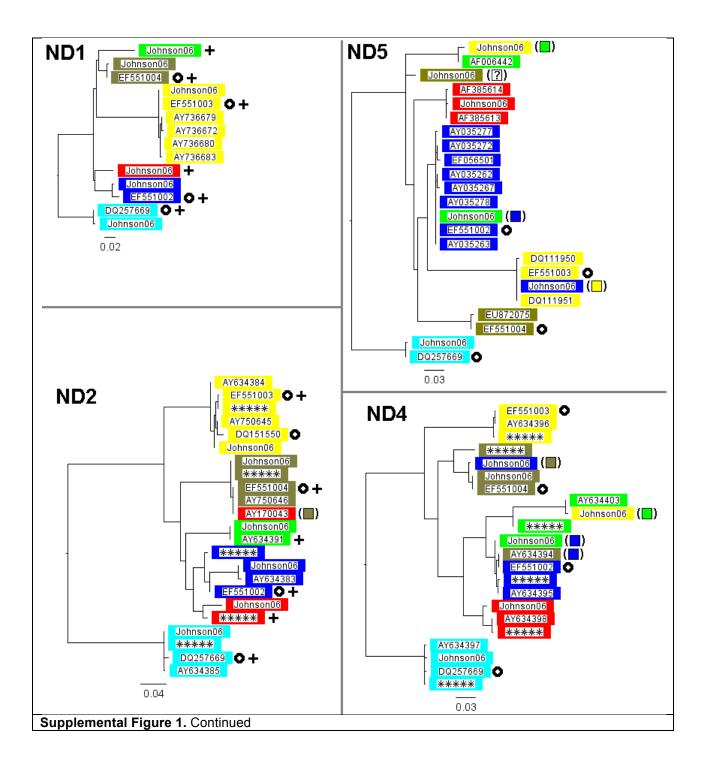
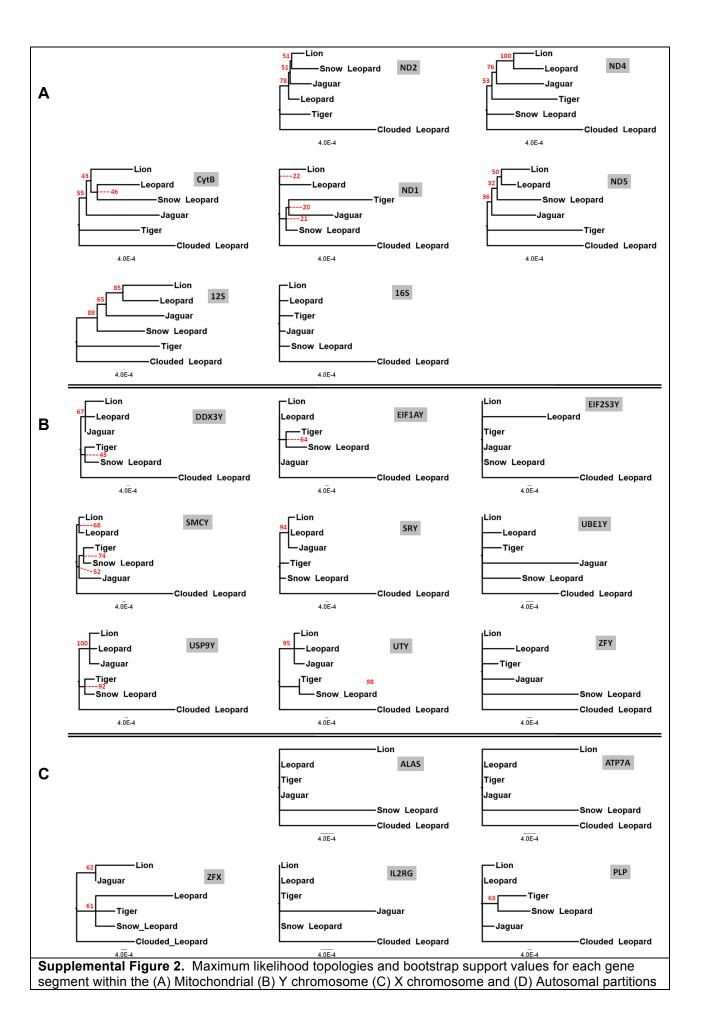
