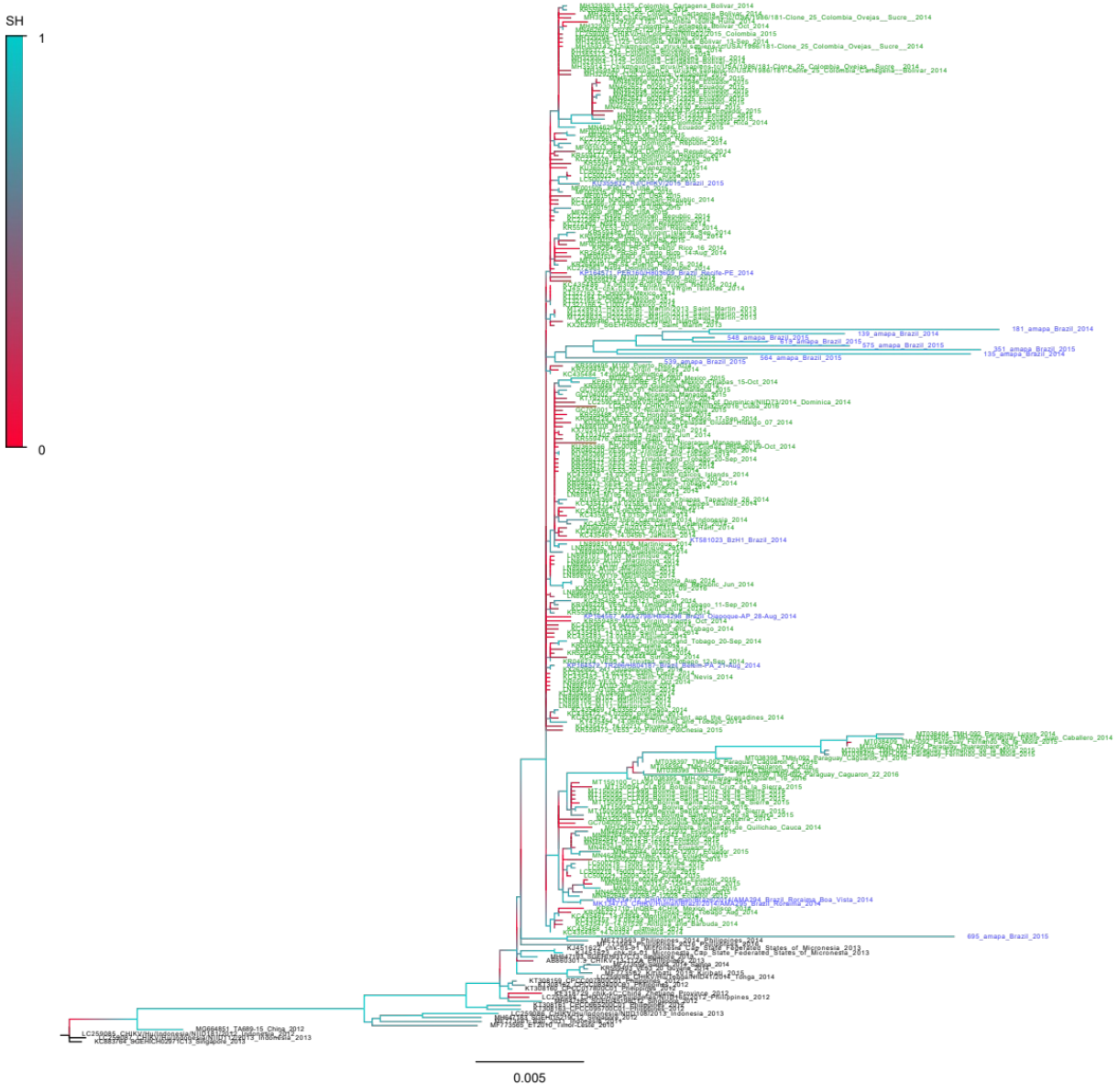
SH
1
0
139_amapa_Brazil_2014
181_amapa_Brazil_2014
548_amapa_Brazil_2015
575_amapa_Brazil_2015
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136_amapa_Brazil_2014
819_amapa_Brazil_2015
584_amapa_Brazil_2015
695_amapa_Brazil_2015
KTS81023_BzH1_Brazil_2014
0.005

