

Supplementary Materials for:

Ancient DNA from the Asiatic wild dog (*Cuon alpinus*) from Europe

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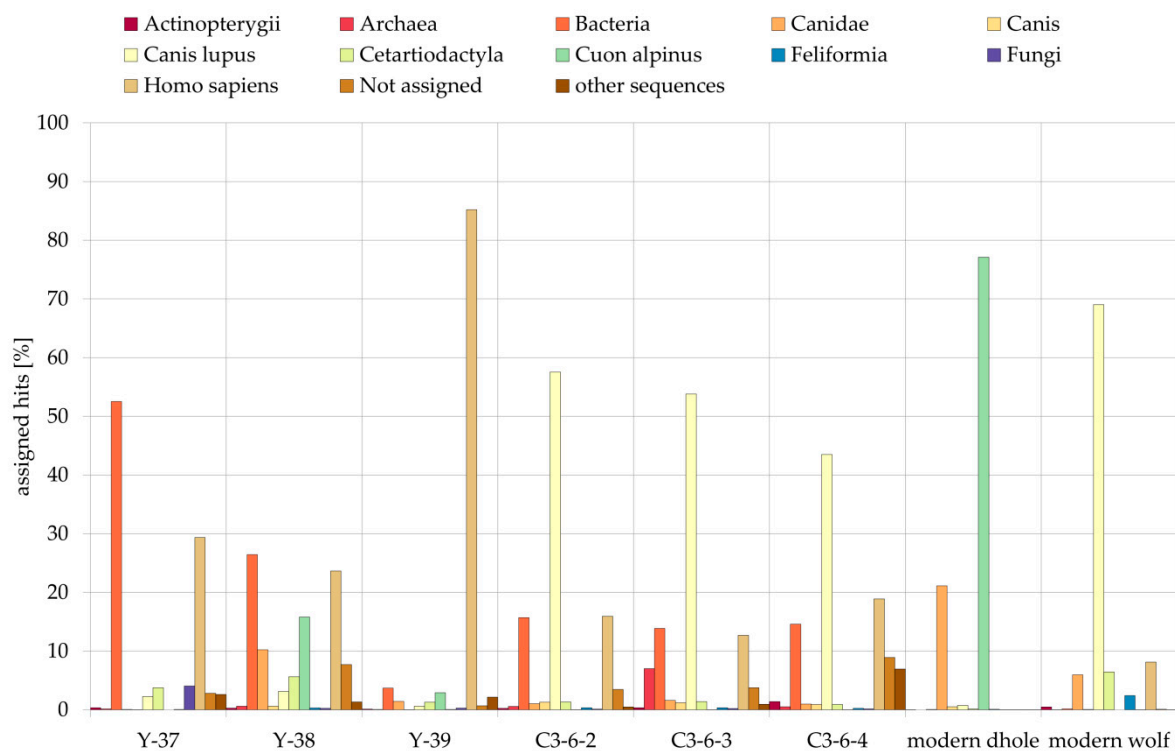


Figure S1. Blast results for pre-processed reads (prior to mapping) of six ancient putative dhole samples, one modern dhole and one modern gray wolf sample. Shown are lineages to which at least one percent of hits were assigned at least for one of the samples. Lineages with less assigned reads are not included.

