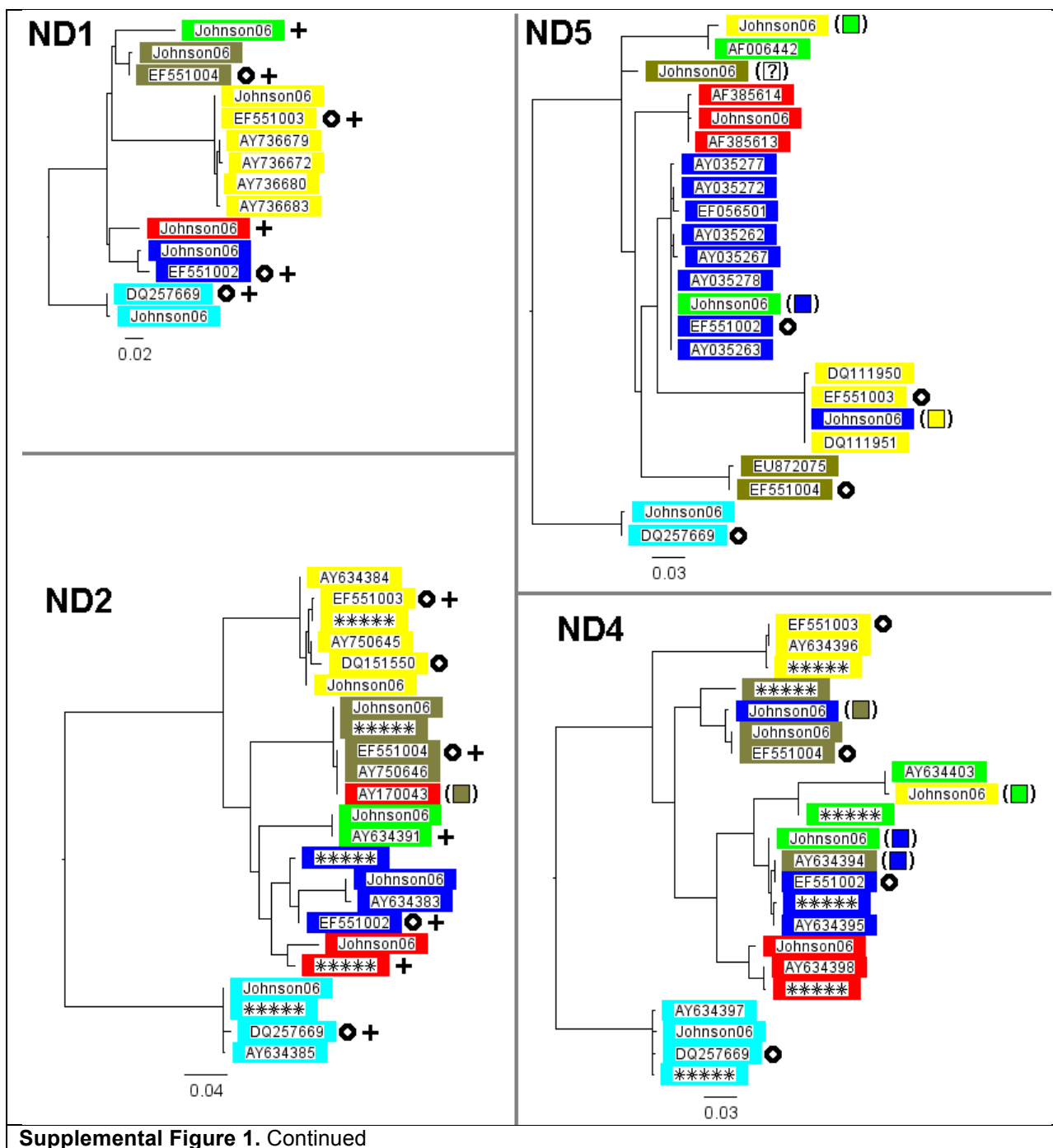
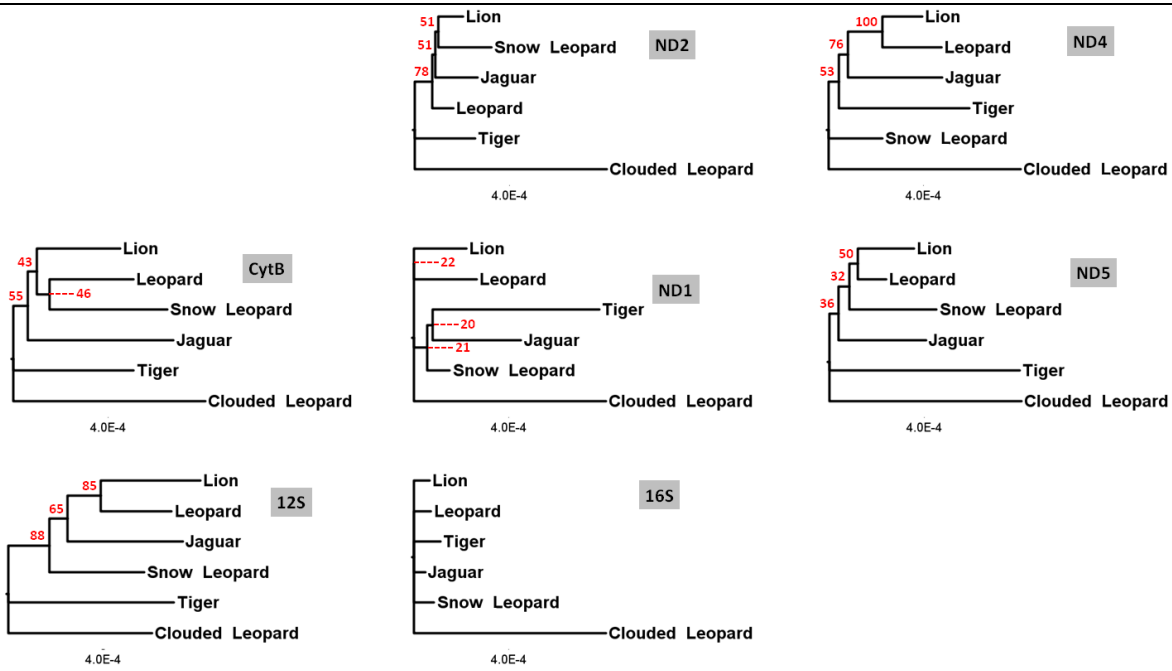


