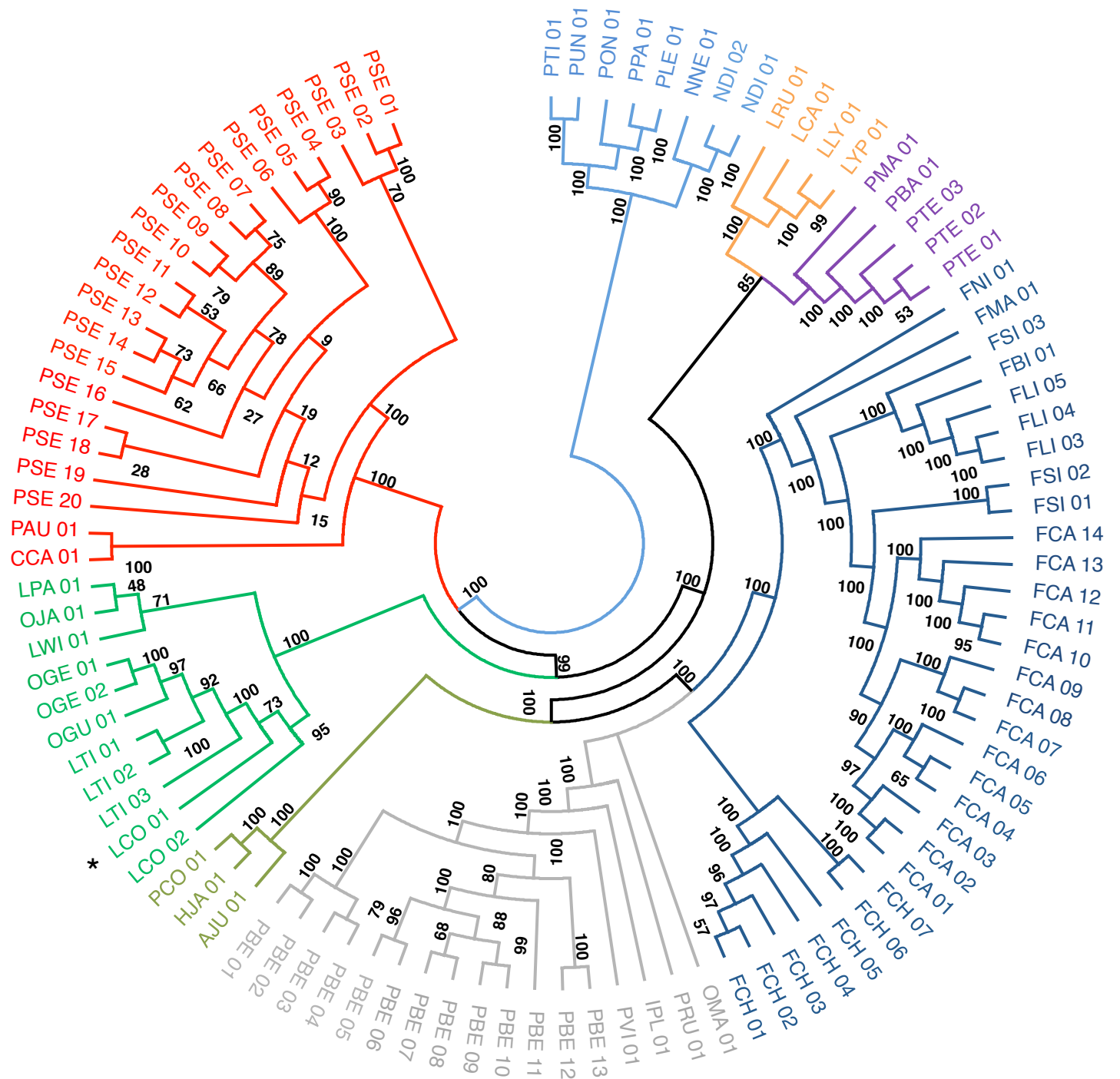


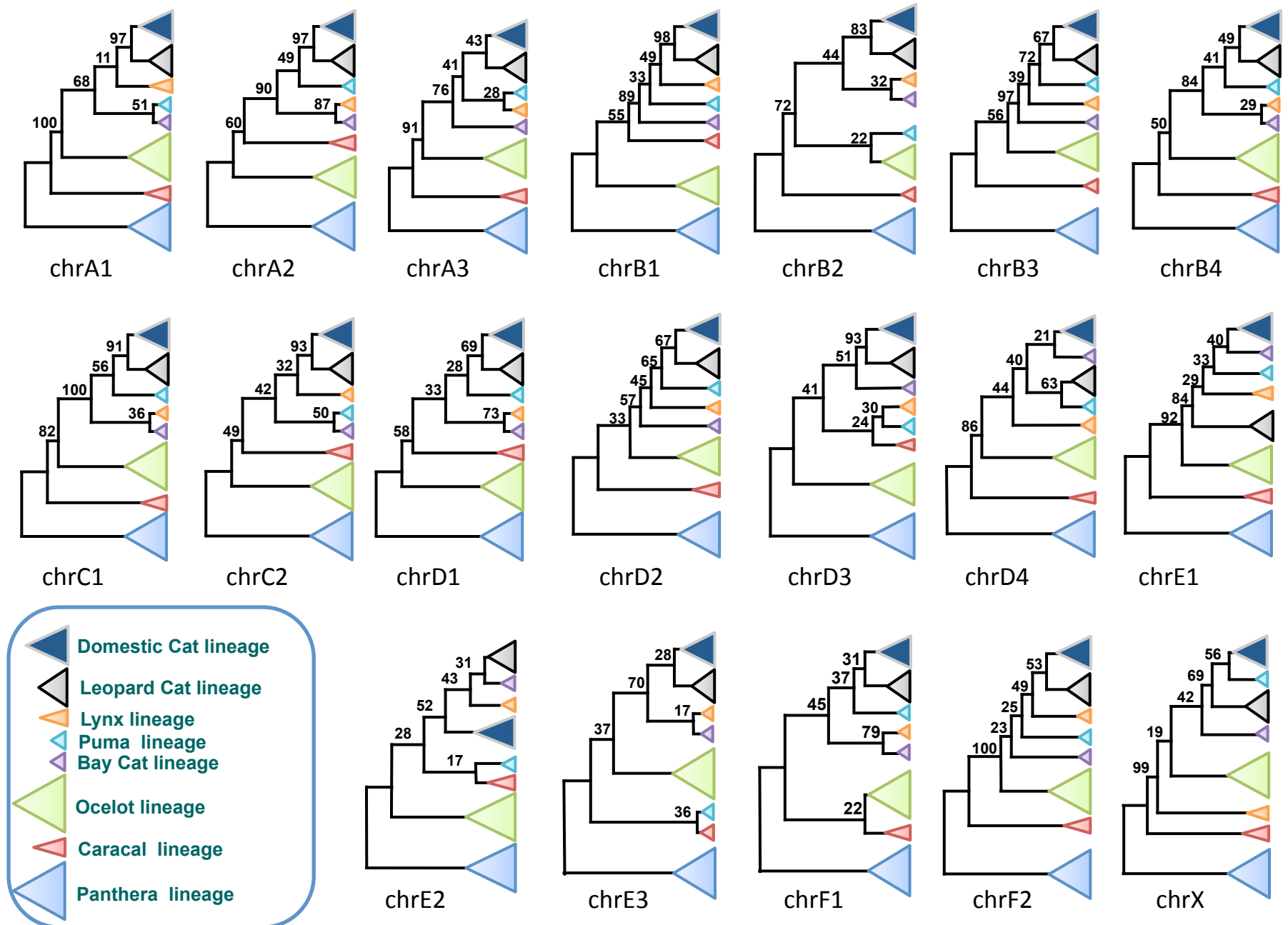
**Supplementary Materials for *Phylogenomic evidence for ancient hybridization in the genomes of living cats (Felidae)*.**

Gang Li, Brian W. Davis, Eduardo Eizirik, and William J. Murphy

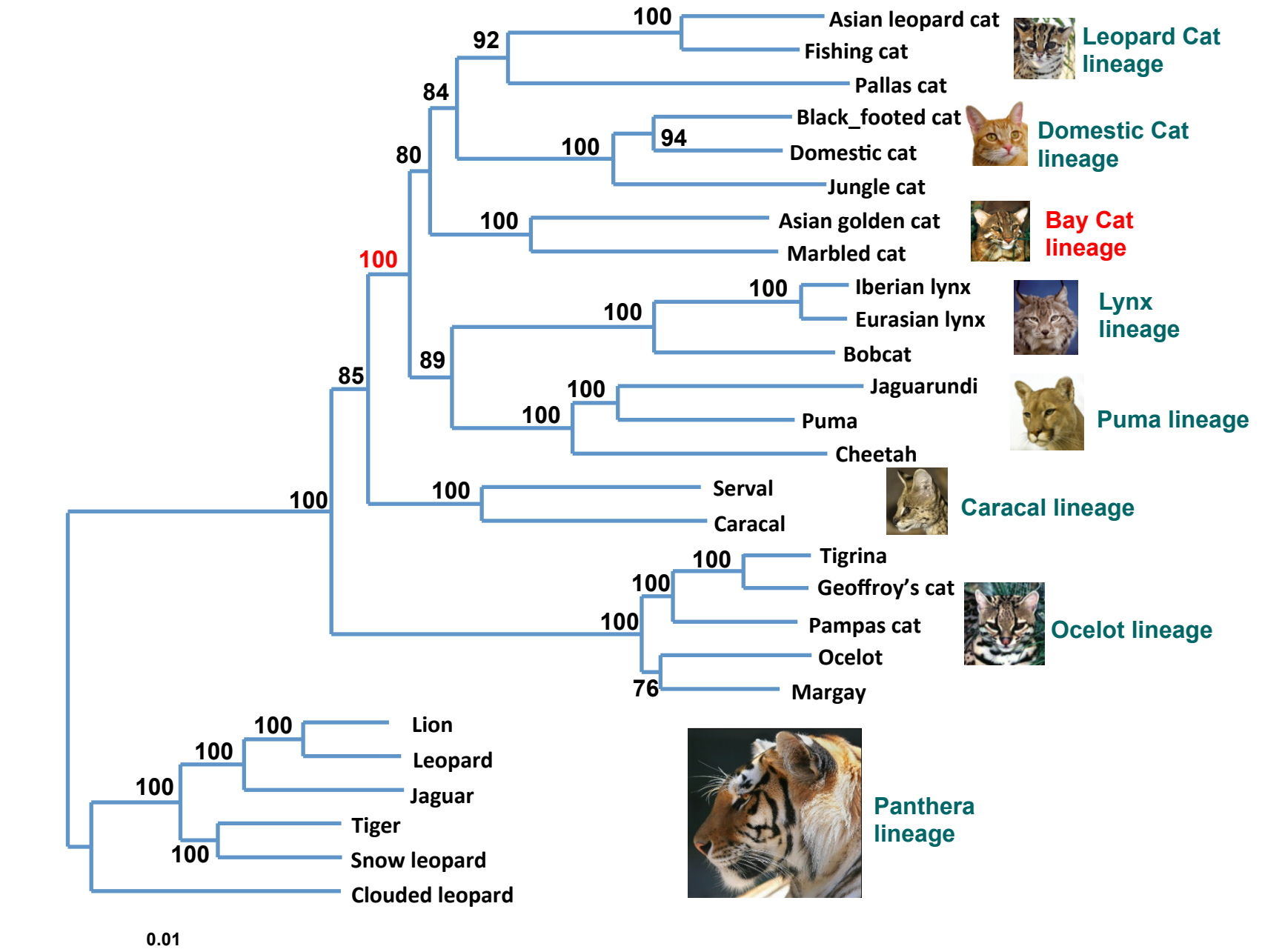
**Figure S1.** SNP-based maximum likelihood tree (GTR+ $\Gamma$ ) based on a matrix of 59,628 SNPs and 101 felid individuals. Refer to Table S1 for the full taxonomic name referenced by each three-letter species code. The asterisk next to pampas cat individual LCO-01 refers to a pampas cat previously documented as a hybrid based on its possession of tigrina mtDNA (the same individual referred to as Lco02 in Johnson et al. [1999]). Because this hybrid is from a captive population it is difficult to ascertain if the hybridization occurred in the wild (Johnson et al. 1999). The genotype of LCO-01 is phylogenetically intermediate to both species, and an analysis of its genome-wide SNP genotype profile indicates it is an early generation hybrid.