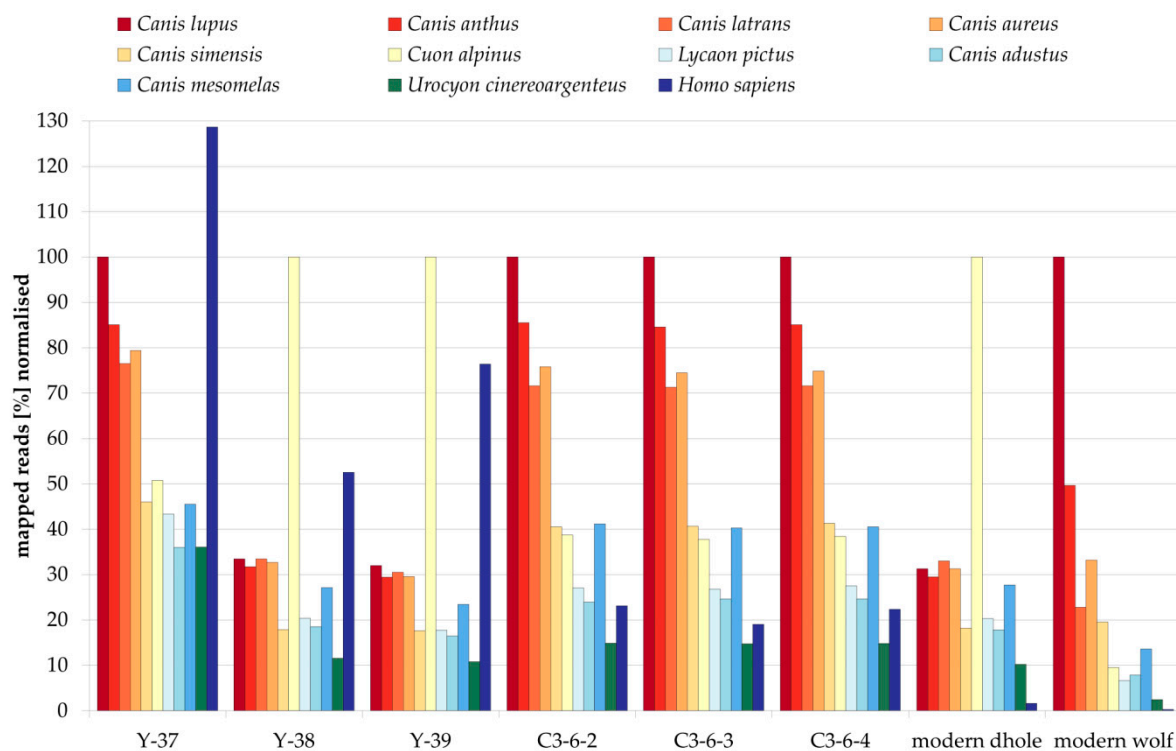


Figure S2. Percentage of reads mapping to various canid mitochondrial genomes and one human mitochondrial genome for six ancient potential dhole samples, one modern dhole, and one modern gray wolf sample. Percentages were normalized to the highest number of mapping reads that was achieved for a canid mitochondrial genome (bars reaching 100 %).

