

Table S1. Total DNA concentration.

Sample	DNA Concentration (ng/μl)
Lib2	9.92
Lib3	0.114
Lib4	0.301
Lib5	0.817
Lib6	0.451
N58	20.9
VS5	>100

Table S2. Sequencing data.

ID	Number of Raw Reads, MM	% Duplicates	Average Reads Length after Trimming, bp
Lib2	168.8	49.9	125
Lib3	69.3	93.0	133
Lib4	101.7	78.6	129
Lib5	69.7	90.0	124
Lib6	117.0	59.0	128
N58	2.9	9.6	124
VS5	14.9	15.0	144

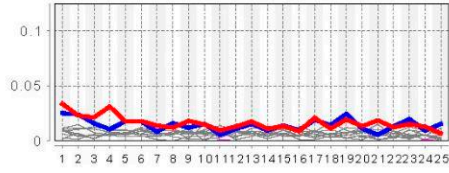
Table S3. Substitution models.

Group	Model	Number of Sites	Partitions
1	GTR+I	7722	pos1_COX2, pos1_CYTB, tRNA-Arg, tRNA-Glu, tRNA-Ile tRNA-Leu, pos1_COX3, tRNA-Pro, pos1_ND3, pos1_ND4l tRNA-Ser, tRNA-Leu, tRNA-Met, tRNA-Cys, rRNA_12S,

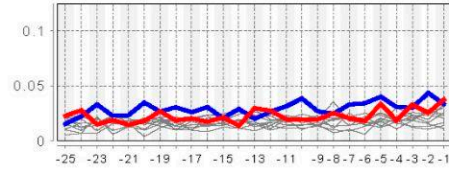
			tRNA-Val, pos1_ATP6, tRNA-Ser, tRNA-Asn, pos1_ND1, pos1_ND2, tRNA-Tyr, pos1_COX1, pos1_ND6, rRNA_16S, tRNA-Lys, pos1_ND5, tRNA-Phe, pos1_ATP8, pos1_ND4, tRNA-Thr, tRNA-His, tRNA-Ala, tRNA-Tyr
2	HKY+I	3940	pos2_ND2, tRNA-Gly, tRNA-Asp, pos2_CYTB, pos2_COX1, pos2_ND5, pos2_ATP6, pos2_ND3, pos2_ND4, tRNA-Gln, pos2_COX2, pos2_ND1, pos2_ND4L, pos2_ND6, pos2_COX3
3	GTR+G	3800	pos3_COX2, pos3_ND2, pos3_COX1, pos3_ATP8, pos3_COX3, pos3_ND5, pos3_ND6, pos3_ND1, pos3_ND4, pos3_CYTB, pos3_ND4L, pos3_ATP6, pos3_ND3
4	GTR+I+G	1339	D-loop, pos2_ATP8

Lib2

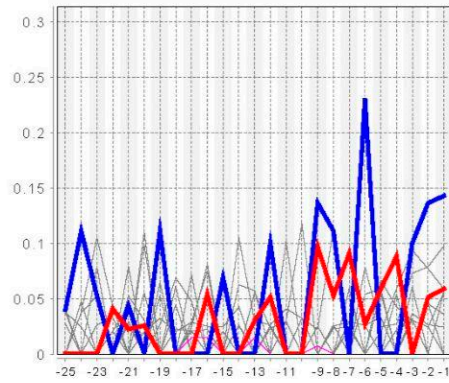
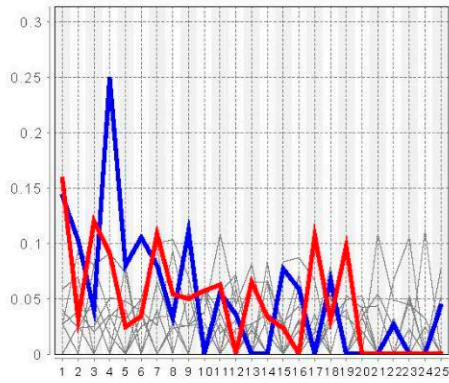
5' end



