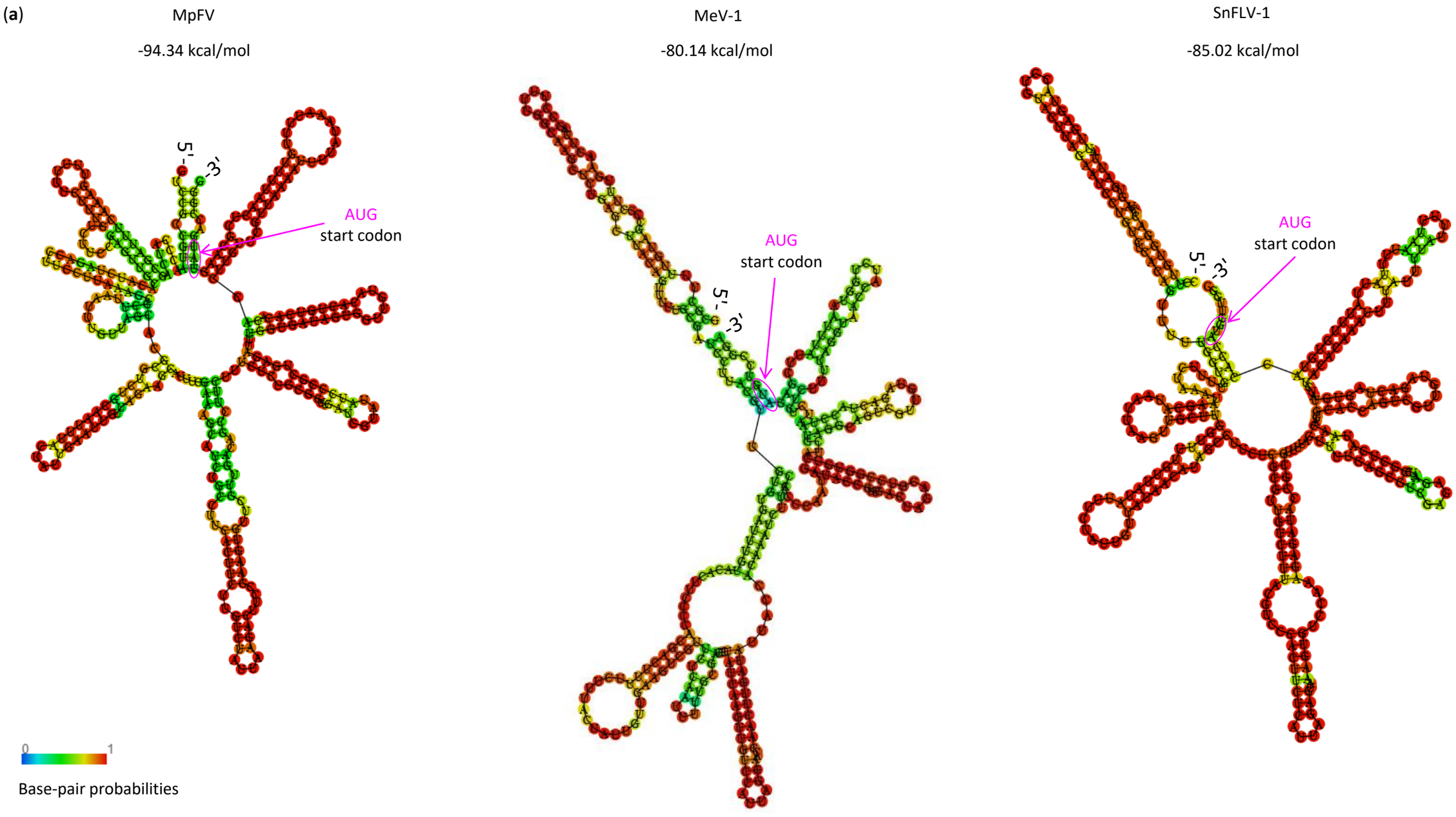
Figure S8. Secondary structure of the genomic RNA 5'- and 3'-untranslated regions (UTRs) of Myzus persicae flavivirus (MpFV), Macrosiphum euphorbiae virus 1 (MeV-1) and Sitobion miscanthi flavi-like virus 1 (SnFLV-1). Secondary structures of the 5'-UTRs (a) and 3'-UTRs (b) of MpFV, MeV-1 and SnFLV-1 genomic RNAs determined using RNA parameters of Turner model 2004 at 30°C at Webserver http://rna.tbi.univie.ac.at/cgi-bin/RNAWebSuite/RNAfold.cgi, are presented as images exported from the Webserver. Positions of 5'- and 3'-termini of the UTR sequences and the AUG start codons at the 5'-UTR ends are indicated. Color code indicates base pair probabilities ranging from 0 (blue) to 1 (red).