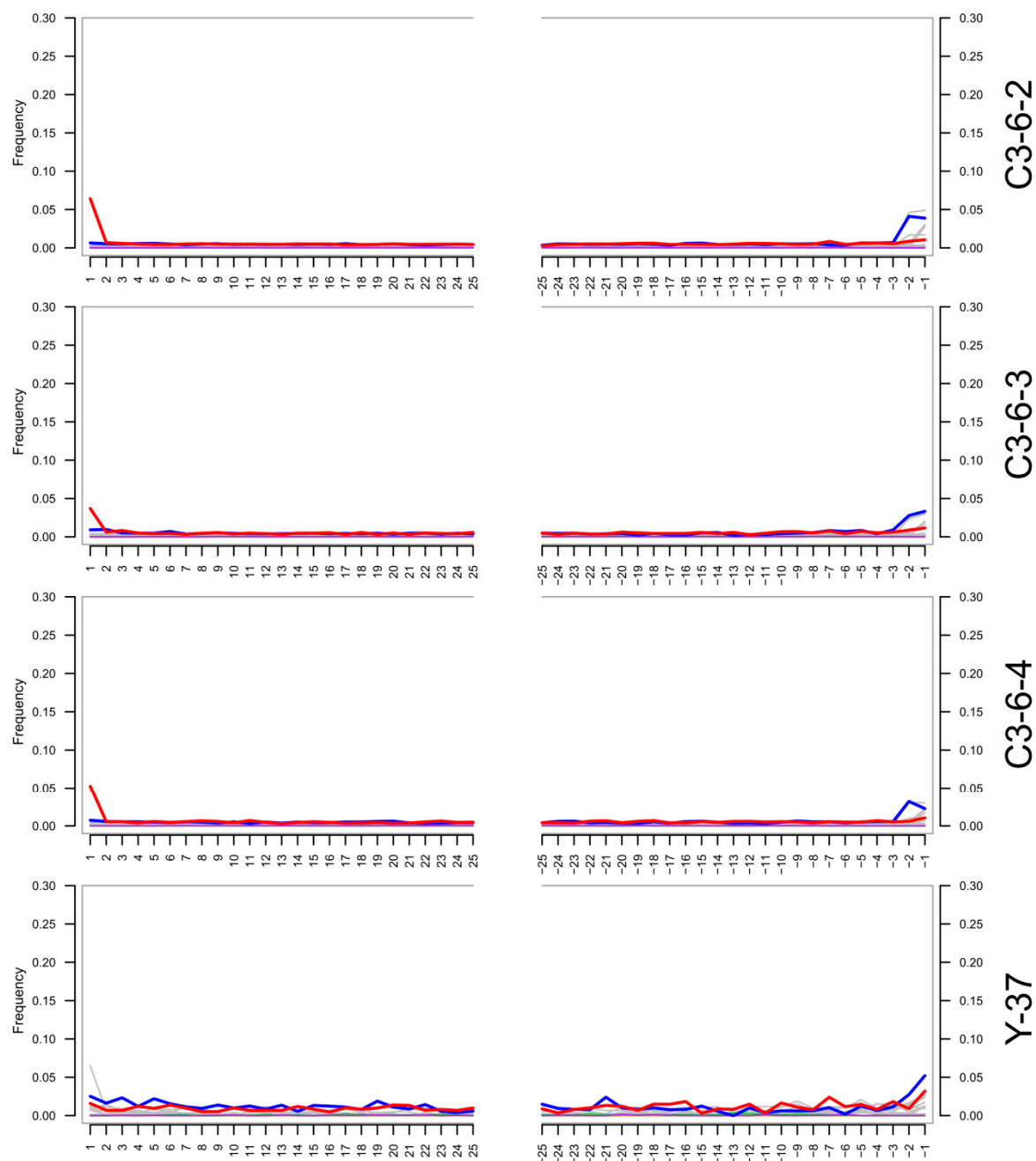


Figure S3. Damage patterns inferred with mapDamage (v2.0.7; [45]) for samples C3-6-2, C3-6-3, C3-6-4 and Y-37. All samples mapped against a gray wolf mitochondrial genome (NC_009686.1). Red: C to T substitutions, blue: G to A substitutions, grey: other substitutions. All samples show slightly elevated substitutions levels at read ends (i.e. C to T and G to A substitutions).

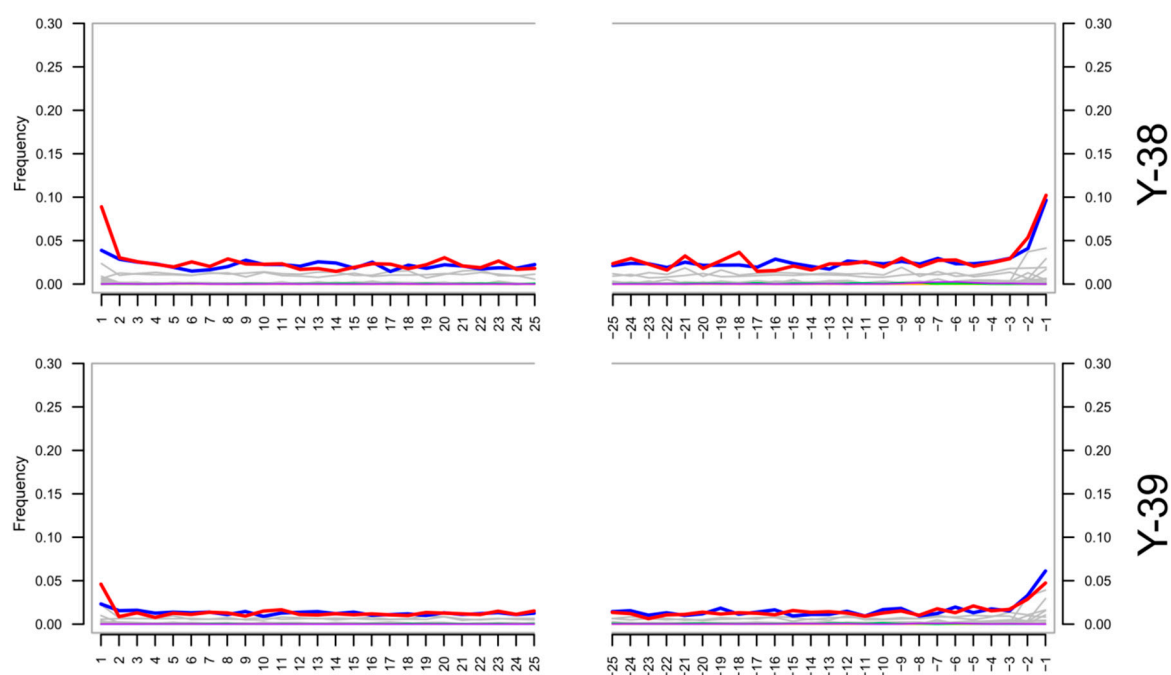


Figure S4. Damage patterns inferred with mapDamage (v2.0.7, [45]) for samples Y-38 and Y-39. Samples mapped against a dhole mitochondrial genome (NC_013445.1). Red: C to T substitutions, blue: G to A substitutions, grey: other substitutions. Y-38 and Y-39 show slightly elevated substitutions levels at read ends (i.e. C to T and G to A substitutions).

