

Supplemental Information

**Genomic Epidemiology Reconstructs
the Introduction and Spread of Zika Virus
in Central America and Mexico**

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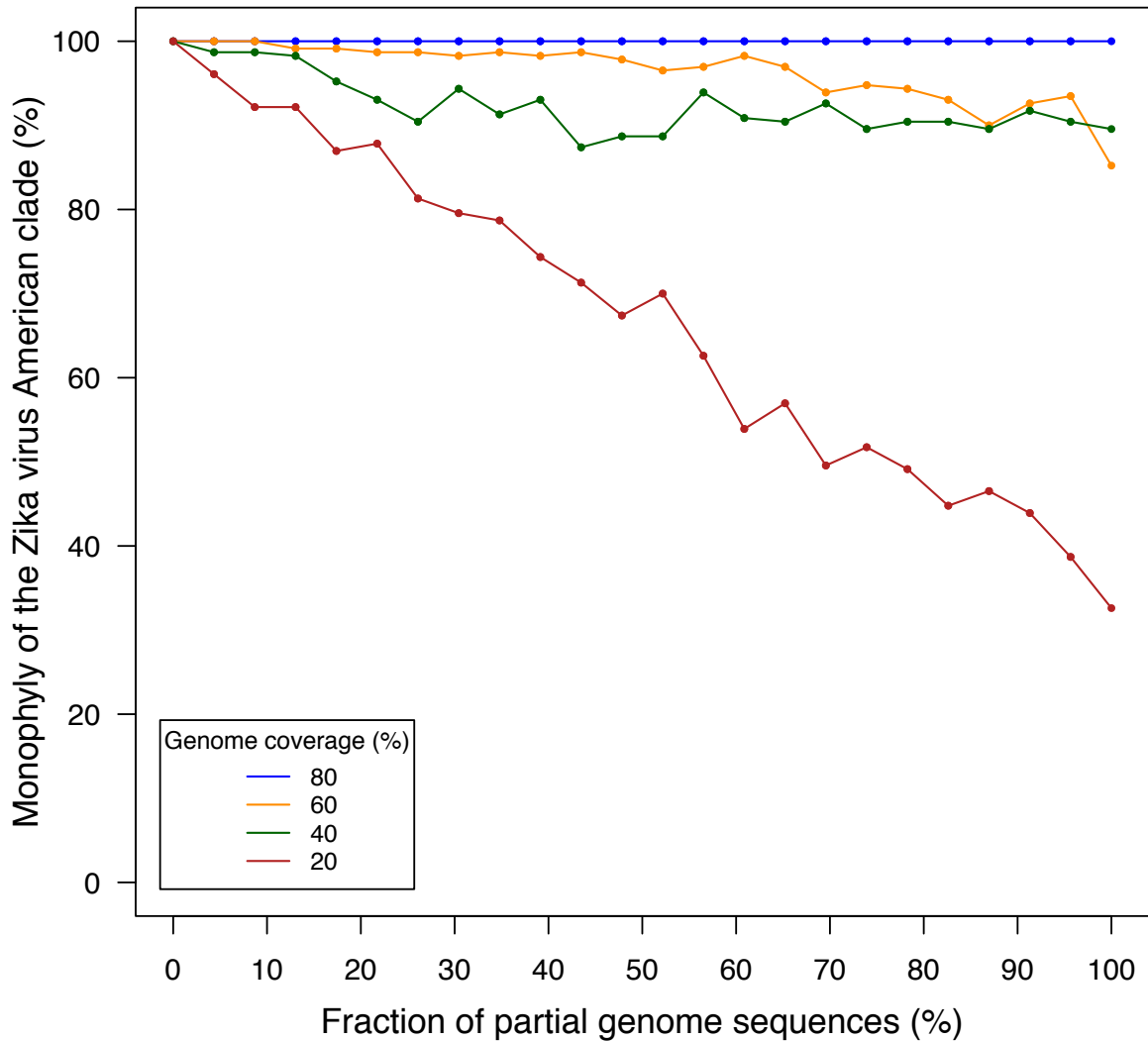


Figure S1. The effect of partial genome sequences on ZIKV phylogenetic inference (related to Figure 1 and Figure 2A). An initial dataset comprising 28 ZIKV complete genome sequences of the Asian genotype was generated (comprising 5 basal genomes from South East Asia and 23 genomes from the Americas, forming the American outbreak clade). Replicate datasets were derived from the initial dataset by subsampling one or more of the 23 American ZIKV genomes, as follows. For each genome that was subsampled, we reduced its coverage from 100% to 20, 40, 60, or 80% (colors; inset) by randomly mapping simulated reads to the genome until the required coverage was reached, then replacing nucleotides at the unmapped sites with the ambiguity code “N”. The read positions and lengths of the simulated reads were chosen to be characteristic of metagenomic sequencing of clinical ZIKV samples. This procedure was then repeated by varying the number of subsampled genomes from 0 to 23 (x-axis). Therefore, for each combination of coverage and fraction of partial genomes (i.e. each dot in the figure), 230 replicate alignments were generated. Maximum likelihood trees were estimated from each replicate alignment and, for each, the percentage of trees in which the American ZIKV outbreak clade is inferred to be monophyletic is shown on the y-axis.

