

DOCUMENT MADE AVAILABLE UNDER THE PATENT COOPERATION TREATY (PCT)

International application number:	PCT/EP2016/082662
International filing date:	23 December 2016 (23.12.2016)
Document type:	Certified copy of priority document
Document details:	Country/Office: EP
	Number: 16176049.1
	Filing date: 23 June 2016 (23.06.2016)
Date of receipt at the International Bureau:	31 January 2017 (31.01.2017)

Remark: Priority document submitted or transmitted to the International Bureau in compliance with Rule 17.1(a),(b) or (b-bis)

Bescheinigung

Die angehefteten
Unterlagen stimmen mit der
als ursprünglich eingereicht
geltenden Fassung der auf
dem nächsten Blatt
bezeichneten europäischen
Patentanmeldung überein.

Certificate

The attached documents are
exact copies of the text in
which the European patent
application described on the
following page is deemed to
have been filed.

Attestation

Les documents joints à la
présente attestation sont
conformes au texte,
considéré comme
initialement déposé, de la
demande de brevet
européen qui est spécifiée à
la page suivante.

Patentanmeldung Nr.

Patent application No.

Demande de brevet n°

16176049.1 / EP16176049

The organization code and number of your priority application, to be used for filing abroad under the Paris Convention, is EP16176049.

Der Präsident des Europäischen Patentamts;
Im Auftrag

For the President of the European Patent Office

Le Président de l'Office européen des brevets
p.o.



V. Joseph

Anmeldung Nr:
Application no.: 16176049.1
Demande no :

Anmeldetag:
Date of filing: 23.06.16
Date de dépôt :

Anmelder / Applicant(s) / Demandeur(s):

Valneva SE
World Trade Center Lyon, Tour Oxygène
10-12 Boulevard Marius Vivier Merle
69003 Lyon/FR

Bezeichnung der Erfindung / Title of the invention / Titre de l'invention:

(Falls die Bezeichnung der Erfindung nicht angegeben ist, oder falls die Anmeldung in einer Nicht-Amtssprache des EPA eingereicht wurde, siehe Beschreibung bezüglich ursprünglicher Bezeichnung.

If no title is shown, or if the application has been filed in a non-EPO language, please refer to the description for the original title.
Si aucun titre n'est indiqué, ou si la demande a été déposée dans une langue autre qu'une langue officielle de l'OEB, se référer à la description pour le titre original.)

VIRUS PURIFICATION

In Anspruch genommene Priorität(en) / Priority(Priorities) claimed / Priorité(s) revendiquée(s)
Staat/Tag/Aktenzeichen / State/Date/File no. / Pays/Date/Numéro de dépôt:

Am Anmeldetag benannte Vertragsstaaten / Contracting States designated at date of filing / Etats contractants désignées lors du dépôt:

AL AT BE BG CH CY CZ DE DK EE ES FI FR GB GR HR HU IE IS IT LI LT LU LV MC MK MT NL NO PL
PT RO RS SE SI SK SM TR

VIRUS PURIFICATION

FIELD OF THE INVENTION

The disclosure relates to methods for the purification of viruses for use in vaccines.

BACKGROUND OF THE INVENTION

Regulatory agencies such as the World Health Organization establish standards and guidelines for the production of pharmaceutical compositions administered to humans, such as vaccines, that limit quantity and components of the compositions. Meeting these standards is particularly challenging with regard to production of vaccines containing biological agents, such as viruses, which must be propagated on cell substrates. Such vaccine preparations must be sterile (*i.e.*, free from independently replicating organisms) and may contain no more than 10 ng of host cell DNA per human dose, among other requirements. These standards are in place in order to ensure safety of the composition for human administration, but may introduce challenges in the development of processes used to produce such compositions.

Protamine was originally isolated from the sperm of salmon and other species of fish but is now produced primarily through recombinant biotechnology. It is a highly cationic peptide that binds to negatively charged molecules such as nucleic acids to form a stable ion pair. Its use in removing host cell nucleic acid is well document.

SUMMARY

During the course of routine virus purification, it was observed that addition of protamine sulfate to a virus harvest produced on a cell substrate removed not only contaminating DNA derived from host cells, as expected, but surprisingly also virtually eliminated immature and otherwise non-infectious virus particles from the preparation. This finding provides a streamlined, gentle, reproducible and broadly-applicable process for obtaining highly-purified infectious virus particles for applications such as vaccine preparation; furthermore, the process is not dependent on the charge of the virus particle.

Disclosed herein are downstream processes for purifying virus particles from a crude preparation. The downstream process can be applied to either a virus which has not adapted for propagation on a particular cell substrate or for a partial / fully cell substrate adapted virus particle.

Aspects of the invention provide processes for the purification of infectious virus particles comprising the steps of (a) providing a crude harvest (a) comprising virus particles and impurities, wherein the impurities are generated from growing said virus particles on a cell substrate; (b) reducing impurities from the crude harvest (a) by precipitation with an agent comprising a protamine salt, preferably a protamine sulphate, to obtain a virus preparation (b); and further purifying the virus preparation (b) by method or methods selecting for size of the virus particles, such as e.g. a sucrose density gradient centrifugation to obtain a virus preparation (c) comprising the infectious virus particles.

In some embodiments, the concentration of protamine sulphate in step (b) is about 1 to 10 mg/ml, more preferably about 1 to 5 mg/ml, more preferably about 1 to 2 mg/ml. In one embodiment, the concentration of protamine sulphate in step (b) is about 2 mg/mL. In one embodiment, the concentration of protamine sulphate is 1.2 to 1.8 mg/ml, more preferably 1.4 to 1.6 mg/ml. In a preferred embodiment, the concentration of protamine sulphate in step (b) is about 1.6 mg/ml or about 2 mg/ml.

In some embodiments, the residual host cell DNA of the virus preparation (e) is less than 1 µg/mL, especially less than 900, 800, 700, 600, 500, 400, 300 or 200 ng/mL, preferably less than 100 ng/mL. In a preferred embodiment, the residual host cell DNA of the virus preparation (c) is less than 10 ng/mL. In some embodiments, the residual host cell protein of the final virus preparation (c) is less than 10 µg/mL, especially less than 9, 8, 7, 6, 5, 4, 3 or 2 µg/mL, preferably less than 1 µg/mL. In a preferred embodiment, the residual host cell protein of the virus preparation (c) is less than 100 ng/mL. In some embodiments, the residual non-infectious virus particles of the final virus preparation (c) is less than 10 µg/mL, especially less than 9, 8, 7, 6, 5, 4, 3 or 2 µg/mL, preferably less than 1 µg/mL. In a preferred embodiment, the residual non-infectious virus particles of the virus preparation (c) is less than 100 ng/mL.

In some embodiments, the crude harvest (a) comprising the virus particles and impurities is subjected to one or more pre-purification step(s) prior to step (b). In some embodiments, the one or more pre-purification step(s) comprises digesting host cell genomic DNA in the crude harvest (a) comprising the virus particles and impurities by enzymatic treatment. In some embodiments, the one or more pre-purification step(s) comprises filtration, ultrafiltration, concentration, buffer exchange and/or diafiltration. In some embodiments, the one or more pre-purification steps is filtration using a filter having a pore size equal to or less than 1 μm . In some embodiments, the filter has a pore size equal to or less than 0.2 μm . In a preferred embodiment, the filter has a pore size of 0.2 μm . In some embodiments, the concentration and/or ultra/diafiltration and/or buffer exchange is performed by tangential flow filtration (TFF). In some embodiments, ultra/diafiltration of the crude harvest (a) comprising the virus particles and impurities is performed using a hollow fiber membrane having a cut-off of equal to or less than 300 kDa. In a preferred embodiment, the hollow fiber membrane has a cut-off of 100 kDa.

In some embodiments, the virus particle is a live virus, a chimeric virus, an attenuated live virus, a modified live virus, or a recombinant live virus. In a further step, the virus particles of the invention may be optionally inactivated. In some embodiments, the virus particle is an attenuated form of the virus particle. For example, the virus may have reduced infectivity, virulence, and/or replication in a host, as compared to a wild-type virus. In some embodiments, the virus is a mutated or modified virus, for example the nucleic acid of the virus may contain at least one mutation relative to the wild-type virus. In some embodiments, the virus is a recombinant live virus, meaning a virus that is generated recombinantly and may contain nucleic acid from different sources.

In some embodiments, the virus particle is a live virus, an attenuated live virus, a modified live virus, or a recombinant live virus. In some embodiments, the virus belongs to a virus family selected from the group consisting of Paramyxoviridae, Orthomyxoviridae, Flaviviridae, Filoviridae, Arenaviridae, Rhabdoviridae, and Coronaviridae. In some embodiments, the virus belongs to a virus family selected from the group consisting of Togaviridae (being live or inactivated), such as alphaviruses, or Flaviviridae (being live or

inactivated). In some embodiments, the virus is a virus of the family Flaviviridae, i.e. a flavivirus. In other embodiments, the virus is a Zika virus or Yellow Fever virus. In preferred embodiments, the virus is a Zika virus. In a most preferred embodiment, the Zika virus is a Zika virus from the Asian lineage.

In some embodiments, the relative reduction of impurity of the final virus preparation relative to the liquid medium (a) comprising the virus particles and impurities is in a range from 60 to 95%. In some embodiments, the residual impurity of the final virus preparation is less than 1%. We observed a decrease in the HCP peaks and the non-infectious aggregate peaks in the HPLC-SEC or SDS-PAGE. An exact quantification is difficult but one can measure the density of the SDS-PAGE bands and other methods.

In some embodiments, the filtration of step in (b)(ii) of claim 1 is performed using a filter having a pore size equal to or greater than 1 μm . In some embodiments, the filter has a pore size equal to or greater than 0.2 μm . In a preferred embodiment, the filter has a pore size of 0.2 μm .

In some embodiments, the virus is propagated in a cell line selected from the group consisting of an EB66 cell line, a Vero cell line, a Vero- α His cell line, a HeLa cell line, a HeLa-S3 cell line, a 293 cell line, a PC12 cell line, a CHO cell line, a 3T3 cell line, a PerC6 cell line, a MDSK cell line, a chicken embryonic fibroblast cell line, a duck cell line, and a diploid avian cell line. In some embodiments, said cell line is a duck cell line. In some embodiments, said cell line is a diploid avian cell line. In some embodiments, said cell line is EB66 cell line. In a preferred embodiment, said cell line is a Vero cell line.

Aspects of the invention provide a use of any of the processes described herein for manufacturing a composition for immunization against a viral infection. In a preferred embodiment, the composition is a vaccine. In one embodiment, the composition or vaccine is directed against Chikungunya virus. In one embodiment, the composition or vaccine is directed against a flavivirus. In one embodiment, the composition or vaccine is directed against Yellow Fever virus. In one embodiment, the composition or vaccine is directed against Zika virus such as e.g. a Zika virus of the Asian lineage.

Other aspects provide compositions comprising the virus particles obtainable by any of the processes described herein for treating and/or preventing a viral infection. In one embodiment, the viral infection is caused by Chikungunya virus. In one embodiment, the viral infection is caused by a flavivirus. In one embodiment, the viral infection is caused by Yellow Fever virus. In one embodiment, the viral infection is caused by Zika virus such as e.g. a Zika virus of the Asian lineage.

In some embodiments, the attenuated form of ChikV is derived from the LR2006-OPY1 ChikV infectious clone (La Reunion isolate). In some embodiments, the attenuated form of ChikV is the Δ 5nsP3 mutant as described by Hallengård et al. (Novel Attenuated Chikungunya Vaccine Candidates Elicit Protective Immunity in C57BL/6 mice (2014) Journal of Virology 88(5):2858–2866) or an immunogenic variant thereof. The immunogenic variant of the Δ 5nsP3 ChikV mutant is herein defined as having at least 80% sequence identity to the nucleotide sequence of the Δ 5nsP3 mutant sequence, especially at least 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or at least 99% sequence identity.

In some embodiments, the Zika virus is derived from the Asian lineage. In some embodiments, the Zika virus is a Zika virus as described partially or fully in Sequence section of this application, i.e. any of sequences SEQ ID Nos 2 to 69, in particular all partly or fully described Zika viruses of the Asian lineages or an immunogenic variant thereof. The immunogenic variants of the Zika virus or Zika virus of the Asian lineages are herein defined as having at least 80% sequence identity to the nucleotide sequence of the sequences described in any of sequences SEQ ID Nos 2 to 69, especially at least 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or at least 99% sequence identity.

In some embodiments, the process of the invention results in an enrichment of infectious virus particles from the crude harvest comprising infectious virus particles and non-infectious virus particles and other virus products such that the enrichment of the infectious virus particles is at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, preferably at least 80%, especially 85% relative to the total virus particle content of the crude harvest (a) comprising the virus particles and impurities.

In some embodiments, the residual impurity of the final virus preparation with respect to all impurities in the crude harvest is less than 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2%, 1%, preferably less than 5% as determined by SEC-HPLC (Size Exclusion Chromatography – HPLC).

In some embodiments, the filtration step of the virus preparation (b) after contact with the solid-phase matrix is performed using a filter having a pore size equal to or greater than 1 μm . In some embodiments, the filter has a pore size equal to or greater than 0.2 μm . In a preferred embodiment, the filter has a pore size of about 0.2 μm , such as 0.22 μm .

In some embodiments, the Zika virus, or Chikungunya virus is propagated in a cell line selected from the group consisting of an EB66 cell line, a Vero cell line, a Vero- α His cell line, a HeLa cell line, a HeLa-S3 cell line, a 293 cell line, a PC12 cell line, a CHO cell line, a 3T3 cell line, a PerC6 cell line, a MDSK cell line, a chicken embryonic fibroblast cell line, a duck cell line, and a diploid avian cell line. In some embodiments, said cell line is a duck cell line. In some embodiments, said cell line is a diploid avian cell line. In some embodiments, said cell line is EB66 cell line. In a preferred embodiment, said cell line is a Vero cell line.

Aspects of the invention provide a use of any of the processes described herein for manufacturing a composition for immunization against a Zika virus, Yellow Fever, or Chikungunya virus infection. In a preferred embodiment, the composition is a vaccine. In preferred embodiments, the vaccine is administered to the subject once, twice or three or more times. In a preferred embodiment, the vaccine is administered once or twice. In a preferred embodiment, the vaccine is administered only once.

Other aspects provide compositions comprising the virus particles obtainable by any of the processes described herein for treating and/or preventing a Chikungunya virus infection.

BRIEF DESCRIPTION OF THE DRAWINGS

The accompanying drawings are not intended to be drawn to scale. The Figures are illustrative only and are not required for enablement of the disclosure. For purposes of clarity, not every component may be labeled in every drawing. In the drawings:

Figure 1 shows the process of flavivirus maturation in the host cell. Full maturation of the particles requires proteolytic cleavage of the precursor membrane glycoprotein (prM) by the host protease furin. Not all prM molecules are cleaved, resulting in the release of mature, mosaic or immature-like conformations from the cells. Mosaic and immature forms are generally not infectious—only mature virions are infective and have hemagglutinin (HA) / TCID₅₀ activity. (Figure adapted from Plevka, et al., Maturation of flaviviruses starts from one or more icosahedrally independent nucleation centres, EMBO reports (2011) 12, 602–606).

Figure 2 shows schematically the genome of the ChikV, including non-structural and structural proteins (labeled “CHIKV”) as well as a schematic representation of the Δ5nsP3 attenuated Chikungunya virus used to exemplify the purification process of the current invention (labeled “Δ5nsP3”). The triangle indicates the approximate location of the deletion in the nsP3 coding region. (Figure adapted from Hallengård et al. 2014, *supra*.)

Figure 3 shows a flow-chart of an exemplary ChikV vaccine downstream purification process from the crude harvest to formulation of the drug substance, a preferred embodiment of the process of the invention.

Figure 4 shows the 214 nm, 260 nm and 280 nm absorbance of the individual SGC fractions of a representative purification run of the process of the invention (A); the SEC-HPLC analysis of the final pooled fractions containing purified infectious ChikV virus particles (B); and a silver-stained SDS-PAGE gel showing the protein content of the virus preparation following different steps of the process of the invention (defined in the table below the figure) (C). The SGC purified pool consisting of SGC fractions F7-F11 is shown in lane 12.

Figure 5 relates the SEC area (mAU*min; right axis) and TCID₅₀ results (log TCID₅₀/mL; left axis) of ChikV production harvests before and after PS treatment. The grey portions of the bars indicate large losses in SEC area following PS treatment, but no corresponding change in the total number of infectious particles (indicated by black portions of the bars) (A); SEC profile

of virus preparation before and after PS addition, showing a complete removal of large size virus aggregates by PS treatment as well as a reduction in host cell proteins (HCP) and LMW impurities (B).

Figure 6 shows electron micrographs of ChikV harvest before and after PS treatment.

Figure 7 shows relative amounts of ChikV particles and other components by SEC-HPLC analysis at the different steps of the process of the invention including, from top to bottom: crude harvest (a); 10X concentrated harvest; diafiltrated harvest; PS treated material; CC700-treated material and SGC purified pool.

Figure 8 shows a flow-chart of an exemplary Zika vaccine downstream purification process from the crude harvest to formulation of the drug substance, a preferred embodiment of the process of the invention.

Figure 9: Change in SEC profile of virus peak after PS addition showing a complete removal of large size aggregates and LMW impurities.

Figure 10: PS treatment results in selective removal of Zika virus aggregates and Vero HCP and LMW impurities (SEC-HPLC of 30x concentrated Zika Virus harvest day 5)

DETAILED DESCRIPTION OF THE INVENTION

Disclosed herein are processes for the purification of infectious virus particles, i.e., mature, functional virus particles, e.g. flavivirus particles (Yellow Fever, Zika Virus) and/or alphavirus particles (Chikungunya virus). The processes disclosed are characterized by the removal of undesired by-products of virus production on host cells, such as non-infectious virus particles and aggregated and immature virus by-products. The processes provided herein allow the production of highly-purified virus preparations comprising mostly infectious virus particles.

During the course of the invention, it was observed that protamine sulphate, added to remove contaminating DNA during virus purification, resulted not only in removal of contaminating DNA, but also in the loss of a high percentage of total virus particles present in the preparation. Surprisingly, however, quantification of total infectious virus particles by TCID50 before and after PS treatment revealed that the absolute number of infectious virus particles did not change following this loss of total virus particles. This observation clearly shows that treatment with PS can facilitate selective removal of non-infectious, aggregated and immature viral by-products, leaving behind the infectious Chikungunya virus particles. Because by-products produced during virus growth on host cells may have different (and undesirable) immunological properties or other unwanted side-effects or safety issues, a simple and robust way to remove these by-products is of high importance for the quality and safety of the final product.

Protamines are small arginine-rich nuclear proteins, present in high amounts in the sperm of fish, which have an important role in DNA packaging during spermatogenesis. Protamine sulfate (or "protamine" or "PS") can form a stable ion pair with heparin and is thus commonly used during certain surgeries when the anti-coagulation effect of heparin is no longer needed. In large doses, protamine sulfate administered alone can also have a weak anticoagulant effect ("Protamine sulfate". Wikipedia: The Free Encyclopedia. Wikimedia Foundation, Inc. 30 Sep 2015 Web. 26 Nov 2015 <https://en.wikipedia.org/wiki/Protamine_sulfate>). Protamine Sulphate is additionally routinely used in biotechnology applications such as DNA precipitation (e.g., removal of host cell DNA from cell culture processes), purification of DNA binding proteins and retroviral-mediated gene transfer.

Protamine is obtained from salmon sperm or produced recombinantly and is used as a sulphate salt. The four major peptides, which constitute almost the entire nitrogen-containing material in salmon protamine, have been fully characterized and found to be polypeptides of 30–32 amino acids in length, of which 21–22 residues are arginine. The average molecular mass is in the range of 4250 Da for the following sequence: PRRRRSSSRP VRRRRRPRVS RRRRRRGGRR RR (SEQ ID NO: 1). Herein, protamine is also referred to as protamine salt, or preferably protamine sulphate.

The present invention relates to the use of protamine sulphate (PS) in a process of purification of a live virus, wherein the protamine sulphate facilitates the removal of impurities from a crude virus harvest, including non-infectious virus particles and aggregates. As seen in Fig. 1, virus production in the host cell can result in the release of virus products which are not mature, infectious particles, which can also be considered impurities according to the present invention. As such, the present invention also relates to the enrichment of infectious virus particles from a crude harvest containing a mix of virus particles and other viral products in various stages of maturation.

The use of protamine sulphate can follow crude cell lysis or any further step after cell lysis wherein the virus particles are further enriched or concentrated and/or other impurities are removed and/or buffer components are exchanged. The further steps may comprise filtration or concentration of the crude cell lysate.

The protamine sulphate may comprise the sequence PRRRRSSSRP VRRRRRPRVS RRRRRRGGR RR (SEQ ID NO: 1) or a variant thereof wherein the amino acid sequence comprises from 28-35 amino acids, preferably 29-34, more preferably 30-33 amino acids, most preferably 31 or 32 amino acids. The protamine sulphate preferably comprises at least 19 arginine residues, more preferably at least 20 arginine residues, more preferably at least 21 arginine residues, even more preferably at least 22 residues, most preferably 20 or 21 arginine residues. Further, other protamine sulphate-like compounds or variants thereof may be used. Therefore, the use of the term "protamine salt" herein shall serve to encompass natural variations on SEQ ID NO: 1, preferably, but not limited to, the protamine sulphate forms.

The process comprising the use of protamine sulphate of the invention can be applied to purification of any virus for use in pharmaceutical compositions, for example, for a pharmaceutical composition such as a vaccine where it is important that the virus is in its infectious form. The virus to be purified may be any live virus, any live attenuated virus or any live chimeric virus, preferably a live wild type virus such as a Zika virus of the Asian lineage. In one embodiment, the virus particle is also be later inactivated. In a preferred embodiment, the virus is inactivated with formaldehyde.

In a preferred embodiment, the produced Zika virus is derived from the Asian lineage (which includes the strains found in South America and all strains derived from any Asian lineage). In some other embodiments, the produced Zika virus is a Zika virus as described in the Sequence section of this application (SEQ ID NO: 2 to 69).

In another preferred embodiment, the live attenuated Chikungunya virus is the protective ChikV-ICRES1-ΔnsP3 described by Hallengård *et al.* (Novel Attenuated Chikungunya Vaccine Candidates Elicit Protective Immunity in C57BL/6 mice (2014) *J. Virology*, 88(5):2858–2866). Briefly, the ChikV genome carries a positive-sense single-stranded RNA genome of 11 Kb containing two open reading frames encoding nonstructural proteins (nsP1 to nsP4) and structural proteins (C, E3, E2, 6K, and E1), respectively (see Fig. 2, top construct). The attenuated virus ΔnsP3, based on the La Reunion ChikV strain LR2006-OPY1, was obtained by the substitution of amino acid residues 1656 to 1717 of the P1234 polyprotein with a small linker (aa sequence AYRAAG) in the hypervariable region of the nsP3 protein (see Fig. 2, bottom construct). The ΔnsP3 ChikV mutant was shown to be infectious, highly immunogenic and protective against challenge with wild type ChikV (Hallengård, *et al.*, *supra* and Hallengård, *et al.*, Prime-Boost Immunization Strategies against Chikungunya Virus (2014) *J. Virology*, 88(22):13333-13343). In one embodiment, the live attenuated Chikungunya virus may be a variant of the ChikV-ICRES1-ΔnsP3 attenuated mutant virus.

A preferred embodiment of the process of the current invention is shown in Figure 3 (Chikungunya virus) and Figure 10 (Zika virus).

Table 1. Overview of process buffers and stock solutions

Buffer	Composition	Final pH	Final conductivity [mS/cm]
A	0.5 M NaOH		n.a.
B	0.1 M NaOH		n.a.
C	25 mM Tris, 150 mM NaCl	7.4±0.2	16.5
D	1 M Tris	7.4±0.2	n.a.
E	4.5 M NaCl	n.a.	n.a.
F	1 M NaCl	n.a.	n.a.
G	1 % SDS	n.a.	n.a.
H	50 % (w/w) Sucrose in 25 mM Tris, 150 mM NaCl	7.4±0.2	n.a.
I	35 % (w/w) Sucrose in 25 mM Tris, 150 mM NaCl	7.4±0.2	n.a.
J	15 % (w/w) Sucrose in 25 mM Tris, 150 mM NaCl	7.4±0.2	n.a.

K	10 x PBS	7.4±0.2	n.a.
L	50 mg/mL Protamine sulphate	7.4±0.2	n.a.
M	Drug substance formulation buffer (10mM Tris(hydroxymethyl)-aminomethan, 5 % Sucrose, 1% (10 mg/mL) rHSA)	7.4±0.2	1.3

Table 2. Abbreviations

CC700	Capto™ Core 700
ChikV	Chikungunya virus
EtOH	Ethanol
EU	Endotoxin units
DS	Drug Substance
DP	Drug Product
DSP	Downstream Process
HCP	Host cell protein
hcDNA	Host cell DNA
hpi	Hours post infection
HPLC	High Pressure Liquid Chromatography
ID	Inner diameter
LDS buffer	Lithium dodecyl sulfate sample loading buffer
MALLS	Multiangle light scattering
mAU	Milli absorbance units
PD	Process development
PFU	Plaque forming units
SEC	Size exclusion chromatography
SGC	Sucrose gradient centrifugation
SDS	Sodium dodecyl sulphate
TBS	Tris buffered saline
TFF	Tangential flow filtration
TCID50	Tissue culture infectious dose 50%
UF/DF	Ultrafiltration/diafiltration
rcf	Relative centrifugal force
rHSA	Recombinant human serum albumin

SEQUENCES

The amino acid sequence of a typical form of protamine is provided by SEQ ID NO: 1:

PRRRRSSSRP VRRRRRPRVS RRRRRRGGRR RR.

Provided below are examples of nucleic acid sequences of the genomes of Zika viruses that may be used in the methods, compositions, and/or vaccines described herein.

KU321639.1 Zika virus strain ZikaSPH2015, Brazil, complete genome (SEQ ID NO: 2)

GTTGTTACTGTTGCTGACTCAGACTGCGACAGTTCGAGTTTGAAGCGAAAGCTAGCAACAGTATCAACAGGTTTTATTTGGATT
 TGGAAACGAGAGTTTCTGGTCATGAAAAACCCAAAAAAGAAATCCGGAGGATTCCGGATTGTCAATATGCTAAACGCGGAG
 TAGCCCGTGTGAGCCCCCTTGGGGGCTTGAAGAGGCTGCCAGCCGACTTCTGCTGGGTCATGGGCCCATCAGGATGGTCTTG
 GCAATTCTAGCCTTTTTGAGATTACGGCAATCAAGCCATCACTGGGTCTCATCAATAGATGGGGTTCAGTGGGGAAAAAGA
 GGCTATGGAAATAATAAAGAAGTTCAAGAAAGATCTGGCTGCCATGCTGAGAATAATCAATGCTAGGAAGGAGAAAGAAGAG
 ACGGGGCGCAGATACTAGTGTGGAATTGTTGGCCTCCTGCTGACCACAGCTATGGCAGCGGAGGTCACTAGACGTGGGAGT
 GCATACTATATGTACTTGGACAGAAACGATGCTGGGGAGGCCATATCTTTCCAACCAATTGGGGATGAATAAGTGTATAT
 ACAGATCATGGATCTTGGACACATGTGTGATGCCACCATGAGCTATGAATGCCCTATGCTGGATGAGGGGGTGGAAACCAGAT
 GACGTCGATTGTTGGTGCAACACGACGTCAACTTGGGTTGTGTACGGAACCTGCCATCACAAAAAGGTGAAGCACGGAGAT
 CTAGAAGAGCTGTGACGCTCCCTCCCATTCCTAGGAAGCTGCAACGCGGTGCGAAACCTGGTTGGAATCAAGAGAATAC
 ACAAGCACTTGATTAGAGTCGAAAATTGGATATTAGGAACCTGGCTTCGCGTTAGCAGCAGCTGCCATCGCTTGGCTTTTG
 GGAAGCTCAACGAGCCAAAAAGTCATATACTTGGTCATGATACTGCTGATTGCCCGGCATACAGCATCAGGTGCATAGGAGT
 CAGCAATAGGGACTTTGTGGAAGGTATGTCAGGTGGGACTTGGGTTGATATTGTCTTGAACATGGAGGTTGTGTACCGTA
 ATGGCACAGGACAAACCGACTGTGACATAGAGCTGGTTACAACAACAGTCAGCAACATGGCGGAGGTAAGATCCTACTGCT
 ATGAGGCATCAATATCAGACATGGCTTCGGACAGCGCTGCCAACACAAGGTGAAGCCTACCTTGACAAGCAATCAGACACT
 CAATATGTCTGCAAAAGAACGTTAGTGGACAGAGGCTGGGGAAATGGATGTGGACTTTTGGCAAAGGGAGTCTGGTGACAT
 GCGCTAAGTTTGCATGCTCCAAGAAAATGACCGGGAAGAGCATCCAGCCAGAGAATCTGGAGTACCGGATAATGCTGTCACT
 TCATGGCTCCAGCACAGTGGGATGATCGTTAATGACACAGGACATGAAACTGATGAGAATAGAGCGAAGGTTGAGATAACG
 CCCAATTCACCAAGAGCCGAAGCCACCCTGGGGGGTTTTTGAAGCCTAGGACTTGATTGTGAACCGAGGACAGGCCTTGACTT
 TTCAGATTGTATTACTTGACTATGAATAACAAGCACTGGTTGGTTTACAAGGAGTGGTTCCACGACATTCCATTACCTTGGCAC
 GCTGGGGCAGACACCGGAACCTCACACTGGAACAACAAAGAAGCACTGGTAGAGTTCAAGGACGCACATGCCAAAAGGCAA
 ACTGTCTGGTTCTAGGGAGTCAAGAAGGAGCAGTTCACACGGCCCTTGTCTGGAGCTCTGGAGGCTGAGATGGATGGTGCAA
 AGGGAAGGCTGTCTCTGCGCCACTTGAAATGTCGCTGAAAATGGATAAATAGATTGAAGGGCGTGCTACTCCTGTGT
 ACCGCAGCGTTCACATTCACCAAGATCCCGGCTGAAACACTGCACGGGACAGTCACAGTGGAGGTACAGTACGCAGGGACAG
 ATGGACCTTGCAAGGTTCCAGTCTAGATGGCGGTGGACATGCAACTCTGACCCAGTTGGGAGGTTGATAACCGTAACCCC
 GTAATCACTGAAAGCACTGAGAACTTAAGATGATGCTGGAACCTTGATCCACCATTTGGGGACTTTACATTGTATAGGAGTC
 GGGGAGAAGAAGATCACCCACACTGGCACAGGAGTGGCAGCACCATTGGAAAAGCATTGGAAGCCACTGTGAGAGGTGCC
 AAGAGAATGGCAGTCTTGGGAGACACAGCCTGGGACTTTGGATCAGTTGGAGGCGCTCTCAACTCATTGGGCAAGGGCATCC
 ATCAAATTTTTGGAGCAGCTTCAAATCATTGTTGGAGGAATGCTCTGGTTCTCAAAATTCTCATTGGAACGTTGCTGATGTG
 GTTGGGTCTGAACACAAAGAATGGATCTATTTCCCTTATGTGCTTGGCCTTAGGGGGAGTGTGATCTTCTTATCCACAGCCGT
 CTCTGCTGATGTGGGTGCTCGGTGGACTTCTCAAAGAAGGAGACGAGATGCGGTACAGGGGTTCGTCTATAACGACGTT
 GAAGCCTGGAGGGACAGGTACAAGTACCATCCTGACTCCCCCGTAGATTGGCAGCAGCAGTCAAGCAAGCCTGGGAAGATG
 GTATCTGCGGGATCTCCTCTGTTTCAAGAATGGAAAACATCATGTGGAGATCAGTAGAAGGGGAGCTCAACGCAATCCTGGAA
 GAGAATGGAGTTCAACTGACGGTCGTTGTGGGATCTGTA AAAAACCCTATGTGGAGAGGTCCACAGAGATTGCCCGTGCTG
 TGAACGAGCTGCCCCACGGCTGGAAGGCTTGGGGGAAATCGCACTTCGTCAGAGCAGCAAAGACAAATAACAGCTTTGTCGT
 GGATGGTGACACACTGAAGGAATGCCACTCAAACATAGAGCATGGAACAGCTTTCTTGTGGAGGATCATGGGTTGCGGGTA
 TTTCACACTAGTGTCTGGCTCAAGGTTAGAGAAGATTATTATTAGAGTGTGATCCAGCCGTTATTGGAACAGCTGTTAAGGGA
 AAGGAGGCTGTACACAGTGTCTAGGCTACTGGATTGAGAGTGAGAAGAATGACACATGGAGGCTGAAGAGGGCCCATCTG
 ATCGAGATGAAAACATGTGAATGGCCAAAGTCCCACACATTGTGGACAGATGGAATAGAAGAGAGTGATCTGATCATACCA
 AGTCTTTAGCTGGGCCACTCAGCCATCACAATACCAGAGAGGGCTACAGGACCCAAATGAAAGGGCCATGGCACAGTGAAGA
 GCTTGAATTCGCTTGGAGGAATGCCAGGCACTAAGGTCCACGTGGAGGAAACATGTGGAACAAGAGGACCATCTCTGAGA

