Supplementary Appendix

Engineered resistance to Zika virus in transgenic *Ae. aegypti* expressing a polycistronic cluster of synthetic small RNAs

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SI Materials and Methods

Synthetic anti-ZIKV small RNAs design and construction

The Drosophila melanogaster miR6.1 stem-loop, which has been previously validated in D. *melanogaster* [1], was modified to target eight unique sites in the ZIKV polyprotein region as previously described [2]. The eight target sites corresponded to regions of capsid (C), membrane precursor (prM), and envelope (E) structural genes, RNA-directed RNA polymerase NS5 (which contained three target sites), and non-structural proteins NS1 and NS2A, of ZIKV strain H/PF/2013 (GenBank: KJ776791.2) [3]. These sites were highly conserved in ZIKV strain FSS13025 (Cambodia 2010, Genbank KU955593)[4] and in ZIKV strain PRVABC59 (isolated from US traveller to Puerto Rico in 2015, GenBank KU501215) (SI Appendix Fig. S1). To generate miR6.1 stem-loop backbones that create mature synthetic small RNAs complementary to each of these target sites, pairs of primers were annealed and products were utilized for two subsequent rounds of PCR and cloned into the pFusA backbone (from the Golden Gate TALEN and TAL Effector Kit 2.0, Addgene #100000024) in sets of four using Golden Gate assembly [5] to generate plasmids OA959A and OA959B. Assembled small RNAs were then digested with either PmeI/BglII (vector OA959A) or with BamHI/PacI (vector OA959B) and were subcloned into a PacI/PmeI-digested final vector OA959C (the anti-ZIKV transgene). The ZIKV target sequences and sequences of primers used in the small RNA cloning are listed in SI Appendix Table S5.

Plasmid Assembly

To generate vector OA959C (the anti-ZIKV transgene), several components were cloned into the *piggyBac* plasmid pBac[3xP3-DsRed] [6] using Gibson assembly/EA cloning [7]. First, a *Drosophila* codon optimized tdTomato marker was amplified with primers 959C.10A and 959C.10B from a gene synthesized vector (GenScript, Piscataway, NJ) and cloned into a XhoI/FseI digested pBac[3xP3-DsRed] backbone using EA cloning. The resulting plasmid was

digested with AscI, and the following components were cloned in via EA cloning: the predicted Aedes aegypti carboxypeptidase promoter [8] amplified from Ae. aegypti genomic DNA using primers 959C.11A and 959C.11B, a GFP sequence amplified from vector pMos[3xP3-eGFP] [9] with primers 959C.12A and 959C.12B, and a 677 bp p10 3' untranslated region (UTR) 959C.13A and 959C.13B from amplified with primers vector pJFRC81-10XUAS-IVS-Syn21-GFP-p10 (Addgene plasmid #36432). Assembled small RNA fourmers were then subcloned into final plasmid OA959C using PacI and PmeI using traditional cloning. All primer sequences are listed in SI Appendix Table S6. Complete annotated plasmid sequence and DNA is available via Addgene (plasmid #104968).

Generation of Transgenic Mosquitoes

Germline transformations were carried out largely as described [10]. Briefly, 0-1 hr old Higgs and Liverpool strain Ae. aegypti pre-blastoderm embryos were injected with a mixture of vector OA959C (200 ng/ul) and a source of *piggyBac* transposase (200 ng/ul) [9]; the injected embryos were hatched in deoxygenated H₂O. A total of 52 surviving Higgs adult males and 64 surviving Higgs adult females, and 61 surviving adult Liverpool males and 75 surviving adult Liverpool females, respectively, were recovered after the injection. Higgs adults were assigned to 35 pools and Liverpool adults were assigned to 39 pools, and outcrossed to Higgs or Liverpool adults, respectively, of the opposite sex in cages. Larvae were fed ground fish food (TetraMin Tropical Flakes, Tetra Werke, Melle, Germany) and adults were fed with 0.3M aqueous sucrose. Adult females were blood fed three to five days after eclosion using anesthetized mice. All animals were handled in accordance with the guide for the care and use of laboratory animals as recommended by the National Institutes of Health and supervised by the local Institutional Animal Care and Use Committee (IACUC). A total of 8,189 Higgs and 10,949 Liverpool G₁s were screened. Larvae with positive fluorescent signals (3xp3-tdTomato) were selected under the fluorescent stereomicroscope (Leica M165FC) and were crossed to establish stable transgenic lines. Four independent lines (termed TZIKV-A, B, and D recovered from Liverpool G₁s, and TZIKV-C recovered from Higgs G_1 s) with the strongest fluorescence expression patterns were selected for further characterization. To determine whether these lines represented single chromosomal insertions, we backcrossed single individuals from each of the lines for four generations to wild-type stock, and measured the Mendelian transmission ratios in each generation; in all cases, we observed a 50% transmission ratio, indicating insertion into single chromosomes. For one of the four lines (TZIKV-C), transgenic mosquitoes were inbred for at least 12 generations to generate a homozygous stock. Mosquito husbandry was performed under standard conditions as previously described [11].

Characterization of Transgene Genomic Insertion Sites

To characterize the insertion site of vector OA959C in transgenic mosquitoes, we adapted a previously described inverse polymerase chain reaction (iPCR) protocol [12] as follows.

Genomic DNA (gDNA) was extracted from 10 transgenic Ae. aegypti fourth instar larvae of each line using the DNAeasy Blood & Tissue Kit (Qiagen #69504) per the manufacturer's protocol. Two separate restriction digests were performed on diluted gDNA to characterize the 5' and 3' ends of the insertion using Sau3AI (5' reaction) or HinP1I (3' reaction) restriction enzymes. A ligation step using NEB T4 DNA Ligase (NEB #M0202S) was performed on the restriction digest products to circularize digested gDNA fragments, and two subsequent rounds of PCR were carried out per ligation using corresponding *piggyBac* primers listed in SI Appendix Table S7. Final PCR products were cleaned up using the MinElute PCR Purification Kit (Qiagen #28004) in accordance with the manufacturer's protocol, and sequenced via Sanger sequencing (Source BioScience, Nottingham, UK). To confirm transgene insertion locus and orientation via PCR, primers were designed based on iPCR mapped genomic regions and used in tandem with *piggyBac* primers based on their location as listed in SI Appendix Table S7. Sequencing data was then blasted to the AaegL5.0 reference genome (NCBI). An alignment of the sequencing data was carried out with SeqManPro (DNASTAR, Madison, WI) to determine orientation of the transgene insertion site. Analysis of the sequencing data indicated that the insertion sites were on chromosome 2 (at approximate position 167,899,561) for line TZIKV-A, on chromosome 3 (at approximate position 402,525,313) for line TZIKV-B, on chromosome 3 (at approximate position 173,647,938) for line TZIKV-C, and on chromosome 1 (at approximate position 228,972,549) for line TZIKV-D. These insertion locations were also confirmed by PCR and sequencing performed on genomic DNA from the transgenic mosquitoes.

