

		CYTB	ND1	ND2	ND4	ND5	12S	16S	ATP8
Lion	Janczewski et al. 1995	Jancz.1995					Jancz.1995		
	Johnson et al. 1997					AF006458		AF006457	
	Mattern et al. 2000	Jancz.1995				AF006458	Jancz.1995	AF006457	
	Yu & Zhang 2005	Jancz.1995		AY170043	AY634398	AF006458	Jancz.1995	AF006457	
	Johnson et al. 2006	John.2006	John.2006	John.2006	John.2006	John.2006	John.2006	John.2006	John.2006
	Wei et al. 2009	S79302		AY170043	AY634398	AF006458	S79300	AF006457	DQ899945
Leopard	Janczewski et al. 1995	Jancz.1995					Jancz.1995		
	Johnson et al. 1997					AF006444		AF006443	
	Mattern et al. 2000	Jancz.1995				AF006444	Jancz.1995	AF006443	
	Yu & Zhang 2005	Jancz.1995		AY634383	AY634395	AF006444	Jancz.1995	AF006443	
	Johnson et al. 2006	John.2006	John.2006	John.2006	John.2006	John.2006	John.2006	John.2006	John.2006
	Wei et al. 2009	EF437590		AY634383	AY634395	AF006444	AM779888	AF006443	DQ899943
Jaguar	Janczewski et al. 1995	Jancz.1995					Jancz.1995		
	Johnson et al. 1997					AF006442		AF006441	
	Mattern et al. 2000	Jancz.1995				AF006442	Jancz.1995	AF006441	
	Yu & Zhang 2005	Jancz.1995		AY634391	AY634403	AF006442	Jancz.1995	AF006441	
	Johnson et al. 2006	John.2006	John.2006	John.2006	John.2006	John.2006	John.2006	John.2006	John.2006
	Wei et al. 2009	EF437582		AY634391	AY634403	AF006442	AY012151	AF006441	DQ899924
Tiger	Janczewski et al. 1995	Jancz.1995					Jancz.1995		
	Johnson et al. 1997					AF006460		AF006459	
	Mattern et al. 2000	Jancz.1995				AF006460	Jancz.1995	AF006459	
	Yu & Zhang 2005	Jancz.1995		AY634384	AY634396	AF006460	Jancz.1995	AF006459	
	Johnson et al. 2006	John.2006	John.2006	John.2006	John.2006	John.2006	John.2006	John.2006	John.2006
	Wei et al. 2009	EF437588		DQ151550	AY634396	AF006460	DQ151550	DQ151550	DQ899931
Snow Leopard	Janczewski et al. 1995	Jancz.1995					Jancz.1995		
	Johnson et al. 1997					AF006450		AF006449	
	Mattern et al. 2000	Jancz.1995				AF006450	Jancz.1995	AF006449	
	Yu & Zhang 2005	Jancz.1995		AY634382	AY634394	AF006450	Jancz.1995	AF006449	
	Johnson et al. 2006	John.2006	John.2006	John.2006	John.2006	John.2006	John.2006	John.2006	John.2006
	Wei et al. 2009	EF551004		EF551004	EF551004	EF551004	EF551004	EF551004	EF551004
Clouded Leopard	Janczewski et al. 1995	Jancz.1995					Jancz.1995		
	Johnson et al. 1997					AF006426		AF006425	
	Mattern et al. 2000	Jancz.1995				AF006426	Jancz.1995	AF006425	
	Yu & Zhang 2005	Jancz.1995		AY634385	AY634397	AF006426	Jancz.1995	AF006425	
	Johnson et al. 2006	John.2006	John.2006	John.2006	John.2006	John.2006	John.2006	John.2006	John.2006
	Wei et al. 2009	DQ257669		DQ257669	DQ257669	DQ257669	DQ257669	DQ257669	DQ257669

Supplemental Table 1. Accession numbers for mitochondrial segments used in prior phylogenetic analysis for *Panthera*. Those segments without accession numbers are referenced by their publication date and primary author.

12S	16S	ND1	ND2	ND5		CytB	
Y08505	AF006457	Johnson06	AY170043	AF006458	AY035271	AF384817	AF053043
S79300	EF152489	EF551002	AY634386	AF385614	AY035270	AF384810	AF053045
EF551002	EF551002	Johnson06	Johnson06	AF385613	AY035269	AF384811	AF053053
AM779888	AF006443	EF551003	AY634383	Johnson06	AY035268	AF384815	AF053054
D28895	AY452108	AY736683	EF551002	EF551002	AY035267	AF053052	AB211408
D28896	EU223367	AY736680	Johnson06	AF006444	AY035266	AY928670	AB211410
EF199741	EF202838	AY736679	Johnson06	EF056501	AY035265	AF384809	EF437588
Jancz95	DQ530062	AY736672	AY634384	AY035292	AY035264	EF437586	Jancz95
EF551003	DQ530061	Johnson06	EF551003	AY035291	AY035263	Jancz95	(Sumatran)
DQ151550	DQ904386	Johnson06	DQ151550	AY035290	AY035262	EF056505	Jancz95
DQ151551	DQ904387	EF551004	DQ151551	AY035289	AY035261	EF056507	Jancz95
Y08504	DQ151550	Johnson06	AY750645	AY035288	AY035260	EF056506	(Siberian)
Jancz95	DQ151551	DQ257669	AY634391	AY035287	Johnson06	AB211401	EF437582
D28898	EF551003	Johnson06	Johnson06	AY035286	EF551003	AB211402	Jancz95
AY736559	AF006459	ND4	DQ257669	AY035285	AF006460	AB211407	EF437584
AY736562	AY452103		AY634385	AY035284	DQ111951	EF551002	EF551004
AY736564	AY452104		Johnson06	AY035283	DQ111950	EF437590	EU872072
AY736566	AY452105		AY634382	AY035282	Johnson06	Jancz95	Jancz95
AY736569	AY452106		EF551004	AY035281	AF006442	Jancz95	Johnson06
EF392685	AY452107		AY750646	AY035280	Johnson06	(Sri Lankan)	DQ257669
FM179470	AY452109		Johnson06	AY035279	EF551004	Johnson06	AJ304497
FM179471	AY452110			AY035278	AF006450	EF551003	AY499337
AY012151	EF392683			AY035277	EU872075	DQ151551	EF434734
AF416456	EF394928			AY035276	Johnson06	AF053042	EF434735
Jancz95	AF006441	AY634403	<div> <div>Lion</div> <div>Leopard</div> <div>Tiger</div> </div> <div> <div>Jaguar</div> <div>Snow Leopard</div> <div>Clouded Leopard</div> </div>		AF006426	AF053039	EF434737
EF551004	AY011185	Johnson06			DQ257669	AF053031	EF437578
D28897	AF006449	AY634394			Johnson06	AF053037	EF437579
Jancz95	EF551004	EF551004				AF053038	EF437575
DQ257669	EU144038	Johnson06				AF053051	EF437580
AY499283	DQ257669	DQ257669				AF053018	EF437576
Jancz95	AF006425	AY634397				AF053024	EF437577
	AY499301	Johnson06				AF053049	Jancz95
							Johnson06