TCAACCACTGCAAGCGGAAGGGTGATCGAGGAATGGTGCTGCAGGGAGTGACAATGCCCCACTGTCGTTCCGGGCTAAAG
 ATGGCTGTTGGTATGGAATGGAGATAAGGCCAGGAAAGAACAGAAAGCAACTAGTAAGGTCAATGGTGACTGCAGGATC
 AACTGATCACATGGATCACTTCTCCCTTGGAGTGCTTGTGATTCTGCTCATGGTGAGGAAGGGCTGAAGAAGAGAATGACCA
 CAAAGATCATATAAGCACATCAATGGCAGTGCTGGTAGCTATGATCCTGGGAGGATTTTCAATGAGTGACCTGGCTAAGCTT
 GCAATTTTGATGGGTGCCACCTTCGCGGAAATGAACACTGGAGGAGATGTAGCTCATCTGGCGTGATAGCGGCATTCAAAGT
 CAGACCAGCGTTGCTGGTATCTTTCATCTTCAGAGCTAATTGGACACCCCGTGAAGCATGCTGCTGGCCTTGGCCTCGTGCT
 TTTGCAAACTGCGATCTCCGCTTGGAAAGGCGACCTGATGGTTCTCATCAATGGTTTTGCTTTGGCCTGGTTGGCAATACGAGC
 GATGGTTGTTCCACGCACTGATAACATCACCTTGGCAATCTGGCTGCTCTGACACCACTGGCCCGGGGCACACTGCTTGTGGC
 GTGGAGAGCAGGCTTGCTACTTGCAGGGGGTTTATGCTCCTCTCTCTGAAGGGAAAAGGCAGTGTAAGAAGAAGCACTTACCA
 TTTGTCATGGCCTGGGACTAACCGCTGTGAGGCTGGTCGACCCCATCAACGTGGTGGGGCTGCTGTTGCTCACAAGGAGTG
 GAAGCGGAGCTGGCCCCCTAGCGAAGTACTCACAGCTGTTGGCTGATATGCGCATTGGCTGGAGGGTTCGCCAAGGCAGAT
 ATAGAGATGGCTGGGCCATGGCCGCGGTCTGCTAATTGTGAGTTACGTGGTCTCAGGAAAGAGTGTTGGACATGTACA
 TTGAAAGAGCAGGTGACATCACATGGGAAAAAGATGCGGAAGTCACTGGAAACAGTCCCCGGCTCGATGTGGCGCTAGATGA
 GAGTGGTGATTTCTCCCTGGTGGAGGATGACGGTCCCCCATGAGAGAGATCATACTCAAGGTGGTCTGATGACCATCTGTG
 GCATGAACCAATAGCCATACCTTTGAGCTGGAGCGTGGTACGTATACGTGAAGACTGGAAAAAGGAGTGGTGCTCTATG
 GGATGTGCTGCTCCCAAGGAAGTAAAAAGGGGGAGACCACAGATGGAGTGACAGAGTAATGACTCGTAGACTGCTAGG
 TTCAACACAAGTTGGAGTGGGAGTTATGCAAGAGGGGGTCTTTCACACTATGTGGCACGTCAAAAAGGATCCGCGCTGAGA
 AGCGGTGAAGGGAGACTTGATCCATACTGGGGAGATGTCAAGCAGGATCTGGTGTACATACTGTGGTCCATGGAAGCTAGATG
 CCGCTGGGACGGGCACAGCGAGGTGCAGCTTGGCCGTGCCCCCGGAGAGAGAGCGAGGAACATCCAGACTCTGCCCCG
 GAATATTTAAGACAAAGGATGGGGACATTGGAGCGGTTGCGCTGGATTACCCAGCAGGAACCTCAGGATCTCCAATCCTAGA
 CAAGTGTGGGAGAGTGATAGGACTTTATGGCAATGGGGTCTGTATCAAAAATGGGAGTTATGTTAGTGCCATCACCAAGGG
 AGGAGGGAGGAAGAGACTCTGTGAGTGCTTCGAGCCTTCGATGCTGAAGAAGAAGCAGCTAACTGTCTTAGACTTGCATC
 CTGGAGCTGGGAAAACAGGAGAGTTCTTCTGAAATAGTCCGTGAAGCCATAAAAACAAGACTCCGTAAGTGTGATCTTAGCT
 CCAACCAGGGTTGTGCTGCTGAAATGGAGGAAGCCCTTAGAGGGCTTCCAGTGCGTTATATGACAACAGCAGTCAATGTAC
 CCACTCTGGAACAGAAATCGTCGACTTAATGTGCCATGCCACCTTCACTTCACGTCTACTACAGCCAATCAGAGTCCCCAATAT
 AATCTGTATATTATGGATGAGGCCCACTTCACAGATCCCTCAAGTATAGCAGCAAGAGGATACATTTCAACAAGGGTTGAGAT
 GGGCGAGGCGGCTGCCATCTTCATGACCGCCACGCCACAGGAACCCGTGACGCATTTCCGGAAGTCCAACTACCAATTATGG
 ACACCGAAGTGGAAGTCCCAGAGAGAGCCTGGAGCTCAGGCTTTGATTGGGTGACGGATTATTCTGGAAAAACAGTTTGGTT
 TGTTCCAAGCGTGAGGAACGGCAATGAGATCGCAGCTTGTCTGACAAAGGCTGGAAAACGGGTATACAGCTCAGCAGAAAG
 ACTTTTGAGACAGAGTTCCAGAAAACAAACATCAAGAGTGGGACTTTGTCTGACAACTGACATTTAGAGATGGGCGCCAA
 CTTTAAAGCTGACCGTGTATAGATTCCAGGAGATGCTTAAAGCCGGTCATACTTGATGGCGAGAGAGTCATTCTGGCTGGAC
 CCATGCCTGTACACATGCCAGCGCTGCCAGAGGAGGGGGCGCATAGGCAGGAATCCAAACAACTGGAGATGAGTATCT
 GTATGGAGGTGGGTGCGCAGAGACTGACGAAGACCATGCACACTGGCTTGAAGCAAGAATGTCCTTGACAATATTTACTCC
 AAGATGGCCTCATAGCCTCGCTCTATCGACCTGAGGCCGACAAAGTAGCAGCCATTGAGGGAGAGTTCAAGCTTAGGACGGA
 GCAAAGGAAGACCTTTGTGGAACCTATGAAAAGAGGAGATCTTCTGTTTGGCTGGCCTATCAGGTTGCATCTGCCGAATAA
 CCTACACAGATAGAAGATGGTGCTTTGATGGCACGACCAACAACACCATAATGGAAGACAGTGTGCCGGCAGAGGTGTGGAC
 CAGACACGGAGAGAAAAGAGTGCTCAAACCGAGGTGGATGGACGCCAGAGTTTGTTCAGATCATGCGGCCCTGAAGTCATTC
 AAGGAGTTTGGCCTGGGAAAAGAGGAGCGGCTTTTGGAGTGATGGAAGCCCTGGGAACACTGCCAGGACACATGACAGAG
 AGATTCAGGAAGCCATTGACAACCTCGCTGTGCTCATGCGGGCAGAGACTGGAAGCAGGCCTTACAAAAGCCGCGGCGGCCC
 AATTGCCGGAGACCTTAGAGACCATATGCTTTTGGGGTTGCTGGGAACAGTCTCGCTGGGAATCTTTTCTGCTTGATGAGG
 AACAAGGGCATAGGGAAGATGGGCTTTGGAATGGTGACTCTTGGGGCCAGCGCATGGCTCATGTGGCTCTCGGAAATTGAGC
 CAGCCAGAATTGCATGTGCTCATTGTTGTGTTCTATTGCTGGTGGTCTCATACCTGAGCCAGAAAAGCAAAGATCTCCCC
 AGGACAACCAATGGCAATCATCATGGTAGCAGTAGGTCTTCTGGGCTTGATTACCGCAATGAAGTGGATGGTTGGAG
 AGAACAAGAGTGACCTAAGCCATCTAATGGGAAGGAGAGAGGAGGGGGCAACCATGGGATTCTCAATGGACATTGACCTG
 CGGCCAGCCTCAGCTTGGGCCATCTATGCTGCCCTGACAACCTTCACTTACCCAGCCGTCCAACATGCAGTGACCACTTCATACA
 ACAACTACTCCTTAATGGCGATGGCCACGCAAGCTGGAGTGTTGTTGGTATGGGCAAAGGGATGCCATTCTACGCATGGGAC

TTTGGAGTCCCGCTGCTAATGATAGGTTGCTACTCACAATTAACGCCCTGACCCTAATAGTGGCCATCATTTTGCTCGTGGCG
 CACTACATGTACTTGATCCCAGGGCTGCAGGCAGCAGCTGCGCGTGTGCCCAGAAGAGAACGGCAGCTGGCATCATGAAGA
 ACCCTGTTGTGGATGGAATAGTGGTGACTGACATTGACACAATGACAATTGACCCCAAGTGGAGAAAAAGATGGGACAGGT
 GCTACTCATGGCAGTAGCCGTCTCCAGCGCCATACTGTGCGGACCCTGGGGGTGGGGGGAGGCTGGGGCCCTGATCACA
 GCCGCAACTTCCACTTTGTGGGAAGGCTCTCCGAACAAGTACTGGAACCTCTCTACAGCCACTTCACTGTGTAACATTTTAGG
 GGAAGTTACTTGGCTGGAGCTTCTAATCTACACAGTAACAAGAAACGCTGGCTTGGTCAAGAGACGTGGGGGTGGAACAG
 GAGAGACCTGGGAGAGAAATGGAAGGCCCGCTTGAACCAGATGTCGGCCCTGGAGTTCTACTCTACAAAAAGTCAGGCAT
 CACCGAGGTGTGCAGAGAAGAGGGCCCGCGCCCTCAAGGACGGTGTGGCAACGGGAGGCCATGCTGTGTCCCAGGGAAG
 TGCAAAGCTGAGATGGTTGGTGGAGCGGGGATACCTGCAGCCCTATGGAAGGTCATTGATCTTGGATGTGGCAGAGGGGG
 CTGGAGTTACTACGCCGCCACCATCCGCAAAGTTCAAGAAGTGAAAGGATACACAAAAGGAGGGCCCTGGTCATGAAGAACCC
 GTGTTGGTGCAAAGCTATGGGTGGAACATAGTCCGTCTTAAGAGTGGGGTGGACGCTTTTCATATGGCGGCTGAGCCGTGTG
 ACACGTTGCTGTGTGACATAGGTGAGTGCATCATCTAGTCTGAAGTGGAAAGACGCGGACGCTCAGAGTCTCTCCATGGTG
 GGGGATTGGCTTGA AAAAGACAGGAGCCTTTGTATAAAAGTGTGTGCCCATACACCAGCACTATGATGGAACCCCTGGA
 GCGACTGCAGCGTAGGTATGGGGGAGGACTGGTCAGAGTGCCACTCTCCGCAACTCTACACATGAGATGTACTGGGTCTCT
 GGAGCGAAAAGCAACACCATAAAAAGTGTGTCCACCACGAGCCAGCTCTCTTGGGGCGCATGGACGGGCCTAGGAGGCCA
 GTGAAATATGAGGAGGATGTGAATCTCGGCTCTGGCAGCGGGCTGTGGTAAGCTGCGCTGAAGCTCCCAACATGAAGATCA
 TTGGTAACCGCATTGAAAGGATCCGCAGTGAGCACGCGGAAACGTGGTTCTTTGACGAGAACCACCCATATAGGACATGGGC
 TTACCATGGAAGCTATGAGGCCCCACACAAGGGTCAGCGTCCTCTCTAATAAACGGGGTTGTGAGGCTCCTGTCAAAACCCT
 GGGATGTGGTGACTGGAGTCAAGGAATAGCCATGACCGACACCACACCGTATGGTCAGCAAAGAGTTTCAAGGAAAAAGT
 GGACACTAGGGTGCCAGACCCCAAGAGGTACTCGTCAGGTTATGAGCATGGTCTCTTCTGGTTGTGGAAAGAGCTAGGC
 AAACACAAACGGCCACGAGTCTGTACCAAGAAGAGTTTCATCAACAAGGTTCTGTAGCAATGCAGCATTAGGGGCAATATTGA
 AGAGGAAAAAGAGTGGAAGACTGCAGTGGAAGCTGTGAACGATCCAAGGTTCTGGGCTAGTGGACAAGGAAAGAGAGCA
 CCACCTGAGAGGAGAGTGCCAGAGTTGTGTGTACAACATGATGGGAAAAAGAGAAAAAGAAACAAGGGGAATTGGAAAGGC
 CAAGGGCAGCCGCGCCATCTGGTATATGTGGCTAGGGGCTAGATTTCTAGAGTTTGAAGCCCTTGGATTCTGAACGAGGATC
 ACTGGATGGGGAGAGAGAACTCAGGAGGTGGTGTGAAGGGCTGGGATTACAAAGACTCGGATATGTCCTAGAAGAGATGA
 GTCGCATACCAGGAGGAAGGATGTATGCAGATGACACTGCTGGCTGGGACACCCGCATCAGCAGGTTTGATCTGGAGAATGA
 AGCTCTAATCACCAACCAATGGAGAAAGGGCACAGGGCCTTGGCATTGGCCATAATCAAGTACACATACCAAAACAAAGTG
 GTAAAGGTCTTAGACCAGCTGAAAAAGGGAAAAACAGTTATGGACATTATTTGAGACAAGACCAAAAGGGGGAGCGGACAA
 GTTGTCACTTACGCTCTTAACACATTTACCAACCTAGTGGTGCAACTCATTGGAATATGGAGGCTGAGGAAGTCTAGAGATG
 CAAGACTTGTGGCTGCTGCGGAGGTGAGAGAAAGTGACCAACTGGTTGCAGAGCAACGGATGGGATAGGCTCAAACGAATG
 GCAGTCAGTGGAGATGATTGCGTTGTGAAGCCAATTGATGATAGGTTTGACATGCCCTCAGGTTCTTGAATGATATGGGAAA
 AGTTAGGAAGGACACACAAGAGTGGAACCCCTCAACTGGATGGGACAACTGGGAAGAAGTTCGGTTTTGCTCCACCACTTCA
 ACAAGCTCCATCTCAAGGACGGGAGGTCCATTGTGGTTCCCTGCGGCCACCAAGATGAAGTATTGGCCGGGCCGCGTCTCT
 CCAGGGGCGGGATGGAGCATCCGGGAGACTGCTTGCTAGCAAAATCATATGCGCAAAATGGGCAGCTCCTTTATTTCCACAG
 AAGGGACCTCCGACTGATGGCCAATGCCATTTGTTTCATCTGTGCCAGTTGACTGGGTTCCAAGTGGGAGAACTACCTGGTCAAT
 CCATGGAAAGGGGAGAAATGGATGACCACTGAAGACATGCTTGTGGTGTGGAACAGAGTGTGGATTGAGGAGAACGACCACAT
 GGAAGACAAGACCCAGTTACGAAATGGACAGACATTCCCTATTTGGGAAAAAGGGGAAGACTTGTGGTGTGGATCTCTATA
 GGGCACAGACCGCGCACCACTGGGCTGAGAACATTA AAAACACAGTCAACATGGTGCGCAGGATCATAGGTGATGAAGAAA
 AGTACATGGACTACCTATCCACCCAAGTTGCTACTTGGGTGAAGAAGGGTCTACACCTGGAGTGCTGTAAGCACCAATCTTA
 ATGTTGTGAGGCCTGCTAGTCAGCCACAGCTTGGGGAAAGCTGTGCAGCCTGTGACCCCCCAGGAGAAGCTGGGAAACCAA
 GCCTATAGTCAGGCCGAGAACGCCATGGCACGGAAGAAGCCATGCTGCCTGTGAGCCCCCTCAGAGGACACTGAGTCAAAAAA
 CCCACGCGCTTGGAGGCGCAGGATGGGAAAAAGAGTGGCGACCTTCCCCACCCTTCAATCTGGGGCCTGAAGTGGAGATC
 AGCTGTGGATCTCCAGAAGAGGGACTAGTGGTTAGAGGAGA

KU497555.1 Zika virus isolate Brazil-ZKV2015, Brazil, complete genome (SEQ ID NO: 3)

CCAATCTGTGAATCAGACTGCGACAGTTCGAGTTTGAAGCGAAAGCTAGCAACAGTATCAACAGGTTTTATTTGGATTGGGA
AACGAGAGTTTCTGGTCATGAAAAACCCAAAAAGAAATCCGGAGGATTCCGGATTGTCAATATGCTAAACGCGGAGTAGC
CCGTGTGAGCCCCCTTTGGGGGCTTGAAGAGGCTGCCAGCCGGACTTCTGCTGGGTCATGGGCCCATCAGGATGGTCTTGGCG
ATTCTAGCCTTTTGGAGATTCACGGCAATCAAGCCATCACTGGGTCTCATCAATAGATGGGGTTGAGTGGGGAAAAAGAGGC
TATGGAAATAATAAAGAAGTTCAAGAAAGATCTGGCTGCCATGCTGAGAATAATCAATGCCAGGAAGGAGAAGAAGAGACG
AGGCGCAGATACTAGTGTGCGAATCGTTGGCCTCTGCTGACCACAGCTATGGCAGCGGAGGTCACTAGACGTGGGAGTGCA
TACTATATGTACTTGGACAGAAACGATGCTGGGGAGGCCATATCTTTTCCAACCACATTGGGGATGAATAAGTGTATATACA
GATCATGGATCTTGGACACATGTGTGATGCCACCATGAGCTATGAATGCCCTATGCTGGATGAGGGGGTGAACCCAGATGAC
GTCGATTGTTGGTGAACACGACGTCAACTTGGGTTGTGTACGGAACCTGCCATCACAAAAAGGTGAAGCACGGAGATCTA
GAAGAGCTGTGACGCTCCCTCCCTCCATTCCACTAGGAAGCTGCAAACCGGGTCGAAACCTGGTTGGAATCAAGAGAATACACA
AAGCACTTGATTAGAGTCAAGAAATGGATATTCAGGAACCTGGCTTCGCGTTAGCAGCAGCTGCCATCGCTTGGCTTTTGGG
AAGCTCAACGAGCCAAAAAGTCATATACTTGGTCATGATACTGCTGATTGCCCGGCATACAGCATCAGGTGCATAGGAGTCA
GCAATAGGGAAGTTTGTGGAAGGTATGTCAGGTGGGACTTGGGTTGATGTTGCTTGGAAACATGGGGGTTGTGTACCCGTAAT
GGCACAGGACAAACCGACTGTGACATAGAGCTGGTTACAACAACAGTCAGCAACATGGCGGAGGTAAGATCCTACTGCTAT
GAGGCATCAATATCAGACATGGCTTCGGACAGCCGCTGCCAACACAAGGTGAAGCCTACCTTGACAAGCAATCAGACACTCA
ATATGCTGCAAAAGAACGTTAGTGGACAGAGGCTGGGGAAATGGATGTGGACTTTTGGCAAAGGGAGCCTGGTGACATGC
GCTAAGTTTGCATGCTCCAAGAAAATGACCGGGAAGAGCATCCAGCCAGAGAATCTGGAGTACCGGATAATGCTGTCAAGTTC
ATGGCTCCAGCACAGTGGGATGATCGTTAATGACACAGGACATGAACTGATGAGAATAGAGCGAAGGTTGAGATAACGCC
CAATTCACCAAGAGCCGAAGCCACCCTGGGGGTTTTGGAAGCTTAGGACTTGATTGTGAACCGAGGACAGGCCTTGACTTT
CAGATTGTATTACTTGACTATGAATAACAAGCACTGGTTGGTTTACAAGGAGTGGTTCCACGACATTCCATTACCTTGGCAGC
CTGGGGCAGACACCGGAATCCCACTGGAACAACAAGAAGCACTGGTAGAGTTCAAGGACGCACATGCCAAAAAGGCAAA
CTGTCTGGTTCTAGGGACTCAAGAAGGAGCAGTTCACACGGCCCTTGTGGAGCTCTGGAGGCTGAGATGGATGGTGCAAA
GGGAAGGCTGTCTCTGGCCACTTGAAATGTGCGCTGAAAATGGATAAACTTAGATTGAAGGGCGTGTACATACTCTTGTGTA
CCGACGCTTCACATTACCAAGATCCCGGCTGAAACACTGCACGGGACAGTCACAGTGGAGGTACAGTACGCAGGGACAGA
TGGACCTTGCAAGGTTCCAGCTCAGATGGCGGTGGACATGCAAACTCTGACCCAGTTGGGAGGTTGATAACCGCTAACCCCG
TAATCACTGAAAGCACTGAGAATCTAAGATGATGCTGGAACCTTGATCCACCATTGGGGACTCTTACATTGTCATAGGAGTCG
GGGAGAAGAAGATACCCACCACTGGCAGAGGAGTGGCAGCACCATTGGAAAAGCATTGAAGCCACTGTGAGAGGTGCCA
AGAGAATGGCAGTCTTGGGAGACACAGCCTGGGACTTTGGATCAGTTGGAGGCGCTCTCAACTCATTGGGCAAGGGCATCCA
TCAAATTTTGGAGCAGCTTCAAATCATTGTTGGAGGAATGCTCTGGTTCTCACAATCTCATTGGAACGTTGCTGATGTGG
TTGGGTCTGAACACAAAGAATGGATCTATTTCCCTTATGTGCTTGGCCTTAGGGGGAGTGTGATCTTCTATCCACAGCCGTC
TCTGCTGATGTGGGGTCTCGGTGGACTTCTCAAAGAAGGAGACGAGATGTGGTACAGGGGTGTTGCTCTATAACGACGTTG
AAGCCTGGAGGGACAGGTACAAGTACCATCCTGACTCTCCCGTAGATTGGCAGCAGCAGTCAAGCAAGCCTGGGAAGATGG
TATCTGCGGGATCTCTCTGTTTCAAGAATGGAAAACATCATGTGGAGATCAGTAGAAGGGGAGCTTAACGCAATCCTGGAAG
AGAATGGAGTTCAACTGACGGTCGTTGTGGGATCTGTAAAAACCCCATGTGGAGAGGTCCACAGAGATTGCCCGTGCCTGT
GAACGAGCTGCCCCACGGCTGGAAGGCTTGGGGGAAATCGTACTTCGTGAGAGCAGCAAAGACAAATAACAGCTTTGTCGTG
GATGGTGACACACTGAAGGAATGCCACTCAAACATAGAGCATGGAACAGCTTCTTGTGGAGGATCATGGGTTCCGGGGTAT
TTCACACTAGTGTCTGGCTCAAGGTTAGAGAAGATTATTCATTAGAGTGTGATCCAGCCGTTATTGGAACAGCTGTTAAGGGA
AAGGAGGCTGTACACAGTGTCTAGGCTACTGGATTGAGAGTGAGAAGAATGACACATGGAGGCTGAAGAGGGCCCATCTG
ATCGAGATGAAAACATGTGAATGGCCAAAGTCCACACATTGTGGACAGATGGAATAGAAGAGAGTGATCTGATCATACCA
AGTCTTAGCTGGGCCACTCAGCCATCACAATACCAGAGAGGGCTACAGGACCCAAATGAAAGGGCCATGGCACAGTGAAGA
GCTTGAATTCGGTTGAGGAATGCCAGGCACTAAGGTCCACGTGGAGGAAACATGTGGAACAAGAGGACCATTCTGAGA
TCAACCACTGCAAGCGGAAGGGTGATCGAGGAATGGTGTGTCAGGGAGTGCACAATGCCCCACTGTGTTCCGGGCTAAAG
ATGGCTGTTGGTATGGAATGGAGATAAGGCCAGGAAGAACCAGAAAGCAACTTAGTAAGGTCAATGGTGACTGCAGGATC
AACTGATCACATGGATCACTTCTCCCTGGAGTGCTTGTGATTCTGCTCATGGTGCAGGAAGGGCTGAAGAAGAGAATGACCA

CAAAGATCATCATAAGCACATCAATGGCAGTGCTGGTAGCTATGATCCTGGGAGGATTTCAATGAGTGACCTGGCTAAGCTT
 GCAATTTTGATGGGTGCCACCTTCGCGGAAATGAACACTGGAGGAGATGTAGCTCATCTGGCGCTGATAGCGGCATTCAAAGT
 CAGACCAGCGTTGCTGGTATCTTCATCTTCAGAGCTAATTGGACACCCCGTGAAGCATGCTGCTGGCCTTGGCCTCGTGTTT
 TTTGCAAACCTGCGATCTCCGCCTTGGAGGGGACCTGATGGTTCTCATCAATGGTTTGGCTTGGCCTGGTTGGCAATACGAGC
 GATGGTTGTTCCACGCACTGACAACATCACCTTGGCAATCCTGGCTGCTCTGACACCACTGGCCCCGGGGCAGCTGCTTGTGGC
 GTGGAGAGCAGGCCCTTGCTACTTGCGGGGGGTTTATGCTCCTCTCTCTGAAGGGAAAAGGCAGTGTGAAGAAGAACTTACCA
 TTTGTCATGGCCCTGGGACTAACCCTGTGAGGCTGGTGGACCCCATCAACGTGGTGGGACTGCTGTTGCTCACAAGGAGTGG
 GAAGCGGAGCTGGCCCCCTAGCGAAGTACTCACAGCTGTTGGCCTGATATGCGCATTGGCTGGAGGGTTCCGCAAGGCAGAT
 ATAGAGATGGCTGGGCCCATGGCCGCGGTGGTCTGCTAATTGTGAGTTACGTGGTCTCAGGAAAGAGTGTGGACATGTACA
 TTGAAAGAGCAGGTGACATCACATGGGAAAAAGATGCGGAAGTCACTGGAAACAGTCCCCGGCTCGATGTGGCGCTAGATGA
 GAGTGGTGACTTCTCCCTGGTGGAGGATGACGGTCCCCCATGAGAGAGATCATACTCAAGGTGGTCTGATGACCATCTGTG
 GCATGAACCAATAGCCATACCTTTGCAGCTGGAGCGTGGTACGTATACGTGAAGACTGGAAAAAGGAGTGGTGTCTATG
 GGATGTGCTGCTCCCAAGGAAGTAAAAAGGGGGAGACCACAGATGGAGGTACAGAGTAATGACTCGTAGACTGCTAGG
 TTCAACACAAGTTGGAGTGGGAGTTATGCAAGAGGGGGTCTTTCACACTATGTGGCACGTCAAAAAGGATCCGCGCTGAGA
 AGCGGTGAAGGGAGACTTGATCCATACTGGGGAGATGTCAAGCAGGATCTGGTGTACTGTGGTCCATGGAAGCTAGATG
 CCGCCTGGGACGGGCACAGCGAGGTGCAGCTTTGGCGTGCCCCCGGAGAGAGAGCGAGGAACATCCAGACTCTGCCCCG
 GAATATTTAAGACAAAGGATGGGGACATTGGAGCGGTTGCGCTGGATTACCCAGCAGGAACCTCAGGATCTCCAATCCTAGA
 CAAGTGTGGGAGAGTGATAGGACTTTATGGCAATGGGGTCGTGATAAAAAATGGGAGTTATGTTAGTGCCATCACCCAAGGG
 AGGAGGGAGGAAGAGACTCCTGTTGAGTGCTTCGAGCCTTCGATGCTGAAGAAGAAGCAGCTAACTGTCTTAGACTTGATC
 CTGGAGCTGGGAAAACAGGAGAGTTCTTCTGAAATAGTCCGTGAAGCCATAAAAAACAAGACTCCGTACTGTGATCTTAGCT
 CCAACCAGGGTTGTCGCTGCTGAAATGGAGGAAGCCCTAGAGGGCTTCCAGTGCGTTATATGACAACAGCAGTCAATGTAC
 CCACTCTGGAACAGAAATCGTCGACTTAATGTGCCATGCCACCTTCACTTACGTCTACTACAGCCAATCAGAGTCCCCAACTAT
 AATCTGTATATTATGGATGAGGCCCACTTACAGATCCCTCAAGCATAGCAGCAAGAGGATACATTTCAACAAGGGTTGAGAT
 GGGCGAGGCGCTGCCATCTTCATGACCGCCACGCCACCAGGAACCCGTGACGCATTTCCGGACTCCAACCTACCAATTATGG
 ACACCGAAGTGGAAGTCCAGAGAGAGCCTGGAGCTCAGGCTTTGATTGGGTGACGGATCATTCTGAAAAACAGTTTGGTT
 TGTTCCAAGCGTGAGGAACGGCAATGAGATCGCAGCTTGTCTGACAAAGGCTGGAACCGGGTCATACAGCTCAGCAGAAAG
 ACTTTTGAGACAGAGTTCCAGAAAAACAAACATCAAGAGTGGGACTTTGTCGTGACAACTGACATTTAGAGATGGGCGCCAA
 CTTTAAAGCTGACCGTGTATAGATTCCAGGAGATGCCAAAGCCGGTCATACTTGATGGCGAGAGAGTCATTCTGGCTGGAC
 CCATGCTGTACACATGCCAGCGCTGCCAGAGGAGGGGGCGCATAGGCAGGAATCCCAACAAACCTGGAGATGAGTACCT
 GTATGGAGGTGGGTGCGCAGAGACTGACGAAGACCATGCACACTGGCTTGAAGCAAGAATGCTCCTTGACAATATTTACCTCC
 AAGATGGCCTCATAGCCTCGCTCTATCGACCTGAGGCCGACAAAGTAGCAGCCATTGAGGGAGAGTTCAAGCTTAGGACGGA
 GCAAAGGAAGACCTTTGTGGAACCTCATGAAAAGAGGAGATCTTCTGTTTGGCTGGCCTATCAGGTTGCATCTGCCGAATAA
 CCTACACAGATAGAAGATGGTGTCTTGTATGGCAGCAACAACACCATAATGGAAGACAGTGTGCCGGCAGAGGTGTGGAC
 CAGACACGGAGAGAAAAGAGTGCTCAAACCGAGGTGGATGGACGCCAGAGTTTGTTCAGATCATGCGGCCCTGAAGTCATT
 AAGGAGTTTGCCGCTGGGAAAAGAGGAGCGGCTTTTGGAGTGATGGAAGCCCTGGGAACACTGCCAGGACACATGACAGAG
 AGATTCCAGGAAGCCATTGACAACCTCGCTGTGCTCATGCGGCAGAGACTGGAAGCAGGCCTTACAAAGCCGCGCGGCC
 AATTGCCGGAGACCTTAGAGACCATTATGCTTTTGGGGTTGCTGGGAACAGTCTCGCTGGGAATCTTTTTCGTCTTGATGAGG
 AACAAGGGCATAGGGAAGATGGGCTTTGGAATGGTACTCTTGGGGCCAGCGCATGGCTCATGTGGCTCTCGGAAATTGAGC
 CAGCCAGAATTGCATGTGCTCTATTGTTGTGTTCTATTGCTGGTGGTGTCTATACCTGAGCCAGAAAAGCAAAGATCTCCCC
 AGGACAACCAATGGCAATCATCATGTTAGCAGTAGGTCTTCTGGGCTTGATTACCGCAATGAACTCGGATGGTTGGAG
 AGAACAAGAGAGTGACCTAAGCCATCTAATGGGAAGGAGAGAGGAGGGGGCAACCATAGGATTCTCAATGGACATTGACTG
 CGGCCAGCCTCAGCTTGGGCCATCTATGCTGCCTTGACAACTTTCATTACCCAGCCGTCCAACATGCAGTGACCACTTCATACA
 ACAACTACTCCTTAATGGCGATGGCCACGCAAGCTGGAGTGTGTTTGGTATGGGCAAAGGGATGCCATTCTACGCATGGGAC
 TTTGGAGTCCCGCTGCTAATGATAGGTTGCTACTACAATTAACACCCCTGACCCTAATAGTGGCCATCATTTTGTCTGCTGGCGC
 ACTACATGTACTTGATCCAGGGCTGCAGGCAGCAGCTGCGCGTGTGCCAGAAAGAGAACGGCAGCTGGCATCATGAAGAA
 CCCTGTTGTGGATGGAATAGTGGTGAAGTACTGACATTGACACAATGACAATTGACCCCAAGTGGAGAAAAAGATGGGACAGGTG