Small RNA Extraction, Isolation, Sequencing, and Bioinformatics

Total RNA was extracted from midguts of 30 ZIKV-C transgenic and WT (Higgs strain) non-blood-fed adult females as well as midguts of 30 ZIKV-C transgenic and WT (Higgs strain) adult females 24 hours post blood-feeding using the Ambion mirVana mRNA Isolation Kit (ThermoFisher Scientific #AM1560). Following extraction, RNA was treated with Ambion Turbo DNase (ThermoFisher Scientific #AM2238). The quality of RNA was assessed using RNA 6000 Pico Kit for Bioanalyzer (Agilent Technologies #5067-1513) and a NanoDrop 1000 UV-vis spectrophotometer (NanoDrop Technologies/Thermo Scientific, Wilmington, DE). Small RNA was then extracted and prepared for sequencing with QIAseq miRNA Library Kit (Qiagen #331502). Libraries were quantified with Qubit dsDNA HS Kit (ThermoFisher Scientific #Q32854) and High Sensitivity DNA Kit for Bioanalyzer (Agilent Technologies #5067-4626) and sequenced on Illumina HiSeq2500 in single read mode with the read length of 75 nt following manufacturer's instructions. After adapter trimming and UMI extraction, reads were aligned to mature Ae. aegypti miRNAs downloaded from miRBase (release 22, [13]) and to each synthetic small RNA's passenger, loop, and guide sequences using bowtie2 in 'very-sensitive-local' mode. (We assumed, based on the design of the synthetic small RNAs, that they are processed as miRNAs; however, it remains possible that they are instead processed as endogenous small RNAs (esiRNA) or some other small RNA species.) Custom Perl scripts were

used to quantify the number of reads that mapped to each target. 5 out of 8 target sites were reliably detected at TPM values between 2 and 91. Sites 3, 5 and 7 were not detected above background in either of the transgenic samples (Table S1). Correlation coefficients of TPM values between WT and transgenic animals were calculated in R[14]. Differential expression analysis was performed with R package DESeq2 using two factor design (design= ~ feeding + genotype). TPM values and MA plots were generated with R package ggplot2 (SI Appendix Fig. S3). Quantification data are shown in SI Appendix Table S1. All sequencing data can be accessed at NCBI SRA (accession ID: SRP150144; BioProject ID: PRJNA475410).

RT-PCR confirmation of anti-ZIKV transgene expression

To assay synthetic small RNA expression in mosquitoes, total RNA was separately extracted from 50 dissected midguts and 6 carcasses (midguts and heads removed) of Higgs WT and ZIKV-C non blood fed females, as well as 30 dissected midguts and 6 carcasses (midguts and heads removed) of Higgs WT and ZIKV-C females 24 hours post blood-feeding using the Ambion mirVana mRNA Isolation Kit (ThermoFisher Scientific #AM1560). Following extraction, total RNA was treated with Ambion Turbo DNase (ThermoFisher Scientific #AM2238). RNA was then converted to cDNA using RevertAid[™] H Minus First Strand cDNA Synthesis Kit (ThermoFisher Scientific #K1631) using a mix of oligo(dT)₁₈ and random hexamer primers. PCR was then performed on the resulting cDNA using standard procedures. To confirm presence of synthetic small RNA transcripts, primers 959.S7 and 959.S8 were used to amplify a fragment from the 5'UTR region of the carboxypeptidase A promoter (downstream of the transcription start site) to the loop-guide strand region of small RNA 1. As a positive control, primers 959.S10 and 959.S11 were used to amplify a short sequence of the Actin1 gene (AAEL011197)[15]. Expression of the anti-ZIKV transgene transcript was observed in both TZIKV-C midgut and carcass tissues regardless of mosquito blood meal state, but was completely absent in Higgs WT mosquito tissues (SI Appendix Figure S4), while Actin1 positive control transcripts were present in all samples. PCR products were sequenced to confirm product identity. All primer sequences are listed in SI Appendix Table S7.

ZIKV Infection of Mosquitoes, Virus Determination and Longevity

All experiments were performed under biosafety level 3 (BSL-3) conditions in the insectary at the Australian Animal Health Laboratory. Insectary conditions were maintained at 27.5°C and 70% in relative humidity with a 12hr light/dark cycle. ZIKV strain FSS13025 (Cambodia 2010, Genbank KU955593)[4] or PRVABC59 (Puerto Rico 2015, GenBank KU501215) were used for viral challenge experiments. Both belong to the Asian/Pacific/American clade and were passaged once in C6/36 cells and twice in Vero cells before using for mosquito infections. WT (Higgs strain for TZIKV-C experiments, Liverpool strain for TZIKV-A, B, and D experiments) and transgenic (confirmed by red fluorescence in the eye) mosquitoes were infected with ZIKV as previously described [16]. Briefly, female mosquitoes were challenged with a chicken blood

meal spiked with ZIKV (TCID₅₀ 10⁶/mL) through chicken skin membrane feeding. Blood-fed female mosquitoes were sorted and maintained at standard conditions in an environmental cabinet with sugar ad libitum. For infection rate and virus titer, mosquito midguts were collected at 4 dpi. For dissemination and transmission rate, mosquito saliva, midguts, and carcasses were collected at 14 dpi. Mosquito saliva was used to determine viral titers using TCID₅₀ assay on Vero cells. Midguts and carcasses were used to determine presence of viral RNA using RT-qPCR against ZIKV NS5 [16] (SI Appendix, Table S7). Mosquito viral challenge, processing, saliva testing, and molecular analyses of infection and dissemination were carried out as previously described [16]. ZIKV infection rate was defined by the number of midguts (4 dpi) found positive for viral nucleic acid over tested midguts. Similarly, the dissemination rate was calculated by the number of carcasses (14 dpi) testing ZIKV positive by qPCR. Transmission rate was defined by the number of $TCID_{50}$ positive saliva samples over the number tested. For each experiment, data from three replicates was pooled. The average TCID₅₀ values were compared by two-tailed unpaired t test. To measure fitness after infection, blood-fed ZIKV-infected females were quickly sorted out after CO₂ anaesthesia and housed in waxed cardboard cup 250 ml containers with a maximum of 25 mosquitoes. Mosquitoes were maintained at standard conditions for 14 days with 10% sugar solution ad libitum. Dead mosquitoes were counted daily. Females surviving at day 14 were marked as censored (status=0) in the database for survival analysis, which was performed using the GraphPad Prism software (GraphPad Software, La Jolla California, USA). The Mantel-Cox test was used to compare the survival of infected mosquitoes at 14 dpi.

Generation of wMel Wolbachia Line and Infection Assay

Eggs of *Ae. aegypti* infected with the *Wolbachia* strain *w*Mel were obtained from the World Mosquito Program (Prof. Scott O'Neill, Monash University). Higgs mosquitoes infected with *w*Mel were generated by crossing *w*Mel+ females with males from the Higgs line, and the resulting offsprings were used for ZIKV infections experiments. At the end of the experiment, *Wolbachia* infection status of these mosquitoes was tested using PCR with primers specific for *w*Mel detection [17] (SI Appendix, Table S7). The PCRs indicated presence of *w*Mel in >90% of mosquitoes, and only results from these positive mosquitoes were used for further analysis.

