAGTCCGGCTGCAGgt		
<i>Equus quagga boehmi</i>	TTCCCGC	--TGGACACGGCCAAGTCCGGCTGCAGgt		
<i>Equus przewalskii</i>	TTCCCGC	--TGGACACGGCCAAGTCCGGCTGCAGgt		
<i>Equus caballus</i>	TTCCCGC	--TGGACACGGCCAAGTCCGGCTGCAGgt		
<i>Manis pentadactyla</i>	-----			

Exon 2

	136	140	150	160	170	180

<i>Homo sapiens</i>	agGTCCAAGGTGAATGCCGACGTCCAGTGTTATTAGGTATAAAAGGTGTCCTG					
<i>Bradypus variegatus</i>	????????	????????	????????	????????	????????	????????
<i>Choloepus hoffmanni</i>	????????	????????	????????	????????	????????	????????
<i>Mylonodon darwini</i>	????????	????????	????????	????????	????????	????????
<i>Cyclopes didactylus</i>	????????	????????	????????	????????	????????	????????
<i>Dasyurus novemcinctus</i>	agATCCAAGGTGAAGGTGAGAAATCCCATGCTATTAAGTACAAAGGTCTCCTG					
<i>Procavia capensis</i>	agATCCAAGGTGAATGGCAGAAGTCCAGTGCCCTTAGCTATAAAAGGCGTCTTG					
<i>Elephas maximus</i>	agATCCAAGGTGAATGCCAGACCTCCAGTGCCATTAGGTATAAAAGGTGTCTTG					
<i>Mammuthus primigenius</i>	agATCCAAGGTGAATGCCAGACCTCCAGTGCCATTAGGTATAAAAGGTGTCTTG					
<i>Loxodonta africana</i>	agATCCAAGGTGAATGCCAGACCTCCAGTGCCATTAGGTATAAAAGGTGTCTTG					
<i>Trichechus manatus</i>	agATCCAAGGTGAATGCCAGACCTCCAGTGCCATTAGGTATAAAAGGTGTCTTG					
<i>Dugong dugon</i>	agATCCAAGGTGAATGCCAGACCTCCAGTGCCATTAGGTATAAAAGGTGTCTTG					
<i>Hydrodamalis gigas</i>	agATCCAAGGTGAGTGCCAGACCTCCAGTGCCATTAGGTATAAAAGGTGTCTTG					
<i>Sus scrofa</i>	agATCCAAGGCAAATGCCGGTCTCCGGTACCATTTCGGTACAAAGACGTCTCTG					
<i>Sus verrucosus</i>	agATCCAAGGCAAATGCCGGTCTCCGGTACCATTTCGGTACAAAGACGTCTCTG					
<i>Sus cebifrons</i>	agATCCAAGGCAAATGCCGGTCTCCGGTACCATTTCGGTACAAAGACGTCTCTG					
<i>Physeter macrocephalus</i>	agATCCAATGCGAATGCCAGACCTCCAGTGCTGTTAGGTATAAAAGGTGTCTCTG					
<i>Delphinapterus leucas</i>	-----					
<i>Lipotes vexillifer</i>	agATCCAATGCGAATGCCAGACCTCCAGTGCTGTTAGGTATAAAAGGTGTCTCTG					
<i>Balaena mysticetus</i>	agATCCAATGCGAATGCCAGATCTCCAGTGCTGTTAGGTATAAAAGGTGTCTCTG					
<i>Balaenoptera acutorostrata</i>	agGTCCAATGCGAATGCCAGACCTCCAGTGCTGTTAGGTATAAAAGGTGTCTCTG					

Balaenoptera physalus
Balaenoptera bonaerensis
Equus asinus
Equus quagga boehmi
Equus przewalskii
Equus caballus
Manis pentadactyla

agATCCAATGCGAATGCCAGACCTCCAGTGCTGTTAGGTATAAAAGTGTCTG
agATCCAATGCGAATGCCAGACCTCCAGTGCTGTTAGGTATAAAAGTGTCTG
agATCCAAGGCGAGCGCCAGACCTCCAGTGCCCTGAGGTATAACGGTATCCTG
agATCCAAGGCGAGCGCCAGACCTCCAGTGCCCTGAGGTATAACGGTATCCTG
agATCCAAGGCGAGCGCCAGACCTCCAGTGCCCTGAGGTATAAAAGGTATCCTG
agATCCAAGGCGAGCGCCAGACCTCCAGTGCCCTGAGGTATAAAAGGTATCCTG

Homo sapiens
Bradypus variegatus
Choloepus hoffmanni
Mylodon darwinii
Cyclopes didactylus
Dasyopus novemcinctus
Procavia capensis
Elephas maximus
Mammuthus primigenius
Loxodonta africana
Trichechus manatus
Dugong dugon
Hydrodamalis gigas
Sus scrofa
Sus verrucosus
Sus cebifrons
Physeter microcephalus
Delphinapterus leucas
Lipotes vexillifer
Balaena mysticetus
Balaenoptera acutorostrata
Balaenoptera physalus
Balaenoptera bonaerensis
Equus asinus
Equus quagga boehmi
Equus przewalskii
Equus caballus
Manis pentadactyla

186 190 200 210 220 230
|...|...|...|...|...|...|...|...|...|...|...|...|
GGAACAATCACCCTGTGGTAAAAACAGAAGGGCGGATGAAACTCTACAG
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GGAACAGTCGCCACTTGGCAAAAACGGAAGGGCCAATGAA--CCTACCG
GAAACAACCACCCTTGACAAAAACAGAGGGGCAATGAAACTATAGCT
GGAACAATCACTACTCTGGCAAAAAGGAAGAGCCAATGAAACTCTATAG
GGAACAATCACTACTCTGGCAAAAAGGAAGAGCCAATGAAACTCTATAG
GGAACAATCACTACTCTGGCAAAAAGGAAGAGCCAATGAAACTCTATAG
GGAACAATCACCCTCTGGCAAAAACAGAAGGGCCAATGAAACGCTATAG
GGAACAATCACCCTCTGGCAAAAACAGAAGGGCCAATGAAACGCTATAG
GGAACAATCACCCTCTGGCAAAAACAGAAGGGCCAATGAAACGCTATAG
GGAACAATCACCCTCTGGCAAAAACAGAAGGGCCAATGAAAGCTCTACAG
GGAACAATCACTACTCTGGCAAAAAGACAGAAGGGCCAATGAAAGCTCTACAG
GGAACAATCACCCTCTGGCAAAAACAGAAGGGCCAATGAAACTCTACAG
GGAACAATCACCCTCTGGCAAAAACAGAAGGGCCAATGAAACTCTACAG

GGAACAATCACCCTCTGGCAAAAACAGAAGGGCCAATGAAACGCTCCAG
GGAACAATCACCCTCTGGCAAAAACAGAAGGGCCAATGAAACTCTACAG
GGAACAATCACCCTCTGGCAAAAACAGAAGGGCCAATGAAACTCTACAA
GGAACAATCACCCTCTGGCAAAAACAGAAGGGCCAATGAAACTCTACAG
GGAACAATCACCCTCTGGCAAAAACAGAAGGGCCAATGAAACTCTACAA
GGGACAATCACCCTCTGGCAAAAACAGAAGGGCCAATGAAACTCTACAG
GGGACAATCACCCTCTGGCAAAAACAGAAGGGCCAATGAAACTCTACAG
GGGACAATCACCCTCTGGCAAAAACAGAAGGGCCAATGAAACTCTACAG
GGGACAATCACCCTCTGGCAAAAACAGAAGGGCCAATGAAACTCTACAG

Homo sapiens
Bradypus variegatus
Choloepus hoffmanni
Mylodon darwinii
Cyclopes didactylus
Dasyopus novemcinctus
Procavia capensis
Elephas maximus
Mammuthus primigenius
Loxodonta africana
Trichechus manatus
Dugong dugon
Hydrodamalis gigas
Sus scrofa
Sus verrucosus
Sus cebifrons
Physeter microcephalus
Delphinapterus leucas
Lipotes vexillifer

236 240 250 260 270 280
|...|...|...|...|...|...|...|...|...|...|...|...|
CGGGCTGCCTGCGGGGCTTCAGCGGCAATCAGCTCCGCCCTCTCTCAGGA
??
??
??
??
CGAGCTGCCTGCTGGCTTCAGAAACAGATGCACTCCACCCT--AGGA
--GCTGCCTGCTGGCTTCAGAGACAAATAAGCTTTGCCTCTCTTAGAA
TGGGCTGCCTGCTGGCTTCAGAGACAAATAAGCTTTGCCTCTCTTAGGA
TGGGCTGCCTGCTGGCTTCAGAGACAAATAAGCTTTGCCTCTCTTAGGA
TGGGCTGCCTGCTGGCTTCAGAGACAAATAAGCTTTGCCTCTCTTAGGA
TGGGCTGCCTGCTGGCTTCAGAGACAAATAAGCTTTGCCTCTCTTAGGA
TGGGCTGCCTGCTGGCTTCAGAGACAAATAAGCTTTGCCTCTCTTAGGA
AGGGCTGCCTGCTGGCTTCAGAGACAAATAAAGCTTCCCTCTCTTAGGA
AGGGCTGCCTGCTGGCTTCAGAGACAAATAAAGCTTCCCTCTCTTAGGA
AGGGCTGCCTGCTGGCTTCAGAGACAAATAAAGCTTCCCTCTCTTAGGA
AGGGCTGCCTGCTGGCTTCAGAGACAAATAAAGCTTCCCTCTCTTAGGA
AGGGCTGCCTGCTGGCTTCAGAGACAAATAAAGCTTCCCTCTCTTAGGA

TGGGCTGCCTGCTGGCTTCAGAGACAAATAAGCTTCCCTCTCTTAGGA

Balaena mysticetus CGGGCTGCCTGCTGGCCTCCAGAGACAAATAAGCTTTGCCTCTCTTAGGA
Balaenoptera acutorostrata CGGGCTGCCTGCTGGCCCCAGAGACAAATAAGCTTTGCCTCTCTTAGGA
Balaenoptera physalus TGGGCTGCCAGCTGGCCTCCAGAGACAAATAAGCTTTGCTTCTCTTAGGA
Balaenoptera bonaerensis CGGGCTGCCTGCTGGCCTCCAGAGACAAATAAGCTTTGCCTCTCTTAGGA
Equus asinus CGGGCTGCCTGCTGGCCTCCAGAGA TAAATAAGCTTCGCCTCTCTGAGGA
Equus quagga boehmi CGGGCTGCCTGCTGGCCTCCAGAGA TAAATAAGCTTCGCCTCTCTGAGGA
Equus przewalskii CGGGCCGCTGCTGGCCTCCAGAGA TAAATAAGCTTCGCCTCTCTGAGGA
Equus caballus CGGGCCGCTGCTGGCCTCCAGAGA TAAATAAGCTTCGCCTCTCTGAGGA
Manis pentadactyla -----

286 290 300 310 320 330
 |...|...|...|...|...|...|...|...|...|...|...
Homo sapiens TCGGCCTCTACGACACGGTCCAGGAGTTCCCTCACCGCAGGGAAAGAAAgT
Bradypus variegatus ???
Choloepus hoffmanni ???
Mylodon darwinii ???
Cyclopes didactylus ???
Dasyus novemcinctus TGGGACTC TACGATACCGTCCCGCGGC TTTCCACCGCAGGGAAACCAGca
Procavia capensis TTGGCTTCTGTGACA GGTTCAGGAGTACTTCACTGGAGGAAAGAAAgT
Elephas maximus CTGGCCTCTATGATATGGCCAGGAGTATTCCACTGCAGAGAAAGAAAgT
Mammuthus primigenius CTGGCCTCTATGATATGGCCAGGAGTATTCCACTGCAGAGAAAGAAAgT
Loxodonta africana CTGGCCTCTATGATATGGCCAGGAGTATTCCACTGCAGAGAAAGAAAgT
Trichechus manatus TTGGCCTCTATGATACTGTCCAGGAGTATTTCACTGCAGGGAAAGAAAgT
Dugong dugon TTGGCCTCTATGATACTGTCCAGGAGTACTTCACTGCAGGG TAAAGAAAgT
Hydrodamalis gigas TTGGCCTCTATGATACTGTA?AGGAGTACTTCACTGCAGGG TAAAGAAAgT
Sus scrofa TCAGCCTCTATGATAACCATCCAGG -----GAGAGAAAgT
Sus verrucosus TCACCCTCTATGATAACCATCCAGG -----GAGAGAAAgT
Sus cebifrons TCAGCCTCTATGATAACCATCCAGG -----GAGAGAAAgT
Physeter macrocephalus TCAGCCTCTATGAGAGCATCCAGGAGCTCTTACCACAGGGAAAGAAAgT
Delphinapterus leucas -----
Lipotes vexillifer TCAGCCTCTATGAGAGCAT CAGGAGTTCTTACCACAGGGAAAGAAAgT
Balaena mysticetus TCAGCATCTATGAAAGCATCCAGGAGTTCTTACCACAGGGAAAGAAAgT
Balaenoptera acutorostrata TCAGCCTCTATGAAAGCATCCAGGAGTTCTTACCACAGGGAAAGAAAgT
Balaenoptera physalus TCAGCCTCTATGAAAGCATCCAGGAGTTCTTACCACAGGGAAAGAAAgT
Balaenoptera bonaerensis TCAGCCTCTATGAAAGCATCCAGGAGTTCTTACCACAGGGAAAGAAAgT
Equus asinus TTGGCCTCTATGATACGGTCCAGGAGTTCTTACCACAGGGAAAGAAAgT
Equus quagga boehmi TTGGCCTCTATGATACGGTCCAGGAGTTCTTACCACAGGGAAAGAAAgT
Equus przewalskii TTGGCCTCTATGATACGGTCCAGGAGTTCTTACCACAGGGAAAGAAAgT
Equus caballus TTGGCCTCTATGATACGGTCCAGGAGTTCTTACCACAGGGAAAGAAAgT
Manis pentadactyla -----

Exon 3

334 340 350 360 370 380
 |.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Homo sapiens agCAGCACCTAGTTTAGGAAGCAAGATTTTAGCTGGTCTAACGACTGGAGGAGT
Bradypus variegatus ???
Choloepus hoffmanni ???
Mylodon darwinii ag-----GTAGTTTAGAAATCAAGATTTTCAAGTTGGCTTAACAAGTGGAGAAGT
Cyclopes didactylus ???
Dasyus novemcinctus -----
Procavia capensis -----
Elephas maximus aaCTCCAGCTAGTTTAGAAAGCAAGATCGCTGCTGGCTTAAGGACTGGAGGAGT
Mammuthus primigenius aaCTCCAGCTAGTTTAGAAAGCAAGATCGCTGCTGGCTTAAGGACTGGAGGAGT
Loxodonta africana aaCTCCAGCTAGTTTAGAAAGCAAGATCGCTGCTGGCTTAAGGACTGGAGGAGT
Trichechus manatus agCACCGGCTAGTTTAGGAAGCAAGATCTCTGCTGGCTTAACGACTGGAGGAGT
Dugong dugon agCACCGGCTAGTTTAGGAAGCAAGATCTCCGCTGGCTTAACGACTGGAGGAGT
Hydrodamalis gigas agCACCGGCTAGTTTAGGAAGCAAGATCTCCGCTGGCTTAATGACTGGAGGAGT
Sus scrofa -----
Sus verrucosus -----