CTACTCATAGCAGTAGCCGTCTCCAGCGCCATACTGTCGCGGACCGCTGGGGGTGGGGGGAGGCTGGGGCCCTGATCACAG
 CCGCAACTTCCACTTTGTGGGAAGGCTCTCCGAACAAGTACTGGAACCTCTACAGCCACTTCACTGTGTAACATTTTAGGG
 GAAGTTACTTGGCTGGAGCTTCTAATCTACACAGTAACAAGAAACGCTGGCTTGGTCAAGAGACGTGGGGGTGGAACAGG
 AGAGACCCTGGGAGAGAAATGGAAGGCCCGCTTGAACCAGATGTCGGCCCTGGAGTTCTACTCTACAAAAAGTCAGGCATC
 ACCGAGGTGTGCAGAGAAGAGGCCCCGCGCCCTCAAGGACGGTGTGGCAACGGGAGGCCATGCTGTGTCCGAGGAAGT
 GCAAAGCTGAGATGGTTGGTGGAGCGGGGATACCTGCAGCCCTATGGAAAGGTCAATTGATCTTGGATGTGGCAGAGGGGGC
 TGGAGTTACTACGCCGCCACCATCCGCAAAGTTCAAGAAGTGAAAGGATACACAAAAGGAGGCCCTGGTCATGAAGAACCCG
 TGTTGGTGCAAAGCTATGGGTGGAACATAGTCCGTCTTAAGAGTGGGGTGGACGCTTTTCATATGGCGGCTGAGCCGTGTGA
 CACGTTGCTGTGTGACATAGGTGAGTCATCATCTAGTCTGAAGTGGAAAGAACGACGGACGCTCAGAGTCTCTCCATGGTGG
 GGGATTGGCTTGAAAAAGACCAGGAGCCTTTTGCAAAAAGTGTGTGCCCATAACACGACTATGATGGAAACCTGGAG
 CGACTGCAGCGTAGGTATGGGGGAGGACTGGTCAGAGTGCCACTCTCCGCAACTCTACACATGAGATGTACTGGGTCTCTG
 GAGCGAAAAGCAACACCATAAAAAAGTGTGTCCACCACGAGCCAGTCTCTTGGGGCGCATGGACGGGCCCTAGGAGGCCAGT
 GAAATATGAGGAGGATGTGAATCTCGGCTCTGGCAGCGGGCTGTGGTAAGCTGCGCTGAAGCTCCCAACATGAAGATCATT
 GGTAAACCGCATTGAAAGGATCCGCAGTGAGCACGCGGAAACGTGGTTCTTTGACGAAAACACCCATATAGGACATGGGCTT
 ACCATGGAAGCTATGTGGCCCCACACAAGGGTCAGCGTCTCTCTAATAAACGGGGTTGTCAGGCTCTGTCAAAACCTGG
 GATGTGGTGAAGTGGAGTCACAGGAATAGCCATGACCGACACCACACCGTATGGTCAGCAAAGAGTTTCAAGGAAAAAGTGG
 AACTAGGGTGCCAGACCCCAAGAAGGCACTCGTCAGGTTATGAGCATGGTCTCTTCTGGTTGTGGAAAGAGCTAGGCAA
 ACACAAACGACCACGAGTCTGTACCAAAGAAGAGTTCATCAACAAGGTTCTAGCAATGCAGCATTAGGGGCAATATTTGAAG
 AGGAAAAAGAGTGGAAAGACTGCAGTGGAAAGCTGTGAACGATCCAAGGTTCTGGGCTCTAGTGGACAAGGAAGAGAGCACC
 ACCTGAGAGGAGAGTGCCAGAGTTGTGTGTACAACATGATGGGAAAAAGAGAAAAAGAAACAAGGGGAATTTGGAAGGCCA
 AGGGCAGCCGCGCCATCTGGTATATGTGGCTAGGGGCTAGATTCTAGAGTTCGAAGCCCTTGGATTCTTGAACGAGGATCAC
 TGGATGGGAGAGAGAACTCAGGAGGTGGTGTGAAGGGCTGGGATTACAAAGACTCGGATATGCTCTAGAAGAGATGAGT
 CGCATACCAGGAGGAAGGATGTATGCAGATGACACTGCTGGCTGGGACACCCGCATCAGCAGGTTTGATCTGGAGAATGAAG
 CTCTAATCACCAACCAATGGAGAAAGGGCACAGGGCCTTGGCATTGGCCATAATCAAGTACACATACCAAAACAAAGTGGTA
 AAGGTCTTAGACCAGCTGAAAAAGGGAAAAACAGTTATGGACATTATTTGAGACAAGACCAAGGGGGAGCGGACAAGTT
 GTCATTACGCTCTTAACACATTTACCAACCTAGTGGTGCAACTCATTGGAATATGGAGGCTGAGGAAGTTCTAGAGATGCAA
 GACTTGTGGCTGCTGCGGAGGTGAGAGAAAGTGACCAACTGGTTGCAGAGCAACGGATGGGATAGGCTCAAACGAATGGCA
 GTCAGTGGAGATGATTGCGTTGTGAAGCCAATTGATGATAGGTTTGACATGCCCTCAGGTTCTTGAATGATATGGGAAAAGT
 TAGGAAGGACACACAAGAGTGGAAACCCCTCAACTGGATGGGACAACCTGGGAAGAGTTCGGTTTGTCTCCACCACTTCAACA
 AGCTCCATCTCAAGGACGGGAGGTCCATTGTGGTTCCCTGCCGCCCAAGATGAAGTGAAGTGGCCGGGCCCGCTCTCTCCA
 GGGGCGGGATGGAGCATCCGGGAGACTGCTTGCCTAGCAAAATCATATGCGCAAATGTGGCAGCTCCTTTATTTCCACAGAA
 GGGACCTCCGACTGATGGCCAATGCCATTTGTCATCTGTGCCAGTTGACTGGGTTCCAAGTGGGAGAACTACCTGGTCAATCC
 ATGGAAAGGGAGAATGGATGACCACTGAAGACATGCTTGTGGTGTGGAACAGAGTGTGGATTGAGGAGAACGACCACATGG
 AAGACAAGACCCAGTTACGAAATGGACAGACATTCCCTATTTGGGAAAAAGGGAAGACTTGTGGTGTGGATCTCTCATAGG
 GCACAGACCGCGCACCACTGGGCTGAGAACATTAAAAATACAGTCAACATGGTGCAGAGGATCATAGGTGATGAAGAAAAG
 TACATGGACTACCTATCCACCAAGTTGCTACTTGGGTGAAGAAGGGTCTACACCTGGAAGTGCTGTGAGCACCATCTTAATG
 TTGTAGGCCCTGCTAGTCAGCCACAGCTTGGGGAAAGCTGTGCAGCCTGTGACCCCTCAGGAGAAAGCTGGGTAACCAAGCCT
 ATAGTCAGGCCGAGAACGCCATGGCAGGAAGAAGCCATGTGCTGTGAGCCCTCAGAGGACACTGAGTCAAAAAACCC
 ACGCGCTTGGAGGCGCAGGATGGGAAAAGAAGGTGGCGACCTTCCCCACCTTCAATCTGGGGCTGAAGTGGAGATCAGCT
 GTGGATCTCAGAAGAGGGACTAGTGGTTAGAGGAGACCCCCGAAAACGAAAACAGCATATTGACGCTGGGAAAGACC
 AGAGACTCCATGAGTTTCCACCACGCTGGCCGCCAGGCACAGATCGCCGAATAGCGGCGGCCGGTGTGGGGAAATCCA

GTTGTGATCTGTGTGAATCAGACTGCGACAGTTCGAGTTTGAAGCGAAAGCTAGCAACAGTATCAACAGGTTTTATTTGGAT
 TTGGAAACGAGAGTTTTCTGGTCATGAAAAACCCAAAAAGAAATCCGGAGGATTCCGGATTGTCAATATGCTAAAAACGCGGA
 GTAGCCCGTGTGAGCCCTTTGGGGGCTTGAAGAGGCTGCCAGCCGACTTCTGCTGGGTCATGGGCCCATCAGGATGGTCTT
 GCGGATTCTAGCCTTTTTGAGATTACGGCAATCAAGCCATCACTGGGTCTCATCAATAGATGGGTTGAGTGGGGAAAAAG
 AGGCTATGGAAACAATAAAGAAGTTCAAGAAAGATCTGGCTGCCATGCTGAGAATAATCAATGCTAGGAAGGAGAAAGA
 GACGAGGCGCAGATACTAGTGTGGAATTGTTGGCTCTGCTGACCACAGCTATGGCAGCGGAGGTCACTAGACGTGGGAG
 TGCATACTATATGTACTTGGACAGAAACGATGCTGGGGAGGCCATATCTTTCCAACCACATTGGGGATGAATAAGTGTATAT
 ACAGATCATGGATCTTGGACACATGTGTGATGCCACCATGAGCTATGAATGCCCTATGCTGGATGAGGGGGTGAACCAGAT
 GACGTCGATTGTTGGTGCAACACGACGTCAACTTGGGTTGTGTACGGAACCTGCCATCACAAAAAGGTGAAGCACGGAGAT
 CTAGAAGAGCTGTGACGCTCCCTCCCATCCACCAGGAAGCTGCAACCGCGTCGCAAACTGGTTGGAATCAAGAGAATAC
 ACAAGCACTTGATTAGAGTCGAAAATTGGATATTGAGGAACCTGGCTTCGCGTTAGCAGCAGCTGCCATCGCTTGGCTTTTG
 GGAAGCTCAACGAGCCAAAAAGTCATATACTTGGTCATGATACTGCTGATTGCCCCGGCATACAGCATCAGGTGCATAGGAGT
 CAGCAATAGGGACTTTGTGGAAGGTATGTCAGGTGGGACTTGGGTTGATGTTGCTTGGAACTGGAGGTTGTGTACCGTA
 ATGGCACAGGACAAACCGACTGTGACATAGAGCTGGTTACAACAACAGTCAGCAACATGGCGGAGGTAAGATCCTACTGCT
 ATGAGGCATCAATATCAGACATGGCTTCTGACAGCCGCTGCCAACACAAGGTGAAGCCTACCTTGACAAGCAATCAGACACT
 CAATATGTCTGCAAAAGAACGTTAGTGGACAGAGGCTGGGGAAATGGATGTGGACTTTTGGCAAAGGGAGCCTGGTGACAT
 GCGCTAAGTTGCTGCTCCAAGAAAATGACCGGGAAGAGCATCCAGCCAGAGAATCTGGAGTACCGGATAATGCTGTCAGT
 TCATGGCTCCCGACACAGTGGGATGATCGTTAATGACACAGGACATGAAACTGATGAGAATAGAGCGAAAGTTGAGATAACG
 CCCAATTCACCGAGAGCCGAAGCCACCTGGGGGGTTTTGGAAGCCTAGGACTTGATTGTGAACCGAGGACAGGCCTTGACTT
 TTCAGATTGTATTACTTGACTATGAATAACAAGCACTGGTTGGTTTACAAGGAGTGGTTCCACGACATTCCATTACCTTGGCAG
 GCTGGGGCAGACACCGGAACCTCCACTGGAACAACAAGCAAGCACTGGTAGAGTTCAAGGACGCACATGCCAAAAGGCAA
 ACTGTCTGGTTCTAGGGAGTCAAGAAGGAGCAGTTCACACGGCCCTTGTGGAGCTCTGGAGGCTGAGATGGATGGTGCAA
 AGGGAAGGCTGTCTCTGGCCACTTGAAATGTCGCTGAAAATGGATAAACTTAGATTGAAGGGCGTGTACACTCCTTGTGT
 ACTGCAGCGTTCACATTACCAAGATCCCGGCTGAAACACTGCACGGGACAGTCACAGTGGAGGTACAGTACGCAGGGACAG
 ATGGACCTTGAAGGTTCCAGCTCAGATGGCGGTGGACATGCAAACTCTGACCCCAAGTTGGGAGGTTGATAACCGCTAACCC
 GTAATCACTGAAAGCACTGAGAACTAAGATGATGCTGGAACCTTATCCACCATTTGGGGACTCTTACATTGTATAGGAGTC
 GGGGAGAAGAAGATCACCCCACTGGCACAGGAGTGGCAGCACCATTGGAAAAGCATTGAAAGCCACTGTGAGAGGTGCC
 AAGAGAATGGCAGTCTTGGGAGACACAGCCTGGGACTTTGGATCAGTTGGAGGCGCTCTCAACTCATTGGGCAAGGGCATCC
 ATCAAATTTTTGGAGCAGCTTCAAATCATTGTTGGAGGAATGTCCTGGTTCTCACAAATTCTCATTGGAACGTTGCTGATGTG
 GTTGGGTCTGAACACAAAGAATGGATCTATTTCCCTTATGTGCTTGGCTTAGGGGGAGTGTGATCTTCTTATCCACAGCCGT
 CTCTGCTGATGTGGGTGCTCGGTGGACTTCTCAAAGAAGGAGACGAGATGCGGTACAGGGGTGTTCTGTCTATAACGACGTT
 GAAGCCTGGAGGGACAGGTACAAGTACCATCTGACTCCCCCGTAGATTGGCAGCAGCAGTCAAGCAAGCCTGGGAAGATG
 GTATCTGCGGGATCTCTGTCTTCAAGAATGGAAACATCATGTGGAGATCAGTAGAAGGGGAGCTCAACGCAATCCTGGAA
 GAGAATGGAGTTCAACTGACGGTCGTTGTGGGATCTGTAAAAAACCCCATGTGGAGAGGTCCACAGAGATTGCCCCTGCTG
 TGAACGAGCTGCCCCACGGCTGGAAGGCTTGGGGGAAATCGTATTTCTGTCAGAGCAGCAAAGACAAATAACAGCTTTGTCGT
 GGATGGTGACACACTGAAGGAATGCCACTCAAACATAGAGCATGGAACAGCTTTCTTGTGGAGGATCATGGGTTCCGGGTA
 TTTCACTAGTGTCTGGCTCAAGGTTAGAGAAGATTATTCATTAGAGTGTGATCCAGCCGTTATTGGAACAGCTGTTAAGGGA
 AAGGAGGCTGTACACAGTGATCTAGGCTACTGGATTGAGAGTGAGAAGAATGACACATGGAGGCTGAAGAGGGGCCATCTG
 ATCGAGATGAAAACATGTGAATGGCCAAAGTCCACACATTGTGGACAGATGGAATAGAAGAGAGTGATCTGATCATACCA
 AGTCTTTAGCTGGGCCACTCAGCCATCAATAACCAGAGAGGGCTACAGGACCCAAATGAAAGGGCCATGGCACAGTGAAGA
 GCTTGAATTCGGTTTGAGGAATGCCAGGCACTAAGGTCCACGTGGAGGAAACATGTGGAACAAGAGGACCATCTCTGAGA
 TCAACCACTGCAAGCGGAAGGGTGATCGAGGAATGGTGTGTCAGGGAGTGACAATGCCCCCACTGTCTTCCGGGCTAAAG
 ATGGCTGTTGGTATGGAATGGAGATAAGGCCAGGAAAGAACCAAGCAAACTTAGTAAGGTCAATGGTGACTGCAGGATC
 AACTGATCACATGGACCCTTCTCCCTTGGAGTGCTTGTGATCTGCTCATGGTGCAGGAAGGGCTGAAGAAGAGAATGACCA
 CAAAGATCATATAAGCACATCAATGGCAGTGCTGGTAGCTATGATCCTGGGAGGATTTCAATGAGTGACCTGGCTAAGCTT
 GCAATTTTGATGGGTGCCACCTTCGCGGAAATGAACACTGGAGGAGATGTAGCTCATCTGGCGCTGATAGCGGCATTCAAAGT

CAGACCAGCGTTGCTGGTATCTTTTCATCTTCAGAGCTAATTGGACACCCCGTGAAAGCATGCTGCTGGCCTTGGCCTCGTGTCT
 TTTGCAAACCTGCGATCTCCGCTTGGAAAGGCGACCTGATGGTTCTCATCAATGGTTTTGCTTTGGCCTGGTTGGCAATACGAGC
 GATGGTTGTTCCACGCACTGATAACATCACCTTGGCAATCCTGGCTGCTCTGACACCACTGGCCCCGGGGCAGACTGCTTGTGGC
 GTGGAGAGCAGGCCTTGTACTTGGGGGGGTTTATGCTCCTCTCTCTGAAGGGAAAAGGCAGTGTGAAGAAGAATTACCA
 TTTGTCATGGCCCTGGGACTAACCCTGTGAGGCTGGTCGACCCCATCAACGTGGTGGGACTGCTGTTGCTCACAAGGAGTGG
 GAAGCGGAGCTGGCCCCCTAGCGAAGTACTCACAGCTGTTGGCCTGATATGCGCATTGGCTGGAGGGTTGCGCAAGGCAGAT
 ATAGAGATGGCTGGGCCCATGGCCGCGGTCTGCTAATTGTGAGTTACGTGGTCTCAGGAAAAGAGTGTGGACATGTACA
 TTGAAAAGAGCAGGTGACATCACATGGGAAAAAGATGCGGAAGTCACTGGAAACAGTCCCCGGCTCGATGTGGCGCTAGATGA
 GAGTGGTGATTTCTCCCTGGTGGAGGATGACGGTCCCCCATGAGAGAGATCATACTCAAGGTGGTCTGATGACCATCTGTG
 GCATGAACCCAATAGCCATACCCTTTCAGCTGGAGCGTGGTACGTATACGTGAAGACTGGAAAAAGGAGTGGTGTCTATG
 GGATGTGCTGCTCCCAAGGAAGTAAAAAGGGGGAGACCACAGATGGAGTGTACAGAGTAATGACTCGTAGACTGCTAGG
 TTCAACACAAGTTGGAGTGGGAGTTATGCAAGAGGGGGTCTTTCACACTATGTGGCACGTACAAAAAGGATCCGCGCTGAGA
 AGCGGTGAAGGGAGACTTGATCCATACTGGGGAGATGTCAAGCAGGATCTGGTGTCTACTGTGGTCCATGGAAAGCTAGATG
 CCGCCTGGGATGGGCACAGCGAGGTGCAGCTCTTGGCCGTGCCCCCGGAGAGAGAGCGAGGAACATCCAGACTCTGCCCC
 GAATATTTAAGACAAAGGATGGGGACATTGGAGCGGTTGCGCTGGATTACCCAGCAGGAACCTTCAGGATCTCCAATCCTAGA
 CAAGTGTGGGAGAGTGATAGGACTTTATGGCAATGGGGTCTGTATCAAAAACGGGAGTTATGTTAGTGCCATCACCAGGG
 AGGAGGGAGGAAGAGACTCCTGTTGAGTGTCTGAGCCCTCGATGCTGAAGAAGAAGCAGCTAACTGTCTTAGACTTGCATC
 CTGGAGCTGGGAAAACAGGAGAGTTCTTCTGAAATAGTCCGTGAAGCCATAAAAACAAGACTCCGTACTGTGATCTTAGCT
 CCAACCAGGGTTGTGCTGCTGAAATGGAGGAGGCCCTTAGAGGGCTTCCAGTGCCTTATATGACAACAGCAGTCAATGTCAC
 CCACTCTGGAACAGAAATCGTCGACTTAATGTGCCATGCCACCTTCACTTACGTCTACTACAGCCAATCAGAGTCCCCAACTAT
 AATCTGTATATTATGGATGAGGCCCCACTTCACAGATCCCTCAAGTATAGCAGCAAGAGGATACATTTCAACAAGGGTTGAGAT
 GGGCGAGGCGGCTGCCATCTTCATGACCGCCACGCCACCAGGAACCCGTGACGCAATTTCCGGACTCCAACCTACCAATTATGG
 ACACCGAAGTGGAAGTCCAGAGAGAGCTGGAGCTCAGGCTTTGATTGGGTGACGGATCATTCTGGAAAAACAGTTTGGTT
 TGTTCCAAGCGTGAGGAACGGCAATGAGATCGCAGCTTGTCTGACAAAGGCTGGAAAACGGGTCATACAGCTCAGCAGAAAAG
 ACTTTTGAGACAGAGTTCCAGAAAACAAAACATCAAGAGTGGGACTTTGTCGTGACAACTGACATTTAGAGATGGGCGCCAA
 CTTTAAAGCTGACCGTGTATAGATTCCAGGAGATGCCATAAGCCGGTCATACTTGATGGCGAGAGAGTCACTTGGCTGGAC
 CCATGCCTGTACACATGCCAGCGCTGCCAGAGGAGGGGGCGCATAGGCAGGAATCCCAACAAACCTGGAGATGAGTATCT
 GTATGGAGGTGGGTGCGCAGAGACTGACGAAGACCATGCACACTGGCTTGAAGCAAGAATGCTCCTTGACAATATTACCTCC
 AAGATGGCCTCATAGCCTCGCTCTATCGACCTGAGGCCGACAAAGTAGCAGCCATTGAGGGAGAGTTCAAGCTTAGGACGGA
 GCAAAGGAAGACCTTTGTGGAACATGAAAAGAGGAGATCTTCTGTTTGGCTGGCCTATCAGGTTGCATCTGCCGAATAA
 CCTACACAGATAGAAGATGGTGTCTTGTGGCAGCAGCAACAACACCATAATGGAAGACAGTGTGCCGGCAGAGGTGTGGAC
 CAGACACGGAGAGAAAAGAGTGTCAAACCGAGGTGGATGGACGCCAGAGTTTGTTCAGATCATGCGGCCCTGAAGTCATTC
 AAGGAGTTTGCCGCTGGGAAAAGAGGAGCGGCTTTTGGAGTGATGGAAGCCCTGGGAACACTGCCAGGACACATGACAGAG
 AGATTCAGGAAGCCATTGACAACCTCGCTGTGCTCATGCGGGCAGAGACTGGAAGCAGGCCCTTACAAAGCCGCGGCGGCCCC
 AATTGCCGGAGACCTAGAGACCATAATGCTTTTGGGTTGCTGGGAACAGTCTCGCTGGGAATCTTCTGCTTGTGATGAGG
 AACAAGGGCATAGGGAAGATGGGCTTTTGAATGGTGAAGTCTTGGGGCCAGCGCATGGCTCATGTGGCTCTCGGAAATTGAGC
 CAGCCAGAATTGCATGTGTCTCATTGTTGTGTTCTATTGCTGGTGGTGTCTATACCTGAGCCAGAAAAGCAAAGATCTCCCC
 AGGACAACCAATGGCAATCATCATGGTAGCAGTAGGCTTCTGGGCTTGATTACCGCAATGAAGTCTGGATGGTTGGAG
 AGAACAAGAGTGACCTAAGCCATCTAATGGGAAGGAGAGAGGAGGGGGCAACCATAGGATTCTCAATGGACATTGACCTG
 CGGCCAGCCTCAGCTTGGGCCATCTATGCTGCCCTGACAACCTTCACTTACCCAGCGTCCAACATGCAGTGACCACTCATACA
 ACACTACTCTTAATGGCGATGGCCACGCAAGCTGGAGTGTGTTTGGCATGGGCAAAGGGATGCCATTCTACGATGGGAC
 TTTGGAGTCCCGTGTCTAATGATAGGTTGCTACTCACAATTAACACCCCTGACCTAATAGTGGCCATCATTTTGTCTGTGGCGC
 ACTACATGTACTTGATCCAGGGCTGCGAGGAGGAGCTGCGCGTGTGCCAGAGAGAAACGGCAGCTGGCATCATGAAGAA
 CCCTGTTGTGGATGGAATAGTGGTGAAGTACATGACACAATGACAATTGACCCCCAAGTGGAGAAAAAGATGGGACAGGTG
 CTACTCATAGCAGTAGCCGTCTCCAGCGCCATACTGTGCGGACCGCCTGGGGTGGGGGGAGGCTGGGGCTGTGATCACAG
 CCGCAACTTCACTTTGTGGGAAGGCTCTCCGAACAAGTACTGGAAGTCTCTACAGCCAATCACTGTGTAACATTTTAGGG

GAAGTTACTTGGCTGGAGCTTCTCTAATCTACACAGTAACAAGAAACGCTGGCTTGGTCAAGAGACGTGGGGGTGGAACAGG
 AGAGACCCTGGGAGAGAAATGGAAGGCCCGCTTGAACCAGATGTGGCCCTGGAGTTCTACTCTACAAAAAGTCAGGCATC
 ACCGAGGTGTGCAGAGAAGAGGCCCGCCGCGCCCTCAAGGACGGTGTGGCAACGGGAGGCCATGCTGTGTCCCGAGGAAGT
 GCAAAGCTGAGATGGTTGGTGGAGCGGGGATACCTGCAGCCCTATGGAAAGGTCATTGATCTTGGATGTGGCAGAGGGGGC
 TGGAGTTACTACGTCGCCACCATCCGCAAAGTTCAGAAGTGAAAGGATACACAAAAGGAGGCCCTGGTCATGAAGAACCCG
 TGTGGTGCAAAGCTATGGGTGGAACATAGTCCGTCTTAAGAGTGGGGTGGACGTCTTTCATATGGCGGCTGAGCCGTGTA
 CACGTTGCTGTGTGACATAGGTGAGTCATCATCTAGTCCTGAAGTGGAAGAAGCACGGACGCTCAGAGTCCTCTCCATGGTGG
 GGGATTGGCTTGA AAAAGACCAGGAGCCTTTTGTATAAAAGTGTGTGCCCATACACCAGCACTATGATGGAAACCTGGAG
 CGACTGCAGCGTAGGTATGGGGGAGGACTGGTCAGAGTGCCACTCTCCGCAACTCTACACATGAGATGTACTGGGTCTCTG
 GAGCGAAAAGCAACACCATAAAAAGTGTGTCCACCACGAGCCAGCTCCTCTGGGGCGCATGGACGGGCTAGGAGGCCAGT
 GAAATATGAGGAGGATGTGAATCTCGGCTCTGGCACGCGGGCTGTGGTAAGCTGCGCTGAAGCTCCCAACATGAAGATCATT
 GGTAACCGCATTGAAAGGATCCGAGTGAGCACGCGGAAACGTGGTTCTTTGACGAGAACCACCCATATAGGACATGGGCTT
 ACCATGGAAGCTATGAGGCCCCCACAAAGGGTCAGCGTCTCTCTAATAAACGGGGTGTGACGGCTCCTGTCAAAACCTGG
 GATGTGGTGACTGGAGTCACAGGAATAGCCATGACCGACACCACACCGTATGGTCAGCAAAGAGTTTTCAAGGAAAAAGTGG
 AACTAGGGTGCCAGACCCCAAGAAGGCACTCGTCAGGTTATGAGCATGGTCTCTTCTGGTTGTGGAAAGAGCTAGGCCAA
 ACACAAACGGCCACGAGTCTGCACCAAAGAAGAGTTTCATCAACAAGGTTCTAGCAATGCAGCATTAGGGGGCAATATTTGAA
 GAGGAAAAAGAGTGGAAGACTGCAGTGGAAGCTGTGAACGATCCAAGGTTCTGGGCTCTAGTGGACAAGGAAAGAGAGCAC
 CACCTGAGAGGAGAGTGCCAGAGCTGTGTGTACAACATGATGGGAAAAAGAGAAAAGAAACAAGGGGAATTTGGAAGGCC
 AAGGGCAGCCGCGCATCTGGTATATGTGGCTAGGGGCTAGATTCTAGAGTTCGAAGCCCTTGGATTCTTGAACGAGGATCA
 CTGGATGGGGAGAGAGAACTCAGGAGGTGGTGTGAAGGGCTGGGATTACAAAGACTCGGATATGTCTAGAAGAGATGAG
 TCGTATACCAGGAGGAAGGATGTATGCAGATGACACTGCTGGCTGGGACACCCGCATTAGCAGGTTTGATCTGGAGAATGAA
 GCTCTAATCACCAACCAATGGAGAAAGGGCACAGGGCCTTGGCATTGGCCATAATCAAGTACACATACCAAAACAAAGTGGT
 AAAGGTCCTTAGACCAGCTGAAAAAGGGAAAAACAGTTATGGACATTATTTGAGACAAGACCAAAGGGGGAGCGGACAAGTT
 GTCATTACGCTCTTAACACATTTACCAACCTAGTGGTGCAACTCATTGGAATATGGAGGCTGAGGAAGTTCTAGAGATGCAA
 GACTTGTGGCTGCTGCGGAGGTGAGAGAAAGTGACCAACTGGTTGCAGAGCAACGGATGGGATAGGCTCAAACGAATGGCA
 GTCAGTGGAGATGATTGCGTTGTGAAGCCAATTGATGATAGGTTTGACATGCCCTCAGGTTCTTGAATGATATGGGAAAAGT
 TAGGAAGGACACACAAGAGTGGAACCCCTCAACTGGATGGGACAACCTGGGAAGAAGTTCCGTTTTGCTCCCAACCACTTCAACA
 AGCTCCATCTCAAGGACGGGAGGTCCATTGTGGTTCCCTGCCGCCACCAAGATGAACTGATTGGCCGGGGCCGCGTCTCTCCA
 GGGGCGGGATGGAGCATCCGGGAGACTGCTTGCTAGCAAAATCATATGCGCAAATGTGGCAGCTCCTTTATTTCCACAGAA
 GGGACCTCCGACTGATGGCCAATGCCATTTGTTATCTGTGCCAGTTGACTGGGTTCCAACCTGGGAGAACTACCTGGTCAATCC
 ATGGAAGGGAGAATGGATGACCACTGAAGACATGCTTGTGGTGTGGAACAGAGTGTGGATTGAGGAGAACGACCACATGG
 AAGACAAGACCCAGTTACGAAATGGACAGACATTCCCTATTTGGGAAAAAGGGAAGACTTGTGGTGTGGATCTCTCATAGG
 GCACAGACCGCGCACCACTGGGCTGAGAACATTAAAAACACAGTCAACATGGTGGCAGGATCATAGGTGATGAAGAAAAG
 TACATGGACTACCTATCCACCCAAGTTGCTACTTGGGTGAAGAAGGGTCTACACCTGGAGTGTCTGAAGCACCATCTTAATG
 TTGTCAGGCCTGCTAGTCAGCCACAGCTTGGGGAAAGCTGTGCAGCCTGTGACCCCCCAGGAGAAGCTGGGAAACCAAGCC
 TATAGTCAGGCCGAGAACGCCATGGCACGGAAGAAGCCATGCTGCCTGTGAGCCCCCTCAGAGGACACTGAGTCAAAAAACC
 CACGCGCTTGGAGGCGCAGGATGGGAAAAGAAGGTGGCGACCTTCCCCACCTTCAATCTGGGGCTGAACTGGAGATCAGC
 TGTGGATCTCCAGAAGAGGGACTAGTGGTTAGAGGA