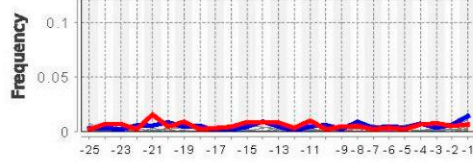
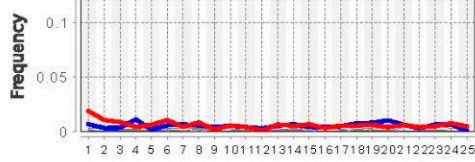
3' end



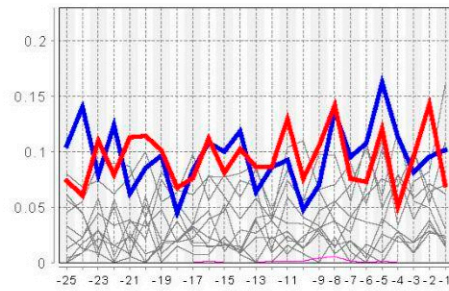
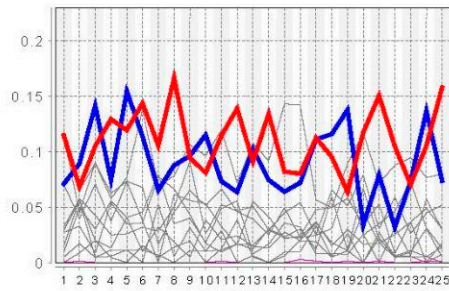
Lib3



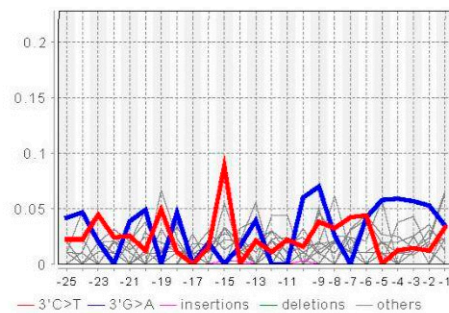
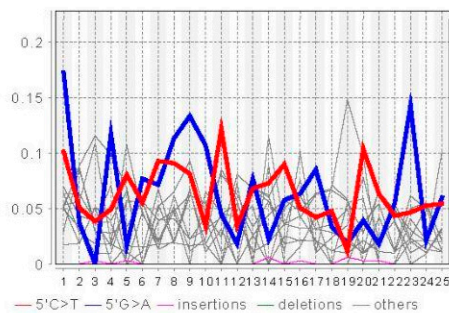
Lib4



Lib5



Lib 6



— 5'C>T — 5'G>A — insertions — deletions — others

— 3'C>T — 3'G>A — insertions — deletions — others

Figure S1. Ancient DNA damage patterns (Lib2–6). The nucleotide positions of the 5' and 3' ends of the reads are shown on the horizontal axis, with the proportion of incorrectly inserted bases represented on the vertical axis. The red and blue colors indicate cytosine-to-thymine substitution and guanine-to-adenine substitution, respectively. Insertions are shown in pink, deletions in green.

Table S4. Metagenomic analysis results of ancient and museum samples of arctic fox.

LAB_ID	Number of Raw Reads	Classified Reads ¹	Unclassified Reads	Microbial Reads	Chordate Reads	Canidae Reads
Lib2	127,039,521	61.8%	38.2%	56%	5.36%	2.21% (2,805,236)
Lib3	53,124,906	48.5%	51.5%	35.3%	11.9%	3.64% (1,933,909)
Lib4	75,597,943	60.1%	39.9%	43.6%	16.1%	11.90% (8,992,487)
Lib5	43,505,102	47.5%	52.5%	35.3%	11.5%	6.11% (2,659,135)
Lib6	85,793,479	57.6%	42.4%	53.8%	3.43%	0.14% (116,518)
N58	2,301,319	86.7%	13.3%	29.9%	55.2%	43.3% (997,317)
VS5	7,483,996	94.6%	5.37%	5.1%	89.4%	84.5% (6,328,500)

¹The percentage in all columns is specified from the total number of reads.

