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Supplementary Information for

Many human RNA viruses show extraordinarily stringent selective constraints on protein evolution

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Other supplementary materials for this manuscript include the following:

Datasets S1 to S4

Fig. S1. Neighbor-Joining tree of the ZIKV strains studied. The phylogeny was built based on the multiple nucleotide sequence alignment of the entire protein coding region of the genomes studied. The synonymous distance (dS) was used as the distance metric. Only bootstrap values > 50 are shown. Each sequence is identified by its accession number in NCBI Genbank, the country from which it was isolated, and the date of isolation.

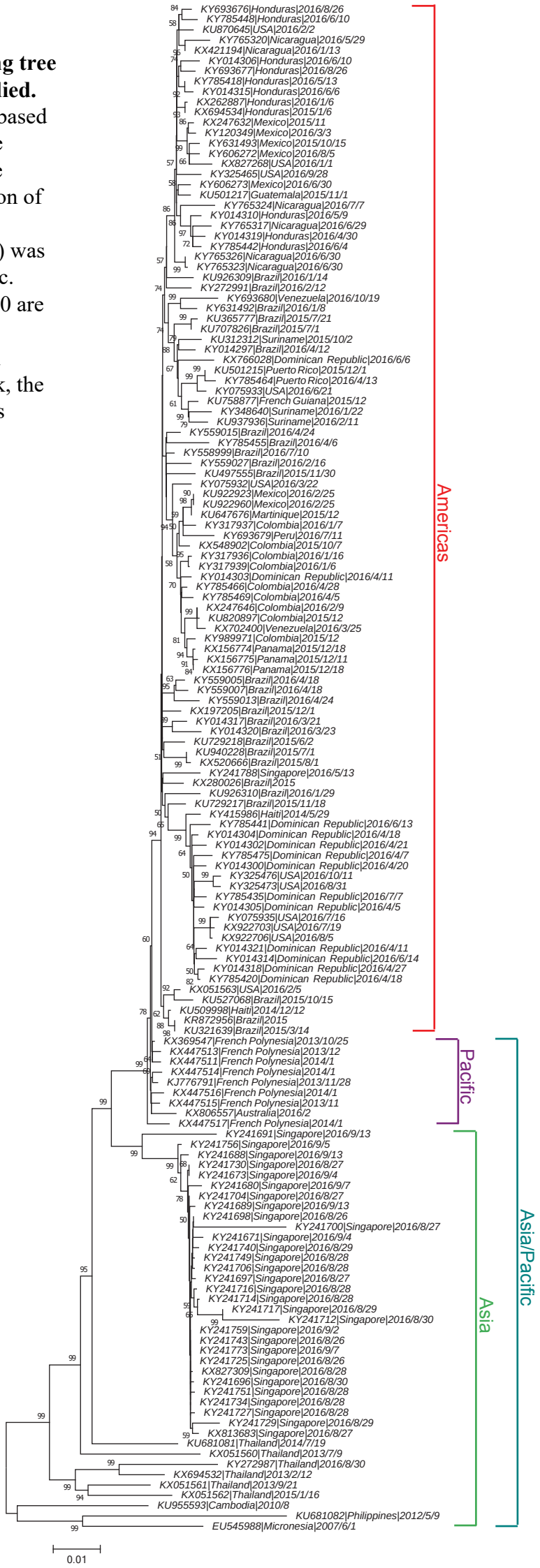

Fig. S2. Neighbor-Joining tree of the WNV strains studied. The phylogeny was built based on the multiple sequence alignment of the entire protein coding region of the genomes studied. The synonymous distance (dS) was used as the distance metric. Only bootstrap values > 50 are shown. Each sequence is identified by the same way as Fig. S1.

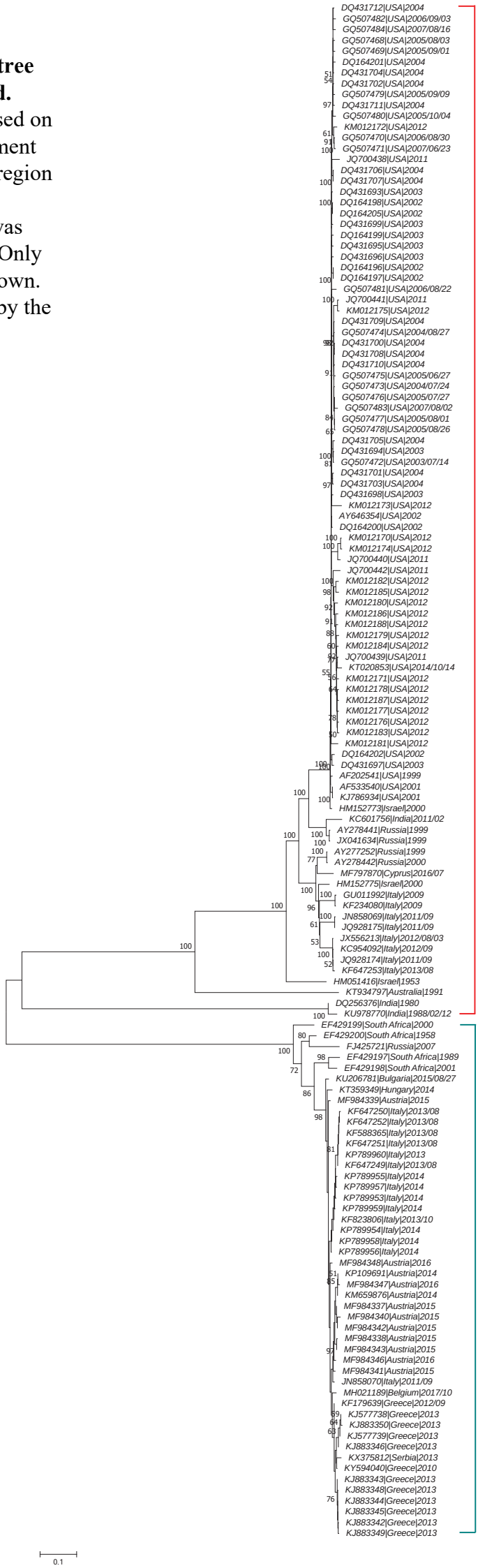

Fig. S3. Neighbor-Joining tree of the hepatitis E virus strains studied.

The phylogeny was built based on the multiple sequence alignment of the entire protein coding region of the genomes studied. The synonymous distance (dS) was used as the distance metric. Only bootstrap values > 50 are shown. Each sequence is identified as in Fig. S1.