Supplemental Figure 1. Phylogenetic analysis based on the envelope 1 gene of chikungunya virus. Analysis was performed using MEGA 5.2.1. Numbers at the branching points are bootstrap values estimated with 1,000 pseudo-replicates. Strain names are shown to the left of the locations, followed by the year of collection. Strains used for mosquito infection are shaded in gray. ECSA = East/Central/South Africa lineage. Scale bar indicates number of nucleotide substitutions per site along the branches.