Supplemental Table 2. List of accession numbers for gene segments used in maximum likelihood mitochondrial analyses. Accession numbers not listed in GenBank are referenced by primary author and publication year. Some sequences were manually entered from within the body text of the Janczewski (1995) study and are denoted 'Jancz95'.

Gene	Model	Maximum Likelihood Parameters
12S	[TrN+I]	Base=(0.3551 0.2384 0.1814) Nst=6 Rmat=(1.0000 31.0720 1.0000 1.0000 93.6756) Rates=equal Pinvar=0.8251
16S	[TIM+I]	Base=(0.3267 0.2209 0.2079) Nst=6 Rmat=(1.0000 37422698496.0 3924018688.0 3924018688.0 83880468480.0) Rates=equal Pinvar=0.7875
CYTB	[HKY+G]	Base=(0.2806 0.3057 0.1449) Nst=2 Tratio=18.6128 Rates=gamma Shape=0.2048 Pinvar=0
ND1	[HKY+G]	Base=(0.3176 0.3059 0.1089) Nst=2 Tratio=26.8145 Rates=gamma Shape=0.1514 Pinvar=0
ND2	[HKY+G]	Base=(0.3604 0.2955 0.0986) Nst=2 Tratio=21.2496 Rates=gamma Shape=0.1200 Pinvar=0
ND4	[K81uf+I]	Base=(0.3135 0.2901 0.1262) Nst=6 Rmat=(1.0000 29.7662 0.0001 0.0001 29.7662) Rates=equal Pinvar=0.6346
ND5	[HKY+G]	Base=(0.3142 0.2664 0.1282) Nst=2 Tratio=28.1177 Rates=gamma Shape=0.2455 Pinvar=0
DDX3Y	[HKY]	Base=(0.3095 0.1776 0.1739) Nst=2 Tratio=3.8930 Rates=equal Pinvar=0
EIF1AY	[TVM]	Base=(0.3290 0.1462 0.1540) Nst=6 Rmat=(0.0001 3.5554 0.2311 6.3969 3.5554) Rates=equal Pinvar=0
EIF2S3Y	[F81]	Base=(0.4137 0.1419 0.1274) Nst=1 Rates=equal Pinvar=0
SMCY	[HKY+I]	Base=(0.2839 0.1902 0.2261) Nst=2 Tratio=1.8734 Rates=equal Pinvar=0.8532
UBE1Y	[GTR]	Base=(0.2795 0.2242 0.1601) Nst=6 Rmat=(0.0000 7.2080 0.0000 2.9950 2.8408) Rates=equal Pinvar=0
USP9Y	[TVM+I]	Base=(0.3336 0.1595 0.1506) Nst=6 Rmat=(0.3694 2.1284 0.3171 1.6664 2.1284) Rates=equal Pinvar=0.7748
UTY	[HKY]	Base=(0.3777 0.1642 0.1372) Nst=2 Tratio=1.4398 Rates=equal Pinvar=0
SRY	[HKY+I]	Base=(0.2948 0.1852 0.2241) Nst=2 Tratio=2.1110 Rates=equal Pinvar=0.9198
ZFY	[HKY]	Base=(0.3266 0.1314 0.1770) Nst=2 Tratio=1.4370 Rates=equal Pinvar=0
FGB	[TVM+I]	Base=(0.2810 0.2031 0.1937) Nst=6 Rmat=(9.6652 14.3298 1.4122 5.3107 14.3298) Rates=equal Pinvar=0.8613
IRBP	[HKY]	Base=(0.1841 0.3147 0.3194) Nst=2 Tratio=3.3512 Rates=equal Pinvar=0
APP	[F81]	Base=(0.2658 0.2023 0.1776) Nst=1 Rates=equal Pinvar=0
CALB	[HKY]	Base=(0.3434 0.1676 0.1856) Nst=2 Tratio=45986922104900543000000000000000000.0000 Rates=equal Pinvar=0
CHRNA	[K80]	Base=equal Nst=2 Tratio=2.0093 Rates=equal Pinvar=0
CLU	[TIMef+I]	Base=equal Nst=6 Rmat=(1.0000 2.0046 0.0000 0.0000 6.1725) Rates=equal Pinvar=0.9214
CMA	[HKY+I]	Base=(0.2468 0.3137 0.1832) Nst=2 Tratio=3.6432 Rates=equal Pinvar=0.9074
DGKG2	[K81uf+I]	Base=(0.2600 0.2224 0.2104) Nst=6 Rmat=(1.0000 1.7658 0.1048 0.1048 1.7658) Rates=equal Pinvar=0.9370
FES	[K81uf+I]	Base=(0.1851 0.2730 0.3349) Nst=6 Rmat=(1.0000 1.3745 0.3449 0.3449 1.3745) Rates=equal Pinvar=0.9038
GATA	[K8luf]	Base=(0.3163 0.1838 0.2507) Nst=6 Rmat=(1.0000 1.4486 0.0000 0.0000 1.4486) Rates=equal Pinvar=0
GHR	[HKY]	Base=(0.3199 0.1935 0.1860) Nst=2 Tratio=4.0249 Rates=equal Pinvar=0
GNAZ	[HKY+I]	Base=(0.2224 0.3260 0.2809) Nst=2 Tratio=7.0577 Rates=equal Pinvar=0.9760
GNB	[HKY]	Base=(0.1949 0.2579 0.2953) Nst=2 Tratio=4.3585 Rates=equal Pinvar=0
HK1	[K8luf]	Base=(0.1878 0.2472 0.3015) Nst=6 Rmat=(1.0000 4.1561 0.0000 0.0000 4.1561) Rates=equal Pinvar=0
NCL	[HKY+I]	Base=(0.3041 0.1614 0.2277) Nst=2 Tratio=4.3783 Rates=equal Pinvar=0.9449
PNOC	[F81]	Base=(0.1442 0.3025 0.3059) Nst=1 Rates=equal Pinvar=0
RAG2	[HKY]	Base=(0.2684 0.1989 0.2325) Nst=2 Tratio=3.0117 Rates=equal Pinvar=0
RASA	[F81]	Base=(0.3330 0.1418 0.1904) Nst=1 Rates=equal Pinvar=0
SILV	[JC]	Base=equal Nst=1 Rates=equal Pinvar=0
TCP	[K8luf]	Base=(0.1833 0.2594 0.2732) Nst=6 Rmat=(1.0000 2.0302 0.0000 0.0000 2.0302) Rates=equal Pinvar=0
TTR	[K8luf]	Base=(0.2822 0.2128 0.1963) Nst=6 Rmat=(1.0000 2.5003 0.0000 0.0000 2.5003) Rates=equal Pinvar=0
CES7	[HKY+I]	Base=(0.2157 0.2583 0.2720) Nst=2 Tratio=2.5185 Rates=equal Pinvar=0.8856 clock=no
ALAS	[K80]	Base=equal Nst=2 Tratio=6.0296 Rates=equal Pinvar=0
ATP7A	[HKY]	Base=(0.2680 0.1873 0.2039) Nst=2 Tratio=5.0100 Rates=equal Pinvar=0
IL2RG	[JC]	Base=equal Nst=1 Rates=equal Pinvar=0
PLP	[HKY]	Base=(0.2209 0.2387 0.2265) Nst=2 Tratio=3.0163 Rates=equal Pinvar=0
ZFX	[HKY]	Base=(0.2969 0.1668 0.2207) Nst=2 Tratio=2.2587 Rates=equal Pinvar=0
Y Chromosome	[TVM+I]	Base=(0.3198 0.1725 0.1767) Nst=6 Rmat=(0.4527 2.7629 0.4131 1.6506 2.7629) Rates=equal Pinvar=0.7683
Mitochondrial	[TrN+I+G]	Base=(0.3233 0.2824 0.1345) Nst=6 Rmat=(1.0000 40.8743 1.0000 1.0000 48.8259) Rates=gamma Shape=0.3345 Pinvar=0.3018
Autosomal	[K81uf+I]	Base=(0.2457 0.2391 0.2479) Nst=6 Rmat=(1.0000 4.1593 0.6009 0.6009 4.1593) Rates=equal Pinvar=0.9371
Mitochondria + Y	[GTR+I+G]	Base=(0.3128 0.1996 0.1773) Nst=6 Rmat=(0.9048 10.2746 0.5547 1.4171 18.0246) Rates=gamma Shape=0.6017 Pinvar=0.8208
Nuclear	[TVM+I]	Base=(0.2938 0.1948 0.2010) Nst=6 Rmat=(0.5782 2.9995 0.3573 1.0300 2.9995) Rates=equal Pinvar=0.9045
Supermatrix	[GTR+I+G]	Base=(0.2868 0.2147 0.2018) Nst=6 Rmat=(0.8165 8.4354 0.4809 0.8814 13.7819) Rates=gamma Shape=0.4110 Pinvar=0.8078
Supplemental Table 3. Maximum likelihood model parameters specified by Modeltest v3.4		

