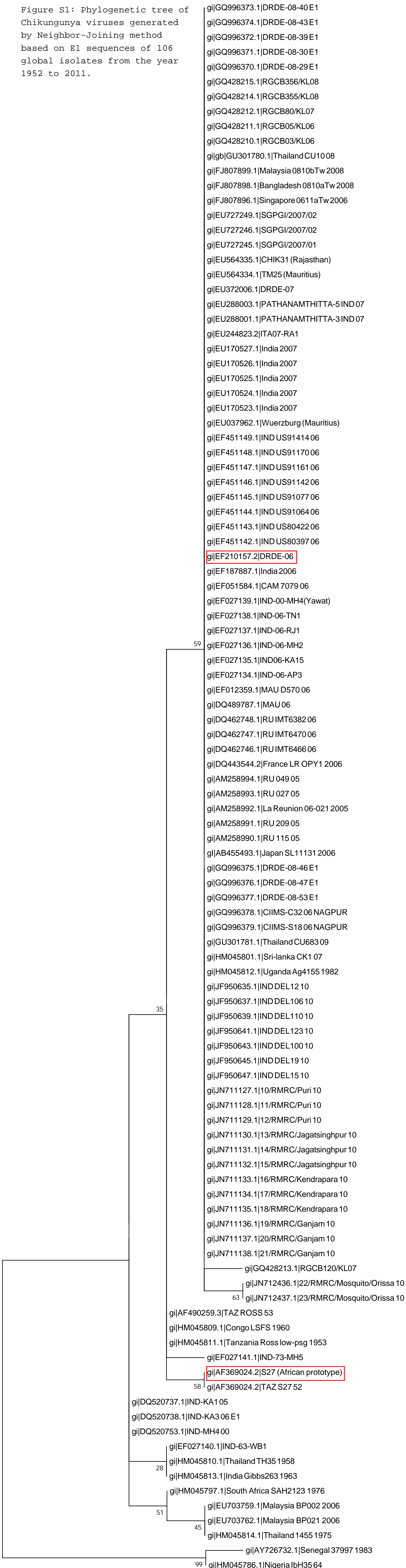


Figure S1: Phylogenetic tree of Chikungunya viruses generated by Neighbor-Joining method based on E1 sequences of 106 global isolates from the year 1952 to 2011.



0.02