KU509998.1 Zika virus strain Haiti/1225/2014, Haiti, complete genome (SEQ ID NO: 5)

GTTGTTACTGTTGCTGACTCAGACTGCGACAGTTCGAGTTTGAAGCGAAAGCTAGCAACAGTATCAACAGGTTTTATTTGGATT
 TGGAACGAGAGTTTCTGGTCATGAAAAACCAAAAAAGAAATCCGGAGGATTCCGGATTGTCAATATGCTAAAACGCGGAG
 TAGCCCGTGTGAGCCCTTTGGGGGCTTGAAGAGGCTGCCAGCCGACTTCTGCTGGGTGATGGGCCCATCAGGATGGTCTTG

GCAATTCAGCCTTTTGGAGATTCACGGCAATCAAGCCATCACTGGGTCTCATCAATAGATGGGGTTCAGTGGGGAAAAAGA
 GGCTATGGAAATAATAAAGAAGTTCAAGAAAGATCTGGCTGCCATGCTGAGAATAATCAATGCTAGGAAGGAGAAGAAGAG
 ACGAGGCGCAGATACTAGTGTGGAATTGTTGGCCTCCTGCTGACCACAGCTATGGCAGCGGAGGTCACTAGACGTGGGAGT
 GCATACTATATGTACTTGGACAGAAACGATGCTGGGGAGGCCATATCTTTCCAACCACATTGGGGATGAATAAGTGTATAT
 ACAGATCATGGATCTTGGACACATGTGTGATGCCACCATGAGCTATGAATGCCCTATGCTGGATGAGGGGGTGGAAACCAGAT
 GACGTCGATTGTTGGTGCAACACGACGTCAACTTGGGTTGTGTACGGAACCTGCCATCACAAAAAGGTGAAGCACGGAGAT
 CTAGAAGAGCTGTGACGCTCCCTCCCATTCACCTAGGAAGCTGCAAAACGCGGTGCAAAACCTGGTTGGAATCAAGAGAATAC
 ACAAAGCACTTGATTAGAGTCGAAAAATTGGATATTAGGAACCTGGCTTCGCGTTAGCAGCAGCTGCCATCGCTTGGCTTTTG
 GGAAGCTCAACGAGCCAAAAAGTCATATACTTGGTCATGATACTGCTGATTGCCCCGGCATACAGCATCAGGTGCATAGGAGT
 CAGCAATAGGGACTTTGTGGAAGGTATGTCAGGTGGGACTTGGGTTGATGTTGCTTGGAAACATGGAGGTTGTGTACCCGTA
 ATGGCACAGGACAAACCGACTGTGACATAGAGCTGGTTACAACAACAGTCAGCAACATGGCGGAGGTAAGATCCTACTGCT
 ATGAGGCATCAATATCAGACATGGCTTCGGACAGCCGCTGCCAACACAAGGTGAAGCCTACCTTGACAAGCAATCAGACACT
 CAATATGTCTGCAAAAGAACGTTAGTGGACAGAGGCTGGGGAAATGGATGTGGACTTTTTGGCAAAGGGAGTCTGGTGACAT
 GCGCTAAGTTTGCATGCTCCAAGAAAATGACCGGGAAGAGCATCCAGCCAGAGAATCTGGAGTACCGGATAATGCTGTCAGT
 TCATGGCTCCCAGCACAGTGGGATGATCGTTAATGACACAGGACATGAACTGATGAGAATAGAGCGAAGGTTGAGATAACG
 CCCAATTCACCAAGAGCCGAAGCCACCCTGGGGGGTTTTGGAAGCCTAGGACTTGATTGTGAACCGAGGACAGGCCTTGACTT
 TTCAGATTTGTATTACTTGACTATGAATAACAAGCACTGGTTGGTTACAAGGAGTGGTTCCACGACATTCATTACCTTGGCAC
 GCTGGGGCAGACACCGGAACCTCCACACTGGAACAACAAGAAGCACTGGTAGAGTTCAAGGACGCACATGCCAAAAGGCAA
 ACTGTCGTGGTTCTAGGGAGTCAAGAAGGAGCAGTTCACACGGCCCTTGGTGGAGCTCTGGAGGCTGAGATGGATGGTGCAA
 AGGGAAGGCTGTCTCTGGCCACTTGAAATGTCGCTGAAATGGATAAACTTAGATTGAAGGGCGTGCATACTCCTTGTGT
 ACCGCAGCGTTCACATTACCAAGATCCCGGCTGAAACACTGCACGGGACAGTCACAGTGGAGGTACAGTACGCAGGGACAG
 ATGGACCTTGCAAGGTTCCAGCTCAGATGGCGGTGGACATGCAAACTCTGACCCAGTTGGGAGGTTGATAACCGCTAACCCC
 GTAATCACTGAAAGCACTGAGAACTTAAGATGATGCTGGAACCTTGATCCACCATTGGGGACTCTTACATTGTCATAGGAGTC
 GGGGAGAAGAAGATCACCCACCACTGGCACAGGAGTGGCAGCACCATTGGAAAAGCATTGAAGCCACTGTGAGAGGTGCC
 AAGAGAATGGCAGTCTTGGGAGACACAGCTGGGACTTTGGATCAGTTGGAGGCGCTCTCAACTCATTGGGCAAGGGCATCC
 ATCAAATTTTGGAGCAGCTTCAAATCATTGTTTGGAGGAATGTCTGGTTCTCACAAATCTCATTGGAACGTTGCTGATGTG
 GTTGGGTCTGAACACAAAGAATGGATCTATTTCCCTTATGTGCTTGGCCTTAGGGGGAGTGTGATCTTCTATCCACAGCCGT
 CTCTGCTGATGTGGGTGCTCGGTGGACTTCTCAAAGAAGGAGACGAGATGCGGTACAGGGGTGTTGCTCTATAACGACGTT
 GAAGCCTGGAGGGACAGGTACAAGTACCATCCTGACTCCCCCGTAGATTGGCAGCAGCAGTCAAGCAAGCCTGGGAAGATG
 GTATCTGCGGGATCTCCTCTGTTTCAAGAATGGAACATCATGTGGAGATCAGTAGAAGGGGAGCTCAACGCAATCCTGGAA
 GAGAATGGAGTTCAACTGACGGTCGTTGTGGGATCTGTAAAAAACCCCATGTGGAGAGGTCCACAGAGATTGCCGTCCTG
 TGAACGAGCTGCCCCACGGCTGGAAGGCTTGGGGGAAATCGCACTTCGTCAGAGCAGCAAAGACAAATAACAGCTTTGTGCT
 GGATGGTGACACACTGAAGGAATGCCACTCAAACATAGAGCATGGAACAGCTTCTTGTGGAGGATCATGGGTTGCGGGTA
 TTTCACTAGTGTCTGGCTCAAGGTTAGAGAAGATTATTATTAGAGTGTGATCCAGCCGTTATTGGAACAGCTGTTAAGGGA
 AAGGAGGCTGTACACAGTGATCTAGGCTACTGGATTGAGAGTGAGAAGAATGACACATGGAGGCTGAAGAGGGCCCATCTG
 ATCGAGATGAAAACATGTGAATGGCCAAAGTCCACACATTGTGGACAGATGGAATAGAAGAGAGTGATCTGATCATACCCA
 AGTCTTTAGCTGGGCCACTCAGCCATCACAATACCAGAGAGGGCTACAGGACCCAAATGAAAGGGCCATGGCACAGTGAAGA
 GCTTGAAATTCGGTTTGAAGGAATGCCAGGCACTAAGGTCACGTGGAGGAAACATGTGGAACAAGAGGACCATCTGTGAGA
 TCAACCACTGCAAGCGGAAGGGTGATCGAGGAATGGTGTGCGAGGAGTGCACAATGCCCCCACTGTGTTCCGGGCTAAAG
 ATGGCTGTTGGTATGGAATGGAGATAAGGCCAGGAAAGAACAGAAAGCACTTAGTAAGGTCAATGGTGACTGCAGGATC
 AACTGATCAGATGGATCACTTCTCCCTTGGAGTGCTTGTGATTCTGCTCATGGTGCAGGAAGGGCTGAAGAAGAGAATGACCA
 CAAAGATCATATAAGCACATCAATGGCAGTGCTGGTAGCTATGATCCTGGGAGGATTTTCAATGAGTGACCTGGCTAAGCTT
 GCAATTTTGATGGGTGCCACCTTCGCGGAAATGAACACTGGAGGAGATGTAGCTCATCTGGCGCTGATAGCGGCATTCAAAGT
 CAGACCAGCGTTGCTGGTATCTTTCATCTTCAGAGCTAATTGGACACCCCGTGAAGAGCATGCTGCTGGCCITGGCCTCGTGTCT
 TTTGCAAACTGCGATCTCCGCTTGGAAAGGCGACCTGATGGTTCTCATCAATGGTTTGTCTTGGCCTGGTTGGCAATACGAGC
 GATGGTTGTTCCACGCACTGATAACATCACCTTGGCAATCCTGGCTGCTGTGACACCACTGGCCCGGGGCACACTGCTTGTGGC

GTGGAGAGCAGGCCTTGCTACTTGCGGGGGGTTTATGCTCCTCTCTCTGAAGGGAAAAGGCAGTGTGAAGAAGAACTTACCA
 TTTGTCATGGCCCTGGGACTAACCCTGTGAGGCTGGTCGACCCCATCAACGTGGTGGGGCTGCTGTTGCTCACAAGGAGTGG
 GAAGCGGAGCTGGCCCCCTAGCGAAGTACTCACAGCTGTTGGCCTGATATGCGCATTGGCTGGAGGGTTCGCCAAGGCAGAT
 ATAGAGATGGCTGGGCCCATGGCCGCGGTCGGTCTGCTAATTGTGAGTTACGTGGTCTCAGGAAAGAGTGTGGACATGTACA
 TTGAAAGAGCAGGTGACATCACATGGGAAAAAGATGCGGAAGTCACTGGAAACAGTCCCCGGCTCGATGTGGCGCTAGATGA
 GAGTGGTGATTTCTCCCTGGTGGAGGATGACGGTCCCCCATGAGAGAGATCATACTCAAGGTGGTCTGATGACCATCTGTG
 GCATGAACCCAATAGCCATACCCTTTCAGCTGGAGCGTGGTACGTATACGTGAAGACTGGAAAAAGGAGTGGTGCTCTATG
 GGATGTGCCTGCTCCCAAGGAAGTAAAAAGGGGGGAGACCACAGATGGAGTGTACAGAGTAATGACTCGTAGACTGCTAGG
 TTCAACACAAGTTGGAGTGGGAGTTATGCAAGAGGGGGTCTTTCACACTATGTGGCACGTACAAAAGGATCCGCGCTGAGA
 AGCGGTGAAGGGAGACTTGATCCATACTGGGGAGATGTCAAGCAGGATCTGGTGTCTACTGTGGTCCATGGAAGCTAGATG
 CCGCTGGGACGGGCACAGCGAGGTGCAGCTCTTGGCGTGCCCCCGGAGAGAGAGCGAGGAACATCCAGACTCTGCCCG
 GAATATTTAAGACAAAGGATGGGGACATTGGAGCGGTTGCGCTGGATTACCCAGCAGGAACCTCAGGATCTCCAATCTAGA
 CAAGTGTGGGAGAGTGATAGGACTTTATGGCAATGGGGTCTGATCAAAAATGGGAGTTATGTTAGTGCCATCACCCAAGGG
 AGGAGGGAGGAAGAGACTCCTGTTGAGTGCTTCGAGCCTTCGATGCTGAAGAAGAAGCAGCTAACTGTCTTAGACTTGATC
 CTGGAGCTGGGAAAACAGGAGAGTTCTTCTGAAATAGTCCGTGAAGCCATAAAAAAGACTCCGTACTGTGATCTTAGCT
 CCAACCAGGGTTGTGCTGCTGAAATGGAGGAAGCCCTTAGAGGGCTTCAGTGCGTTATATGACAACAGCAGTCAATGTCAC
 CCACTCTGGAACAGAAATCGTCGACTTAATGTGCCATGCCACCTTCACTTCACGTCTACTACAGCCAATCAGAGTCCCCAACTAT
 AATCTGTATATTATGGATGAGGCCCACTTACAGATCCCTCAAGTATAGCAGCAAGAGGATACATTTCAACAAGGGTTGAGAT
 GGGCGAGGCGGCTGCCATCTTCATGACCGCCACGCCACCAGGAACCCGTGACGCATTTCCGGACTCCAACCTACCAATTATGG
 ACACCGAAGTGGAAGTCCCAGAGAGAGCCTGGAGCTCAGGCTTTGATTGGGTGACGGATTATTCTGGAAAAACAGTTTGGTT
 TGTTCCAAGCGTGAGGAACGGCAATGAGATCGCAGCTTGTCTGACAAAGGCTGGAAAAAGGGTGCATACAGCTCAGCAGAAAG
 ACTTTTGAGACAGAGTTCCAGAAAAACAAACATCAAGAGTGGGACTTTGCTGTCGACAACTGACATTTAGAGATGGGCGCCAA
 CTTTAAAGCTGACCGTGTCTAGATTCCAGGAGATGCCTAAAGCCGGTGCATCTTATGGCGAGAGAGTCATTCTGGCTGGAC
 CCATGCCTGTCACACATGCCAGCGCTGCCAGAGGAGGGGGCGCATAGGCAGGAATCCCAACAAACCTGGAGATGAGTATCT
 GTATGGAGGTGGGTGCGCAGAGACTGACGAAGACCATGCACACTGGCTTGAAGCAAGAATGCTCCTTGACAATATTACCTCC
 AAGATGGCCTCATAGCCTCGCTCTATCGACCTGAGGCCGACAAAGTAGCAGCCATTGAGGGAGAGTTCAAGCTTAGGACGGA
 GCAAAGGAAGACCTTTGTGGAACCTATGAAAAGAGGAGATCTTCTGTTTGGCTGGCCTATCAGGTTGCATCTGCCGGAATAA
 CCTACACAGATAGAAGATGGTGCTTTGATGGCAGCACCAACAACACCATAATGGAAGACAGTGTGCCGGCAGAGGTGTGGAC
 CAGACACGGAGAGAAAAGAGTGTCTCAAACCGAGGTGGATGGACGCCAGAGTTTGTTCAGATCATGCGGCCCTGAAGTCATT
 AAGGAGTTTCCGCTGGGAAAAGAGGAGCGGCTTTTGGAGTGATGGAAGCCCTGGGAACCTGCCAGGACACATGACAGAG
 AGATTCCAGGAAGCCATTGACAACCTCGCTGTGCTCATGCGGGCAGAGACTGGAAGCAGGCCTTACAAAGCCGCGCGGCC
 AATTGCGGAGACCTAGAGACCATTATGCTTTTGGGTTGCTGGGAACAGTCTCGCTGGGAATCTTTTCTGCTTGTATGAGG
 AACAAGGGCATAGGGAAGATGGGCTTTGGAATGGTGACTCTGGGGCCAGCGCATGGCTCATGTGGCTCTCGGAAATTGAGC
 CAGCCAGAATTGCATGTGCTCCTATTGTTGTGTTCTATTGCTGGTGGTGTCTATACCTGAGCCAGAAAAGCAAAGATCTCCCC
 AGGACAACCAAATGGCAATCATCATGTTAGCAGTAGGTCTTCTGGGCTTGATTACCGCCAATGAACCTGGATGGTTGGAG
 AGAACAAAGAGTGACCTAAGCCATCTAATGGGAAGGAGAGAGGAGGGGGCAACCATGGGATTCTAATGGACATTGACCTG
 CGGCCAGCCTCAGCTTGGGCCATCTATGCTGCTTGACAACCTTCACTACCCAGCCGTCCAACATGAGTGACCACTTCATACA
 ACAACTACTCCTTAATGGCGATGGCCACGCAAGCTGGAGTGTGTTTGGTATGGGCAAAGGGATGCCATTCTACGCATGGGAC
 TTTGGAGTCCCGCTGCTAATGATAGGTTGCTACTCACAAATTAACGCCCTGACCCTAATAGTGGCCATCATTTTCTCGTGGCG
 CACTACATGTACTTGATCCCAGGGCTGCAGGCAGCAGCTGCGCGTGTGCCCAGAAGAGAACGGCAGCTGGCATCATGAAGA
 ACCCTGTTGTGGATGGAATAGTGGTGACTGACATTGACACAATGACAATTGACCCCAAGTGAGAAAAAGATGGGACAGGT
 GCTACTCATGGCAGTAGCCGTCTCAGCGCCATACTGTGCGGACCGCCTGGGGTGGGGGGAGGCTGGGGCCCTGATCACA
 GCCGCAACTTCCACTTTGTGGGAAGGCTCTCGGAACAAGTACTGGAACCTCTACAGCCACTTCACTGTGTAACATTTTAGG
 GGAAGTTACTTGGCTGGAGCTTCTAATCTACACAGTAACAAGAAACGCTGGCTTGGTCAAGAGACGTGGGGGTGGAACAG
 GAGAGACCTGGGAGAGAAATGGAAGGCCGCTTGAACCAGATGTGCGCCCTGGAGTTCTACTCTACAAAAAGTCAGGCAT
 CACCGAGGTGTGCAGAGAAGAGGCCCGCGCCCTCAAGGACGGTGTGGCAACGGGAGGCCATGCTGTGTCCCGAGGAAG

TGCAAAGCTGAGATGGTTGGTGGAGCGGGGATACCTGCAGCCCTATGGAAAGGTCATTGATCTTGGATGTGGCAGAGGGGG
 CTGGAGTTACTACGCCGCCACCATCCGCAAAGTTCAAGAAGTGAAAGGATACACAAAAGGAGGCCCTGGTCATGAAGAACCC
 GTGTTGGTGCAAAGCTATGGGTGGAACATAGTCCGTCTTAAGAGTGGGGTGGACGCTTTTCATATGGCGGCTGAGCCGTGTG
 ACACGTTGCTGTGTGACATAGGTGAGTCATCATCTAGTCCTGAAGTGGAAGAAGCACGGACGCTCAGAGTCCTCTCCATGGTG
 GGGGATTGGCTTGAAAAAAGACCAGGAGCCTTTGTATAAAAGTGTGTGCCCATACACCAGCACTATGATGGAAACCCTGGA
 GCGACTGCAGCGTAGGTATGGGGGAGGACTGGTCAGAGTGCCACTCTCCCGCAACTCTACACATGAGATGTACTGGGTCTCT
 GGAGCGAAAAAGCAACACCATAAAAAAGTGTGTCCACCAGAGCCAGCTCCTCTTGGGGCGCATGGACGGGCCTAGGAGGCCA
 GTGAAATATGAGGAGGATGTGAATCTCGGCTCTGGCACGCGGGCTGTGGTAAGCTGCGCTGAAGCTCCCAACATGAAGATCA
 TTGGTAACCGCATTGAAAGGATCCGCAGTGAGCACGCGGAAACGTGGTTCTTTGACGAGAACCACCCCATATAGGACATGGGC
 TTACCATGGAAGCTATGAGGCCCCACACAAGGGTCAGCGTCCTCTCTAATAAACGGGGTTGTCAGGCTCCTGTCAAAACCT
 GGGATGTGGTGAAGTACAGGAATAGCCATGACCGACACCACACCGTATGGTCAGCAAAGAGTTTCAAGGAAAAAGT
 GGACACTAGGGTGCAGACCCCCAAGAAGGCACTCGTCAGGTTATGAGCATGGTCTCTTCTGGTTGTGAAAGAGCTAGGC
 AAACACAAACGGCCACGAGTCTGTACCAAAGAAGAGTTCATCAACAAGGTTCTGTAAGCAATGCAGCATTAGGGGCAATATTGA
 AGAGGAAAAAGAGTGGAAGACTGCAGTGGAAGCTGTGAACGATCCAAGGTTCTGGGCTCTAGTGGACAAGGAAAGAGAGCA
 CCACCTGAGAGGAGAGTGCCAGAGTTGTGTGTACAACATGATGGGAAAAAGAGAAAAAGAAACAGGGGAATTTGGAAAGGC
 CAAGGGCAGCCGCGCATCTGGTATATGTGGCTAGGGGCTAGATTTCTAGAGTTTGAAGCCCTTGGATTCTTGAACGAGGATC
 ACTGGATGGGGAGAGAGAACTCAGGAGGTGGTGTGAAGGGCTGGGATTACAAAGACTCGGATATGTCCTAGAAGAGATGA
 GTCGCATACCAGGAGGAAGGATGTATGCAGATGACACTGCTGGCTGGGACACCCGCATCAGCAGGTTTGATCTGGAGAATGA
 AGCTCTAATCACCAACCAATGGAGAAAGGGCACAGGGCCTTGGCATTGGCCATAATCAAGTACACATACCAAAACAAAGTG
 GTAAAGGTCCTTAGACCAGCTGAAAAAGGGAAGACAGTTATGGACATTATTTGAGACAAGACCAAGGGGGAGCGGACAA
 GTTGTCACTTACGCTCTTAACACATTTACCAACCTAGTGGTGCAACTCATTGGAATATGGAGGCTGAGGAAAGTTCTAGAGATG
 CAAGACTTGTGGCTGCTGCGGAGGTCAGAGAAAGTGACCAACTGGTTGCAGAGCAACGGATGGGATAGGCTCAAACGAATG
 GCAGTCAGTGGAGATGATTGCGTTGTGAAGCCAATTGATGATAGGTTTGCACATGCCCTCAGGTTCTTGAATGATATGGGAAA
 AGTTAGGAAGGACACACAAGAGTGGAAACCCTCAACTGGATGGGACAAGTGGGAAGAAGTCCGTTTTGCTCCCACTTCA
 ACAAGCTCCATCTCAAGGACGGGAGGTCCATTGTGGTTCCCTGCGGCCACCAAGATGAACTGATTGGCCGGGCGCGCTCTCT
 CCAGGGGCGGGATGGAGCATCCGGGAGACTGCTTGCTAGCAAAATCATATGCGCAAATGTGGCAGCTCCTTATTTCCACAG
 AAGGGACCTCCGACTGATGGCCAATGCCATTTGTTTCATCTGTGCCAGTTGACTGGGTTCCAAGTGGGAGAACTACCTGGTCAAT
 CCATGGAAAGGGAGAAATGGATGACCACTGAAGACATGCTTGTGGTGTGGAAACAGAGTGTGGATTGAGGAGAACGACCACAT
 GGAAGACAAGACCCAGTTACGAAATGGACAGACATTCCTATTTGGGAAAAAGGGAAGACTTGTGGTGTGGATCTCTCATA
 GGGCACAGACCGCGCACCACCTGGGCTGAGAACATTAACAAACACAGTCAACATGGTGCGCAGGATCATAGGTGATGAAGAAA
 AGTACATGGACTACCTATCCACCAAGTTCGCTACTTGGGTGAAGAAGGGTCTACACCTGGAGTGTGTAAGCACCAATCTTA
 ATGTTGTGAGGCTGTAGTCAGCCACAGCTTGGGGAAAGCTGTGACGCTGTGACCCCCCAGGAGAAGCTGGGAAACCAA
 GCCTATAGTCAGGCCGAGAACGCCATGGCACGGAAGAAGCCATGCTGCTGTGAGCCCCCTCAGAGGACACTGAGTCAAAAAA
 CCCCACGCGCTTGGAGGCGCAGGATGGGAAAGAAGGTGGCGACCTTCCCCACCTTCAATCTGGGGCCTGAAGTGGAGATC
 AGCTGTGGATCTCCAGAAGAGGGACTAGTGGTTAGAGGAGA

KU527068.1 Zika virus strain Natal RGN, Brazil: Rio Grande do Norte, Natal, complete genome (SEQ ID
 NO: 6)

AGTTGTTGATCTGTGTGAATCAGACTGCGACAGTTCGAGTTGAAGCGAAAGCTAGCAACAGTATCAACAGGTTTTATTTGG
 ATTTGGAAACGAGAGTTTCTGGTCATGAAAAACCCAAAAAGAAATCCGGAGGATTCCGGATTGTCAATATGCTAAACGCGG
 AGTAGCCCGTGTGAGCCCCCTTGGGGGCTTGAAGAGGCTGCCAGCCGACTTCTGCTGGGTGATGGGCCCATCAGGATGGTC
 TTGGCAATTCTAGCCTTTTGTAGATTACGGCAATCAAGCCATCACTGGGTCTCATCAATAGATGGGGTTCAGTGGGGAAAAA

AGAGGCTATGGAAATAATAAAGAAGTTCAAGAAAGATCTGGCTGCCATGCTGAGAATAATCAATGCTAGGAAGGAGAAGAA
 GAGACGAGGCGCAGATACTAGTGTCGGAATTGTTGGCCTCCTGCTGACCACAGCTATGGCAGCGGAGGTCACTAGACGTGGG
 AGTGCATACTATATGTACTTGGACAGAAACGATGCTGGGGAGGCCATATCTTTTCCAACCACATTGGGGATGAATAAGTGTTA
 TATACAGATCATGGATCTTGGACACATGTGTGATGCCACCATGAGCTATGAATGCCCTATGCTGGATGAGGGGGTGGAAACCAG
 ATGACGTCGATTGTTGGTGCAACACGACGTCAACTTGGGTTGTGTACGGAACCTGCCATCACAAAAAGGTGAAGCACGGAG
 ATCTAGAAGAGCTGTGACGCTCCCTCCATTCCACTAGGAAGCTGCAAAACGCGGTCGCAAACTGGTTGGAATCAAGAGAAT
 ACACAAAGCACTTGATTAGAGTCGAAAATTGGATATTCAGGAACCTGGCTTCGCGTTAGCAGCAGCTGCCATCGCTTGGCTTT
 TGGGAAGCTCAACGAGCCAAAAAGTCATATACTTGGTCATGATACTGCTGATTGCCCGGCATACAGCATCAGGTGCATAGGA
 GTCAGCAATAGGGACTTTGTGGAAGGTATGTCAGGTGGGACTTGGGTTGATGTTGTCTTGGAACATGGAGGTTGTGTACCG
 TAATGGCACAGGACAAACCGACTGTCGACATAGAGCTGGTTACAACAACAGTCAGCAACATGGCGGAGGTAAGATCCTACTG
 CTATGAGGCATCAATATCAGACATGGCTTCGGACAGCCGCTGCCAACACAAGGTGAAGCCTACCTTGACAAGCAATCAGACA
 CTCAATATGCTGCAAAAGAACGTTAGTGGACAGAGGCTGGGGAAATGGATGTGGACTTTTGGCAAAGGGAGCCTGGTGAC
 ATGCGCTAAGTTTGCATGCTCCAAGAAAATGACCGGGAAGAGCATCCAGCCAGAGAATCTGGAGTACCGGATAATGCTGTCA
 GTTCATGGCTCCAGCACAGTGGGATGATCGTTAATGACACAGGACATGAAACTGATGAGAATAGAGCGAAGGTTGAGATAA
 CGCCCAATTCACCAAGAGCCGAAGCCACCCTGGGGGGTTTTGGAAGCCTAGGACTTGATTGTGAACCGAGGACAGGCCTTGA
 CTTTTCAGATTGTATTACTTGACTATGAATAACAAGCACTGGTTGGTCCACAAGGAGTGGTCCACGACATTCATTACCTTGG
 CACGCTGGGGCAGACACCGGAATCCCACTGGAACAACAAAGAAGCACTGGTAGAGTTCAAGGACGCACATGCCAAAAGG
 CAAACTGTCGTGGTTCTAGGGAGTCAAGAAGGAGCAGTTCACACGGCCCTTGCTGGAGCTCTGGAGGCTGAGATGGATGGTG
 CAAAGGGAAGGCTGTCTCTGGCCACTTGAAATGTCGCTGAAAATGGATAAACTTAGATTGAAGGGCGTGTCTACTCTCTTG
 TGTACCGCAGCGTTCACATTACCAAGATCCCGGCTGAAACACTGCACGGGACAGTCACAGTGGAGGTACAGTACGCAGGGA
 CAGATGGACCTTGCAAGGTTCCAGCTCAGATGGCGGTGGACATGCAAACTCTGACCCAGTTGGGAGGTTGATAACCGCTAAC
 CCCGTAATCACTGAAAGCACTGAGAACTCTAAGATGATGCTGGAACCTTGATCCACCATTGGGGACTCTTACATTGTCATAGGA
 GTCGGGGAGAAGAAGATACCCACCCTGGCACAGGAGTGGCAGCACCATTGGAAGGCACTTTGAAGCCACTGTGAGAGGT
 GCCAAGAGAATGGCAGTCTTGGGAGACACAGCTGGGACTTTGGATCAGTTGGAGGCGCTCTCAACTCATTGGGCAAGGGCA
 TCCATCAAATTTTGGAGCAGCTTTCAAATCATTGTTTGGAGGAATGTCCTGTTCTCACAATCCTCATTGGAACGTTGCTGAT
 GTGGTTGGGCTGAACACAAAGAATGGATCTATTTCCCTATGTGCTTGGCCTTAGGGGGAGTGTGATCTTCTTATCCACAGC
 CGTCTCTGCTGATGTGGGGTGCTCGGTGGACTTCTCAAAGAAGGAGACGAGATGCGGTACAGGGGTGTTCTGTATAACGAC
 GTTGAAGCCTGGAGGGACAGGTACAAGTACCATCCTGACTCCCCCGTAGATTGGCAGCAGCAGTCAAGCAAGCCTGGGAAG
 ATGGTATCTGCGGGATCTCTCTGTTTCAAGAATGGAGAACATCATGTGGAGATCAGTAGAAGGGGAGCTCAACGCAATCTTG
 GAAGAGAATGGAGTTCAACTGACGGTCTGTGTGGGATCTGTAAAAAACCCCATGTGGAGAGGTCCACAGAGATTGCCCGTGC
 CTGTGAACGAGCTGCCCCAGGCTGGAAGGCTTGGGGGAAATCGTACTTCGTCAGAGCAGCAAAGACAAATAACAGCTTGT
 CGTGGATGGTGACACACTGAAGGAATGCCCACTCGAACATAGAGCATGGAACAGCTTCTGTGGAGGATCATGGGTTCCGG
 GTATTTCACTAGTGTCTGGCTCAAGGTTAGAGAAGATTATTATTAGAGTGTGATCCAGCCGTATTGGAACAGCTGTTAAG
 GGGAAGGAGGCTGTACACAGTGTCTAGGCTACTGGATTGAGAGTGAGAAGAATGACACATGGAGGCTGAAGAGGGCCCAT
 CTAATCGAGATGAAAACATGTGAATGGCCAAAGTCCACACATTGTGGGCAGATGGAATAGAAGAGAGTGATCTGATCATTCC
 CAAGTCTTTAGCTGGGCCACTCAGCCATCACAATACCAGAGAGGGCTACAGGACCCAAATGAAAGGGCCATGGCACAGTGAA
 GAGCTTGAATTCGTTTGAAGGAATGCCCGGCACTAAGGTCCACGTGGAGGAAACATGTGGAACAAGAGGACCATCTCTGA
 GATCAACCACTGCAAGCGGAAGGGTGATCGAGGAATGGTGCTGCAGGGAGTGACAATGCCCCACTGTGCTTCCGGGCTAA
 AGATGGCTGTTGGTATGGAATGGAGATAAGGCCCAGGAAAGAACCAAGCACTTAGTAAGGTCAAGTGGTGACTGCAGG
 ATCAACTGATCACATGGATCACTTCTCCCTTGGAGTGCTTGTGATTCTGCTCATGGTGCAAGGAAGGGCTGAAGAAGAGAATGA
 CCACAAAGATCATATAAGCACATCAATGGCAGTGCTGGTAGCTATGATCCTGGGAGGATTTCAATGAGTGACCTGGCTAAG
 CTTGCAATTTTGTGGGCGCCACCTTCGCGGAAATGAACACTGGAGGAGATGTAGCTCATCTGGCGCTGATAGCGGCATTCAA
 AGTCAGACCAGCGTTGCTGGTATCTTTCATCTTCAGAGCTAATTGGACACCCCGTGAAGCATGCTGCTGGCCTTGGCCTCGTG
 TCTTTTGAACACTGCGATCTCGCCTTGAAGGCGACCTGATGGTTCTCATCAATGGTTTTGCTTGGCCTGGTTGGCAATACG
 AGCGATGGTTGTCCACGCACTGATAACATCACCTTGGCAATCCTGGCTGCTGACACCACTGGCCCGGGGCACACTGCTTGT
 GCGTGGAGAGCAGGCCTTGTACTTGGGGGGGTTATGCTCCTCTCTGAAGGGAAAAGGCAGTGTGAAGAAGAACTTA