Gene	Model	Bayesian Parameters		
DDX3Y	[HKY]	nst=2	rates=equal;	statefreqpr=dirichlet(1,1,1,1);
EIF1AY	[GTR]	nst=6	rates=equal;	statefreqpr=dirichlet(1,1,1,1);
EIF2S3Y	[F81]	nst=1	rates=equal;	statefreqpr=dirichlet(1,1,1,1);
SMCY	[HKY+I]	nst=2	rates=propinv;	statefreqpr=dirichlet(1,1,1,1);
UBE1Y	[GTR+I]	nst=6	rates=propinv;	statefreqpr=dirichlet(1,1,1,1);
USP9Y	[GTR]	nst=6	rates=equal;	statefreqpr=dirichlet(1,1,1,1);
UTY	[HKY]	nst=2	rates=equal;	statefreqpr=dirichlet(1,1,1,1);
SRY	[HKY+I]	nst=2	rates=propinv;	statefreqpr=dirichlet(1,1,1,1);
ZFY	[HKY]	nst=2	rates=equal;	statefreqpr=dirichlet(1,1,1,1);
FGB	[GTR+I]	nst=6	rates=propinv;	statefreqpr=dirichlet(1,1,1,1);
IRBP	[HKY]	nst=2	rates=equal;	statefreqpr=dirichlet(1,1,1,1);
APP	[F81]	nst=1	rates=equal;	statefreqpr=dirichlet(1,1,1,1);
CALB	[HKY]	nst=2	rates=equal;	statefreqpr=dirichlet(1,1,1,1);
CHRNA	[K80]	nst=2	rates=equal;	statefreqpr=fixed(equal);
CLU	[K80]	nst=2	rates=equal;	statefreqpr=fixed(equal);
CMA	[HKY+I]	nst=2	rates=propinv;	statefreqpr=dirichlet(1,1,1,1);
DGKG2	[HKY+G]	nst=2	rates=gamma;	statefreqpr=dirichlet(1,1,1,1);
FES	[HKY+I]	nst=2	rates=propinv;	statefreqpr=dirichlet(1,1,1,1);
GATA	[F81]	nst=1	rates=equal;	statefreqpr=dirichlet(1,1,1,1);
GHR	[HKY]	nst=2	rates=equal;	statefreqpr=dirichlet(1,1,1,1);
GNAZ	[HKY+I]	nst=2	rates=propinv;	statefreqpr=dirichlet(1,1,1,1);
GNB	[HKY]	nst=2	rates=equal;	statefreqpr=dirichlet(1,1,1,1);
HK1	[HKY]	nst=2	rates=equal;	statefreqpr=dirichlet(1,1,1,1);
NCL	[HKY+I]	nst=2	rates=propinv;	statefreqpr=dirichlet(1,1,1,1);
PNOC	[HKY]	nst=2	rates=equal;	statefreqpr=dirichlet(1,1,1,1);
RAG2	[HKY]	nst=2	rates=equal;	statefreqpr=dirichlet(1,1,1,1);
RASA	[F81]	nst=1	rates=equal;	statefreqpr=dirichlet(1,1,1,1);
SILV	[JC]	nst=1	rates=equal;	statefreqpr=fixed(equal);
TCP	[F81]	nst=1	rates=equal;	statefreqpr=dirichlet(1,1,1,1);
TTR	[HKY]	nst=2	rates=equal;	statefreqpr=dirichlet(1,1,1,1);
CES7	[HKY+I]	nst=2	rates=propinv;	statefreqpr=dirichlet(1,1,1,1);
ALAS	[K80]	nst=2	rates=equal;	statefreqpr=fixed(equal);
ATP7A	[HKY]	nst=2	rates=equal;	statefreqpr=dirichlet(1,1,1,1);
IL2RG	[JC]	nst=1	rates=equal;	statefreqpr=fixed(equal);
PLP	[HKY]	nst=2	rates=equal;	statefreqpr=dirichlet(1,1,1,1);
ZFX	[HKY]	nst=2	rates=equal;	statefreqpr=dirichlet(1,1,1,1);
12S	[GTR+I+G]	nst=6	rates=invgamma;	statefreqpr=dirichlet(1,1,1,1);
16S	[HKY+I]	nst=2	rates=propinv;	statefreqpr=dirichlet(1,1,1,1);
CYTB	[HKY+G]	nst=2	rates=gamma;	statefreqpr=dirichlet(1,1,1,1);
ND1	[HKY+G]	nst=2	rates=gamma;	statefreqpr=dirichlet(1,1,1,1);
ND2	[HKY+G]	nst=2	rates=gamma;	statefreqpr=dirichlet(1,1,1,1);
ND4	[GTR+I]	nst=6	rates=propinv;	statefreqpr=dirichlet(1,1,1,1);
ND5	[HKY+G]	nst=2	rates=gamma;	statefreqpr=dirichlet(1,1,1,1);
Y Chromosome	[GTR+I]	nst=6	rates=propinv;	statefreqpr=dirichlet(1,1,1,1);
Autosomes	[GTR+I]	nst=6	rates=propinv;	statefreqpr=dirichlet(1,1,1,1);
X Chromosome	[HKY]	nst=2	rates=equal;	statefreqpr=dirichlet(1,1,1,1);
Mitochondria	[HKY+G]	nst=2	rates=gamma;	statefreqpr=dirichlet(1,1,1,1);
Nuclear	[GTR+I]	nst=6	rates=propinv;	statefreqpr=dirichlet(1,1,1,1);
Uniparental	[GTR+I]	nst=6	rates=propinv;	statefreqpr=dirichlet(1,1,1,1);
Supplemental Table 4. Bayesian model parameters specified by MrModeltest v2				