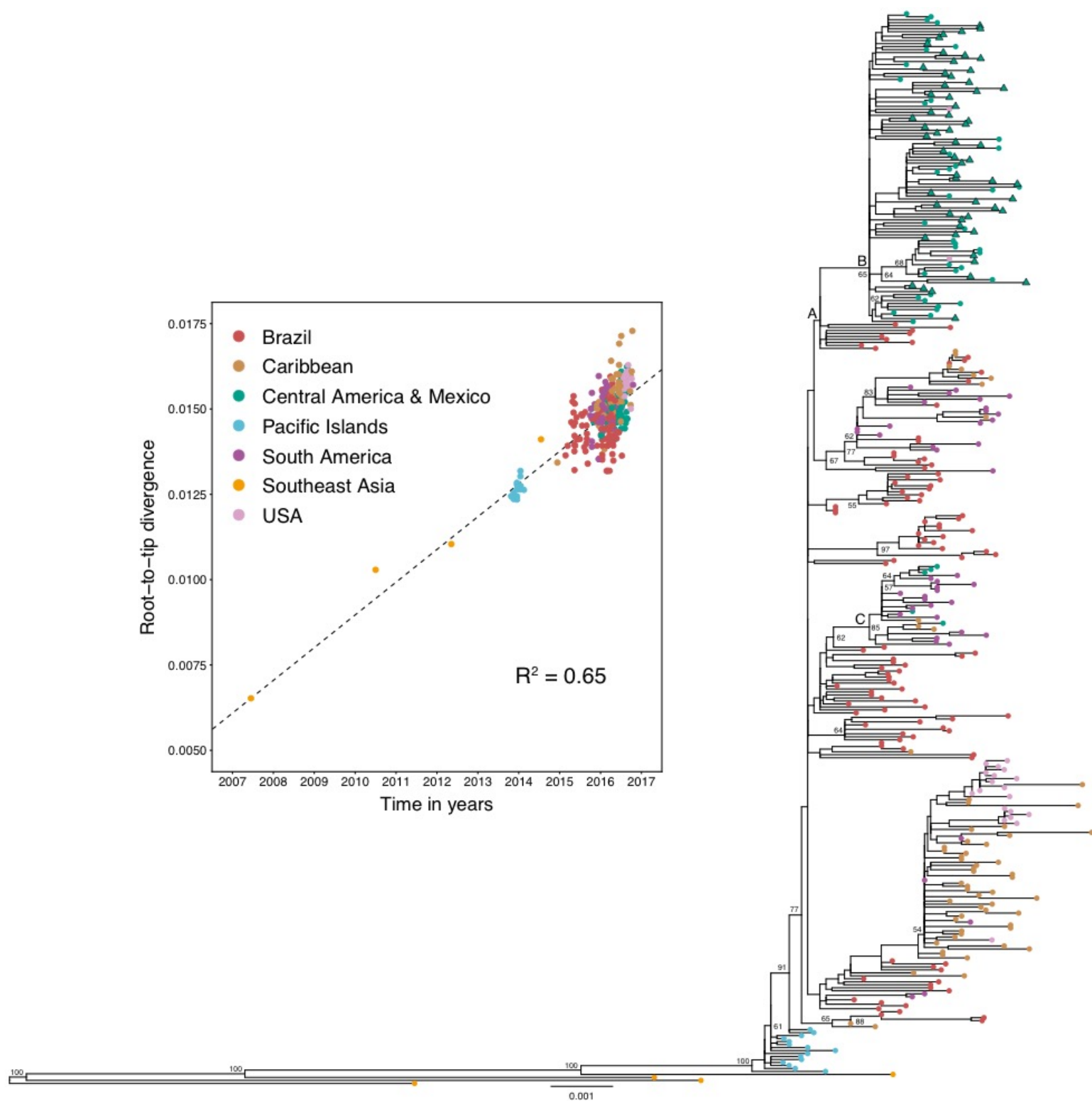


Figure S2. Maximum likelihood phylogeny and temporal signal of the Zika virus Asian genotype lineage (related to Figure 2A). The phylogeny was estimated using PhyML (Guindon and Gascuel, 2003) based on complete and partial (>1500 nt) coding genome sequences. Statistical supports for nodes were assessed using a bootstrap approach (100 replicates). Only bootstrap supports >50 at internal nodes are displayed. Colored symbols at phylogenetic tips denote sampling locations of the sequences. Circles and triangles denote sequences publicly available and sequences generated in this study, respectively. The regression plot shows the correlation between the sampling date of each sequence and the genetic distance of that sequence from the root of the phylogeny. Colored circles denote tips of the phylogeny with its corresponding sampling location.