Supplemental Figure 1. Maximum likelihood clustering trees for all mitochondrial segments after the removal of all putative numt sequences.

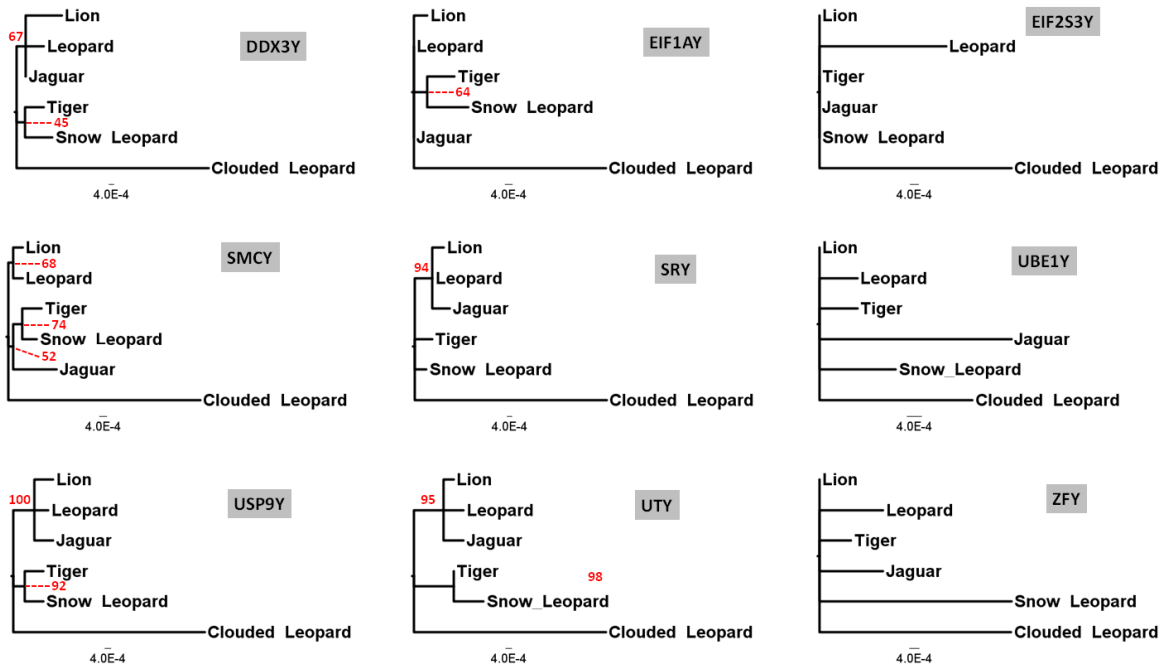


Supplemental Figure 1. Continued

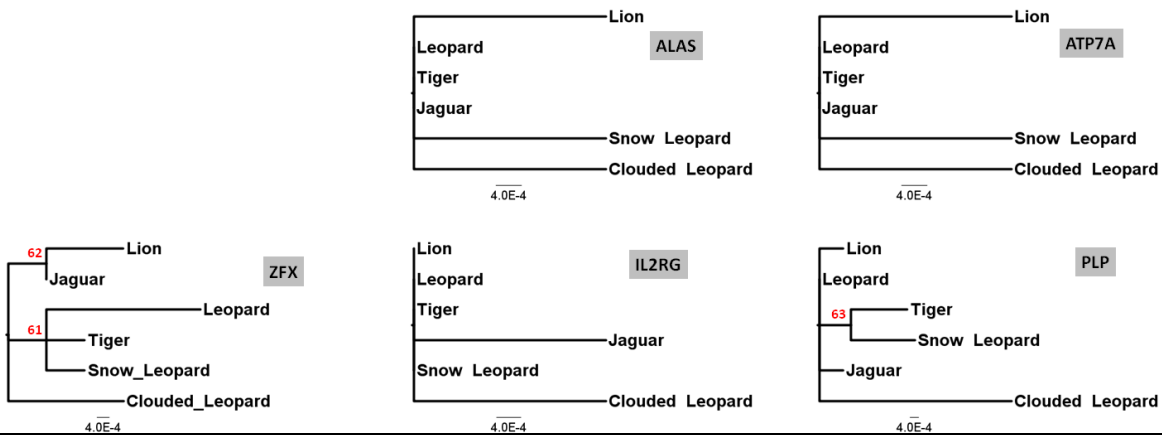
A



B

