



Fig. S1. Mutation frequency. The frequency of mutations in (A) S-segment with N, NSs, intergenic region (IGR), S-untranslated region (UTR), (B) M-segment with pre-glycoregion (ORF at the upstream of Gn cleavage site), Gn, Gc and M-UTR, and (C) L-segment with L ORF and L-UTR are shown. The frequency of mutations is represented by the number of mutations divided by the length of corresponding genome element.