CCATTTGTCATGGCCCTGGGACTAACCGCTGTGAGGCTGGTCGACCCCATCAACGTGGTGGGACTGCTGTTGCTCACAAGGAG
 TGGGAAGCGGAGCTGGCCCCCTAGCGAAGTACTCACAGCTGTTGGCCTGATATGCGCATTGGCTGGAGGGTTGCGCAAGGCA
 GATATAGAGATGGCTGGGCCCATGGCCGCGGTCGGTCTGCTAATTGTCAGTTACGTGGTCTCAGGAAAGAGTGTGGACATGT
 ACATTGAAAGAGCAGGTGACATCACATGGGAAAAAGATGCGGAAGTCACTGGAAACAGTCCCCGGCTCGATGTGGCGCTAGA
 TGAGAGTGGTGATTTCTCCCTGGTGGAGGATGACGGTCCCCCATGAGAGAGATCATACTCAAGGTGGTCTCTGATGACCATCT
 GTGGCATGAACCCAATAGCCATACCCTTTGCAGCTGGAGCGTGGTACGTATACGTGAAGACTGGAAAAAGGAGTGGTGCTCT
 ATGGGATGTGCTGCTCCCAAGGAAGTAAAAAGGGGGAGACCACAGATGGAGTGTACAGAGTAATGACTCGTAGACTGCTA
 GGTTCACACAAGTTGGAGTGGGAGTTATGCAAGAGGGGGTCTTTCACACTATGTGGCACGTCAAAAAAGGATCCGCGCTGA
 GAAGCGGTGAAGGGAGACTTGATCCATACTGGGGAGATGTCAAGCAGGATCTGGTGTCTACTGTGGTCCATGGAAGCTAGA
 TGCCGCTGGGACGGGCACAGCGAGGTGCAGCTCTTGCCCGTGCCCCCGGAGAGAGAGCGAGGAACATCCAGACTCTGCCC
 GGAATATTTAAGACAAAGGATGGGGACATTGGAGCGGTTGCGCTGGATTACCCAGCAGGAACCTCAGGATCTCCAATCCTAG
 ACAAGTGTGGGAGAGTGATAGGACTTTATGGCAATGGGGTCTGATCAAAAATGGGAGTTATGTTAGTGCCATCACCCAAGG
 GAGGAGGGAGGAAGAGACTCCTGTTGAGTGCTTCGAGCCTCGATGCTGAAGAAGAAGCAGCTAACTGTCTTAGACTTGCTAT
 CCTGGAGCTGGGAAAACAGGAGAGTTCTTCTGAAATAGTCCGTGAAGCCATAAAAAAAGACTCCGTACTGTGATCTTAGC
 TCCAACCAGGGTTGTGCTGCTGAAATGGAGGAAGCCCTTAGAGGGCTTCCAGTGCGTTATATGACAACAGCAGTCAATGTCA
 CCCACTCTGGAACAGAAATCGTCGACTTAATGTGCCATGCCACCTTCACTTCACGTCTACTACAGCCAATCAGAGTCCCCAACTA
 TAATCTGTATATTATGGATGAGGCCCACTTCACAGATCCCTCAAGTATAGCAGCAAGAGGATACATTTCAACAAGGGTTGAGA
 TGGGCGAGGCGGTGCCATCTTCATGACCGCCACGCCACAGGAACCCGTGACGCATTCCGGACTCCAACCTACCAATTATG
 GACACCGAAGTGGAAGTCCAGAGAGAGCCTGGAGCTCAGGCTTTGATTGGGTGACGGATCATTCTGGAAAAACAGTTTGGT
 TTGTTCCAAGCGTGAGGAACGGCAATGAGATCGCAGCTTGTCTGACAAAGGCTGGAAAACGGGTATACAGCTCAGCAGAAA
 GACTTTTGAGACAGAGTTCCAGAAAAACAAACATCAAGAGTGGGACTTTGTCTGACAACCTGACATTTAGAGATGGGCGCCA
 ACTTTAAAGCTGACCGTGTATAGATTCCAGGAGATGCCTAAAGCCGGTCATACTTGATGGCGAGAGAGTCAATTTGGCTGGA
 CCCATGCTGTACACATGCCAGCGCTGCCAGAGGAGGGGGCGCATAGGCAGGAATCCCAACAAACCTGGAGATGAGTATC
 TGATGGAGGTGGGTGCGCAGAGACTGACGAAGACCATGCACACTGGCTTGAAGCAAGAATGCTCCTTGACAATATTTACCTC
 CAAGATGGCTCATAGCCTCGCTCTATCGACCTGAGGCCGACAAAGTAGCAGCCATTGAGGGAGAGTTCAAGCTTAGGACGG
 AGCAAAGGAAGACCTTTGTGGAACCTCATGAAAAGAGGAGATCTTCTGTTGGCTGGCCTATCAGGTTGCATCTGCCGAATA
 ACCTACACAGATAGAAGATGGTGCTTGTATGGCAGCAGCAACACCCATAATGGAAGACAGTGTGCCGGCAGAGGTGTGGA
 CCAGACACGGAGAGAAAAGAGTGCTCAAACCGAGGTGGATGGACGCCAGAGTTTGTTCAGATCATGCGGCCCTGAAGTCATT
 CAAGGAGTTTGCCGCTGGGAAAAGAGGAGCGGCTTTTGGAGTGATGGAAGCCCTGGGAACACTGCCAGGACACATGACAGA
 GAGATTCAGGAAGCCATTGACAACCTCGCTGTGCTCATGCGGGCAGAGACTGGAAGCAGGCTTACAAAGCCGCGCGCGCC
 CAATTGCCGAGACCCTAGAGACCATTATGCTTTTGGGGTTGCTGGGAACAGTCTCGCTGGGAATCTTTTCTGCTTGATGAGG
 AACAAGGGCATAGGGAAGATGGGCTTTGGAATGGTGACTCTGGGGCCAGCGCATGGCTCATGTGGCTCTCGGAAATTGAGC
 CAGCCAGAATTGCATGTGCTCTCATTGTTGTTCTATTGCTGGTGGTGCTCATACCTGAGCCAGAAAAGCAAAGATCTCCCC
 AGGACAACCAAATGGCAATCATCATCATGGTAGCAGTAGGTCTTCTGGGCTTGATTACCGCCAATGAACCTCGGATGGTTGGAG
 AGAACAAAGAGTGACCTAAGCCATCTAATGGGAAGGAGAGAGGAGGGAGCAACCATAGGATTCTCAATGGACATTGACCTG
 CGGCCAGCCTCAGCTTGGGCCATCTATGCTGCCCTTGACAACCTTCAATACCCAGCCGTCACATGCAGTGACCACTTCATACA
 ACACTACTCCTAATGGCGATGGCCACGCAAGCTGGAGTGTTGTTGGTATGGGCAAAGGGATGCCATTCTACGCATGGGAC
 TTTGGAGTCCCGCTGCTAATGATAGGTTGCTACTCACAATTAACACCCCTGACCCCTAATAGTGGCCATCATTTTGTCTGTGGCGC
 ACTACATGTACTTGATCCCAGGGCTGCAGGCAGCAGCTGCGCGTGCTGCCAGAGAGAACGGCAGCTGGCATCATGAAGAA
 CCCTGTTGTGGATGGAATAGTGGTGACTGACATTGACACAATGACAATTGACCCCAAGTGGAGAAAAAGATGGGACAGGTG
 CTACTCATAGCAGTAGCAGTCTCCAGCGCCATACTGTGCGGACCGCCTGGGGGTGGGGGGAGGCTGGGGCCCTGATCACAG
 CCGCAACTTCACTTTGTGGGAAGGCTCTCCGAACAAGTACTGGAACCTCTACAGCCACTTCACTGTGTAACATTTTAGGG
 GAAGTTACTTGGCTGGAGCTTCTCTAATCTACATAGTAACAAGAAACGCTGGCTTGGTCAAGAGACGTGGGGGTGGAACAGG
 AGAGACCCTGGGAGAGAAATGGAAGGCCCGCTGAAACCAGATGTGCGCCCTGGAGTTCTACTCTACAAAAAGTCAGGCATC
 ACCGAGGTGTGCAGAGAAGAGGGCCCGCGCCCTCAAGGATGGTGTGGCAACGGGAGGCCATGCTGTGTCCGAGGGAAGT
 GCAAAGCTGAGATGGTTGGTGGAGCGGGGATACCTGCAGCCCTATGAAAGGTCAATTGATCTTGGATGTGGCAGAGGGGGC

PAT022-EP-PR

TGGAGTTACTACGCCGCCACCATCCGCAAAGTTC AAGAAGTGAAAGGATACACAAAAGGAGGCCCTGGTCATGAAGAACCCG
 TGTGGTGCAAAGCTATGGGTGGAACATAGTCCGTCTTAAGAGTGGGGTGGACGTCTTTCATATGGCGGCTGAGCCGTGTGA
 CACGTTGCTGTGTGACATAGGTGAGTCATCATCTAGTCCTGAAGTGGAAGAAGCACGGACGCTCAGAGTCTCTCCATGGTGG
 GGGATTGGCTTGAAAAAGACCAAGAGCCTTTTGTATAAAAGTGTTGTGCCATACACCAGCACTATGATGGAAACCTGGAG
 CGACTGCAGCGTAGGTATGGGGGAGGACTGGTCAGAGTGCCACTCTCCGCAACTCTACACATGAGATGTAAGTGGGTCTCTG
 GAGCGAAAAGCAACACCATAAAAAGTGTGTCCACCACGAGCCAGCTCCTCTTGGGGCGCATGGACGGGCTAGGAGGCCAGT
 GAAATATGAGGAGGATGTGAATCTCGGCTCTGGCACGCGGGCTGTGGTAAGCTGCGCTGAAGCTCCCAACATGAAGATCATT
 GGTAACCGCATTGAAAGGATCCGAGTGAGCACGCGGAAACGTGGTTCTTTGACGAGAACCACCCATATAGGACATGGGCTT
 ACCATGGAAGCTATGAGGCCCCCACAAGGGTACGCGTCTCTCTAATAAACGGGGTGTGACGGCTCCTGTCAAAACCTGG
 GATGTGGTGACTGGAGTCACAGGAATAGCCATGACCGACACCACACCGTATGGTCAGCAAAGAGTTTCAAGGAAAAAGTGG
 ACACTAGGGTGCCAGACCCCCAAGAAGGCACTCGTCAGGTTATGAGCATGGTCTCTCTGGTTGTGGAAAGAGCTAGGCAA
 ACACAAACGGCCACGAGTCTGTACCAAAGAAGAGTTCATCAACAAGGTTCTGAGCAATGCAGCATTAGGGGCAATATTTGAA
 GAGGAAAAAGAGTGGAAAGACTGCAGTGGAAAGCTGTGAACGATCCAAGGTTCTGGGCTCTAGTGGACAAGGAAAGAGAGCAC
 CACCTGAGAGGAGAGTGCCAGAGTTGTGTGTACAACATGATGGGAAAAAGAGAAAAGAAACAAGGGGAATTTGGAAAGGCC
 AAGGGCAGCCGCGCCATCTGGTATATGTGGCTAGGGGCTAGATTCTAGAGTTCGAAGCCCTTGGATTCTTGAACGAGGATCA
 CTGGATGGGGAGAGAGAACTCAGGAGGTGGTGTGAAGGGCTGGGATTACAAAGACTCGGATATGTCTAGAAGAGATGAG
 TCGCATACCAGGAGGAAGGATGTATGCAGATGACACTGCTGGCTGGGACACCCGCATCAGCAGGTTCTGATCTGGAGAATGAA
 GCTCTAATCACCAACCAATGGAGAAAAGGCATAGGGCCTTGGCATTGGCCATAATCAAGTACACATACCAAAACAAAGTGGT
 AAAGGTCCTTAGACCAGCTGAAAAAGGGAAAACAGTTATGGACATTATTTGAGACAAGACCAAAGGGGGAGCGGACAAGTT
 GTCATTACGCTCTTAACACATTTACCAACCTAGTGGTGCAACTCATTGGAATATGGAGGCTGAGGAAGTTCTAGAGATGCAA
 GACTTGTGGCTGCTGCGGAGGTGAGAGAAAGTGACCAACTGTTGTCAGAGCAACGGATGGGATAGGCTCAAACGAATGGCA
 GTCAGTGGAGATGATTGCGTTGTGAAGCCAATTGATGATAGGTTTGACATGCCCTCAGGTTCTTGAATGATATGGGAAAAGT
 TAGGAAGGACACACAAGAGTGGAAACCTCAACTGGATGGGACAACCTGGGAAGAAGTCCGTTTTGCTCCCACTTCAACA
 AGCTCCATCTCAAGGACGGGAGGTCCATTGTGGTTCCCTGCCGCCACCAAGATGAACTGATTGGCCGGGGCCGCTCTCTCA
 GGGGCGGGATGGAGCATCCGGGAGACTGCTTGCTAGCAAAATCATATGCGCAAATGTGGCAGCTCCTTTATTTCCACAGAA
 GGGACCTCCGACTGATGGCCAATGCCATTTGTTCTGTGCCAGTTGACTGGGTTCCAACCTGGGAGAACTACCTGGTCAATCC
 ATGGAAAGGGAGAATGGATGACCACTGAAGACATGCTTGTGGTGTGGAACAGAGTGTGGATTGAGGAGAACGACCACATGG
 AAGACAAGACCCAGTTACGAAATGGACAGACATTCCTATTTGGGAAAAAGGGAAGACTGTGGTGTGGATCTCTCATAGG
 GCACAGACCGCGCACCACCTGGGCTGAGAACATTA AAAACACAGTCAACATGGTGCAGGATCATAGGTGATGAAGAAAAG
 TACATGGACTACCTATCCACCCAAGTTCGCTACTTGGGTGAAGAAGGGTCTACACCTGGAGTGCTGTAAAGCACCAATCTTAATG
 TTGTCAGGCCTGCTAGTCAGCCACAGCTTGGGGAAAGCTGTGCAGCCTGTGACCCCCCAGGAGAAGCTGGGAAACCAAGCC
 TATAGTCAGGCCGAGAACGCCATGGCACGGAAGAAGCCATGCTGCTGTGAGCCCTCAGAGGACACTGAGTCAAAAAACCC
 CATGCGCTTGGAGGCGCAGGATGGGAAAAGAAGGTGGCGACCTTCCCCACCTTCAATCTGGGGCCTGAACTGGAGATCAGC
 TGTGGATCTCCAGAAGAGGGACTAGTGGTTAGAGGAGACCCCCGGAAAACGCAAAACAGCATATTGACGCTGGGAAAGAC
 CAGAGACTCCATGAGTTTCCACCACGCTGGCCGCGAGGCACAGATCGCCGAATAGCGGCGCGCGGTGTGGGAAATCCATGG
 GTCTT

KU681081.3 Zika virus isolate Zika virus/H.sapiens-tc/THA/2014/SV0127- 14, Thailand, complete
 genome (SEQ ID NO: 7)

AGTTGTTGATCTGTGTGAATCAGACTGCGACAGTTCGAGTTTGAAGCGAAAGCTAGCAACAGTATCAACAGGTTTTATTTGG
 ATTTGGAAACGAGAGTTTCTGGTCATGAAAAACCCAAAAAGAAATCCGGAGGATTCCGGATTGTCAATATGCTAAACGCGG
 AGTAGCCCGTGTGAGCCCTTTGGGGCTTGAAGAGGCTGCCAGCCGACTTCTGCTGGGTGATGGGCCCATCAGGATGGTC

TTGGCGATTCTAGCCTTTTTGAGATTCACGGCAATCAAGCCATCACTGGGTCTCATCAATAGATGGGGTTCAGTGGGAAAAA
 AGAGGCTATGGAAATAATAAAGAAGTTCAAGAAAGATCTGGCTGCCATGCTGAGAATAATCAATGCTAGGAAGGAGAAGAA
 GAGACGAGGCACAGATACTAGTGTGGAATTGTTGGCCTCCTGCTGACCACAGCTATGGCAGCGGAGGTCACTAGACGTGGG
 AGTGCATACTATATGTACTTGGACAGAAGCGATGCTGGGGAGGCCATATCTTTCCAACCACACTGGGGATGAATAAGTGTTA
 TATACAGATCATGGATCTTGGACACATGTGTGATGCCACCATGAGCTATGAATGCCCTATGCTGGATGAGGGGGTAGAACCAG
 ATGACGTGCGATTGTTGGTGCAACACGACGTCAACTTGGGTTGTGTACGGAACCTGCCATCACAAAAAGGTGAAGCACGGAG
 ATCCAGAAGAGCTGTGACGCTCCCTCCCTCCATTCCACTAGGAAGCTGCAAAACGCGGTGCGAGACCTGGTTGGAATCAAGAGAAT
 ACACAAAGCACTTGATTAGAGTCGAAAATTGGATATTCAGGAACCTGGCTTCGCGTTAGCAGCAGCTGCCATCGCTTGGCTTT
 TGGGAAGCTCAACGAGCCAAAAAGTCATATACTTGGTCATGATACTGCTGATTGCCCGGCATACAGCATCAGGTGCATAGGA
 GTCAGTAATAGGGACTTTGTGGAAGGTATGTCAGGTGGGACTTGGGTTGATGTTGTCTTGAACATGGAGGTTGTGTACCCGT
 AATGGCACAGGACAAACCGACTGTGACATAGAGCTGGTTACAACAACAGTCAGCAACATGGCGGAGGTAAGATCCTACTGC
 TATGAGGCATCAATATCGGACATGGCTTCGGACAGCCGCTGCCAACACAAGGTGAAGCCTACCTTGACAAGCAATCAGACAC
 TCAATATGTCTGCAAAAGAAGCTTAGTGACAGAGGCTGGGGAAATGGATGTGGACTTTTGGCAAAGGGAGCCTGGTGACA
 TCGCTAAGTTTGCATGCTCCAAGAAAATGACCGGGAAGAGCATCCAGCCAGAGAATCTGGAGTACCGGATAATGCTGTGAG
 TTCATGGCTCCAGCACAGTGGGATGATCGTTAATGACACAGGACATGAACTGATGAGAATAGAGCGAAGGTTGAGATAAC
 GCCCAATTCACCAAGAGCCGAAGCCACCCTGGGGGTTTGGGAAGCCTAGGACTTGATTGTGAACCGAGGACAGGCCCTTGAC
 TTTTCAGATTTGTATTACTTGACTATGAACAACAAGCACTGGTTGGTTCAAGGAGTGGTTCCACGACATTCATTACCTTGGC
 AACTGGGGCAGACACCGGAATCCACACTGGAACAACAAAGAAGCACTGGTAGAGTTCAAGGACGCACATGCCAAAAGGC
 AAAGTTGCTGTTCTAGGGAGTCAAGAAGGAGCAGTTCACACGGCCCTTCTGGAGCTCTGGAGGCTGAGATGGATGGTGC
 AAAGGGAAGGCTGTCTCTGGCCACTTGAAATGTCGCTGAAAATGGATAAACTTAGATTGAAGGGCGTGCATACTCCTTGT
 GTACCGCAGCGTTCACATTACCAAGATCCCGGCTGAAACACTGCACGGGACAGTCACAGTGGAGGTACAGTACGCAGGGAC
 AGATGGACCTTGAAGGTTCCAGCTCAGATGGCGGTGGACATGCAAACTCTGACCCAGTTGGGAGGTTGATAACCGCTAACC
 CCGTAATCACTGAAGGCACTGAGAACTCTAAGATGATGCTGGAACCTGATCCACCATTGGGGACTCTTACATTGTGATAGGA
 GTCGGGGAGAAGAAGATCACCCACCACTGGCACAGGAGTGGCAGCACCATTGGAAGGCACTTGAAGCCACTGTGAGAGGT
 GCCAAGAGAATGGCAGTCTTGGGAGACACAGCCTGGGACTTTGGATCAGTTGGAGGCGTTCTTAATCATTGGGCAAGGGCA
 TCCATCAAATTTTGGAGCAGCTTCAAATCATTGTTGGAGGAATGTCTGGTTCTCACAATTTCTATTGGAACGTTGCTGAT
 GTGGTTGGGTCTGAATACAAAGAATGGATCTATTTCCCTATGTGCTTGGCCTTAGGGGGAGTGTGATCTTCTATCCACAGC
 CGTCTCCGCTGATGTGGGGTGCTCGGTGGACTTCTCAAAGAAGGAAACGAGATGCGGTACAGGGGTGTTCTGTATAACGAC
 GTTGAAGCCTGGAGGGACAGGTACAAGTACCATCTGACTCCCTCGTAGATTGGCAGCAGTAGTCAAGCAAGCCTGGGAAG
 ATGGTATCTGTGGGATCTCCTCTGTTTCAAGAATGGAACCATCATGTGGAGATCAGTAGAAGGGGAGCTCAACGCAATCTG
 GAAGAGAATGGAGTTCAACTGACGGTCGTTGTGGGATCTGTAAAAACCCCATGTGGAGAGGTCCACAGAGATTGCCCGTGC
 CTGTGAACGAGCTGCCCAAGGCTGGAAGGCTTGGGGGAAATCGTACTTCTGTCAGAGCAGCAAAGACAAATAACAGCTTTGT
 CGTGGATGGTGACACACTGAAGGAATGCCCACTCAAACATAGAGCATGGAACAGCTTTCTTGTGGAGGATCATGGGTTGGGG
 GTATTTACACTAGTGTCTGGCTCAAGGTTAGAGAAGATTATTCAGTAGAGTGTGATCCAGCCGTCATTGGAACAGCTGTTAAG
 GGAAGGAGGCTGTACACAGTGTCTAGGCTACTGGATTGAGAGTGAGAAGAACGACACATGGAGGCTGAGGAGGGCCAC
 CTGATCGAGATGAAAACATGTGAATGGCCAAAGTCCACACATTGTGGACAGATGGAATAGAAGAGAGTGTCTGATCATAC
 CCAAGTCTTAGCTGGGCCACTCAGCCATCACAACACCAGAGAGGGGTACAGGACCCAAATGAAAGGGCCATGGCAGAGTGA
 AGAGCTTGAAATTCGGTTTGGGAATGCCCAGGCACTAAGGTCCACGTGGAGGAAACATGTGGAACAAGAGGACCATCTCTG
 AGATCAACCACTGCAAGCGGAAGGGTGATCGAGGAATGGTGCTGCAGGGAGTGACAATGCCCCCACTGTCTGTTCCGGGCTA
 AAGATGGCTGTTGGTATGGAATGGAGATAAGGCCAGGAAAGAACAGAAAGTAAGTCAATGGTACTGTCAG
 GATCAACTGATCACATGGATCACTTTCCCTTGGAGTGCTTGTGATTCTGCTCATGGTGCAGGAAGGGCTGAAGAAGAGAATG
 ACCACAAAGATCATATAAGCACATCAATGGCAGTGTGGTAGCTATGATCCTGGGAGGATTTCAATGAGTGTCTGGCTAA
 GCTTGCAATTTTGTGGGTGCCACCTTTCGGAAATGAACACTGGAGGAGATGTAGCTCATCTGGCGCTGGTAGCGGCATTCA
 AAGTCAGACCAGCGTTGCTGGTATCTTTCATCTTCAGAGCTAATTGGACACCCCGTGAAGCATGCTGCTGGCCTTGGCCTCGT
 GTCTTTTGCAAACTGCGATCTCCGCTTGGGAAGGGACCTGATGGTTCTCATCAATGGTTTTGCTTGGCCTGGTTGGCAATAC
 GAGCGATGGTTGTTCCACGCACTGACAATATCACCTTGGCAATCCTGGCTGCTTGACACCACTGGCCCGGGCACACTGCTTG

TGGCGTGGAGAGCAGGCCCTTGCTACTTGCGGGGGGTTTCATGCTCCTCTCTCTGAAGGGGAAAGGCAGTGTGAAGAAGAACTT
 ACCATTTGTCATGGCCCTGGGACTAACCGCTGTGAGGCTGGTCGACCCCATCAACGTGGTGGGACTGCTGTTGCTCACAAGGA
 GTGGGAAGCGGAGCTGGCCCCCTAGCGAAGTACTCACAGCTGTTGGCCTGATATGCGCATTGGCTGGAGGGTTCCGCCAAGGC
 AGATATAGAGATGGCTGGGCCCATGGCCGCGGTGGTCTGCTAATTGTCAGTTACGTGGTCTCAGGAAAGAGTGTGGACATG
 TACATTGAAAGAGCAGGTGACATCACATGGGAAAAAGATGCGGAAGTTACTGGAAACAGTCCCCGGCTCGATGTGGCACTAG
 ATGAGAGTGGTGATTTCTCCCTGGTGGAGGATGACGGTCCCCCATGAGAGAGATCATACTCAAAGTGGTCCTGATGACCATC
 TGTGGCATGAACCAATAGCCATACCCCTTGCGAGCTGGAGCGTGGTACGTATACGTGAAAACTGGAAAAAGGAGTGGTGCTCT
 ATGGGATGTGCTGCTCCCAAGGAAGTAAAAAAGGGGGAGACCACAGATGGAGTGTACAGAGTAATGACTCGTAGACTGCTA
 GGTTCACACAAGTTGGAGTGGGAGTTATGCAAGAGGGGGTCTTTCACTATGTGGCATGTCAAAAAGGATCCGCGCTGA
 GAAGCGGTGAAGGGAGACTTGATCCATACTGGGGAGATGTCAAGCAGGATCTGGTGTACACTGTGGTCCATGGAAGCTAGA
 TGCCGCTGGGACGGGCACAGCGAGGTGCAGCTCTTGCCGTGCCCGGAGAGAGAGCGAGGAACATCCAGACTCTGCC
 GGAATATTTAAGACAAAGGATGGGGACATTGGAGCGGTTGCGCTGGACTATCCAGCAGGAACCTCAGGATCTCCAATCCTAG
 ACAAGTGTGGGAGAGTGATAGGACTCTATGGCAATGGGGTCTGATCAAGAATGGGAGTTATGTAGTGCCATCACCCAAGG
 GAGGAGGGAGGAAGAGACTCCTGTTGAGTGCTTCGAGCCTTCGATGCTGAAGAAGAAGCAGCTAACTGTCTTAGACTTGCT
 CCTGGAGCTGGGAAAACAGGAGAGTTCTTCCTGAAATAGTCCGTGAAGCCATAAAAACGAGACTCCGTACTGTGATCTTAGC
 TCCAACCAAGGTTGTGCTGCTGAAATGGAGGAAGCCCTTAGAGGGCTTCAGTGCGTTATATGACAACAGCAGTCAATGTCA
 CCCATTCTGGGACAGAAATCGTTGACTTAATGTGCCATGCCACCTTCACTTCAGCTACTACAGCCAATCAGAGTCCCCAATA
 TAATCTGTATATTATGGATGAGGCCCACTTCACAGATCCCTCAAGTATAGCAGCAAGAGGATACATTTCAACAAGGGTTGAGA
 TGGGCGAGGCAGCTGCCATCTTCATGACCGCCACGCCACCAGGAACCCGTGACGCATTCCCGGACTCCAACCTACCAATTATG
 GACACCGAAGTGGAAGTCCCAGAGAGAGCCTGGAGCTCAGGCTTTGATTGGGTGACGGATCATCTGGAAAAACAGTTTGGT
 TTGTCCCAAGCGTGAGGAACGGCAATGAGATCGCAGCTTGTCTGACAAAGGCTGGAAAACGGGTACACAGCTCAGCAGAAA
 GACTTTTGAGACAGAGTTCCAGAAAACAAAACATCAAGAGTGGGACTTCGTCGTGACAACTGACATTTAGAGATGGGCGCCA
 ACTTTAAAGCTGACCGTGTATAGATTCCAGGAGATGCTAAAGCCGGTCACTACTGATGGCGAGAGAGTCACTCTGGCTGGA
 CCCATGCTGTACACATGCCAGCGCTGCCAGAGGAGGGGGCGCATAGGCAGGAATCCCAACAAACCTGGAGATGAGTATC
 TGTATGGAGGTGGGTGCGCAGAGACTGATGAAGACCATGCACACTGGCTGAAGCAAGAATGCTCCTTGACAATATTTACCTC
 CAAGATGGCCTCATAGCCTCGCTCTATCGACCTGAGGCCGACAAAGTAGCAGCCATTGAGGGAGAGTTCAAGCTTAGGACGG
 AGCAAAGGAAGACCTTTGTGGAACCTCATGAAAAGAGGAGATCTTCTGTTGGCTGGCCTATCAGGTTGCATCTGCCGGAATA
 ACCTACACAGATAGAAGATGGTGCTTGATGGCATGACCAACAACACCATAATGGAAGACAGTGTGCCGGCAGAGGTGTGGA
 CCAGACACGGAGAGAAAAGAGTGCTCAAACCGAGGTGGATGGACGCCAGAGTTTGTTGAGATCATGCGGCCCTGAAGTCATT
 CAAGGAGTTTGCCGCTGGGAAAAGAGGAGCGGCTTTGGAGTGATGGAAGCCCTGGGAACACTGCCAGGACACATGACGGA
 GAGATTCCAGGAAGCCATTGACAACCTCGCTGTGCTCATGCGGGCAGAGACTGGAAGCAGGCCTTACAAAGCCGCGGCGGCC
 CAATTGCCGAGACCCTAGAGACCATTATGCTTTTGGGGTTGCTGGGAACAGTCTCGCTGGGAATCTTTTCTGTTGATGCGG
 AACAGGGCATAGGGAAGATGGGCTTTGGAATGGTGACTCTGGGGCAGCGCATGGCTCATGTGGCTCTCGGAAATTGAGC
 CAGCCAGAATTGCATGCGTCTCATTGTTGTGTTCTATTGCTGGTGGTGCTCATACCTGAGCCAGAAAAGCAAAGATCCCCC
 AGGACAACCAATGGCAATCATCATCATGGTAGCAGTAGGTCTTCTGGGCTTGATTACCGCCAATGAACCTCGGATGGTTGGAG
 AGAACAAAGAGTGACCTAAGCCATCTAATGGGAAGGAGAGAGGAGGGGGCAACCATAGGATTCTCAATGGACATTGACCTG
 CGGCCAGCCTCGGCCCTGGGCCATCTATGCTGCCCTGACAACTTTCATTACCCAGCCGTCCAACATGCAGTGACCACTTCATAC
 AACAACTACTCCTAATGGCGATGGCCACGCAAGCTGGAGTGTGTTTGGTATGGGCAAAGGGATGCCATTCTACGCATGGGA
 CTTTGGAGTCCCGCTGCTAATGATAGGTTGCTACTACAATTAACACCCCTGACCCTAATAGTGGCTATCATTTTCTGCTGGCG
 CACTACATGTACTTGATCCCAGGGCTGCAGGCAGCAGCTGCGCGTGTGCTGCCAGAAGAGAACGGCAGCTGGCATCATGAAGA
 ACCCTGTTGTGGATGGAATAGTGGTGACTGACATTGACACAATGACTATTGACCCCAAGTGGAGAAAAAGATGGGACAGGT
 GCTACTCATAGCAGTAGCCGTCTCCAGCGCCATACTGTGCGGACCGCCTGGGGTGGGGGGAAGCTGGGGCCCTGATCACA
 GCTGCAACTTCCACTTTGTGGGAAGGCTCTCGAACAAGTACTGGAACCTCTACAGCCACTTCACTGTGCAACATTTTAGG
 GGAAGTTACTTGGCTGGAGCTTCTAATCTACACAGTAACAAGAAACGCTGGCTTGTTCAAGAGACGTGGGGGTGGAACAG
 GAGAGACCCTGGGAGAGAAATGGAAGGCCCGCTTGAACCAGATGTGCGCCCTGGAGTTCTACTCTACAAAAAGTCAGGCAT
 CACCGAGGTGTGCAGAGAAGAGGCCCGCGCCCTCAAGGACGGTGTGGCAACGGGAGGCCATGCTGTGTCCTCCGAGGAAG