Mouse Transmission Assays

All experiments were performed under biosafety level 3 (BSL-3) conditions in the insectary at NHRI. Insectary conditions were maintained at 29°C and 80% relative humidity with a 12 hr light/dark cycle, and mosquitoes were maintained as previously described [18]. For experimental assays, transgenic anti-TZIKV-C mosquitoes were outcrossed to WT (Higgs strain) for a generation to obtain heterozygotes. Non-transgenic sibling mosquitoes from the above cross were used as Higgs WT controls. ZIKV strain PRVABC59 (Puerto Rico 2015, GenBank KU501215) was used for viral challenge experiments. It was obtained from the Taiwan Center

for Disease Control, and maintained/amplified as previously described [18]. For direct ZIKV infection, 7-10 day-old female TZIKV-C and Higgs WT mosquitoes were inoculated with 200 plaque forming units (pfu) of ZIKV by thoracic injection as previously described [18] and maintained under standard housing conditions for 7 days prior to their use in assays. Infection via artificial membrane blood feeding was carried out as described above, and infected mosquitoes were then maintained under standard conditions for 14 days prior to their use in transmission assays. Viral titers were measured at 7 dpi (for thoracic injection infections) or 14 dpi (for membrane blood feeding infection) by plaque assay as previously described [18,19]. Briefly, 2x10⁵ cells/well of Vero cells (a kind gift from Dr. Guann-Yi Yu) were incubated for one day (in serum-free 1xDMEM medium (HyClone, SH30022), at 37°C) before being infected with ZIKV. At two hours post infection, unbound virus particles were removed, and cells were gently washed by PBS and overlaid with 3 ml of 1xDMEM medium containing 2% FBS (Gibco, 16000044), 10 mM HEPES, 10nM sodium pyruvate, 2mM L-Glutamine (Gibco, 25030081), 1xPenicillin-Streptomycin (Gibco, 15140122), and 1% Methyl cellulose (Sigma, M0512-250G). The infected cells were then incubated at 37°C and 5% CO₂ for 4 days until plaque formation. Cells were fixed and stained with 0.5mL crystal violet/methanol mixed solution (ASK®Gram Stain Reagent) for 2 hours, and washed with H₂O. Number of plaques was then calculated, and viral titers were determined as plaque forming units per mosquito and were compared by one-way ANOVA.

All mouse-related experiments were conducted in compliance with the guidelines of the Laboratory Animal Center of NHRI. The animal protocol (NHRI-IACUC-105111) was approved by the Institutional Animal Care and Use Committee of NHRI, according to the Guide for the Care and Use of Laboratory Animals (NRC 2011). Management of animal experiments and animal care and use practices of NHRI have been accredited by the AAALAC International. *Stat1-/-* (C57BL/6 background) mice were provided by Dr. Guann-Yi Yu (NTU, Taiwan). Both male and female mice between the ages of 11-12 weeks were used in the study.

Mosquito-mediated ZIKV mouse infections were carried out as previously described [18,19]. Briefly, mice were anesthetized with Ketalar (100 mg/Kg, Pfizer, New York, NY) via intraperitoneal injection, and their ventral surfaces were shaved. Then, mice were placed on top of a polyester mesh covering a mosquito-housing cage that permitted female mosquitoes to take a blood meal. Female mosquitoes were starved for 10h before they were allowed to take blood meals from mice, and each mouse was fed on by 6–11 mosquitoes. Mouse body weight and mortality were then recorded for 6-30 days. Mouse weights were compared by the Mann Whitney test to evaluate for significant weight loss.

Fitness Assessment and Conditions

To determine if the anti-ZIKV transgene confers a fitness cost, several fitness parameters were evaluated in Higgs WT and TZIKV-C mosquitoes. For these experiments, homozygous TZIKV-C mosquito stock obtained after 12 generations of inbreeding (see above) and the Higgs

WT stock utilized to obtain transgenic lines were used. Evaluation of all experimental and control replicates were performed simultaneously. Insectary conditions were maintained at 28°C and 70-80% in relative humidity with a 12hr light/dark cycle. To assess larval to pupal development time, eggs were vacuum hatched and larvae were distributed into pans (50 larvae per pan) containing 2.5L of ddH₂O and 0.6mL of fish food slurry. To determine the development time of TZIKV-C and Higgs WT control mosquitoes, 4th instar larvae were sorted according to fluorescence phenotype and reared until pupation. Pupae were collected and counted every day until no pupae were left. To assess female fertility and fecundity, 90 TZIKV-C or Higgs WT females were mated to 20 Higgs WT males in a cage. After four days, females were blood fed and individually transferred into plastic vials filled with water and lined with egg paper. After three days, egg papers were collected, and eggs were counted and vacuum hatched in 9-ounce plastic cups. Starting on the fourth day, larvae were counted every day until no larvae were present. Female fecundity refers to the number of eggs laid per female, and fertility reflects the number of eggs hatching to produce larvae. To measure male mating success, fecundity, and fertility, one TZIKV-C or Higgs WT male was mated to five Higgs WT females in a single cup filled with water and lined with egg paper. Three days post blood meal, cups were checked for the presence of eggs, which were collected, counted, and hatched. Hatched larvae were then counted every day until no larvae were present. Male mating success was calculated as the percentage of single male outcrosses that produced larvae. Fecundity was measured as the number of eggs laid per cup; fertility was determined by the number of hatching larvae in each cup. To asses wing length as a proxy for body size, images of TZIKV-C and Higgs WT mosquito wings were taken with a Leica M165 FC microscope (Leica Microsystems). Wing length measurements were done by using the measurement tool on the Leica Application Suite X, measuring from the axial incision to the intersection of the R 4+5 margin. Finally, to assess mosquito longevity, equal numbers of male and female TZIKV-C or Higgs WT mosquitoes were placed in medium sized cages (in triplicate). Mosquitoes that died were counted and removed daily until all mosquitoes had died. Statistical analyses were performed using the GraphPad Prism software (GraphPad Software, La Jolla California, USA). Means were compared using unpaired t tests with Welch's correction except for male mating success (no Welch's correction). Analyses of mosquito survivorship utilized the Mantel-Cox test. P-values>0.05 were considered non-significant.

Confirmation of Transgene Zygosity

To molecularly confirm zygosity of transgenic mosquitoes, mosquito heads were homogenised using bead-beater for DNA extraction in 30 ul extraction buffer (1x Tris-EDTA, 0.1M EDTA, 1M NaCl and 2.5 uM proteinase K), and incubated at 56°C for 5 minutes and then at 98°C for 5 minutes. PCR was then performed on each line to detect the presence of the transgene by pairing a *piggyBac* primer with a genomic primer as follows: primers 1018.S46 and 991.5R2 for TZIK-A, 1018.S26 and 991.3F2 for TZIK-B, 1018.S8 and 991.5R1 for TZIK-C, and 1018.S50

and 991.3F2 for TZIK-D (SI Appendix Table S7). To determine zygosity, we amplified the WT locus of each transgenic line using corresponding forward and reverse primers listed in SI Appendix Table S7. WT mosquitoes (Higgs strain for TZIKV-C assays, Liverpool for TZIKV-A, B, and D assays) served as controls to ensure that the WT locus was successfully amplified in each genetic background. A PCR kit (ThermoFisher Scientific #F553S) with 57°C annealing temperature and standard protocols was used for all PCRs.