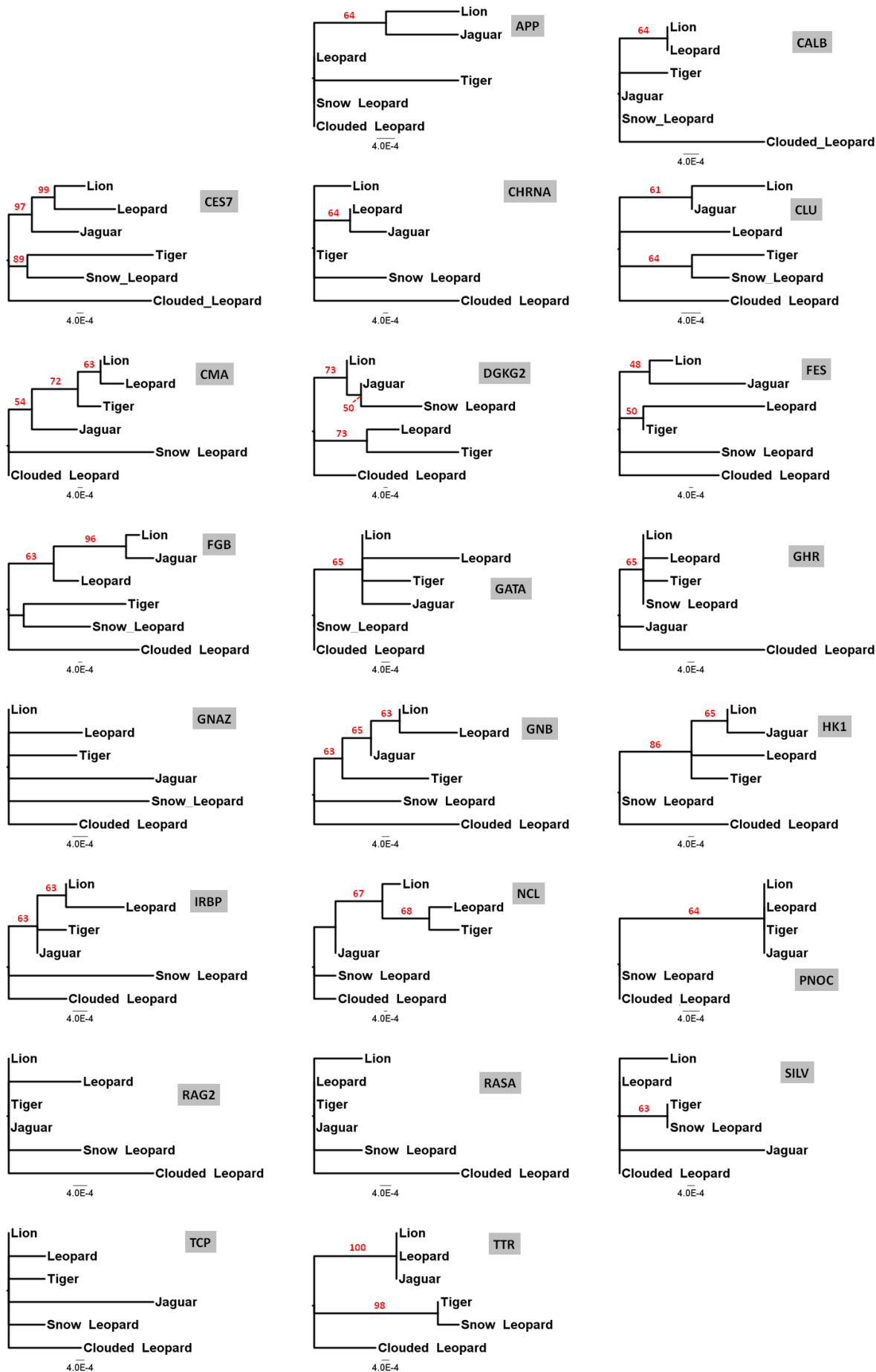


C

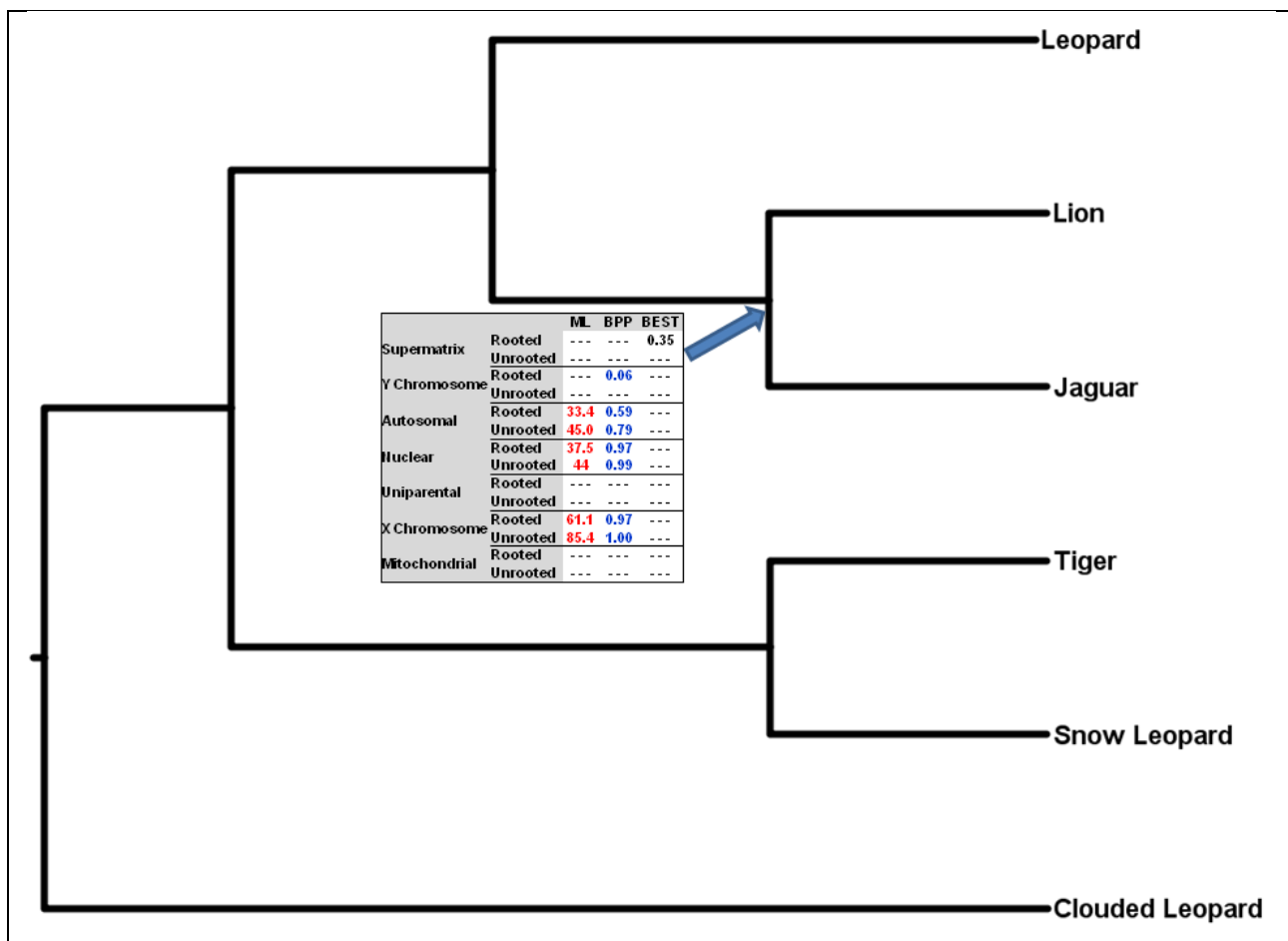


Supplemental Figure 2. Maximum likelihood topologies and bootstrap support values for each gene segment within the (A) Mitochondrial (B) Y chromosome (C) X chromosome and (D) Autosomal partitions