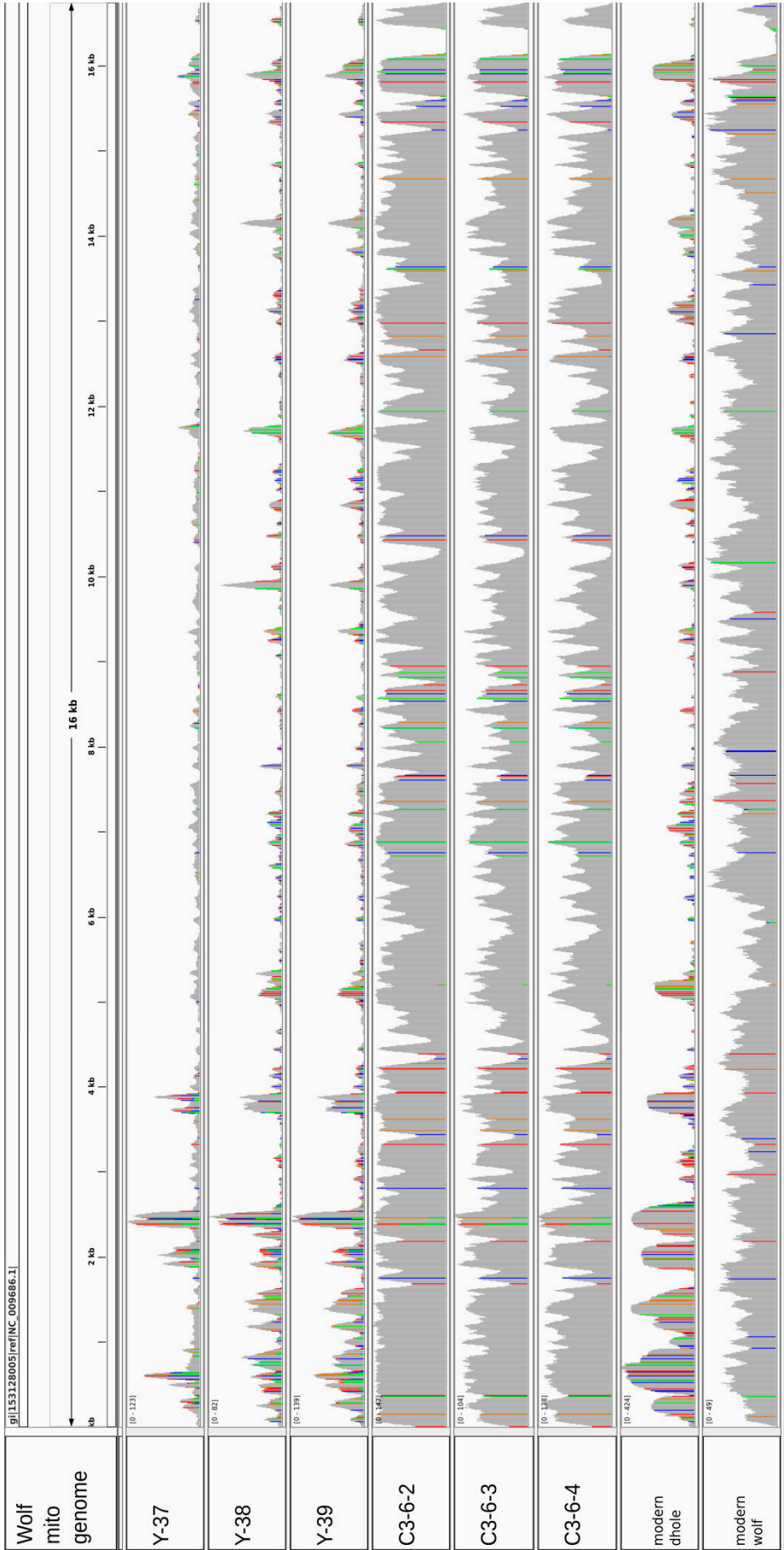


Figure S5. Coverage of the wolf mitochondrial reference genome when mapping reads of six ancient samples, one modern dhole and one modern wolf sample. Taken from the "Coverage track" in IGV (v2.3.68; [66]). Y axes are differing across panels (note minimum and maximum read depth given in the left upper corner of each coverage track). Coloured lines indicate variable positions (i.e. differences between reference and reads aligned).