Data Availability Statement

All sequencing data associated with this study are available from NCBI sequence read archive (SRA) accession ID: SRP150144; BioProject ID: PRJNA475410. Complete annotated plasmid sequence and DNA is publically available at Addgene (plasmid #104968). Transgenic mosquitoes will be made available by corresponding author upon request.



SI Appendix Figures and Tables

SI Appendix Fig. S1. small RNA target site conservation between ZIKV strains H/PF/2013, FSS13025, and PRVABC59. small RNA target sites between the ZIKV strain used for small RNA target selection (H/PF/2013, top sequence) and the strains used for mosquito challenges (FSS13025, middle sequence; PRVABC59, bottom sequence) are highly conserved, with only one base pair mismatch in one target site in each strain (shown in red).



SI Appendix Fig. S2: Effect of anti-ZIKV transgene on ZIKV titres in four independent mosquito lines. ZIKV virus titres in wildtype (Liverpool WT and Higgs WT), anti-ZIKV transgenic mosquito lines (TZIKV-A, TZIKV-B, TZIKV-C, TZIKV-D) following a blood meal infected with a Cambodian (FSS13025) are shown. ZIKV genome equivalent from mosquito midgut (day 4 post infection) of Liverpool WT, Higgs WT, and transgenic mosquitoes were determined using real-time RT-qPCR and calculated using previously published methods. Circles represent WT mosquitoes; black diamonds represent anti-ZIKV Hm transgenic mosquitoes; red colored diamonds represent anti-ZIKV Ht transgenic mosquitoes. Horizontal bars represent the mean virus titer. Mantel-Cox test was used for statistical analysis. **represents p<0.001.









SI Appendix Fig. S3. Differential expression analysis of small RNAs from Higgs WT and TZIKV-C mosquito midguts. TPM (transcripts per million) values for transgenic versus Higgs WT animals without a blood meal (**A**) and 24 hours after a blood meal (**B**) are shown. Expression of synthetic small RNAs does not affect expression levels of endogenous miRNAs significantly (correlation coefficients of 0.9761 and 0.9757, respectively). MA (log2FoldChange vs. baseMean) (**C**) plot demonstrates that detected synthetic small RNAs are strongly differentially expressed between Higgs WT and transgenic animals.



SI Appendix Fig. S4. RT-PCR analysis on non blood fed and 24-hr post blood fed Higgs WT and TZIKV-C female midgut and carcass samples. A 195bp region of the anti-ZIKV transgene, from the 5'UTR region of the carboxypeptidase A (AAEL010782) promoter to the loop-target site-1 region, was amplified to confirm expression of the anti-ZIKV transgene (odd numbered lanes, labeled in red). A 175bp region of the *Actin1* gene was amplified as a control (even numbered lanes, labeled in white). Higgs WT midgut (lanes 1 and 2), Higgs WT carcass (lanes 3 and 4), TZIKV-C midgut (lanes 5 and 6), and TZIKV-C carcass (lanes 7 and 8) samples were assayed in both a non blood fed (top panel) and 24-hr blood fed (bottom panel) state. All PCR products were sequenced to confirm product identity.

Daily survival of mosquitoes



SI Appendix Fig. S5. Survivorship curve of Higgs WT and TZIKV-C male and female mosquitoes. The x-axis indicates the number of elapsed days after the start of the experiment, and the y-axis indicates the percent of mosquitoes surviving on each elapsed day. Each line represents accumulated results from 120-130 adult mosquitoes combined from 3 biological replicates.

SI Appendix Table S1. Quantification of endogenous and engineered small RNA expression on read and UMI (Unique Molecular Identifiers) levels in Higgs WT and TZIKV-C mosquitoes prior to blood meal (NBF) and 24 hr post blood feeding (PBM). Both raw read or UMI counts and normalized TPM (Transcripts Per Million) values are shown.

	NBF.	NBF.trans	PBM.	PBM.trans	NBF.	NBF.tran	PBM.	PBM.tran
	WT.co	genic.coun	WT.co	genic.coun	WT.T	sgenic.TP	WT.T	sgenic.TP
ID	unts	ts	unts	ts	PM	Μ	PM	Μ
target_site_						31.879374		90.868653
1	0	164	0	124	0	67	0	03
target_site_								
1_passenge						15.162141		30.045280
r	0	78	0	41	0	61	0	44
					0.2954			
target_site_					39041	6.4147522		5.1296820
2	1	33	0	7	6	2	0	26

target_site_								
2_passenge						0.5831592		0.7328117
r	0	3	0	1	0	927	0	18
target_site_						0.9719321		
3	0	5	0	0	0	545	0	0
target_site_								
3_passenge						18.855483		17.587481
r	0	97	0	24	0	8	0	23
					0.2954			
target_site_					39041	66.285772		16.854669
4	1	341	0	23	6	93	0	51
target_site_					0.2954			
4_passenge					39041	24.687076		33.709339
r	1	127	0	46	6	72	0	03
target_site_						0.5831592		0.7328117
5	0	3	0	1	0	927	0	18
target_site_								
5_passenge						0.1943864		
r	0	1	0	0	0	309	0	0
					0.2954			
target_site_					39041	27.019713		8.7937406
6	1	139	0	12	6	89	0	15
target_site_								
6_passenge						6.0259793		4.3968703
r	0	31	0	6	0	58	0	08
target_site_						0.1943864		1.4656234
7	0	1	0	2	0	309	0	36
target_site_								
7_passenge						0.7775457		
r	0	4	0	0	0	236	0	0
target_site_						1.9438643		2.1984351
8	0	10	0	3	0	09	0	54
target_site_								
8_passenge						11.274412		5.1296820
r	0	58	0	7	0	99	0	26
						0.3887728		
loop	0	2	0	0	0	618	0	0

aae-bantam					23045.	31427.426	33832.	34544.011
-3p	78005	161675	33520	47139	72244	21	20357	57
aae-bantam					876.56	1106.0587	1795.5	2816.1954
-5p	2967	5690	1779	3843	76365	92	69515	32
					43641.	33906.047	64252.	87095.405
aae-let-7	147717	174426	63660	118851	36891	6	926	49
					49405.	35735.612	39220.	44815.100
aae-miR-1	167227	183838	38859	61155	38461	68	93075	61
					863.56	831.19637	1182.9	190.53104
aae-miR-10	2923	4276	1172	260	83187	85	15948	67
aae-miR-10					8028.2	5055.6022	6768.4	4188.0189
0	27174	26008	6706	5715	60517	95	59343	68
aae-miR-10					297.21	173.19830	677.24	565.73064
00	1006	891	671	772	16759	99	96599	63
aae-miR-11					20095.	22788.115	13554.	14449.581
-3p	68020	117231	13429	19718	76361	68	07702	45
aae-miR-11					443.45	262.03290	321.97	383.99334
-5p	1501	1348	319	524	40015	88	11498	02
aae-miR-11					95989.	101887.84	58616.	66338.513
74	324904	524151	58076	90526	32638	21	91691	58
aae-miR-11					5841.4	13038.275	11868.	9581.5132
75-3p	19772	67074	11759	13075	20731	47	52273	12
aae-miR-11					7132.7	7119.7918	6275.9	7501.0607
75-5p	24143	36627	6218	10236	84782	04	14136	45
aae-miR-12					1168.4	1273.0367	1177.8	861.05376
-3p	3955	6549	1167	1175	6141	36	69379	86
aae-miR-12					31639.	23889.509	15872.	12690.100
-5p	107093	122897	15726	17317	45328	2	47116	52
aae-miR-12								0.7328117
4	0	0	0	1	0	0	0	18
aae-miR-12					4676.5	8181.7248	8592.2	4016.5410
5-5p	15829	42090	8513	5481	0459	76	89649	26
aae-miR-13					4170.1	4185.1398	3109.6	3584.9149
-3p	14115	21530	3081	4892	22072	57	96277	24
aae-miR-13					399.13	337.84361	457.21	668.32428
-5p	1351	1738	453	912	81452	69	9219	68
aae-miR-13					18.317	15.939687	17.158	5.8624937
3	62	82	17	8	22058	33	33714	44