	CI	RI	HI	RCI
Autosomes	0.6287	0.5118	0.3713	0.4465
Y Chromosome	0.9838	0.8889	0.1364	0.8745
Mitochondria	0.5565	0.3238	0.4435	0.2478
Total	0.5661	0.3624	0.4339	0.2930
Supplemental Table 5. Consistency Index (CI) Retention Index (RI), Homoplasy Index (HI) and Rescaled Consistency Index (RCI) values for the autosomal, Y chromosome, and mitochondrial partitions, as well as the complete matrix.				

	Johnson Leopard											
Yu Leopard	0.007	Yu Leopard										
Johnson Lion	0.089	0.087	Johnson Lion									
Yu Lion	0.104	0.096	0.091	Yu Lion								
Johnson Jaguar	0.099	0.097	0.089	0.105	Johnson Jaguar							
Yu Jaguar	0.101	0.094	0.092	0.102	0.003	Yu Jaguar						
Johnson Tiger	0.129	0.127	0.124	0.126	0.117	0.12	Johnson Tiger					
Yu Tiger	0.126	0.117	0.125	0.116	0.116	0.113	0.009	Yu Tiger				
Johnson Snow L.	0.093	0.091	0.088	0.01	0.097	0.1	0.118	0.115	Johnson Snow L.			
Yu Snow L.	0.106	0.098	0.093	0.116	0.084	0.081	0.126	0.116	0.118	Yu Snow L.		
Johnson Clouded	0.159	0.157	0.155	0.169	0.177	0.181	0.184	0.196	0.159	0.168	Johnson Clouded	
Yu Clouded	0.16	0.155	0.156	0.168	0.179	0.179	0.185	0.194	0.16	0.166	0.005	

Supplemental Table 6. LogDet pairwise distances between published Johnson et al. (2006) and Yu and Zhang (2005) sequences for the *ND2* gene for all species.

	A	C	G	T
12S	0.3575	0.2360	0.1815	0.2250
16S	0.3280	0.2240	0.2066	0.2414
CYTB	0.2878	0.2970	0.1400	0.2752
ND1	0.3165	0.3457	0.0878	0.2500
ND2	0.3602	0.2938	0.0981	0.2479
ND4	0.3140	0.2894	0.1245	0.2722
ND5	0.3119	0.2669	0.1233	0.2980
Average	0.3251	0.2790	0.1374	0.2585
Supplemental Table 7. Base frequencies for each segment of the final mitochondrial matrix show a distinct anti-G bias, indicating true mitochondrial sequence.				