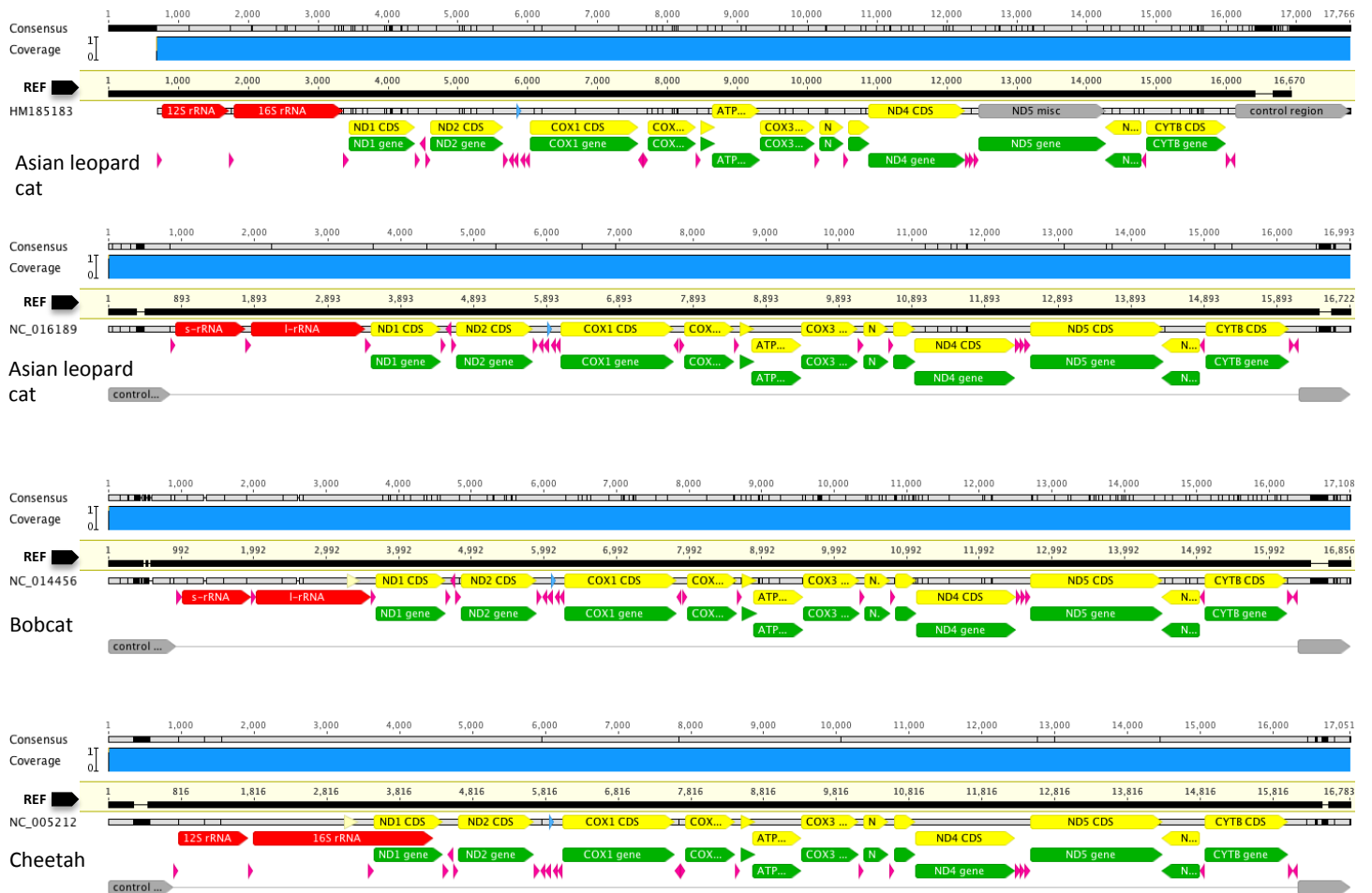
**Figure S2.** SNP-based maximum likelihood trees for each chromosome (w/bootstrap support). All support values for monophyly of each lineage were greater than 90% (not shown).



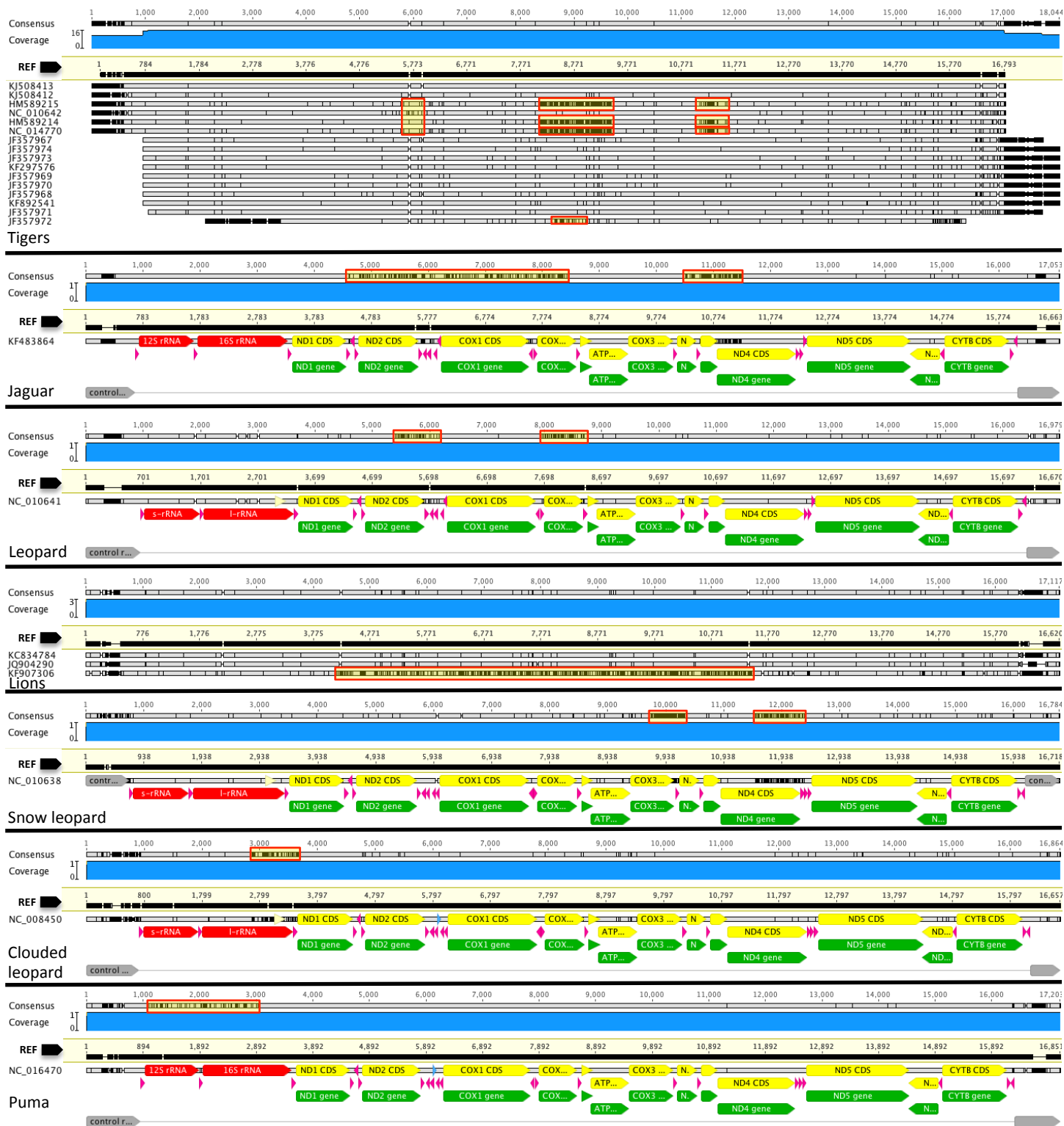
**Figure S3.** *VIR* gene maximum likelihood tree (GTR+ $\Gamma$ ) based on a 49,708-bp supermatrix of 26 vomeronasal receptor genes and pseudogenes, sequenced from 27 felids across all felid lineages (Montague et al. 2014).