aae-miR-13					571.37	465.16672	700.46	419.90111
7	1934	2393	694	573	91065	91	38807	44
					82922.	98991.289	34150.	32953.810
aae-miR-14	280675	509250	33835	44969	35301	93	13747	14
aae-miR-18					38905.	30137.089	60539.	
4	131686	155037	59981	79673	18563	09	65998	58385.308
aae-miR-18					25.407	28.963578	22.204	23.449974
89-3p	86	149	22	32	75758	2	90688	97
aae-miR-18					42568.	37516.775	18877.	16244.237
89-5p	144086	193001	18703	22167	62975	55	19879	35
aae-miR-18					857.65	773.07483	415.83	378.86365
90	2903	3977	412	517	95378	57	7347	82
aae-miR-18					24.226	46.847129	31.288	29.312468
91	82	241	31	40	00141	85	73242	72
aae-miR-19					303.41	321.90392	162.49	161.21857
0	1027	1656	161	220	58957	96	95458	79
aae-miR-19						0.1943864		
3	0	1	0	0	0	309	0	0
aae-miR-21								0.7328117
0	0	0	0	1	0	0	0	18
					0.2954			
aae-miR-21					39041		5.0465	5.8624937
9	1	0	5	8	6	0	69746	44
aae-miR-25					2.6589	1.3607050	5.0465	2.9312468
2-3p	9	7	5	4	51375	16	69746	72
aae-miR-25								0.7328117
2-5p	0	0	0	1	0	0	0	18
aae-miR-26						0.1943864		
3a-3p	0	1	0	0	0	309	0	0
aae-miR-26					138.56	103.80235	133.22	99.662393
3a-5p	469	534	132	136	09105	41	94413	64
					0.2954			
aae-miR-26					39041	0.1943864		
3b-3p	1	1	0	0	6	309	0	0
aae-miR-26					50.815	53.845041	48.447	24.182786
3b-5p	172	277	48	33	51516	36	06956	69
aae-miR-27					15751.	13760.809	98832.	98135.946
5-3p	53314	70791	97920	133917	03706	83	0219	83

aae-miR-27					42.543	27.019713	1113.2	1149.0487
5-5p	144	139	1103	1568	22199	89	73286	74
aae-miR-27					18945.	28574.610	65367.	46020.575
6- 3 p	64126	146999	64764	62800	32398	95	2086	89
aae-miR-27					156.58	267.08695	469.33	375.19959
6-5p	530	1374	465	512	26921	6	09863	96
aae-miR-27					4.1361	2.7214100	3.0279	2.9312468
65	14	14	3	4	46583	33	41847	72
aae-miR-27					4783.1	5816.2363	3040.0	2945.1702
7-3p	16190	29921	3012	4019	58084	99	53615	94
aae-miR-27					100.44	113.13290	23.214	19.785916
7-5p	340	582	23	27	92742	28	22083	38
aae-miR-27					2607.5	3919.0248	3781.8	3993.8238
8-3p	8826	20161	3747	5450	44981	33	99367	63
aae-miR-27					226.89	180.19622	202.87	309.97935
8-5p	768	927	201	423	7184	14	21038	67
aae-miR-27					5298.1	4575.8565	3471.0	3409.0401
9	17933	23540	3439	4652	08333	83	30671	12
aae-miR-28					76127.	96416.641	81540.	56411.846
1-3p	257677	496005	80788	76980	84593	66	45532	05
aae-miR-28					67.655	74.644389	128.18	102.59364
1-5p	229	384	127	140	54053	46	28715	05
aae-miR-28					6.2042	9.5249351	7.0651	6.5953054
2-3p	21	49	7	9	19874	14	97644	62
aae-miR-28					76.223	60.648566	62.577	30.045280
2-5p	258	312	62	41	27274	44	46485	44
aae-miR-28					13871	110109.02	66597.	59554.875
3	469526	566444	65983	81269	6.3115	75	5623	51
aae-miR-28					13.294	0.3887728	73.679	82.074912
5	45	2	73	112	75687	618	91829	41
aae-miR-28								
6a	0	0	0	0	0	0	0	0
aae-miR-28								0.7328117
6b	0	0	0	1	0	0	0	18
aae-miR-29					1021.0	1142.0202	2500.0	2224.0835
40-3p	3456	5875	2477	3035	37328	82	70652	64
aae-miR-29					10286.	7760.1007	21025.	18396.505
40-5p	34818	39921	20831	25104	59655	08	01887	37

					0.8863			
aae-miR-29					17124	0.5831592	30.279	1.4656234
41	3	3	30	2	9	927	41847	36
aae-miR-29					398.84	814.09037	557.14	528.35724
42	1350	4188	552	721	27062	26	12999	86
aae-miR-29								
43	0	0	0	0	0	0	0	0
aae-miR-29								
44a-3p	0	0	0	0	0	0	0	0
aae-miR-29					1.4771	0.5831592	1.0093	0.7328117
44a-5p	5	3	1	1	95208	927	13949	18
					0.2954			
aae-miR-29					39041	0.1943864	1.0093	
44b-3p	1	1	1	0	6	309	13949	0
					0.8863			
aae-miR-29					17124	1.1663185	3.0279	
44b-5p	3	6	3	0	9	85	41847	0
aae-miR-29					274.46	363.89139	268.47	253.55285
45-3p	929	1872	266	346	28697	86	75105	44
aae-miR-29					39.588	42.765014	60.558	65.953054
45-5p	134	220	60	90	83158	8	83695	62
aae-miR-29					1.1817	1.5550914	31.288	9.5265523
46	4	8	31	13	56166	47	73242	33
aae-miR-2a					3693.2	4270.8642	2285.0	2054.8040
-3p	12501	21971	2264	2804	83459	73	86781	57
aae-miR-2a					115.22	94.471805	84.782	95.265523
-5p	390	486	84	130	12262	41	37173	33
					423.36	591.71229	360.32	351.01681
aae-miR-2b	1433	3044	357	479	41466	56	50798	29
					365.45	530.48056	317.93	284.33094
aae-miR-2c	1237	2729	315	388	80945	99	3894	66
aae-miR-30					109.90	87.668280	2640.3	2481.3004
5-3p	372	451	2616	3386	33235	33	65291	77
aae-miR-30					853.81	638.55942	23818.	28740.142
5-5p	2890	3285	23599	39219	88303	55	79989	77
aae-miR-30					30.725	49.179767	35.325	
6-3p	104	253	35	39	66033	02	98822	28.579657

