

Supporting Information

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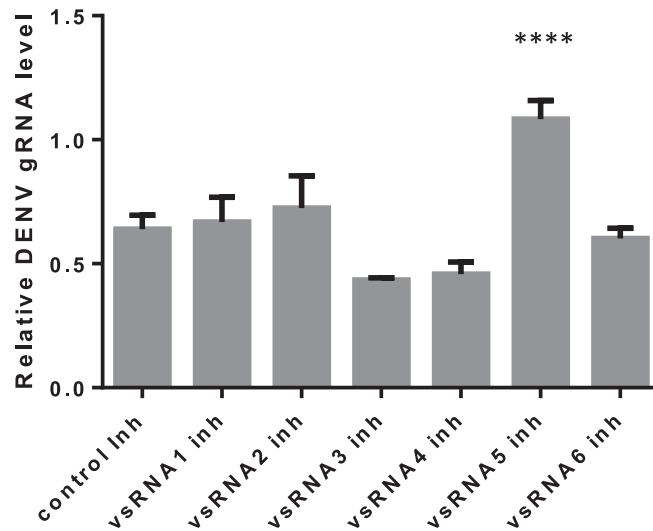


Fig. S1. Quantitative RT-PCR analysis to examine the levels of viral genomic RNA (gRNA) in *Aedes albopictus* RML-12 cells transfected with synthetic inhibitors of the six vsRNAs as shown in Fig. 1A followed by Dengue virus-2 infection at 7 d after infection. Data were normalized against RPS17. **** $P < 0.0001$, ANOVA.

Table S1. DENV-2 miRNA-like viral small RNAs (vsRNAs) identified in the 5' and 3'UTRs of the viral genome

DENV- vsRNAs	Genomic position	Sequence	PremiRNA (RNAfold)
vsRNA-1	14–35	CGUGGACCGACAAAGACAGAUU	AGUCUACGUGGACCGACAAAGACAGAUUCUUUGAGGGAGC UAAGCUCAACGU
vsRNA -2	10697–10723	AAUGGUGCUGUUGAAUACAACAGGUUCU	UCUCCUCAGCAUCAUCCAGGCACAGAACGCCAGAAAUG GAAUGGUGCUGUUGAAUACAACAGGUUCU
vsRNA -3	10488–10507	GUAGUGGACUAGCGGUUAGA	AUCUGGGAGGCCACAAACCAUGGAAGCUGUACGCAUGGCCGUA GUGGACUAGCGGUUAGAGGAG
vsRNA -4	10526–10546	AAUCGCAGCAACAAUGGGGGC	AUGGCGUAGUGGACUAGCGGUUAGAGGAGACCCUCCUUACA AAUCGCAGCAACAAUGGGGGC
vsRNA -5	10299–10321	CAGAAGUCAGGUCGGAUUAGCC	ACAAGGCAGAAGUCAGGUCGGAUUAGCCAUAGUACGGAAAAA CUAUGCACUCCUGUGAGCCC
vsRNA -6	10582–10602	ACUAGAGGUUAGAGGAGACC	AGGUGAGAUGAAGCUGUAGUCUCACUGGAAGGACUAGAGGUUA GAGGAGACCCCCCA

The vsRNA sequences were obtained from deep sequencing of DENV-infected *Aedes aegypti* mosquitoes. Potential sequences forming precursor stem loops (premiRNA) were predicted in RNAfold.

