Supplementary figure S4 – Phylogenetic tree of Zika virus including African and Asian isolates based on the partial envelope gene (773bp).

Phylogenetic tree computed using MrBayes with a dataset that included 5 African lineage ZIKV isolates as an outgroup in addition to 83 Asian lineage ZIKV sequences (one partial Asian ZIKV sequence was removed due to missing data). Two parallel runs with four MCMC chains were run for 5M MCMC generations using a GTR+I+G(4) model of nucleotide evolution, Dirichlet priors, sampling every 1000 generations, discarding the first 25 % as burn-in before computing a consensus tree. Numbers on branches indicate posterior probability support.