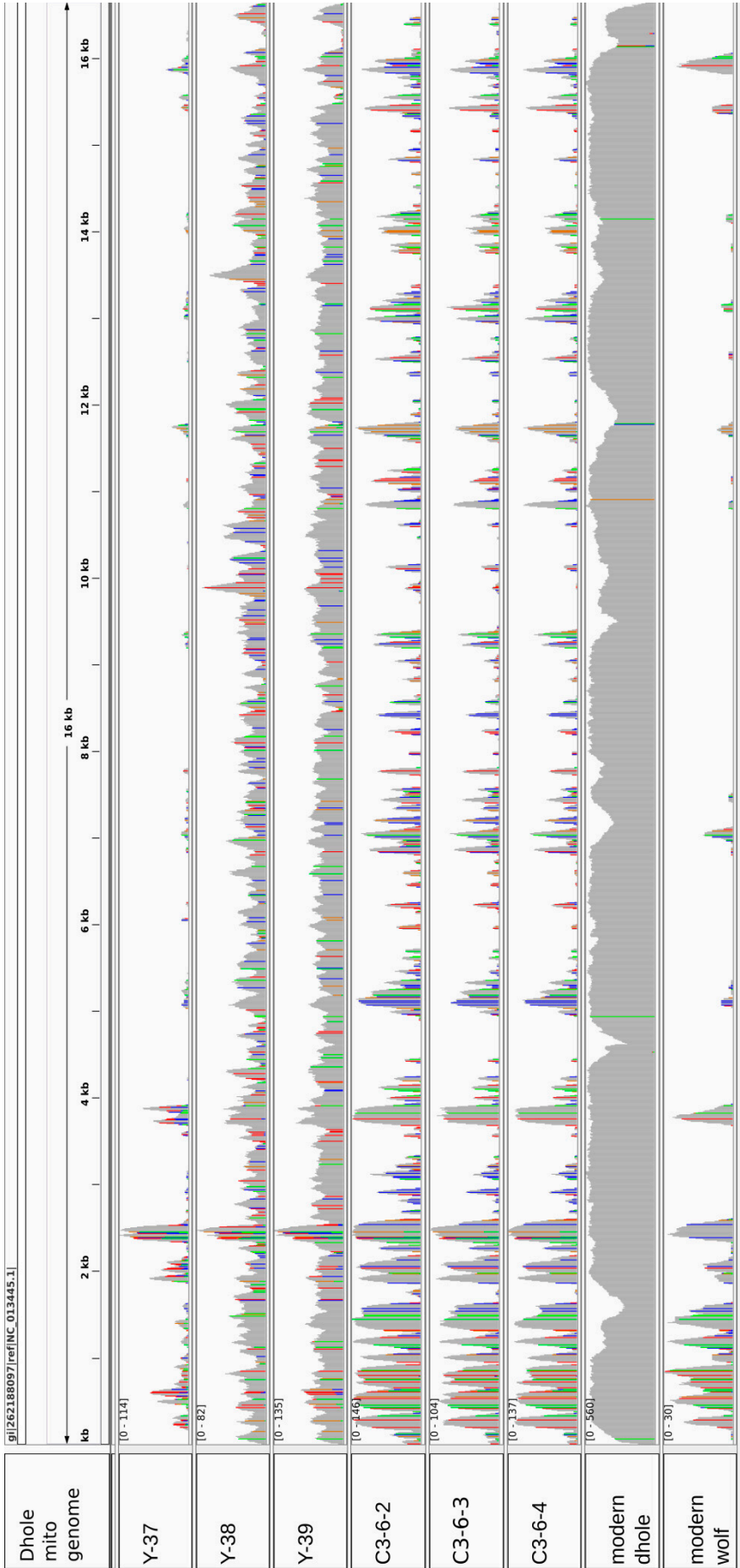


Figure S6. Coverage of the dhole mitochondrial reference genome when mapping reads of six ancient samples, one modern dhole and one modern wolf sample. Taken from the "Coverage track" in IGV (v2.3.68; [66]). Y axes are differing across panels (note minimum and maximum read depth given in the left upper corner of each coverage track). Coloured lines indicate variable positions (i.e. differences between reference and reads aligned).

