

Figure S1.

Saturation plots of transitions (red diamonds; dotted line) and transversions (green squares) calculated through pairwise sequence comparisons. Maximum-likelihood distances calculated using the substitution model that best fitted the data are plotted against the percent number of substitutions all codon positions.

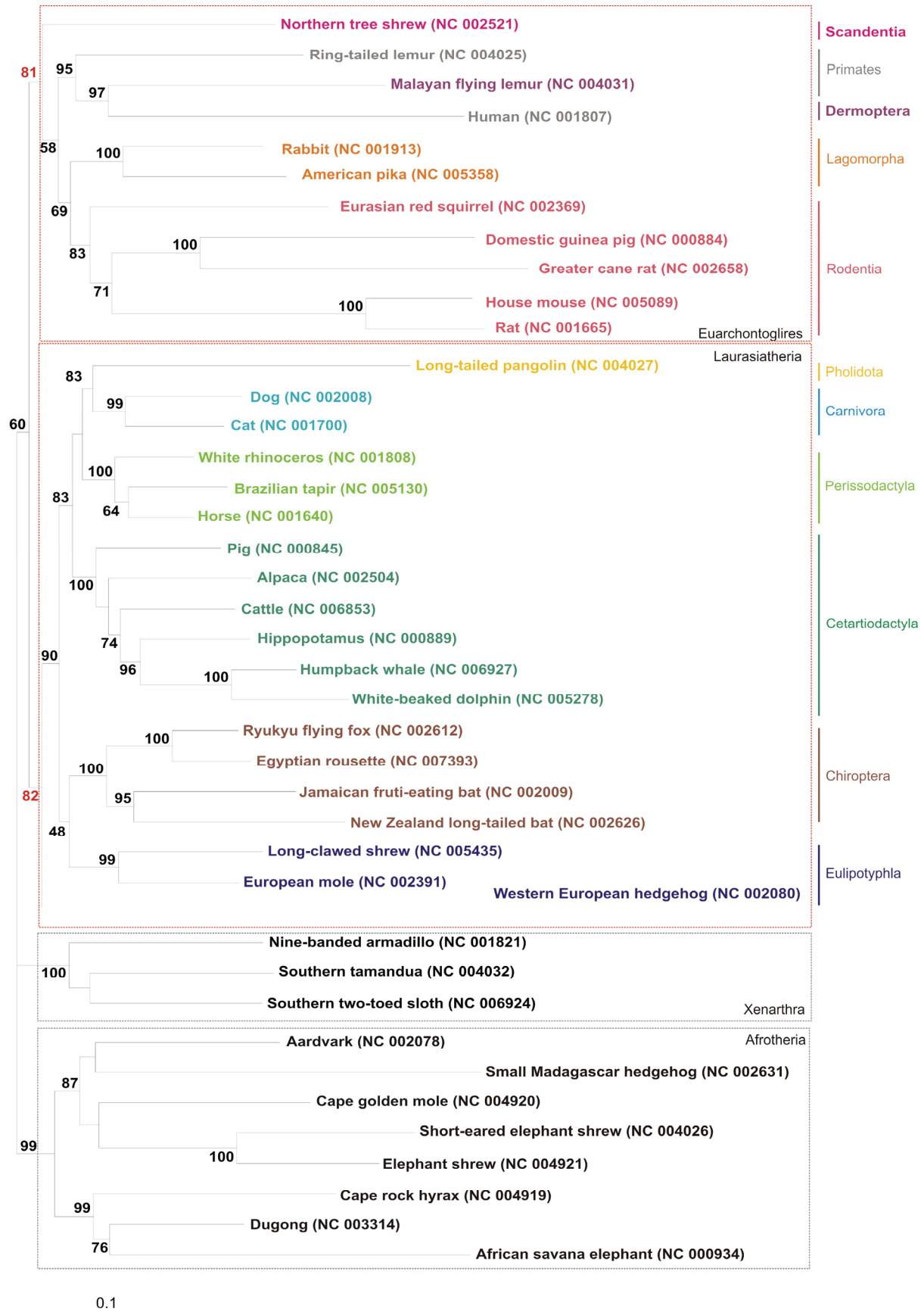


Figure S2. Maximum likelihood tree obtained using the TVM+I+G model of sequence substitution. Maximum likelihood (ML) bootstrap values were obtained through 1000 pseudoreplicates in PHYML.