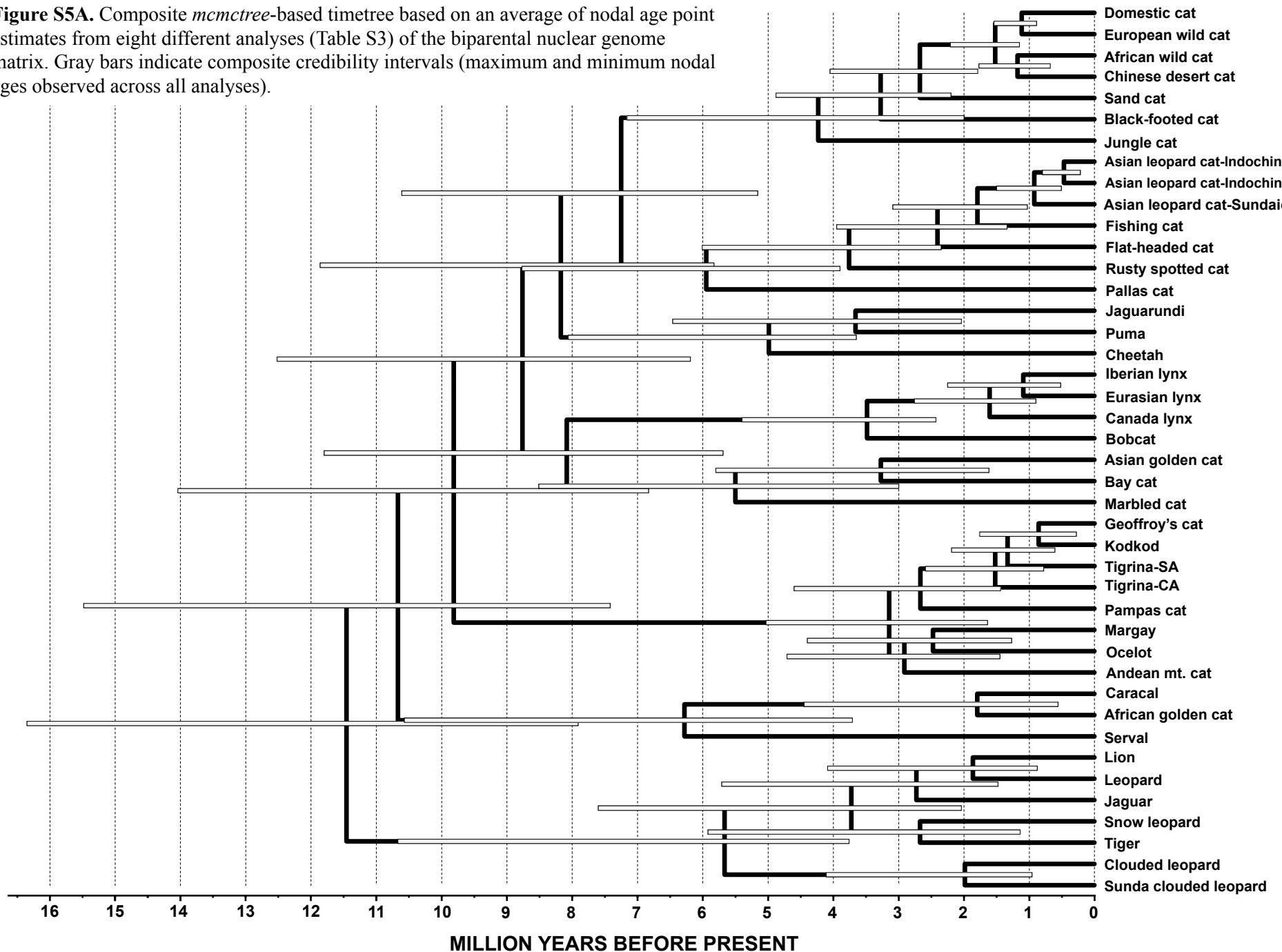
**Figure S4A.** Alignment between reference mitogenomes generated in the present study and mitogenomes from GenBank. The consensus sequence between the reference mitogenome sequence (top black line denoted with REF and black arrowhead) and the GenBank reference sequence(s) (bottom gray bars) is shown on the top of each subfigure. Felid mitochondrial genomes shown below possess no numt contamination.



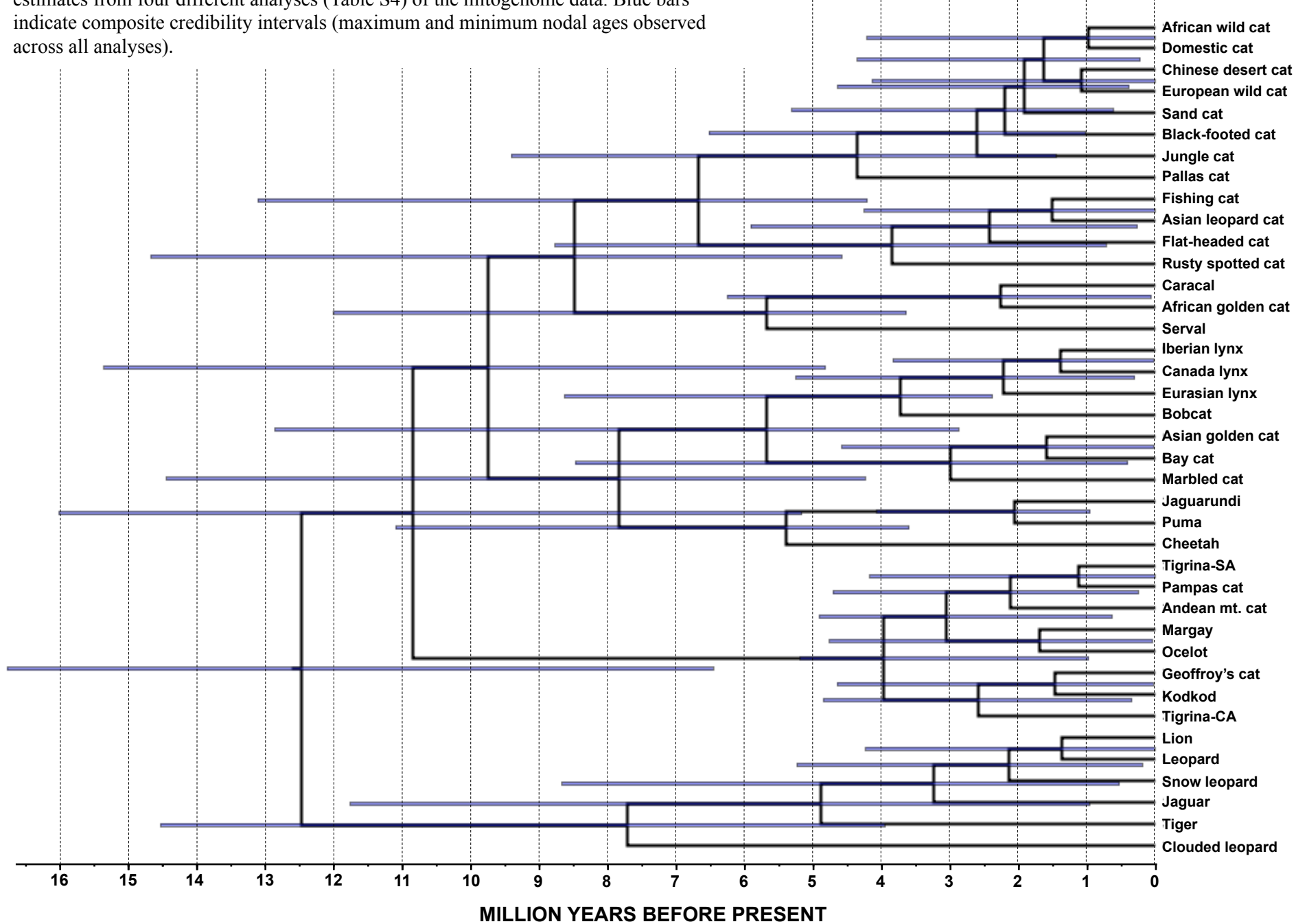
**Figure S4B.** Felid mitochondrial genomes with probable numt contamination. The consensus sequence between the reference mitogenome sequence (top black line denoted with REF and black arrowhead) and the GenBank reference sequence(s) (bottom gray bars) is shown on the top of each subfigure. Vertical black lines within the consensus and individual GenBank reference sequences indicate nucleotide substitutions relative to the reference. Red boxes highlight regions with significantly elevated nucleotide divergence compared to the reference, and represent probable numts. Mitochondrial gene annotation is indicated with colored arrowheads.



**Figure S5A.** Composite *mcmctree*-based timetree based on an average of nodal age point estimates from eight different analyses (Table S3) of the biparental nuclear genome matrix. Gray bars indicate composite credibility intervals (maximum and minimum nodal ages observed across all analyses).

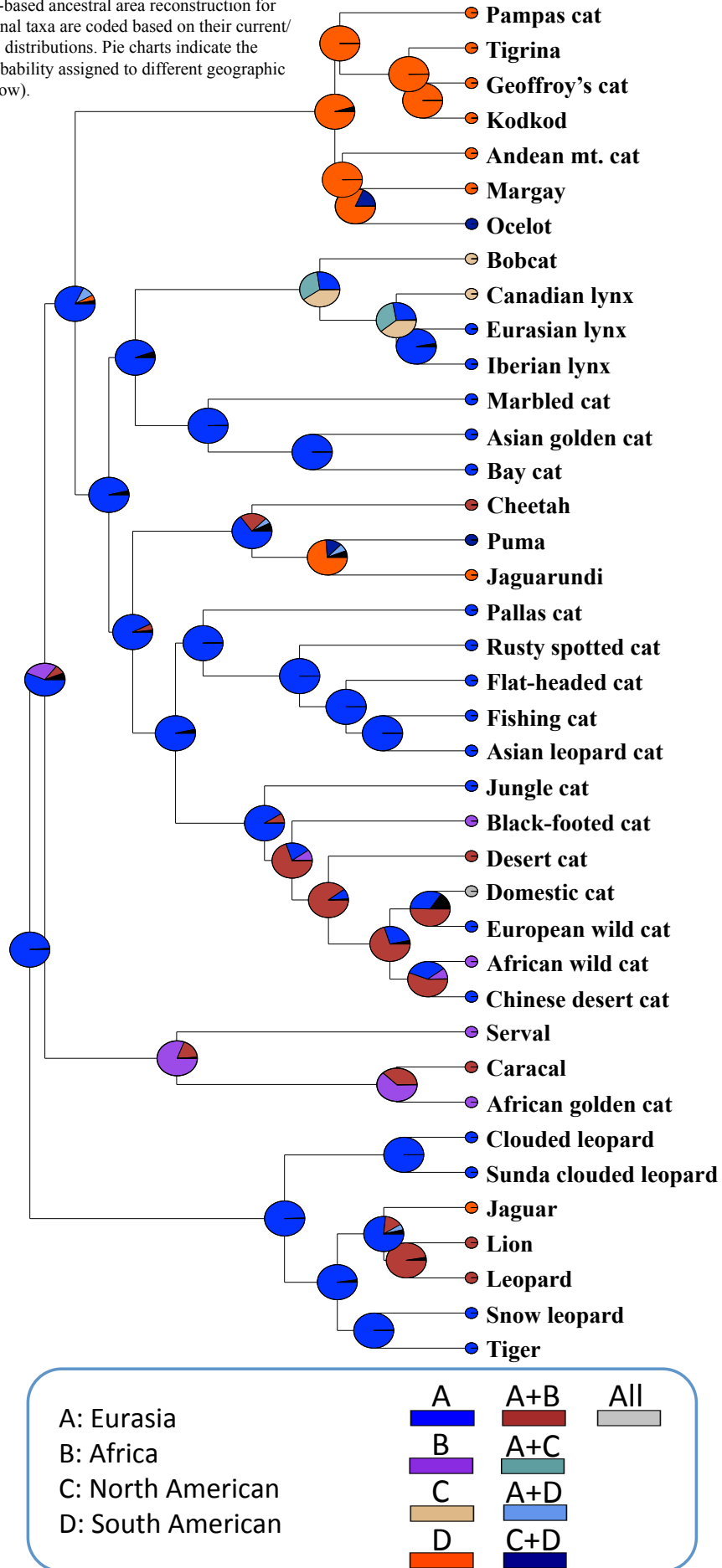


**Figure S5B.** Composite *mcmctree*-based timetree based on an average of nodal age point estimates from four different analyses (Table S4) of the mitogenome data. Blue bars indicate composite credibility intervals (maximum and minimum nodal ages observed across all analyses).