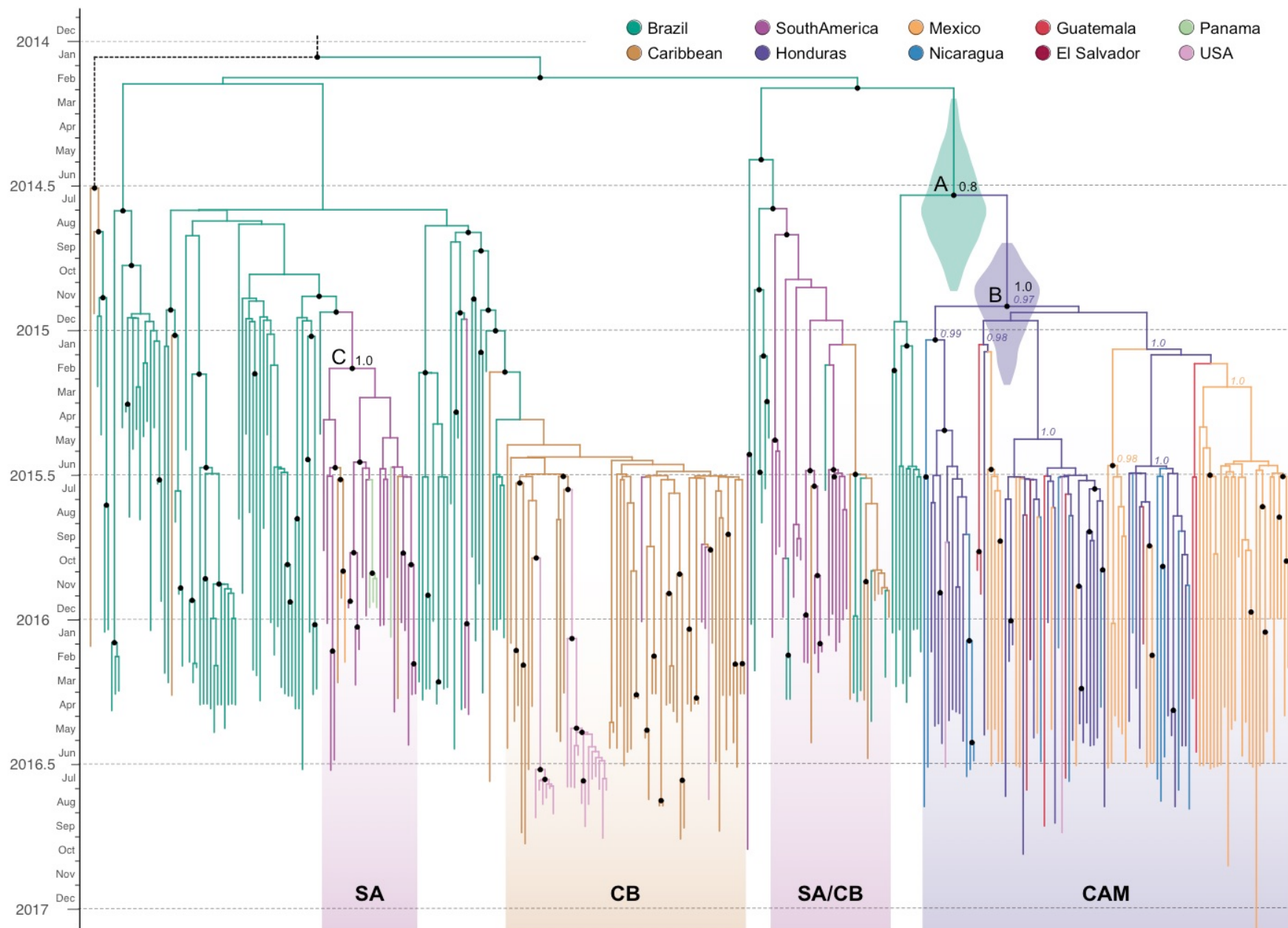


Figure S3. Maximum clade credibility phylogeny estimated from complete and partial ZIKV sequences from the Americas (related to Figure 2A). For visual clarity, basal Asian and Pacific lineages are not displayed. Violin plots show the posterior distributions of the estimated dates of nodes A and B (see main text). Branch colors indicate the most probable ancestral lineage locations. Circles at internal nodes denote clade posterior probabilities >0.75 . For selected nodes, colored numbers show the posterior probabilities of inferred ancestral locations, whilst black numbers are the clade posterior probabilities. Clades from outside Brazil are highlighted and denoted CB (Caribbean), SA (South America), and CAM (Central America and Mexico).