Sus cebifrons
Physeter macrocephalus
Delphinapterus leucas
Lipotes vexillifer
Balaena mysticetus
Balaenoptera acutorostrata
Balaenoptera physalus
Balaenoptera bonaerensis
Equus asinus
Equus quagga boehmi
Equus przewalskii
Equus caballus
Manis pentadactyla

aa caac ag CTAGTTTAGGAAGCCAGGTCTCAGCGGGCCTAACGACTGGCGGTGT

aa caac gg CTAGTTTAGTGAGAAGCAGGGTCTCAGCGGGCCTAACGACTGGCGG
aa caac gg CTAGTTTAGGAAGCAGGGTCTCAGCGGGCCTAACGAATGGCGGCGT
aa caac gg CTAGTTTAGGAAGCAGGGTCTCAGCGAGCCTAACGAATGGCGGCGT
aa caac gg CTAGTTTAGGAAGCAGGGTCTCAGCGGGCCTAACGAMTGGCGGCGT
aa caac gg CTAGTTTAGGAAGCAGGGTCTCAGCGGGCCTAACGACTGGCAGCAT
ag-----CTAGTTTAGGAAGCAAGGTCTCAGCTGGCCTAACGACTGGAGGAGT
ag-----CTAGTTTAGGAAGCAAGGTCTCAGCTGGCCTAACGACTGGAGGAGT
ag-----CTAGTTTAGGAAGCAAGGTCTCAGCTGGCCTAACGACTGGAGGAGT
ag-----CTAGTTTAGGAAGCAAGGTCTCAGCTGGCCTAACGACTGGAGGAGT
agCAACACTTCAGTTAGGAAGTAAGATCTCAGCTGAGCTAA GACTAAAGGAGA

385 390 400 410 420 430

Homo sapiens
Bradypus variegatus
Choloepus hoffmanni
Mylonodon darwinii
Cyclopes didactylus
Dasyptes novemcinctus
Procavia capensis
Elephas maximus
Mammuthus primigenius
Loxodonta africana
Trichechus manatus
Dugong dugon
Hydrodamalis gigas
Sus scrofa
Sus verrucosus
Sus cebifrons
Physeter microcephalus
Delphinapterus leucas
Lipotes vexillifer
Balaena mysticetus
Balaenoptera acutorostrata
Balaenoptera physalus
Balaenoptera bonaerensis
Equus asinus
Equus quagga boehmi
Equus przewalskii
Equus caballus
Manis pentadactyla

|...|...|...|...|...|...|...|...|...|...|...|...|...|...|
GGCAGTATTCATTGGGGCAACCCACAGAGGTCTGTAAGTCAGACTTCAAG
??
??
GGCCAT??
??

GGCAGTGTTCACT GGC A ACCC ACAGAGGTCTGGAGGCTAGACTTCAAG
GGCAGTGTTCACT GGC A ACCC ACAGAGGTCTGGAGGCTAGACTTCAAG
GGCAGTGTTCACT GGC A ACCC ACAGAGGTCTGGAGGCTAGACTTCAAG
GGCGGTATTCATTGGGGCAACCCACAGAGGTCTGCAGGTCAAGCATCAAG
GGTGGTATTCATTGGGGCAACCCACAGAGGTCTGCAGGTCAAGCATCAAG
GGCGGTATTTGCTGGGGCAACCCACAGAGGTCTGCAGGTCAAGCATCAAG

GGCCGTGTTCATTGGGGCAACGCACAGAGGTAGTGAAGGTCAAGACTTCAAG
-----TGGTGAAGGTCAAGACTTCAAG
GGCCGTGTTCGTTGGGGCAACCCACAGAGGTAGTGATGGTCAAGACTTCAAG
GGCCGTGTTCATTGGGGCAACCCACAGAGGTAGTGAAGGTCAAGACTTCAAG
GGCTGTGTTCATTGGGGCAACCCACAGAGGTAGTGAAGGTCAAGACTTCAAG
GGCCGTGTTCATTGGGGCAACCCACAGAGGTAGTGAAGGTCAAGACTTCAAG
GGCAGTATTCATTGGGGCAACCCACCAGAGGTCTGAAGGTCAAGACTTCAAG
GGCAGTATTCATTGGGGCAACCCACAGAGGTCTGAAGGTCAAGACTTCAAG
GGCAGTATTCATTGGGGCAACCCACCAGAGGTCTGAAGGTCAAGACTTCAAG
GGCAGTATTCATTGGGGCAACCCACCAGAGGTCTGAAGGTCAAGACTTCAAG
GACAGTATTTATTTGGGCAAC CACAGAGGTTGTGAAGGTCAAGACTTCAAG

436 440 450 460 470 480

Homo sapiens
Bradypus variegatus
Choloepus hoffmanni
Mylonodon darwinii
Cyclopes didactylus
Dasyptes novemcinctus
Procavia capensis
Elephas maximus
Mammuthus primigenius
Loxodonta africana
Trichechus manatus
Dugong dugon

|...|...|...|...|...|...|...|...|...|...|...|...|...|...|
CACAGAGCCATCTCCACGGAACTCAAACCTCGCTACACGGGACTTATAAT
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??
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??

CACAGAGCCATCTACATGGTCTCAAACCGTGCTACACTGGGACTTACAAT
CACAGAGCCATCTACATGGTCTCAAACCATGCTACACTGGGACTTACAAT
CACAGAGCCATCTACATGGTCTCAAACCGTGCTACACTGGGACTTACAAT
TGCAGAGCCATCTATGTGGTCTCAAACCGTGCTACACTGGGACTTACAAT
TGCAGAGCCATCTGTGTGGTCTCAAACCGCGCTACACTGGGACTTACAAT

Mammuthus primigenius agGGACTACTCTCAGTCTGACAAGAAATATCATCATCAGTTGTACAGAGCTAG
Loxodonta africana agGGACTACTCTCAATCTGACAAGAAATATCATCATCAGTTGTACAGAGCTAG
Trichechus manatus agGGATTACTCCCAATCTGACAAGAAATGTCATCATCAATTTGTACAGAGCTAG
Dugong dugon agGGACTACTCCCAATCTGACAAGAAATGTCATCATCAATTTGTACAGAGCTAG
Hydrodamalis gigas agGGACTACTCCCAATCTGACAAGAAATGTCATCATCAATTTGTACAGAGCTAG
Sus scrofa -----
Sus verrucosus -----
Sus cebifrons -----
Physeter macrocephalus agGTTTCTACTCCAAATCTGACAAGAATTGTCATCATCGGCTGTACAGAGCTAG
Delphinapterus leucas tcACTTTTATATAGTGCTTCAGCAATTTACTACCGATTTGCTTTCTAGTATGTC
Lipotes vexillifer agGTTTCTACTCCAAATCTGACAAGAATTGTCATCATCAGCTGTACAGAGCTAG
Balaena mysticetus agGTTTCTACTCCGAATCTGACAAGAATTGTCATCATCAGCTGTACAGAGCTAG
Balaenoptera acutorostrata agGTTTCTACTCCGAATCTGACAAGAATTGTCATCATCAGCTGTACAGAGCTAG
Balaenoptera physalus agGTTTCTACTCCGAATCTGACAAGAATTGTCATCATCAGCTGTACAGAGCTAG
Balaenoptera bonaerensis agGTTTCTACTCCGAATCTGACAAGAATTGTCATCATCAGCTGTATAGAGCTAG
Equus asinus agGGACCCTCTCAATCTGACAAGAATTGTCATCATCAATTTGTACAGAGCTAG
Equus quagga boehmi agGGACCCTCTCAATCTGACAAGAATTGTCATCATCAATTTGTACAGAGCTAG
Equus przewalskii agGGACCCTCTCAATCTGACAAGAATTGTCATCATCAATTTGTACAGAGCTAG
Equus caballus agGGACCCTCTCAATCTGACAAGAATTGTCATCATCAATTTGTACAGAGCTAG
Manis pentadactyla atGGTCTACTCCCAATCTGATGAGAAATGTCATCATGAATTTGTGCAGAGCTAG

586 590 600 610 620 630
 |...|...|...|...|...|...|...|...|...|...|
Homo sapiens TAACATATGATCTAATGAAGGAGGCCTTTGTGAAAAACAACATATTAGCAGgt
Bradypus variegatus ???
Choloepus hoffmanni ???
Mylodon darwini ???
Cyclopes didactylus ???

Dasypus novemcinctus -----
Procavia capensis -----
Elephas maximus TAACATATGACCTGATGAAGGAGACCTTTGTGAAAAACAACCTACTAGCAGct
Mammuthus primigenius TAACATATGACCTGATGAAGGAGACCTTTGTGAAAAACAACCTACTAGCAGct
Loxodonta africana TAACATATGACCTGATGAAGGAGACCTTTGTGAAAAACAACCTACTAGCAGct
Trichechus manatus TAACACATGACCTAATGAAGGAGACCTTTGTGAAAAACAATCTACTGGCAGgt
Dugong dugon TAACACATGACCTAATGAAGGAGACCTTTGTGAAAAACAATCTACTGGCAGgt
Hydrodamalis gigas TAACACATGACCTAATGAAGGAGACCTTTGTGAAAAACAATCTACTGGCAGat
Sus scrofa -----
Sus verrucosus -----
Sus cebifrons -----
Physeter macrocephalus TAACATATGACCTAATGAAGGAGGCCCTTTGTGAAAAACA----ATTAACAGgt
Delphinapterus leucas ACTATCTCATTGACATGCTCCTGCCCTTTGTGAAAAACA----ATTAACAGgt
Lipotes vexillifer TAACATATGACCTAATGAAGGAGACCTTTGTGAAAAACA----ATTAACAGgt
Balaena mysticetus TAACGTATGACCTAATGAAGGAGACCTTTGTGAAAAACA----ATTAACAGgt
Balaenoptera acutorostrata TAACGTATGACCTAATGAAGGAGGCCCTTTGTGAAAAACA----ATTAACAGgt
Balaenoptera physalus TAACGTATGTCCTAATGAAGGAGGCCCTTTGTGAAAAACA----ATTAACAGgt
Balaenoptera bonaerensis TAACGTATGACCTAATGAAGGAGGCCCTTTGTGAAAAACA----ATTAACAGgt
Equus asinus TAACCCATGACCTAATGAAGGAGGCCCTTTGTGAAAAACCAACTATTAGCAGgt
Equus quagga boehmi TAACCCATGACCTAATGAAGGAGGCCCTTTGTGAAAAACCAACTATTAGCAGgt
Equus przewalskii TAACCCATGACCTAATGAAGGAGGCCCTTTGTGAAAAACCAACTATTAGCAGgt
Equus caballus TAACCCATGACCTAATGAAGGAGGCCCTTTGTGAAAAACCAACTATTAGCAGgt
Manis pentadactyla TAA--GTATGACCTAATGAAGGAGGCACCTCTAAACAAGA----CTTACCAGct

Exon 5

636 640 650 660 670 680
 |...|...|...|...|...|...|...|...|...|...|
Homo sapiens agATGACGTCCCCTGCCACTTGGTGTGGCTCTTATCGCTGGATTTTGC---

<i>Homo sapiens</i>	ATTCTCCACCAGGACAG---TACAAAAGTGTGCCAACTGTGCAATGAAA
<i>Bradypus variegatus</i>	??
<i>Choloepus hoffmanni</i>	??
<i>Mylodon darwinii</i>	??
<i>Cyclopes didactylus</i>	??
<i>Dasypus novemcinctus</i>	-----
<i>Procavia capensis</i>	ATTCTCCACCAAGATAC---TAAACTAGTGTACCCAAACATGCAACCATC
<i>Elephas maximus</i>	ATTCTCCACCAGGATAC---TACACGAGTGTACCCAAATGCGCAGTGACC
<i>Mammuthus primigenius</i>	ATTCTCCACCAGGATAC---TACACGAGTGTACCCAAATGCGCAGTGACC
<i>Loxodonta africana</i>	ATTCTCCACCAGGATAC---TACACGAGTGTACCCAAATGCGCAGTGACC
<i>Trichechus manatus</i>	ATTCTCCACCAGGATAC---TACACAAGCATACCCAAATGTGCAATGACC
<i>Dugong dugon</i>	ATTCTCCACCAGGATAC---TACACAAGCATGCCCCAAATGTGCAATGACC
<i>Hydrodamalis gigas</i>	ATTCTCCACCAGGATAC---TACACAAGCATACCCAAATGTGCAATGACC
<i>Sus scrofa</i>	-----
<i>Sus verrucosus</i>	-----
<i>Sus cebifrons</i>	-----
<i>Physeter microcephalus</i>	ACTGTCTACCGGGACAG---TACACAAGTGTGTCCAACCTGTGCAATGATG
<i>Delphinapterus leucas</i>	ACTGTCTACCGGGACAG---TACACAAGTGTGTCCAACCTGTGCAATGATG
<i>Lipotes vexillifer</i>	ACTGTCTACCGAGACAG---TACATAAGCGTGTCCAACCTGTGCAATGATG
<i>Balaena mysticetus</i>	ACTGTCTACCGGGACGGACACACAAGTGTGTCCGACTGCGCAATGATG
<i>Balaenoptera acutorostrata</i>	ACTGTCTACCGGGACGG---TACACAAGTGTGTCCGACTGCGCAATGTTG
<i>Balaenoptera physalus</i>	ACTGTCTACCRGGACGG---TACACAAGTGTGTCCGACTGCGCAATGTTG
<i>Balaenoptera bonaerensis</i>	ACTGTCTACCGGGACGG---TACACAAGTGTGTCCGACTGCGCAATGTTG
<i>Equus asinus</i>	ATTCTCCACCAGGACAG---TACACAAGTGTGCCAACTGTGCAACGACA
<i>Equus quagga boehmi</i>	ATTCTCCACCAGGACAG---TACACAAGTGTGCCAACTGTGCAACGACA
<i>Equus przewalskii</i>	ATTCTCCACCAGGACAG---TACACAAGTGTGCCAACTGTGCAACGACA
<i>Equus caballus</i>	ATTCTCCACCAGGACAG---TACACAAGTGTGCCAACTGTGCAACGACA
<i>Manis pentadactyla</i>	ATTCTCTACCAGGACAA---TGCACAAGTGTGCCCACTGTGCAATGACA