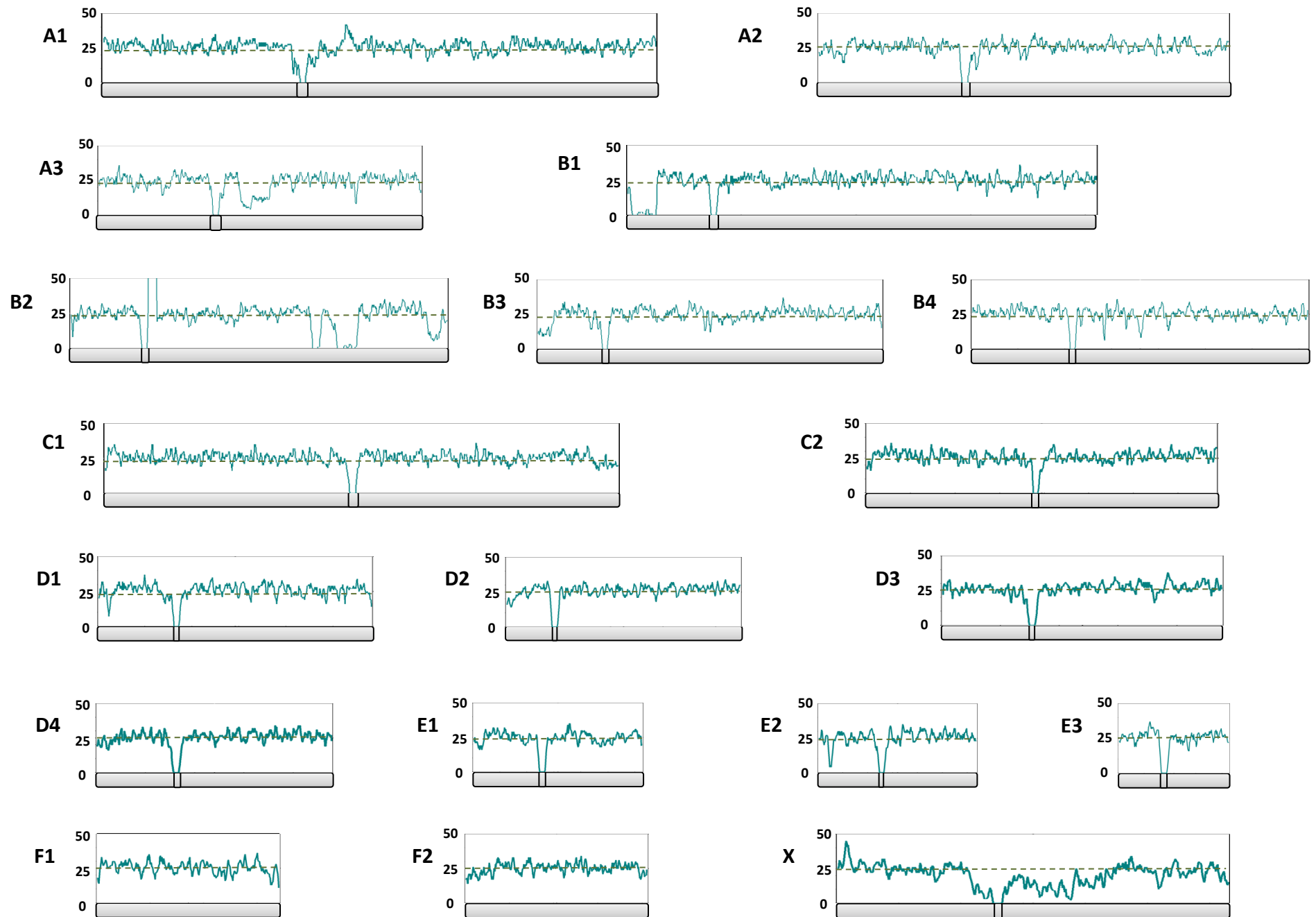




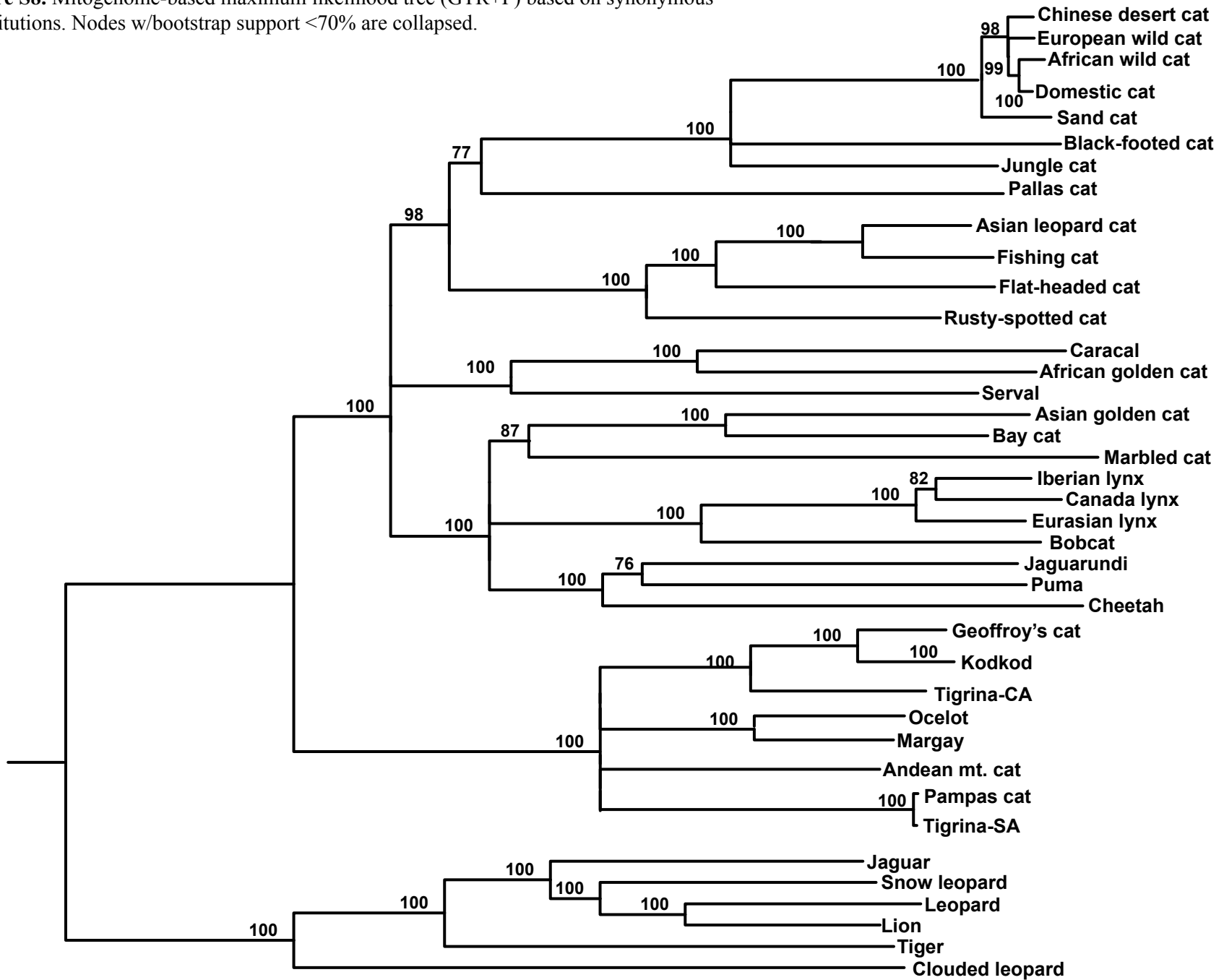
**Figure S6.** Bayesian-based ancestral area reconstruction for living Felidae. Terminal taxa are coded based on their current/historical geographic distributions. Pie charts indicate the relative posterior probability assigned to different geographic areas (see legend below).