(**b**)

MpFV

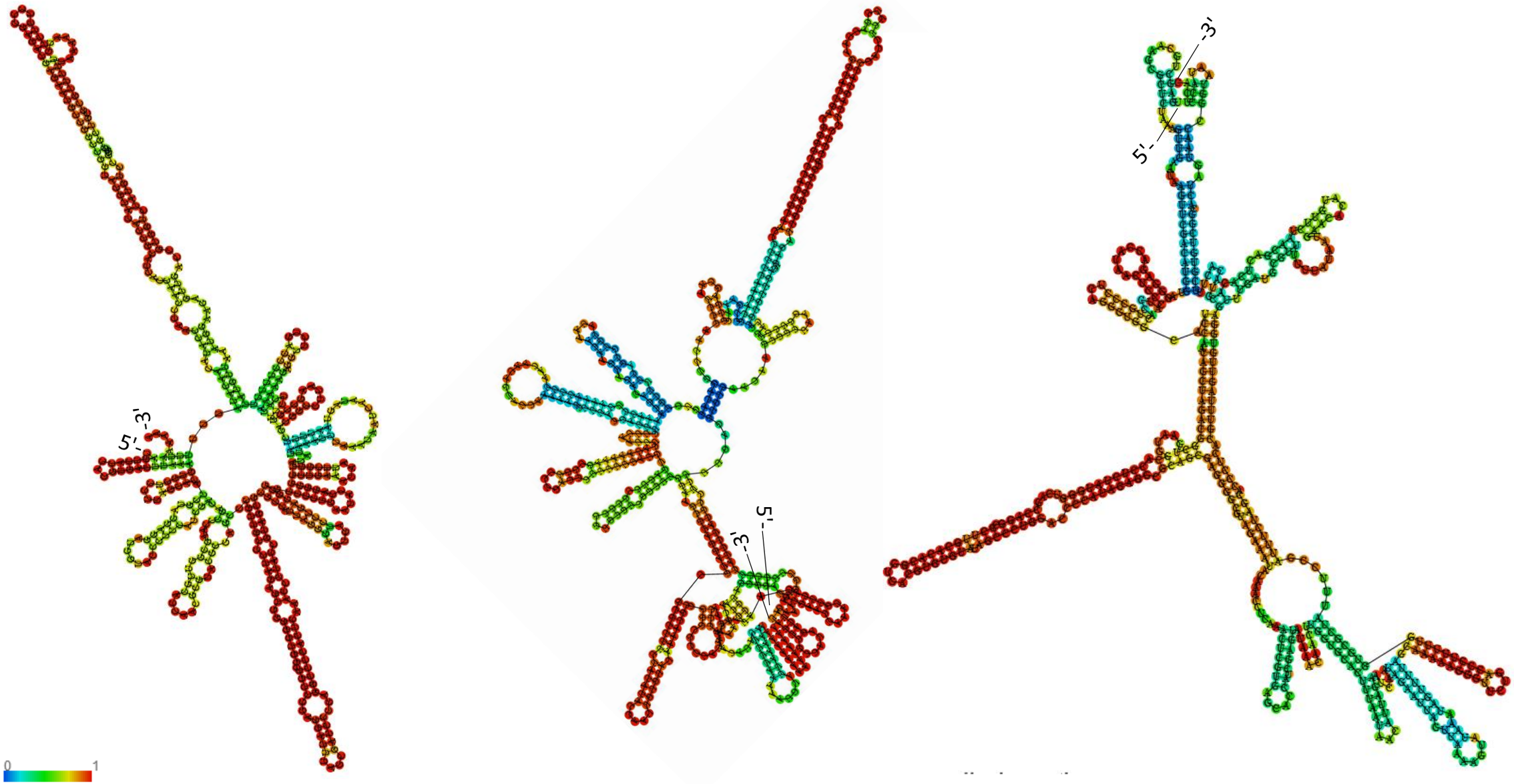
-183.46 kcal/mol

MeV-1

-155.42 kcal/mol

SnFLV-1

-160.2 kcal/mol



Base-pair probabilities