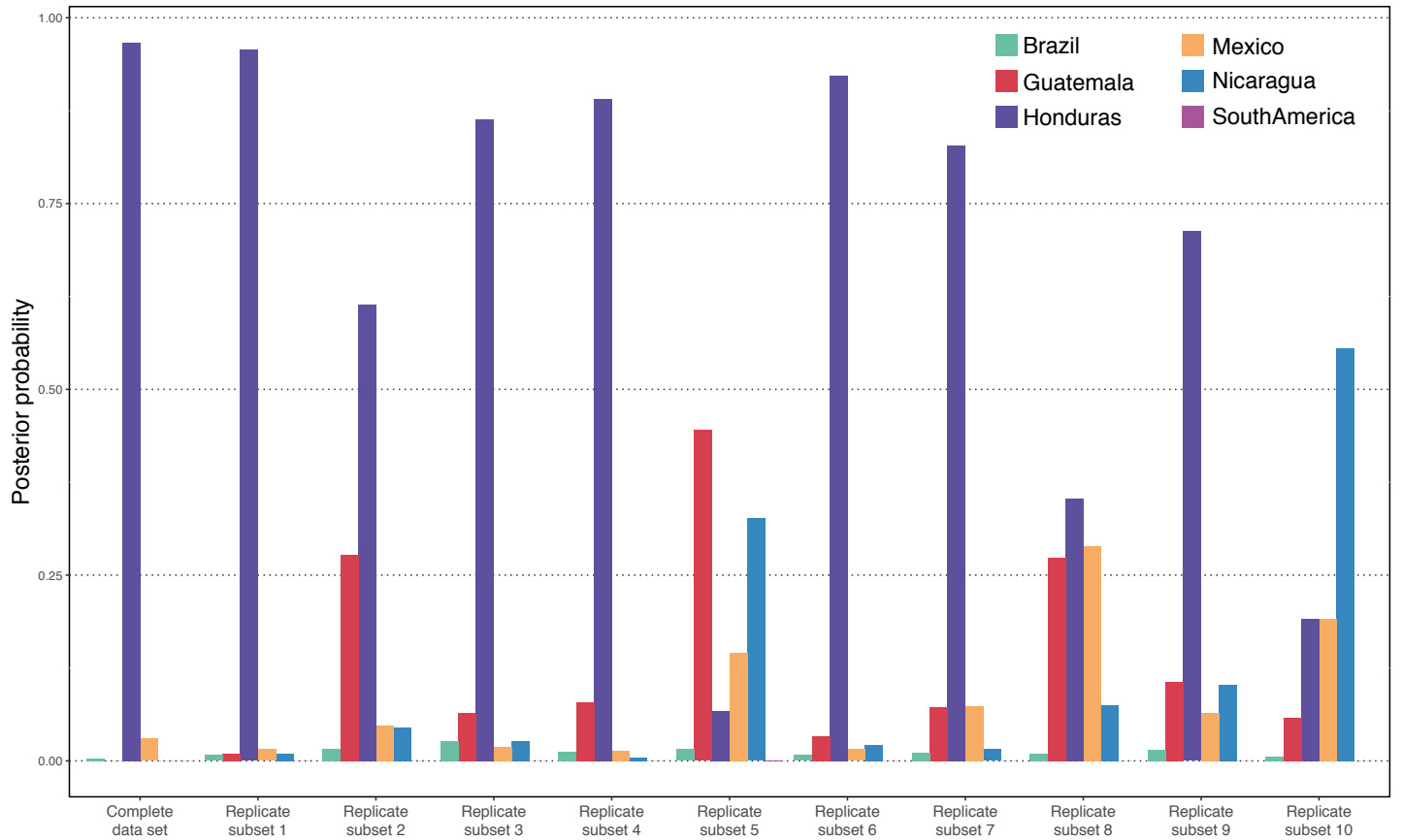


Figure S4. Ancestral node location posterior probabilities for node B (related to Figure 2A), estimated using the full dataset, and on ten jackknife resampled datasets (see STAR Methods for details). For each dataset, a Bayesian asymmetric discrete trait evolution model was used to estimate ancestral node locations.

Table S1. Sample and sequencing information (related to Figure 1)