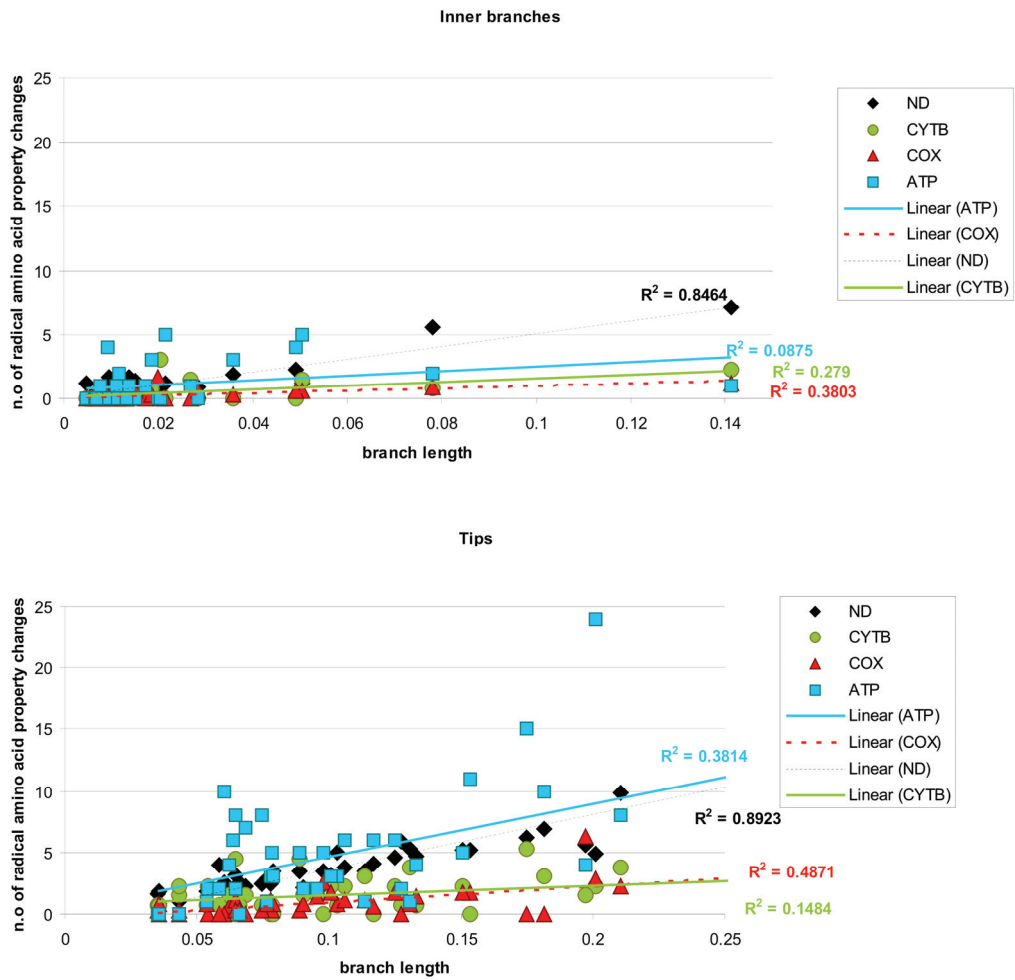


Figure S3.
 Number of strong positively selected amino acid properties vs branch length.

