

Global transmission and evolutionary dynamics of the Chikungunya virus

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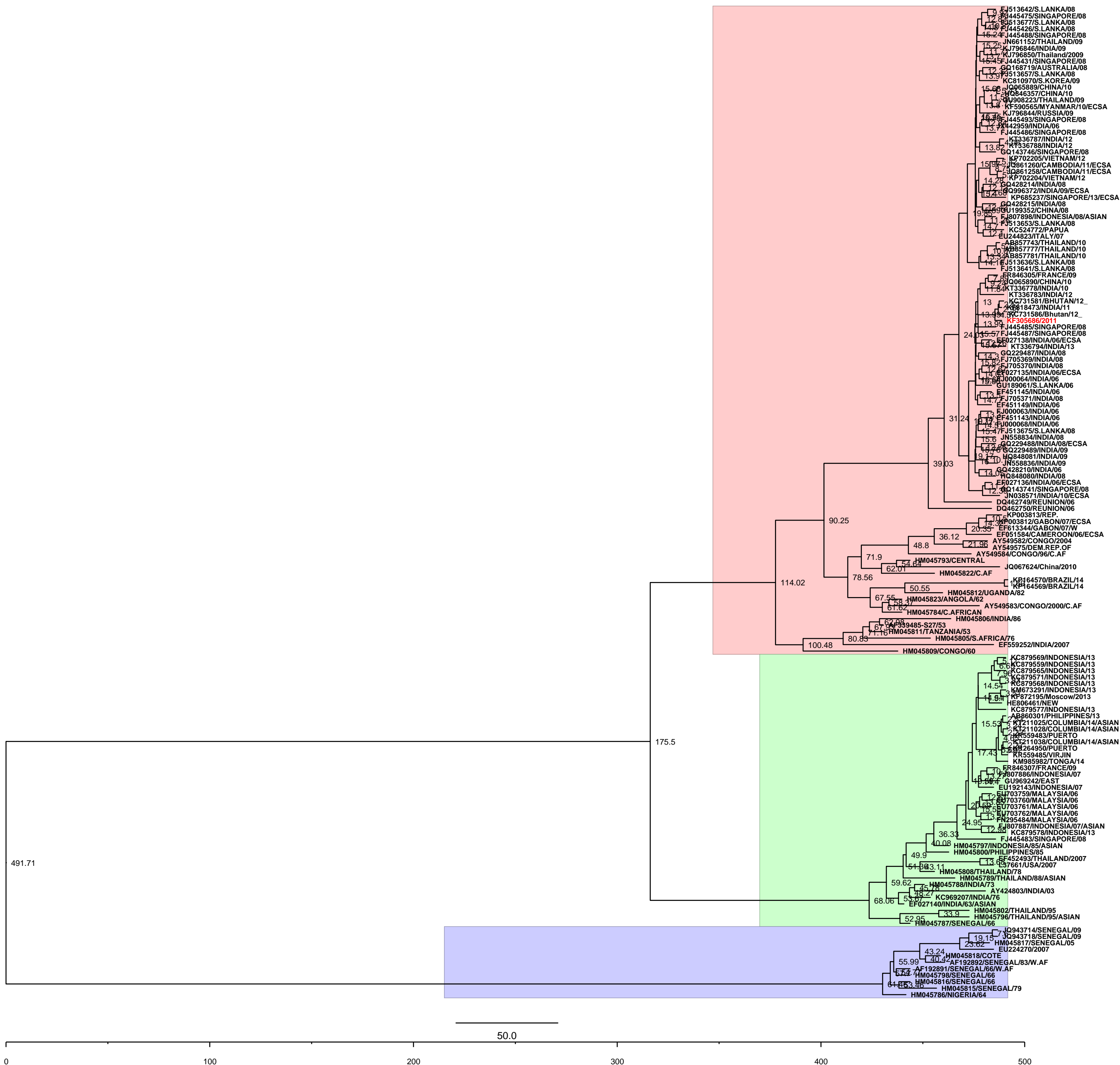
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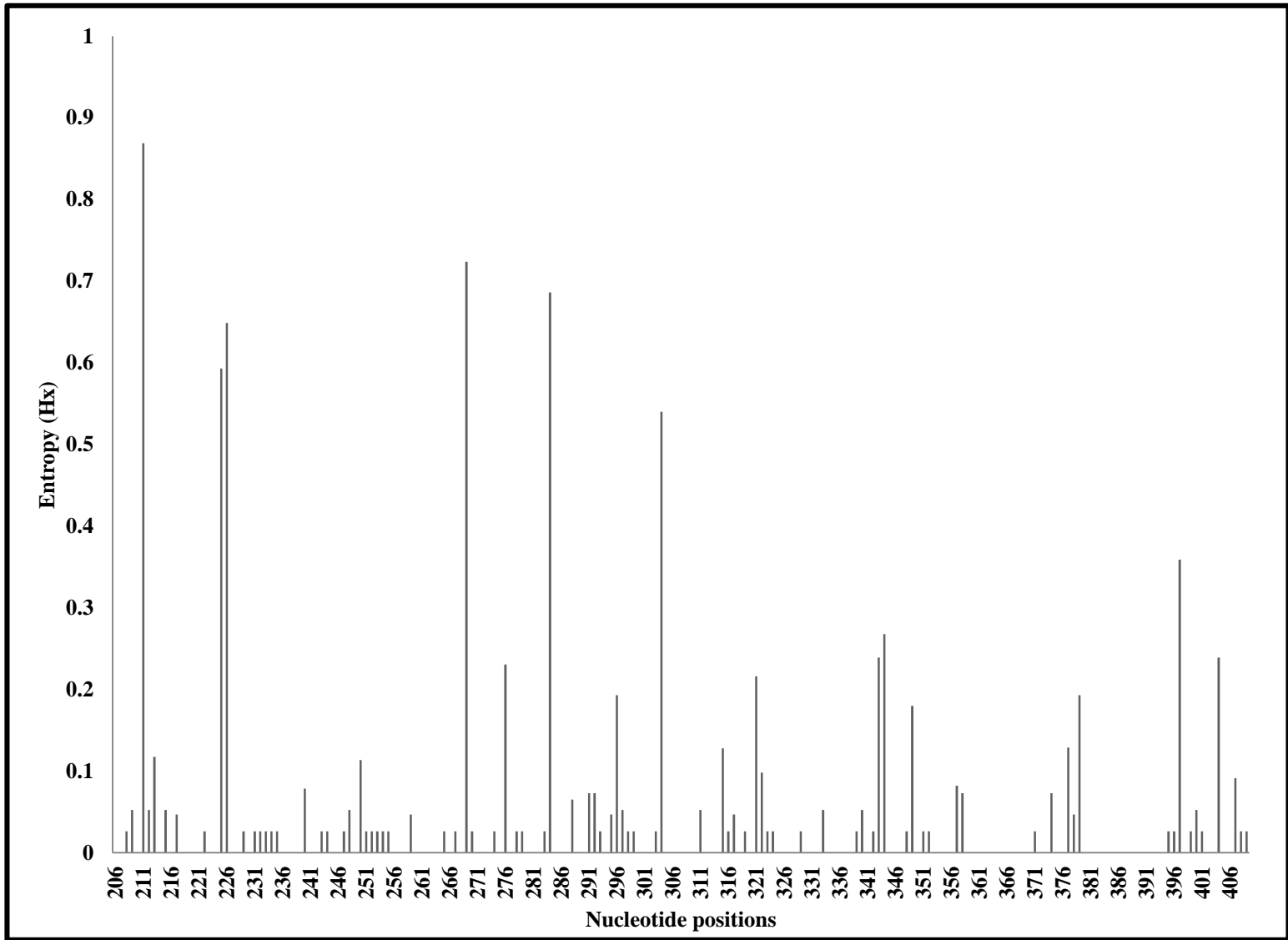
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Supplementary figures: 4 (S1-S4)