Sequencing Method	Accession Number	Sample Name	Source	Sample type	Region	Collection Date	Days between symptom onset and date of sampling	ZIKV Ct value during sequencing (diagnostic Ct)	Illumina					Illumina with Probe Enrichment					Merged		Used in phylogenetic analyses
									Reads mapped	Average coverage depth	Deduplicated reads mapped	Deduplicated average coverage depth	Reference coverage (%)	Reads mapped	Average coverage depth	Deduplicated reads mapped	Deduplicated average coverage depth	Reference coverage (%)	Reference coverage (%)		
Bait capture mNGS	MF434516	1304.13.A.1	HCSFV	Serum	Nicaragua: Managua	2016-08-05		31	162,621	2,168.25	829	19.86	99.95	-	-	-	-	-	-	yes	
	MF434517	1659.13.A.1	HCSFV	Serum	Nicaragua: Managua	2016-08-19	2	28	131,556	1,765.42	11,065	154.78	99.99	-	-	-	-	-	-	yes	
	NA	4445.13.A.1	HCSFV	Serum	Nicaragua: Managua	2016-08-03	2	28	19	1.09	19	1.09	4.61	-	-	-	-	-	-	no	
	NA	4858.13.A.1	HCSFV	Serum	Nicaragua: Managua	2016-07-13	3	35	5	1.00	5	1.00	1.40	-	-	-	-	-	-	no	
	MF434518	5256.13.A.1	HCSFV	Serum	Nicaragua: Managua	2016-08-26	1	36	145,718	2,072.49	269	6.23	92.60	-	-	-	-	-	-	yes	
	MF434519	5338.13.A.1	HCSFV	Serum	Nicaragua: Managua	2016-07-22	1	29	14,369	325.58	91	2.04	58.96	-	-	-	-	-	-	yes	
	NA	5376.13.A.1	HCSFV	Serum	Nicaragua: Managua	2016-07-07	2	36	4	1.00	4	1.00	1.98	-	-	-	-	-	-	yes	
	NA	5604.12.B.1	HCSFV	Serum	Nicaragua: Managua	2016-02-07	4	26	9	1.33	9	1.33	2.28	-	-	-	-	-	-	no	
	NA	5660.13.A.1	HCSFV	Serum	Nicaragua: Managua	2016-07-27	2	32	4,088	304.40	18	1.33	16.05	-	-	-	-	-	-	no	
	MF434520	5847.12.B.1	HCSFV	Serum	Nicaragua: Managua	2016-02-07	1	39	258,362	2,564.90	202	4.72	53.18	-	-	-	-	-	-	yes	
	NA	5953.13.A.1	HCSFV	Serum	Nicaragua: Managua	2016-08-11	1	37	704	35.41	36	1.79	26.93	-	-	-	-	-	-	no	
	MF434521	6547.13.A.1	HCSFV	Serum	Nicaragua: Managua	2016-05-19	1	21	158,162	2,142.25	5,861	83.79	100.00	-	-	-	-	-	-	yes	
	NA	7208.13.A.1	HCSFV	Serum	Nicaragua: Managua	2016-07-15	1	38	20	1.38	20	1.38	6.33	-	-	-	-	-	-	no	
	MF434522	7253.13.A.1	HCSFV	Serum	Nicaragua: Managua	2016-08-29	1	32	41,299	554.15	3,803	52.75	99.96	-	-	-	-	-	-	yes	
Spiked primers mNGS	MF801381	CDPH_CentralAm-24	CDPH	urine	Honduras	2016		NA	32	6,846	66.15	2,185	22.30	-	-	-	-	-	-	yes	
	MF801380	CDPH_CentralAm-2411	CDPH	urine	Guatemala	2016-04-11		NA	39	844	9.12	366	4.14	-	-	-	-	-	-	yes	
	MF801382	CDPH_CentralAm-25	CDPH	urine	Honduras	2016		NA	28	408	5.15	241	3.20	-	-	-	-	-	-	yes	
	NA	CDPH_CentralAm-3263	CDPH	urine	Guatemala	2016-04-11		NA	38	123	4.37	32	1.24	-	-	-	-	-	-	no	
	MF801426	CDPH_CentralAm-3912	CDPH	urine	Nicaragua	2016-07-25		NA	29	89,647	844.26	4,826	70.40	-	-	-	-	-	-	yes	
	MF801378	CDPH_CentralAm-3921	CDPH	urine	Guatemala	2016-07-21		NA	33	10,510	88.46	1,889	20.21	-	-	-	-	-	-	yes	
	NA	CDPH_ElSalvador-0528	CDPH	serum	El Salvador	2016-02-22		NA	No Ct (37)	-	-	-	-	-	-	-	-	-	-	NA	
	MF801377	CDPH_ElSalvador-1055	CDPH	urine	El Salvador	2016-02-22		NA	35	856	9.43	131	2.20	-	-	-	-	-	-	yes	
	NA	CDPH_ElSalvador-5261	CDPH	serum	El Salvador	2016-02-03		NA	No Ct (38)	-	-	-	-	-	-	-	-	-	-	NA	
	NA	CDPH_Guatemala-S840	CDPH	urine	Guatemala	2016-02-11		NA	39	-	-	-	-	-	-	-	-	-	-	no	
	MF801379	CDPH_Guatemala-3294	CDPH	urine	Guatemala	2016-06-18		NA	35	171	5.01	78	2.47	-	-	-	-	-	-	yes	
	NA	CDPH_Guatemala-4516	CDPH	serum	Guatemala	2016-06-19		NA	41	548	151.93	6	1.68	-	-	-	-	-	-	no	
	NA	CDPH_Guatemala-4530	CDPH	serum	Guatemala	2016-06-18		NA	40	129	7.18	21	1.35	-	-	-	-	-	-	no	
	NA	CDPH_Guatemala-5559	CDPH	serum	Guatemala	2016-02-17		NA	No Ct (37)	-	-	-	-	-	-	-	-	-	-	NA	
	MF801383	CDPH_Honduras-4102	CDPH	serum	Honduras	2016-06-03		NA	33	4,567	38.85	907	8.35	-	-	-	-	-	-	yes	
Spiked primers mNGS	NA	CDPH_Mexico_S085	CDPH	serum	Mexico: Chiapas	2016-01-24		NA	37	-	-	-	-	-	-	-	-	-	-	no	
	MF801390	CDPH_Mexico-1	CDPH	urine	Mexico	2016		NA	36	229	4.02	131	2.55	-	-	-	-	-	-	yes	
	NA	CDPH_Mexico-20	CDPH	urine	Mexico	2016		NA	Not Ct (37)	-	-	-	-	-	-	-	-	-	-	NA	