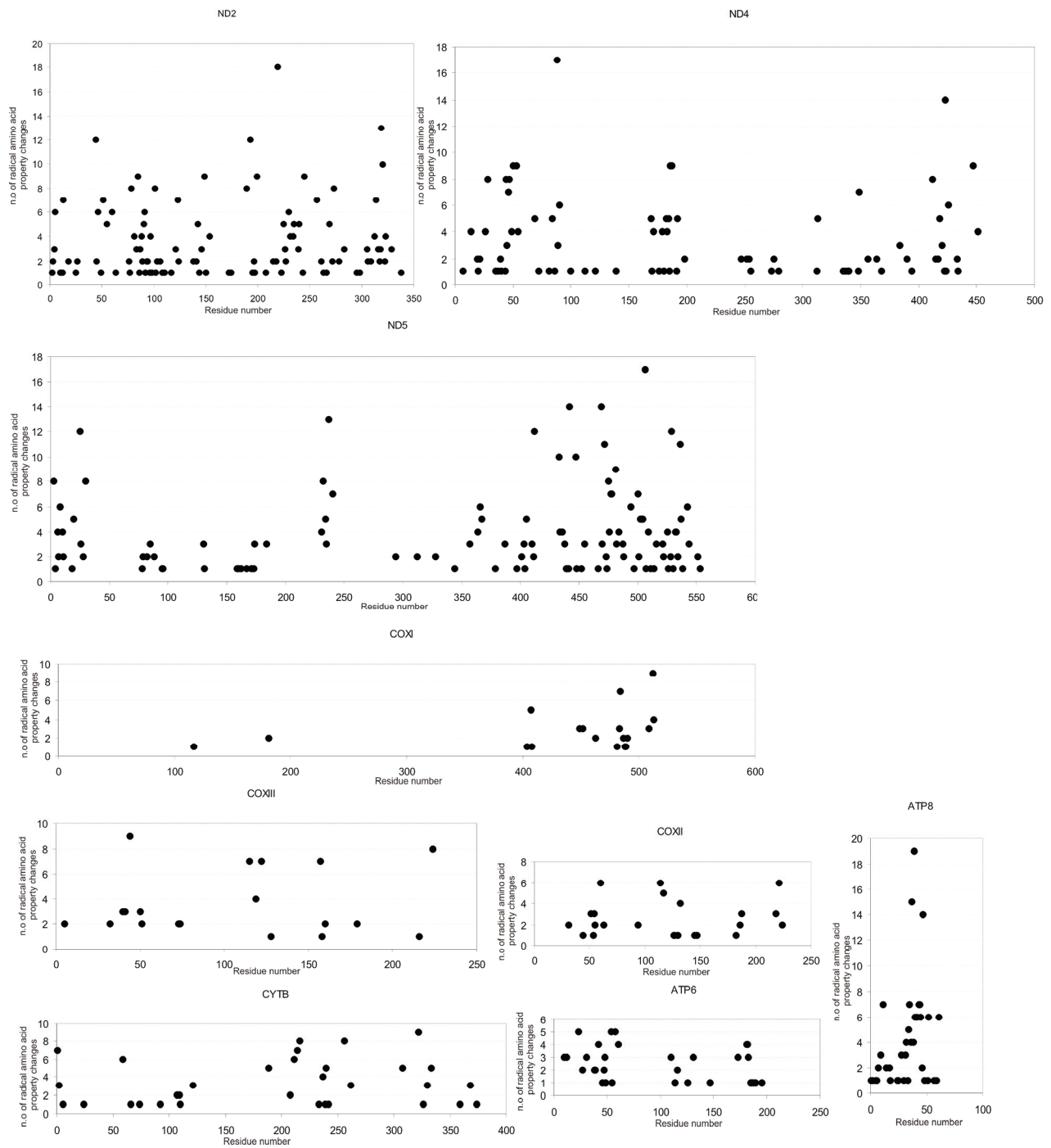


Figure S4.
 Number of strong positively selected amino acid properties (y-axis) across all sites (x-axis) in each mammalian mtDNA-encoded subunit of the respiratory chain.

NC 005129	<i>E maximus</i>	16 K-SE-TN-E-D-N-L-A
AJ224821	<i>L africana</i>	110 K-SE-TN-E-D-N-L-A
AY741079	<i>L cyclotis</i>	111 K-SE-MS-E-D-N-L-A
NC 007596	<i>M primigenius</i>	158 K-SE-TD-E-D-N-L-A
NC_009574	<i>M americanum</i>	159 K-SE-TS-E-D-N-P-A
		162
		260
		263
		266
		277
U06429	<i>L glama</i>	N-LE-TT-E-N-N-P-A
Y08812	<i>L guanicoe</i>	N-LE-TT-E-N-N-P-A
U06430	<i>V vicugna</i>	N-LE-TT-E-N-N-P-A
NC 002504	<i>L pacos</i>	N-LE-TT-E-N-S-P-P
U06427	<i>C bactrianus</i>	D-LE-TT-E-N-N-P-A
U06426	<i>C dromedarius</i>	D-SE-TT-E-N-N-P-A

Figure S5. Sites indicated in Figure 8 in four elephant relatives and 6 alpaca relatives.