

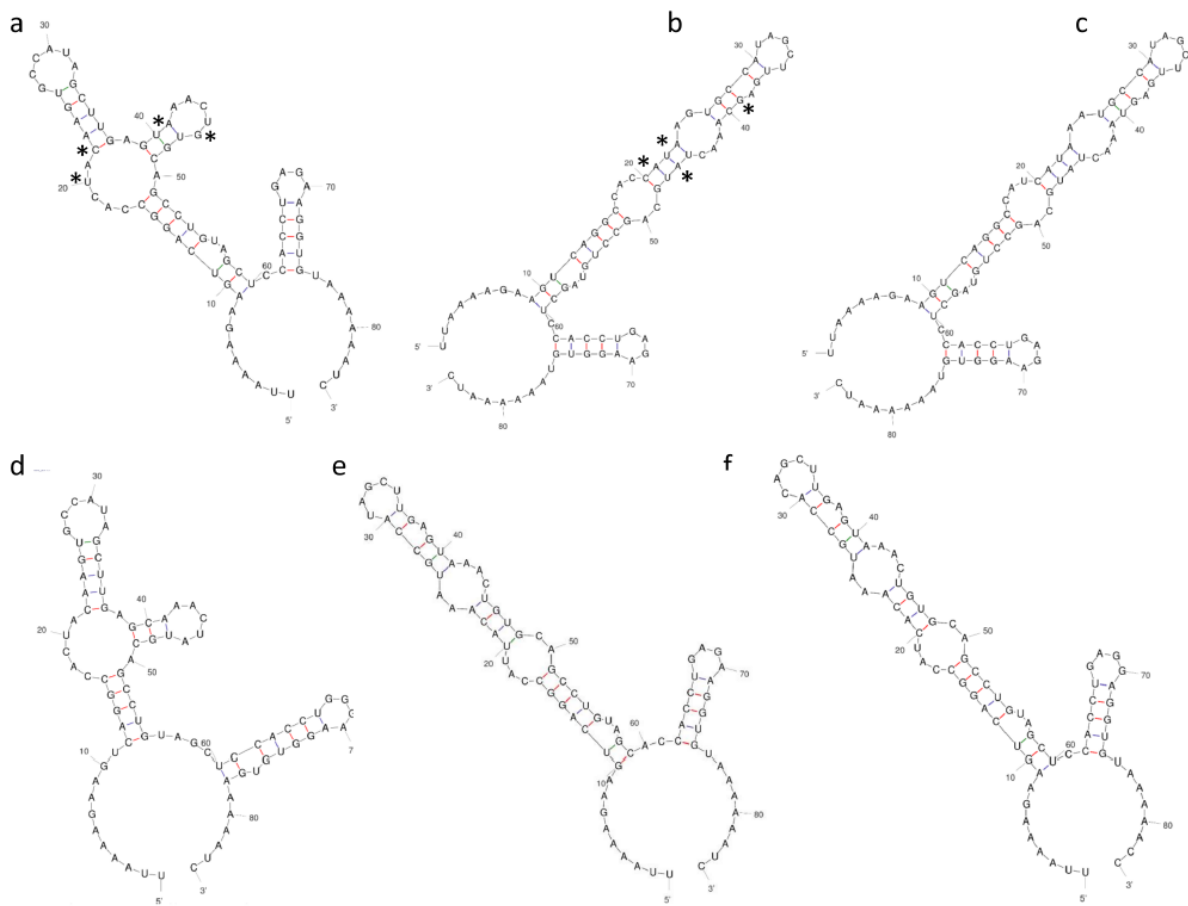
## Lineage replacement associated with fitness gain in mammalian cells and *Aedes*

### *aegypti*: A catalyst for dengue virus type 2 transmission

Cheong Huat Tan<sup>1£</sup>, Li Kiang Tan<sup>1£</sup>, Hapuarachchige Chanditha Hapuarachchi<sup>1£\*</sup>, Pei

Sze Jeslyn Wong<sup>1</sup>, Mei Zhi Irene Li<sup>1</sup>, Wing Yan Wong<sup>1</sup>, Lee Ching Ng<sup>1,2\*</sup>

\*Corresponding authors



**Figure S1. Comparison of RNA secondary structures of the variable region of 3'UTR.**

The complete sequence of 3'UTR was used to draw the secondary structure as predicted

by the MFOLD web server <sup>21</sup>. Only the region predicted to be structurally different between clades I and II viruses is shown. Positions shown correspond to respective nucleotides from the beginning of 3'UTR. (a). Clade I (SGEHI(D2)0232Y06) (b). Clade II (SG(EHI)D2/0866Y07) (c). DENV-2 Asian I genotype (GenBank accession no. NC001474) (d). DENV-2 cosmopolitan genotype – Indian sub-continent lineage (e). DENV-2 Asian II genotype (GenBank accession no. AF204178) and (f). DENV-2 American/Asian genotype (GenBank accession no. AF208496). Asian I genotype was not included as the structure was vastly different. The 3' UTR sequences of American genotype were not available in the GenBank database. Substitutions in clade I and II viruses are indicated with asterisks. Stem loop structures were named as illustrated elsewhere <sup>26,27</sup>.