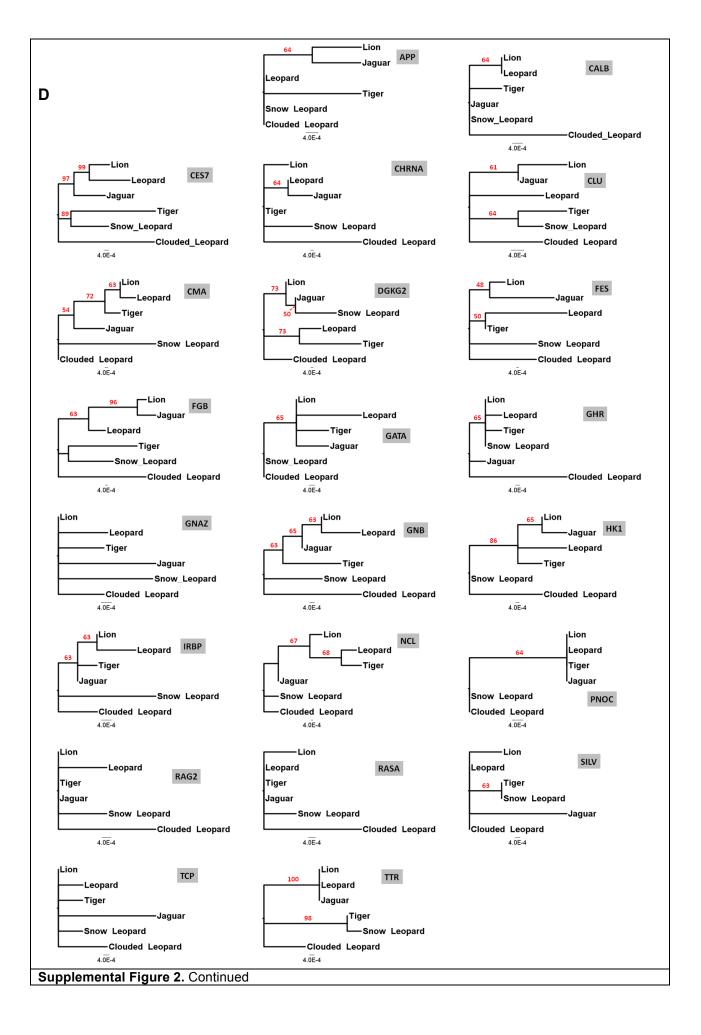
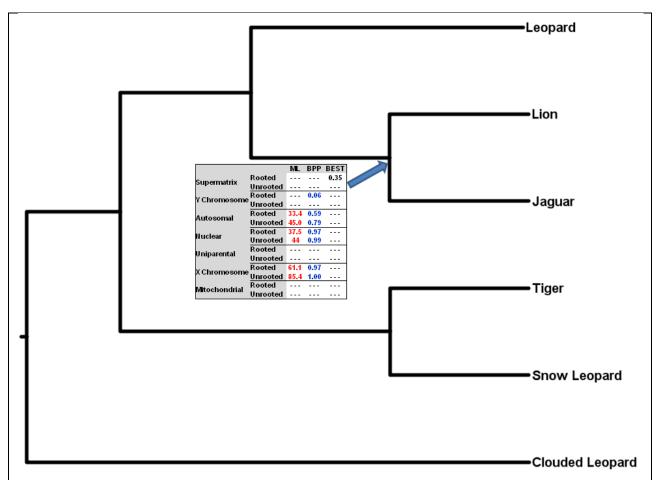