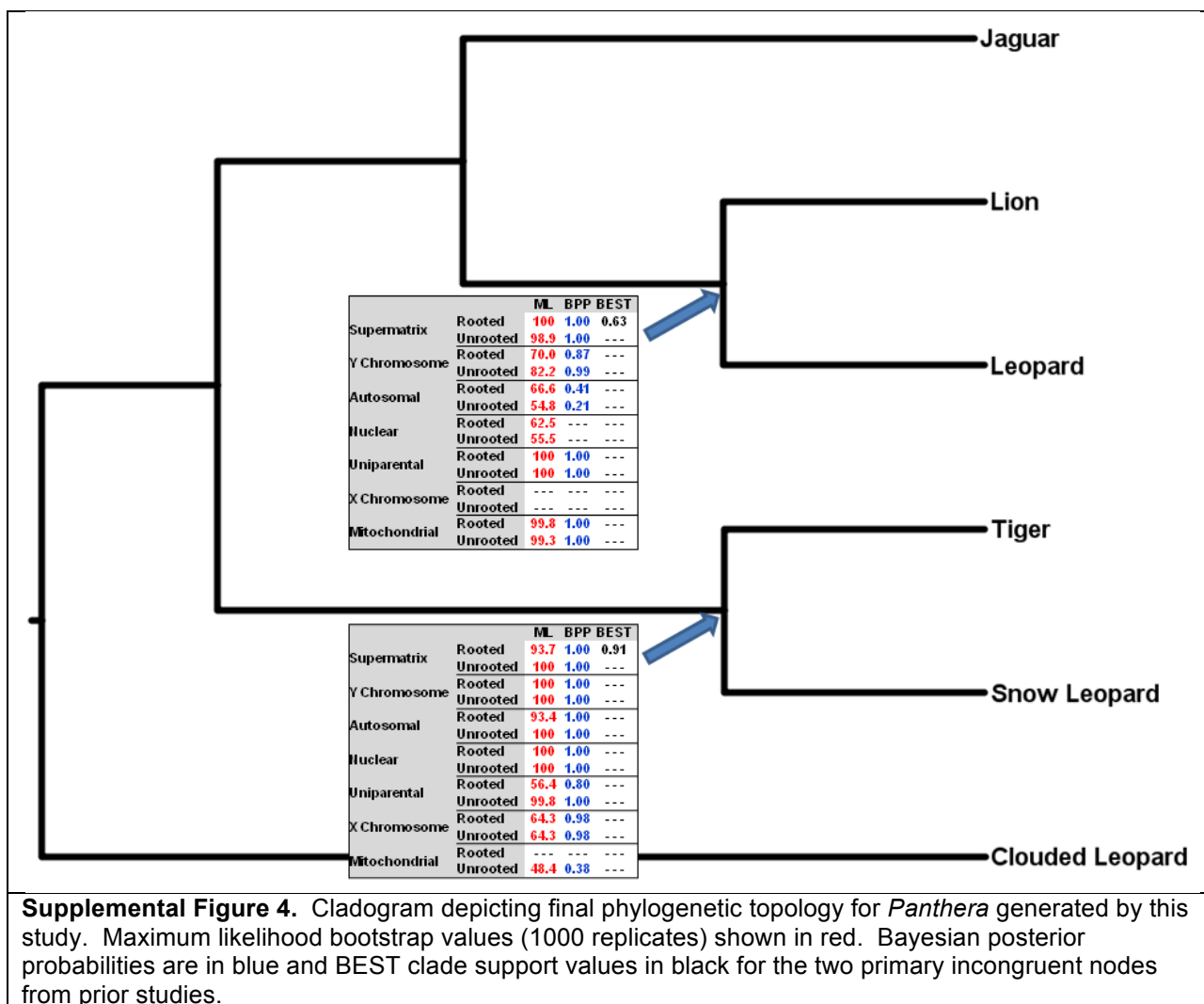
D



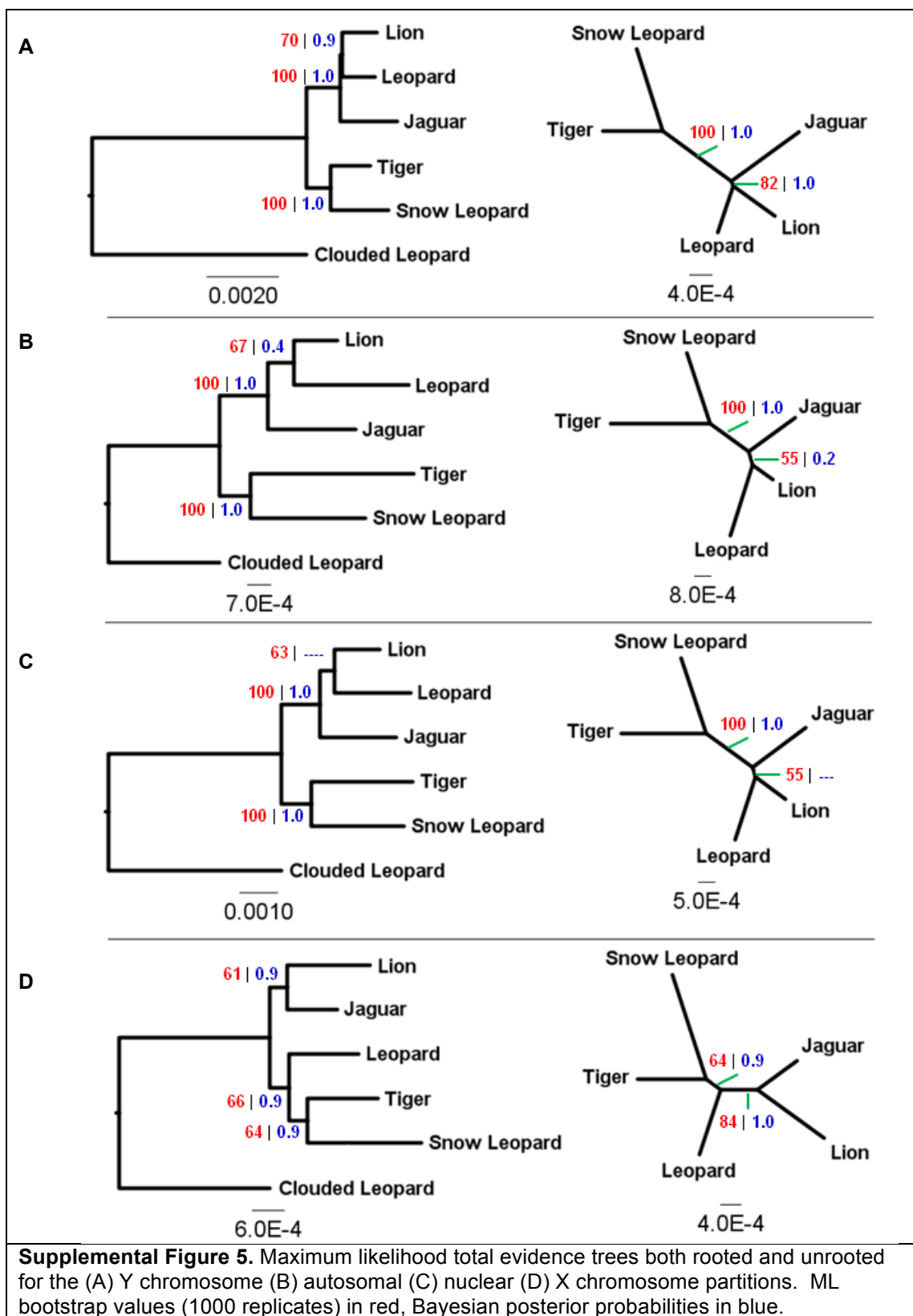
Supplemental Figure 2. Continued

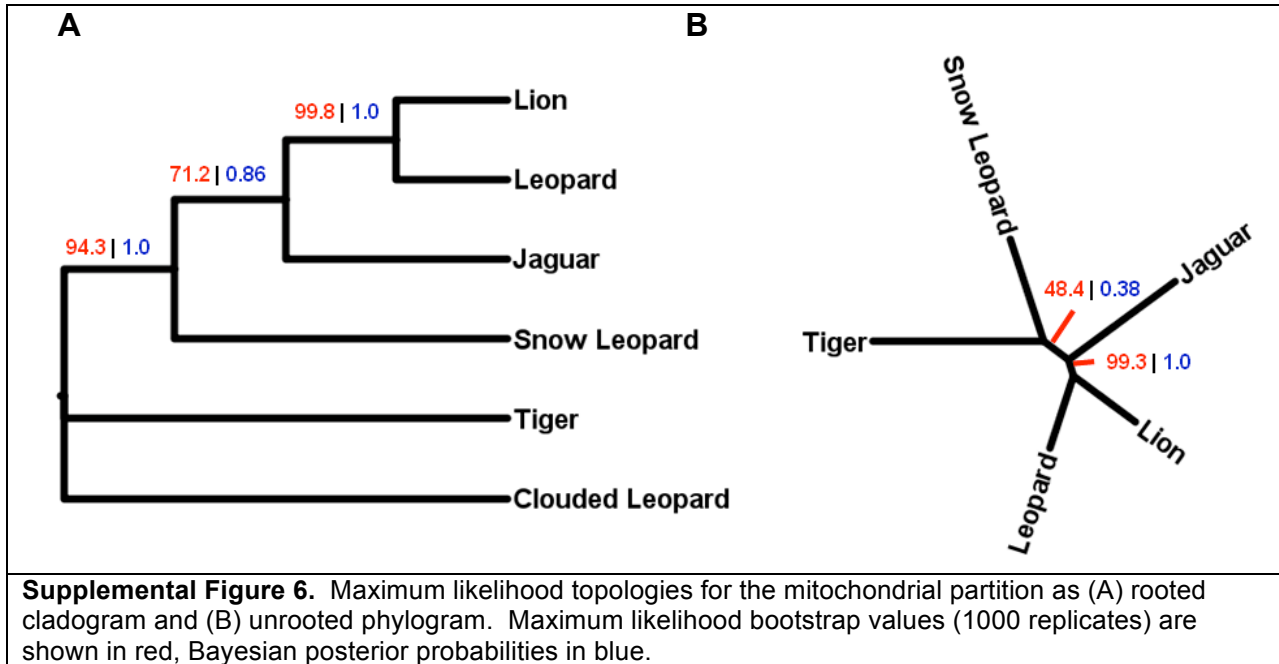