	NA	CDPH_Mexico-21	CDPH	urine	Mexico	2016		NA	31	619	29.08	46	3.96	-	-	-	-	-	-	no	
	NA	CDPH_Mexico-22	CDPH	urine	Mexico	2016		NA	36	14	14.48	4	2.57	-	-	-	-	-	-	no	
	NA	CDPH_Mexico-23	CDPH	urine	Mexico	2016		NA	34	96	13.89	11	1.49	-	-	-	-	-	-	no	
	MF801391	CDPH_Mexico-3502	CDPH	urine	Mexico: Oaxaca	2016-07-06		NA	31	17,002	196.13	700	15.28	-	-	-	-	-	-	yes	
	MF801392	CDPH_Mexico-4227	CDPH	urine	Mexico	2016-08-13		NA	34	136	3.79	42	1.46	-	-	-	-	-	-	yes	
	NA	CDPH_Mexico-5	CDPH	urine	Mexico	2016		NA	37	45	10.30	8	1.32	-	-	-	-	-	-	no	
	MF801425	CDPH_Nicaragua-3358	CDPH	urine	Nicaragua	2016-06-24		NA	34	3,059	78.68	82	5.35	-	-	-	-	-	-	yes	
	MF801384	Hond-1031	BSRI	Serum	Honduras: Roatán	2016-02-03		NA	26	4,462	39.57	1,825	18.98	-	-	-	-	-	-	yes	
	MF801385	Hond-1055	BSRI	Serum	Honduras: Roatán	2016-02-12		NA	30	704	8.07	400	4.79	-	-	-	-	-	-	yes	
	MF801386	Hond-1083	BSRI	Serum	Honduras: Roatán	2016-02-24		NA	4	20	29,644	303.93	1,048	32.73	-	-	-	-	-	yes	
	MF801387	Hond-1122	BSRI	Serum	Honduras: Roatán	2016-03-29		2	23	15,511	148.90	2,086	28.45	-	-	-	-	-	-	yes	
	MF801388	Hond-1138	BSRI	Serum	Honduras: Roatán	2016-04-25		1	32	1,985	73.93	32	8.33	-	-	-	-	-	-	yes	
	MF801389	Hond-1162	BSRI	Serum	Honduras: Roatán	2016-05-10		2	29	1,944	19.23	1,178	12.03	-	-	-	-	-	-	yes	
Spiked primers mNGS	MF801393	mex01	CLE	Serum	Mexico: Chiapas	2016-04-22		2	37	4,142	68.73	444	7.24	-	-	-	-	-	-	yes	
	NA	mex02	CLE	Serum	Mexico: Chiapas	2016-04-29		3	40	620	425.10	4	4.51	-	-	-	-	-	-	no	
	KY606271	mex03	CLE	Serum	Mexico: Chiapas	2016-05-03		2	35	3,715	42.25	1,365	16.13	-	-	-	-	-	-	yes	
	MF801394	mex04	CLE	Serum	Mexico: Chiapas	2016-05-03		4	34	31,022	676.55	231	23.33	-	-	-	-	-	-	yes	
	MF801395	mex05	CLE	Serum	Mexico: Chiapas	2016-05-09		1	34	10,769	136.99	3,183	40.37	-	-	-	-	-	-	yes	
	NA	mex06	CLE	Serum	Mexico: Chiapas	2016-05-06		4	No Ct (33)	-	-	-	-	-	-	-	-	-	-	NA	
	KY606272	mex07	CLE	Serum	Mexico: Oaxaca	2016-05-11		5	32	14,099	187.73	3,343	46.96	-	-	-	-	-	-	yes	
	NA	mex08	CLE	Serum	Mexico: Chiapas	2016-05-11		2	No Ct (40)	-	-	-	-	-	-	-	-	-	-	NA	
	NA	mex09	CLE	Serum	Mexico: Guerrero	2016-05-16		3	40	475	119.72	12	2.91	-	-	-	-	-	-	no	
	NA	mex10	CLE	Serum	Mexico: Chiapas	2016-05-12		3	37	1,908	216.62	28	3.26	-	-	-	-	-	-	no	
	NA	mex11	CLE	Serum	Mexico: Chiapas	2016-05-16		5	No Ct (33)	-	-	-	-	-	-	-	-	-	-	NA	
	NA	mex12	CLE	Serum	Mexico: Chiapas	2016-05-16		2	37	352	235.71	4	2.68	-	-	-	-	-	-	no	
	NA	mex13	CLE	Serum	Mexico: Chiapas	2016-05-16		1	No Ct (34)	-	-	-	-	-	-	-	-	-	-	NA	
	MF801396	mex14	CLE	Serum	Mexico: Chiapas	2016-05-17		3	37	2,081	28.10	681	9.59	-	-	-	-	-	-	yes	
	NA	mex15	CLE	Serum	Mexico: Guerrero	2016-05-20		3	41	42	2.01	27	1.31	-	-	-	-	-	-	no	
Spiked primers mNGS	MF801397	mex16	CLE	Serum	Mexico: Campeche	2016-05-20		2	38	715	9.42	402	5.36	-	-	-	-	-	-	yes	
	MF801398	mex17	CLE	Serum	Mexico: Chiapas	2016-05-20		3	35	2,434	31.34	1,343	17.69	-	-	-	-	-	-	yes	
	NA	mex18	CLE	Serum	Mexico: Chiapas	2016-05-24		1	No Ct (31)	-	-	-	-	-	-	-	-	-	-	NA	
	MF801399	mex19	CLE	Serum	Mexico: Chiapas	2016-05-20		5	37	406	6.22	150	2.38	-	-	-	-	-	-	yes	
	MF801400	mex20	CLE	Serum	Mexico: Chiapas	2016-05-20		3	35	1,227	17.70	377	5.56	-	-	-	-	-	-	yes	
	NA	mex21	CLE	Serum	Mexico: Chiapas	2016-05-21		0	No Ct (30)	-	-	-	-	-	-	-	-	-	-	yes	
	NA	mex22	CLE	Serum	Mexico: Chiapas	2016-05-23		3	38	23	1.75	14	1.06	-	-	-	-	-	-	no	
	MF801401	mex23	CLE	Serum	Mexico: Chiapas	2016-05-23		1	35	31,247	423.50	860	23.09	-	-	-	-	-	-	yes	
	MF801402	mex24	CLE	Serum	Mexico: Chiapas	2016-05-26		1	36	2,614	33.76	1,293	17.05	-	-	-	-	-	-	yes	
	MF801403	mex25	CLE	Serum	Mexico: Chiapas	2016-05-25		4	34	150,375	1,965.38	2,402	73.63	-	-	-	-	-	-	yes	
	MF801404	mex26	CLE	Serum	Mexico: Guerrero	2016-07-08		4	38	2,623	41.57	462	7.32	-	-	-	-	-	-	yes	
	MF801405	mex27	CLE	Serum	Mexico: Guerrero	2016-07-09		37	3,070	76.11	159	4.70	39.99	-	-	-	-	-	-	yes	
	MF801406	mex28	CLE	Serum	Mexico: Oaxaca	2016-07-07		1	36	23,110	250.45	5,636	66.58	-	-	-					