**Supplemental Figure 1.** Maximum likelihood clustering trees for all mitochondrial segments after the removal of all putative numt sequences.

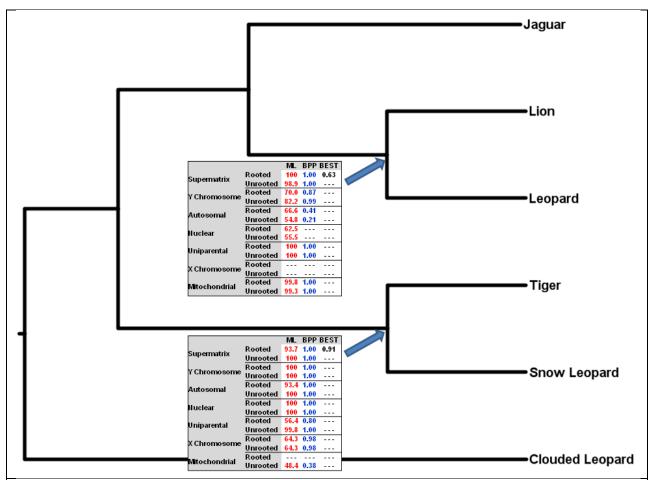




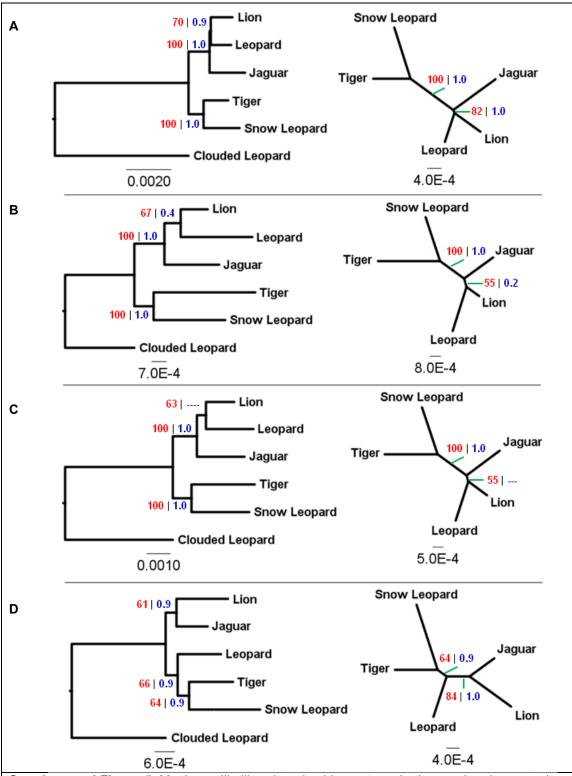




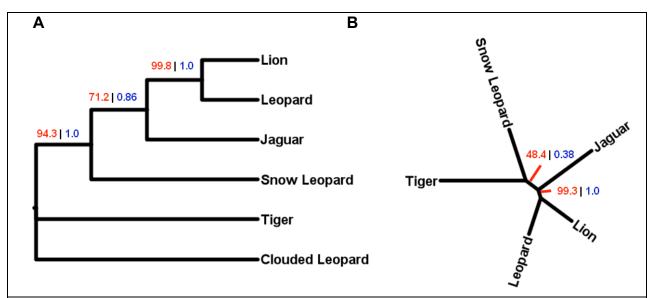
**Supplemental Figure 3.** Cladogram depicting phylogenetic topology for *Panthera* generated by Johnson et al. (2006). Maximum likelihood bootstrap values from this study (1000 replicates) shown in red; Bayesian posterior probabilities in blue; and BEST clade support values in black.



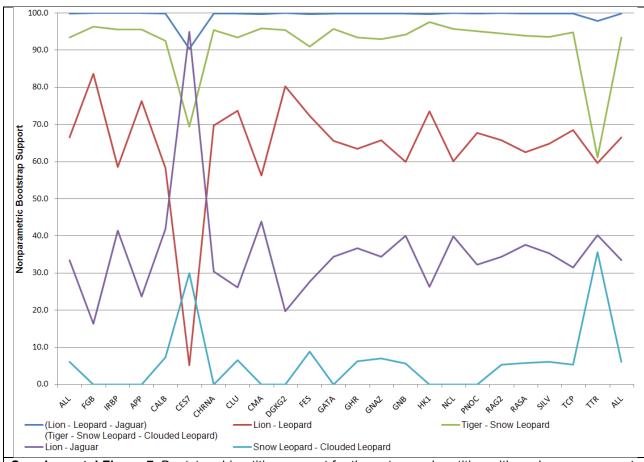
**Supplemental Figure 4.** Cladogram depicting final phylogenetic topology for *Panthera* generated by this study. Maximum likelihood bootstrap values (1000 replicates) shown in red. Bayesian posterior probabilities are in blue and BEST clade support values in black for the two primary incongruent nodes from prior studies.



