

***Babesia duncani* Cytochrome *b* Gene**

1 TTAGTGAAGG AACTTGACAG GTATAAAAAT TTTTATATATA TTTGTTATAA AAATGAATTA
61 GGATACAGGG CTATAACCAA CAAGTTAACA TTTGCATTTA ATATGATTAA ATCACATCTT
121 ACAAACTATT TAGTACCAGA TAATATAAAT GGTAATTGGA ATTACGGATT CCTTTTGGCT
181 ATGCTTTTAT TACTGCAGAT TTTCTCAGGA ATATTAGCTG CCACAATATA TTCTCCTTAT
241 GGAGGAAATG CTTTTGAGAG CCTTCTAACA CTTTACGTTA GTAAAAATAT AGGATGGTTA
301 GTCCGCTATT TTCACGCTGT ATGTGTTTCA ATTTACTTTT TGGTCATGTA TTTTCATGTC
361 ACAAAAGGTT TGTCTTATTC TACAAGATAC ATCCCTTGGG TGTGGTATAC TGGATGGGCA
421 ATTCTTGTCT TAAGTATTAT TATCGCATTC TTGGGTTATA CTCTTCCAAA CGGTCAGATG
481 AGCTTTTGGG GAGCAACAGT TATATTAAAT TTATTTTATT GGGTTGGAGA CTTTGTGAGT
541 CTTCTAATGG GAGGATTTAG TGTTGAATCA GAGACACTTG GTAGATTTTA TATTCTACAT
601 TTTTCTCTTC CTTTTGTTTT ATTAATTCTT GTTCTTATAC ATATATTTTA CTTGCATGT
661 CAAGGAAGTA CAAATCCTGT AATTAATCTT GACGCACTAT TAGGTGAGAG ATTTTGTGTA
721 AATCCAGCAT TTTGCGATTT AAAATGCATA ATTATTTTAT TTGTTGGAAT TTCACTTCAA
781 ATTGCATATG GAATACTGCC TATATTTCAA GGTGATCACG ACAATTCGAT CGAAGCAAAT
841 AGCTCACAAA CTCCTGAACA TATTGTTCCCT GAGTGGTATT TACTTGTGTT TTATGCAGCA
901 TTGAAATTAT GTCCTGGAAG ATTCGCAGGA CTATTAGCAA TGATTGCAAT TATGGAACCT
961 CTGGTAATTT TATCAGAAGC TAGAGCTTTT GCTGCAATAG TATCATGTGC CGTCCATCAT
1021 AGAAATTGGA CTACAGCACT TTCTGTGCGTA CTACCAGCCC TTTTATATATT GGGTTCATTA
1081 GGACAAATTG CAATCAATTT GTATATCCTA AAGGTAGGTG CATATATAAT ATGTGCAGTC
1141 ACTTGCTGTA TTACTAGACT GCTTGATCTA GCAATTATAG AAAGAGTCTA TTAA

***Babesia duncani* Cytochrome *b* Protein**

MVKELDRYKNFLYICYKNELGYRAITNKLTFAFNMIKSHLTNYLVPDNINGNWNWYGFLLA
MLLLLQIFSGILAATIYSPYGGNAFESLLTLVSKNIGWLVRYFHAVCVSIYFLVMYFHV
TKGLSYSTRYIPWMWYTGWAILVLSIIIAFLGYTLPNGQMSFWGATVILNLFYVWVDFVS
LLMGGFSVESETLGRFYILHFSLPFVLLILVLIHIFYHLHCQGSTNPVINLDALLGERFLL
NPAFCDLKCIILFVGISLQIAYGILPIFQGDHNSIEANSSQTPEHIVPEWYLLVFYAA
LKLCPGKFAGLLAMIAIMELLVILSEARAFAAIVSCAVHHRNWTALSVVLPALFILGSL
GQIAINLYILKVGAYIICAVTCCITRLLDLAIIERVY

