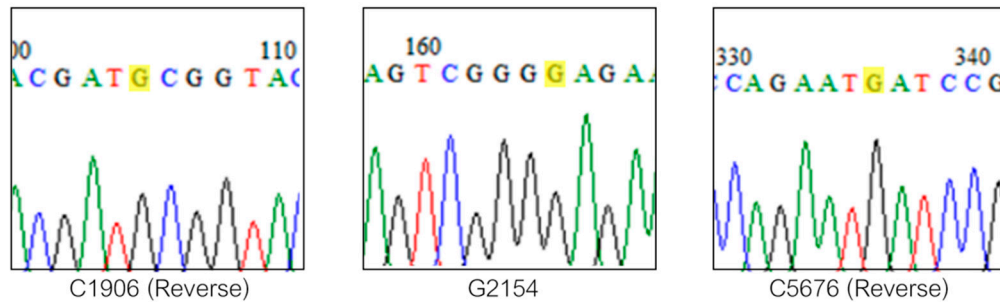
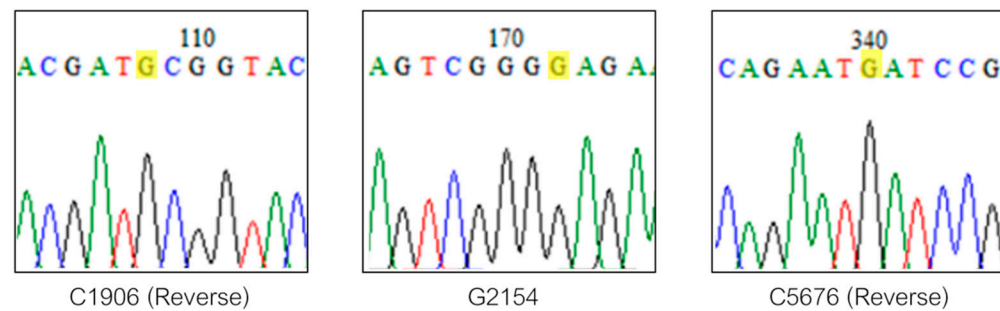


## Supplementary Materials

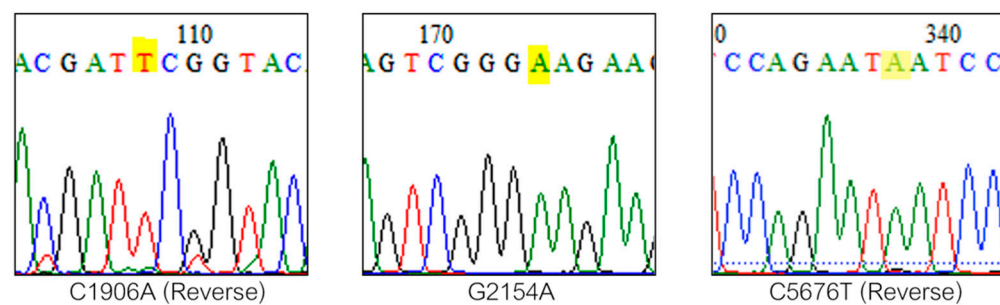
(a) ZIKV-CVD\_06-020



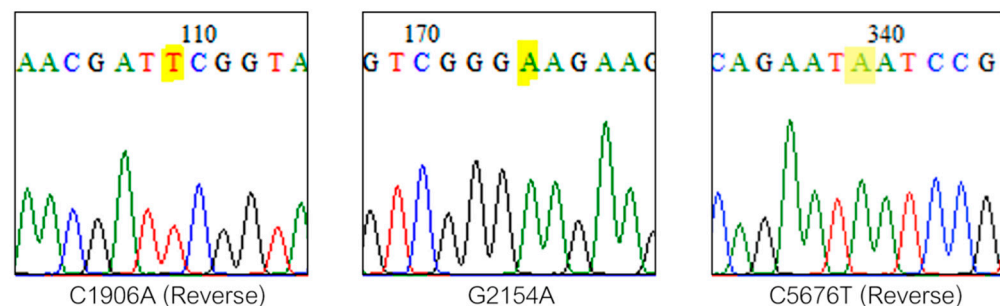
(b) ZIKV-PDK7-B5



(c) ZIKV-PDK7-S3



(d) ZIKV-PDK7-S1.4



**Figure S1.** Chromatograms of mutations **a)** ZIKV-CVD\_06-020 or wild-type, **b)** ZIKV-PDK7-B5, **c)** ZIKV-PDK7-S3, and **d)** ZIKV-PDK7-S1.4. The nucleotide positions at 1906, 2154, and 5676 represent the mutation points A310E, E393K, in E protein and H355Y in NS3, respectively. “(Reverse)” indicates that a reverse primer was used to read that sequence portion