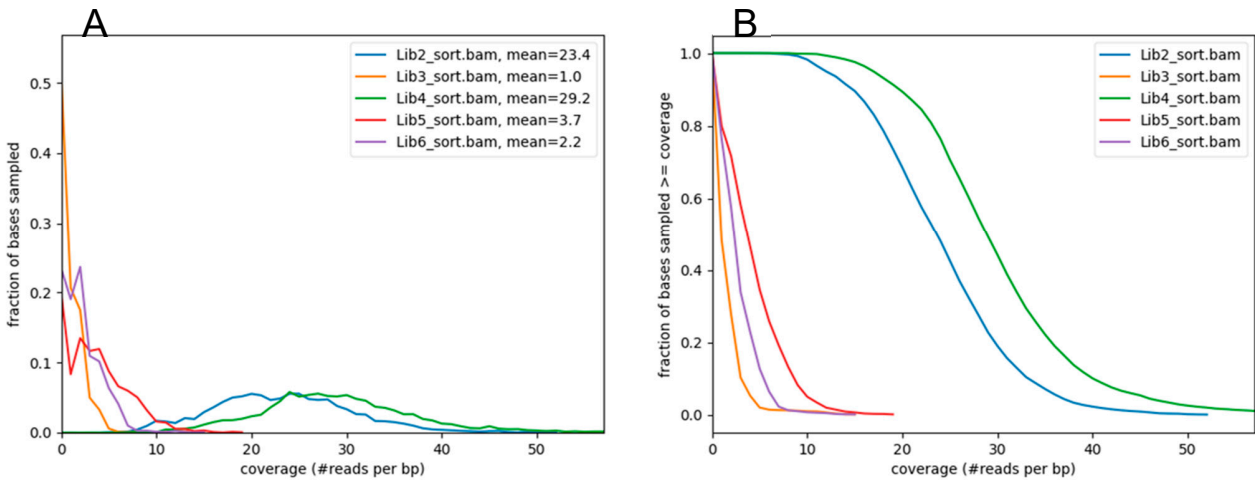
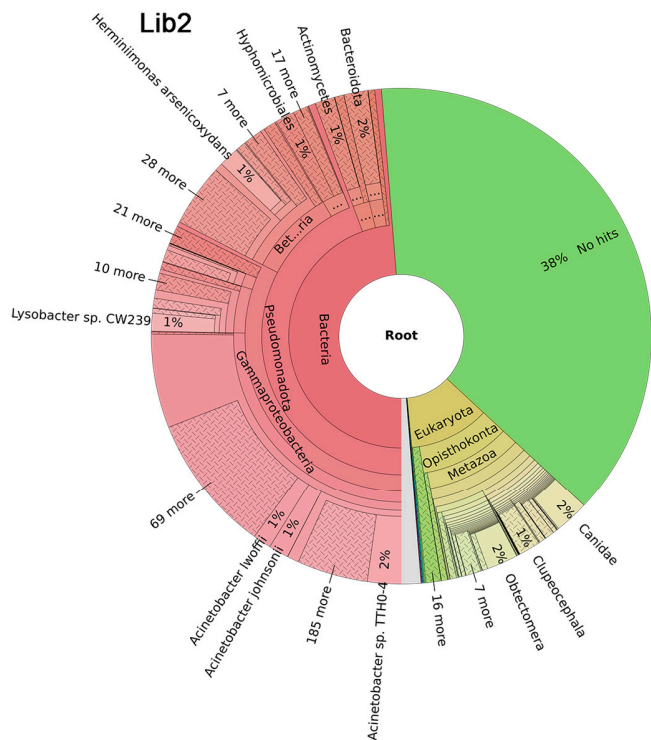
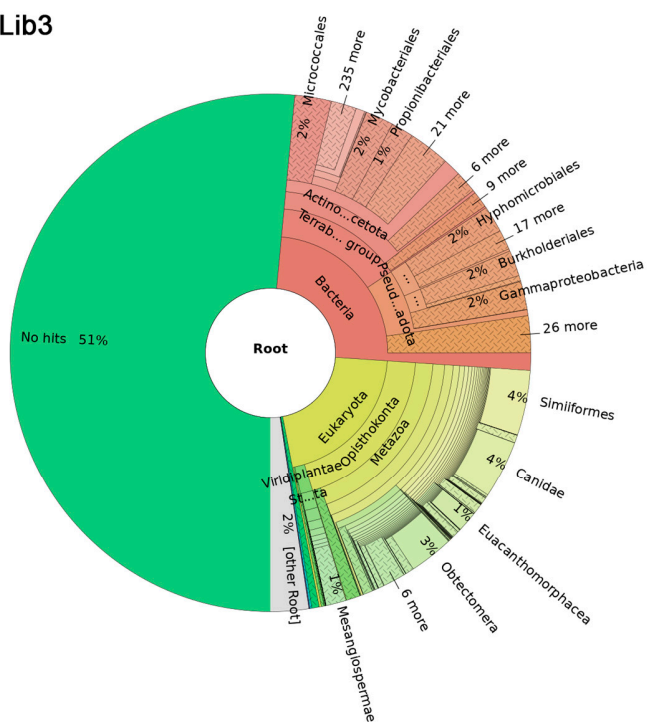