Partition	Sequence Length	# Partitions	P-value
Supermatrix	47,628 bp	4	P = 0.001*
Supermatrix	47,628 bp	29	P = 0.346
Supermatrix	47,628 bp	43	P = 0.981
Autosomes	19,124 bp	22	P = 0.002*
Y Chromosome	19,140 bp	9	P = 1.000
X Chromosome	3,223 bp	5	P = 1.000
Mitochondria	6,141 bp	7	P = 0.893
Uniparental	25,281 bp	16	P = 0.936
Nuclear	41,487 bp	36	P = 0.008*
Mitochondria + X	9,364 bp	12	P = 0.999
Mitochondria + Autosomes	25,265 bp	29	P = 0.955
Autosomes + Y	38,264 bp	31	P = 0.001*
Autosomes + X	22,347 bp	27	P = 0.016
Chromosomes X + Y	22,363 bp	14	P = 0.780
Mitochondria + X + Y	28,504 bp	21	P = 0.998
Mitochondria + Autosomes + Y	44,405 bp	28	P = 0.907
Mitochondria + Autosomes + X	28,488 bp	34	P = 0.998
Supplemental Table 8. Partition homogeneity results ($\alpha=0.01$). Supermatrix dataset is internally incompatible when partitioned into the four genomic regions. Incongruence is seen for the autosomal, autosomal + Y and nuclear partitions. The autosomal + X partition was very close to statistical incongruence.			

	Y	Autosomes	X	Mitochondria	Supermatrix	Total # PI sites
Chromosome			Chromosome			
(Lion-Leopard) (Jaguar-Tiger-Snow)	2.99%	14.94%	0.00%	11.16%	11.13%	118
(Tiger-Snow) (Lion-Leopard-Jaguar)	88.06%	36.36%	33.33%	10.68%	19.43%	206
(Lion-Jaguar) (Leopard-Tiger-Snow)	1.49%	11.69%	66.67%	5.64%	6.60%	70
(Leopard-Tiger) (Lion-Jaguar-Snow)	0.00%	9.09%	0.00%	8.52%	8.02%	85
(Leopard-Jaguar) (Lion-Tiger-Snow)	0.00%	5.84%	0.00%	6.48%	5.94%	63
(Jaguar-Snow) (Lion-Leopard-Tiger)	0.00%	5.19%	0.00%	10.32%	8.87%	94
(Lion-Tiger) (Leopard-Jaguar-Snow)	0.00%	2.60%	0.00%	5.28%	4.53%	48
(Leopard-Snow) (Lion-Tiger-Jaguar)	0.00%	2.60%	0.00%	6.60%	5.57%	59
(Tiger-Jaguar) (Lion-Leopard-Snow)	0.00%	0.00%	0.00%	8.88%	0.00%	106
(Lion-Snow) (Leopard-Tiger-Jaguar)	0.00%	0.00%	0.00%	2.52%	0.00%	42

Supplemental Table 9. Percentage of phylogenetically informative sites within each partition supporting each species relationship. Monophyly supported by the final tree topology in this study is highlighted in green. The topology from Johnson et al. 2006 is in orange.

Gene	ALAS 513	ATP7A 670	IL2RG 318	PLP 899	ZFX 823	12S 964	16S 376	CYTB 1140	ND1 548	ND2 1038	ND4 1368	ND5 707
Length												
% Total Length	1.08%	1.41%	0.67%	1.89%	1.73%	2.02%	0.79%	2.39%	1.15%	2.18%	2.87%	1.48%
% Partition Length	15.92%	20.79%	9.87%	27.89%	25.54%	15.70%	6.12%	18.57%	8.93%	16.91%	22.28%	11.51%
% Informative Sites (Total)	0.00%	0.00%	0.00%	0.16%	0.31%	5.15%	2.03%	18.41%	6.71%	12.95%	22.62%	11.39%
% Informative Sites (Partition)	0.00%	0.00%	0.00%	33.33%	66.67%	6.50%	2.56%	23.23%	8.46%	16.34%	28.54%	14.37%
% Total Sites / % Seq Length	0.00	0.00	0.00	0.08	0.18	2.54	2.57	7.69	5.83	5.94	7.88	7.67
% Partition Sites / % Seq Length	0.00	0.00	0.00	1.20	2.61	0.41	0.42	1.25	0.95	0.97	1.28	1.25
(Lion, Leopard)						5	1	12	3	4	20	4
(Jaguar, Tiger, Snow)						5	1	10	3	3	19	3
(Tiger, Snow)				1		5	2	7	2	12	13	5
(Lion, Leopard, Jaguar)				1		4	2	7	2	10	13	5
(Lion, Jaguar)					2	1	1	7	1	4	5	4
(Leopard, Tiger, Snow)					2							
(Leopard, Tiger)						2	1	9	5	11	9	3
(Lion, Jaguar, Snow)						1	1	9	5	3	9	3
(Leopard, Jaguar)						1	1	9	2	2	9	5
(Lion, Tiger, Snow)						1	1	8	2		8	5
(Jaguar, Snow)						2		6	2	13	15	9
(Lion, Leopard, Tiger)						2		6	2	6	15	8
(Lion, Tiger)						1		7	1	2	6	3
(Leopard, Jaguar, Snow)						1		7	1	6	6	3
(Leopard, Snow)						2	1	12	1	4	6	2
(Lion, Tiger, Jaguar)						2	2	12	1	2	6	2
(Lion, Leopard, Tiger, Jaguar)								7		8	11	6
(Lion, Leopard, Tiger, Snow)							1	10	2	1	6	6
(Lion, Leopard, Jaguar, Snow)						5	1	7	7	7	16	1
(Leopard, Tiger, Jaguar, Snow)						1		5	2	3	3	5
(Lion, Tiger, Jaguar, Snow)						2	1	5	1	5	9	2
(Tiger-Jaguar)						3		14	6	8	11	11
(Lion, Leopard, Snow)						3	2	13	6	6	11	12
Lion-Snow						3		6	5	4	3	
(Leopard-Tiger-Jaguar)						3		5	5	6	2	

Supplemental Table 10. Phylogenetically informative sites for each species relationship within each gene segment for the X chromosome and mitochondrial partitions.

