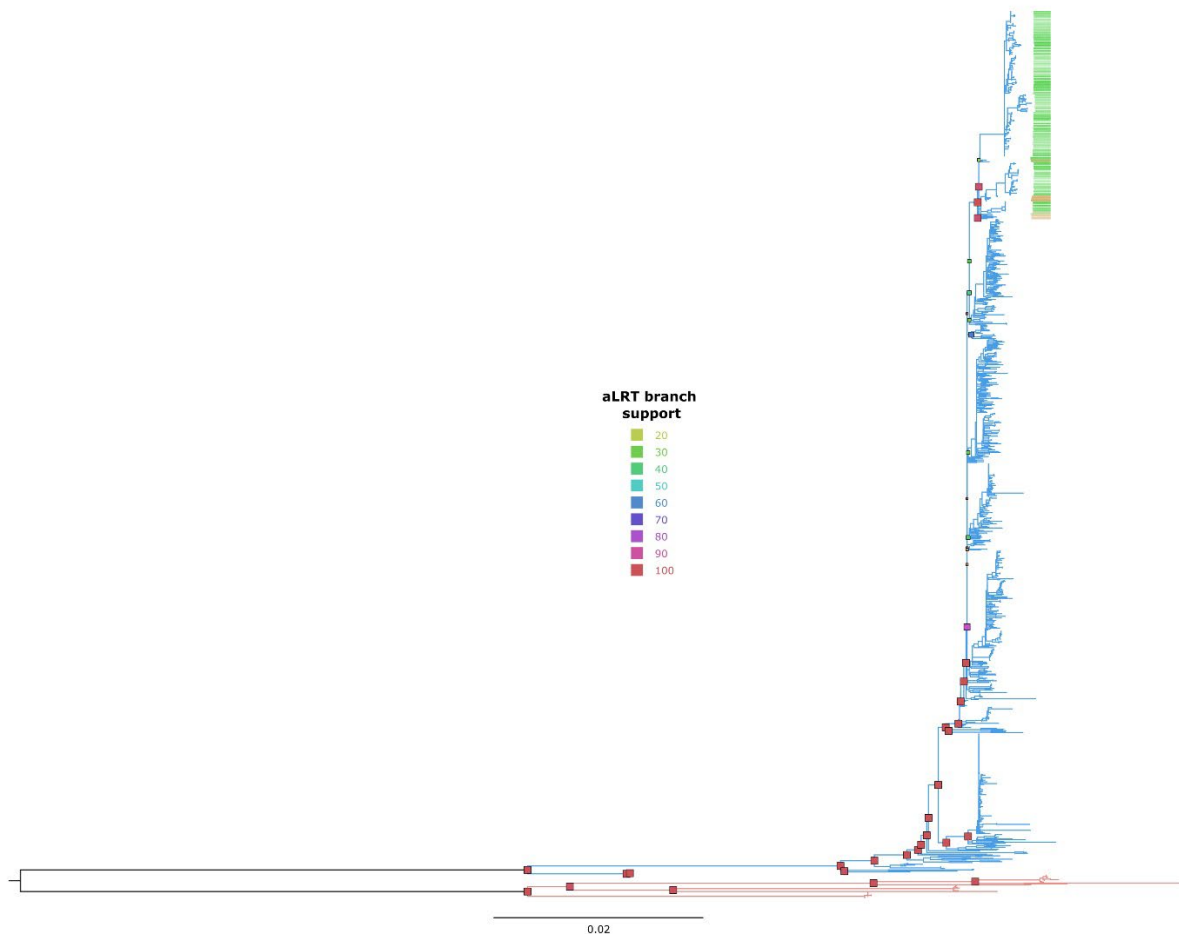
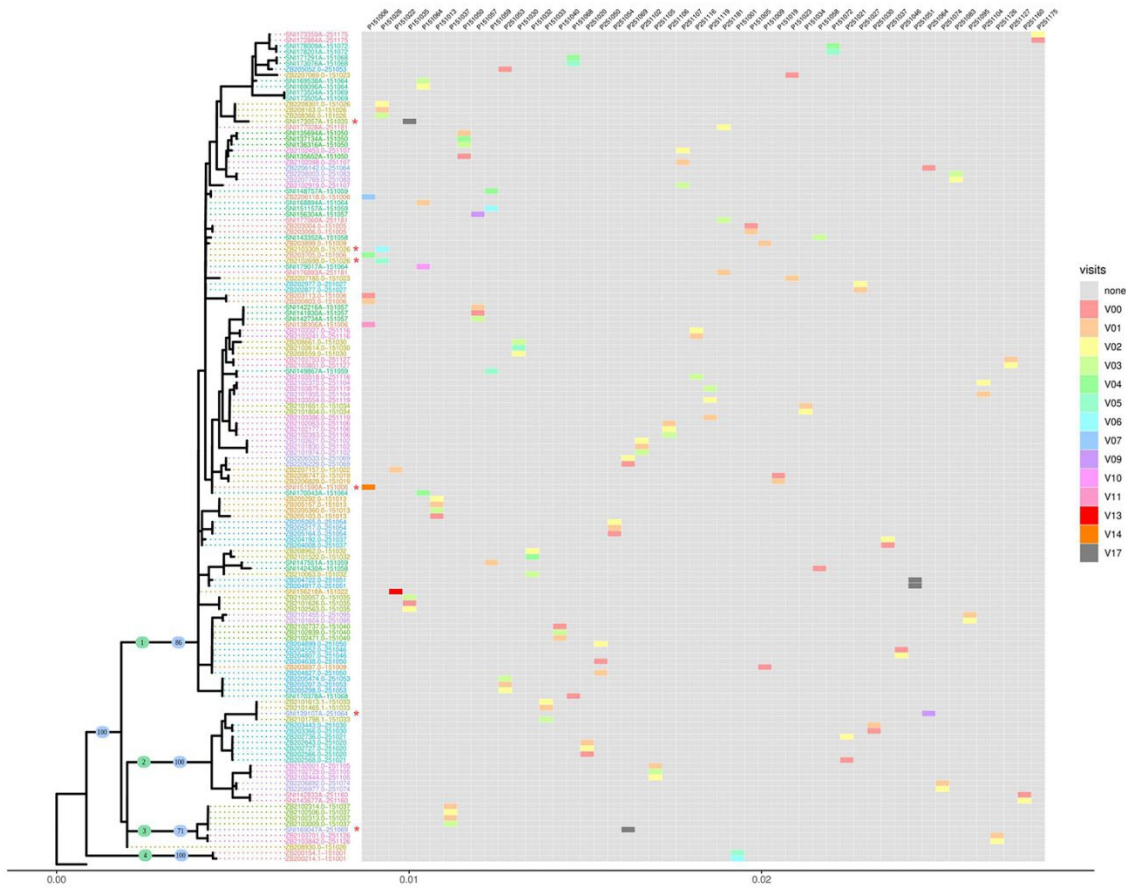


Evidence of Zika Virus Reinfection by Genome Diversity and Antibody Response Analysis

Appendix 1



Appendix Figure 1. Maximum likelihood phylogenetic tree reconstructed based on the coding nucleotide region of eight hundred fourteen ZIKV genomes sequences downloaded from ViPR database and all genomes generated in this study. Red and blue bars denote genomes belonging to African and Asian ZIKV lineages while green bars are samples generated in this study.



Appendix Figure 2. Maximum likelihood phylogenetic tree including all ZIKV genomes generated in this study. Participant identifications (IDs) are color-coded in the tip labels, the same color represents multiple samples obtained at different time points from the same participant. Green numbers in the tree branches (1 to 4) represent the different ZIKV clades as identified in our analysis and blue numbers are the aLRT branch support of each defined clade. Columns represent the study participants with at least one persistent associated sample. Color-coded columns represent the study visit, as described in Table 1. Reinfection-associated genomes are marked with a red asterisk. Pattern of minor variant accumulation.