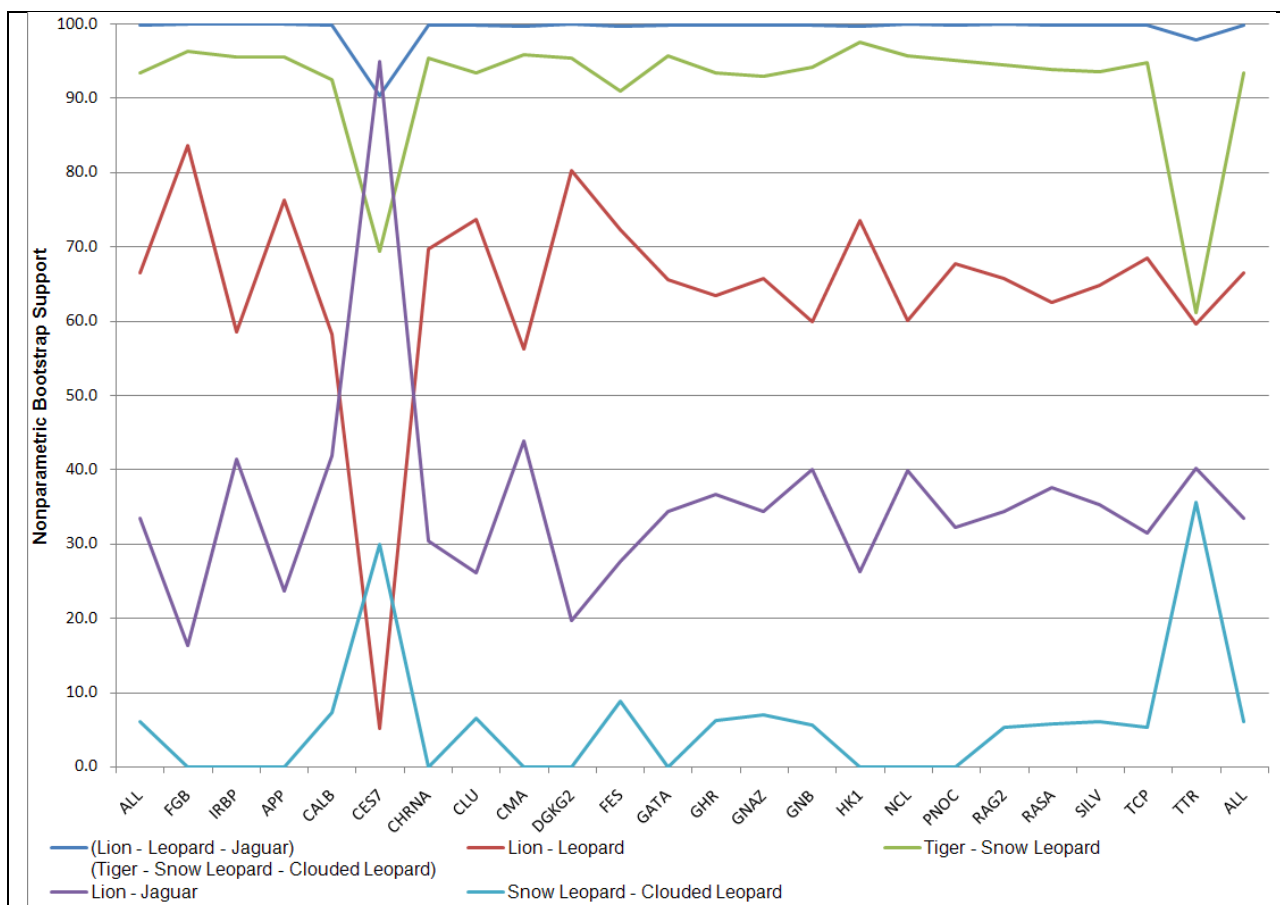
Supplemental Figure 3. Cladogram depicting phylogenetic topology for *Panthera* generated by Johnson et al. (2006). Maximum likelihood bootstrap values from this study (1000 replicates) shown in red; Bayesian posterior probabilities in blue; and BEST clade support values in black.



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.