TGCAAAGCTGAGATGGTTGGTGGAGCGGGGATACCTGCAGCCCTATGGAAAGGTCATTGATCTTGGATGTGGCAGAGGGGG
 CTGGAGTTACTACGCCGCCACCATCCGCAAAGTTCAAGAAGTGAAAGGATACACAAAAGGAGGCCCTGGTCATGAAGAACCC
 ATGTTGGTGCAAAGCTATGGGTGGAACATAGTCCGTCTTAAGAGTGGGGTGGACGTCTTTCATATGGCGGCTGAGCCGTGTG
 ACACGTTGCTGTGTGACATAGGTGAGTCATCATCTAGTCTGAAGTGGAAGAAGCACGGACGCTCAGAGTCTCTCCATGGTG
 GGGGATTGGCTTGAAAAAGACCAGGAGCCTTTTGTGAAAAGTGTGTGCCCATACACCAGCACTATGATGGAAACCTGGA
 GCGACTGCAGCGTAGGTATGGGGGAGGACTGGTCAGAGTGCCACTCTCCCGCAACTCTACACATGAGATGTACTGGGTCTCT
 GGAGCGAAAAGCAACACCATAAAAAAGTGTGCCACCACGAGCCAGCTCCTCTTGGGGCGCATGGACGGGCCAGGAGGCCA
 GTGAAATATGAGGAGGATGTGAATCTCGGCTCTGGCACGCGGGCTGTGGTAAGCTGCGCTGAAGCTCCCAACATGAAGATCA
 TTGGTAACCGCATTGAAAGGATCCGAGTGAGCACGCGGAAACGTGGTTCTTTGACGAGAACCACCCATATAGGACATGGGC
 TTACCATGGAAGCTATGAGGCCCTACACAAGGGTCAGCGTCTCTCTAATAAACGGGGTTGTCAGGCTCCTGTCAAACCT
 GGGATGTGGTGACTGGAGTCACAGGAATAGCCATGACCGACACCACCCGATGGTCAGCAAAGAGTTTCAAGGAAAAAGT
 GGACACCAGGGTGCCAGACCCCCAAGAAGGCACTCGTCAGGTTATGAGCATGGTCTCTTCTGGTTGTGGAAGAGCTAGGC
 AAACACAAACGGCCACGAGTCTGTACCAAGAAGAGTTCATCAACAAGGTTCTGAGCAATGCAGCATTAGGGGCAATATTTGA
 AGAGGAAAAAGAGTGGAAGACCGCAGTGGAAGCTGTGAACGATCCAAGGTTCTGGGCTCTAGTGGACAAGGAAAGAGAGC
 ACCACCTGAGAGGAGAGTGCCAGAGCTGTGTGTACAACATGATGGGAAAAAGAGAAAAGAAACAAGGGGAATTTGAAAG
 GCCAAGGGCAGCCGCGCATCTGGTATATGTGGCTAGGGGCTAGATTCTAGAGTTCGAAGCCCTTGGATTCTTAATGAGGA
 TCACTGGATGGGGAGAGAGAAGTCAAGAGGTGGTGTGAAGGGCTGGGATTACAAAGACTCGGATATGTCCTAGAAGAGAT
 GAGTCGCATACCAGGAGGAAGGATGTATGCAGATGACACTGCTGGCTGGGACACCCGCATCAGCAGGTTTGATCTGGAGAAT
 GAAGCTTTAATCACCAACCAATGGAGAAAGGGCACAGGGCCTTAGCATTGGCCATAATCAAGTACACATACCAAAACAAAGT
 GGTAAAGGTCCTTAGACCAGCTGAAAAAGGGAAGACAGTTATGGACATTATTTCAAGACAAGACCAAGGGGGAGCGGACA
 AGTTGTCACTTACGCTCTTAACACATTACCAACCTAGTGGTGCAACTCATTGGAATATGGAGGCTGAGGAAGTTCTAGAGAT
 GCAAGACTGTGGCTGTGCGGAGGTGAGAGAAAGTGACCAACTGGTTGCAGAGCAACGGATGGGATAGGCTCAAACGAAT
 GGCAGTCAGTGGAGATGATTGCGTTGTGAAGCCAATTGATGATAGGTTTGACATGCCCTCAGGTTCTTGAATGATATGGGAA
 AAGTTAGGAAGGACACACAAGAGTGGAACCTCAACTGGATGGGACAACCTGGGAAGAAGTTCGTTTTGTTCCCACTTC
 AACAAGCTCCATCTCAAGGACGGGAGGTCCATTGTGGTTCCCTGCCGCCACCAAGATGAAGTGAATGGCCGGGCCGTGTCTC
 TCCAGGGGCGGGATGGAGCATCCGGGAGACTGCTTGCTAGCAAAGTCATATGCGCAAATGTGGCAGCTCCTTTATTTCCACA
 GAAGGGACCTCCGACTGATGGCCAATGCCATCTGTTATCTGTGCCAGTTGACTGGGTCCAAGTGGGAGAACTACCTGGTCA
 ATCCATGGAAAGGGAGAATGGATGACCACTGAAGACATGCTTGTGGTGTGGAACAGAGTGTGGATTGAGGAGAACGACCAC
 ATGGAAGACAAGACCCAGTTACGAAATGGACAGACATTCCCTATCTGGGAAAAAGGGAAGACTGTGGTGTGGATCTCTCA
 TAGGGGCACAGACCGCGACCACTGGGCTGAGAACATTAAAAACACAGTCAACATGGTGGCAGGATCATAGGTGATGAAGA
 AAAGTACATGGACTACCTATCCACCAAGTTCGCTACTTGGGTGAAGAAGGGTCTACACCTGGAGTGCTATAAGCACCAATCTT
 AGTGTGTGAGGCTGTAGTCAGCCACAGCTTGGGGAAGCTGTGCAGCCTGTGACCCCCCAGGAGAGGCTGGGAAACCA
 AGCCCATAGTCAGGCCGAGAACGCCATGGCACGGAAGAAGCCATGCTGCCTGTGAGCCCCCTCAGAGGACACTGAGTCAAAAA
 ACCCCACGCGCTTGGAGGCGCAGGATGGGAAAAGAAGGTGGCGACCTTCCCCACCTTCAATCTGGGGCTGAAGTGGAGAT
 CAGCTGTGGATCTCCAGAAGAGGGACTAGTGGTTAGAGGAGACCCCCCGGAAAACGCAAAACAGCATATTGACGCTGGGAA
 AGACCAGAGACTCCATGAGTTTCCACCACGCTGGCCGCCAGGCACAGATCGCCGAATAGCGGCGGCCGGTGTGGGGAAATCC
 ATGGGTCT

KU681082.3 Zika virus isolate Zika virus/H.sapiens-tc/PHL/2012/CPC-0740, Philippines, complete
 genome (SEQ ID NO: 8)

AGTTGTTGATCTGTGTGAATCAGACTGCGACAGTTCGAGTTTGAAGCGAAAGCTAGCAACAGTATCAACAGGTTTTATTTGG
 ATTTGGAAACGAGAGTTTCTGGTCATGAAAAACCCAAAAAGAAATCCGGAGGATTCCGGATTGTCAATATGCTAAAACGCGG

AGTAGCCCGTGTGAGCCCCCTTTGGGGGCTTGAAGAGGCTGCCAGCCGGACTTCTGCTGGGCCATGGGCCCATCAGGATGGTC
 TTGGCGATACTAGCCTTTTTGAGATTCACGGCAATCAAGCCATCACTGGGTCTCATCAATAGATGGGGTTCAGTGGGGAAAAA
 AGAGGCTATGGAATAATAAAGAAGTTCAAGAAAGATCTGGCTGCCATGCTGAGAATAATCAATGCTAGGAAGGAGAAGAA
 GAGACGAGGCGCAGATACTAGCGTCGGAATTGTTGGCCTCCTCTGACCACAGCCATGGCAGTAGAGGTCACTAGACGTGGG
 AGTGCATACTATATGTACTTGGACAGAAGCGATGCTGGGGAGGCCATATCTTTCCAACCACACTGGGGATGAATAAGTGTTA
 CATACAAATCATGGATCTTGGACACATGTGTGATGCCACCATGAGCTATGAATGCCCTATGTTGGATGAGGGGGTAGAACCAG
 ATGACGTCGATTGCTGGTGAACACGACATCAACTTGGGTTGTGTATGGAACCTGCCACCACAAAAAAGGTGAAGCACGGAG
 ATCTAGAAGAGCTGTGACGCTCCCTCCCATTCCTAGGAAGCTGCAAACGCGGTGCGAGACCTGGTTGGAATCAAGAGAAT
 ACACAAAGCAGCTGATTAGAGTTGAAAATTGGATATTGAGGAACCTGGCTTCGCTTAGCAGCAGCTGTCTGCTTGGCTTT
 TGGGAAGTTCAACGAGCCAAAAAGTCATATATCTGGTCATGATACTGCTGATTGCCCCGCATACAGCATCAGGTGCATAGGA
 GTCAGCAATAGGGACTTTGTGGAAGGTATGTCAGGTGGGACTTGGGTTGATGTTGTCTTGGAACATGGAGGTTGTGTTACCGT
 AATGGCACAGGACAAACCGACTGTGACATAGAGCTGGTTACAACAACAGTCAGCAACATGGCGGAGGTAAGATCCTACTGC
 TATGAGGCATCAATATCGGATATGGCTTCGGACAGCCGCTGCCAACACAAAGGTGAGGCCTACCTTGACAAGCAGTCAGACAC
 TCAATATGTCTGCAAAAGAACGTTAGTGGACAGAGGCTGGGGAAATGGATGTGGACTTTTGGCAAAGGGAGCCTGGTGACA
 TGGCGTAAGTTTGCATGCTCCAAGAAAATGACCGGGAAGAGCATCCAGCCAGAGAATCTGGAGTACCGGATAATGCTGTGAG
 TTCATGGCTCCAGCACAGTGGGATGATCGTTAATGACACAGGACATGAACTGATGAGAATAGAGCGAAGGTTGAGATAAC
 GCCCAATTCACCAAGAGCCGAAGCCACCCTGGGGGGTTTTGGGAGCCTAGGACTTGATTGTGAACCGAGGACAGGCCCTTGAC
 TTTTCAGATTTGTATTACCTGACTATGAATAACAAGCACTGGTTGGTTCAAGGAGTGGTTCCACGACATTCATTACCTTGGC
 ATGCTGGGGCAGACACTGGAACCTCACATTGGAACAACAAAGAAGCACTGGTAGAGTTCAAGGACGACATGCAAAAAGGCA
 AACTGTCGTGGTTCTAGGGAGTCAAGAAGGAGCAGTTACACGGCCCTTGCTGGAGCTCTGGAGGCTGAGATGGATGGAGCC
 AAGGGAAGGCTGTCTCTGGCCACTTGAAATGTCGCTGAAATGGATAAACTTAGATTGAAGGGCGTGTCTACTCTTGTG
 CACTGCAGCGTTACATTACCAAGATCCCGCTGAAACACTGCACGGGACAGTCACAGTGGAGGTACAGTACGCAGGGACA
 GATGGACCTTGCAAGGTTCCAGCTCAGATGGCGGTGGATATGCAAACTCTGACCCAGTTGGGAGGTTGATAACCGCTAACCC
 TGTAATCACTGAAAGCACCGAGAAGCTAAGATGATGCTGGAACCTTGATCCACCATTTGGGGACTCTTACATTGTATAGGAGT
 CGGGGAGAAGAAGATACCCATCACTGGCACAGGAGTGGCAGCACCATTGGAAAAGCATTGAAGCCACTGTGAGAGGTGC
 CAAGABAATGGCAGTCTTGGGAGACACAGCCTGGGACTTTGGATCAGTTGGGGGTGCTCTCAACTATTGGGCAAGGGCATC
 CATCAATTTTTGGAGCAGCTTCAAATCATTGTTCCGAGGAATGTCTGGTTCTCAAAATCTCATTGGAACGTTGCTGGTGT
 GGTGGGTCTGAATACAAAGAATGGATCTATTTCCCTTACGTGCTTGGCCTTAGGGGGAGTGTGATCTTCTATCCACAGCCG
 TTTCTGCTGATGTGGGGTGCTCGGTGGACTTCTCAAAGAAGGAAACGAGATGCGGTACAGGGGTGTTCTGTCTATAACGACGTT
 GAAGCCTGGAGGGACAGGTACAAGTACCATCTGACTCCCTCGTAGATTGGCAGCAGCAGTCAAGCAAGCCTGGGAAGATG
 GGATCTGTGGGATCTCTCTCTCAAGAATGGAACATCATGTGGAGATCAGTAGAAGGGGAGCTCAACGCAATCTGGA
 AGAGAATGGAGTTCAACTGACGGTCTTGTGGGATCTGTAAAAAACCCCATGTGGAGAGGTCCACAGAGATTGCCCGTGCT
 GTGAACGAGCTGCCCCACGGCTGGAAGGCTTGGGGGAAATCGTACTTCGTGAGAGCAGCAAGACAAATAACAGCTTTGTG
 TGGATGGTGACACACTGAAGGAATGCCCACTCAAACATAGAGCATGGAACAGCTTTCTTGTGGAGGATCATGGGTTTGGGGT
 ATTTACACTAGTGTCTGGCTCAAGGTTAGAGAAGATTATTCATTAGAGTGTGATCCAGCCGTATTGGAACAGCTGCTAAGG
 GAAAGGAGGCTGTGCACAGCGATCTAGGCTACTGGATTGAGAGTGAGAAGAACGACACATGGAGGCTGAAGAGGGCCACC
 TGATCGAGATGAAAACATGTGAATGGCCAAAGTCCCACACATTGTGGACAGATGGAGTAGAAGAAAGTGATCTGATCATACC
 CAAGTCTTTAGCTGGGCCACTCAGCCATCACAACACCAGAGAGGGCTACAGGACTCAAATGAAAGGGCCATGGCACAGTGAA
 GAGCTTGAAATTCGGTTTGAGGAATGCCAGGCACTAAGGTCCACGTGGAGGAAACATGTGGGACAAGAGGACCATCCCTGA
 GATCAACCACTGCAAGCGGAAGGGTGATCGAGGAATGGTGCTGCAGGGAATGCACAATGCCCCACTGCTGTTCCGAGCTAA
 AGATGGCTGTTGGTATGGAATGGAGATAAGGCCCAGGAAAGAACCAGAAAGTAAGTTAGTAAGGTCAATGGTGACTGCAGG
 ATCAACTGATCATATGGATCACTTCTCTTGGAGTGCTTGTGATTTTGCTCATGGTGAGGAAGGGCTGAAGAAGAGAATGA
 CCACAAAGATCATATAAGCACATCAATGGCAGTGCTGGTAGCCATGATCTGGGAGGATTTTCAATGAGTGACCTGGCTAAG
 CTTGCAATTTTGATGGGTGCCACCTTCGCGGAAATGAACACTGGAGGAGATGTAGCTCATTGGCGCTGATAGCGGCATTCAA
 AGTCAGACCTCGGTTGCTGGTATCTTTCATCTTCAGAGCTAATTGGACACCCCGTGAGAGCATGCTGCTGGCCTTGCCCTCGTG
 TCTTCTGCAAACTGCGATCTCCGCTTGGAAGGCGACCTGATGGTTCTCATCAATGGTTTTGCTTTGGCCTGGTTGGCAATACG

AGCGATGGTTGTTCCACGCACTGACAACATCACCTTGGCAATCCTGGCTGCTCTGACACCACTGGCCCCGGGGCACACTGCTTGT
 GCGTGGAGAGCAGGCCCTTGCTACTTGCAGGGGGTTCATGCTCCTCTCTCTGAAGGGGAAAGGCAGTGTGAAGAAGAACCTA
 CCATTGTGTCATGGCCTTGGGACTAACTGCTGTGAGGCTGGTCGACCCCATCAACGTGGTGGGACTGCTGTTGCTCACAAGGAG
 TGGGAAGCGGAGCTGGCCCCCTAGTGAAGTACTCACAGCTGTTGGCCTGATATGCGCATTGGCTGGAGGGTTCCGCAAGGCG
 GATATAGAGATGGCTGGGCCCATGGCCGCGTCTGGTCTGCTAATTGTCAGTTACGTGGTCTCAGGAAAGAGTGTGGACATGT
 ACATTGAAAGAGCAGGTGACATCACATGGGAAAAAGATGCGGAAATCACTGGAAACAGTCCCCGGCTCGATGTGGCACTAGA
 TGAGAGTGGTGATTTCTCCCTAGTGGAGGATGATGGTCCACCCATGAGAGAGATCATACTCAAAGTGGTCTCTGATGACCATCT
 GCGGCATGAACCCAATAGCCATACCTTTGCAGCTGGAGCGTGGTACGTGTATGTGAAGACTGGAAAAAGGAGTGGTGCTCT
 ATGGGATGTGCTGCTCCCAAGGAAGTAAAAAGGGGGAGACCACAGATGGAGTGTACAGAGTAATGACTCGTAGACTGCTT
 GGTTCAACACAAGTTGGAGTGGGAGTCATGCAAGAGGGGGTCTTCCACACTATGTGGCACGTCACAAAAGGATCCGCGCTGA
 GAAGCGGTGAAGGGAGACTTGATCCATACTGGGAGATGTCAAGCAGGATCTGGTGTCTACTGTGGTCCGTGGAAAGCTAGA
 CGCCGCTGGGACGGGCACAGCGAGGTGCAGCTCTTGGCCGTGCCCCCGGAGAGAGAGCGAGGAACATCCAGACTCTGCC
 CGGAACATTAAAGACAAAGGATGGGACATTGGAGCAGTTGCGCTGGACTACCCAGCAGGAACCTCAGGATCTCCAATCCTA
 GACAAGTGTGGGAGAGTGATAGGACTCTATGGTAATGGGGTCTGTGATAAAAAATGGGAGTTATGTTAGTGCCATCACCCAAG
 GGAGGAGGGAGGAAGAGACTCCTGTTGAGTGCTTCGAGCCTTCGATGCTGAAGAAGAAGCAGCTAACTGTCTTAGACCTGCA
 TCCTGGAGCCGGGAAAACAGGAGAGTTCTCTGAAATAGTCCGTGAAGCCATAAAAAACAAGACTCCGTACTGTGATCTTAG
 CTCCAACCAAGGTCGTGCTGCTGAAATGGAGGAAGCCCTTAGAGGGCTTCCAGTTCGTTATATGACAACAGCAGTCAATGTC
 ACCCATCTGGGACAGAAATCGTTGACTTAATGTGCCATGCTACCTTCACTTACGCGCTACTACAACCAATCAGAGTCCCCAAGT
 ATAATTTGATATTATGGATGAGGCCCACTTACAGATCCCTCAAGTATAGCAGCAAGAGGATACATTCAACAAGGGTTGAG
 ATGGGCGAGGCGGCTGCCATCTTCATGACCGCCACGCCACAGGAACCCGTGACGCATTCCCGGACTCCAACCTACCAATTAT
 GGACACCGAGGTGGAAGTCCAGAGAGAGCCTGGAGCACAGGCTTTGATTGGGTGACGGATCATCTGGGAAAACAGTCTG
 GTTTGTTCCAAGCGTGAGGAACGGCAATGAGATCGCAGCTTGTCTGACAAAGGCTGGAAACGGGTCTACAGCTCAGCAGA
 AAGACTTTTGAGACAGAGTTCCAGAAAACGAAAAATCAAGAGTGGGACTTCGTCTGTGACAACCGACATTTAGAGATGGGCG
 CCAACTTTAAAGCTGACCGTGTATAGATTCCAGGAGATGCTTAAAGCCGGTCTACTTGATGGCGAGAGAGTCATTTGGCT
 GGACCCATGCCTGTACACATGCCAGCGCTGCTCAGAGGAGGGGGCGCATAGGCAGGAATCCCAACAAACCTGGAGATGAGT
 ATCTGTATGGAGGTGGGTGCGCAGAGACTGATGAAGATCAGCACACTGGCTTGAAGCAAGAATGCTTCTTGACAACATTTAC
 CTCCAAGATGGCCTCATAGCTTCGCTCTATCGACCTGAGGCCGACAAAGTAGCAGCTATTGAGGGAGAGTTCAAGCTTAGGAC
 GGAGCAAAGGAAGACCTTTGTGGAACCTCATGAAAAGAGGAGATCTCCGGTTTGGTTGGCCTATCAGGTTGCATCTGCCGGA
 ATAACCTACACAGATAGAAGATGGTGCTTTGATGGCATGACCAACAACACCATAATGGAAGACAGTGTGCCGGCAGAGGTGT
 GGACCAGATACGGAGAGAAAAGAGTGCTCAAACCGAGGTGGATGGACGCCAGAGTTTGTTCAGATCATGCGGCCCTGAAGT
 CATTCAAAGAGTTTCCGCTGGGAAAAGAGGAGCGGCCCTTGGAGTGATAGAAGCCCTGGGAACACTGCCAGGACACATGAC
 AGAGAGATTCCAGGAAGCCATTGACAACCTCGCTGTGCTCATGCGGGCAGAGACTGGAAGCAGGCTTACAAAGCCGCGGCG
 GCCCAATTGCCGGAGACCCTAGAGACCATTATGCTTTTGGGGTGTCTGGGAACAGTCTCGCTGGGAATCTTTTCTGCTTGATG
 CGGAACAAGGGCATGGGGAAGATGGGCTTTGGAATGGTGACTCTTGGGGCCAGCGCATGGCTTATGTGGCTCTCGGAAATTG
 AGCCAGCCAGAATTGCATGTGTCTCATTGTCTGTTCTTATTGCTGGTGGTGTCTACCTGAGCCAGAAAAGCAAAGATCTC
 CTCAGGACAACCAATGGCAATCATCATGTTAGCAGTGGGTCTTCTGGGCTTGATTACCGCCAATGAACTCGGATGGTTG
 GAGAGAACAAAAAGTGACCTAAGCCATCTAATGGGAAGGAGAGAGGAGGGGCAACCACAGGATTCTCAATGGACATTGAC
 CTGCGGCCAGCTCAGCTTGGGCTATCTATGCTGCTGCTGACAACCTTTCATCACCCAGCCGTCCAACATGCGGTGACCACTTCAT
 ACAACAACACTACTCTTAATGGCGATGGCCACGCAAGCTGGGGTGTGTTGTTGGTATGGGCAAAGGGATGCCATTCTACGCATGG
 GACTTTGGAGTCCCCTGCTAATGATGGGTGCTACTCACAATTAACACCTCTGACCCTAATAGTGCCATCATTTTGTCTGTG
 GCGCACTACATGTACTTGATCCAGGGCTGCAGGCAGCAGCTGCGCGGGCTGCCAGAAGAGAACGGCAGCTGGCATCATGA
 AGAACCCTGTTGTGGATGGAATAGTGGTGACTGACATTGACACAATGACAATTGACCCCCAAGTGGAAGAAAAGATGGGGCA
 GGTGCTACTCATAGCAGTAGCCGTCTCCAGCGCCATACTGTGCGGAGCCGCTGGGGGTGGGGGGAGGCTGGGGCCCTGATC
 ACAGCTGCAACTTCCACCTTGTGGGAAGGCTCTCCGAACAAGTACTGGAACCTCTCACAGCCACTTCACTGTGTAACATTTTAA
 GGGGAAGTTACTTGGCTGGAGCTTCTAATCTACACAGTAACAAGAAACGCTGGCTTGGTCAAGAGACGTGGGGGTGGAAC
 GGGAGAGACCCTGGGAGAGAAATGGAAGGCCCGCTGAACCAGATGTGCGCCCTGGAGTTCTACTCTACAAAAAGTCAGGC

PAT022-EP-PR

ATCACCGAGGTGTGCAGAGAAGAGGCCCGCCGTGCCCTCAAGGACGGTGTGGCAACAGGAGGCCATGCTGTGTCCCAGGA
AGTGCAAAGCTTAGATGGCTGGTGGAGAGAGGATACCTGCAGCCCTATGGAAAGGTCATTGATCTTGGATGTGGCAGAGGG
GGCTGGAGTTACTATGCCGCCACCATCCGCAAAGTTCAGGAAGTGAAAGGATACACAAAAGGAGGCCCTGGTCATGAAGAAC
CCATGTTGGTGCAAAGCTATGGGTGGAACATAGTCCGTCTTAAGAGTGGGGTGGACGTCTTTCACATGGCGGCTGAGCCGTG
TGACACTTTGCTGTGTGATATAGGTGAGTCATCATCTAGTCTGAAGTGGGAAGAAGCACGGACGCTCAGAGTCCTCTCCATGG
TGGGGGATTGGCTTGAAAAAGACCAGGAGCCTTTGTATAAAAGTGTGTGCCCATACACCAGCACTATGATGGAAACCTG
GAGCGACTGCAGCGTAGGTATGGGGGAGGACTGGTCAGGGTGCCACTCTCCCGCAACTCTACACATGAGATGTAAGTGGTCT
CTGGAGCGGAAAAGCAACACCATAAAAAGTGTGTCCACCACGAGCCAGCTCTCTTGGGGCGCATGGACGGGCCAGGAGGCC
AGTGAAATATGAGGAGGATGTGAATCTCGGCTCTGGCAGCGGGGCTGTGGTAAGCTGCGCTGAAGCTCCCAACATGAAGATC
ATTGGTAACCGCATTGAGAGGATCCGCAGTGAGCACGCGGAAACGTGGTCTTTGACGAGAACCACCCATATAGGACATGGG
CTTACCATGGAAGCTATGAGGCCCTACACAAGGGTCAGCGTCTCTCTAATAAACGGGGTTGTGAGGCTCTGTCAAAACCT
GGGATGTGGTGACTGGAGTCACAGGAATAGCCATGACTGACACCACACCGTATGGTCAGCAAAGAGTTTCAAGGAAAAAGT
GGACACTAGGGTGCCAGACCCCCAAGAAGGCACTCGTCAGGTTATGAGCATGGTCTCTTCTGGTTATGGAAGGAGCTAGGC
AAACACAAACGGCCACGAGTCTGTACCAAAGAAGAGTTCATCAACAAGGTTCTGTAGCAATGCAGCATTAGGGGCAATATTTGA
AGAGGAAAAAGAGTGGAAGACTGCAGTGGAAGCTGTGAATGATCCAAGGTTCTGGGCTCTAGTGGACAAGGAAAGAGAGCA
TCACCTGAGAGGAGAGTGTGAGAGCTGTGTGTACAACATGATGGGAAAAAGAGAAAAAGAAAGGGGAATTTGGAAGGC
CAAGGGCAGCCGCGCCATCTGGTATATGTGGCTAGGGGCTAGATTCTTAGAGTTTCAAGCCCTTGGATTCTTGAATGAGGATC
ATTGGATGGGGAGAGAGAATTCAGGAGGTGGTGTGGAAGGACTGGGATTACAAAGACTCGGATATGTCCTAGAAGAGATGA
GTCGCATACCAGGAGGAAGGATGTATGCAGATGATACTGCTGGCTGGGACACCCGCATCAGCAGGTTTGATCTGGAGAATGA
AGCTCTAATCACCAACCAATGGAGAAAGGGCACAGGGCCTTGGCATTGGCCATAATCAAGTACACATACCAAAACAAAGTG
GTAAAGGTCTTAGACCAGCTGAAAAAGGGAAGACAGTTATGGACATTATTTCAAGACAAGACCAAGGGGGAGCGGACAA
GTTGTCACTTACGCTCTTAATACATTACCAACCTGGTGGTGCAGCTCATTGGAATATGGAGGCTGAGGAAGTTCTAGAGATG
CAAGACTTGTGGCTGTGCGGAGGCCAGAGAAAGTGACCAACTGGTTGCAAAGCAACGGATGGGATAGGCTCAAAAGAATG
GCAGTCAGTGGAGATGATTGCGTTGTGAAACCAATTGATGATAGGTTTGACATGCCCTCAGGTTCTTGAATGATATGGGAAA
AGTTAGGAAGGACACACAAGAGTGGAACCCCTCAACTGGATGGGACAACTGGGAAGAAGTTCCGTTTTGCTCCACCACTTCA
ACAACTCCATCTTAAGGACGGGAGGTCCATTGTGGTTCCTGCGCCACCAAGATGAACTGATTGGCCGAGCCCGCGTATCA
CCAGGGGCGGGATGGAGCATCCGGGAGACTGCTTGCTAGCAAAATCATATGCGCAAAATGTGGCAGCTCCTTATTTCCACAG
AAGGGACCTCCGACTGATGGCCAATGCCATTTGTTATCTGTGCCAGTTGATTGGGTTCCAAGTGGGAGAACTACCTGGTCAAT
CCATGGAAAGGGAGAATGGATGACCACTGAAGACATGCTTGTGGTATGGAACAGAGTGTGGATTGAGGAAAACGACCACAT
GGAAGACAAGACCCAGTTACAAATGGACAGACATTCCTATTTGGGAAAAAGAGAAGACTTGTGGTGTGGATCTCTCATAG
GGCACAGACCGCTACTACCTGGGCTGAGAACATCAAAATACAGTCAACATGATGCGCAGGATCATAGGTGATGAAGAAAA
GTACATGGACTACCTATCCACCCAGGTTGCTACTTGGGTGAAGAAGGGTCCACACCTGGAGTGTGTAAGCACCAATCTTAG
TGTTGTCAGGCCTGTAGTCAGCCACAGCTTGGGGAAAGCTGTGCAGCCTGTGACCCCCCAGGAGAAGCTGGGAAACCAAG
CCTATAGTCAGGCCGAGAACGCCATGGCACGGAAGAAGCCATGCTGCTGTGAGCCCTCAGAGGACACTGAGTCAAAAAAC
CCCACGCGCTTGGAGGCGCAGGATGGGAAAAGAAGGTGGCGACCTTCCCAACCTTCAATCTGGGGCTGAACTGGAGATCA
GCTGTGGATCTCAGAAGAGGGACTAGTGGTTAGAGGAGACCCCCGAAAAACGCAAAACAGCATATTGACGCTGGGAAAG
ACCAGAGACTCCATGAGTTTCCACCACGCTGGCCGCCAGGCACAGATCGCCGAATAGCGGCGGCCGGTGTGGGAAATCCAT
GGGTCT

KU707826.1 Zika virus isolate SSABR1, Brazil, complete genome (SEQ ID NO: 9)

GACAGTTCGAGTTTGAAGCGAAAGCTAGCAACAATATCAACAGGTTTTATTTGGATTGGAAACGAGAGTTTCTGGTCATGAA
AAACCCAAAAAGAAATCCGGAGGATTCCGGATTGTCAATATGCTAAAACGCGGAGTAGCCCGTGTGAGCCCTTTGGGGGC
TTGAAGAGGCTGCCAGCCGGACTTCTGCTGGGTATGAGGCCATCAGGATGGTCTTGGCGATTCTAGCCTTTTGAATTAC