Figure S2. Ancient samples reference genome mapping coverage (Lib2–Lib6). (A) Plot represents the frequencies of the found read coverages and the mean coverage value in the upper right corner. (B) Plot represents the fraction of the genome that has a specified depth of sequencing.

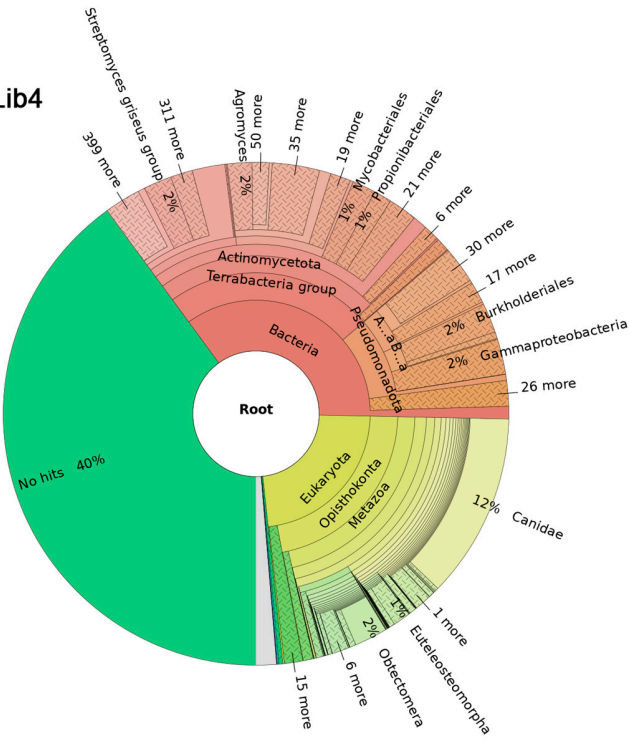