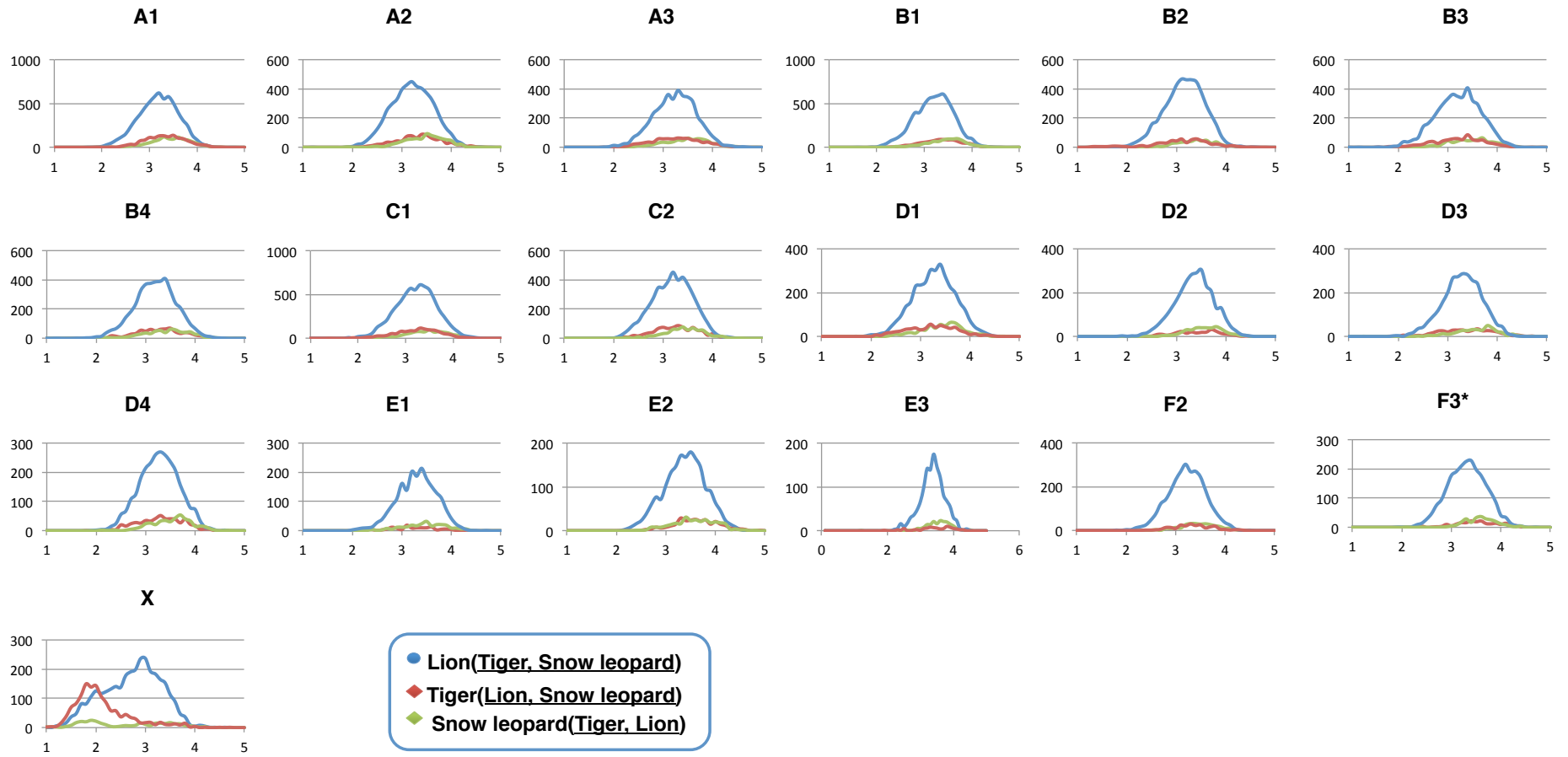
**Figure S7.** SNP density across all chromosomes within the domestic cat version 6.2 (felCat5) genome assembly. chrUN is not shown. The y-axis displays no. SNPs/Mb, calculated across the length of each felid chromosome (gray horizontal bars, with the centromere depicted as a box). Chromosomes F1 and F2 are acrocentric. Note the reduced SNP density within the central portion of the X chromosome which is within the low recombining region indicated in Fig. 4. Image is from Davis et al. 2015.



**Figure S8.** Mitogenome-based maximum likelihood tree (GTR+ $\Gamma$ ) based on synonymous substitutions. Nodes w/bootstrap support <70% are collapsed.



**Figure S9.** Frequency distribution of topologies (y axis) and divergence time point estimates (x axis, in millions of years) for each chromosome based on the tiger/snow leopard/lion whole genome analysis. Blue, green and red lines indicate trees with topologies grouping tiger + snow leopard, lion + tiger, and lion + snow leopard, respectively.



\**Panthera* chromosome F3 is orthologous to domestic cat chromosome F1 (Wurster-Hill and Centerwall, 1982).

**Table S1. Illumina 63K SNP array and mitochondrial genome statistics for different felid specimens. The percentage of heterozygous SNPs in each felid species was negatively correlated with genome divergence from the domestic cat. The results demonstrate the expected low genome-wide heterozygosity of these markers among non-*Felis silvestris* complex species of the Felidae. Only two individuals had call rates <90%: Sunda clouded leopard, and the Andean mountain cat. The Andean mountain cat DNA extract is from preserved hide (Johnson et al. 2006), thus relatively poor DNA quality may have contributed to the reduced call rates and increased heterozygosity.**

Species/3-letter code	Common name	# of individuals genotyped on array	% post-QC filtered SNPs	Within lineage average SNP call rates $\pm$ SEM	% Heterozygous SNPs	Mitogenome Length	Mean mitogenome coverage*
<i>Felis catus</i> /FCA	Domestic cat	14	99.7		12.0	17009	NA
<i>Felis lybica</i> /FLI	African wild cat	3	99.3		11.7	16741	236.5
<i>Felis silvestris</i> /FSI	European wild cat	3	99.3		6.2	16584	273.5
<i>Felis bieti</i> /FBI	Chinese desert cat	1	99.4	98.7 $\pm$ 0.34	1.5	16922	272.4
<i>Felis margarita</i> /FMA	Sand cat	1	98.1		0.1	16942	639.2
<i>Felis nigripes</i> /FNI	Black-footed Cat	1	97.4		0.3	16833	517.7
<i>Felis chaus</i> /FCH	Jungle cat	7	97.6		0.5	16725	800.8
<i>Prionailurus planiceps</i> /IPL	Flat-headed cat	1	95.1		0.3	16690	185.2
<i>Prionailurus rubiginosus</i> /PRU	Rusty-spotted cat	1	95.0		0.4	16914	398.0
<i>Prionailurus viverrinus</i> /PVI	Fishing cat	1	94.8	94.8 $\pm$ 0.07	0.3	16914	398.0
<i>Prionailurus bengalensis</i> /PBE	Asian leopard cat	13	94.7		0.9	16718	437.2
<i>Otocolobus manul</i> /OMA	Pallas's cat	1	94.6		0.2	16710	174.3
<i>Acinonyx jubatus</i> /AJU	Cheetah	1	94.4		0.4	16790	449.6
<i>Puma concolor</i> /PCO	Puma	1	94.4	94.3 $\pm$ 0.06	0.3	16897	188.2
<i>Puma yagouaroundi</i> /HJA	Jaguarundi	1	94.2		0.7	16780	288.7
<i>Pardofelis temminckii</i> /PTE	Asian golden cat	3	94.4		0.4	16949	198.7
<i>Pardofelis badia</i> /PBA	Bay cat	1	94.3	94.3 $\pm$ 0.10	0.5	16828	502.4
<i>Pardofelis marmorata</i> /PMA	Marbled cat	1	94.0		0.3	16871	367.8
<i>Lynx rufus</i> /LRU	Bobcat	1	94.9		0.6	17027	192.1
<i>Lynx lynx</i> /LLY	Eurasian lynx	1	94.4	94.0 $\pm$ 0.42	0.4	16718	1109.3
<i>Lynx canadensis</i> /LCA	Canada lynx	1	94.2		0.2	16665	435.5
<i>Lynx pardinus</i> /LYP	Iberian lynx	1	92.6		0.2	16841	79.9
<i>Leopardus pardalis</i> /LPA	Ocelot	1	94.2		0.8	16695	80.0
<i>Leopardus wiedii</i> /LWI	Margay	1	93.8		0.7	16718	187.6
<i>Leopardus colocolo</i> /LCO	Pampas cat	2	93.6		0.4	16649	338.7
<i>Leopardus geoffroyi</i> /OGE	Geoffroy's cat	2	93.4	93.6 $\pm$ 0.10**	0.6	16750	340.4
<i>Leopardus tigrinus</i> /LTI 01&02	Tigrina-NE Brazil/S.Am.	2	93.4		0.4	16644	316.4
<i>Leopardus "tigrinus"/LTI 03</i>	Tigrina-CostaRica/C.Am.	1	93.5		0.5	16852	87.0
<i>Leopardus guigna</i> /OGU	Kodkod	1	93.4		0.3	16772	274.4
<i>Leopardus jacobitus</i> /OJA	Andean mountain cat	1	83.7		1.9	16605	20.2
<i>Profelis serval</i> /PSE	Serval	20	94.4		0.8	16707	2446.5
<i>Profelis aurata</i> /PAU	African golden cat	1	93.6	93.8 $\pm$ 0.22	0.6	16917	267.5
<i>Profelis caracal</i> /CCA	Caracal	1	93.5		0.7	16899	219.9
<i>Panthera leo</i> /PLE	Lion	1	92.3		0.4	16619	195.5
<i>Panthera uncia</i> /PUN	Snow leopard	1	92.1		0.2	16709	238.1
<i>Panthera pardus</i> /PPA	Leopard	1	92.0		0.2	16678	508.8
<i>Panthera tigris</i> /PTI	Tiger	1	92.0	91.9 $\pm$ 0.13***	0.4	16792	831.6
<i>Panthera onca</i> /PON	Jaguar	1	91.3		0.3	16708	270.1
<i>Neofelis nebulosa</i> /NNE	Clouded leopard	1	91.8		0.2	16681	226.0
<i>Neofelis diardi</i> /NDI	Sunda clouded leopard	2	86.2		2.3	NA	NA

\*Estimated from mapping single-end Illumina 100-bp reads

\*\*excluding *Leopardus jacobitus*

\*\*\*excluding *Neofelis diardi*

**Table S2. Felid mitogenomes in GenBank with apparent numts.**

<b>Species</b>	<b>Acc. No.</b>	<b>Sequencing Method</b>	<b>PCR-based</b>	<b>Mitochondrial Enrichment?</b>	<b>Genes with numt origin</b>	<b>Publication (PubMed id)</b>
Jaguar	KF483864	Sanger	Yes	?	<i>ND2, COX1, COX2, ND3, ND4, ATP8, tRNAs</i>	25010076
Leopard	NC_010641	Sanger	Yes	Yes	<i>ND2, tRNAs, COX2</i>	22038004
Snow leopard	NC_010638	Sanger	Yes	Yes	<i>COX3, ND3</i>	18431688
African Lion	KF907306	Illumina	No	?	<i>ND2, COX1, COX2, ND2, ND3, ND4, ATP6</i>	24438244*
Clouded leopard	NC_008450	Sanger	Yes	No	<i>16SrRNA</i>	17546090
Puma	NC_016470	?	?	?	<i>12SrRNA, tRNAval, 16SrRNA</i>	unpublished
Tiger	HM589214	Sanger	Yes	No	<i>COX2, ATP8, ATP6, COX3, ND4</i>	21110106
Tiger	NC_014770	Sanger	Yes	No	<i>COX2, ATP8, ATP6, COX3, ND4</i>	21110106
Tiger	JF357972	Sanger	Yes	No	<i>COX2, ATP8, ATP6, COX3, ND4</i>	21723800

\* withdrawn from PubMed due to an unspecified error in the data.

Table S3. Results of multidivtime analyses performed on the biparental nuclear DNA genome partition, with different partitions and constraints.