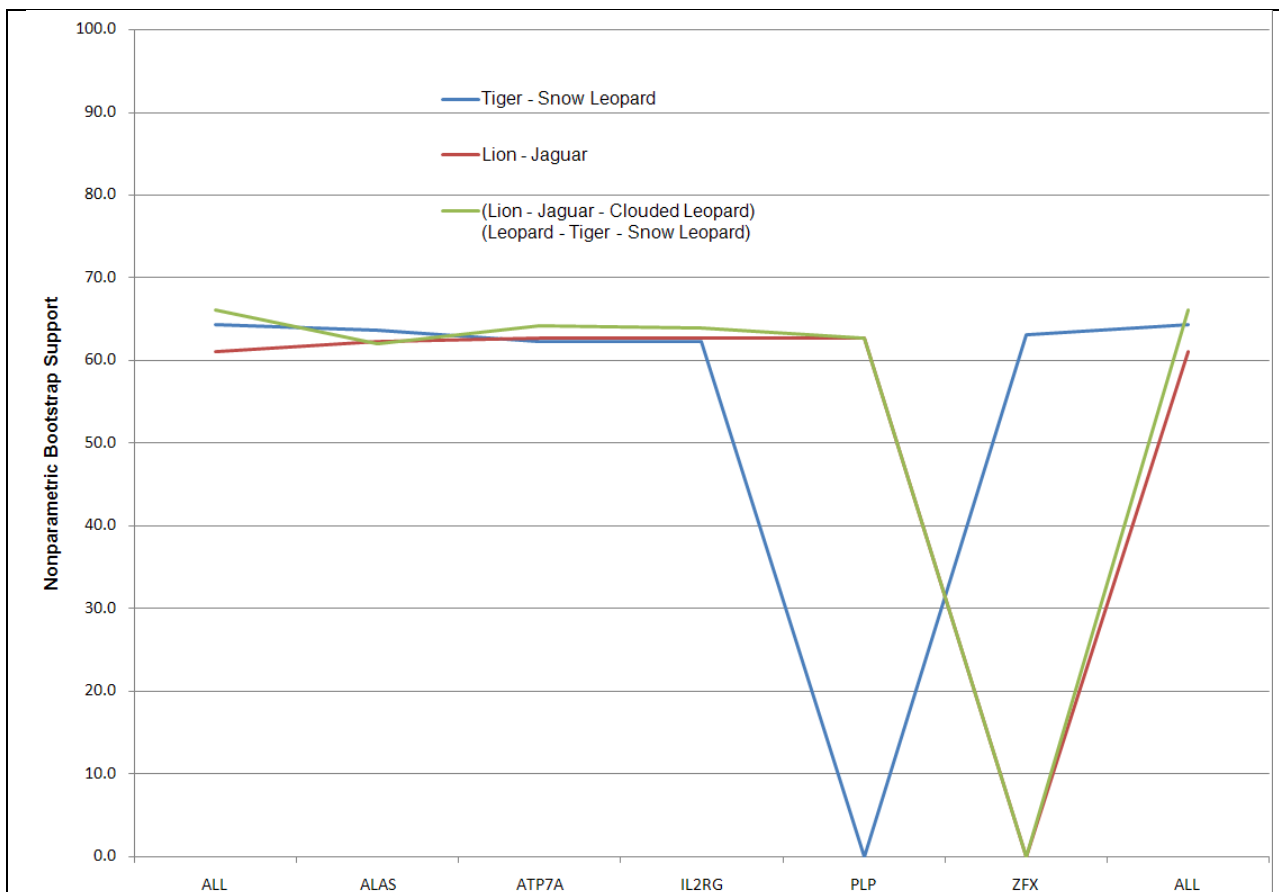




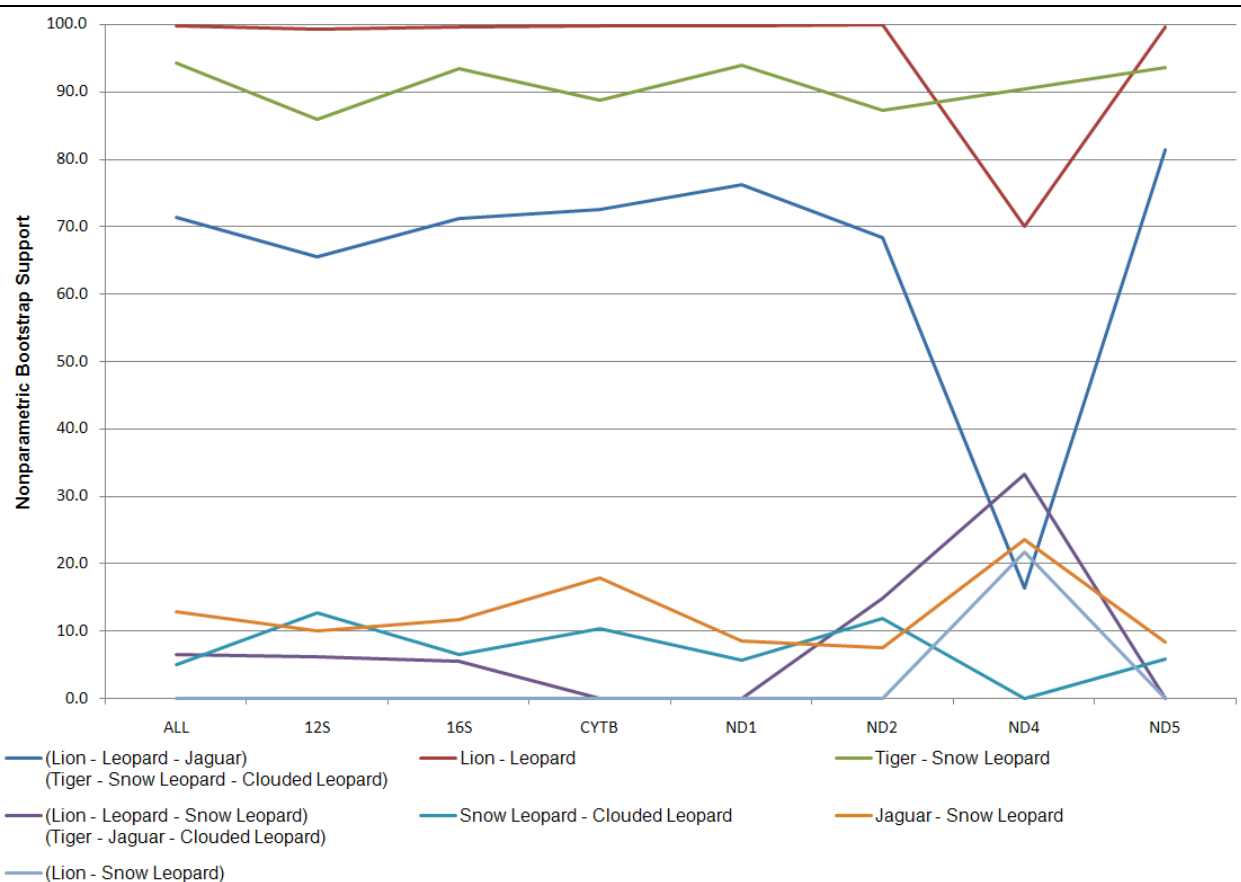
Supplemental Figure 7. Bootstrap bipartition support for the autosomal partition with each gene segment jackknifed out. Y-axis is bootstrap percentages from 1000 replicates. The change in topology is evident when either *TTR* or the much larger *CES7* is jackknifed from the dataset.