GGCAATCAAGCCATCACTGGGTCTCATCAATAGATGGGGTTCAGTGGGGAAAAAGAGGCTATGGAAATAATAAAGAAGTTC
 AAGAAAGATCTGGCTGCCATGCTGAGAATAATCAATGCTAGGAAGGAGAAGAAGAGACGAGGCGCAGATACTAGTGTGGA
 ATTGTTGGCCTCCTGCTGACCACAGCTATGGCAGCGGAGGTCACTAGACGTGGGAGTGCATACTATATGTACTTGGACAGAAA
 CGATGCTGGGGAGGCCATATCTTTTCCAACCACATTGGGGATGAATAAGTGTATATACAGATCATGGATCTTGGACACATGT
 GTGATGCCACCATGAGCTATGAATGCCCTATGCTGGATGAGGGGGTGAACCAGATGACGTCGATTGTTGGTGAACACGAC
 GTCAACTTGGGTTGTGTACGGAACCTGCCATCAGAAAAAGGTGAAGCACGGAGATCTAGAAGAGCTGTGACGCTCCCTCCC
 ATTCCTACTAGGAAGCTGCAACGCGGTGCAAACTGTTGGAATCAAGAGAATACACAAAGCACTTGATTAGAGTCGAAAAT
 TGGATATTCAGGAACCTGGCTTCGCGTTAGCAGCAGCTGCCATCGCTTGGCTTTTGGGAAGCTCAACGAGCCAAAAAGTCAT
 ATACTTGGTCATGATACTGCTGATTGCCCCGGCATAACAGCATCAGGTGCATAGGAGTCAGCAATAGGGACTTTGTGGAAGGTA
 TGTGAGGTGGGACCTGGGTTGATGTTGCTTGGAAACATGGAGGTTGTGTACCGTAATGGCACAGGACAAACCGACTGTGCA
 CATAGAGCTGGTTACAACAACAGTCAGCAACATGGCGGAGGTAAGATCCTACTGCTATGAGGCATCAATATCAGACATGGCTT
 CGGACAGCCGCTGCCAACACAAGGTGAAGCCTACCTTGACAAGCAATCAGACACTCAATATGTCTGCAAAAGAACGTTAGTG
 GACAGAGGCTGGGGAAATGGATGTGGACTTTTGGCAAAGGGAGCCTGGTGACATGCGCTAAGTTGTCATGCTCCAAGAAAA
 TGACCGGGAAGAGCATCCAGCCAGAGAATCTGGAGTACCGGATAATGCTGTGCTAGTTCATGGCTCCAGCACAGTGGGATGAT
 TGTTAATGACACAGGACATGAACTGATGAGAATAGAGCGAAAGTTGAGATAACGCCCAATTCACCAAGAGCCGAAGCCACC
 CTGGGGGGTTTGGGAAGCCTAGGACTTGATTGTGAACCGAGGACAGGCCTTGACTTTTCAGATTTGTATTACTTGACTATGAAT
 AACAAGCACTGGTTGGTTCACAAGGAGTGGTTCACGACATTCATTACCTTGGCACGCTGGGGCAGACACCGGAACTCCACA
 CTGGAACAACAAAGAAGCACTGGTAGAGTTCAAGGACGCACATGCCAAAAGGCCAACTGTGCTGGTTCTAGGGAGTCAAGAA
 GGAGCAGTTCACACGGCCCTTGCTGGAGCTCTGGAGGCTGAGATGGATGGTGCAAAGGGAAGGCTGTCTCTGGCCACTTGA
 AATGTCGCTGAAAAATGGATAAATCTAGATTGAAGGGCGTGCATACTCCTTGTTGTAAGTGCAGCGTTCACATTCACCAAGATCC
 CGGCTGAAACACTGCACGGGACAGTCACAGTGGAGGTACAGTACGCAGGGACAGATGGACCTTGCAAGGTTCCAGCTCAGAT
 GCGGTTGACATGCAAACTCTGACCCAGTTGGGAGGTTGATAACCGCTAACCCTGTAATCACTGAAAGCACTGAGAACTCTA
 AGATGATGCTGGAACCTGATCCACCATTGTTGGGACTCTTACATTGTCATAGGAGTGGGGGAGAAGAAGATCACCCACCACTGG
 CACAGGAGTGGCAGCACCATTTGAAAAGCATTGGAAGCCACTGTGAGAGGTGCCAAGAGAATGGCAGTCTTGGGAGACACA
 GCCTGGGACTTTGGATCAGTTGGAGGCGCTCTCAACTCATTGGGCAAGGGCATCCATCAAAATTTTGGAGCAGCTTTCAAATCA
 TTGTTTGGAGGAATGCTGCTGTTCTCACAATCTCATTGGAACGTTGCTGATGTGGTTGGGTCTGAACACAAAGAATGGATCT
 ATTTCCCTTATGTGCTTGGCCTTAGGGGGAGTGTGATCTTCTTATCCACAGCCGTCTCTGCTGATGTGGGGTGTCTGGTGGAC
 TTCTCAAAGAAGGAGACGAGATGCGGTACAGGGGTGTTGCTCTATAACGACGTTGAAGCCTGGAGGGACAGGTACAAGTACC
 ATCCTGACTCCCCCGTAGATTGGCAGCAGCAGTCAAGCAAGCCTGGGAAGATGGTATCTGCGGGATCTCTCTGTTTCAAGA
 ATGGAAAACATCATGTGGAGATCAGTAGAAGGGGAGCTCAACGCAATCCTGGAAGAGAATGGAGTTCAACTGACGGTCTGTTG
 TGGGATCTGTAAAAACCCCATGTGGAGAGGTCCACAGAGATTGCCGTGCTGTGAACGAGCTGCCCCACGGCTGGAAGGC
 TTGGGGGAAATCGTACTTCGTGACAGCAGCAAAAGACAAATAACAGCTTTGTCGTGGATGGTGACACACTGAAGGAATGCCCA
 CTCAAACATAGAGCATGGAACAGCTTTCTTGAGGAGTATGAGGTTGCGGGGATTTCACACTAGTGTCTGGCTCAAGGTTAG
 AGAAGATTATTCATTAGAGTGTGATCCAGCCGTTATTGGAACAGCTGTTAAGGGAAAGGAGGCTGTACACAGTGTCTAGGCT
 ACTGGATTGAGAGTGAGAAGAATGACACATGGAGGCTGAAGAGGGCCCATCTGATCGAGATGAAAACATGTGAATGGCCAA
 AGTCCACACATTGTGGACAGATGGAATAGAAGAGAGTGATCTGATCATACCCAAGTCTTAGCTGGGCCACTCAGCCATCAC
 AATACCAGAGAGGGCTACAGGACCCAAATGAAAGGGCCATGGCACAGTGAAGAGCTTGAAATTCGGTTTGAGGAATGCCCA
 GGCACTAAGGTCCACGTGGAGGAAAAATGTGGAACAAGAGGACCATCTCTGAGATCAACCACTGCAAGCGGAAGGGTGATC
 GAGGAATGGTGTGTCAGGGAGTGACAATGCCCCACTGTGCTTCCGGGTAAAGATGGCTGTTGGTATGGAATGGAGATAA
 GGCCACAGGAAAGAACAGAAAGCAACTTAGTAAGGTCAATGGTGACTGCAGGATCAACTGATCAGATGGACCACTTCTCCCTT
 GGAGTGTCTGTGATTCTGCTCATGGTGCAGGAAGGGCTGAAGAAGAGAATGACCACAAAGATCATCATAAGCACATCAATGG
 CAGTGTGGTAGCTATGATCCTGGGAGGATTTTCAATGAGTGACCTGGCTAAGCTTGCAATTTTGATGGGTGCCACCTTCGCG
 GAAATGAACACTGGAGGAGATGTAGCTCATCTGGCGTGATAGCGGCATTCAAAGTCAGACCAGCGTTGCTGGTATCTTTCAT
 CTTAGAGCTAATTGGACACCCCGTGAAGCATGCTGCTGGCCTTGGCCTGCTGCTTTTGCAAACTGCGATCTCCGCTTGGGA
 AGGCGACCTGATGTTCTCATCAATGGTTTTGCTTGGCCTGTTGGCAATACGAGCGATGGTTGTTCCACGCACTGATAACAT
 CACCTTGGCAATCCTGGCTGCTCTGACACCCTGGCCCGGGGCACACTGCTTGTGGCGTGGAGAGCAGGCCCTTGTACTTGGG

GGGGGTTTATGCTCCTCTCTCTGAAGGGAAAAGGCAGTGTGAAGAAGAACTTACCATTGTGTCATGGCCCTGGGACTAACCCT
 GTGAGGCTGGTCGACCCCATCAACGTGGTGGGACTGCTGTTGCTCACAAGGAGTGGGAAGCGGAGCTGGCCCCCTAGCGAA
 GTACTCACAGCTGTTGGCCTGATATGCGCATTGGCTGGAGGGTTGCGCAAGGCAGATATAGAGATGGCTGGGCCCATGGCCG
 CGGTGGTCTGCTAATTGTCAGTTACGTGGTCTCAGGAAAGAGTGTGGACATGTACATTGAAAGAGCAGGTGACATCACATG
 GGAAAAAGATGCGGAAGTCACTGGAAACAGTCCCCGGCTCGATGTGGCGCTAGATGAGAGTGGTGATTCTCCCTGGTGGAG
 GATGACGGTCCCCCATGAGAGAGATCATACTCAAGGTGGTCTGATGACCATCTGTGGCATGAACCAATAGCCATACCCTTT
 GCAGCTGGAGCGTGGTACGTATACGTGAAGACTGGAAAAAGGAGTGGTGTCTATGGGATGTGCCTGCTCCCAAGGAAGTAA
 AAAAGGGGGAGACCACAGATGGAGTGACAGAGTAATGACTCGTAGACTGCTAGGTTCAACACAAGTTGGAGTGGGAGTTA
 TGCAAGAGGGGGTCTTTCACACTATGTGGCACGTCAAAAAGGATCCGCGCTGAGAAGCGGTGAAGGGAGACTTGATCCATA
 CTGGGGAGATGTCAAGCAGGATCTGGTGTCTACTGTGGTCCATGGAAGCTAGATGCCGCTGGGACGGGCACAGCGAGGT
 GCAGCTCTTGGCCGTGCCCCCGGAGAGAGAGCGAGGAACATCCAGACTCTGCCCGGAATATTTAAGACAAAGGATGGGGAC
 ATTGGAGCGGTTGCGCTGGATTACCCAGCAGGAACCTCAGGATCTCCAATCCTAGACAAGTGTGGGAGAGTGATAGGACTTTA
 TGGCAATGGGGTCTGATCAAAAATGGGAGTTATGTTAGTGCCATCACCAAGGGAGGAGGGAGGAAGAGACTCCTGTTGA
 GTGCTTCGAGCCTTCGATGCTGAAGAAGAAGCAGCTAACTGTCTTAGACTTGATCCTGGAGCTGGGAAAACCAGGAGAGTTC
 TTCTGAAATAGTCCGTGAAGCCATAAAAACAAGACTCCGTACTGTGATCTTAGCTCCAACCAGGGTTGTGCTGCTGAAATGG
 AGGAGGCCCTTAGAGGGCTTCCAGTGCCTTATATGACAACAGCAGTCAATGTACCCACTCTGGAACAGAAATCGTCGACTTA
 ATGTGCCATGCCACCTTCACTTCACGTCTACTACAGCCAATCAGAGTCCCCAACTATAATCTGTATATTATGGATGAGGCCCACT
 TCACAGATCCCTCAAGTATAGCAGCAAGAGGATACATTTCAACAAGGGTTGAGATGGGCGAGGCGGCTGCCATCTTCATGACC
 GCCACGCCACCAGGAACCCGTGACGCATTTCCGACTCCAACCTACCAATTATGGACACCGAAGTGGAGTCCCAGAGAGAGC
 CTGGAGCTCAGGCTTTGATTGGGTGACGGATCATTCTGGA AAAACAGTTTGGTTTGTCCAAGCGTGAGGAACGGCAATGAG
 ATCGCAGCTTGTCTGACAAAGGCTGGAAAACGGGTATACAGCTCAGCAGAAAGACTTTTGAGACAGAGTTCCAGAAAACAA
 AACATCAAGAGTGGGACTTTGTGCTGACAACCTGACATTTAGAGATGGGCGCAACTTTAAAGCTGACCGTGTATAGATTCC
 AGGAGATGCCTAAAGCCGGTCATACTTGATGGCGAGAGAGTCATTCTGGCTGGACCCATGCCTGTACACATGCCAGCGCTGC
 CCAGAGGAGGGGGCGCATAGGCAGGAATCCCAACAAACCTGGAGATGAGTATCTGTATGGAGGTGGGTGCGCAGAGACTGA
 CGAAGACCATGCACACTGGCTTGAAGCAAGAATGCTCCTTGACAATATTTACCTCCAAGATGGCCTCATAGCCTCGCTCTATCG
 ACCTGAGGCCGACAAAGTAGCAGCCATTGAGGGAGAGTTCAAGCTTAGGACGAGCAAGGAGAACCTTTGTGGAACCTATG
 AAAAGAGGAGATCTTCTGTTTGGCTGGCCTATCAGGTTGCATCTGCCGGAATAACCTACACAGATAGAAGATGGTGCTTTGA
 TGGCACGACCAACAACACCATAATGGAAAGACAGTGTGCCGCGAGAGGTGTGGACCAGACACGGAGAGAAAAGAGTGTCAA
 ACCGAGGTGGATGGACGCCAGAGTTTGTTCAGATCATGCGGCCCTGAAGTCATTCAAGGAGTTTGCCGCTGGGAAAAGAGGA
 GCGGCTTTTGGAGTGATGGAAGCCCTGGGAACACTGCCAGGACACATGACAGAGAGATTCCAGGAAGCCATTGACAACCTCG
 CTGTGCTCATGCGGGCAGAGACTGGAAGCAGGCCCTTACAAAGCCGCGCGGCCCAATTGCCGAGACCTTAGAGACCATTAT
 GCTTTTGGGGTTGCTGGGAACAGTCTCGCTGGGAATCTTCTCTGCTTGATGAGGAACAAGGGCATAGGGAAGATGGGCTTT
 GGAATGGTGACTCTTGGGGCCAGCGCATGGCTCATGTGGCTCTCGGAAATTGAGCCAGCCAGAATTGCATGTGTCTCATTGT
 TGTGTTTCTATTGCTGGTGGTGCTCATACCTGAGCCAGAAAAGCAAGATCTCCCCAGGACAACCAAATGGCAATCATCATCAT
 GGTAGCAGTAGGTCTTCTGGGCTTGATTACCGCCAATGAACTCGGATGGTTGGAGAGAACAAGAGTGACCTAAGCCATCTA
 ATGGGAAGGAGAGAGGAGGGGGCAACCATAGGATTCTCAATGGACATTGACCTGCGGCCAGCCTCAGCTTGGGCCATCTATG
 CTGCCCTTGACAACCTTCAATTACCCAGCCGTCCAACATGCACTGACCACTTCATACAACAATACTCCTTAATGGCGATGGCCAC
 GCAAGCTGGAGTGTTGTTTGGTATGGGCAAGGGATGCCATTCTACGCATGGGACTTTGGAGTCCCGCTGCTAATGATAGGTT
 GCTACTACAATTAACACCCCTGACCCTAATAGTGGCCATCATTTTGCTCGTGGCGCACTACATGTACTTGATCCCAGGGCTGCA
 GGCAGCAGCTGCGCGTGCTGCCAGAAGAGAACGGCAGCTGGCATCATGAAGAACCCTGTTGTGGATGGAATAGTGGTGACT
 GACATTGACACAATGACAATTGACCCCCAAGTGGAGAAAAAGATGGGACAGGTGCTACTCATAGCAGTAGCCGTCTCCAGCG
 CCATACTGTGCGGACCGCCTGGGGTGGGGGGAGGCTGGGGCCCTGATCACAGCCGCAACTTCCACTTTGTGGGAAGGCTC
 TCCGAACAAGTACTGGAACCTCTACAGCCACTTCACTGTGTAACTTTTAAAGGGAAAGTTACTTGGCTGGAGCTTCTCTAATC
 TACACAGTAACAAGAAACGCTGGCTTGGTCAAGAGACGTGGGGGTGGAACAGGAGAGACCCTGGGAGAGAAATGGAAGGC
 CCGCTTGAACCAAGATGTGCGCCCTGGAGTTCTACTCTACAAAAAGTCAGGCATCACCGAGGTGTGCAGAGAAGAGGCCCGC
 CGCGCCCTCAAGGACGGTGTGGCAACGGGAGGCCATGCTGTGTCCCGAGGAAGTGCAAGCTGAGATGGTTGGTGGAGCGG

PAT022-EP-PR

GGATACCTGCAGCCCTATGGAAAGGTCATTGATCTTGGATGTGGCAGAGGGGGCTGGAGTTACTACGCCGCCACCATCCGCA
AAGTTCAAGAAGTGAAAGGATACACAAAAGGAGGCCCTGGTCATGAAGAACCCGTGTTGGTGCAAAGCTATGGGTGGAACAT
AGTCCGCTTAAGAGTGGGGTGGACGTCTTTCATATGGCGGCTGAGCCGTGTGACACGTTGCTGTGTGACATAGGTGAGTCAT
CATCTAGTCCTGAAGTGGAAGAAGCACGGACGCTCAGAGTCCTCTCCATGGTGGGGGATTGGCTTGAAAAAGACCAGGAGC
CTTTGTATAAAGGTGTTGTGCCATACACCAGCACTATGATGGAAACCCCTGGAGCGACTGCAGCGTAGGTATGGGGGAGGA
CTGGTCAGAGTGGCACTCTCCCGCAACTCTACACATGAGATGTATTGGGTCTCTGGAGCGAAAAGCAACACCATAAAAAAGTGT
GTCCACCACGAGCCAGCTCCTCTTGGGGCGCATGGACGGGCCTAGGAGGCCAGTGAAATATGAGGAGGATGTGAATCTCGGC
TCTGGCACGCGGGCTGTGGTAAGCTGCGCTGAAGCTCCCAACATGAAGATCATTGGTAACCGCATTGAAAGGATCCG CAGTG
AGCACGCGGAAACGTGGTTCTTTGACGAGAACCACCCATATAGGACATGGGCTTACCATGGAAGCTATGAGGCCCCACACAA
GGGTGAGCGTCTCTCTAATAAACGGGGTTGTCAGGCTCTGTCAAAACCCCTGGGATGTGGTGACTGGAGTCACAGGAATAGC
CATGACCGACACCACACCGTATGGTCAGCAAAGAGTTTCAAGGAAAAAGTGGACACTAGGGTGCCAGACCCCAAGAAGGC
ACTCGTCAGGTTATGAGCATGGTCTCTTCTGGTTGTGAAAGAGCTAGGCCAAACACAAACGCCACGAGTCTGTACCAAAGA
AGAGTTTCATCAACAAGTTCTGATCAATGCAGCATTAGGGGCAATATTTGAAGAGGAAAAAGAGTGGAAAGACTGCAGTGGGA
AGCTGTGAACGATCCAAGTTCTGGGCTCTAGTGGATAAGGAAAGAGAGCACCACCTGAGAGGAGAGTGCCAGAGTTGTGT
GTACAACATGATGGGAAAAAGAGAAAAGAAACAAGGGGAATTTGGAAAGGCCAAGGGCAGCCGCGCCATCTGGTATATGTG
GCTAGGGGCTAGATTTCTAGAGTTCGAAGCCCTTGATTCTTGAACGAGGATCACTGGATGGGGAGAGAGAACTCAGGAGGT
GGTGTGAAGGGCTGGGATTACAAAGACTCGGATATGTCTAGAAAGAGATGAGTCGTATACCAGGAGGAAGGATGTATGCA
GATGACACTGCTGGCTGGGACACCCGCATCAGCAGGTTTGATCTGGAGAATGAAGCTCTAATCACCAACCAATGGAAAAAG
GGCACAGGGCCCTTGGCATTGGCCATAATCAAGTACACATACCAAAACAAAGTGGTAAAGGTCCTTAGACCAGCTGAAAAAGG
GAAAACAGTTATGGACATTATTCGAGACAAGACCAAGGGGGAGCGGACAAGTTGTCACCTACGCTCTTAACACATTTACCA
ACCTAGTGGTGCAACTCATTGGGAATATGGAGGCTGAGGAAGTTCTAGAGATGCAAGACTTGTGGCTGTGCGGAGGTGAGA
GAAAGTGACCAACTGGTTGCAGAGCAACGGATGGGATAGGCTCAAACGAATGGCAGTCAGTGGAGATGATTGCGTTGTGAA
GCCAATTGATGATAGGTTTGACATGCCCTCAGGTTCTTGAATGATATGGGAAAAGTTAGGAAGGACACACAAGAGTGGAAA
CCCTCAACTGGATGGGACAACCTGGGAAGAGTTCCGTTTGTCTCCACCCTTCAACAAGCTCCATCTCAAGGACGGGAGGTC
CATTGTGGTTCCCTGCCGCCACCAAGATGAAGTGAAGTGGCCGGGGCCCGCTCTCTCCAGGGGCGGGATGGAGCATCCGGGAG
ACTGCTTGCTAGCAAAATCATATGCGCAAATGTGGCAGCTCCTTTATTTCCACAGAAGGGACCTCCGACTGATGGCCAATGCC
ATTTGTTATCTGTGCCAGTTGACTGGGTTCCAAGTGGGAGAACTACCTGGTCAATCCATGGAAAGGGAGAATGGATGACCAC
TGAAGACATGCTTGTGGTGTGGAACAGAGTGTGGATTGAGGAGAACGACCACATGGAAGACAAGACCCCGATTACGAAATG
GACAGACATCCCTATTTGGGAAAAAGGGAAGACTTGTGGTGTGGATCTCTCATAGGGCACAGACCGCGCACCACTCTGGCT
GAGAACATTAACACAGTCAACATGGTGCGCAGGATCATAGGTGATGAAGAAAAGTACATGGACTACCTATCCACCAAG
TTCGCTACTTGGGTGAAGAAGGGTCTACACCTGGAGTGTGTAAAGCACCAGTCTTAATGTTGTGAGGCTGCTAGTCAGCCAC
AGCTTGGGGAAGCTGTGCAGCCTGTGACCCCCCAGGAGAAGCTGGGAAACCAAGCCTATAGTCAGGCCGAGAACGCCATG
GCACGGAAGAAGCCATGCTGCCTGTGAGCCCCCTCAGAGGACACTGAGTCAAAAAACCCACGCGCTTGGAGGCGCAGGATG
GGAAAAGAAGGTGGCGACCTTCCCACCTTCAATCTGGGGCTGAAGTGGAGATCAGCTGTGGATCTCCAGAAGAGGGACT
AGTGGTTAGAGGAG

KU744693.1 Zika virus isolate VE_Ganxian, China, complete genome (SEQ ID NO: 10)

GTTGTTACTGTTGCTGACTCAGACTGCGACAGTTCGAGTTTGAAGCGAAAGCTAGCAACAGTATCAACAGGTTTATTTGGATT
TGGAAACGAGAGTTTCTGGTCATGAAAAACCAAAAAAGAAATCCGGAGGATTCCGGATTGTCAATATGCTAAACCGGGAG
TAGCCCGTGTGAGCCCCCTTGGGGGCTTGAAGAGGCTGCCAGCCGACTTCTGCTGGGTGATGGGCCCATCAGGATGGTCTTG
GCAATTCTAGCCTTTTTGAGATTCACGGCAATCAAGCCATCACTGGGTCTCATCAATAGATGGGGTTCAAGTGGGGAAAAAGA
TGCTATGGAATAATAAAGAAGTTCAAGAAAGATCTGGCTGCCATGCTGAGAATAATCAATGCTAGGAAGGAGAAGAAGAGA
CGAGGCGCAGATACTAGTGTGGAATTGTTGGCCTCTGCTGACCACAGCTATGGCAGCGGAGGTCACTAGACGTGGGAGTG

CATACTATATGTACTTGGACAGAAACGATGCTGGGGAGGCCATATCTTTCCAACCACATTGGGGATGAATAAGTGTATATAC
 AGATCATGGATCTTGGACACATGTGTGATGCCACCATGAGCTATGAATGCCCTATGCTGGATGAGGGGGTGAACCAGATGA
 CGTCGATTGTTGGTGCAACACGACGTCAACTTGGGTTGTACGGAACCTGCCATCACAAAAAGGTGAAGCACGGAGATCTA
 GAAGAGCTGTGACGCTCCCTTCCATTCCACTAGGAAGCTGCAAACGCGTGC AAAACCTGGTTGGAATCAAGAGAATACACA
 AAGCACTTGATTAGAGTCGAAAATTGGATATTAGGAACCTGGCTTCGCGTTAGCAGCAGCTGCCATCGCTTGGCTTTGGG
 AAGCTCAACGAGCCAAAAAGTCATATACTTGGTCATGATACTGCTGATTGCCCCGGCATACAGCATCAGGTGCATAGGAGTCA
 GCAATAGGGACTTTGTGGAAGGTATGTCAGGTGGGACTTGGGTTGATGTTGCTTGGAACATGGAGGTTGTGTACCGCAAT
 GGCACAGGACAAACCGACTGTCGACATAGAGCTGGTTACAACAACAGTCAGCAACATGGCGGAGGTAAGATCTACTGCTAT
 GAGGCATCAATATCAGACATGGCTTCGGACAGCCGCTGCCAACACAAGGTGAAGCCTACCTTGACAAGCAATCAGACACTCA
 ATATGTTTGCAAAAGAACGTTAGTGGACAGAGGCTGGGGAATGGATGTGGACTTTTGGCAAAGGGAGTCTGGTGACATGC
 GCTAAGTTTGCATGCTCCAAGAAAATGACCGGGAAGAGCATCCAGCCAGAGAATCTGGAGTACCGGATAATGCTGTCAAGTTC
 ATGGCTCCAGCACAGTGGGATGCTCGTTAATGACACAGGACATGAACTGATGAGAATAGAGCGAAGGTTGAGATAACGCC
 CAATTCACCAAGAGCCGAAGCCACCCTGGGGGTTTTGGAAGCCTAGGACTTGATTGTGAACCGAGGACAGGCCTTGACTTTT
 CAGATTTGTATTACTTGACTATGAATAACAAGCACTGGTTGGCTCACAAGGAGTGGTTCCACGACATTCCATTACCTTGGCAG
 CTGGGGCAGCCACCGGAACCTCCACTGGAACAACAAGAACGACTGGTAGAGTTCAAGGACGCACATGCCAAAAGGCCAAAC
 TGTCGTGGTTCTAGGGAGTCAAGAAGGAGCAGTTCACACGGCCCTTGCTGGAGCTCTGGAGGCTGAGATGGATGGTGCAAAG
 GGAAGGCTGTCTCTGGCCACTTGAAATGTCGCTGAAAATGGATAAATTAGATTGAAGGGCGTGTCACTCCTTGTTGTAC
 CGCAGCGTTCACATTACCAAGATCCCGGCTGAAACAGTGGACGGGACAGTCACAGTGGAGGGACAGTACGGAGGGACAGA
 TGGACCTTGCAAGGTTCCAGCTCAGATGGCGGTGGACATGCAGACTCTGACCCAGTTGGGAGGTTGATAACCGCTAACCCCG
 TAATCACTGAAAGCACTGAGAAGCTAAGATGATGCTGGAACCTTGATCCACCTTTGGGGACTTTACATTGTCATAGGAGTGC
 GGGAGAAGAAGATCAACCACTGGCACAGGAGTGGCAGCACCATTGAAAAGCATTGAAAGCACTGTGAGAGGTGCCA
 AGAGAATGGCAGTCTTGGGAGACACAGCCTGGGACTTTGGATCAGTTGGAGGCGCTCTCACTCATTGGGCAAGGGCATCCA
 TCAAATTATTGGAGCAGCTTCAAATCATTGTTGGAGGAATGTCCTGGTTCTCACAATTCTCATTGGGACGTTGCTGATGTG
 GTTGGGTCTGAACACAAGAATGGATCTATTTCCCTTATGTGCTTGGCCTTAGGGGGAGTGTGATCTTCTTATCCACAGCCGT
 CTCAGGTGGTGTGGGGTGCTCGGTGGACTTCTCAAAGAAGGAGACGAGATGCGGTACAGGGGTGTTCTGTATAACGATGTT
 GAAGCCTGGAGGGACAGGTACAAGTACCATCCTGACTCCCCCGTAGATTGGCAGCAGCAGTCAAGCAAGCCTGGGAAGATG
 GTATCTGCGGGATCTCCTCTGTTTCAAGAATGGAACATCATGTGGAGATCAGTAGAAGGGGAGCTCAACGCAATCCTGGAA
 GAGAATGGAGTTCAACTGACGGTCGTTGTGGGATCTGTA AAAAACCCCATGTGGAGAGGTCCACAGAGATTGCCGTCGCTG
 TGAACGAGCTGCCCCACGGCTGGAAGGCTTGGGGGAATCGTACTTCGTCAGAGCAGCAAAGACAAATAACAGCTTTGTCTG
 GGATGGTGACACACTGAAGGAATGCCACTCAAACATAGAGCATGGAACAGCTTTCTGTGGAGGATCATGGGTTCCGGGTA
 TTTCACTAGTGTCTGGCTCAAGGTTAGAGAAGACTATTGGTTAGAGTGTGATCCAGCCGTTATTGGAACAGCTGTTAAGGG
 AAAGGAGGCTGTACACAGTGTCTAGGCTACTGGATTGAGAGTGAGAAGAATGACACATGGTGGCTGAAGAGGGCCCATCT
 GATCGAGATGAAAACATGTGAATGGCCAAAGTCCACACATTGTGGACAGATGGAATAGAAGAGAGTGATCTGATCATACCC
 AAGTCTTTAGCTGGGCCACTCAGCCATCACAATGCCAGAGAGGGCTACAGGACCCAAATGAAAGGGCCATGGCACAGTGAAG
 AGCTTGAAATTGCGTTTGAGGAATGCCAGGCACTAAGGTCCACGTGGAGGAAACATGTGGAACAAGAGGACCATCTCTGAG
 ATCAACCACTGCAAGCGGAAGGGTGATCGAGGAATGGTCTCAGGGAGTGCACAATGCCCCACTGTCTTCCAGGCTAAA
 GATGGCTGTTGGTATGGAATGGAGATAAGGCCAGGAAGAACCAGAAAGCAACTTAGTAAGGTCAATGGTGAETGCAGGA
 TCAACTGATCAGATGGATCACTTCTCCCTTGGAGTGCTTGTGATTCTGCTCATGGTGCAGGAAGGGCTGAAGAAGAGAATGAC
 CACAAAGATCATATAAGCACATCAATGGCAGTGCTGGTAGCTATGATCCTGGGAGGATTTTCAATGAGTGACCTGGCTAAGC
 TTGCAATTTTGATGGGTGCCACCTTCGCGGAAATGAACACTGGAGGAGATGTAGCTCATCTGGCGCTGATAGCGGCATTCAA
 GTCAGACCAGCGTTGCTGGTATCTTTCTCTCAGAGCTAATTGGACACCCCGTGAAGCATGCTGCTGGCCTTGGCCTCGTGT
 CTTTGGCAAACCTGCGATCTCCGCTTGGAAAGGCGACCTGATGGTTCTCATCAATGGTTTGGCTTTGGCCTGGTTGGCAATACGA
 GCGATGGTTGTTCCACGCACTGATAACATCACCTTAGCAATCTGGCTGCTCTGACACCACTGGCCGGGGCACACTGCTTGTG
 GCGTGGAGAGCAGGCTTGTACTTGGGGGGGTTTATGCTCTCTCTCTGAAGGGAAAAGGCAGTGTGAAGAAGAACTTAC
 CATTTGTCATGGCCCTGGGACTAACCGCTGTGAGGCTGGTCGACCCCATCAACGTGGTGGGACTGCTGTTGCTCACAAGGAGT
 GGGGAAGCGGAGCTGGCCCCCTAGCGAAGTACTCACAGCTGTTGGCTGATATGCGCATTGGCTGGAGGGTTCCGAAGGCAG