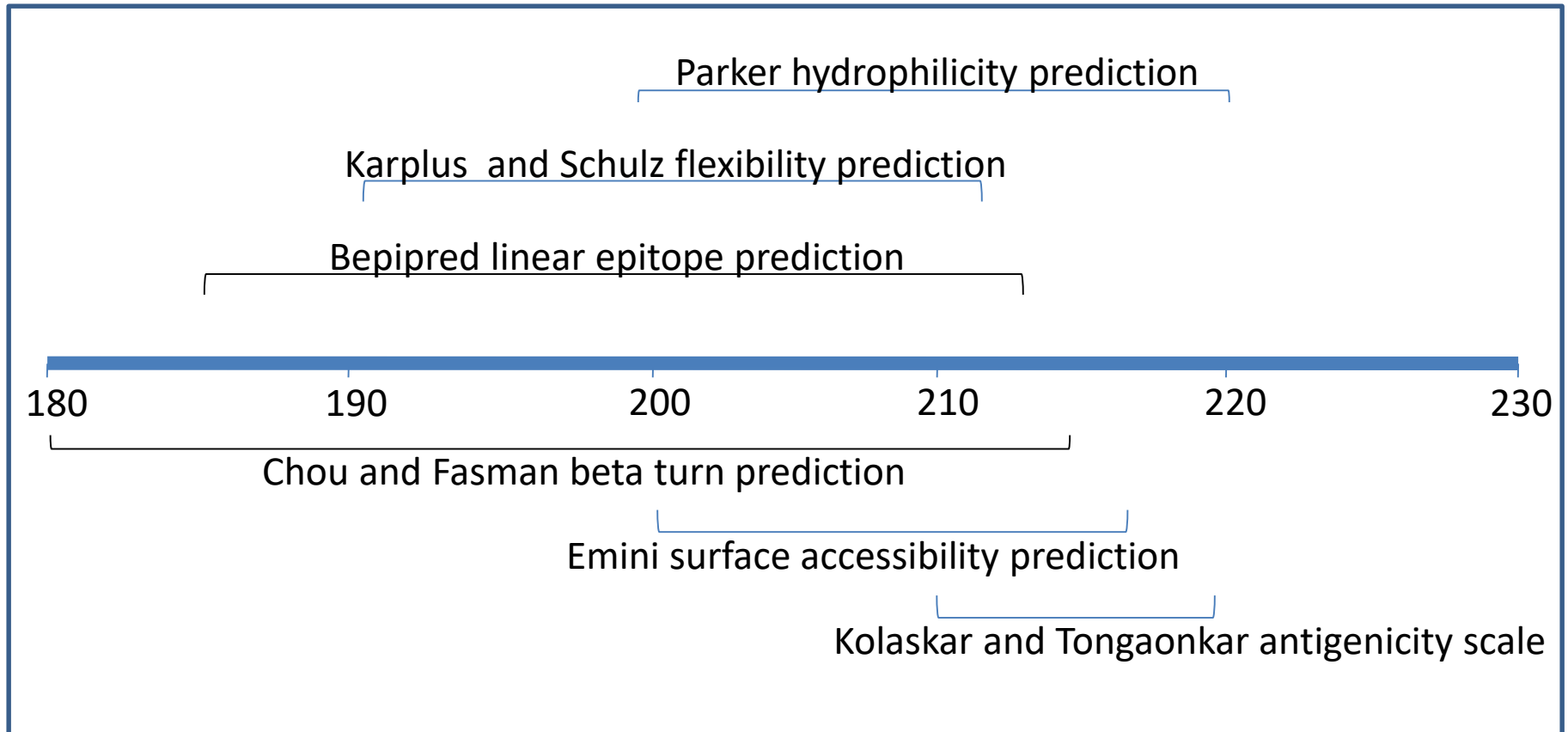
Supplementary figure S1: The detailed version of ML phylogenetic tree of Chikungunya virus. The bootstrap values above 80% are displayed on the nodes. The strains have been represented by their respective accession number followed by country and year of isolation.