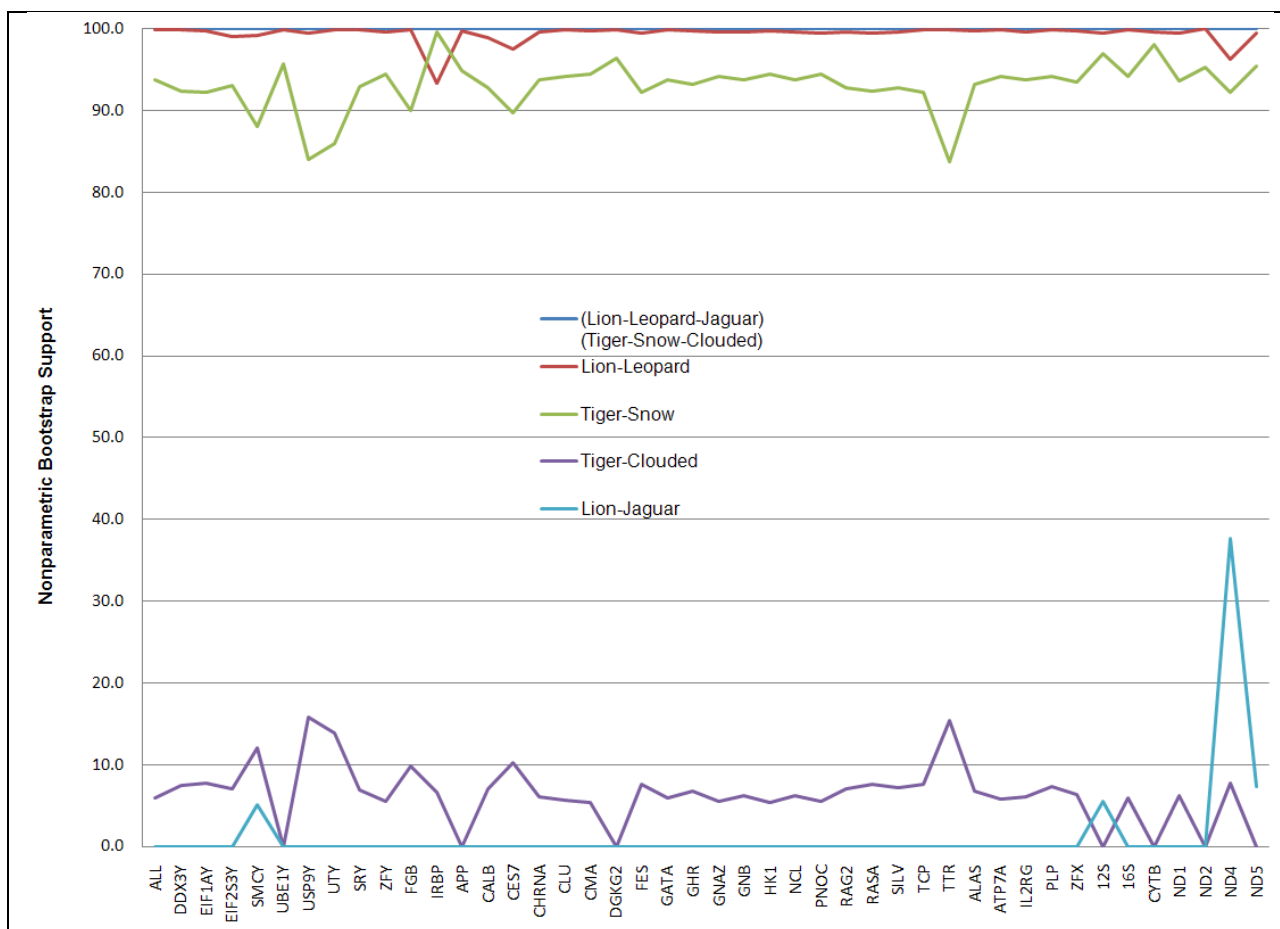
Supplemental Figure 8. Bootstrap bipartition support for the Y chromosome partition with each gene segment jackknifed out. Y-axis is bootstrap percentages from 1000 replicates. The change in topology is evident when *SMCY* is jackknifed from the dataset.



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



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



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