aae-miR-30					16271.	20953.885	18218.	20672.618
6-5p	55076	107795	18050	28210	60066	32	11678	56
aae-miR-30					1.4771	2.5270236	3.0279	1.4656234
7	5	13	3	2	95208	02	41847	36
aae-miR-30					1.7726	2.9157964	2.0186	2.1984351
8-3p	6	15	2	3	3425	63	27898	54
aae-miR-30					3407.2	4217.7967	2547.5	4205.6064
8-5p	11533	21698	2524	5739	98467	78	08408	49
					0.2954			
aae-miR-30					39041	1.3607050	7.0651	2.9312468
9a	1	7	7	4	6	16	97644	72
					0.2954			
aae-miR-30					39041	0.3887728		1.4656234
9b-3p	1	2	0	2	6	618	0	36
aae-miR-30								
9b-5p	0	0	0	0	0	0	0	0
					6513.8	4442.5074	5226.2	3960.8473
aae-miR-31	22048	22854	5178	5405	3999	92	27629	36
aae-miR-31								
5-3p	0	0	0	0	0	0	0	0
aae-miR-31					3.2498	2.3326371	11.102	2.1984351
5-5p	11	12	11	3	29458	71	45344	54
aae-miR-31					5619.8	9280.0082	3134.9	2822.0579
6	19022	47740	3106	3851	4145	11	29126	26
aae-miR-31					10046.	19786.594	15986.	14665.028
7	34006	101790	15839	20012	70005	8	52364	1
					28.066	54.233814	54.502	54.228067
aae-miR-33	95	279	54	74	70895	22	95325	13
aae-miR-34					25.407	13.023890	26.242	20.518728
-3p	86	67	26	28	75758	87	16268	1
aae-miR-34					40730.	42281.381	25560.	24656.183
-5p	137865	217512	25325	33646	70347	36	87576	06
aae-miR-37					5.6133	3.6933421	11.102	2.9312468
5	19	19	11	4	41791	87	45344	72
					8043.0	3633.2767	9084.8	13296.868
aae-miR-7	27224	18691	9001	18145	32469	8	34856	62
aae-miR-71					2800.4	3535.3060	1777.4	1862.8073
-3p	9479	18187	1761	2542	66676	19	01864	87

aae-miR-71					1885.1	1471.8940	1311.0	1566.0186
-5p	6381	7572	1299	2137	96525	55	9882	41
aae-miR-79					40.179	82.808619	55.512	54.960878
-3p	136	426	55	75	70966	56	2672	85
aae-miR-79					45.497	43.931333	21.195	35.174962
-5p	154	226	21	48	61241	38	59293	46
aae-miR-8-					59847.	52455.955	53965.	64277.847
3p	202571	269854	53468	87714	3821	92	99823	03
aae-miR-8-					2362.0	2666.7874	3200.5	3985.7629
5p	7995	13719	3171	5439	35138	45	34533	34
					115.51	148.51123	90.838	
aae-miR-87	391	764	90	117	66653	32	25542	85.738971
aae-miR-92					8.8631	8.7473893	12.111	10.259364
7	30	45	12	14	71249	9	76739	05
aae-miR-92								
9	0	0	0	0	0	0	0	0
aae-miR-92					173.42	228.59844	14991.	16261.824
a-3p	587	1176	14853	22191	27174	27	34009	83
aae-miR-92					3.2498	12.051958	10.093	6.5953054
a-5p	11	62	10	9	29458	72	13949	62
aae-miR-92					23.930		227.09	205.92009
b-3p	81	123	225	281	56237	23.909531	56386	27
aae-miR-92					20.976	14.578982	24.223	15.389046
b-5p	71	75	24	21	17195	32	53478	08
					0.8863			
aae-miR-93					17124	0.5831592	5.0465	0.7328117
2-3p	3	3	5	1	9	927	69746	18
aae-miR-93					2.3635	2.3326371	10.093	5.1296820
2-5p	8	12	10	7	12333	71	13949	26
aae-miR-95				_	15.067	9.1361622	22.204	5.8624937
7	51	47	22	8	39112	52	90688	44
aae-miR-96					141.51	228.01528	268.47	205.18728
5	479	1173	266	280	53009	34	75105	1
aae-miR-97		e 4 6 6 -			6328.3	6027.5344	4716.5	4598.3935
0	21420	31008	4673	6275	04271	49	24084	3
aae-miR-98			_	_	20.385	35.961489	34.316	25.648410
0-3p	69	185	34	35	29387	72	67427	13

					2 05 42	1 0 4 2 9 (4 2	4 0 2 7 2	2 100 4251
aae-mik-98	10	10		2	2.9545	1.9438043	4.0372	2.1984331
0-5p	10	10	4	3	90416	09	55796	54
aae-miR-98					9.4540	15.162141	14.130	16.121857
1	32	78	14	22	49332	61	39529	79
aae-miR-98					37.520	144.81789	99.922	43.968703
8-3p	127	745	99	60	75829	1	08096	08
aae-miR-98					90.404	101.66410	57.530	75.479606
8-5p	306	523	57	103	34674	34	8951	95
aae-miR-98					7.6814	7.3866843	160.48	7.3281171
9	26	38	159	10	15082	74	09179	8
aae-miR-99						0.1943864		
3	0	1	0	0	0	309	0	0
aae-miR-99					2390.3	3800.2547	2208.3	2085.5821
6	8091	19550	2188	2846	97286	24	78921	49
aae-miR-99					31.316	38.099740	55.512	51.296820
8	106	196	55	70	53841	46	2672	26
aae-miR-99					4084.4	2991.0240	3454.8	3653.7992
9	13825	15387	3423	4986	4475	12	81648	26
					22269.	21307.668	22466.	22784.581
aae-miR-9a	75376	109615	22259	31092	0132	62	31919	93
					30090.	26028.731	23456.	29476.618
aae-miR-9b	101849	133902	23240	40224	17095	87	45618	54
aae-miR-9c					1467.1	1583.4718	1085.0	1300.0079
- 3 p	4966	8146	1075	1774	50281	66	12495	88
aae-miR-9c					30301.	32098.059	24866.	31590.780
-5p	102564	165125	24637	43109	40986	4	46776	35
aae-miR-ia					2.0680	2.1382507		0.7328117
b-4-3p	7	11	0	1	73291	4	0	18
aae-miR-ia					36.339	41.015536	33.307	24.182786
b-4-5p	123	211	33	33	00212	92	36032	69

SI Appendix Table S2. Anti-ZIKV transgene effect on ZIKV infection, dissemination, and transmission rates. ZIKV infection rates were quantified in the midgut at 4 days post infection (dpi). Dissemination rates were quantified in both the midgut and carcass at 14 dpi. Transmission rates were calculated by measuring prevalence of ZIKV in the saliva at 14 dpi. For each experiment, data from three replicates is pooled.