Lib2



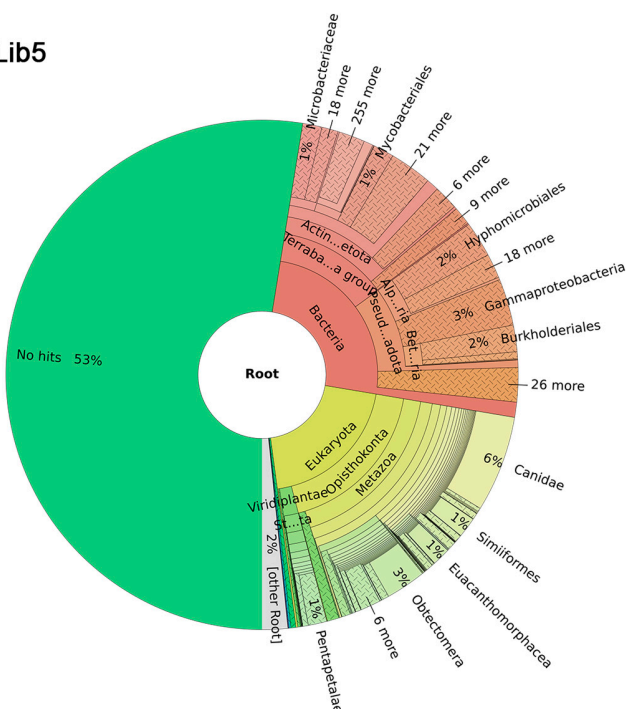
Lib3



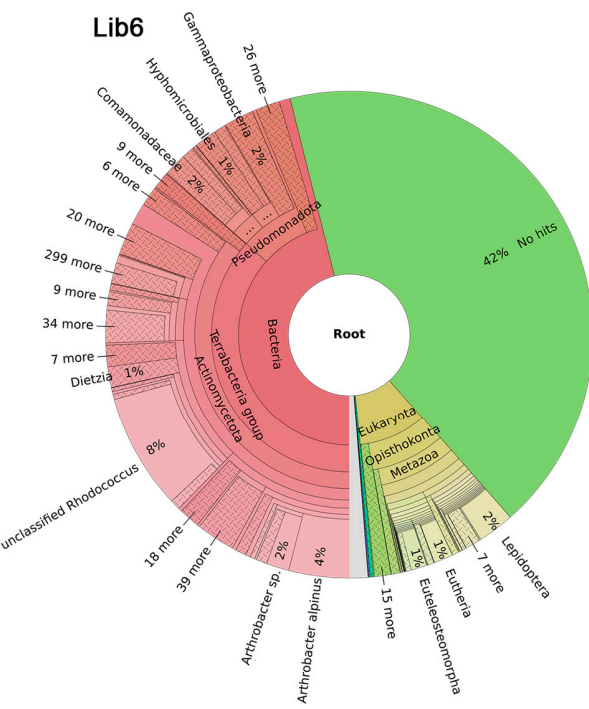
Lib4



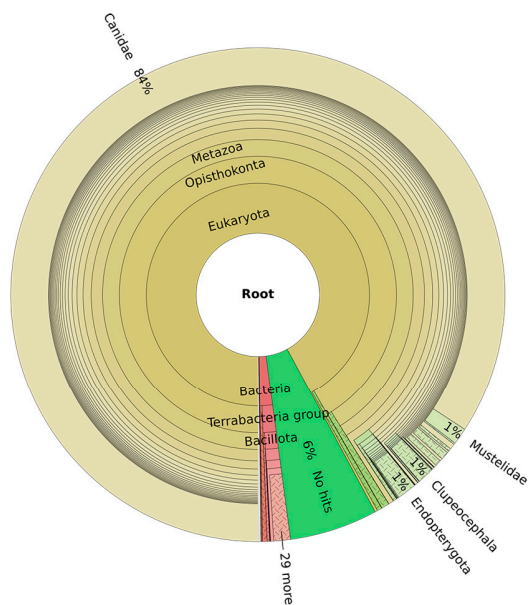
Lib5



Lib6



VS5



58

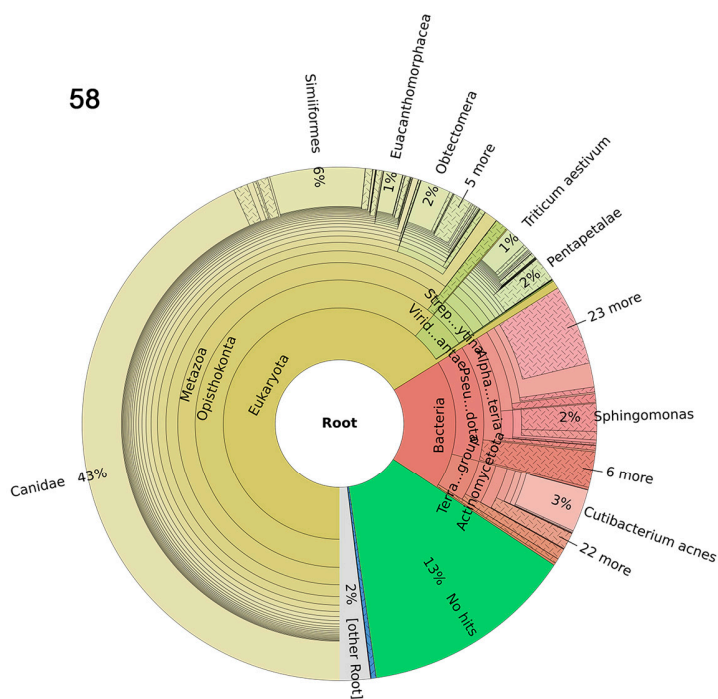


Figure S3. Pie charts illustrate results of metagenomic analysis for all specimens.

