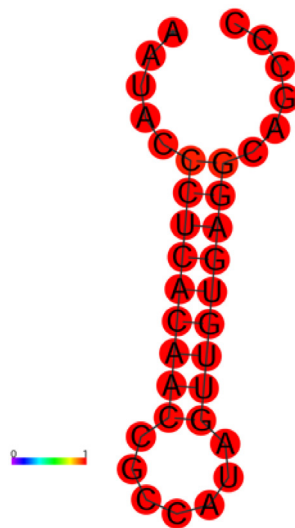


Supplementary Fig. 1. Conserved nucleotide region of hibiscus chlorotic ringspot virus (HCRSV) isolates predicted with BioEdit software. Conserved nucleotide regions were indicated with different colors.



Supplementary Fig. 2. The stem-loop secondary structures of a well-characterized and highly conserved sequences in the 3'-untranslated region of hibiscus chlorotic ringspot virus (HCRSV) genome predicted with RNAfold server (<http://rna.tbi.univie.ac.at/>). Color bar with No. 0-1 denotes the possibilities of base pairing.