Figure S1. Maximum likelihood tree of CHIKV-Asian lineage. The unrooted tree was constructed using reference genomes of CHIKV-Asian lineage. Sequences from Brazil are indicated in blue. Sequences from Caribbean countries are in green color and sequences from South Asia/Oceania are in black color. The cluster composed by Caribbean sequences plus almost all Brazilian sequences is labeled. The Brazilian sequence related with a Philippine sequences is highlighted. The branch support is indicated by a color scale of 0 to 1, and is based on the Shimodaira-Hasegawa-like test. The tree was inferred using the TN-93 model plus gamma correction. Horizontal bar indicate the nucleotide substitution per base.

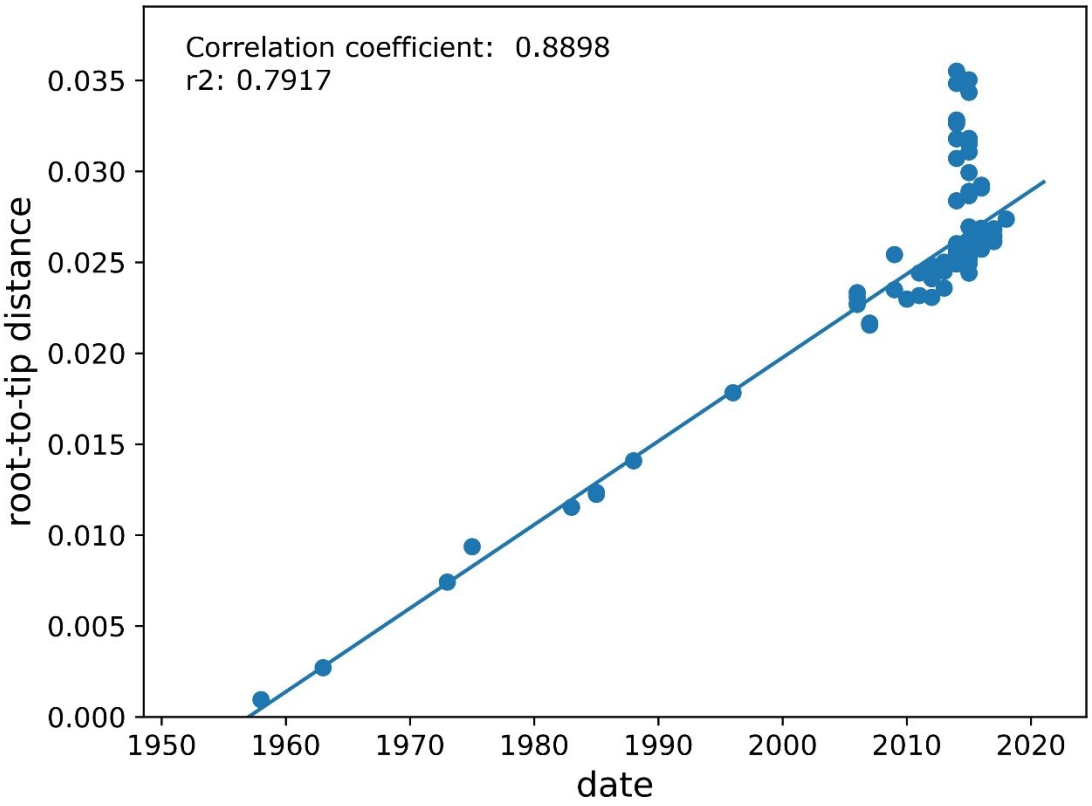

Figure S2. Linear regression analysis. root-to-tip genetic distance against year of sampling fof 297 CHIKV Asian lineage sequences. Linear regression was performed and the trend line and R-squared value (r2) are indicated.