Table S2. Association between mosquito climatic vector suitability and Zika virus notified cases (related to Figure 3)

Country	Belize	Costa Rica	El Salvador	Guatemala	Honduras	Mexico	Nicaragua	Panama
Period	Jan 2016 - May 2017	Jan 2016 - May 2017	Oct 2015 - May 2017	Nov 2015 - May 2017	Jan 2016 - Mar 2017	Jan 2016 - Apr 2017	Jan 2016 - May 2017	Nov 2015 - Apr 2017
<i>P</i> -value	0.0352	0.000213	0.381	0.127	0.0656	2.24E-07	1.61E-06	0.438
Adjusted-R ²	0.214	0.585	< 0	0.0806	0.179	0.851	0.78	< 0
Time lag (months)	1.06	0.81	5.91	-5.98	4.62	0.62	0.69	-2.58

For each country, the table provides the estimated correlated time period (*T*), *P*-value of the linear term of suitability in *T*, adjusted R^2 of the model, and time lag (*I*).

Table S3. 13-mer primers used in the metagenomic next-generation sequencing (related to Figure 1)

Primer Name	Primer Direction	Primer Sequence (without adapter)	Primer Sequence (with adapter)
ZIKV-13mer_251R	reverse	CTGCCATAGCTGT	GTTTCCCCTGGAGGATACTGCCATAGCTGT
ZIKV-13mer_501R	reverse	TTGTGATGGCAGG	GTTTCCCCTGGAGGATATTGTGATGGCAGG
ZIKV-13mer_751R	reverse	GTATGCCGGGGCA	GTTTCCCCTGGAGGATAGTATGCCGGGGCA
ZIKV-13mer_1001R	reverse	CAAGGTAGGCTTC	GTTTCCCCTGGAGGATAACAAGGTAGGCTTC
ZIKV-13mer_1251R	reverse	TTCGCTCTATTCT	GTTTCCCCTGGAGGATATTTCGCTCTATTCT
ZIKV-13mer_1501R	reverse	ATGTGCGTCCTTG	GTTTCCCCTGGAGGATAATGTGCGTCCTTG
ZIKV-13mer_1751R	reverse	CGTACTGTACCTC	GTTTCCCCTGGAGGATACGTACTGTACCTC
ZIKV-13mer_2001R	reverse	CTCACAGTGGCTT	GTTTCCCCTGGAGGATACTCACAGTGGCTT
ZIKV-13mer_2251R	reverse	GGATAAGAAGATC	GTTTCCCCTGGAGGATAGGATAAGAAGATC
ZIKV-13mer_2501R	reverse	GGATTGCGTTGAG	GTTTCCCCTGGAGGATAGGATTGCGTTGAG
ZIKV-13mer_2751R	reverse	ACCCCGAACCCAT	GTTTCCCCTGGAGGATAACCCCGAACCCAT
ZIKV-13mer_3001R	reverse	CTTGGGTATGATC	GTTTCCCCTGGAGGATACTTGGGTATGATC
ZIKV-13mer_3251R	reverse	AGCCATCTTTAGC	GTTTCCCCTGGAGGATAAGCCATCTTTAGC
ZIKV-13mer_3501R	reverse	AAAATTGCAAGCT	GTTTCCCCTGGAGGATAAAAATTGCAAGCT
ZIKV-13mer_3751R	reverse	AACCATCGCTCGT	GTTTCCCCTGGAGGATAAACCATCGCTCGT
ZIKV-13mer_4001R	reverse	TCCGCTTCCCCT	GTTTCCCCTGGAGGATATCCGCTTCCCCT
ZIKV-13mer_4251R	reverse	AAATCACCCTCT	GTTTCCCCTGGAGGATAAAATCACCCTCT
ZIKV-13mer_4501R	reverse	TCCAACCTGTGTT	GTTTCCCCTGGAGGATATCCAACCTGTGTT
ZIKV-13mer_4751R	reverse	CATCCTTTGTCTT	GTTTCCCCTGGAGGATACATCCTTTGTCTT