Gene	DDX3Y	EIF1AY	EIF2S3Y	SMCY	UBE1Y	USP9Y	UTY	SRY	ZFY
Length	1428	1314	817	3793	977	6135	1575	2371	730
% Total Length	3.00%	2.76%	1.72%	7.96%	2.05%	12.88%	3.31%	4.98%	1.53%
% Partition Length	7.46%	6.87%	4.27%	19.82%	5.10%	32.05%	8.23%	12.39%	3.81%
% Informative Sites (Total)	0.47%	0.16%	0.00%	0.78%	0.78%	2.18%	0.78%	0.47%	0.00%
% Informative Sites (Partition)	8.33%	2.78%	0.00%	13.89%	13.89%	38.89%	13.89%	8.33%	0.00%
% Total Sites / % Seq Length	0.16	0.06	0.00	0.10	0.38	0.17	0.24	0.09	0.00
% Partiton Sites / % Seq Length	1.12	0.40	0.00	0.70	2.72	1.21	1.69	0.67	0.00
(Lion, Leopard)				1					
(Jaguar, Tiger, Snow)				1					
(Tiger, Snow)	2	1		3	3	14	5	2	
(Lion, Leopard, Jaguar)	2	1		3	3	13	5	2	
(Lion, Jaguar)									
(Leopard, Tiger, Snow)								1	
(Leopard, Tiger)									
(Lion, Jaguar, Snow)									
(Leopard, Jaguar)									
(Lion, Tiger, Snow)									
(Jaguar, Snow)									
(Lion, Leopard, Tiger)									
(Lion, Tiger)									
(Leopard, Jaguar, Snow)									
(Leopard, Snow)									
(Lion, Tiger, Jaguar)	1								
(Lion, Leopard, Tiger, Jaguar)					1				
(Lion, Leopard, Tiger Snow)				1					
(Lion, Leopard, Jaguar, Snow)					1				
(Leopard, Tiger, Jaguar, Snow)						1			
(Lion, Tiger, Jaguar, Snow)									
(Tiger-Jaguar)									
(Lion, Leopard, Snow)									
Lion-Snow									
(Leopard-Tiger-Jaguar)									

Supplemental Table 11. Phylogenetically informative sites for each species relationship within each gene segment for the Y chromosome.

Gene Length	FGB 678	IRBP 1254	APP 642	CALB 817	CHRNA 326	CLU 1369	CMA 518	DGKG2 710	FES 413	GATA 457	GHR 670
% Total Length	1.42%	2.63%	1.35%	1.72%	0.68%	2.87%	1.09%	1.49%	0.87%	0.96%	1.41%
% Partition Length	3.54%	6.55%	3.35%	4.26%	1.70%	7.15%	2.70%	3.71%	2.16%	2.39%	3.50%
% Informative Sites (Total)	1.72%	0.31%	0.16%	0.16%	0.16%	0.62%	0.47%	1.09%	0.47%	0.16%	0.16%
% Informative Sites (Partition)	11.70%	2.13%	1.06%	1.06%	1.06%	4.26%	3.19%	7.45%	3.19%	1.06%	1.06%
% Total Sites / % Seq Length	1.21	0.12	0.12	0.09	0.23	0.22	0.43	0.73	0.54	0.16	0.11
% Partiton Sites / % Seq Length	3.31	0.33	0.32	0.25	0.63	0.60	1.18	2.01	1.48	0.45	0.30
(Lion, Leopard)		1		1			1				
(Jaguar, Tiger, Snow)				1			1				
(Tiger, Snow)	2					1		1			
(Lion, Leopard, Jaguar)	2					1		1			
(Lion, Jaguar)	1		1			2		1	1		
(Leopard, Tiger, Snow)	1		1			2		1	1		
(Leopard, Tiger)	1				1			4	1		
(Lion, Jaguar, Snow)								4	1		
(Leopard, Jaguar)					1				1		
(Lion, Tiger, Snow)						1			1		
(Jaguar, Snow)											
(Lion, Leopard, Tiger)							1	1			
(Lion, Tiger)							1	1			
(Leopard, Jaguar, Snow)											
(Leopard, Snow)											
(Lion, Tiger, Jaguar)											
(Lion, Leopard, Tiger, Jaguar)		1								1	
(Lion, Leopard, Tiger, Snow)							1				1
(Lion, Leopard, Jaguar, Snow)											
(Leopard, Tiger, Jaguar, Snow)	1										
(Lion, Tiger, Jaguar, Snow)											
(Tiger-Jaguar)											
(Lion, Leopard, Snow)											
Lion-Snow											
(Leopard-Tiger-Jaguar)											

Supplemental Table 12. Phylogenetically informative sites for each species relationship within each gene segment for the autosomes.

Gene Length	GNAZ 622	GNB 674	HK1 350	NCL 297	PNOC 290	RAG2 473	RASA 551	SILV 371	TCP 596	TTR 885	CES7 6161
% Total Length	1.31%	1.42%	0.73%	0.62%	0.61%	0.99%	1.16%	0.78%	1.25%	1.86%	12.94%
% Partition Length	3.25%	3.52%	1.83%	1.55%	1.51%	2.47%	2.88%	1.94%	3.11%	4.62%	32.16%
% Informative Sites (Total)	0.00%	0.47%	0.47%	0.62%	0.16%	0.00%	0.00%	0.16%	0.00%	1.56%	5.77%
% Informative Sites (Partition)	0.00%	3.19%	3.19%	4.26%	1.06%	0.00%	0.00%	1.06%	0.00%	10.64%	39.36%
% Total Sites / % Seq Length	0.00	0.33	0.64	1.00	0.26	0.00	0.00	0.20	0.00	0.84	0.45
% Partiton Sites / % Seq Length	0.00	0.91	1.75	2.74	0.70	0.00	0.00	0.55	0.00	2.30	1.22
(Lion, Leopard)		1									8
(Jaguar, Tiger, Snow)		1									8
(Tiger, Snow)		1		1				1		10	12
(Lion, Leopard, Jaguar)		1						1		10	12
(Lion, Jaguar)			1								2
(Leopard, Tiger, Snow)			1								2
(Leopard, Tiger)				1							
(Lion, Jaguar, Snow)				1							
(Leopard, Jaguar)				1							2
(Lion, Tiger, Snow)											2
(Jaguar, Snow)				2							
(Lion, Leopard, Tiger)				2							
(Lion, Tiger)											
(Leopard, Jaguar, Snow)											2
(Leopard, Snow)											2
(Lion, Tiger, Jaguar)											2
(Lion, Leopard, Tiger, Jaguar)	1		2		1						2
(Lion, Leopard, Tiger Snow)											2
(Lion, Leopard, Jaguar, Snow)											3
(Leopard, Tiger, Jaguar, Snow)											1
(Lion, Tiger, Jaguar, Snow)											1
(Tiger-Jaguar)											
(Lion, Leopard, Snow)											
Lion-Snow											
(Leopard-Tiger-Jaguar)											