Mosquito Line	Zygosity	Viral Strain	Infection (Midgut 4 dpi)	Dissemination		Transmission (Saliva 14 dpi)
				Midgut (14 dpi)	Carcass (14 dpi)	
Higgs WT	N/A	FSS13025	42/50 (84%)	52/65 (80%)	52/65 (80%)	48/65 (73.8%)
TZIKV-C	Heterozygote	FSS13025	28/32 (87.5%)	29/39 (74.4%)	29/39 (74.4%)	29/39 (74.4%)
TZIKV-C	Homozygote	FSS13025	0/32 (0%)	0/46 (0%)	0/46 (0%)	0/46 (0%)
Higgs WT	N/A	PRVABC 59	28/32 (87.5%)	53/70 (75.7%)	53/70 (75.7%)	53/70 (75.7%)
TZIKV-C	Heterozygote	PRVABC 59	26/32 (81.25%)	49/70 (70%)	49/70 (70%)	49/70 (70%)
TZIKV-C	Homozygote	PRVABC 59	0/32 (0%)	0/70 (0%)	0/70 (0%)	0/70 (0%)
Higgs-wMel	N/A	PRVABC 59	42/50 (84%)	38/50 (76%)	38/50 (76%)	38/50 (76%)

SI Appendix Table S3. Fitness evaluation of Higgs WT and TZIKV-C mosquitoes. Comparisons of several fitness parameters (leftmost column) between Higgs WT (second column from left) and TZIKV-C mosquitoes (third column from left) suggest that there are few significant differences (rightmost column) between the two groups, indicating that the anti-ZIKV transgene does not have a major impact on mosquito fitness.

	Mosq	Mosquito Strain		
Fitness Parameter	Higgs WT (N)	TZIKV-C (N)	<i>P</i> -value	
Female fecundity□ ^{†§}	102.5 ± 3.8 (65;	113.2 ± 4.4 (65; 7,117)	0.0708	

	6,648)		
Egg hatchability□ ^{∥§}	70.9 ± 2.7 (63; 4,684)	58.5 ± 2.8 (63; 4,130)	0.0019
Male mating success□°¶	92 ± 0.05 (25)	92 ± 0.05 (25)	>0.9999
Male fecundity□ ^{1§}	118.2 ± 11.8 (25; 2,846)	119.2 ± 12.7 (25; 3,089)	0.9580
Egg hatchability□ ^{Ⅲ§}	61 ± 5.8 (23; 1,562)	60.7 ± 4.8 (23; 1,771)	0.9709
Larval to pupal development in days \Box^{\S}	$10.35 \pm 0.07 \\ (1,224)$	9.836 ± 0.10 (904)	0.002
Female wing length □§	3.65 ± 0.02 (56)	3.62 ± 0.08 (58)	0.1489
Male wing length □ [§]	2.76 ± 0.01 (54)	2.79 ± 0.01 (55)	0.0600
Female median survival in days ^{††}	64 (124)	52 (124)	<0.0001
Male median survival in days ^{††}	18 (130)	20 (120)	0.2195
% Survival at 14 dpi with ZIKV 🗆 ‡††	80.6 ± 3.5 (129)	75 ± 4.6 (88)	0.3636

SI Appendix Table S4. The survivorship of ZIKV-infected TZIKV-C mosquitoes at 14 days post infection (dpi). Higgs WT, Higgs *w*Mel+, and TZIKV-C mosquitoes infected with ZIKV strain FSS13025 or PRVABC59 were assessed for survival at 14 dpi. The mean percentage±SEM of surviving mosquitoes and number of mosquitoes tested (in parentheses) are reported. No assay was performed for Higgs *w*Mel mosquitoes infected with strain FSS13025. The Mantel-Cox test was used to compare the survival of infected Higgs WT, Higgs *w*Mel (for PRVABC59 strain only), and TZIKV-C mosquitoes.

		_		
Virus strain	Higgs WT	Higgs WT	TZIKV-C	P-value

		wMel		
FSS13025 (Cambodia)	64.1% ± 6.6 (53)		73.6% ± 6.1 (53)	0.2528
PRVABC59 (Puerto Rico)	92.1% ± 3.0 (76)	86.9% ± 5.0 (46)	77.1% ± 7.0 (35)	0.0817

SI Appendix Table S5. Primer sequences and small RNA target sites utilized to generate synthetic small RNA constructs used in this study. Self annealing primers are listed first, and consist of forward and reverse target site sequences flanking the stem loop region of the synthetic small RNA. Primers amplifying flanking regions, BsaI cut sites, and multiple cloning sites are listed below.

Primer	Primer Sequence, 5' to 3'	Source
small RNA 1 959C.1A	ATCACAGCCTTTAATGTACACAAAGCACTTGATTAGCGTTAAGTTAAT ATACCATATCTA	Self annealing primers
959C1.B	TTAGGCACTTTAGGTACACACAAAGCACTTGATTAGAGTTAGATATGG TATATTAACTTA	
small RNA 2 959C.2A	ATCACAGCCTTTAATGTGGAATGCCCACTCAAACATCGATAAGTTAAT ATACCATATCTA	Self annealing primers
959C.2B	TTAGGCACTTTAGGTACGGAATGCCCACTCAAACATAGATAG	
small RNA 3 959C.3A	ATCACAGCCTTTAATGTGGATTGTCAATATGCTAAACCGTAAGTTAAT ATACCATATCTA	Self annealing primers
959C.3B	TTAGGCACTTTAGGTACGGATTGTCAATATGCTAAAACGTAAGTTAAT ATACCATATCTA	

small RNA 4 959C.4A	ATCACAGCCTTTAATGTATAGAGCGAAGGTTGAGATCACTAAGTTAAT ATACCATATCTA	Self annealing primers
959C.4B	TTAGGCACTTTAGGTACATAGAGCGAAGGTTGAGATAACTAGATATGG TATATTAACTTA	
small RNA 5 959C.5A	ATCACAGCCTTTAATGTGGAGAATGAAGCTCTAATCCCCTAAGTTAAT ATACCATATCTA	Self annealing primers
959C.5B	TTAGGCACTTTAGGTACGGAGAATGAAGCTCTAATCACCTAGATATGG TATATTAACTTA	
small RNA 6 959C.6A	ATCACAGCCTTTAATGTCGAATGGCAGTCAGTGGAGCTGTAAGTTAAT ATACCATATCTA	Self annealing primers
959C.6B	TTAGGCACTTTAGGTACCGAATGGCAGTCAGTGGAGATGTAGATATGG TATATTAACTTA	
small RNA 7 959C.7A	ATCACAGCCTTTAATGTAGAAGTGAAAGGATACACATAATAAGTTAAT ATACCATATCTA	Self annealing primers
959C.7B	TTAGGCACTTTAGGTACAGAAGTGAAAGGATACACAAAATAGATATG GTATATTAACTTA	
small RNA 8 959C.8A	ATCACAGCCTTTAATGTTGACCACAAAGATCATCATCAGTAAGTTAAT ATACCATATCTA	Self annealing primers
959C.8B	TTAGGCACTTTAGGTACTGACCACAAAGATCATCATAAGTAGATATGG TATATTAACTTA	
720C	TTTAAAGTCCACAACTCATCAAGGAAAATGAAAGTCAAAGTTGGCAGC TTACTTAAACTTAATCACAGCCTTTAATGT	Self-annealed products of
720D	AAAACGGCATGGTTATTCGTGTGCCAAAAAAAAAAAAAA	959C.#A/959C .#B
small RNAs 1,5 959C.C1	TCTAGAGGTCTCGCTATCGGCGGCCGCGCGTTTAAACAACCGGATCCT TTAAAGTCCACAACTCATC	Self-annealed products of 720C/720D-1 and 720C/720D-5
720F.1	CTCGAGGGTCTCCCATGGTCAAAACGGCATGGTTATTCGTG	120C/120D-3

