



Supplementary Figure S1: Predicted RNA secondary structures of homologous regions of 5' untranslated regions of hepatitis C virus, genotype 1 (HCV; GenBank accession number NC_004102), bald eagle hepacivirus (BeHV; GenBank accession number MN062427), and the human pegivirus GB virus C (HPgV; GenBank accession number NC_001710). Structures are minimum free energy predictions (-110.12, -87.67, and -118.62 kcal/mol, respectively) generated by the RNAfold algorithm on the Vienna RNA Website server^{92,93}; colored scales indicate base-pair probabilities.