786 790 800 810 820

<i>Homo sapiens</i>	GTGTTCACTAACGAAGGACCAACGGC-TTTCTTCAAGGgt
<i>Bradypus variegatus</i>	??
<i>Choloepus hoffmanni</i>	??
<i>Mylodon darwinii</i>	??
<i>Cyclopes didactylus</i>	??
<i>Dasypus novemcinctus</i>	-----
<i>Procavia capensis</i>	ATGTTTACCAAGAAAAGACCACCAGC-TTTTTTCAAAGGgt
<i>Elephas maximus</i>	ATGTTTACCAAGAAAAGGACTGCCGGC-TTTTTTCAAACGGgt
<i>Mammuthus primigenius</i>	ATGTTTACCAAGAAAAGGACTGCCGGC-TTTTTTCAAACGGgt
<i>Loxodonta africana</i>	ATGTTTACCAAGAAAAGGACTGCCGGC-TTTTTTCAAACGGgt
<i>Trichechus manatus</i>	GTGTTTACCAAGGAAGGACTGCCGGC-TTTTTTCAAAGGgt
<i>Dugong dugon</i>	GCGTTTACCAAGGAAGGACTGCCGGC-TTTTTTCAAAGGgt
<i>Hydrodamalis gigas</i>	GTGTTTACCAAGGAAGGACTGCCGGC-TTTTTTCAAAGGgt
<i>Sus scrofa</i>	-----
<i>Sus verrucosus</i>	-----
<i>Sus cebifrons</i>	-----
<i>Physeter microcephalus</i>	GTCCTTCTAAGGAAGGACCATCGGC-TTTTTTCAAAGGgt
<i>Delphinapterus leucas</i>	ATGCCCCTAAGGAAGGACCATCGGC-TTTTTTCAAAGGgt
<i>Lipotes vexillifer</i>	ATGCTCACTAAGGAAGGACCATCGGC-TTTTTTCAAAGGgt
<i>Balaena mysticetus</i>	ATGCTCACTAAGGAAGGACCATCGGC-TTTTTTCAAAGGgt
<i>Balaenoptera acutorostrata</i>	ATGCTCACTAAGGAAGGACCATCGGC-TTTTTTCAAAGGgt
<i>Balaenoptera physalus</i>	ATGCTCACTAAGGAAGGACCATCGGC-TTTTTTCAAAGGgt
<i>Balaenoptera bonaerensis</i>	ATGCTCACTAAGGAAGGACCATCGGC-TTCTTTCAAAGGgt
<i>Equus asinus</i>	ATGCTCACTAAGGAAGGACCGTCAGC-TTTTTTCAAAGGgt
<i>Equus quagga boehmi</i>	ATGCTCACTAAGGAAGGACCGTCAGC-TTTTTTCAAAGGgt
<i>Equus przewalskii</i>	ATGCTCACTAAGGAAGGACCGTCAGC-TTTTTTCAAAGGgt
<i>Equus caballus</i>	ATGCTCACTAAGGAAGGACCGTCAGC-TTTTTTCAAAGGgt
<i>Manis pentadactyla</i>	GTGCTCACTAAGGAAGGACCATCGGC-TTTTTTCAAAGGgc

Exon 6

825 830 840 850 860 870
|. . .|. . .|. . .|. . .|. . .|. . .|. . .|. . .|. . .|. . .|
Homo sapiens agGTTGGTACCTTCCTTCTTGCGACTTGGATCCTGGAACGTCATTATGTTTGT
Bradypus variegatus agGTTTGTGCCTTCCTTCTTGCGACTTAGATCCTGGAATGTCATCATGTTTGA
Choloepus hoffmanni agGTTTGTGCCTTCCTTCTTGAGACTTGGATCC**TGA**AATGTCATCATGTTTGT
Mylodon darwinii ???
Cyclopes didactylus agATTTGTACCTTCCTTCTTGCAACTAGGATCCTGGAATGTCATCATGTTTGT
Dasypus novemcinctus agTCTTATGCCTTCCTTCTTG**TGA**CTCAGATCCTGGAATGTTGTCATGTTTGT
Procavia capensis agGTTTGTACCTTCCTTCTTG**TGA**CTAAGACTGGAAGCATCATTAAGTTCAT
Elephas maximus agGCTTGTGCCTTCCTTCTTGCGACTGGGATCCTGGAACGCCATTATGTTTTT
Mammuthus primigenius agGCTTGTGCCTTCCTTCTTGCGACTGGGATCCTGGAACGCCATTATGTTTTT
Loxodonta africana agGCTTGTGCCTTCCTTCTTGCGACTGGGATCCTGGAACGCCATTATGTTTTT
Trichechus manatus agGTTTGTGCCTTCCTTCTTGCGACTCGGTTCCCTGGAATGTCATTATGTT---T
Dugong dugon agGTTTGTGCCTTCCTTCTTG**TGA**CTCGGATCCTGGAATGTCATTATGTT---T
Hydrodamalis gigas agGTTTGTGCCTTCCTTCTTGCGACTCGGATCCTGGAATGTCATTATGTT---T
Sus scrofa agATTTGTACCTTCCTTCTGG**TGA**CTGGGATCCTGGAACGTCATCCCATTGTT
Sus verrucosus agATTTGTACCTTCCTTCTGG**TGA**CTGGGATCCTGGAACGTCATCCCATTGTT
Sus cebifrons agATTTGTACCTTCCTTCTGG**TGA**CTGGGATCCTGGAACGTCATCCCATTGTT
Physeter microcephalus agATTTGTACCTTCCTTCT**TGAGTGA**CTGGGATCCTGGAACATCATCGTGT---GT
Delphinapterus leucas agATTTGTACCTTCCTTCTTG**TGA**CTGGGGTCTGGAACATCATCGTGT---GT
Lipotes vexillifer agATTTGTACCTTCCTTCTTG**TGA**CTGGGATCCTGGAACATCATCGTGT---GT
Balaena mysticetus agATTTGTACCTTCCTTCTTG**TGA**CTGGGATCCTGGAACATCATCGTGT---GT
Balaenoptera acutorostrata agATTTGTACCTTCCTTCTTG**TGA**CTGGGATCCTGGAACATCATCGTGT---GT
Balaenoptera physalus agATTTGTACCTTCCTTCTTG**TGA**CTGGGATCCTGGAACATCATCGTGT---GT
Balaenoptera bonaerensis ???
Equus asinus agATTTGTGCCTTCCTTCTTGCGACTCGGATCCTGGCATGTCATCATGTTTGT
Equus quagga boehmi agATTTGTGCCTTCCTTCTTGCGACTCGGATCCTGGCATGTCATCATGTTTGT
Equus przewalskii agATTTGTGCCTTCCTTCTTGCGACTCGGATCCTGGCATGTCATCATGTTTGT
Equus caballus agATTTGTGCCTTCCTTCTTGCGACTCGGATCCTGGCATGTCATCATGTTTGT
Manis pentadactyla agATTTG----TCCCTTCTTGACCTTGGGTCTCCAGACGTCATTATATTTGT

876 880 890 900 910 920
|. . .|. . .|. . .|. . .|. . .|. . .|. . .|. . .|. . .|. . .|
Homo sapiens GTGCTTTGAACAACCTGAAACGAGAAGTGTCAAAGTCAAGGCAGACTATGGA
Bradypus variegatus GTA---CTGAACAGCTAAAACAGGAAAGGATGACATCAAGGCGGACTATGGA
Choloepus hoffmanni GTG---TTGAACAGCTAAAACAGGAAATGATGACATCAAGGCA---ACTATGAA
Mylodon darwinii ???
Cyclopes didactylus GTG---TTGAACAGCTAAAACAAGAAGTGTGATGACATCAAGGCAGACTATGGA
Dasypus novemcinctus GTACTTTGAACAGCTGAAAACAAGAATTGATGAAGCCAAGGCAGACTATGGA
Procavia capensis GTGCTTTGAACAGCTGAAAAAAGAATTGATGAAGTCGAGGCAGATGATGGA
Elephas maximus GTGCTCTGAACAGCTGAAAACAAGAATTGATGAAGTCAAGGCAGACTATGGG
Mammuthus primigenius GTGCTCTGAACAGCTGAAAACAAGAATTGATGAAGTCAAGGCAGACTATGGG
Loxodonta africana GTGCTCTGAACAGCTGAAAACAAGAATTGATGAAGTCAAGGCAGACTATGGG
Trichechus manatus GTGCTTTGAA**TAG**CTGAAACGAGAATTGATGAAGTCGAGGGAGACTATGGA
Dugong dugon GTGCTTTGAACAGCTGAAACGAGAATTGATGAAGTCGAGGCAGACTATGGA
Hydrodamalis gigas GTGCTTTGAACAGCTGAAACGAGAATTGATGAAGTCGAGGCAGACTATGGA
Sus scrofa GTGCTTTGAACAGCTGAAACAAGAGTTGATGGAGTCAAGGCAGACTGTGGA
Sus verrucosus GTGCTTTGAACAGCTGAAACAAGAGTTGATGGAGTCAAGGCAGACTGTGGA
Sus cebifrons GTGCTTTGAACAGCTGAAACAAGAGTTGATGGAGTCAAGGCAGACTGTGGA
Physeter microcephalus GTGCCTTGAACAGCTGAAGCGAGAAGTCTGAAGTCGAGGCAGACCATGGA
Delphinapterus leucas GTGCTTTGAACAGCTGAAGCGAGAATTGATGAAGTTGAGGCAGACCATGGA
Lipotes vexillifer GTGCTTTGAACAGCTGAAG**TGA**GAATTGATGAAGTTGAGGCAGACCATGGA
Balaena mysticetus GTGCTTTGAACAGCTGAAGCGAGAATTGATGAAGTCGAGGCAGACCACGGA
Balaenoptera acutorostrata GTGCTCTGAACAGCTGCAGCGAGAATTGATGAAGTCGAGGCAGACCATGGA
Balaenoptera physalus GTGCTTTGAACAGCTGAAGMGAGAATTGATGAAGTCGAGGCAGACCATGGA
Balaenoptera bonaerensis ???
Equus asinus GTGCTTTGAACAGCTGAAGCGAGAATTGATGAAGTCAAGGCAGACCAGGGA

<i>Equus quagga boehmi</i>	GTGCTTTGAACAGCTGAAGCGAGAATTGATGAAGTCAACGCAGACCATGGA
<i>Equus przewalskii</i>	GTGCTTTGAACAGCTGAAGCGAGAATTGATGAAGTCAACGCAGACCATGGA
<i>Equus caballus</i>	GTGCTTTGAACAGCTGAAGCGAGAATTGATGAAGTCAACGTGACAGACCAT
<i>Manis pentadactyla</i>	GTGCTCTGAACAAGGAAAA TGA AAATTGACGAACTCAAGG -----
	925 930 940 950

<i>Homo sapiens</i>	CTGTGCCACA-----TAA
<i>Bradypus variegatus</i>	CTGTGCCACAGCTTCAGGAAAAGAATG -TAA
<i>Cyclopes didactylus</i>	CTTTGCCACA ACTTCAGGAAAAGGATG-T TA
<i>Choloepus hoffmanni</i>	CTGTGTCACAGCTTCAGGAAAAGAATGTTAA
<i>Mylodon darwinii</i>	????????????????????????????????
<i>Dasypus novemcinctus</i>	CTGTGCTACA-----TAA
<i>Procavia capensis</i>	CTGTGCCACA-----TAA
<i>Elephas maximus</i>	CTGTACCACA-----TAA
<i>Mammuthus primigenius</i>	CTGTACCACA-----TAA
<i>Loxodonta africana</i>	CTGTACCACA-----TAA
<i>Trichechus manatus</i>	CTGTGCCACA-----TAA
<i>Dugong dugon</i>	CTGTGCCACA-----TAA
<i>Hydrodamalis gigas</i>	CTGTGCCACA-----TAA
<i>Sus scrofa</i>	CTGTGCTGCA-----TAA
<i>Sus verrucosus</i>	CTGTGCTGCA-----TAA
<i>Sus cebifrons</i>	CTGTGCTGCA-----TAA
<i>Physeter microcephalus</i>	CTGTGCTACC-----TAA
<i>Delphinapterus leucas</i>	CTGTGCTACC-----TAA
<i>Lipotes vexillifer</i>	CTGTGCTACC-----TAA
<i>Balaena mysticetus</i>	CTGTGCTACC-----TAA
<i>Balaenoptera acutorostrata</i>	CTGTGCTACC-----TAA
<i>Balaenoptera physalus</i>	CTGTGCTACC-----TAA
<i>Balaenoptera bonaerensis</i>	????????????????????????????????
<i>Equus asinus</i>	CTGTGCCACA-----TAA
<i>Equus quagga boehmi</i>	CTGTGCCACA-----TAA
<i>Equus przewalskii</i>	CTGTGCCACA-----TAA
<i>Equus caballus</i>	CTGTGCCACA-----TAA
<i>Manis pentadactyla</i>	CTGTGTCATA-----TAA

fig. S2. Exon alignments depicting deleterious mutations found in *UCPI* sequences of placental mammal taxa. The intact human *ucp1* sequence is provided for reference. Mutated initiation codons (green), premature stop codons (red), frameshift insertions (turquoise), deletions (dashes), frameshift deletions (pink), mutated splice sites (yellow), and mutated stop codons (teal) are indicated. Note insert from ~800 bp upstream of *ucp1* in exon 4 of beluga (grey). Missing data are denoted by question marks.