Supplementary figure S2: The detailed version of MCMC Bayesian tree generated using different Chikungunya virus strains from various parts of the world. The respective ages are shown on each node. Pink, green and blue regions show the clusters of ECSA, Asian and West African genotypes respectively.



Supplementary figure S3: Shannon Entropy analysis plot showing entropy values of different amino acid residues. The higher entropy value depicts enhanced probability of being a variable site.



Supplementary figure S4: The amino acid scale showing the most common region between all the B-cell epitope prediction methods having high prediction score.

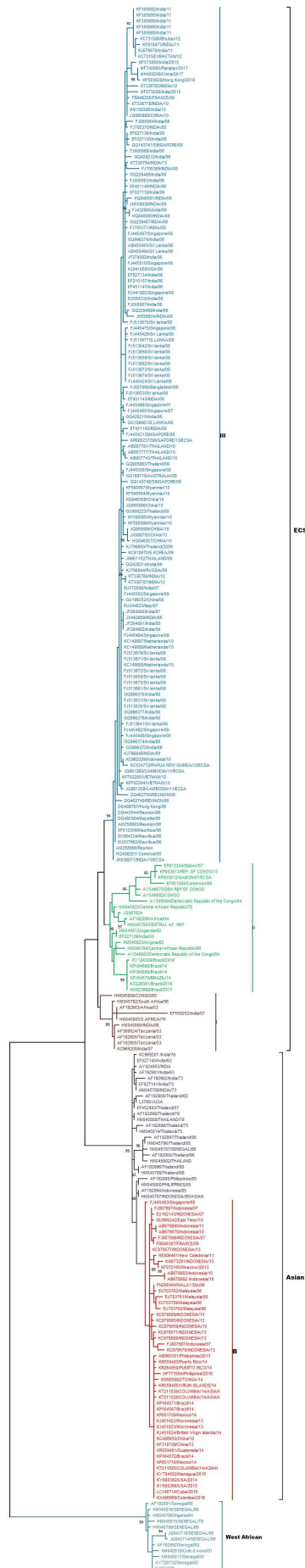


Figure S5: Maximum likelihood tree with thousand bootstrap values generated in Mega X 10.1.5 software