	HARD-BOUNDED CONSTRAINTS											
	No SNPs						SNPs w/out <i>Felis sylvestris</i> complex					
	Autocorrelated rates			Independent rates			Autocorrelated rates			Independent rates		
<b>Felidae</b>	10.59	8.38	13.74	9.91	7.91	12.77	11.66	9.26	15.10	10.20	8.34	12.84
<b>Felinae</b>	9.93	7.85	12.80	9.06	7.42	11.49	11.02	8.93	14.03	9.62	7.85	12.04
<b>Ocelot lineage/Lynx+Puma+ALC+DC lineages</b>	9.19	7.29	11.86	8.38	6.83	10.65	9.92	8.07	12.56	8.90	7.23	11.22
<b>Ocelot lineage</b>	3.02	2.01	4.14	2.98	2.22	3.98	3.57	2.77	4.63	2.12	1.64	2.81
<b>Pampas cat/tigrinas+Geoffroy's cat+kodkod</b>	2.41	1.60	3.33	2.37	1.71	3.21	3.24	2.52	4.21	1.90	1.44	2.56
<b>C.Am. tigrina/S. Am. tigrina+Geoffroy's cat+kodkod</b>							1.58	1.10	2.21	1.47	1.00	2.13
<b>tigrina/Geoffroy's cat+kodkod</b>	1.28	0.81	1.82	1.30	0.87	1.84	1.46	1.07	1.98	0.91	0.61	1.28
<b>Geoffroy's cat/kodkod</b>	0.61	0.28	1.17	0.71	0.30	1.35	1.14	0.83	1.58	0.69	0.43	1.05
<b>Andean mountain cat/ocelot+margay</b>	2.83	1.86	3.91	2.75	1.98	3.74	3.31	2.56	4.31	1.92	1.45	2.56
<b>ocelot/margay</b>	2.24	1.47	3.10	2.10	1.42	2.97	3.09	2.37	4.04	1.76	1.27	2.40
<b>Lynx+Bay Cat lineage/Puma+ALC+DC lineages</b>	8.19	6.51	10.52	7.55	6.19	9.52	8.66	7.05	10.99	8.06	6.60	10.07
<b>Lynx lineage/Bay cat lineage</b>	7.70	6.13	9.90	7.03	5.69	8.96	7.95	6.49	10.09	7.26	5.85	9.16
<b>Lynx lineage</b>	3.39	2.61	4.50	3.28	2.57	4.42	3.26	2.57	4.35	3.02	2.52	4.00
<b>lynx clade</b>	1.49	1.03	2.15	1.59	1.05	2.46	1.48	1.09	2.09	1.48	0.92	2.23
<b>Eurasian lynx/Iberian Lynx</b>	1.03	0.70	1.43	1.02	0.61	1.57	1.04	0.76	1.49	1.00	0.53	1.70
<b>Bay cat lineage</b>	5.31	4.18	6.90	4.38	3.00	5.99	5.81	4.66	7.46	4.82	3.48	6.58
<b>Bay cat/Asian golden cat</b>	3.45	2.48	4.79	2.81	1.73	4.14	3.31	2.58	4.33	2.55	1.65	3.90
<b>Puma lineage/ALC+Domestic cat lineages</b>	7.76	6.22	9.94	7.14	5.83	9.03	7.90	6.46	10.03	7.43	6.12	9.27
<b>Puma lineage</b>	5.11	4.05	6.67	4.49	3.83	5.78	4.59	3.84	5.91	4.42	3.82	5.68
<b>puma/jaguarundi</b>	4.06	3.16	5.33	3.38	2.48	4.50	3.26	2.64	4.30	2.84	2.04	3.84
<b>Domestic cat lineage/Leopard cat lineage</b>	6.93	5.56	8.86	6.40	5.16	8.21	6.86	5.62	8.73	6.60	5.35	8.24
<b>Leopard cat lineage</b>	5.37	4.26	6.89	5.09	3.90	6.68	5.97	4.87	7.61	5.47	4.22	7.00
<b><i>Prionailurus</i> clade</b>	3.46	2.53	4.73	3.75	2.70	5.11	3.30	2.61	4.27	3.27	2.35	4.58
<b>flat-headed cat/Asian leopard cat+fishing cat</b>	1.83	1.34	2.49	2.28	1.57	3.19	2.41	1.87	3.18	2.28	1.57	3.39
<b>Asian leopard cat/fishing cat</b>	1.40	1.07	1.86	1.62	1.11	2.28	1.85	1.40	2.46	1.68	1.03	2.56
<b>Sundaic/Indochinese Asian leopard cats</b>												
<b>Indochinese Asian leopard cats</b>												
<b>Domestic cat lineage</b>	4.26	3.36	5.50	3.89	2.97	5.23	3.38	2.68	4.47	3.93	2.00	5.40
<b>black-footed cat/sand cat+domestic cat clade</b>	3.22	2.52	4.17	2.89	2.20	3.91						
<b>sand cat/domestic cat clade</b>	2.64	2.05	3.44	2.37	1.79	3.22						
<b>domestic cat clade</b>	1.48	1.19	1.92	1.45	1.17	1.89						
<b>domestic cat/European wild cat</b>	1.10	1.00	1.35	1.11	1.00	1.36						
<b>African wild cat/Chinese desert cat</b>	1.15	0.82	1.52	1.12	0.68	1.55						
<b>Caracal lineage</b>	6.73	5.12	8.88	5.08	3.87	7.43	6.82	5.11	9.22	4.82	3.84	6.43
<b>caracal/African golden cat</b>	2.52	1.61	3.74	1.71	1.05	2.78	1.45	0.89	2.26	1.01	0.57	1.81
<b>Pantherinae</b>	5.27	4.04	7.11	5.33	4.06	7.23	5.42	4.05	7.44	4.57	3.83	6.14
<b><i>Neofelis</i></b>							1.87	1.27	2.78	1.71	0.96	2.52
<b><i>Panthera</i></b>	3.51	2.67	4.76	3.59	2.69	4.83	3.66	2.73	5.15	2.72	2.04	3.56
<b>jaguar/lion+leopard</b>	2.55	1.91	3.46	2.64	1.89	3.64	2.70	1.97	3.85	1.99	1.48	2.71
<b>lion/leopard</b>	1.68	1.23	2.33	1.73	1.15	2.57	1.93	1.38	2.79	1.42	0.88	2.05
<b>tiger/snow leopard</b>	2.61	1.95	3.56	2.41	1.51	3.49	2.79	2.05	3.97	1.78	1.14	2.55

	SOFT-BOUNDED CONSTRAINTS											
	No SNPs						SNPs w/out <i>Felis sylvestrus</i> complex					
	Autocorrelated rates			Independent rates			Autocorrelated rates			Independent rates		
<b>Felidae</b>	12.64	9.37	15.96	11.21	8.37	14.92	13.67	10.26	16.35	11.76	8.66	15.46
<b>Felinae</b>	11.75	8.76	15.14	10.24	7.82	13.43	12.56	9.60	15.48	11.16	8.28	14.76
<b>Ocelot lineage/Lynx+Puma+ALC+DC lineages</b>	10.89	8.10	14.02	9.53	7.28	12.47	11.35	8.67	14.04	10.33	7.65	13.69
<b>Ocelot lineage</b>	3.62	2.58	4.82	3.40	2.44	4.65	3.85	2.03	5.03	2.59	1.85	3.64
<b>Pampas cat/tigrinas+Geoffroy's cat+kodkod</b>	2.89	2.06	3.90	2.69	1.88	3.72	3.50	1.84	4.60	2.32	1.63	3.26
<b>C.Am. tigrina/S. Am. tigrina+Geoffroy's cat+kodkod</b>							2.02	1.41	2.59	1.30	0.83	1.92
<b>tigrina/Geoffroy's cat+kodkod</b>	1.54	1.06	2.15	1.47	0.97	2.15	1.59	0.82	2.19	1.12	0.71	1.70
<b>Geoffroy's cat/kodkod</b>	0.78	0.35	1.41	0.82	0.34	1.51	1.25	0.64	1.76	0.85	0.48	1.35
<b>Andean mountain cat/ocelot+margay</b>	3.39	2.40	4.54	3.15	2.21	4.37	3.58	1.85	4.71	2.35	1.66	3.33
<b>ocelot/margay</b>	2.68	1.89	3.61	2.42	1.57	3.46	3.33	1.71	4.40	2.17	1.49	3.13
<b>Lynx+Bay Cat lineage/Puma+ALC+DC lineages</b>	9.72	7.24	12.52	8.63	6.58	11.34	9.96	7.64	12.30	9.30	6.97	12.24
<b>Lynx lineage/Bay cat lineage</b>	9.15	6.80	11.80	8.06	6.07	10.69	9.15	7.01	11.35	8.35	6.11	11.09
<b>Lynx lineage</b>	4.05	2.90	5.40	3.75	2.59	5.28	3.80	2.74	5.20	3.31	2.43	4.94
<b>lynx clade</b>	1.77	1.16	2.57	1.76	1.14	2.64	1.74	1.17	2.53	1.54	0.90	2.76
<b>Eurasian lynx/Iberian Lynx</b>	1.22	0.80	1.70	1.14	0.67	1.72	1.22	0.81	1.81	1.06	0.52	2.25
<b>Bay cat lineage</b>	6.31	4.61	8.27	5.01	3.29	7.19	6.70	5.05	8.43	5.65	3.71	8.51
<b>Bay cat/Asian golden cat</b>	4.13	2.78	5.80	3.19	1.89	4.81	3.81	2.77	4.93	2.92	1.62	4.95
<b>Puma lineage/ALC+Domestic cat lineages</b>	9.22	6.87	11.86	8.18	6.22	10.75	9.10	6.98	11.28	8.65	6.48	11.41
<b>Puma lineage</b>	6.13	4.54	8.06	5.10	3.79	7.03	5.34	3.96	6.87	4.71	3.65	6.55
<b>puma/jaguarundi</b>	4.88	3.60	6.46	3.91	2.55	5.56	3.80	2.79	5.00	3.14	2.04	4.72
<b>Domestic cat lineage/Leopard cat lineage</b>	8.22	6.13	10.61	7.32	5.55	9.71	7.92	6.06	9.87	7.74	5.79	10.24
<b>Leopard cat lineage</b>	6.38	4.70	8.33	5.84	4.27	7.83	6.90	5.26	8.61	6.54	4.81	8.77
<b><i>Prionailurus</i> clade</b>	4.14	2.86	5.82	4.33	2.99	6.01	3.82	2.84	4.87	3.99	2.77	5.53
<b>flat-headed cat/Asian leopard cat+fishing cat</b>	2.18	1.51	3.09	2.65	1.69	3.84	2.79	2.05	3.62	2.80	1.93	3.95
<b>Asian leopard cat/fishing cat</b>	1.66	1.18	2.27	1.89	1.18	2.85	2.14	1.56	2.79	2.09	1.33	3.09
<b>Sundaic/Indochinese Asian leopard cats</b>	0.90	0.65	1.26	0.82	0.51	1.21	1.04	0.71	1.42	0.93	0.53	1.50
<b>Indochinese Asian leopard cats</b>	0.46	0.32	0.66	0.42	0.22	0.67	0.53	0.36	0.76	0.46	0.24	0.80
<b>Domestic cat lineage</b>	4.96	3.68	6.50	4.48	3.23	6.14	3.95	2.94	5.09	5.00	3.44	7.16
<b>black-footed cat/sand cat+domestic cat clade</b>	3.71	2.74	4.88	3.28	2.36	4.56						
<b>sand cat/domestic cat clade</b>	3.01	2.18	4.05	2.67	1.88	3.73						
<b>domestic cat clade</b>	1.61	1.19	2.21	1.54	1.15	2.14						
<b>domestic cat/European wild cat</b>	1.14	0.92	1.54	1.11	0.89	1.48						
<b>African wild cat/Chinese desert cat</b>	1.25	0.85	1.77	1.19	0.74	1.73						
<b>Caracal lineage</b>	8.01	5.84	10.57	5.44	3.82	8.07	7.84	5.64	10.34	5.49	3.71	9.00
<b>caracal/African golden cat</b>	2.98	1.84	4.45	1.87	1.10	3.10	1.66	1.02	2.53	1.16	0.56	2.29
<b>Pantherinae</b>	6.28	4.25	9.08	6.32	4.45	8.96	7.03	4.56	10.67	5.10	3.76	7.20
<b><i>Neofelis</i></b>							2.46	1.41	4.11	1.90	1.09	2.98
<b><i>Panthera</i></b>	4.18	2.79	6.13	4.22	2.97	5.90	4.81	3.07	7.60	3.10	2.18	4.42
<b>jaguar/lion+leopard</b>	3.03	2.01	4.48	3.07	2.12	4.30	3.56	2.23	5.71	2.28	1.58	3.34
<b>lion/leopard</b>	2.00	1.30	2.99	2.01	1.28	2.96	2.55	1.56	4.09	1.58	0.98	2.41
<b>tiger/snow leopard</b>	3.11	2.07	4.62	2.89	1.83	4.39	3.69	2.31	5.92	2.09	1.37	3.13