small RNAs 2,6 720E-2 720-F2	TCTAGAGGTCTCCCATGGCTTTAAAGTCCACAACTCATCAAGGA CTCGAGGGTCTCGGTCCTGAAAACGGCATGGTTATTCGTGTGC	Self-annealed products of 720C/720D-2 and 720C/720D-6
small RNA 3,7 720-E3 720-F3	TCTAGAGGTCTCAGGACCATTTAAAGTCCACAACTCATCAAGGAA CTCGAGGGTCTCCCTGGCAAAAACGGCATGGTTATTCGTGTGC	Self-annealed products of 720C/720D-3 and 720C/720D-7
small RNA 4,8 720-E4 959C.C2	TCTAGAGGTCTCGCCAGGATTTAAAGTCCACAACTCATCAAGGA CTCGAGGGTCTCCCGCCACTGCGGCCGCTTAATTAATGGCCGGCC	Self-annealed products of 720C/720D-4 and 720C/720D-8
small RNA target site	Target Sequence (5' to 3')	Viral Region Targeted
		0
small RNA target site 1	ACACAAAGCACTTGATTAGAGT	Membrane glycoprotein precursor M
small RNA target site 1 small RNA target site 2	ACACAAAGCACTTGATTAGAGT GGAATGCCCACTCAAACATAGA	Membrane glycoprotein precursor M Nonstructural protein NS1
small RNA target site 1 small RNA target site 2 small RNA target site 3	ACACAAAGCACTTGATTAGAGT GGAATGCCCACTCAAACATAGA GGATTGTCAATATGCTAAAACG	Membrane glycoprotein precursor M Nonstructural protein NS1 Capsid protein C

small RNA target site 5	GGAGAATGAAGCTCTAATCACC	RNA-depende nt RNA polymerase NS5
small RNA target site 6	CGAATGGCAGTCAGTGGAGATG	RNA-depende nt RNA polymerase NS5
small RNA target site 7	AGAAGTGAAAGGATACACAAAA	RNA-depende nt RNA polymerase NS5
small RNA target site 8	TGACCACAAAGATCATCATAAG	Nonstructural protein NS2A

Fragment and Primers	Primer Sequence, 5' to 3'	Source
tdTomato marker 959C.10A 959C.10B	GACGGTACGATCCACCGGTCGCCACCATGGTGAGCAAGGGCGAGGA GGTCATCAAAGAGT TGGTATGGCTGATTATGATCTAGAGTCGCGGCCGCCTACTTGTACAG CTCGTCCATGCCG	Gene synthesized vector
Carboxypeptidase promoter 959C.11A 959C.11B	ATGGTTAATTCGAGCTCGCCCGGGGTCCTAGGGAATTCGTCAATAA AAAAATACGTTCAA CTCCTCGCCCTTGCTCACCATGTTTAAACTTTCCCAACTAACCGATA CACACTAACCTG	Genomic <i>Ae.</i> <i>aegypti</i> DNA
GFP marker 959C.12A 959C.12B	AGTGTGTATCGGTTAGTTGGGAAAGTTTAAACATGGTGAGCAAGGG CGAGGAGCTGTTCAC TGATTTGTTATTTTAAAAACGATTCATTCTAGTTAATTAA	pMos[3xP3- eGFP]
p10 3' UTR 959C.13A 959C.13B	GGACGAGCTGTACAAGTAATTAATTAACTAGAATGAATCGTTTTTA AAATAACAAAT TCCCCGGGCGAGCTCGAATTGGCGCGCCCGGCCGTTAACTCGAATC GCTATCCAAGC	pJFRC81-10 XUAS-IVS- Syn21-GFP- p10

SI Appendix Table S6. Primers used to assemble plasmid OA959C (the anti-ZIKV transgene).

piggyBac Primers				
Reaction	Primer Name		Primer Sequence, 5' to 3'	
5' (1st Round PCR)	991.5F1		GACGCATGATTATCTTTTACGTGAC	
	ļ	991.5R1	TGACACTTACCGCATTGACA	
5'(2nd Round PCR)	991.5F2		GCGATGACGAGCTTGTTGGTG	
	9	991.5R2	TCCAAGCGGCGACTGAGATG	
3' (1st Round PCR)		991.3F1	CAACATGACTGTTTTTAAAGTACAAA	
	991.3R1		GTCAGAAACAACTTTGGCACATATC	
3' (2nd Round PCR)	991.3F2		CCTCGATATACAGACCGATAAAAC	
	991.3R2		TGCATTTGCCTTTCGCCTTAT	
Zygosity Primers				
Reaction	Line	Primer Name	Primer Sequence, 5' to 3'	
Forward primer	TZIK-A	1018.S46	GTACTGGCACCCATAGCTCG	
	TZIK-B	1018.S27	GCAAATCCTAAAACCTCATCGAACCG	
	TZIK-C	1018.S8	TTTCCACGAAATGAACTCAAACGC	
	TZIK-D	1018.S48	ACGTTATGCAAATCTCTCGGAT	

Supplementary Table S7. Diagnostic primers used for inverse PCR (iPCR) assays, zygosity confirmation, ZIKV NS5 RT-qPCR, and *w*Mel infection confirmation.

Reverse primer	TZIK-A	1018.S47.1	CGAAAATTGCGTTTACCTTATACGT
	TZIK-B	1018.S26	AATCGAATGAACGAATTTCTGATTAAATCC
	TZIK-C	1018.S10	AGAAGAACAGAGGCAATCAACTACATTGA
	TZIK-D	1018.850	CCATCTTTCGATGGAAATGCATT
ZIKV NS5 RT-qPCR Primers			
Primer name			Primer Sequence, 5' to 3'
NS5-F		GAACGAGGATCACTGGATGG	
NS5-R		CTCCTGGTATGCGACTCATC	
wMel Primers			
Primer name		Primer Sequence, 5' to 3'	
wMel-F		CAAATTGCTCTTGTCCTGTGG	
wMel-R		GGGTGTTAAGCAGAGTTACGG	
RT-PCR Primers			
Primer name		Primer Sequence, 5' to 3'	
<i>Actin1</i> -F 959.S10		CGTTCGTGACATCAAGGAAA	
Actin1-R 959.S11		GAACGATGGCTGGAAGAGAG	
Synthetic small RN 959.S7	A-F	ATGGCACCTGATTGCAATTGGC	

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