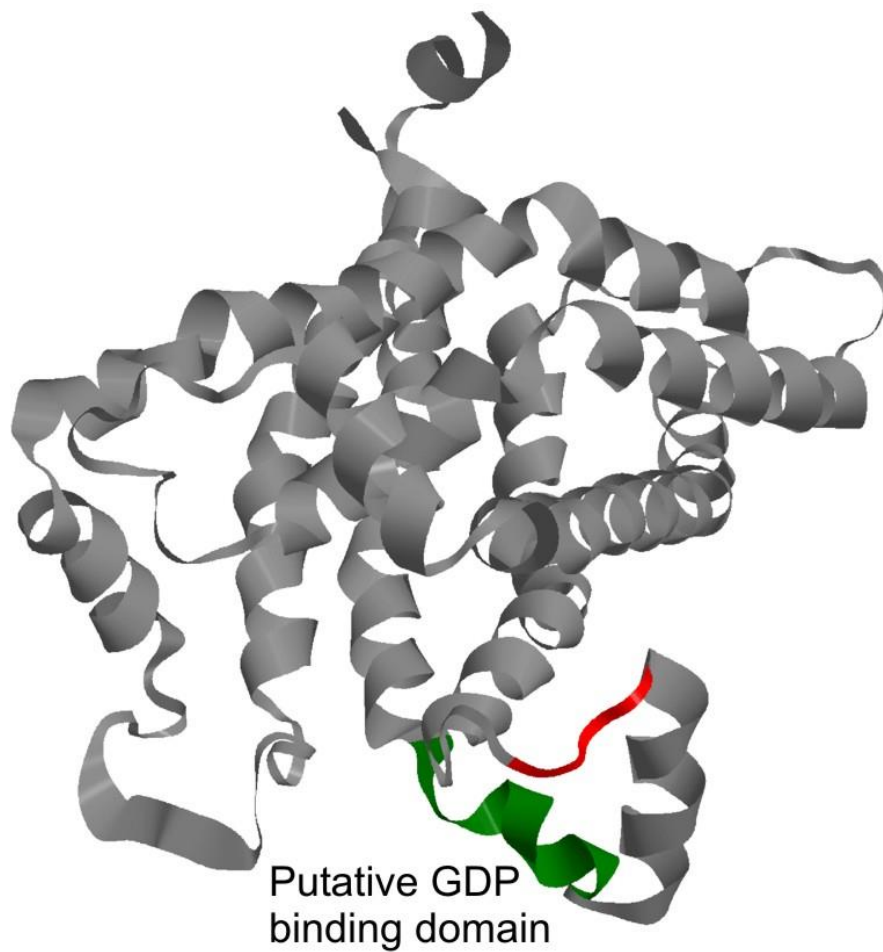


fig. S3. Ribbon diagram of residues 13 to 304 of human UCP1 (UniProt accession number P25874) structurally modelled by SWISS-MODEL. Residues highlighted in red denote the position of a four amino acid deletion in the third matrix loop of the camel (*Camelus ferus*) UCP1 protein which borders the putative GDP-binding domain (green).

<i>Saimiri boliviensis</i>	M	E	T	N	T	R	E	L	F	L	N	F	T	I	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	Y
<i>Nomascus leucogenys</i>	M	G	I	N	T	R	E	L	F	L	N	F	T	I	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	Y
<i>Colobus angolensis</i>	M	G	I	N	T	R	E	L	F	L	N	F	T	I	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	Y
<i>Mandrillus leucophaeus</i>	M	G	I	N	T	R	E	L	F	L	N	F	T	I	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	Y
<i>Cercocebus atys</i>	M	G	I	N	T	R	E	L	F	L	N	F	T	I	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	Y
<i>Pongo abelii</i>	M	G	I	N	T	R	E	L	F	L	N	F	T	I	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	Y
<i>Gorilla gorilla</i>	M	G	I	N	T	R	E	L	F	L	N	F	T	I	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	Y
<i>Homo sapiens</i>	M	G	I	N	T	R	E	L	F	L	N	F	T	I	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	Y
<i>Pan troglodytes</i>	M	G	I	N	T	R	E	L	F	L	N	F	T	I	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	Y
<i>Pan paniscus</i>	M	G	I	N	T	R	E	L	F	L	N	F	T	I	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	Y
<i>Nasalis larvatus</i>	M	G	I	N	T	R	E	L	F	L	N	F	T	I	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	Y
<i>Rhinopithecus roxellana</i>	M	G	I	N	T	R	E	L	F	L	N	F	T	I	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	Y
<i>Chlorocebus sabaues</i>	M	G	I	N	T	R	E	L	F	L	N	F	T	I	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	Y
<i>Macaca fascicularis</i>	M	G	I	N	T	R	E	L	F	L	N	F	T	I	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	Y
<i>Macaca mulatta</i>	M	G	I	N	T	R	E	L	F	L	N	F	T	I	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	Y
<i>Macaca nemestrina</i>	M	G	I	N	T	R	E	L	F	L	N	F	T	I	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	Y
<i>Papio anubis</i>	M	G	I	N	T	R	E	L	F	L	N	F	T	I	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	Y
<i>Condylura cristata</i>	M	E	L	S	T	R	E	L	F	L	N	F	T	V	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	Y
<i>Erinaceus europaeus</i>	M	E	R	S	T	R	E	L	F	L	N	F	T	V	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	Y
<i>Sorex araneus</i>	M	E	R	S	T	R	E	L	F	L	N	F	T	V	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	Y
<i>Eptesicus fuscus</i>	M	D	L	S	A	R	E	L	C	L	N	F	T	V	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	S
<i>Myotis lucifugus</i>	M	D	L	S	A	R	E	L	C	L	N	F	T	V	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	S
<i>Myotis brandtii</i>	M	D	L	S	A	R	E	L	C	L	N	F	T	V	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	S
<i>Myotis davidii</i>	M	D	L	S	A	R	E	L	C	L	N	F	T	V	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	S
<i>Rhinolophus ferrumequinum</i>	M	E	H	S	T	R	E	L	C	L	N	F	T	I	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	S
<i>Megaderma lyra</i>	M	E	R	S	T	R	E	L	C	L	N	F	T	V	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	S
<i>Eidolon helvum</i>	M	E	L	S	T	R	E	L	C	L	N	F	T	V	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	Y
<i>Pteropus vampyrus</i>	M	E	L	S	T	R	E	L	C	L	N	F	T	I	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	Y
<i>Pteropus alecto</i>	M	E	L	S	T	R	E	L	C	L	N	F	T	I	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	Y
<i>Manis pentadactyla</i>	M	E	R	S	T	R	E	L	C	L	N	F	T	V	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	Y
<i>Felis catus</i>	M	G	I	S	T	R	E	L	F	L	N	F	T	I	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	Y
<i>Acinonyx jubatus</i>	M	G	I	S	T	R	E	L	F	L	N	F	T	I	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	Y
<i>Panthera uncia</i>	M	G	I	S	T	R	E	L	F	L	N	F	T	I	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	Y
<i>Panthera tigris</i>	M	G	I	S	T	R	E	L	F	L	N	F	T	I	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	Y
<i>Canis lupus</i>	M	G	I	S	T	R	E	L	F	L	N	F	T	I	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	Y
<i>Ursus maritimus</i>	M	G	I	S	T	R	E	L	F	L	N	F	T	I	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	Y
<i>Ailuropoda melanoleuca</i>	M	G	I	S	T	R	E	L	F	L	N	F	T	I	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	Y
<i>Mustela putorius</i>	M	G	I	S	T	R	E	L	F	L	N	F	T	I	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	Y
<i>Odobenus rosmarus</i>	M	G	I	S	T	R	E	L	F	L	N	F	T	I	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	Y
<i>Leptonychotes weddellii</i>	M	G	I	S	T	R	E	L	F	L	N	F	T	I	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	Y
<i>Tapirus indicus</i>	M	E	W	T	T	R	E	L	F	L	N	F	T	V	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	Y
<i>Ceratotherium simum</i>	M	E	W	T	T	R	E	L	F	L	N	F	T	V	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	Y
<i>Diceros bicornis</i>	M	E	W	T	T	R	E	L	F	L	N	F	T	V	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	?
<i>Rhinoceros unicornis</i>	M	E	W	T	T	R	E	L	F	L	N	F	T	V	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	Y
<i>Dicerorhinus sumatrensis</i>	M	E	W	T	T	R	E	L	F	L	N	F	T	V	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	Y
<i>Coelodonta antiquitatis</i>	M	E	W	T	T	R	E	L	F	L	N	F	T	V	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	Y
<i>Equus przewalskii</i>	M	E	W	R	-	R	E	L	F	L	N	F	T	V	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	-
<i>Equus caballus</i>	M	E	W	R	-	R	E	L	F	L	N	F	T	V	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	-
<i>Equus asinus</i>	M	E	W	R	-	R	E	L	F	L	N	F	T	V	V	L	I	T	V	I	L	M	W	L	L	V	R	S	Y	Q	-
<i>Camelus ferus</i>	M	E	R	S	T	R	E	L	C	L	N	F	T	V	V	L	I	T	V	I	L	I	W	L	L	V	R	S	Y	Q	Y
<i>Vicugna pacos</i>	M	E	R	S	T	R	E	L	C	L	N	F	T	V	V	L	I	T	V	I	L	I	W	L	L	V	R	S	Y	Q	Y
<i>Sus scrofa</i>	M	E	R	S	T	R	E	L	C	L	N	F	T	V	V	L	I	T	V	I	L	I	W	L	L	V	R	S	Y	Q	Y
<i>Sus cebifrons</i>	M	E	R	S	T	R	E	L	C	L	N	F	T	V	V	L	I	T	V	I	L	I	W	L	L	V	R	S	Y	Q	Y
<i>Sus verrucosus</i>	M	E	R	S	T	R	E	L	C	L	N	F	T	V	V	L	I	T	V	I	L	I	W	L	L	V	R	S	Y	Q	Y
<i>Balaenoptera acutorostrata</i>	M	E	R	S	T	R	E	L	C	L	N	F	T	V	V	L	I	T	V	I	L	I	W	L	L	V	R	S	Y	Q	Y
<i>Balaenoptera physalus</i>	M	E	R	S	T	R	E	L	C	L	N	F	T	V	V	L	I	T	V	I	L	I	W	L	L	V	R	S	Y	Q	Y
<i>Balaenoptera bonaerensis</i>	M	E	R	S	T	R	E	L	C	L	N	F	T	V	V	L	I	T	V	I	L	I	W	L	L	V	R	S	Y	Q	Y
<i>Physeter macrocephalus 1 & 2</i>	M	E	R	S	T	R	E	L	C	L	N	F	T	V	V	L	I	T	V	I	L	I	W	L	L	V	R	S	Y	Q	Y
<i>Lipotes vexillifer</i>	M	E	R	S	T	R	E	L	C	L	N	F	T	V	V	L	I	T	V	I	L	I	W	L	L	V	R	S	Y	Q	Y
<i>Orcinus orca</i>	M	E	R	S	T	R	E	L	C	L	N	F	T	V	V	L	I	T	V	I	L	I	W	L	L	V	R	S	Y	Q	Y
<i>Tursiops truncatus</i>	M	E	R	S	T	R	E	L	C	L	N	F	T	V	V	L	I	T	V	I	L	I	W	L	L	V	R	S	Y	Q	Y
<i>Capreolus capreolus</i>	M	E	R	S	T	R	E	L	C	L	N	F	T	V	V	L	I	T	V	I	L	I	W	L	L	V	R	S	Y	Q	Y

<i>Pantholops hodgsonii</i>	M	E	R	S	T	R	E	L	C	L	N	F	T	V	V	L	I	T	V	I	L	I	W	L	L	V	R	S	Y	Q	Y
<i>Ovis aries</i>	M	E	R	S	A	R	E	I	C	L	N	F	T	V	V	L	I	T	V	M	L	I	W	L	L	V	R	S	Y	Q	Y
<i>Capra hircus</i>	M	E	R	S	T	R	E	I	C	L	N	F	T	V	V	L	I	T	V	I	L	I	W	L	L	V	R	S	Y	Q	Y
<i>Capra aegagrus</i>	M	E	R	S	T	R	E	I	C	L	N	F	T	V	V	L	I	T	V	I	L	I	W	L	L	V	R	S	Y	Q	Y
<i>Bubalus bubalis</i>	M	E	R	S	T	R	E	L	C	L	N	F	T	V	V	L	I	T	V	I	L	I	W	L	L	V	R	S	Y	Q	Y
<i>Bison bison</i>	M	E	R	S	T	R	E	L	C	L	N	F	T	V	V	L	I	T	V	I	L	I	W	L	L	V	R	S	Y	Q	Y
<i>Bos grunniens</i>	M	E	R	S	T	R	E	L	C	L	N	F	T	V	V	L	I	T	V	I	L	I	W	L	L	V	R	S	Y	Q	Y
<i>Bos indicus</i>	M	E	R	S	T	R	E	L	C	L	N	F	T	V	V	L	I	T	V	I	L	I	W	L	L	V	R	S	Y	Q	Y
<i>Bos taurus</i>	M	E	R	S	T	R	E	L	C	L	N	F	T	V	V	L	I	T	V	I	L	I	W	L	L	V	R	S	Y	Q	Y

fig. S4. Amino acid alignment of vertebrate sln. The mutated start codons (ATG→CTG) in the two-toed sloth (*Choleopus hoffmannii*) and brown-throated sloth (*Bradypus variegatus*) were verified from the NCBI sequence read archive and polymerase chain reaction amplification, respectively. Amino acid deletions in the equid lineage are highlighted in red. Note that two sarcolipin gene copies were found in the *Xenopus tropicalis*, *Monodelphis domestica*, and *Physeter macrocephalus* assemblies. Missing data denoted by question marks.

table S1. GenBank accession numbers of species used in this study.

<i>Species name</i>	<i>ucp1 Source</i>	<i>ucp2 Source</i>	<i>ucp3 Source</i>	<i>sln Source</i>
Osteichthyes				
<i>Astyanax mexicanus</i>	APWO01100404.1 APWO01100403.1	APWO01075838.1	APWO01075838.1	Missing
<i>Cyprinus carpio</i>	AY461434.2	AJ243486.1	AY505343.1	Missing
<i>Danio rerio</i>	CABZ01073633.1 CABZ01073634.1	CABZ01017713.1	CABZ01012840.1 CABZ01017713.1	NM_001302745.1
<i>Latimeria chalumnae</i>	AFYH01226130.1 AFYH01226129.1	BAHO01089108.1 AFYH01155949.1	Missing	AFYH01102483.1
<i>Lepisosteus oculatus</i>	AHAT01015452.1	AHAT01003069.1	AHAT01003069.1	AHAT01003063.1
<i>Takifugu rubripes</i>	CAAB02001533.1	CAAB02000575.1	CAAB02000575.1	CAAB02007733.1
<i>Xiphophorus maculatus</i>	AGAJ01004818.1 AGAJ01004819.1	AGAJ01021216.1	AGAJ01021216.1	AGAJ01040366.1
Amphibia				
<i>Xenopus tropicalis</i>	AAMC02004107.1	NM_203848.1	NM_001095178.1	AAMC02008311.1 AAMC02008313.1
Montremata				
<i>Ornithorhynchus anatinus</i>	NW_001794248.1	AAPN01056149.1 AAPN01056148.1 AAPN01056147.1 AAPN01382618.1	AAPN01178604.1 AAPN01178605.1	AAPN01035927.1
Marsupialia				
<i>Monodelphis domestica</i>	AAFR03015618.1	AAFR03050488.1	AAFR03050488.1	AAFR03009954.1 AAFR03043596.1
<i>Macropus eugenii</i>	ABQO020217652.1 ABQO020162103.1 ABQO020106554.1 ABQO020051005.1 ABQO021106434.1	ABQO020850797.1 ABQO020012246.1	ABQO020339531.1 ABQO020395080.1 ABQO020450629.1 ABQO020707648.1 ABQO020652099.1	ABQO020365261.1
<i>Sarcophilus harrisii</i>	AEFK01228715.1 AEFK01215941.1	AFEY01422591.1	AFEY01409403.1 AFEY01344314.1 AFEY01422590.1	AFEY01139015.1
<i>Sminthopsis crassicaudata</i>	EF622232.1	Missing	Missing	Missing
Xenarthra				
<i>Choloepus hoffmanni</i>	ABVD02364175.1	ABVD01312484.1	ABVD02315747.1	ABVD02284044.1
<i>Bradypus variegatus</i>	KY886638	Missing	Missing	KY886670
<i>Cyclopes didactylus</i>	KY886639	Missing	Missing	Missing
<i>Dasybus novemcinctus</i>	AAGV03181320.1	AAGV03150769.1	AAGV03292997.1 AAGV03292996.1	AAGV03173212.1
<i>Myiodon darwini</i>	SRX327588	SRX327588 SRX327589	SRX327588 SRX327589 SRX465052	SRX327588

