

Figure S1. Phylogenetic relationships among several CHIKV and ones from French cases (Genbank accession number pending) based on complete genome (11,237 nucleotides) analysis. Bootstrap support values (1,000 replicates) are indicated at major nodes. Gray shading indicates the two French CHIKV isolates. Scale bar indicates number of base substitutions per site. ECSA, East/Central/South Africa.