ZIKV-13mer_5001R	reverse	ACTCTCCTGGTTT	GTTTCCCCTGGAGGATAACTCTCCTGGTTT
ZIKV-13mer_5251R	reverse	GGCCTCATCCATA	GTTTCCCCTGGAGGATAGGCCTCATCCATA
ZIKV-13mer_5501R	reverse	CATTGCCGTTCT	GTTTCCCCTGGAGGATACATTGCCGTTCT
ZIKV-13mer_5751R	reverse	GCAGCGCTGGCAT	GTTTCCCCTGGAGGATAGCAGCGCTGGCAT
ZIKV-13mer_6001R	reverse	TTTCATGAGTTCC	GTTTCCCCTGGAGGATATTTTCATGAGTTCC
ZIKV-13mer_6251R	reverse	AAGCCGCTCCTCT	GTTTCCCCTGGAGGATAAAGCCGCTCCTCT
ZIKV-13mer_6501R	reverse	GTCACCATCCAA	GTTTCCCCTGGAGGATAGTCACCATCCAA
ZIKV-13mer_6751R	reverse	TCTCCTTCCCATT	GTTTCCCCTGGAGGATATCTCCTTCCCATT
ZIKV-13mer_7001R	reverse	TTGTGAGTAGCAA	GTTTCCCCTGGAGGATATTGTGAGTAGCAA
ZIKV-13mer_7251R	reverse	GCGACAGTATGGC	GTTTCCCCTGGAGGATAGCGACAGTATGGC
ZIKV-13mer_7501R	reverse	ATCTGGTTCAAGC	GTTTCCCCTGGAGGATAATCTGGTTCAAGC
ZIKV-13mer_7751R	reverse	TCCTTTCCTTCT	GTTTCCCCTGGAGGATATCCTTTCCTTCT
ZIKV-13mer_8001R	reverse	GGCACAACACCTT	GTTTCCCCTGGAGGATAGGCACAACACCTT
ZIKV-13mer_8251R	reverse	CAGCTTACCACAG	GTTTCCCCTGGAGGATACAGCTTACCACAG
ZIKV-13mer_8501R	reverse	CTGACCATACGGT	GTTTCCCCTGGAGGATACTGACCATACGGT
ZIKV-13mer_8751R	reverse	CTAGAGCCCAGAA	GTTTCCCCTGGAGGATACTAGAGCCCAGAA
ZIKV-13mer_9001R	reverse	ACATATCCGAGTC	GTTTCCCCTGGAGGATAACATATCCGAGTC
ZIKV-13mer_9251R	reverse	CCCCCTTGGTCT	GTTTCCCCTGGAGGATACCCCCCTTGGTCT
ZIKV-13mer_9501R	reverse	TATCATTCAAGAA	GTTTCCCCTGGAGGATATATCATTCAAGAA
ZIKV-13mer_9751R	reverse	AAATAAAGGAGCT	GTTTCCCCTGGAGGATAAAATAAAGGAGCT
ZIKV-13mer_10001R	reverse	GAGAGATCCACAC	GTTTCCCCTGGAGGATAGAGAGATCCACAC
ZIKV-13mer_10251R	reverse	TTGGTTTCCCAGC	GTTTCCCCTGGAGGATATTGGTTTCCCAGC
ZIKV-13mer_10501R	reverse	TGGTCTTCCCAG	GTTTCCCCTGGAGGATATGGTCTTCCCAG
ZIKV-13mer_10751R	reverse	GGATTTCCCCACA	GTTTCCCCTGGAGGATAGGATTTCCCCACA
ZIKV-13mer-3prime_7R	reverse	TCACAGCTAGTCT	GTTTCCCCTGGAGGATATCACAGCTAGTCT
ZIKV-13mer-3prime_6R	reverse	ATGCTGTTTTGCG	GTTTCCCCTGGAGGATAATGCTGTTTTGCG
ZIKV-13mer-3prime_5R	reverse	GGCGGCCAGCGTG	GTTTCCCCTGGAGGATAGGCGGCCAGCGTG
ZIKV-13mer-3prime_4R	reverse	GCGATCTGTGCCT	GTTTCCCCTGGAGGATAGCGATCTGTGCCT
ZIKV-13mer-3prime_3R	reverse	CCGCCGAAGTTCG	GTTTCCCCTGGAGGATACCGCCGAAGTTCG
ZIKV-13mer-3prime_1R	reverse	AGAAACCATGGAT	GTTTCCCCTGGAGGATAAGAAACCATGGAT
ZIKV-13mer-3prime_1R	reverse	AGAAACCATGGAT	GTTTCCCCTGGAGGATAAGAAACCATGGAT
ZIKV-13mer-3prime_3R	reverse	CCGCCGAAGTTCG	GTTTCCCCTGGAGGATACCGCCGAAGTTCG

[illegible][illegible]