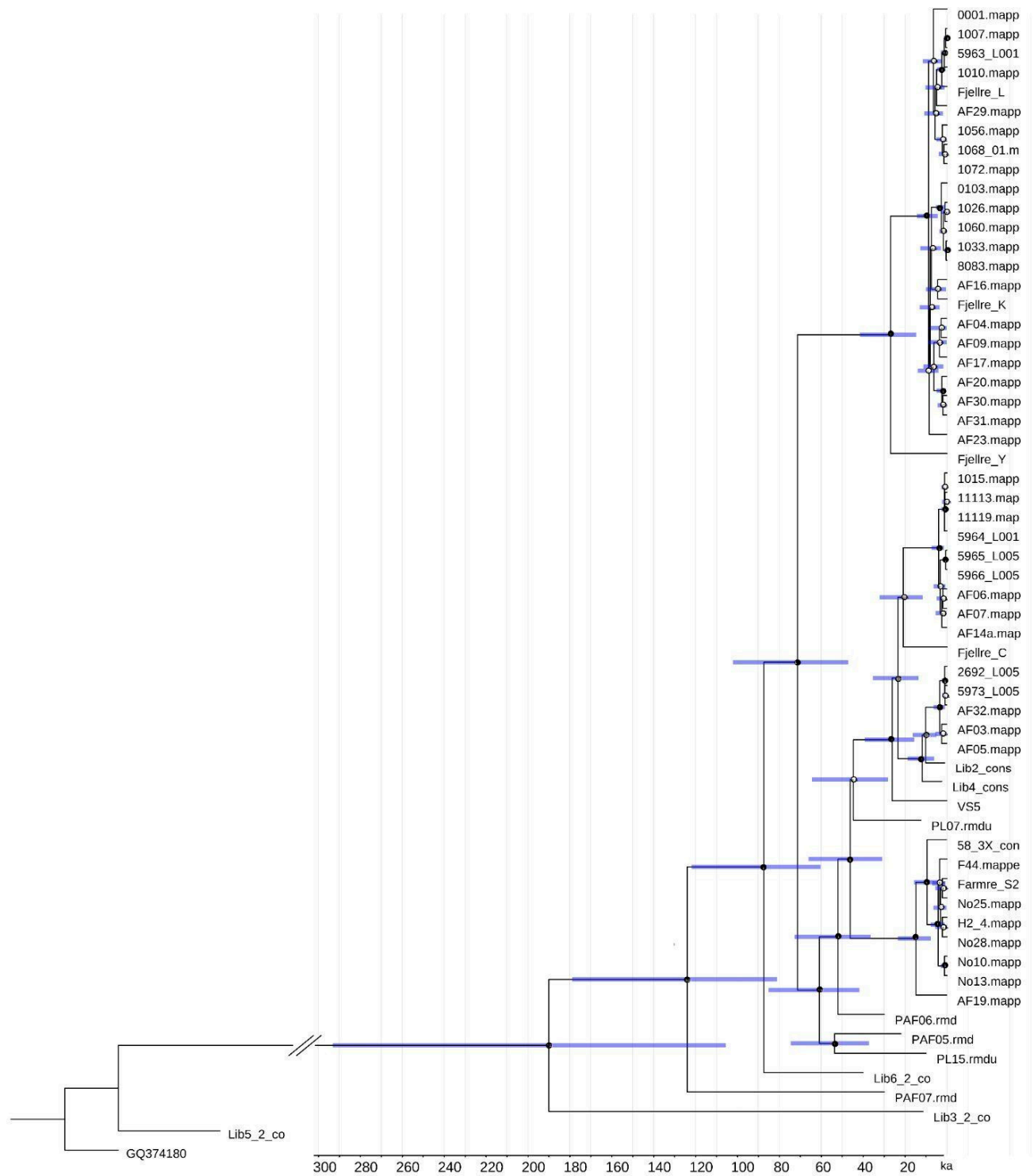


Figure S4. Phylogenetic tree without labels compression.