Afrotheria

<i>Chrysochloris asiatica</i>	AMDV01244955.1 AMDV01244956.1	AMDV01302651.1	AMDV01302653.1	AMDV01027313.1
<i>Dugong dugon</i>	KY886640	KY886652	KY886661	KY886671
<i>Echinops telfairi</i>	AAIY02209271.1	AAIY02169770.1	AAIY02169772.1	AAIY02172361.1
<i>Elephantulus edwardii</i>	AMGZ01097263.1	AMGZ01085574.1	AMGZ01085576.1; AMGZ01085575.1	AMGZ01226582.1
<i>Elephas maximus</i>	KY886642	ERX334764 ERX334765	ERX334764 ERX334765	ERX334764 ERX334765
<i>Hydrodamalis gigas</i>	KY886641	KY886653	KY886662	KY886672
<i>Loxodonta africana</i>	AAGU03034821.1	AAGU03079300.1	AAGU03079300.1	AAGU03058675.1
<i>Mammuthus primigenius</i>	ERP008929	ERP008929	ERP008929	ERP008929
<i>Orycteropus afer</i>	ALYB01104541.1 ALYB01104543.1	ALYB01103367.1	ALYB01103365.1	ALYB01161748.1
<i>Procavia capensis</i>	ABRQ02143236.1	ABRQ02011699.1	ABRQ02011697.1	ABRQ02037372.1
<i>Trichechus manatus latirostris</i>	AHIN01109623.1 AHIN01109624.1	AHIN01084584.1	AHIN01084587.1	AHIN01088368.1

Laurasiatheria

<i>Acinonyx jubatus</i>	LLWD01000416.1	LLWD01000509.1	LLWD01000509.1	LLWD01000070.1
<i>Ailuropoda melanoleuca</i>	ACTA01016457.1	ACTA01146014.1	ACTA01130015.1	ACTA01090054.1
<i>Balaena mysticetus</i>	KY886643	Missing	Missing	Missing
<i>Balaenoptera acutorostrata</i>	ATDI01065547.1	ATDI01094623.1	ATDI01094627.1	ATDI01043778.1
<i>Balaenoptera bonaerensis</i>	BAUQ01197845.1 BAUQ01696173.1 BAUQ01341929.1	BAUQ01410165.1	BAUQ01284797.1	BAUQ01341977.1
<i>Balaenoptera physalus</i>	SRX323050	SRX323050	SRX323050	SRX323050
<i>Bison bison</i>	JPYT01100523.1	JPYT01642782.1	JPYT01019071.1	JPYT01254401.1
<i>Bos grunniens</i>	AGSK01075302.1	AGSK01058532.1 [Misassembled]	AGSK01132661.1 AGSK01132663.1 [Misassembled]	AGSK01136949.1
<i>Bos indicus</i>	AGFL01142555.1 AGFL01142556.1	AGFL01131821.1	AGFL01131836.1 AGFL01131835.1	AGFL01128732.1
<i>Bos taurus</i>	DAAA02044420.1 DAAA02044421.1	AAFC03092999.1	NM_174210.1	AAFC03004956.1
<i>Bubalus bubalis</i>	AWWX01630119.1	AWWX01596091.1	AWWX01532946.1	AWWX01539210.1
<i>Camelus ferus</i>	AGVR01051296.1	AGVR01023127.1	AGVR01023127.1	AGVR01041834.1
<i>Canis lupus familiaris</i>	NM_001003046.1	AAEX03012810.1	NM_001003047.1	AOCS01147984.1
<i>Capra aegagrus</i>	CBYH010071014	CBYH010041467.1	CBYH010041467.1	JXYW01145092.1
<i>Capra hircus</i>	AJPT01162993.1	JN986832.1	AJPT01151377.1	AJPT01148506.1
<i>Capreolus capreolus</i>	CCMK010104759.1 CCMK012865005.1 CCMK010278719.1	CCMK010138775.1	CCMK010008945.1	CCMK010366203.1
<i>Ceratotherium simum</i>	AKZM01017598.1	AKZM01032604.1	AKZM01032604.1	AKZM01019766.1
<i>Choeropsis liberiensis</i>	KY886644	KY886654	KY886663	Missing
<i>Coelodonta antiquitatis</i>	KY886645	KY886655	KY886664	KY886673
<i>Condylura cristata</i>	AJFV01047153.1	AJFV01042335.1	AJFV01042336.1	AJFV01057960.1
<i>Delphinapterus leucas</i>	KY886646	KY886656	KY886665	Missing

<i>Diceros bicornis</i>	KY886647	KY886657	KY886666	KY886674
<i>Dicerorhinus sumatrensis</i>	KY886648	KY886658	KY886667	KY886675
<i>Eidolon helvum</i>	AWHC01029981.1	AWHC01218500.1	AWHC01218502.1 AWHC01218501.1	AWHC01196379.1
<i>Eptesicus fuscus</i>	ALEH01005956.1	ALEH01084492.1	ALEH01084495.1; ALEH01084494.1	ALEH01120006.1
<i>Equus asinus</i>	SRX290673 SRX290675 SRX290677	SRX290673 SRX290675 SRX290677	SRX290673 SRX290675 SRX290677	ERX607030 ERX607036 ERX607001
<i>Equus caballus</i>	AAWR02018851.1	AAWR02018167.1	AAWR02018167.1	AAWR02020714.1
<i>Equus przewalskii</i>	ATBW01036321.1 ATBW01036320.1	ATBW01058700.1 ATBW01058701.1	ATBW01058699.1	ATBW01057363.1
<i>Equus quagga boehmi</i>	KY886649	Missing	Missing	Missing
<i>Erinaceus europaeus</i>	AMDU01193160.1 AMDU01193161.1 AMDU01193162.1	AANN01307683.1	AMDU01063251.1 AMDU01063252.1 AMDU01063253.1	AANN01527796.1
<i>Felis catus</i>	ACBE01132808.1 ACBE01132809.1	AANG02100994.1	AANG02100994.1	ACBE01332355.1
<i>Leptonychotes weddellii</i>	APMU01141180.1 APMU01115166.1	APMU01037391.1	APMU01037393.1	APMU01115847.1
<i>Lipotes vexillifer</i>	AUPI01000024.1 AUPI01000025.1	AUPI01017650.1	AUPI01017651.1	AUPI01060449.1
<i>Manis pentadactyla</i>	JPTV01131901.1	JPTV01099221.1	JPTV01146288.1	JPTV01082441.1
<i>Megaderma lyra</i>	AWHB01348443.1 AWHB01348444.1	AWHB01174334.1 AWHB01174333.1	AWHB01278871.1 AWHB01278872.1	AWHB01215178.1
<i>Mustela putorius furo</i>	AGTQ01041845.1	AGTQ01009941.1	AGTQ01009939.1	AEYP01061363.1
<i>Myotis brandtii</i>	ANKR01273868.1 ANKR01273869.1	ANKR01210024.1	ANKR01210023.1	ANKR01318413.1
<i>Myotis davidii</i>	ALWT01125743.1	ALWT01314732.1 ALWT01314733.1	ALWT01314729.1	ALWT01118440.1
<i>Myotis lucifugus</i>	AAPE02001462.1	AAPE02040816.1	AAPE02040815.1 AAPE02040816.1	AAPE02047638.1
<i>Neovison vison</i>	EU360729.1	EU360730.1	Missing	Missing
<i>Odobenus rosmarus</i>	ANOP01028105.1	ANOP01000820.1	ANOP01000821.1	ANOP01017035.1
<i>Orcinus orca</i>	ANOL02004931.1 (Deleted gene - Synteny analysis)	ANOL02054064.1	ANOL02054065.1	ANOL02064465.1
<i>Ovis aries</i>	JN604985.1	CBYI010055183.1	CBYI010055184.1	ACIV011354444.1
<i>Panthera tigris altaica</i>	ATCQ01112915.1	ATCQ01048793.1	ATCQ01048791.1	ATCQ01029167.1
<i>Panthera uncia</i>	SRX273036	SRX273036	SRX273036	SRX273036
<i>Pantholops hodgsonii</i>	AGTT01188813.1	AGTT01169141.1	AGTT01169136.1	AGTT01037849.1
<i>Phoca vitulina</i>	AB921529.1	Missing	Missing	Missing
<i>Physeter macrocephalus</i>	AWZP01062081.1	AWZP01062236.1	AWZP01062236.1	AWZP01043685.1 AWZP01078901.1
<i>Pteropus alecto</i>	ALWS01011689.1	ALWS01169197.1	ALWS01169198.1 ALWS01169197.1	ALWS01050977.1
<i>Pteropus vampyrus</i>	ABRP02126915.1	ABRP02138358.1	ABRP02138358.1	ABRP02100214.1
<i>Rhinoceros unicornis</i>	KY886650	KY886659	KY886668	KY886676
<i>Rhinolophus</i>	AWHA01040305.1	AWHA01096410.1	AWHA01092973.1	AWHA01130749.1

<i>ferrumequinum</i>	AWHA01040304.1		AWHA01092975.1	
<i>Sorex araneus</i>	AALT02056093.1	AALT02155451.1	AALT02155448.1 AALT02155449.1	AALT02042376.1
<i>Suncus murinus</i>	AB244816.1	Missing	Missing	Missing
<i>Sus cebriifrons</i>	ERX149172	ERX149172	ERX149172	ERX149172
<i>Sus scrofa</i>	DQ372918.1	NM_214289.1	NM_214049.1	AJJKK01191606.1
<i>Sus verrucosus</i>	ERX1054048- ERX1054067	ERX1054048- ERX1054067	ERX1054048- ERX1054067	ERX1054048- ERX1054067
<i>Tapirus indicus</i>	KY886651	KY886660	KY886669	KY886677
<i>Tursiops truncatus</i>	ABRN02199412.1 (Deleted gene - Synteny analysis)	ABRN02011700.1	ABRN02011697.1	ABRN02379235.1
<i>Ursus maritimus</i>	AVOR01014285.1	AVOR01090225.1	AVOR01090228.1	AVOR01032007.1
<i>Vicugna pacos</i>	ABRR02134987.1	ABRR02047266.1	ABRR02047266.1	ABRR02146164.1

Euarchontoglires

<i>Aotus nancymae</i>	JYKP01215429.1	JYKP01068224.1	JYKP01068227.1	JYKP01155709.1
<i>Apodemus sylvaticus</i>	LIPJ01014497.1 LIPJ01184746.1	LIPJ01041350.1	LIPJ01000433.1	LIPJ01004285.1
<i>Callithrix jacchus</i>	ACFV01002817.1 ACFV01002818.1	ACFV01035072.1	ACFV01035065.1 ACFV01035066.1 ACFV01035067.1	JRUL010233331.1
<i>Cavia aperea</i>	AVPZ01000778.1	AVPZ01000005.1	AVPZ01000005.1	AVPZ01000041.1
<i>Cavia porcellus</i>	AAKN02011801.1	AAKN02051191.1	AAKN02051190.1	AAKN02053822.1
<i>Cercocebus atys</i>	JZLG01060688.1	JZLG01056565.1	JZLG01056561.1	JZLG01010897.1
<i>Chinchilla lanigera</i>	AGCD01027651.1 AGCD01027652.1	AGCD01015245.1	AGCD01015243.1	AGCD01012756.1
<i>Chlorocebus sabaeus</i>	AQIB01017419.1	AQIB01134135.1	AQIB01134133.1	AQIB01093034.1
<i>Colobus angolensis</i>	JYKR01122839.1 JYKR01122838.1 JYKR01122837.1	JYKR01062401.1	JYKR01062397.1	JYKR01171003.1
<i>Cricetulus griseus</i>	AFTD01128394.1	AFTD01106142.1	AFTD01106142.1	APMK01041211.1
<i>Daubentonia madagascariensis</i>	AGTM011584996.1 AGTM011708528.1 AGTM012010142.1 AGTM011594144.1	AGTM010366851.1 AGTM012942927.1 AGTM010409851.1 AGTM011996042.1 AGTM011949823.1	AGTM010372645.1 AGTM011680642.1	AGTM011625695.1
<i>Dicrostonyx groenlandicus</i>	AF515781.1	Missing	Missing	Missing
<i>Dipodomys ordii</i>	ABRO02057411.1	ABRO02020382.1	ABRO02020382.1	ABRO02010842.1
<i>Eulemur flavifrons</i>	LGHW01000184.1	LGHW01005764.1	LGHW01005764.1	LGHW01001219.1
<i>Eulemur macaco</i>	LGHX01000184.1	LGHX01005675.1	LGHX01005675.1	LGHX01001209.1
<i>Fukomys damarensis</i>	AYUG01151055 AYUG01151056	AYUG01134562.1 AYUG01134563.1	AYUG01134566.1 AYUG01134565.1	AYUG01150094.1
<i>Galeopterus variegatus</i>	JMZW01045216.1 JMZW01045217.1	JMZW01159785.1 JMZW01159786.1	JMZW01159781.1	JMZW01093471.1
<i>Gorilla gorilla gorilla</i>	NW_004002547.1	NW_004005093.1	NW_004005093.1	CABD030081410.1
<i>Heterocephalus glaber</i>	AFSB01162372.1	AFSB01032172.1	AFSB01032171.1	AFSB01080593.1
<i>Homo sapiens</i>	NG_012139.1	U82819.1	U84763.1	U96094.1