**Table S1.** Primers for whole genome ZIKV sequencing

Region	Primer name	Primer sequence (5'-3')
5'UTR-E	ZIKV_F1	AGTTGTTGATCTGTGTGAATCAGACTGC <sup>1,2</sup>
	ZIKV_R213	CCATGACCCAGCAGAAAGTCC <sup>1</sup>
	ZIKV_F774	TCCACTAGGAAGCTGCAAA <sup>1</sup>
	ZIKV_F1084	GAGATGGATGGTGCAAAGGGAAG <sup>1</sup>
	ZIKV_R1_2040	CTGGGGTCAGAGTTTGCATG <sup>1,2</sup>
E-NS1	ZIKV_F2_1957	CAGTGGAGGTACAGTACGCAGG <sup>1, 2</sup>
	ZIKV_NS1F	GATGTGGGGTGCTCGGTGGACT <sup>1</sup>
	ZIKV_R2_4123	TTCTTCACACTGCCTTTCCCC <sup>1,2</sup>
NS1-NS3	ZIKV_F3_3978	CCACGCACTGACAAYATCACCTTGG <sup>1,2</sup>
	ZIKV_NS3F	AGTGGTGCTCTATGGGATGTG <sup>1</sup>
	ZIKV_R3_6040	CCACCTCCATACAGATACTCATCTC <sup>1,2</sup>
NS3-NS5	ZIKV_F4_5942	TGGACCCATGCCTGTCACAC <sup>1, 2</sup>
	ZIKV_F5886	AGATTCCAGGAGATGCCTAAAG <sup>1</sup>
	ZIKV_NS4AF	GGAGCGGCTTTTGGAGTGATGG <sup>1</sup>
	ZIKV_NS4BF	AATGAACTCGGATGGTTGGAG <sup>1</sup>
	ZIKV_F7418	AAAGATGGGACAGGTGCTACTC <sup>1</sup>
	ZIKV_R4_9037	CCCATCATGTTGTACACACAGCTC <sup>1,2</sup>
NS5-5'UTR	ZIKV_F5_8800	CGTAGCAATGCAGCATTAGGGG <sup>1,2</sup>
	ZIKV_NS5R	GAAGGGTCTACACCTGGAGTGCTA <sup>1</sup>
	ZIKV_F10117	GAGTGTGGATTGAGGAGAACGAC <sup>1</sup>
	ZIKV_R5	AGACCCATGGATTCCCCAC <sup>1,2,3</sup>

<sup>1</sup> Primers for sequencing<sup>2</sup> Primers for both amplification and sequencing of each fragment<sup>3</sup> Primer for cDNA synthesis

**Table S2.** Primers and probes for real-time PCR

	Detection	Primer and probe	Primer and probe sequences (5'-3')
Virus	Zika envelope	ZIKV_BonE_F*	AGYCGYTGYCCAACACAAG
		ZIKV_BonE_R*	CACCARRCTCCCYTTGCCA
		ZIKV_BonE probe*	FAM-CCTMCCTYGAYAAGCARTCAGACACYCAA-BHQ1
Housekeeping	40SRibosomal	RPS17_F**	ACATCTGATGAAGCGCCTGC
	Protein S17	RPS17_R**	ACACTTCCGGCACGTAGTTGT
	<i>A. aegypti</i>	RPS17_probe**	JOE-CACTCCCAGGTCCGTGGTATCTCCATC-BHQ1
	MusM_18srR	MusM_18srRNA_F	GTAACCCCGT TGAACCCCAT
	NA	MusM_18srRNA_R	CCATCCAATCGGTAGTAGCG
		MusM_18srRNA_probe	JOE-TCCCAGTAAGTGCGGGTCATAAGC-BHQ1

\*Corman VM, Rasche A, Baronti C, et al. Assay optimization for molecular detection of Zika virus. Bull World Health Organ. 2016;94(12):880-892. doi:10.2471/BLT.16.175950

\*\*Cox J, Brown HE, Rico-Hesse R. Variation in vector competence for dengue viruses does not depend on mosquito midgut binding affinity. PLoS Negl Trop Dis. 2011;5(5):e1172. doi:10.1371/journal.pntd.0001172

**Table S3.** Energy and vibrational entropy changes

Region	Mutations <sup>1</sup>	$\Delta\Delta G$ (kcal.mol <sup>-1</sup> .K <sup>-1</sup> ) <sup>2</sup>	$\Delta\Delta S_{Vib}$ (kcal.mol <sup>-1</sup> .K <sup>-1</sup> ) <sup>3</sup>
Envelope	A310E	1.861	-2.326
	E393K	1.629	-2.036
NS3	H355Y	-0.059	0.073

<sup>1</sup> Mutations of small-plaque isolates

<sup>2</sup> Energy changing between wild-type and mutation

<sup>3</sup> Vibrational Entropy Energy changing between wild-type and mutation