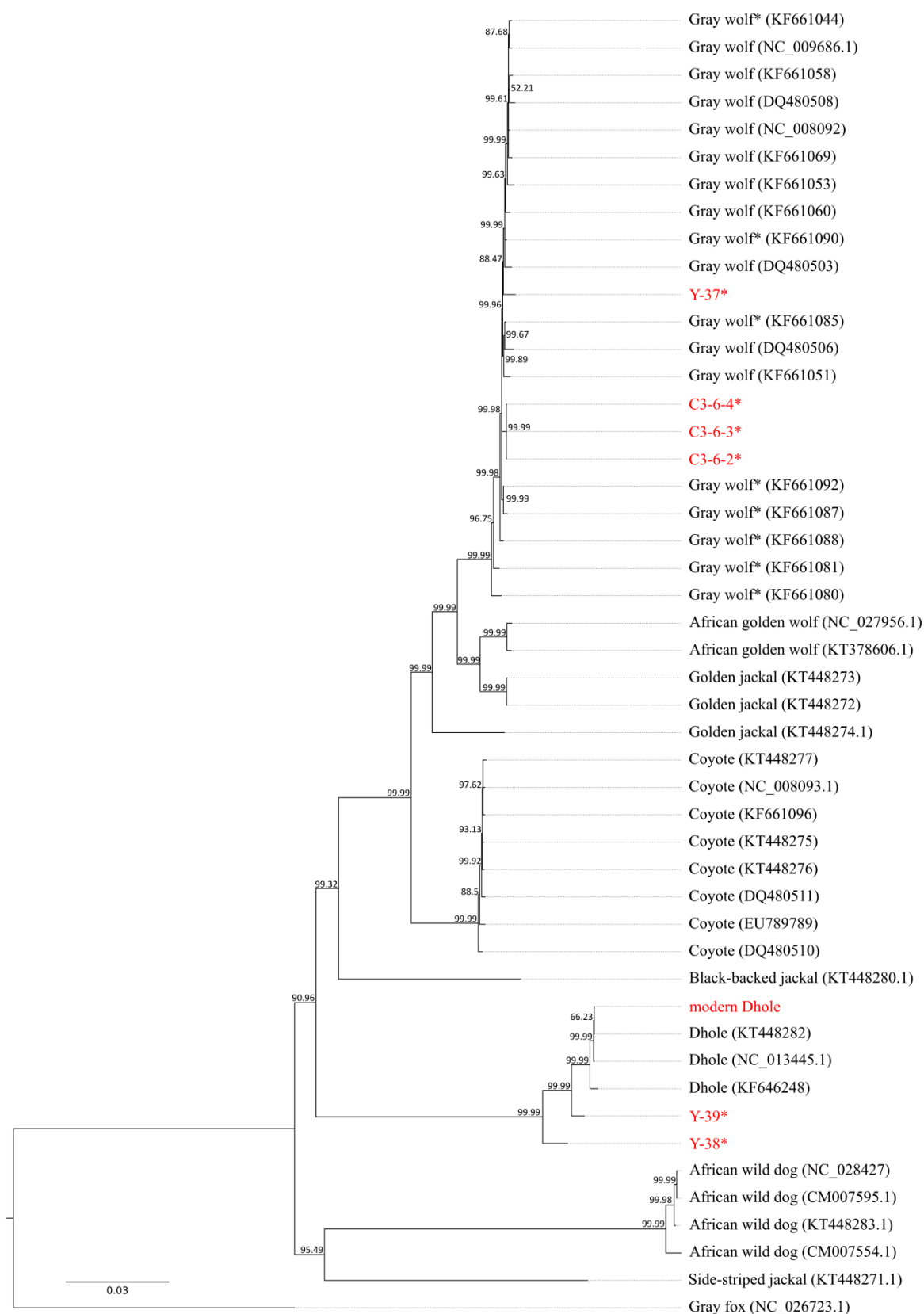


Figure S7. Bayesian tree using an MSA of 48 sequences and 10,582 bp length as input, applying a chain length of 11,000,000 with a subsampling frequency of 10,000. The consensus tree was created using a support threshold of 50% and a burn-in of 10%. Posterior probabilities are given at nodes. Red: samples. Asterisk: ancient sequences

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