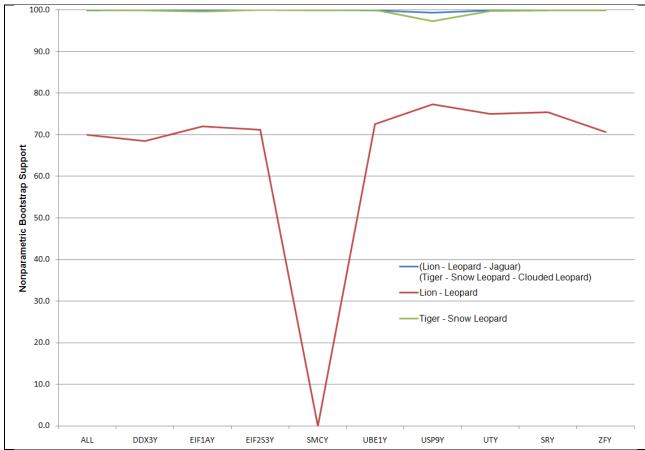
**Supplemental Figure 5.** Maximum likelihood total evidence trees both rooted and unrooted for the (A) Y chromosome (B) autosomal (C) nuclear (D) X chromosome partitions. ML bootstrap values (1000 replicates) in red, Bayesian posterior probabilities in blue.



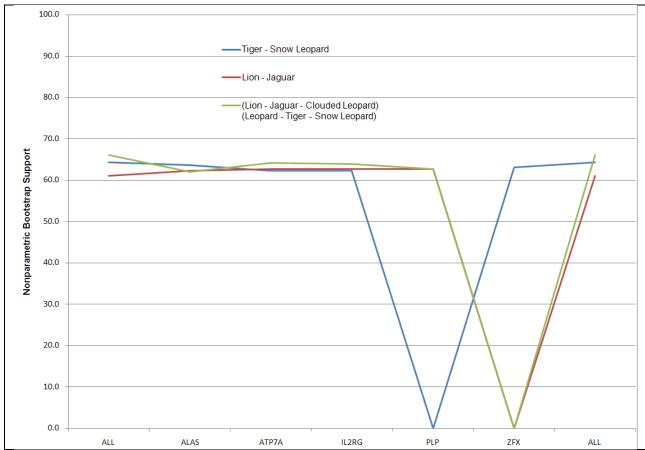
**Supplemental Figure 6.** Maximum likelihood topologies for the mitochondrial partition as (A) rooted cladogram and (B) unrooted phylogram. Maximum likelihood bootstrap values (1000 replicates) are shown in red, Bayesian posterior probabilities in blue.



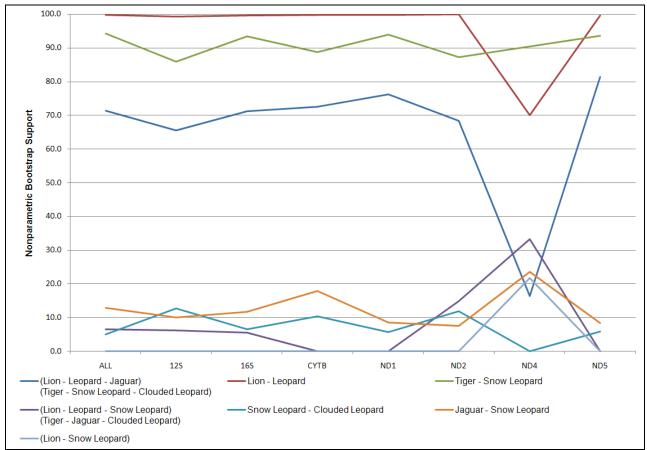
**Supplemental Figure 7.** Bootstrap bipartition support for the autosomal partition with each gene segment jacknifed out. Y-axis is bootstrap percentages from 1000 replicates. The change in topology is evident when either *TTR* or the much larger *CES7* is jackknifed from the dataset.



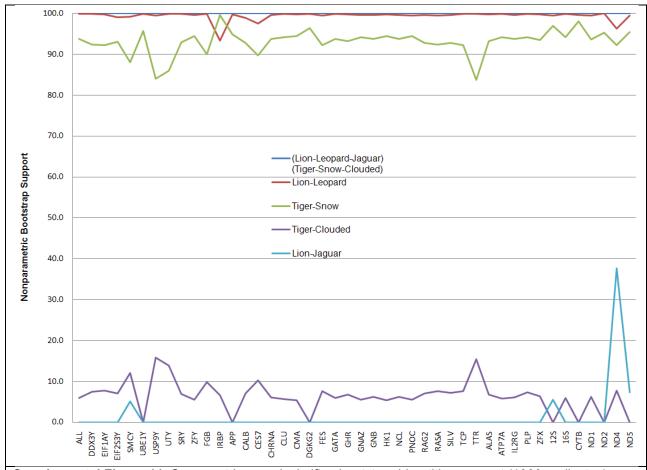
**Supplemental Figure 8.** Bootstrap bipartition support for the Y chromosome partition with each gene segment jacknifed out. Y-axis is bootstrap percentages from 1000 replicates The change in topology is evident when *SMCY* is jacknifed from the dataset.