AVERAGE DATES ACROSS RUNS			Johnson et al. 2006 dates			
Mean	min	max	Mean	min	max	
11.46	7.91	16.35	10.78	8.38	14.45	<b>Felidae</b>
10.67	7.42	15.48	NA	NA	NA	<b>Felinae</b>
9.81	6.83	14.04	NA	NA	NA	<b>Ocelot lineage/Lynx+Puma+ALC+DC lineages</b>
3.14	1.64	5.03	2.91	2.02	4.25	<b>Ocelot lineage</b>
2.67	1.44	4.60	NA	NA	NA	<b>Pampas cat/tigrinas+Geoffroy's cat+kodkod</b>
						<b>C.Am. tigrina/S. Am. tigrina+Geoffroy's cat+kodkod</b>
1.33	0.61	2.19	0.93	0.56	1.48	<b>tigrina/Geoffroy's cat+kodkod</b>
0.86	0.28	1.76	0.74	0.41	1.21	<b>Geoffroy's cat/kodkod</b>
2.91	1.45	4.71	NA	NA	NA	<b>Andean mountain cat/ocelot+margay</b>
2.47	1.27	4.40	1.58	1.01	2.41	<b>ocelot/margay</b>
8.76	6.19	12.52	NA	NA	NA	<b>Lynx+Bay Cat lineage/Puma+ALC+DC lineages</b>
8.08	5.69	11.80	NA	NA	NA	<b>Lynx lineage/Bay cat lineage</b>
3.48	2.43	5.40	3.24	2.53	4.74	<b>Lynx lineage</b>
1.61	0.90	2.76	1.61	1.06	2.6	<b>lynx clade</b>
1.09	0.52	2.25	1.18	0.7	1.98	<b>Eurasian lynx/Iberian Lynx</b>
5.50	3.00	8.51	5.86	4.27	8.42	<b>Bay cat lineage</b>
3.27	1.62	5.80	4.3	2.96	6.42	<b>Bay cat/Asian golden cat</b>
8.17	5.83	11.86	NA	NA	NA	<b>Puma lineage/ALC+Domestic cat lineages</b>
4.99	3.65	8.06	4.92	3.86	6.92	<b>Puma lineage</b>
3.66	2.04	6.46	4.17	3.16	6.01	<b>puma/jaguarundi</b>
7.25	5.16	10.61	6.18	4.8	8.55	<b>Domestic cat lineage/Leopard cat lineage</b>
5.95	3.90	8.77	5.86	4.53	8.16	<b>Leopard cat lineage</b>
3.76	2.35	6.01	4.59	3.42	6.54	<b>Prionailurus clade</b>
2.40	1.34	3.95	2.94	2.04	4.31	<b>flat-headed cat/Asian leopard cat+fishing cat</b>
1.79	1.03	3.09	NA	NA	NA	<b>Asian leopard cat/fishing cat</b>
						<b>Sundaic/Indochinese Asian leopard cats</b>
						<b>Indochinese Asian leopard cats</b>
4.23	2.00	7.16	3.36	2.41	4.88	<b>Domestic cat lineage</b>
3.28	2.20	4.88	3.04	2.16	4.44	<b>black-footed cat/sand cat+domestic cat clade</b>
2.67	1.79	4.05	2.49	1.72	3.67	<b>sand cat/domestic cat clade</b>
1.52	1.15	2.21	1.4	0.89	2.16	<b>domestic cat clade</b>
1.12	0.89	1.54	0.99	0.59	1.62	<b>domestic cat/European wild cat</b>
1.18	0.68	1.77	1.17	0.72	1.86	<b>African wild cat/Chinese desert cat</b>
6.28	3.71	10.57	5.59	4.14	7.91	<b>Caracal lineage</b>
1.80	0.56	4.45	1.88	1.19	2.93	<b>caracal/African golden cat</b>
5.67	3.76	10.67	6.37	4.47	9.32	<b>Pantherinae</b>
1.99	0.96	4.11	NA	NA	NA	<b>Neofelis</b>
3.72	2.04	7.60	3.72	2.44	5.79	<b>Panthera</b>
2.73	1.48	5.71	2.87	1.81	4.63	<b>jaguar/lion+leopard</b>
1.86	0.88	4.09	NA	NA	NA	<b>lion/leopard</b>
2.67	1.14	5.92	2.88	1.82	4.62	<b>tiger/snow leopard</b>

Table S4. Results of multidivtime analyses performed on the mitogenome matrix, with different partitions and constraints

HARD-BOUNDED CONSTRAINTS				SOFT-BOUNDED CONSTRAINTS				AVERAGE DATES ACROSS RUNS						
Independent rates			Autocorrelated rates			Independent rates			Autocorrelated rates			Mean	min	max
10.90	7.45	15.50	11.93	6.46	15.81	13.08	7.18	16.53	13.98	9.73	16.76	12.47	6.46	16.76 Felidae
9.28	5.17	13.76	10.53	6.09	14.98	11.23	5.67	15.77	12.31	7.17	16.00	10.84	5.17	16.00 Felinae
8.24	4.82	12.67	9.50	5.63	14.28	10.18	5.13	15.19	11.07	6.06	15.34	9.75	4.82	15.34 Lynx + Bay cat + Puma + Caracal + Asian leopard cat + Domestic Cat lineages
6.64	4.24	11.26	7.58	4.24	13.17	8.35	4.27	14.26	8.73	4.35	14.43	7.83	4.24	14.43 Lynx + Bay cat + Puma lineages
4.97	3.83	8.98	5.23	3.85	9.23	5.69	3.60	11.05	5.68	3.61	11.09	5.39	3.60	11.09 Puma lineage
2.44	1.82	3.42	2.51	1.82	4.07	1.66	0.96	3.54	1.64	0.96	3.57	2.06	0.96	4.07 puma/jaguarundi
4.94	2.93	8.95	5.47	3.04	10.64	6.09	2.88	12.28	6.20	2.98	12.85	5.68	2.88	12.85 Lynx + Bay cat lineage
2.98	1.84	5.40	2.89	0.45	7.39	2.98	0.41	8.03	3.17	0.45	8.47	3.01	0.41	8.47 Bay cat lineage
2.23	0.39	3.31	1.33	0.04	4.20	1.27	0.05	4.37	1.52	0.04	4.58	1.59	0.03	4.58 Bay cat/Asian golden cat
3.34	2.52	5.51	3.56	2.55	6.63	4.00	2.42	8.62	4.01	2.39	8.45	3.73	2.39	8.62 Lynx lineage
2.66	1.84	4.28	1.92	0.31	4.44	2.16	0.36	5.00	2.18	0.38	5.25	2.23	0.31	5.25 lynx clade
2.36	0.91	3.41	0.99	0.03	2.99	1.11	0.04	3.83	1.13	0.04	3.81	1.40	0.03	3.83 Canada lynx+Iberian lynx
7.20	4.58	11.46	8.19	4.90	13.21	8.94	4.78	14.22	9.61	5.22	14.66	8.49	4.58	14.66 Caracal lineage/Domestic cat + Asian leopard cat lineages
5.10	3.85	8.56	5.57	3.86	10.13	5.89	3.64	10.82	6.17	3.68	11.99	5.68	3.64	11.99 Caracal lineage
2.65	0.90	4.88	2.02	0.08	5.35	2.14	0.08	6.25	2.24	0.07	5.98	2.26	0.07	6.25 caracal+African golden cat
5.93	4.27	9.80	6.29	4.29	10.87	7.09	4.21	12.56	7.39	4.31	13.10	6.68	4.21	13.10 Domestic cat + Asian leopard cat lineages
4.02	2.04	6.91	3.57	0.73	7.32	3.92	0.73	8.65	3.92	0.80	8.76	3.86	0.73	8.76 Prionailurus clade
2.86	1.84	4.78	2.18	0.27	4.95	2.29	0.27	5.74	2.39	0.31	5.91	2.43	0.27	5.91 flat-headed cat/Asian leopard cat+fishing cat
2.38	1.26	3.43	1.14	0.02	3.85	1.20	0.05	4.19	1.33	0.03	4.25	1.51	0.02	4.25 Asian leopard cat/fishing cat
4.26	2.27	7.27	3.94	1.46	8.16	4.55	1.64	9.06	4.67	1.65	9.40	4.36	1.46	9.40 Pallas cat+Domestic cat lineage
2.81	1.84	5.08	2.11	1.03	5.32	2.65	1.05	5.92	2.85	1.04	6.52	2.61	1.03	6.52 Domestic cat lineage
2.61	1.83	4.46	1.77	0.62	4.48	2.14	0.69	4.71	2.33	0.73	5.31	2.21	0.62	5.31 black-footed cat/sand cat+domestic cat clade
2.50	1.81	4.09	1.47	0.39	3.83	1.76	0.43	4.20	1.96	0.47	4.64	1.92	0.39	4.64 sand cat/domestic cat clade
2.37	1.14	3.39	1.18	0.23	3.22	1.39	0.24	3.93	1.61	0.26	4.35	1.64	0.23	4.35 domestic cat clade
1.36	0.06	2.83	0.74	0.02	2.82	0.80	0.02	3.27	1.05	0.02	4.21	0.99	0.02	4.21 domestic cat/African wild cat
1.94	0.12	3.16	0.67	0.02	2.60	0.76	0.02	2.48	0.97	0.02	4.14	1.09	0.02	4.14 European wild cat+Chinese desert cat
4.31	2.46	4.99	3.85	1.25	4.97	3.84	0.98	5.19	3.88	1.57	5.15	3.97	0.98	5.19 Ocelot lineage
3.16	1.67	4.85	2.32	0.35	4.63	2.41	0.35	4.79	2.44	0.39	4.74	2.58	0.35	4.85 Central Am. tigrina/Geoffroy's cat+kodkod
2.16	0.11	4.64	1.16	0.04	3.76	1.27	0.04	4.03	1.33	0.04	4.26	1.48	0.04	4.64 Geoffroy's cat/kodkod
3.67	1.94	4.91	2.85	0.73	4.74	2.84	0.64	4.91	2.88	0.83	4.83	3.06	0.64	4.91 ocelot+margay/Andean mountain cat+Pampas cat+S. Am. tigrina
2.84	1.16	4.71	1.84	0.26	4.29	1.90	0.26	4.48	1.92	0.27	4.41	2.13	0.26	4.71 Andean mountain cat/Pampas cat+S. Am. tigrina
1.62	0.06	4.17	0.92	0.02	3.10	0.97	0.03	3.71	1.04	0.03	3.28	1.14	0.02	4.17 Pampas cat+S. Am. tigrina
2.45	0.14	4.76	1.38	0.06	4.03	1.40	0.05	4.27	1.58	0.05	4.34	1.70	0.05	4.76 ocelot+margay
6.63	4.04	11.09	7.22	3.99	12.95	8.30	3.96	14.20	8.67	4.09	14.52	7.71	3.96	14.52 Pantherinae
4.66	2.06	8.53	4.53	0.97	10.21	5.12	1.03	11.44	5.24	1.09	11.75	4.89	0.97	11.75 Panthera
3.40	1.86	6.81	3.00	0.53	7.87	3.25	0.55	8.50	3.29	0.56	8.66	3.24	0.53	8.66 jaguar/snow leopard+lion+leopard
2.66	1.82	4.48	1.83	0.20	5.07	1.98	0.22	5.21	2.11	0.23	5.23	2.15	0.20	5.23 snow leopard/lion+leopard
2.32	0.49	3.45	0.89	0.02	3.06	1.09	0.02	4.03	1.21	0.02	4.23	1.38	0.02	4.23 lion/leopard

