Supplementary figure S1 – Phylogenetic tree of Zika virus including African and Asian isolates based on partial and complete genomes

The tree was computed with MrBayes using a dataset that included 5 African lineage ZIKV isolates as an outgroup in addition to 84 Asian lineage ZIKV sequences. Two parallel analyses 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.