Supplemental Table 12. Continued

	Y				X		
	Supermatrix	Chromosome	Autosomal	Mitochondrial	Chromosome	Uniparental	Nuclear
Supermatrix		1.0000	0.5411	0.2948	0.1210	1.0000	1.0000
Y							
Chromosome	1.0000		0.5411	0.2948	0.1210	1.0000	1.0000
Autosomal	1.0000	1.0000		0.2948	0.1210	1.0000	1.0000
Mitochondrial	0.3169	0.1067	0.2485		0.0880	0.6023	0.0776
X							
Chromosome	0.0001	0.0132	0.0574	0.0090		0.0010	0.0073
Uniparental	1.0000	1.0000	0.5411	0.2948	0.1210		1.0000
Nuclear	1.0000	1.0000	0.5411	0.2948	0.1210	1.0000	

Supplemental Table 13. Results of the Shimodaira-Hasegawa test. Significant topological differences ($\alpha=0.05$) between partitions indicated in yellow. The maximum likelihood topology used is listed in the vertical column with the compared maximum likelihood topology in the horizontal row.

Supermatrix					
	(Lion-Leopard-Jaguar) (Tiger-Snow-Clouded)	Lion-Leopard	Tiger-Snow	Tiger-Clouded	Lion-Jaguar
ALL	100.0	99.9	93.7	6.0	0.0
DDX3Y	100.0	99.9	92.3	7.5	0.0
EIF1AY	100.0	99.7	92.2	7.8	0.0
EIF2S3Y	100.0	99.0	93.0	7.0	0.0
SMCY	100.0	99.1	88.0	12.0	5.1
UBE1Y	100.0	99.8	95.7	0.0	0.0
USP9Y	100.0	99.5	84.0	15.8	0.0
UTY	100.0	99.9	85.9	13.9	0.0
SRY	100.0	99.9	92.9	6.9	0.0
ZFY	100.0	99.6	94.4	5.5	0.0
FGB	100.0	99.9	90.0	9.9	0.0
IRBP	100.0	93.3	99.6	6.7	0.0
APP	100.0	99.7	94.9	0.0	0.0
CALB	100.0	98.9	92.8	7.1	0.0
CES7	100.0	97.5	89.7	10.3	0.0
CHRNA	100.0	99.6	93.7	6.1	0.0
CLU	100.0	99.9	94.1	5.7	0.0
CMA	100.0	99.7	94.5	5.4	0.0
DGKG2	100.0	99.9	96.4	0.0	0.0
FES	100.0	99.4	92.2	7.6	0.0
GATA	100.0	99.9	93.8	6.0	0.0
GHR	100.0	99.7	93.2	6.8	0.0
GNAZ	100.0	99.6	94.2	5.5	0.0
GNB	100.0	99.6	93.8	6.2	0.0
HK1	100.0	99.7	94.5	5.4	0.0
NCL	100.0	99.6	93.8	6.2	0.0
PNOC	100.0	99.4	94.4	5.5	0.0
RAG2	100.0	99.6	92.8	7.0	0.0
RASA	100.0	99.5	92.3	7.6	0.0
SILV	100.0	99.6	92.7	7.2	0.0
TCP	100.0	99.9	92.2	7.6	0.0
TTR	100.0	99.8	83.7	15.4	0.0
ALAS	100.0	99.7	93.2	6.8	0.0
ATP7A	100.0	99.8	94.2	5.8	0.0
IL2RG	100.0	99.6	93.8	6.1	0.0
PLP	100.0	99.8	94.2	7.3	0.0
ZFX	100.0	99.7	93.5	6.4	0.0
12S	100.0	99.4	97.0	0.0	5.5
16S	100.0	99.9	94.1	5.9	0.0
CYTB	100.0	99.6	98.0	0.0	0.0
ND1	100.0	99.5	93.6	6.3	0.0
ND2	100.0	100.0	95.3	0.0	0.0
ND4	100.0	96.2	92.2	7.8	37.7
ND5	100.0	99.4	95.4	0.0	7.4

Supplemental Table 14. Gene jackknife bootstrap bipartition support for the complete supermatrix

Y Chromosome

	(Lion-Leopard-Jaguar) (Tiger-Snow-Clouded)	Lion-Leopard	Tiger-Snow
ALL	99.9	70.0	100.0
DDX3Y	100.0	68.5	99.9
EIF1AY	100.0	72.0	99.6
EIF2S3Y	100.0	71.2	100.0
SMCY	100.0	0.0	99.8
UBE1Y	99.9	72.5	100.0
USP9Y	99.4	77.3	97.3
UTY	99.9	75.0	99.7
SRY	100.0	75.4	99.9
ZFY	100.0	70.7	99.8

Supplemental Table 15. Gene jackknife bootstrap bipartition support for the Y chromosome partition