**Table S5. Results of ABBA/BABA tests based on the genus *Felis* whole genome SNV data.**

Chromosome	((Domestic cat, Sand cat), Jungle cat), Asian leopard cat					((Sand cat, Domestic cat), Black-footed cat), Asian leopard cat				
	ABBA	BABA	<i>D</i>	<i>Z</i>	<i>P</i>	ABBA	BABA	<i>D</i>	<i>Z</i>	<i>P</i>
A1	40229	33462	0.092 ± 0.001	64.14	0	49604	40370	0.103 ± 0.002	63.77	0
A2	28759	23590	0.099 ± 0.002	53.39	0	35532	28126	0.116 ± 0.002	71.62	0
A3	22430	18941	0.084 ± 0.002	39.26	0	28403	22053	0.126 ± 0.002	68.33	0
B1	35956	29217	0.103 ± 0.002	55.21	0	44054	34812	0.117 ± 0.001	89.86	0
B2	25992	21632	0.092 ± 0.002	38.20	0	32626	25544	0.122 ± 0.002	72.06	0
B3	23394	19359	0.094 ± 0.002	42.95	0	28968	23096	0.113 ± 0.002	47.78	0
B4	24639	19555	0.115 ± 0.002	47.41	0	30420	23551	0.127 ± 0.003	50.53	0
C1	35207	29150	0.094 ± 0.002	59.10	0	43851	34779	0.115 ± 0.001	79.56	0
C2	26403	22354	0.083 ± 0.002	43.59	0	32789	26323	0.109 ± 0.002	62.84	0
D1	19005	15559	0.100 ± 0.002	42.02	0	23805	19123	0.109 ± 0.003	35.30	0
D2	17142	13793	0.108 ± 0.002	48.16	0	21262	16181	0.134 ± 0.003	41.38	0
D3	17556	14181	0.106 ± 0.003	42.44	0	22004	17175	0.123 ± 0.003	44.64	0
D4	16188	13817	0.079 ± 0.003	29.41	0	20777	16175	0.125 ± 0.003	38.43	0
E1	12263	9399	0.132 ± 0.005	26.54	0	14742	11568	0.121 ± 0.003	34.50	0
E2	10598	8327	0.120 ± 0.005	23.65	0	13263	10168	0.132 ± 0.004	30.44	0
E3	8546	6824	0.112 ± 0.005	21.79	0	10288	8013	0.124 ± 0.005	23.74	0
F1	12960	10328	0.113 ± 0.004	26.98	0	16141	12327	0.134 ± 0.003	46.16	0
F2	14649	12301	0.087 ± 0.004	23.28	0	18239	14598	0.111 ± 0.003	35.89	0
X	8081	7122	0.063 ± 0.004	17.43	0	10743	8551	0.113 ± 0.004	26.28	0

**Table S6. Results of the ABBA/BABA tests using a reduced set of high confidence orthologous SNPs.**

<b>Species Tree (P1,P2) P3</b>	<b>Outgroup</b>	<b>ABBA</b>	<b>BABA</b>	<b><i>D</i></b>	<b><i>Z</i></b>	<b><i>P</i></b>
(Sand cat, Domestic cat), Black-footed cat	Asian leopard cat	1002	761	0.137 ± 0.028	4.88	1.05E-06
(Black-footed cat, Sand cat), Jungle cat	Asian leopard cat	607	482	0.115 ± 0.032	3.63	0.000283
(Domestic cat, Sand cat), Jungle cat	Asian leopard cat	895	602	0.196 ± 0.02	9.73	0

**Table S7. Summary of SNP-based *D*-statistics based on jackknifing the outgroup taxon for non-Domestic cat lineage comparisons (only significant results from Table 1 were evaluated).**

<b>P1</b>	<b>P2</b>	<b>P3</b>	<b>number of tested outgroups</b>	<b>range of Z-scores</b>	<b>range of ABBA sites</b>	<b>range of BABA sites</b>	<b>range of <i>D</i>-scores</b>	<b>range of <i>P</i> values</b>
Malay/Sunda ALC	Indochinese ALC	Fishing cat	16	3.5—7.7	302—359	192—222	0.16—0.29	0.0004—1.58e-14
Iberian lynx	Eurasian lynx	Canada lynx	16	4.8—7.9	264—330	142—175	0.23—0.34	1.53E-06—3.55e-15
Iberian lynx	Canada lynx	Bobcat	16	3.1—6.2	202—262	122—148	0.18—0.30	0.0022—5.94e-10
Kodkod	Geoffroy's cat	Tigrina (S.Am.)	16	2.0—3.5	220—235	164—186	0.09—0.17	0.047—0.0005

**Table S8. Results of ABBA/BABA tests between tiger (P1), snow leopard (P2) and lion (P3), using domestic cat as the outgroup species. Positive *D* scores support P2+P3, while negative scores support P1+P3.**

Chromosome	SNV	ABBA	BABA	<i>D</i>	<i>Z</i>	<i>P</i>
A1	2305655	41567	37017	0.0579 ± 0.0022	27.31	0
A2	1492397	25516	22562	0.0614 ± 0.0032	19.26	0
A3	1210659	19950	17983	0.0519 ± 0.0046	11.35	0
B1	1884034	34089	31771	0.0352 ± 0.0033	16.09	0
B2	1408000	24421	22447	0.0421 ± 0.0038	11.01	0
B3	1250800	20979	18519	0.0623 ± 0.0042	14.88	0
B4	1215044	21210	19210	0.0495 ± 0.0036	13.84	0
C1	1860373	31250	27894	0.0567 ± 0.0027	21.11	0
C2	1430423	25797	23095	0.0553 ± 0.0038	14.72	0
D1	944433	16591	15641	0.0295 ± 0.0044	6.68	2.40E-11
D2	832379	14658	15526	-0.0288 ± 0.0053	5.39	7.13E-08
D3	856445	15066	14875	0.0064 ± 0.005	1.28	0.2013 <sup>NS</sup>
D4	793931	14208	12731	0.0548 ± 0.006	9.18	0
E1	453453	7179	7423	-0.0167 ± 0.0101	1.65	0.0996 <sup>NS</sup>
E2	457214	7933	7340	0.0388 ± 0.0064	6.02	1.74E-09
E3	282299	4504	4950	-0.0472 ± 0.0091	5.17	2.39E-07
F1	633514	11041	11284	-0.0109 ± 0.0076	1.43	0.1516 <sup>NS</sup>
F2	774198	13645	13370	0.0102 ± 0.006	1.69	0.0914 <sup>NS</sup>
X	687121	8271	5872	0.1696 ± 0.014	11.76	0

<sup>NS</sup>Not significant.

**Table S9. Summary of per-lineage variable sites in the SNP matrix and within sliding windows used for Fig. 2A.**

<b>Lineage name</b>	<b>All variable sites</b>	<b>Average # sites/window</b>
Asian Leopard Cat	3359	14.6
Domestic	20201	87.8
Lynx	1076	4.7
Bay Cat	2022	8.8
Puma	1823	7.9
Ocelot	1636	7.1
Caracal	1261	5.5
Panthera	2441	7.4

## Literature Cited

Davis BW, Seabury CM, Brashear W, Li G, Roelke-Parker M, Murphy WJ. 2015. Mechanisms underlying mammalian hybrid sterility in two interspecies models. *Mol. Biol. Evol.* May 25. pii: msv124. [Epub ahead of print]

Johnson WE, Slattery JP, Eizirik E, Kim JH, Raymond MM, Bonacic C, Cambre R, Crawshaw P, Nunes A, Seuanez HN *et al.* 1999. Disparate phylogeographic patterns of molecular genetic variation in four closely related South American small cat species. *Mol Ecol* **8**: S79-S94.

Johnson WE, Eizirik E, Pecon-Slattery J, Murphy WJ, Antunes A, Teeling E, O'Brien SJ. 2006. The Late Miocene radiation of modern Felidae: a genetic assessment. *Science* **311**: 73-77.

Montague MJ, Li G, Gandolfi B, Khan R, Aken BL, Searle SM, Minx P, Hillier LW, Koboldt DC, Davis BW *et al.* 2014. Comparative analysis of the domestic cat genome reveals genetic signatures underlying feline biology and domestication. *Proc Natl Acad Sci USA* **111**: 17230-17235.

Wurster-Hill DH, Centerwall WR. 1982. The interrelationships of chromosome-banding patterns in canids, mustelids, hyena, and felids. *Cytogenet Cell Genet* **34**: 178-192.