<i>Jaculus jaculus</i>	AKZC01091543.1	AKZC01100636.1 AKZC01100637.1	AKZC01100628.1 AKZC01100629.1 AKZC01100630.1 AKZC01100632.1	AKZC01057088.1
<i>Macaca fascicularis</i>	CAEC01514737.1	AEHL01150243.1	AEHL01150254.1; AEHL01150253.1	CAEC01142624.1
<i>Macaca mulatta</i>	AANU01271750.1	AANU01189618.1	AANU01189616.1	AEHK01077455.1
<i>Macaca nemestrina</i>	JZLF01028562.1	JZLF01057018.1	JZLF01057022.1	JZLF01029339.1
<i>Mandrillus leucophaeus</i>	JYKQ01107155.1 JYKQ01107156.1	JYKQ01166891.1	JYKQ01166885.1	JYKQ01102438.1
<i>Marmota marmota</i>	CZRN01000015.1	CZRN01000004.1	CZRN01000004.1	CZRN01000026.1
<i>Mesocricetus auratus</i>	NM_001281332.1	APMT01084061.1	APMT01084061.1	APMT01047702.1
<i>Microcebus murinus</i>	ABDC01082367.1	ABDC01179060.1	ABDC01179052.1 ABDC01179053.1	ABDC02015405.1
<i>Microtus agrestis</i>	LIQJ01004042.1	LIQJ01014426.1	LIQJ01014426.1	LIQJ01000448.1
<i>Microtus ochrogaster</i>	AHZW01157106.1	AHZW01107615.1	AHZW01107615.1	AHZW01020748.1
<i>Mus musculus</i>	CAAA01024310.1	CAAA01006333.1	AAHY01064811.1	AAHY01078220.1
<i>Myodes glareolus</i>	LIPI01003929.1	LIPI01011290.1	LIPI01011290.1	LIPI01022398.1
<i>Nannospalax galili</i>	AXCS01128925.1	AXCS01188952.1	AXCS01188951.1	AXCS01045434.1
<i>Nasalis larvatus</i>	JMHX01319533.1	JMHX01319543.1	CM003003.1	JMHX01319543.1
<i>Nomascus leucogenys</i>	ADFV01177960.1 ADFV01177959.1	ADFV01111583.1	ADFV01111578.1 ADFV01111580.1	ADFV01056290.1
<i>Ochotona dauurica</i>	AB283043.1	Missing	Missing	Missing
<i>Ochotona princeps</i>	ALIT01060999.1	AAYZ01137505.1	AAYZ01237828.1	AAYZ01218708.1
<i>Octodon degus</i>	AJSA01193670.1 AJSA01193671.1	AJSA01174660.1	AJSA01174659.1 AJSA01174660.1	AJSA01031476.1
<i>Oryctolagus cuniculus</i>	NM_001171077.1	AAGW02008192.1	AAGW02008192.1	AAGW02009195.1
<i>Otolemur garnettii</i>	AAQR03074138.1	AAQR03001165.1	AAQR03001162.1	AAQR03181843.1
<i>Pan paniscus</i>	AJFE01070904.1		AJFE01047917.1	AJFE01100549.1
<i>Pan troglodytes</i>	AACZ03032212.1 AACZ03032211.1	AACZ03079660.1	AADA01222375.1	AADA01279835.1
<i>Papio anubis</i>	AHZZ01043343.1	AHZZ01024419.1	AHZZ01024424.1	AHZZ01040054.1
<i>Papio hamadryas</i>	PreEnsembl	Missing	Missing	Missing
<i>Peromyscus maniculatus</i>	AYHN01134223.1 AYHN01134224.1	AYHN01057054.1	AYHN01057054.1	AYHN01010930.1
<i>Phodopus sungorus</i>	AF271263.1	AF271264.1	AF271265.2	Missing
<i>Pongo abelii</i>	ABGA01062109.1 ABGA01062111.1	ABGA01223176.1 ABGA01223175.1	ABGA01223178.1	ABGA01383648.1
<i>Propithecus coquereli</i>	JZKE01017273.1 JZKE01017272.1 JZKE01017271.1	JZKE01114303.1	JZKE01114303.1	JZKE01236593.1
<i>Rattus norvegicus</i>	AAHX01097782.1	AAHX01007471.1	AABR06007535.1	AAHX01054738.1
<i>Rhinopithecus roxellana</i>	JABR01098768.1	JABR01036514.1	JABR01036511.1	JABR01016757.1
<i>Saimiri boliviensis</i>	AGCE01051213.1	AGCE01022106.1	AGCE01022109.1	AGCE01023439.1
<i>Spermophilus tridecemlineatus</i>	AGTP01049379.1	AAQQ01149310.1	AGTP01028875.1	AAQQ01672914.1
<i>Tarsius syrichta</i>	ABRT02355485.1 ABRT02355484.1	ABRT02455082.1	ABRT02455086.1 ABRT02455085.1	ABRT02333009.1
<i>Tupaia belangeri chinensis</i>	ALAR01031044.1	ALAR01010153.1	ALAR01010154.1	ALAR01067265.1

table S2. Likelihood ratio tests for *ucp1* CODEML models. The M2 pseudogene branch model was tested against individual branch models (M2), with additional branch categories for the camel, pygmy hippopotamus, stem rhinoceros, and stem pinniped branches. The pseudogene branch model (M2) analyses with and without the stem placental branch as its own category were tested against each other showing that ω of the stem placental branch ($\omega = 0.6333$) is significantly different than all placental branches with functional *ucp1* ($\omega = 0.1591$). Branch categories for the pseudogene analysis included non-mammalian vertebrates, non-placental mammals, placental branches with intact *ucp1* loci, individual transitional branches (M2 ω values displayed in Fig. 3), and pseudogenic branches. Site and branch-site models were performed with pseudogenes pruned from the dataset. The site model M2a revealed no sites under positive selection and no difference from the null model M1a. The branch site model A was performed to identify sites on the stem placental branch that may have contributed to the gain of NST function. While eight sites were found to have a posterior probability >0.95 , model A was not significantly different from the corresponding null model where ω is fixed at 1 for foreground branch sites in the positive selection site category. Site and branch-site model parameters include the proportion of sites (p_0, p_1, p_2, p_{2a} , and p_{2a}) and omega values ($\omega_0, \omega_1, \omega_2, \omega_{2a}$ and ω_{2b}) for all site classes.

LRT models	Parameter estimates	$2\Delta\ell$	df	p-value	Sites (posterior probability >0.95)
Branch models					
M2 pseudogene vs. M2 camel branch	<p>M2 pseudogene:</p> <ul style="list-style-type: none"> ω functional non-mammal branches = 0.0501 ω functional non-placental branches = 0.1238 ω functional placental branches = 0.1591 ω pseudogenic placental branches = 0.9443 <p>M2 camel branch:</p> <ul style="list-style-type: none"> ω functional non-mammal branches = 0.0501 ω functional non-placental branches = 0.1238 ω functional placental branches = 0.1585 ω pseudogenic placental branches = 0.9438 ω <i>C. ferus</i> = 1.0330 	4.66614	1	0.030762959	
M2 pseudogene vs. M2 pygmy hippo branch	<p>M2 pseudogene:</p> <ul style="list-style-type: none"> ω functional non-mammal branches = 0.0501 ω functional non-placental branches = 0.1238 ω functional placental branches = 0.1591 ω pseudogenic placental branches = 0.9443 <p>M2 pygmy hippo branch:</p> <ul style="list-style-type: none"> ω functional non-mammal branches = 0.0501 ω functional non-placental branches = 0.1238 ω functional placental branches = 0.1585 ω pseudogenic placental branches = 0.9439 ω <i>C. liberiensis</i> = 0.2530 	1.45469	1	0.227776571	

M2 pseudogene vs. M2 stem pinniped branch	M2 pseudogene: ⊖ functional non-mammal branches = 0.0501 ⊖ functional non-placental branches = 0.1238 ⊖ functional placental branches = 0.1591 ⊖ pseudogenetic placental branches = 0.9443 M2 pinniped branch: ⊖ functional non-mammal branches = 0.0501 ⊖ functional non-placental branches = 0.1238 ⊖ functional placental branches = 0.1580 ⊖ pseudogenetic placental branches = 0.9439 ⊖ stem pinniped branch = 0.2866	0.074304175	1	0.074304175
M2 pseudogene vs. M2 stem rhinoceros branch	M2 pseudogene: ⊖ functional non-mammal branches = 0.0501 ⊖ functional non-placental branches = 0.1238 ⊖ functional placental branches = 0.1591 ⊖ pseudogenetic placental branches = 0.9443 M2 stem rhinoceros branch: ⊖ functional non-mammal branches = 0.0501 ⊖ functional non-placental branches = 0.1238 ⊖ functional placental branches = 0.1585 ⊖ pseudogenetic placental branches = 0.9438 ⊖ stem rhinoceros branch = 0.2851	1.459344	1	0.227034526
M2 pseudogene vs. M2 stem placental branch	M2 pseudogene: ⊖ functional non-mammal branches = 0.0501 ⊖ functional non-placental branches = 0.1238 ⊖ functional placental branches = 0.1591 ⊖ pseudogenetic placental branches = 0.9443 M2 stem placental branch: ⊖ functional non-mammal branches = 0.0502 ⊖ functional non-placental branches = 0.1183 ⊖ functional placental branches = 0.1536 ⊖ pseudogenetic placental branches = 0.9437 ⊖ stem placental branch = 0.6333	36.676754	1	1.39432E-9

Site models

M1a vs. M2a	M1a: $p_0 = 0.92037$ $p_1 = 0.07963$ $\omega_0 = 0.11041$ $\omega_1 = 1.00000$ M2a: $p_0 = 0.92037$ $p_1 = 0.05616$ $p_2 = 0.02347$ $\omega_0 = 0.11038$ $\omega_1 = 1.00000$ $\omega_2 = 1.00004$	0	2	1	None
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Branch-site models

Model A null vs. Model A - stem placental branch	Model A null: $p_0 = 0.47004$ $p_1 = 0.04251$ $p_{2a} = 0.44702$ $p_{2b} = 0.04043$ ω_0 & ω_{2a} background = 0.10531 ω_1 & ω_{2b} background = 1.00000 ω_0 foreground = 0.10531 ω_1, ω_{2a} & ω_{2b} foreground = 1.00000 Model A: $p_0 = 0.54398$ $p_1 = 0.04910$ $p_{2a} = 0.37323$ $p_{2b} = 0.03369$ ω_0 & ω_{2a} background = 0.10532	0.63447	1	0.425720414	15L, 22S, 76K, 124L, 153I, 170T, 224I, 261M
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Ω_1 & Ω_{2b} background = 1.00000
 Ω_0 foreground = 0.10532
 Ω_1 foreground = 1.00000
 Ω_{2a} & Ω_{2b} foreground = 1.40522

table S3. Calculated *ucp1* inactivation dates (Ma) within the placental mammal lineage.

Inactivation date ranges were calculated using the two sets of formulas specified by Meredith *et al.* (26) with branch model CODEML analyses using species divergences and branch lengths arising from our 51 kb maximum likelihood species timetree analysis (data file S1). The first dating method assumes the rate of “synonymous substitution are neutral and equal on functional and pseudogene branches” while the second assumes “the rate synonymous substitution on functional branches is non-neutral and 70% of the rate of synonymous substitution on pseudogene branches”. Inactivation date calculations utilized ω values for placental branches with functional *ucp1* ($\omega=0.1591$), transitional branches (ω values displayed in Fig. 3), and pseudogenetic branches ($\omega=0.9435$). As ω values calculated for *Dasybus novemcinctus*, *Manis pentadactyla*, and the stem cetacean branch ($\omega=1.0567$, 0.9849, and 0.9872, respectively) exceeded the mean value of pseudogenized branches, we placed their inactivation dates at the base of each clade. Conversely, the ω value (0.0805) for the stem Pilosa branch was below that for functional branches; shared inactivating mutations in three-toed sloth (*Bradypus*), two-toed sloth (*Choleopus*), and silky anteater (*Cyclopes didactylus*), however, indicate *ucp1* was pseudogenized prior to their radiation ~55.03 Ma. Note that since only remnants of *ucp1* (exon 6) were identified from representative Pilosa, it is possible that *ucp1* pseudogenization preceded its divergence from Cingulata.

Transitional branch	Inactivation date (Ma)
<i>Dasybus novemcinctus</i>	65.55
Pilosa	>55.03
<i>Procavia capensis</i>	33.5–27.3
Proboscidea	42.9–37.5
Sirenia	46.0–44.8
Suidae (<i>Sus spp.</i>)	41.2–36.4
Cetacea	52.75
Equus	25.1–20.7
<i>Manis pentadactyla</i>	74.69

table S4. Results of BiSSE models with and without constraints on the diversification rate for five trees from the work of Faurby and Svenning (56).

Tree #	Model	Constraints	lambda0	lambda1	mu0	mu1	q01	q10	parameters	Ln Lik	AIC	p value
1	No reversal	$q_{10} = 0$	0.2990537	0.2118425	0.2301557	0.1818380	0.0001916	0	5	-14264	28539	2.32E-05
1	No reversal, equal diversification	lambda0 = lambda1, mu0 = mu1, $q_{10} = 0$	0.2985928	0.2985928	0.2333964	0.2333964	0.0001907	0	3	-14275	28556	
2	No reversal	$q_{10} = 0$	0.2979023	0.1557338	0.2310627	0.1124779	0.0001479	0	5	-14334	28679	1.31E-07
2	No reversal, equal diversification	lambda0 = lambda1, mu0 = mu1, $q_{10} = 0$	0.292754	0.292754	0.228024	0.228024	0.0001891	0	3	-14350	28707	
3	No reversal	$q_{10} = 0$	0.2724713	0.1950414	0.1966417	0.1611570	0.0001922	0	5	-14467	28944	1.27E-05
3	No reversal, equal diversification	lambda0 = lambda1, mu0 = mu1, $q_{10} = 0$	0.2714773	0.2714773	0.1993568	0.1993568	0.0001890	0	3	-14478	28963	
4	No reversal	$q_{10} = 0$	0.3102003	0.1427713	0.2429003	0.0985164	0.0001410	0	5	-14178	28366	9.45E-10
4	No reversal, equal diversification	lambda0 = lambda1, mu0 = mu1, $q_{10} = 0$	0.3041617	0.3041617	0.2393333	0.2393333	0.0001951	0	3	-14199	28404	
5	No reversal	$q_{10} = 0$	0.2789428	0.1652951	0.2083545	0.1242601	0.0001596	0	5	-14518	29047	3.37E-06
5	No reversal, equal diversification	lambda0 = lambda1, mu0 = mu1, $q_{10} = 0$	0.2755167	0.2755167	0.2074114	0.2074114	0.0001844	0	3	-14531	29068	

table S5. BiSSE results for neutral character simulations. Neutral characters were simulated on the same five trees (5138 taxa) as in table S4. In each case, a model with no reversal ($q_{10} = 0$) and no constraints on diversification rates was compared to a model with no reversal ($q_{10} = 0$), equal speciation rates ($\lambda_0 = \lambda_1$), and equal extinction rates ($\mu_0 = \mu_1$). Significance levels are indicated (* = $p < 0.5$; ** = $p < 0.01$; *** = $p < 0.0001$).