Fig S1. Nucleotide and Protein Sequence of *Babesia duncani* Cytochrome *b*

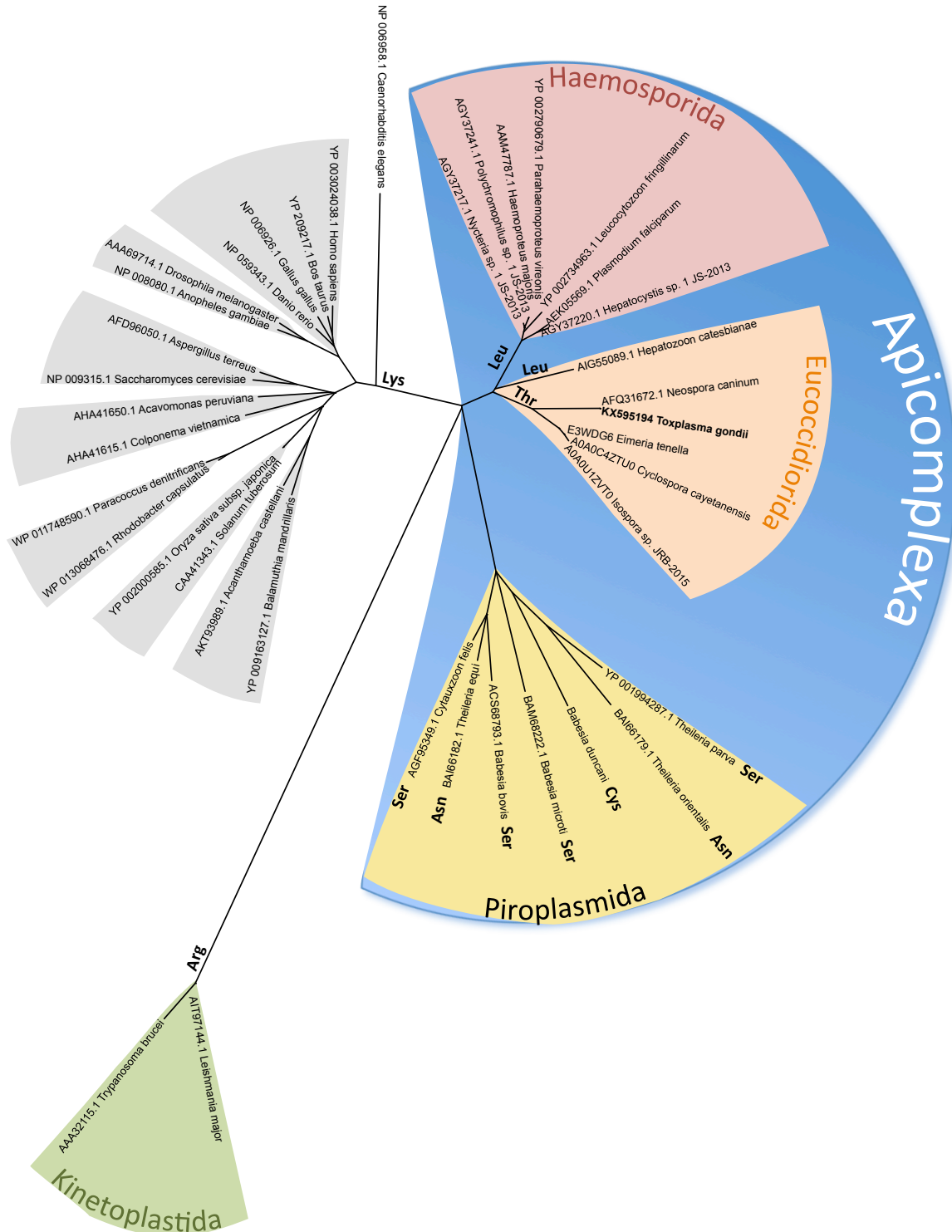


Fig S2. Divergence of Amino Acid 222 among Apicomplexa Compared to a Broad Representative Sample of Cytochrome b Protein Sequences.

Amino acid abbreviations indicate the amino acids that are analogous to *T. gondii* *Cytb* Thr222. Within the order Eucoccidiorida, the family Sarcocystidae, which includes *T. gondii*, and the family Eimeriidae possess a threonine at *T. gondii* position 222. *Hepatozoon catesbianae* possesses a leucine like the Haemosporida. The Piroplasmida demonstrate further diversity in that *Babesia* species have a serine or cysteine, while *Theileria* species have either serine or asparagine. Outside of the Apicomplexa, the vast majority of *Cytb* sequences, including non-apicomplexan Alveolata, contain a lysine residue. The highly divergent *Cytb* of kinetoplastids have an arginine similar to lysine. Phylogenetic analysis of *Cytb* was performed by the Maximum Likelihood method using MEGA7 as noted in the methods.