



Figure S1. Phylogenetic analysis of a partial sequence from the E ZIKV gene. The consensus of the forward and reverse sequences (293 bp) segment from the E gene (nt 1595 to 1887, ref KJ776791). The phylogenetic tree was constructed based on neighbor-joining method by using the ZIKV typing tool Ref [31]. The black square represent the Nicaraguan sequence (Subject B, 7DPSO, NIC, November 2016).