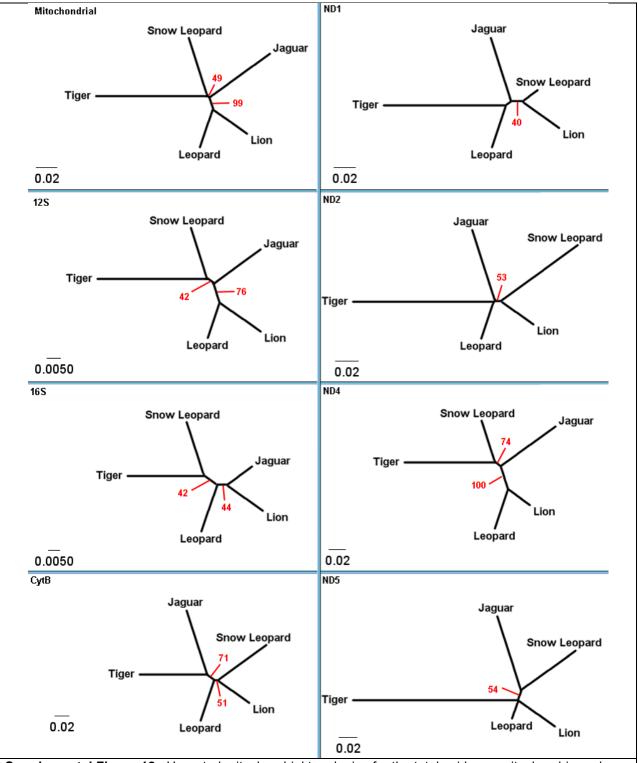
**Supplemental Figure 9.** Bootstrap bipartition support for the X chromosome partition with each gene segment jacknifed out. Y-axis is bootstrap percentages from 1000 replicates. The change in topology is evident when either *ZFX* or *PLP* is jacknifed from the dataset.



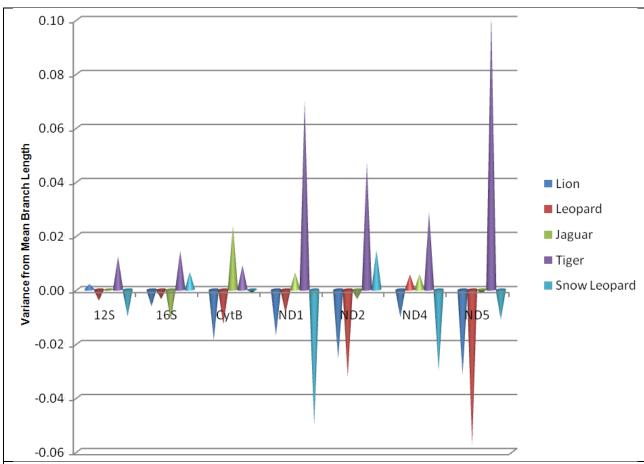
**Supplemental Figure 10** Bootstrap bipartition support for the mitochondrial partition with gene each gene segment jacknifed out. Y-axis is bootstrap percentages from 1000 replicates. The change in topology is evident when *ND4* is jacknifed from the dataset.



**Supplemental Figure 11.** Supermatrix gene jacknifing bootstrap bipartition support (1000 replicates) plotted across all gene segments with respect to each species relationship.



**Supplemental Figure 12.** Unrooted mitochondrial topologies for the total evidence mitochondria and each component gene segment. 1,000 bootstrap replicate percentages shown in red.



**Supplemental Figure 13.** Conical graph showing the consistently accelerated mitochondrial mutation rate of the tiger. The y-axis depicts the percentage divergence from the mean outgroup-to-tip branch length. Each gene segment and each taxa are shown. The higher the positive percentage divergence from the mean, the more accelerated the lineage's mutation rate for that gene.