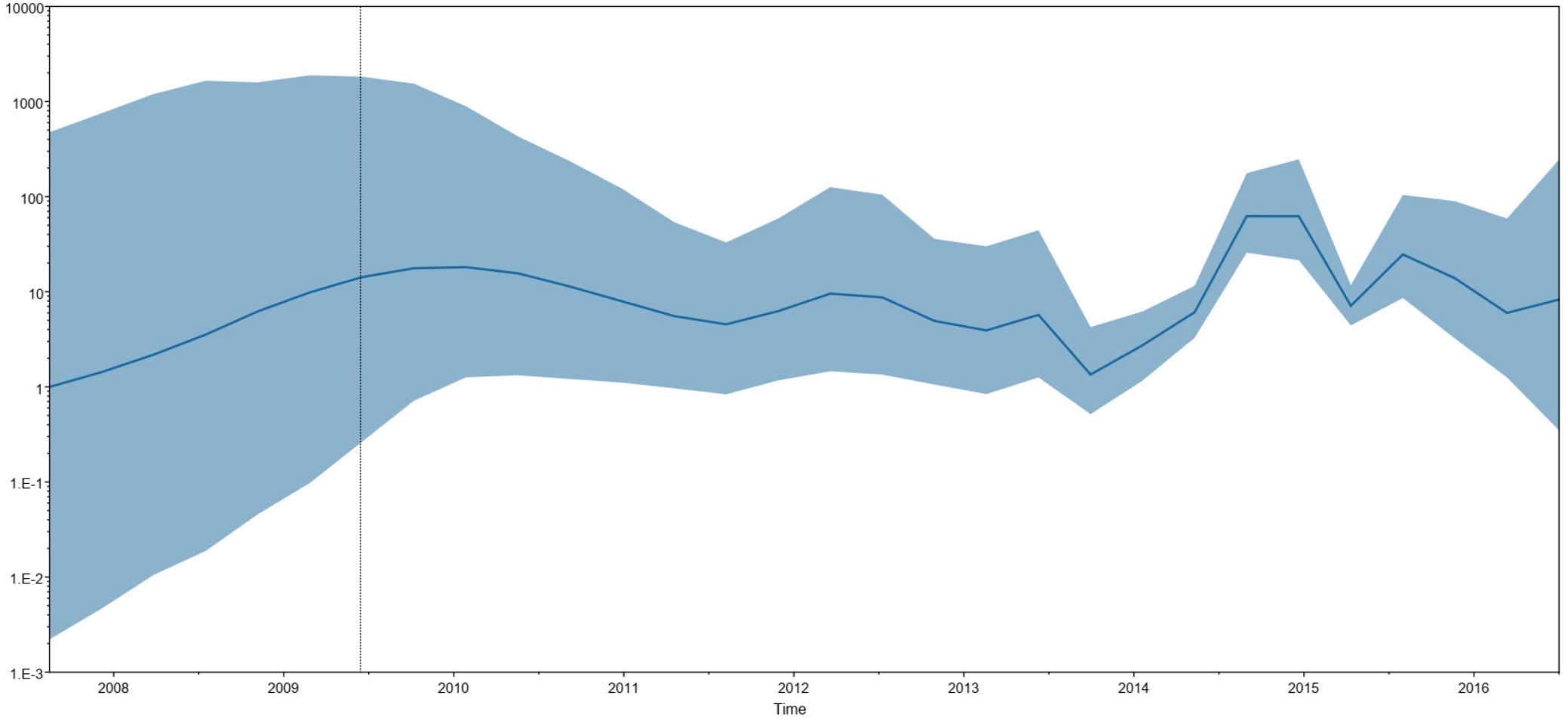

Figure S3. Skygrid demographic of CHIKV. The reconstruction plot, based on relaxed-clock coalescent analysis. X-axis represents time in years, while Y-axis shows the Effective population size at time t (Ne(t)). The thick black line represents the median, while the blue band represents 95% highest posterior density (HPD) intervals.