Tree #	Ln Lik	AIC	ChiSq	p value	Significance level
1	-14287	28580	8.3649	0.01526	*
1	-14290	28585	17.882	0.0001309	***
1	-14283	28571	25.832	2.46E-06	***
1	-14268	28541	1.6061	0.448	
1	-14297	28600	5.7015	0.0578	
1	-14279	28564	2.7851	0.2484	
1	-14268	28543	6.1693	0.04575	*
1	-14279	28564	0.68013	0.7117	
1	-14267	28539	1.6509	0.438	
1	-14288	28582	2.1826	0.3358	
1	-14262	28531	1.4547	0.4832	
1	-14311	28628	0.24268	0.8857	
1	-14268	28543	1.2025	0.5481	
1	-14291	28588	15.569	0.0004162	***
1	-14254	28514	4.3205	0.1153	
1	-14268	28542	8.56	0.01384	*
1	-14284	28574	5.711	0.05753	
1	-14304	28615	4.7037	0.0952	
1	-14276	28558	15.226	0.0004939	***
1	-14301	28608	2.1298	0.3448	
2	-14321	28648	2.2439	0.3256	
2	-14352	28709	12.725	0.001725	**
2	-14368	28742	1.9207	0.3828	
2	-14360	28725	0.30942	0.8567	
2	-14360	28726	2.7076	0.2583	
2	-14342	28690	7.9521	0.01876	*
2	-14332	28669	3.5106	0.1729	
2	-14321	28648	2.2393	0.3264	
2	-14356	28717	2.5266	0.2827	
2	-14340	28686	1.5311	0.4651	
2	-14340	28687	3.4521	0.178	
2	-14347	28700	11.566	0.00308	**
2	-14339	28685	7.5964	0.02241	*
2	-14355	28715	12.958	0.001535	**
2	-14348	28703	13.494	0.001174	**
2	-14354	28714	3.9504	0.1387	

2	-14349	28704	19.476	5.90E-05	***
2	-14360	28727	2.1532	0.3408	
2	-14348	28703	15.847	0.0003622	***
2	-14353	28713	0.42811	0.8073	
3	-14447	28899	24.473	4.85E-06	***
3	-14509	29024	4.2386	0.1201	
3	-14525	29056	16.217	0.0003009	***
3	-14488	28982	7.0465	0.0295	*
3	-14514	29034	7.2817	0.02623	*
3	-14494	28995	0.22603	0.8931	
3	-14470	28947	1.5699	0.4561	
3	-14498	29001	3.105	0.2117	
3	-14481	28967	7.1922	0.02743	*
3	-14472	28950	3.9134	0.1413	
3	-14477	28961	2.3794	0.3043	
3	-14472	28950	0.68295	0.7107	
3	-14455	28916	6.5718	0.03741	*
3	-14500	29007	17.326	0.0001729	***
3	-14477	28960	14.934	0.0005715	***
3	-14471	28947	13.084	0.001441	**
3	-14504	29014	3.9079	0.1417	
3	-14523	29051	7.2379	0.02681	*
3	-14476	28958	23.591	7.54E-06	***
3	-14501	29008	1.8208	0.4024	
4	-14178	28362	0.90767	0.6352	
4	-14220	28446	25.795	2.51E-06	***
4	-14212	28431	7.0962	0.02878	*
4	-14214	28433	18.623	9.04E-05	***
4	-14208	28423	0.68958	0.7084	
4	-14210	28426	22.513	1.29E-05	***
4	-14188	28382	1.5229	0.467	
4	-14215	28436	6.0754	0.04794	*
4	-14202	28410	4.4862	0.1061	
4	-14187	28380	1.037	0.5954	
4	-14200	28406	26.321	1.93E-06	***
4	-14187	28380	2.1832	0.3357	
4	-14176	28358	2.4273	0.2971	
4	-14187	28380	6.1279	0.0467	*
4	-14191	28388	8.889	0.01174	*
4	-14199	28403	9.5794	0.008315	**
4	-14188	28382	13.933	0.0009428	***
4	-14213	28432	20.863	2.95E-05	***
4	-14194	28393	4.8134	0.09011	

4	-14200	28405	5.7027	0.05777	
5	-14527	29060	1.4141	0.4931	
5	-14546	29098	3.5835	0.1667	
5	-14536	29078	5.8842	0.05275	
5	-14549	29105	2.5866	0.2744	
5	-14525	29057	1.59	0.4516	
5	-14555	29116	107.64	<2.2e-16	***
5	-14550	29106	0.29186	0.8642	
5	-14526	29058	4.8953	0.0865	
5	-14557	29119	2.5245	0.283	
5	-14530	29066	1.7002	0.4274	
5	-14546	29098	8.3536	0.01535	*
5	-14552	29109	4.0583	0.1314	
5	-14545	29096	4.2978	0.1166	
5	-14546	29098	3.0219	0.2207	
5	-14534	29074	10.38	0.005572	**
5	-14510	29025	9.9686	0.006845	**
5	-14570	29147	32.984	6.88E-08	***
5	-14562	29129	6.778	0.03374	*
5	-14545	29096	4.8771	0.08729	
5	-14526	29058	0.23807	0.8878	

table S6. Deleterious mutations found in *ucp2* and *ucp3* sequences of placental mammal taxa. Base numbers correspond to position in multiple species alignments (data files S7 and S8). Note that the coding region of several *ucp2* and *ucp3* sequences in GenBank (*ucp2*: Tammar wallaby [ABQO020850797.1], orangutan [ABGA01223176.1, ABGA01223175.1], and thirteen-lined ground squirrel [AAQQ01149310.1]; *ucp3*: Northern white-cheeked gibbon [ADFV01111578.1]) showed signs of disruption (indels), though these were not present in the NCBI sequence read archive and thus likely represent assembly errors.

Gene	Species name	Base number	Inactivating mutation	
<i>ucp2</i>	<i>Dasypus novemcinctus</i>	1	Mutated initiation codon	
		96	1 bp deletion	
		348-349	2 bp deletion	
		396-397	2 bp deletion	
		463	1 bp deletion	
		646-648	Nonsense mutation	
		653-654	2 bp deletion	
		673	1 bp deletion	
		889	1 bp deletion	
		906	1 bp deletion	
		930	1 bp deletion	
<i>ucp3</i>	<i>Dasypus novemcinctus</i>	752	1 bp deletion	
		<i>Oryctolagus cuniculus</i>	54	1 bp deletion
			78	1 bp deletion

table S7. Specimen data and sources of tissue samples used for PCR amplification and DNA hybridization capture.

Common name	Scientific name	Sample	Provided by
Xenarthra			
Brown-throated sloth	<i>Bradypus variegatus</i>	Genomic DNA, previously extracted	M. Springer, University of California, Riverside
Silky anteater	<i>Cyclopes didactylus</i>	Genomic DNA, previously extracted (46)	M. Springer, University of California, Riverside
Paenungulata			
Dugong	<i>Dugong dugon</i>	Two genomic DNA samples, Female, Mabuiag Island, Torres Straits, Australia, previously extracted (69); Sample codes: MD33 and MD118	D. McDonald, James Cook University, Australia
Steller's sea cow	<i>Hydrodamalis gigas</i>	Three bone samples housed in the Zoological Institute of the Russian Academy of Sciences (St. Petersburg, Russian Federation), previously extracted (64, 70) ZI 6852: Mandible collected from Bering Island, Komandorskii in 1884 ZI6853: Humerus, no collection information ZI 17170: Scapula, no collection information	R. MacPhee, American Museum of Natural History
Asian elephant	<i>Elephas maximus</i>	Genomic DNA, Male, previously extracted (69)	W. Korver, Bowmanville Zoo, Ontario, Canada
African elephant	<i>Loxodonta africana</i>	Genomic DNA, Female, previously extracted (69)	W. Korver, Bowmanville Zoo, Ontario, Canada
Laurasiatheria			
Pygmy hippopotamus	<i>Choeropsis liberiensis</i>	Genomic DNA, previously extracted (79)	New York Zoological Society
Bowhead whale	<i>Balaena mysticetus</i>	Genomic DNA	SWFSC
Beluga whale	<i>Delphinapterus leucas</i>	Genomic DNA, previously extracted (79)	New York Zoological Society
Grant's zebra	<i>Equus quagga boehmi</i>	Skeletal muscle from stillborn calf	S. Petersen, Assiniboine Park Zoo, Manitoba, Canada
Malayan tapir	<i>Tapirus indicus</i>	Blood	M. Bertelsen, Copenhagen Zoo, Frederiksberg, Denmark T. Gilbert and E. Willerslev, University of Copenhagen
Woolly rhinoceros	<i>Coelodonta antiquitatis</i>	Permafrost preserved tooth and bone samples housed at the Centre for GeoGenetics at the Natural History museum of Denmark (Copenhagen, Denmark) CGG_1_000024: Tooth, Bol'shoi Lyakhovsky Island, Novaya Sibir' Island, Siberia, Russia CGG_1_000029: Bone, Badyarikha, Indigirka Lowland, Russia CGG_1_000031: Bone, Khetachan Creek Mine, Kolyma Lowland, Russia	T. Gilbert and E. Willerslev, University of Copenhagen
Black rhinoceros	<i>Diceros bicornis</i>	Genomic DNA, previously extracted	CRES
Sumatran rhinoceros	<i>Dicerorhinus sumatrensis</i>	Blood excised from a leech that fed on a Sumatran rhinoceros	R. Havmøller, T. Gilbert, and E. Willerslev, University of Copenhagen Leibniz-Institute for Zoo and Wildlife Research, Berlin, Germany
Indian rhinoceros	<i>Rhinoceros unicornis</i>	Genomic DNA, previously extracted	CRES

table S8. Fossil constraints used in timetree analysis.^A

Constrained Clade	Min Age	Max Age	Basis for Max Age	Oldest Fossil	Comments/References
1. Metatheria	65.18	83.8	SB	<i>Peradectes</i> (Puercan); <i>Minoperadectes</i> (Early Wasatchian)	Horovitz <i>et al.</i> (81) reported Puercan <i>Peradectes</i> (age = 65.18 Ma) as the oldest crown metatherian and recovered this taxon as a stem didelphimorphian. Benton <i>et al.</i> (78) cited Horovitz <i>et al.</i> (81) in support of a younger age for Metatheria but failed to describe their rationale for excluding <i>Peradectes</i> from crown Metatheria.
2. Xenarthra	47.8	66.0	PB	<i>Riostegotherium</i>	<i>Riostegotherium</i> is from the Itaboraian (82). The Itaboraian was originally considered equivalent to the Selandian stage (83), but Woodburne <i>et al.</i> (84) suggested an early Eocene age (minimum = 47.8 Ma). The first outgroup to Xenarthra is Afrotheria, Boreoeutheria, or Epitheria, all of which have early Paleocene representatives.
3. Proboscidea (= <i>Loxodonta</i> to <i>Elephas</i>)	6.8	11.62	SB	<i>Loxodonta</i>	Vignaud <i>et al.</i> (85) reported <i>Loxodonta</i> in their faunal list for a hominid locality in Chad. Vignaud <i>et al.</i> 's (85) locality was radiometrically dated by Lebatard <i>et al.</i> (86) to have an age between 6.8 and 7.2 Ma. The oldest <i>Elephas</i> lineage fossils have a minimum age of 5.332 Ma (87, 88).
4. <i>Dugong</i> to <i>Hydrodamalis</i>	28.1	38.0	SB	<i>Crenatosiren</i>	The minimum age is based on the inclusion of early Oligocene taxa (<i>e.g.</i> , <i>Crenatosiren olseni</i>) in crown Dugongidae (64, 89).
5. Sirenia (<i>Dugong</i> to <i>Trichechus</i>)	41.3	59.2	SB	<i>Eotheroides</i>	The minimum age is based on the inclusion of Lutetian age <i>Eotheroides aegyptiacum</i> in crown Sirenia (64, 89-91).
6. Tethytheria	59.2	72.3	SB	<i>Eritherium</i>	<i>Eritherium</i> is a stem proboscidean and is no younger than the late Selandian (92), which has a minimum age of 59.1 Ma.
7. Paenungulata	59.2	72.3	SB	<i>Eritherium</i>	<i>Eritherium</i> is a stem proboscidean and is no younger than the late Selandian (92), which has a minimum age of 59.1 Ma.
8. Chiroptera	47.8	66.0		<i>Dizzya</i>	<i>Dizzya</i> (Phyllitidae, Vespertilionoidea) is among the oldest crown chiropterans and is from the Ypresian (93). We used the top of the Ypresian as a minimum age for Yangochiroptera. Phillips (94) suggested a maximum age of 58.9 Ma for Chiroptera. The oldest bats (earliest Eocene, ~55 Ma) were already highly specialized fliers with fully developed wings (95, 96). Bats are one of the least common groups of mammals in the fossil record (93, 95, 97, 98), and in our view it is unnecessarily restrictive to enforce a maximum of 58.9 Ma on crown Chiroptera. Furthermore, molecular studies have rearranged the evolutionary tree for bats and recovered numerous higher-level clades that were previously unrecognized based on morphological data (97, 99, 100). The relationships of several early Eocene fossils (<i>e.g.</i> , <i>Palaeochiropteryx</i> , <i>Archaeonycteris</i> , <i>Hassianonycteris</i>), in turn, lack robust support, and their inclusion or exclusion from crown Chiroptera is sensitive to the enforcement of molecular scaffolds (96, 97, 101). Phylogenetic uncertainties, convergent evolution, and a depauperate fossil record conspire together to limit our understanding of the early evolutionary history of bats and caution against employing a maximum that is younger than the KPg boundary (66 Ma).
9. Megadermatidae to Rhinolophidae+ Hipposideridae	38.0	56	SB	<i>Hipposideros</i>	<i>Hipposideros</i> and <i>Rhinolophus</i> are both known from the Eocene of Europe (102). Eiting and Gunnell (93) indicate that <i>Hipposideros</i> first occurs in the Bartonian whereas <i>Rhinolophus</i> first occurs in the Priabonian.
10. Caniformia (=Canidae to Arctoidea)	38.0	56	SB	<i>Hesperocyon gregarius</i>	<i>Hesperocyon gregarius</i> fossils are known from the Duchesnean (~Bartonian) land mammal age in the middle Eocene (103). <i>H. gregarius</i> is a stem canid (104).
11. Ursidae to other Arctoidea	28.1	41.3	SB	<i>Cephalogale</i>	<i>Cephalogale</i> belongs to the ursid subfamily Hemicyoninae and has emerged as a stem ursid in phylogenetic analyses (105); also see