Autosomal					
	(Lion-Leopard-Jaguar) (Tiger-Snow-Clouded)	Lion-Leopard	Tiger-Snow	Lion-Jaguar	Snow-Clouded
ALL	99.8	66.6	93.4	33.4	6.1
FGB	100.0	83.7	96.3	16.3	0.0
IRBP	99.9	58.6	95.5	41.4	0.0
APP	100.0	76.3	95.5	23.7	0.0
CALB	99.8	58.2	92.5	41.8	7.4
CES7	90.3	5.1	69.5	94.9	30.0
CHRNA	99.9	69.7	95.3	30.3	0.0
CLU	99.9	73.8	93.4	26.1	6.5
CMA	99.7	56.2	95.8	43.8	0.0
DGKG2	100.0	80.4	95.4	19.6	0.0
FES	99.7	72.4	90.9	27.6	8.8
GATA	99.8	65.6	95.7	34.4	0.0
GHR	99.9	63.4	93.4	36.6	6.3
GNAZ	99.9	65.7	92.9	34.3	7.0
GNB	99.9	60.0	94.2	40.0	5.7
HK1	99.7	73.6	97.5	26.3	0.0
NCL	100.0	60.1	95.7	39.9	0.0
PNOC	99.8	67.8	95.1	32.2	0.0
RAG2	100.0	65.7	94.4	34.3	5.4
RASA	99.9	62.5	93.8	37.5	5.8
SILV	99.8	64.8	93.5	35.2	6.1
TCP	99.9	68.5	94.7	31.5	5.3
TTR	97.9	59.7	61.2	40.1	35.6
ALL	99.8	66.6	93.4	33.4	6.1

Supplemental Table 16. Gene jackknife bootstrap bipartition support for the autosomal partition

X Chromosome			
	(Tiger-Snow)	(Lion-Jaguar)	(Lion-Jaguar-Clouded)
ALL	64.3	61.1	66.0
ALAS	63.6	62.3	61.9
ATP7A	62.3	62.7	64.1
IL2RG	62.3	62.7	63.8
PLP	0.0	62.7	62.6
ZFX	63.1	0.0	0.0
ALL	64.3	61.1	66.0

Supplemental Table 17. Gene jackknife bootstrap bipartition support for the X chromosome partition

Mitochondria							
	(Lion-Leopard-Jaguar) (Tiger-Snow-Clouded)	Lion-Leopard	Tiger-Snow	Snow-Clouded	Jaguar-Snow	(Lion-Snow)	(Lion-Leopard-Snow) (Tiger-Jaguar-Clouded)
ALL	71.2	99.8	94.3	5.0	12.9	0.0	6.5
12S	65.4	99.3	85.9	12.7	10.1	0.0	6.2
16S	71.1	99.6	93.4	6.5	11.7	0.0	5.5
CYTB	72.4	99.9	88.8	10.4	18.0	0.0	0.0
ND1	76.2	99.9	93.9	5.7	8.6	0.0	0.0
ND2	68.2	100.0	87.2	11.9	7.6	0.0	14.8
ND4	16.3	70.1	90.5	0.0	23.6	21.7	33.2
ND5	81.3	99.7	93.6	5.8	8.5	0.0	0.0

Supplemental Table 18. Gene jackknife bootstrap bipartition support for the mitochondrial partition

Autosomal - NoCES7

	(Lion-Leopard-Jaguar) (Tiger-Snow-Clouded)	Lion-Leopard	Tiger-Snow	Lion-Jaguar	Snow-Clouded	Leopard-Tiger
ALL	90.3	5.1	69.5	94.9	30.0	8.9
FGB	84.0	19.1	66.0	78.3	33.9	14.4
IRBP	90.1	0.0	72.9	97.1	26.2	8.8
TTR	44.2	0.0	8.3	96.0	86.2	54.4
APP	90.6	9.9	69.9	89.1	30.0	8.2
CALB	87.0	0.0	64.4	96.8	35.4	11.4
CHRNA	90.5	6.9	66.6	92.0	33.0	8.6
CLU	90.2	10.4	60.5	88.3	39.2	9.1
CMA	91.2	0.0	75.6	97.3	23.5	7.9
DGKG2	96.9	12.6	72.7	86.8	27.2	0.0
FES	94.7	7.4	63.2	92.2	36.6	0.0
GATA	90.7	5.0	72.1	94.6	27.2	7.8
GHR	91.1	5.5	67.5	94.4	31.9	7.8
GNAZ	90.1	6.4	69.0	93.0	30.7	8.7
GNB	85.4	0.0	68.6	96.5	30.5	12.8
HK1	92.4	8.7	78.3	90.7	20.6	6.8
NCL	94.3	0.0	78.7	96.1	20.9	0.0
PNOC	90.9	6.0	74.1	93.7	25.4	7.9
RAG2	90.2	7.7	67.8	92.0	31.6	8.9
RASA	90.7	5.3	65.3	94.4	34.5	8.8
SILV	89.0	5.2	58.1	94.2	41.2	10.0
TCP	90.8	7.0	66.8	92.8	32.3	8.0

Supplemental Table 19. Gene jackknife bootstrap bipartition support for the autosomal partition without CES7

		-ln L	L_0-L_1	$2(L_0-L_1)$	P value (df=4)
Supermatrix	L_0	79776.83	344.004	688.01	0.00000
	L_1	80120.84			
Nuclear	L_0	61892.37	219.756	439.51	0.00000
	L_1	62112.13			
Uniparental	L_0	45148.36	299.84	599.68	0.00000
	L_1	45448.20			
Y	L_0	27591.79	198.425	396.85	0.00000
	L_1	27790.22			
X	L_0	4775.93	8.79662	17.593	0.00148
	L_1	4784.73			
Mitochondria	L_0	15818.45	139.333	278.67	0.00000
	L_1	15957.78			
Autosomal	L_0	29010.00	60.332	120.66	0.00000
	L_1	29070.33			
Supplemental Table 20. Molecular clock test results. L_0 is the unconstrained likelihood value and L_1 is the likelihood value when the topology is constrained using the molecular clock hypothesis.					

Species	Individual ID (San Diego Zoo)
<i>Panthera leo krugeri</i>	KB13712
<i>Panthera tigris</i>	OR602
<i>Panthera pardus</i>	KB13453
<i>Panthera uncia</i>	OR2735
<i>Neofelis nebulosa nebulosa</i>	OR1017
Supplemental Table 21. Species and unique individual identifier information for DNA samples used in analyses. All samples were obtained from Dr. Oliver Ryder of the San Diego Zoological Society/CRES.	