					Wang <i>et al.</i> (106). <i>Cephalogale</i> is known from the early Oligocene (107). We used the top of the early Oligocene as the minimum for Urside to other arctoids.
12. Musteloidea to Pinnipedia	23.03	38.0	SB/PB/PU	<i>Promartes</i> , <i>Enaliarctos</i>	<i>Mustelavus priscus</i> is first known from the latest Eocene (108). <i>M. priscus</i> is either a stem musteloid (106, 108, 109), and the oldest representative of the crown taxon that includes musteloids and pinnipeds, or a deeper lineage within Caniformes (110). Tomiya's analysis is at odds with molecular studies and recovered <i>Ursus</i> inside of crown Musteloidea. Nevertheless, given the uncertainty regarding <i>Mustelavus</i> based on Tomiya (110), we implemented a minimum of 23.03 Ma for the musteloid-pinniped split based on the oldest musteloid (<i>Promartes</i>) (105, 108) and oldest pinniped (<i>Enaliarctos</i>) (111), both of which are from the late Oligocene.
13. Pinnipedia	20.43	33.9	SB	<i>Desmatophoca brachycephala</i>	<i>Desmatophoca brachycephala</i> is Aquitanian (20.43-23.03 Ma) in age (112). The oldest stem pinnipeds are Chattian (e.g., <i>E. tedfordi</i>). SB yields an older maximum than PB.
14. Carnivora	38.0	66.0	PU	<i>Hesperocyon gregarius</i>	<i>Hesperocyon gregarius</i> is a basal canid in constrained (113) and unconstrained (104, 113) analyses. Viverravids from the early Paleocene are probably stem carnivorans (113), but phylogenetic uncertainty allows for the possibility that they are stem feliforms (114-116). Benton <i>et al.</i> (78) also suggested a maximum of 66 Ma for Carnivora.
15. Perissodactyla	55.5	61.6	SB	<i>Hyracotherium</i>	<i>Hyracotherium</i> first appears in Wa-0 at the beginning of the Eocene (117) and is the oldest crown Perissodactyla.
16. Erinaceidae to Soricidae	61.6	83.8	SB	<i>Adunator</i>	<i>Adunator</i> is the oldest erinaceomorph (118) and is known from the Torrejonian (contained within Danian). The minimum age is 61.6 Ma and the maximum is the base of the Campanian (83.6 +/-0.2 = 83.8 Ma) based on SB.
17. Cetartiodactyla	52.5	66.0	PB/PU	<i>Himalayacetus</i>	<i>Himalayacetus</i> is from shallow benthic zone SB8, which has a minimum age of 52.5 Ma within the Ypresian (53, 118). Mesonychids are a possible sister taxon to Cetartiodactyla, or may even be nested with Cetartiodactyla as the sister to Cetacea (119). The oldest mesonychids are early Paleocene in age and establish a maximum age for Cetartiodactyla.
18. Whippomorpha	52.5	61.6	SB	<i>Himalayacetus</i>	<i>Himalayacetus</i> is from shallow benthic zone SB8, which has a minimum age of 52.5 Ma within the Ypresian (53, 118).
19. Cetacea	34.0	47.8	SB	<i>Llanocetus denticrenatus</i>	<i>Llanocetus</i> is known from the La Meseta Formation of Seymour Island, Antarctica, and is latest Eocene in age (53, 120). <i>Llanocetus</i> is the oldest crown cetacean and a primitive stem mysticete. The oldest odontocetes are stem odontocetes from the Rupelian (early Oligocene) or more precisely from the late early Oligocene (53), although there are also older forms that have not been described. Uhen (53) doesn't provide ages.
20. Mysticeti	20.43	33.9	SB	<i>Morenocetus parvus</i>	<i>Morenocetus parvus</i> is the oldest described species belonging to crown-group Mysticeti, and is from the Aquitanian (minimum age = 20.43 Ma) in the early Miocene of Patagonia (121). There is also an unnamed balaenid (~28 Ma) from the late Oligocene of New Zealand (Kokoamu Greensand) (122), but the phylogenetic position of this taxon is unclear and awaits phylogenetic analysis (J. Geisler, communication to J. Gatesy).
21. Bovinae to Antilopinae	16	28.1	SB	<i>Pseudoeotragus</i>	<i>Pseudoeotragus</i> is a stem antelope and is known from the Burdigalian (78).
22. Haplorrhini (=Tarsiidae to Anthroidea)	38.0	59.2	PU	Numerous eosimiids	<i>Altialasius</i> is known from the late Paleocene and is a stem anthropoid in recent cladistic analyses (123, 124), although not in Bloch <i>et al.</i> (125). <i>Anthrasimias</i> (54-55 Ma, Sparnacian) (123, 126) is another putative stem anthropoid, although its anthropoid status has been questioned (124). <i>Algeripithecus</i> is younger (> 45 Ma) and has been referred to Anthroidea (127). However, recent discoveries of more complete specimens of <i>Algeripithecus</i> suggest that it is not anthropoid (128). Instead, it may belong to the Azibiidae, which are argued to be adapiforms, early euprimates, plesiadapiforms (possible stem

					primates), or even nonprimates (128). As many as 11 species and six genera of Asian eosimiids are known from the middle Eocene of Asia (128). The oldest tarsiid is <i>Tarsius eoceanus</i> (129, 130) from the middle Eocene of China (minimum age = 38.0 Ma). We used the top of the middle Eocene as a minimum for crown Haplorhini based on the occurrence of numerous eosimiids from the middle Eocene (128). The maximum age allows for the possibility that the late Paleocene <i>Altiatlasius</i> from Morocco is a stem anthropoid (128).
23. Anthropeidea	28.1	56.0	PU	<i>Aegyptopithecus</i>	<i>Aegyptopithecus</i> (early Oligocene~Rupelian) is a stem catarrhine in Kay <i>et al.</i> 's (131) cladistic analyses with molecular scaffolds. The oldest stem platyrrhine is <i>Branisella</i> (131) from the late Oligocene of Bolivia (Salla Beds, Chron 8, age = 25.82-27.02 Ma) (124). Some authors have suggested that <i>Catopithecus browni</i> from the Priabonian is a stem catarrhine, but other authors (<i>e.g.</i> , Williams <i>et al.</i> ; 128) have suggested a stem anthropoid position for this taxon. Seiffert <i>et al.</i> (127) recovered a polytomy with catarrhines, platyrrhines, Parapithecoidea, Proteopithecidae, and <i>Algeripithecus minutus</i> . The age of the latter taxon is Ypresian to basal Lutetian, which established a maximum of 56.0 Ma for the base of Anthropeidea if we allow for phylogenetic uncertainty, <i>i.e.</i> , that <i>Algeripithecus</i> is either a crown anthropoid or one of the first two outgroups. In contrast, Tabuce <i>et al.</i> (132) place <i>Algeripithecus</i> as a stem strepsirrhine based on more complete material.
24. Catarrhini	20.55	38.0	PB/PU	<i>Afropithecus</i>	<i>Afropithecus turkanensis</i> , previously <i>Morotopithecus bishop</i> (133), is dated at 20.6 +/- 0.05 = 20.55 Ma based on overlying lava (134) and is the oldest crown-group catarrhine. It is a stem hominoid (135) or even a crown hominoid (134). The oldest cercopithecoid is <i>Victoriapithecus</i> (136) at ~19 Ma. Oligopithecids (including <i>Catopithecus</i>) are sometimes regarded as stem catarrhines (<i>e.g.</i> , see review of alternate hypotheses in Seiffert and Simons; 137) where <i>Catopithecus</i> is sometimes part of second outgroup to crown catarrhines). The age of <i>Catopithecus</i> is 34.8-33.7 Ma (Chron C13r) based on Seiffert (138), which is mostly within the Priabonian. We used the base of the Priabonian (38.0 Ma) as the maximum age for the base of Catarrhini.
25. Hominoidea	11.608	28.1	SB	<i>Sivapithecus</i>	<i>Sivapithecus</i> is the oldest crown hominoid in Finarelli and Clyde's (135) cladistic and stratocladistic analyses.
26. Strepsirrhini	38.0	56	SB/PB	<i>Saharagalago</i>	<i>Saharagalago misrensis</i> is known from the Bartonian (139) and is assigned to Galagidae; <i>Karanisia</i> is as a crown lorissid in Seiffert <i>et al.</i> 's (139) analysis, although these authors also allow for the possibility that this taxon is a stem lorissid or stem lorissiform. These are the oldest crown strepsirrhines. Adapiforms are paraphyletic at the base of crown Strepsirrhini (see 140). The oldest adapiforms are early Eocene and establish a maximum age for Strepsirrhini.
27. Chinchillidae to Octodontidae	24.5	38.0	SB/PB	<i>Sallamys</i> , <i>Xylechimys</i> , <i>Deseadomys</i>	Molecular studies (141, 142) suggest that <i>Myocastor</i> , and possibly <i>Capromys</i> , are nested within Echimyidae. The fossil taxa <i>Sallamys</i> , <i>Xylechimys</i> , and <i>Deseadomys</i> (family Echimyidae) are all known from the Deseadean (143), which is mostly late Oligocene and has a minimum age of 24.5 Ma (144, 145). These fossils establish the minimum age for Echimyidae (inclusive of <i>Capromys</i> and <i>Myocastor</i>). <i>Eosallamys</i> , <i>Eoespina</i> , <i>Eosachacui</i> , and <i>Eodelphomys</i> were assigned to Echimyidae and are known from the Santa Rosa Local Fauna of Peru (146, 147). The putative age of this fauna is late Eocene, but this age is based on stage of evolution arguments and remains to be firmly established using more rigorous stratigraphic methods. Hence, we incorporate this information into our maximum age but not our minimum age.
28. Phiomorpha + Caviomorpha	40.94	56	SB/PB	Stem caviomorphs in Antoine <i>et al.</i> (146) including <i>Cachiyacuy</i> and other stem Caviomorpha	This calibration was suggested by Phillips (94) based on fossils that were described by Antoine <i>et al.</i> (148) including <i>Cachiyacuy contamanensis</i> . We retained minimum and maximum ages suggested by Phillips (94). Hartenberger (149) contends that specimens of the early Eocene <i>Glibia</i> are instead the oldest representatives of

					Phiomoridae. Given this possibility we used the base of the early Eocene as the maximum age for Phiomorpha to Caviomorpha.
29. Myomorpha (=Muroidea to Dipodidae)	45	59.2	SB	<i>Pappocricetodon</i>	Eocene deposits in China with <i>Pappocricetodon</i> have been biocorrelated with Bridgerian and early Uintan LMAs of North America (130), and suggest an age of ~45 Ma. SB yields a maximum age of 59.2 Ma for Muroidea + Dipodidae.
30. <i>Mus</i> to <i>Rattus</i>	10.4	15.97		<i>Karmimata</i>	<i>Karmimata darwini</i> is known from the Dhok Pathan Formation, which has an absolute age in the vicinity of 10.4 Ma (78) within the Tortonian stage. <i>K. darwini</i> is closer to <i>Rattus</i> than <i>Mus</i> (78). We used 10.4 Ma as the minimum age for <i>Rattus</i> to <i>Mus</i> following Benton <i>et al.</i> (78). Benton <i>et al.</i> (78) suggested a maximum constraint of 14.0 Ma based on the oldest record of <i>Antemurus</i> , which is found in the Langhian stage. We used the base of the Langhian stage (15.97 Ma) rather than 14.0 Ma for the maximum age of <i>Mus</i> to <i>Rattus</i> .
31. Rodentia	56.0	66.0	SB	<i>Acritoparamys</i> , <i>Paramys</i>	The earliest crown rodents (<i>e.g.</i> , <i>Acritoparamys</i> , <i>Paramys</i>) are late Thanetian in age (78) and establish a minimum age of 56.0 Ma for Rodentia. Given this age, stratigraphic bounding supports a maximum age of 66.0 Ma, which agrees with Benton <i>et al.</i> (78).
32. Lagomorpha	47.6	61.6	SB/PB	Ypresian tarsals	Tarsals from the Vastan mine, India, belong to crown Lagomorpha in phylogenetic analyses (150; p. 1205). The age of the Vastan mine deposits is Ypresian (minimum = 47.6 Ma). The first and second outgroups to crown Lagomorpha are <i>Palaeolagus</i> and <i>Mimotona</i> (151, 152). The latter is from the late Paleocene, which includes the Selandian and Thanetian. <i>Dawsonolagus</i> (153) is another stem lagomorph, but has not been included in cladistic analyses.
33. Mammalia	160.7	227	PB/PU	<i>Ambondro</i>	<i>Ambondro</i> , from the Bathonian, is a crown mammal in a variety of analyses (<i>e.g.</i> , Lou <i>et al.</i> (154) and Woodburne <i>et al.</i> (155); reviewed in Benton <i>et al.</i> (78)), although its affinities with monotremes versus therians remain controversial. We followed Benton <i>et al.</i> (78) and used the top of the Bathonian, <i>i.e.</i> , 166.1 +/- 1.2 Ma = 164.9 Ma. Multituberculata are generally placed inside of crown Mammalia (<i>e.g.</i> , Kielan-Jaworowska <i>et al.</i> ; 156). Haramiyids, in turn, may be related to multituberculates (156-158). The oldest haramiyid is <i>Thomasia</i> from the Norian (159). The oldest mammal fossils are <i>Adelobasileus</i> (159), <i>Gondwanadon</i> (160), and <i>Tikitherium</i> (160) from the Carnian, but there is no suggestion that any of these taxa belong to crown Mammalia. Given the uncertainty associated with the placement of Haramiyidae, including <i>Thomasia</i> , we employed a maximum of 227 Ma (base of Norian).
34. Neognathae	66	86.8	SB	<i>Vegavis iaai</i>	Clarke <i>et al.</i> (161); Benton <i>et al.</i> (78, 118)
35. Amniota	318	332.9	SB	<i>Hylonomus lyelli</i>	<i>Hylonomus</i> is from the Joggins Formation of Nova Scotia. The most recent estimates for the age of the Joggins Formation are in the range of 318-319 Ma (78) (based on Gradstein <i>et al.</i> ; 162). The maximum age is based on the absence of crown amniotes in well-sampled, fossiliferous deposits that occur below the strata with <i>Hylonomus</i> (78).
36. Archosauria to Lepidosauria	255.9	295.9	SB	<i>Protorosaurus speneri</i>	<i>Protorosaurus speneri</i> is the oldest archosauromorph and has a minimum age estimate of 255.9 Ma (78, 118), which falls within the Wuchiapingian stage of the Permian. Benton <i>et al.</i> (78) suggested a maximum age of 295.9 Ma.
37. Tetrapoda	337	351	SB	<i>Lethiscus stocki</i>	<i>Lethiscus</i> is the oldest reptilomorph (stem amniote) and is from the Wardie Shales, which belong to the Lower Oil Shale Group. The age of the Wardie Shales is ~343.5-337 Ma (78) (based on Gradstein <i>et al.</i> ; 162). The maximum age for Tetrapoda is from Benton <i>et al.</i> (78).

^ATable modified and updated after Meredith *et al.* (46). Abbreviations: PB, phylogenetic bracketing; PU, phylogenetic uncertainty; SB, stratigraphic bounding; Ma, million years.