ATATAGAGATGGCTGGGCCCATGGCCGCGGTGCGTCTGCTAATTGTGAGTTACGTGGTCTCAGGAAAGAGTGTGGACATGTA
 CATTGAAAGAGCAGGTGACATCACATGGGAAAAAGATGCGGAAGTCACTGGAAACAGTCCCCGGCTCGATGTGGCGCTAGAT
 GAGAGTGGTGATTTCTCCCTGGTGGAGGATGACGGTCCCCCATGAGAGAGATCATACTCAAGGTGGTCTGATGACCATCTG
 TGGCATGAACCAATAGCCATACCTTTGCAGCTGGAGCGTGGTACGTATACGTGAAGACTGGAAAAAGGAGTGGTGTCTAT
 GGGATGTGCTGCTCCCAAGGAAGTAAAAAGGGGGAGACCACAGATGGAGTGTACAGAGTAATGACTCGCAGACTGCTAG
 GTTCAACACAAGTTGGAGTGGGAGTTATGCAAGAGGGGGTCTTTCACACTATGTGGCACGTCACAAAAGGATCCGCGCTGAG
 AAGCGGTGAAGGGAGACTTGATCCATACTGGGGAGATGTCAAGCAGGATCTGGTGTCTACTGTGGTCCATGGAAGCTAGAT
 GCCGCTGGGACGGGCACAGCGAGGTGCAGCTCTTGGCCGTGCCCCCGGAGAGAGAGCGAGGAACATCCAGACTCTGCCC
 GGAATATTTAAGACAAAGGATGGGGACATTGGAGCGGTGCACTGGATTACCCAGCAGGAACCTCAGGATCTCCAATCCTAG
 ACAAGTGTGGGAGAGTGATAGGACTTTATGGCAATGGGGTCTGTATCAAAAATGGGAGTTATGTTAGTGCCATCACCAAGG
 GAGGAGGGAGGAAGAGACTCCTGTTGAGTGCTTCGAGCCTTCGATGCTGAAGAAGAAGCAGCTAACTGTCTTAGACTTGAT
 CCTGGAGCTGGGAAAACAGGAGAGTCTTCTGAAATAGTCCGTGAAGCCATAAAAAACAAGACTCCGTACTGTGATCTTGGC
 TCCAACAGGGTTGTGCTGCTGAAATGGAGGAGGCCCTTAGAGGGCTTCCAGTGCGTTATATGACAACAGCAGTCAATGTCA
 CCCACTCTGGAACAGAAATCGTCGACTTAATGTGCCATGCCACCTTCACTTCACGTCTACTACAGCCAATTAGAGTCCCCAACTA
 TAATCTGTATATTATGGATGAGGCCCACTTCACAGATCCCTCAAGTATAGCAGCAAGAGGATACATTTCAACAAGGGTTGAGA
 TGGGCGAGGCGGCTGCCATCTTCATGACCGCCACGCCACAGGAACCGTGACGCATTTCCGACTCCAACCTACCAATTATG
 GACACCGAAGTGGAAGTCCAGAGAGAGCCTGGAGCTCAGGCTTTGATTGGGTGACGGAGTATCTGGAAAAACAGTTTGGT
 TTGTTCCACGCGTGAGGAACGGCAATGAGATCGCAGCTTGTCTGACAAAGGCTGGAAAACGGGTCTACAGCTCAGCAGAAA
 GACTTTTGAGACAGAGTTCCAGAAAAACAAACATCAAGAGTGGGACTTTGTCTGACAACTGACATTTCCAGAGATGGGCGCCA
 ACTTTAAAGCTGACCGTGTCTAGATTCCAGGAGATGCCTAAAGCCGGTCTACTTGGTGGCGAGAGAGTATTCTGGCTGGA
 CCCATGCTGTACACATGCCAGCGCTGCCAGAGGAGGGGGCGCATAGGCAGGAATCCCAACAAACCTGGAGATGAGTATC
 TGTATGGAGGTGGGTGCGCAGAGACTGACGAAGACCATGCACACTGGCTTGAAGCAAGAATGCTCCTTGACAATATTTACCTC
 CAAGATGGCTCATAGCCTCGCTCTATCGACCTGAGGCCGACAAAGTAGCAGCCATTGAGGGAGAGTTCAAGCTTAGGACGG
 AGCAAAGGAAGACCTTTGTGGAACCTCATGAAAAGAGGAGATCTTCTGTTTGGCTGGCCTATCAGGTTGCATCTGCCGGAATA
 ACCTACACAGATAGAAGATGGTGCTTGTATGGCAGCAGCAACACCATTAATGGAAGACAGTGTGCCGGCAGAGGTGTGGA
 CCAGACACGGAGAGAAAAGAGTGCTCAAACCGAGGTGGATGGACGCCAGAGTTTGTTCAGATCATGCGGCCCTGAAGTCATT
 CAAGGAGTTTGCCGCTGGGAAAAGAGGAGCGGCTTTTGGAGTGATGGAAGCCCTGGGAACACTGCCAGGACACATGACAGA
 GAGATTCCAGGAAGCCATTGACAACCTCGCTGTGCTCATGCGGGCAGAGACTGGAAGCAGGCCCTACAAAGCCGCGGCGGCC
 CAATTGCCGGAGACCCTAGAGACCATTATGCTTTTGGGGTGTCTGGGAACAGTCTCGCTGGGAATCTTTTCTGCTTGATGAGG
 AACAAGGGCATAGGGAAGATGGGCTTTGGAATGGTGACTCTTGGGGCCAGCGCATGGCTCATGTGGCTCTCGGAAATTGAGC
 CAGCCAGAATTGCATGTGCTCTATTGTTGTGTTCTATTGCTGGTGGTCTCATACCTGAGCCAGAAAAGCAAAGATCTCCCC
 AGGACAACCAATGGCCATCATCATGTTAGCAGTAGGTCTTCTGGGCTTGATTACCGCCAATGAACTCGGATGTTGGAG
 AGAACAAAGAGTGACCTAAGCCATCTAATGGGAAGGAGAGAGGAGGGGGCAACCATGGGATTCTAATGGACATTGACCTG
 CGGCCAGCCTCAGCTTGGGCCATCTATCCTGCCCTGACATCTTTCATTACCCAGCCGTCCAACATGCAGTGACCACTTCATACA
 ACAACTACTCCTTAATGGCGATGGCCACGCAAGCTGGAGTGTGTTTGGTATGGGCAAAGGGATGCCATTCTACGCATGGGAC
 TTTGGAGTCCCGCTGCTAATGATAGGTTGCTACTCACAATTAACGCCCTGACCTAATAGTGGCCATCATTTTCTGCTGGCG
 CACTACATGTACTTGATCCCAGGGCTGCAGGCAGCAGCTGCGCGTGTGCCCAGAAGAGAACGGCAGCTGGCATCATGAAGA
 ACCCTGTTGTGGAGGGAATAGTGGTGACTGACATTGACACAATGACAATTGACCCCAAGTGGAGAAAAAGATGGGACAGGT
 GCTACTCATGGCAGTAGCCGTCTCCAGCGCCATACTGTGAGGACCGCTGGGGGTGGGGGGAGGCTGGGGGCCCTGATCACA
 GCCGCAACTTCCACTTTGTGGGAAGGCTCTCCGAACAAGTACTGGAACCTCTCTACAGCCACCTCACTGTGTAACATTTTAGG
 GGAAGTTACTTGGCTGGAGCTTCTAATCTACACAGTAACAAGAACGCTGGCTTGGTCAAGAGACGTGGGGGTGGAACAG
 GAGAGACCCTGGGAGAGAAATGGAAGGCCGCTTGAACCAGATGTGGCCCTGGAGTTCTACTCTACAAAAAGTCAGGCAT
 CACCGAGGTGTGCAGAGAAGAGGCCCGCGCCCTCAAGGACGGTGTGGCAACGGGAGGCCATGCTGTGTCCCGAGGAAG
 TGCAAAGCTGAGATGGTTGGTGGAGCGGGGATACCTGCAGCCCTATGGAAAGGTCAATGATCTGGATGTGGCAGAGGGGG
 CTGGAGTTACTACGCCGCCACCATCCGCAAAGTTCAAGAAAGTGAAGGATACACAAAAGGAGGCCCTGGTCAAGAAACCC
 GTGTTGGTGCAAAGCTATGGGTGGAACATAGTCCGTCTTAAGAGTGGGGTGGACGCTTTCATATGGCGGCTGAGCCGTGTG

ACACGTTGCTGTGTGACATAGGTGAGTCATCATCTAGTCCTGAAGTGAAGAAGCACGGACGCTCAGAGTCCTCTCCATGGTG
 GGGGATTGGCTTGAAAAAGACCAGGAGCCTTTTGTATAAAAGTGTGTGCCCATACACCAGCACTATGATGGAAACCTGGA
 GCGACTGCAGCGTAGGTATGGGGGAGGACTGGTCAGAGTGCCACTCTCCCGCAACTCTACACATGAGATGTACTGGGTCTCT
 GGAGCGAAAAGCAACACCATAAAAAGTGTGTCCACCACGAGCCAGCTCCTCTTGGGGCGCATGGACGGGCCTAGGAGGCCA
 GTGAAATATGAGGAGGATGTGAATCTCGGCTCTGGCACGCGGGCTGTGGTAAGCTGCGCTGAAGCTCCCAACATGAAGATCA
 TTGGTAACCGCATTGAAAGGATCCGCGCTGAGAAAGCGGAAACGTGGTCTTTGACGAGAACCACCCATATAGGACATGGGC
 TTACCATGGAAGCTATGATGCCGCCACACAAGGGTCAGCGTCCTCTCTAATAAACGGGGTTGTCAAGGCTCCTGTCAAAACCT
 GGGATGTGGTGACTGGAGTCACAGGAATAGCCATGACCGACACACACCGTATGGTCAGCAAAGAGTTTCAAGGAAAAAGT
 GGACACTAGGGTGCCAGACCCCCAAGAAGGCACTCGTCAGGTTATGAGCATGGTCTCTTCTGGTTGTGGAAAGAGCTAGGC
 AAACACAAACGGCCACGAGTCTGTACCAAAGAAGAGTTCATCAACAAGGTTCTGTAGCAATGCAGCATTAGGGGCAATATTGA
 AGAGGAAAAAGAGTGGAAGACTGCAGTGGAAGCTGTGAACGATCCAAGGTTCTGGGCTCTAGTGGACAAGGAAAGAGAGCA
 CCACCTGAGAGGAGAGTGCCAGAGTTGTGTGTACATCACAATGGGAAAAAGAGAAAAACAAGGGGAATTTGAAAGGC
 CAAGGGCAGCGCGCCATCTGGTATATGTGGCTAGGGGCTAGATTCTAGAGTTTGAAGCCCTTGGATTCTTGAACGAGGATC
 ACTGGATGGGAGAGAGAACTCAGGAGGTGGTGTGAAGGGCTGGGATTACAAAGACTCGGATATGTCCTAGAAGAGATGA
 GTCGCATACCAGGAGGAAGGATGTATGCAGATGACACTGCTGGCTGGGACACCCGCATCAGCAGGTTTGTCTGGAGAATGA
 AGCTCTAATCACCAACCAATGGAGAAAGGGCACAGGGCCTTGGCATTGGCCATAATCAAGTACACATACCAAAACAAAGTG
 GTAAAGGTCTTAGACCAGCTGAAAAAGGGAAGACAGTTATGGACATTATTTGAGACAAGACCAAAGGGGGAGCGGACAA
 GTTGTCACTTACGCTCTCAACACATTTACCAACCTAGTGGTGCAACTCATTGGGAATATGGAGGCTGAGGAAGTTCTAGAGATG
 CAAGACTTGTGGCTGCTGCGGAGGTGAGAGAAAGTGACCAACTGGTTGCAGAGCAACGGATGGGATAGGCTCAAACGAATG
 GCGGTCACTGGAGATGATTGCGTTGTGAAACCAATTGATGATAGGTTTGCACATGCCCTCAGGTTCTTGAATGATATGGGAAA
 AGTTAGGAAGGACACACAAGAGTGGAACCCCTCAACTGGATGGGACAACTGGGAAGAAGTTCCCTTCTGCTCCCACCACTTCA
 ACAAGCTCCATCTCAAGGACGGGAGGTCCATTGTGTTCCCTGCCGCCACCAAGATGAAGTATTGGCCGGGCCCGCTCTCT
 CCAGGGGCGGGATGGAGCATCCGGGAGACTGCTTGCCTAGCAAAATCATATGCGCAAAATGTGGCAGCTCCTTTATTTCCACAG
 AAGGGACCTCCGACTGATGGCCAATGCCATTTGTTTATCTGTGCCAGTTGACTGGGTTCCAAGTGGGAGAACTACCTGGTCAAT
 CCATGGAAAGGGAGAATGGATGACCACTGAAGACATGCTTGTGGCGTGGAACAGAGTGTGGATTGAGGAGAACGACCACAT
 GGAAGACAAGACCCAGTCACGAAATGGACAGACATTCCCTATTTGGGAAAAAGGGAAAGACTTGTGGTGTGGATCTCTCATA
 GGGCACAGACCGCGCACCACTGGGCTGAGAACATTAACACAGTCAACATGGTGCGCAGGATCATAGGTGATGAAGAAA
 AGTACATGGACTACCTATCCACCCAAGTTCGCTACTTGGGTGAAGAAGGGTCTACACCTGGAGTGCTGTAAAGCACCAATCTTA
 ATGTTGTGAGGCCTGCTAGTCAGCCACAGCTTGGGGAAAGCTGTGCAGCCTGTGACCCCCCAGGAGAAGCTGGGAAACCAA
 GCCTATAGTCAGGCCGAGAACGCCATGGCACGGAAGAAGCCATGCTGCCTGTGAGCCCCCAGAGGACACTGAGTCAAAAAA
 CCCACGCGCTTGGAGGCGCAGGATGGGAAAAAGAGTGGCGACCTTCCCCACCCTTCAATCTGGGGCCTGAACTGGAGATC
 AGCTGTGGATCTCCAGAAGAGGGACTAGTGGTTAGAGGAGA

LC002520.1 Zika virus genomic RNA, strain: MR766-NIID, Uganda, complete genome (SEQ ID NO: 11)

AGTTGTTGATCTGTGTGAGTCAGACTGCGACAGTTCGAGTCTGAAGCGAGAGCTAACAACAGTATCAACAGGTTAATTGGAA
 TTTGGAAACGAGAGTTTCTGGTCATGAAAAACCAAGAAGAAATCCGGAGGATTCCGGATTGTCAATATGCTAAAACGCGG
 AGTAGCCCGTGTAACCCCTTGGGAGGTTTGAAGAGGTTGCCAGCCGACTTCTGCTGGGTGATGGACCCATCAGAATGGTTT
 TGGCGATACTAGCCTTTTGTAGATTACAGCAATCAAGCCATCACTGGGCTTATCAACAGATGGGGTTCCGTGGGGAAAAAA
 GAGGCTATGGAAATAATAAAGAAGTTCAAGAAAGATCTGCTGCCATGTTGAGAATAATCAATGTAGGAAAGAGAGGAAGA
 GACGTGGCGCAGACACCAGCATCGGAATCATTGGCCTCTGCTGACTACAGCCATGGCAGCAGAGATCACTAGACGCGGGAG
 TGCATACTACATGTACTTGGATAGGAGCGATGCCGGGAAGGCCATTTGTTTGTACCACATTGGGAGTGAACAAGTGCCACG
 TACAGATCATGGACCTCGGGCACATGTGTGACGCCACCATGAGTTATGAGTGCCCTATGCTGGATGAGGGAGTGGAAACCAGA
 TGATGTGCGATTGCTGGTGCAACACGACATCAACTTGGGTTGTGTACGGAACTGTGCATCACAACAAAGGTGAGGACGCGCAT

CTAGAAGAGCCGTGACGCTCCCTTCTCACTCTACAAGGAAGTTGCAAACGCGGTGCGAGACCTGGTTAGAATCAAGAGAATAC
 ACGAAGCACTTGATCAAGGTTGAAAAGTGGATATTGAGGAACCCCGGGTTTGGCTAGTGGCCGTGCCATTGCCTGGCTTTT
 GGGAAAGCTCGACGAGCCAAAAAGTCATATACTTGGTCATGATACTGCTGATTGCCCCGGCATACAGTATCAGGTGCATTGGAG
 TCAGCAATAGAGACTTCGTGGAGGGCATGTGAGGTGGGACCTGGGTTGATGTTGTCTTGGAAACATGGAGGCTGCGTTACCGT
 GATGGCACAGGACAAGCCAACAGTTGACATAGAGTTGGTCACGACGACGGTTAGTAACATGGCCGAGGTAAGATCCTATTGC
 TACGAGGCATCGATATCGGACATGGCTTCGGACAGTCGTTGCCAACACAAGGTGAAGCCTACCTTGACAAGCAATCAGACAC
 TCAATATGTCTGCAAAAGAACATTAGTGGACAGAGGTTGGGGAACGCGTTGTGGACTTTTTGGCAAAGGGAGCTTGGTGACA
 TGTGCCAAGTTTACGTGTTCTAAGAAGATGACCGGGAAGAGCATTCAACCGGAAAATCTGGAGTATCGGATAATGCTATCAGT
 GCATGGCTCCCAGCATAGCGGGATGACTGTCAATGATATAGGATATGAAACTGACGAAAATAGAGCGAAAAGTCGAGGTTACG
 CCTAATTCACCAAGAGCGGAAGCAACCTTGGGAGGCTTTGGAAGCTTAGGACTTGACTGTGAACCAAGGACAGGCCTTGACTT
 TTCAGATCTGTATTACCTGACCATGAACAATAAGCATTGGTTGGTGACAAAGAGTGGTTTCATGACATCCCATTGCCTTGGCA
 TGCTGGGGCAGACACTGGAAGTCCACACTGGAACAACAAAGAGGCTTGGTAGAATTCAAGGATGCCACGCCAAGAGGCAA
 ACCGTCGTCGTTCTGGGAGCCAGGAAGGAGCCGTTACACGGCTCTCGCTGGAGCTCTAGAGGCTGAGATGGATGGTGCAA
 AGGGAAAGCTGTTCTTGGCCATTTGAAATGCCGCTAAAAATGGACAAGCTTAGATTGAAGGGCGTGTATATTCTTGTGC
 ACTGCGGCATTACATTACCAAGGTCCCAGCTGAAACACTGCATGGAACAGTCACAGTGGAGGTGCAGTATGCAGGGACAG
 ATGGACCTGCAAGATCCAGTCCAGATGGCGGTGGACATGCAGACCTGACCCAGTTGGAAGGCTGATAACCGCCAACCC
 CGTGATTACTGAAAGCACTGAGAACTCAAAGATGATGTTGGAGCTTGACCCACCATTTGGGGATTCTTACATTGTATAGGAG
 TTGGGGACAAGAAAATCACCCACCACTGGCATAGGAGTGGTAGCACCATCGGAAAAGGCAATTTGAGGGCACTGTGAGAGGCGC
 CAAGAGAATGGCAGTCTGGGGGATACAGCCTGGGACTTCGGATCAGTCGGGGGTGTGTTCAACTCACTGGGTAAGGGCATT
 CACCAGATTTTGGAGCAGCCTTCAAATCACTGTTTGGAGGAATGTCCTGGTTCTCACAGATCCTCATAGGCACGCTGCTAGTG
 TGGTTAGGTTTGAACACAAAGAATGGATCTATCTCCCTCACATGCTTGGCCCTGGGGGGAGTGATGATCTTCTCTCCACGGCT
 GTTCTGCTGACGTGGGGTGCTCAGTGGACTTCTCAAAAAAGGAAACGAGATGTGGCACGGGGGATTTCATCTATAATGATGT
 TGAAGCCTGGAGGGACCGGTACAAGTACCATCCTGACTCCCCCGCAGATTGGCAGCAGCAGTCAAGCAGGCCTGGGAAGAG
 GGGATCTGTGGATCTCATCGTTTCAAGAATGGAACATCATGTGGAAATCAGTAGAAGGGGAGCTCAATGCTATCCTAGA
 GGAGAATGGAGTTCAACTGACAGTTGTTGTGGGATCTGTAAAAAACCCATGTGGAGAGGTTCCACAAAGATTGCCAGTGCCT
 GTGAATGAGCTGCCCATGGCTGGAAGCCTGGGGGAAATCGTATTTGTTAGGGCGGCAAAGACCAACAACAGTTTGTGTTGT
 CGACGGTGACACACTGAAGGAATGTCGCTTGAGCACAGAGCATGGAATAGTTTTCTGTGGAGGATCACGGGTTTGGAGTC
 TTCCACACCACTGTCTGGCTTAAGGTGAGAGAAGATTACTCATTAGAATGTGACCCAGCCGTCATAGGAACAGCTGTTAAGGG
 AAGGGAGGCCGCGCACAGTGATCTGGGCTATTGGATTGAAAGTGAAAAGAATGACACATGGAGGCTGAAGAGGGCCACCT
 GATTGAGATGAAAACATGTGAATGGCCAAAGTCTCACACATTGTGGACAGATGGAGTAGAAGAAAGTGATCTTATCATACCCA
 AGTCTTAGCTGGTCCACTCAGCCACCACAACACCAGAGAGGGTTACAGAACCCAAAGTGAAAGGGCCATGGCAGTGAGA
 GCTTGAATCCGGTTTGAGGAATGTCCAGGCACCAAGGTTTACGTGGAGGAGACATGCGGAAGTACAGGACCATCTCTGAGA
 TCAACTACTGCAAGTGAAGGGTCATTGAGGAATGGTGCTGTAGGGAATGCACAATGCCCCACTATCGTTTCGAGCAAAAG
 ACGGCTGCTGGTATGGAATGGAGATAAGGCCCAGGAAAGAACAGAGAGCAACTTAGTGAGGTCAATGGTGACAGCGGGGT
 CAACCGATCATATGGACCATTCTCTCTTGGAGTGCTTGTGATTCTACTCATGGTGCAGGAGGGGTTGAAGAAGAGAATGACC
 ACAAGATCATCATGAGCACATCAATGGCAGTGCTGGTAGTCATGATCTTGGGAGGATTTTCAATGAGTGACCTGGCCAAGCT
 TGTGATCCTGATGGGTGCTACTTTCGAGAAATGAACACTGGAGGAGATGTAGCTCACTTGGCATTGGTAGCGGCATTTAAAG
 TCAGACCAGCCTTGCTGGTCTCCTTCATTTTCAGAGCCAATTGGACACCCCGTGAGAGCATGCTGCTAGCCCTGGCTTCGTGTC
 TTCTGCAAACTGCGATCTCTGCTCTTGAAGGTGACTTGATGGTCTCATTAAATGGATTGCTTTGGCCTGGTTGGCAATTCGAGC
 AATGGCCGTGCCACGCACTGACAACATCGCTCTACCAATCTTGGCTGCTCTAACACCACTAGCTCGAGGCACACTGCTCGTGGC
 ATGGAGAGCGGGCTGGCTACTTGTGGAGGGATCATGCTCTCTCCCTGAAAGGGGAAAGGTAGTGTGAAGAAGAACTGCCA
 TTTGTGATGGCCCTGGGATTGACAGCTGTGAGGGTAGTAGACCTATTAATGTGGTAGGACTACTGTTACTACAAGGAGTGG
 GAAGCGGAGCTGGCCCCCTAGTGAAGTTCTCACAGCCGTTGGCTGATATGTGCACTGGCCGGAGGGTTTGCAAGGCAGAC
 ATTGAGATGGCTGGACCATGGCTGCAGTAGGCTTGCTAATTGTGAGCTATGTGGTCTCGGGAAGAGTGTGGACATGTACAT
 TGAAAGAGCAGGTGACATCACATGGGAAAAGGACGCGGAAGTCACTGGAAACAGTCTCGGCTTGACGTGGCACTGGATGA
 GAGTGGTGATTTCTCTTGGTAGAGGAAGATGGTCCACCCATGAGAGAGATCATCTTAAGGTGGTCTGATGGCCATCTGTG

GCATGAEECCAATAGCTATACCTTTTGCTGCAGGAGCGTGGTATGTGTATGTGAAGACTGGGAAAAGGAGTGGCGCCCTCTG
GGACGTGCCTGCTCCCAAAGAAGTGAAGAAAAGGAGAGACCACAGATGGAGTGTACAGAGTGATGACTCGCAGACTGCTAGG
TTCAACACAGGTTGGAGTGGGAGTCATGCAAGAGGGAGTCTTCCACACCATGTGGCACGTTACAAAAGGAGCCGCACTGAGG
AGCGGTGAGGGAAGACTTGATCCATACTGGGGGGATGTCAAGCAGGACTTGGTGTCTACTGTGGGCCCTTGGAAAGTTGGATG
CAGCTTGGGATGGACTCAGCGAGGTACAGCTTTTGGCCGTACCTCCCGGAGAGAGGGCCAGAAACATTAGACCCCTGCCTGG
AATATTCAAGACAAAGGACGGGGACATCGGAGCAGTTGCTCTGGACTACCTGCAGGGACCTCAGGATCTCCGATCCTAGAC
AAATGTGGAAGAGTGATAGGACTCTATGGCAATGGGGTTGTGATCAAGAATGGAAGCTATGTTAGTGCTATAACCCAGGGAA
AGAGGGGAGGAGGAGACTCCGTTGAATGTTTCGAACCTCGATGCTGAAGAAGAAGCAGCTAAGTGTCTTGGATCTGCATCC
AGGAGCCGGAAAAACCAGGAGAGTCTTCTCTGAAATAGTCCGTGAAGCCATAAAAAAGAGACTCCGGACAGTGATCTTGGCA
CCAAGTAGGGTTGCTGCTGCTGAGATGGAGGAGGCCCTTGAGAGGACTTCCGGTGCCTTACATGACAACAGCAGTCAACGTCA
CCCAATCTGGGACAGAAATCGTTGATTTGATGTCCATGCCACTTTCACCTCACGCTTACTACAACCCATCAGAGTCCCTAATTA
CAATCTCTACATCATGGATGAAGCCCACTTCACAGACCCCTCAAGTATAGCTGCAAGAGGATATATATCAACAAGGGTTGAAAT
GGGCGAGGCGGCTGCCATTTTATGACTGCCACACCACAGGAACCCGTGATGCGTTTCTGACTCTAAGTCAACATCATGGA
CACAGAAGTGGAACTCCAGAGAGAGCCTGGAGCTCAGGCTTTGATTGGGTGACAGACCATTCTGGGAAAACAGTTTGGTTC
GTTCCAAGCGTGAGAAACGGAATGAAATCGCAGCCTGTCTGACAAAGGCTGGAAAGCGGGTCATACAGCTCAGCAGGAAG
ACTTTTGAGACAGAAATTCAGAAAAACAAAAATCAAGAGTGGGACTTTGTACATAACAACTGACATCTCAGAGATGGGCGCCAA
CTTCAAGGCTGACCGGGTCATAGACTCTAGGAGATGCCTAAACCCAGTCATACTTGATGGTGAGAGAGTCATCTTGGCTGGGC
CCATGCCTGTACGCATGCTAGTGCTGCTCAGAGGAGAGGACGTATAGGCAGGAACCCCTAACAAACCTGGAGATGAGTACAT
GTATGGAGGTGGGTGTGACAGACTGATGAAGGCCATGCACACTGGCTTGAAGCAAGAATGCTTCTTGACAACATCTACCTCC
AGGATGGCCTCATAGCCTCGCTCTATCGGCCTGAGGCCGATAAGGTAGCCGCCATTGAGGGAGAGTTTAAAGCTGAGGACAGA
GCAAAGGAAGACCTTCGTGGAACCTCATGAAGAGAGGAGACCTTCCCGTCTGGCTAGCCTATCAGGTTGCATCTGCCGAATAA
CTTACACAGACAGAAGATGGTGCTTTGATGGCACAACCAACAACACCATAATGGAAGACAGCGTACCAGCAGAGGTGTGGAC
AAAGTATGGAGAGAAGAGAGTGTCAAACCGAGATGGATGGATGCTAGGGTCTGTTTCAAGACCATGCGGCCCTGAAGTCTGTC
AAAGAATTGCGCGCTGGAAAAAGAGGAGCGGCTTTGGGAGTAATGGAGGCCCTGGGAACACTGCCAGGACACATGACAGAG
AGGTTTCAGGAAGCCATTGACAACCTCGCCGTGCTCATGCGAGCAGAGACTGGAAGCAGGCCCTTATAAGGCAGCGGCAGCCC
AACTGCCGGAGACCCCTAGAGACCATTTATGCTCTTAGGTTTGTCTGGGAACAGTTTCACTGGGGATCTTCTTCTGCTTGATGCGGA
ATAAGGGCATCGGGAAGATGGGCTTTGGAATGGTAACCTTGGGGCCAGTGATGGCTCATGTGGCTTTTCGGAATTGAACC
AGCCAGAATTGCATGTGCTCCTATTGTTGTGTTTTATTACTGGTGGTGCTCATACCCGAGCCAGAGAAGCAAAGATCTCCCA
AGATAACCAGATGGCAATTATCATCATGGTGGCAGTGCGGCTTCTAGGTTTGATAACTGCAAACGAACCTGGATGGCTGGAAA
GAACAAAAAATGACATAGCTCATCTAATGGGAAGGAGAGAAGAAGGAGCAACCATGGGATTCTCAATGGACATTGATCTGCG
GCCAGCCTCCGCTGGGCTATCTATGCCGATTGACAACCTCTCATACCCAGCTGTCCAACATGCGGTAACCACTTCATAACA
AACTACTCCTTAATGGCGATGGCCACACAAGCTGGAGTGCTGTTTGGCATGGGCAAAGGGATGCCATTTTATGCATGGGACCT
TGGAGTCCCGCTGCTAATGATGGGTTGCTATTACAAATTAACACCCCTGACTCTGATAGTAGCTATCATTCTGCTTGTGGCGCA
CTACATGTACTTGATCCAGGCCCTACAAGCGGCAGCAGCGCTGCTGCCAGAAAAGGACAGCAGCTGGCATCATGAAGAAT
CCCGTTGTGGATGGAATAGTGGTAAGTACATTGACACAATGACAATAGACCCCCAGGTGGAGAAGAAGATGGGACAAGTGT
TACTCATAGCAGTAGCCATCTCCAGTGTCTGTGCTGCTGCGGACCGCTGGGGATGGGGGAGGCTGGAGCTCTGATCACAGC
AGCGACCTCCACCTTGTGGGAAGGCTCTCCAAACAAATACTGGAACCTCTACAGCCACCTCACTGTGCAACATCTTCAGAGG
AAGCTATCTGGCAGGAGCTTCCCTTATCTATACAGTGACGAGAAACGCTGGCCTGGTTAAGAGACGTGGAGGTGGGACGGGA
GAGACTCTGGGAGAGAAGTGGAAAGCTCGTCTGAATCAGATGTGCGCCCTGGAGTTCTACTCTTATAAAAAAGTCAGGTATCAC
TGAAGTGTGTAGAGAGGAGGCTCGCGTGCCCTCAAGGATGGAGTGGCCACAGGAGGACATGCCGTATCCCGGGGAAGTGC
AAAGCTCAGATGGTTGGTGGAGAGAGGATATCTGCAGCCCTATGGGAAGGTTGTTGACCTCGGATGTGGCAGAGGGGGCTG
GAGCTATTATGCCGCCACCATCCGCAAGTGACGAGGTTGAGAGGATACACAAGGGAGGTCCCGGTGATGAAGAACCCTATG
CTGGTGCAAAGCTATGGGTGGAACATAGTTCGTCTCAAGAGTGGAGTGGACGCTTCCACATGGCGGCTGAGCCGTGTGACA
CTCTGCTGTGTGACATAGGTGAGTCATCATAGTCTGAAGTGGAAAGAGACGAACACTCAGAGTGCTCTCTATGGTGGGG
GACTGGCTTGAAAAAGACCAGGGGCCCTTCTGTATAAAGGTGCTGTGCCCATACACCAGCACTATGATGGAAACCATGGAGC
GACTGCAACGTAGGCATGGGGGAGGATTAGTCAGAGTGCCATTGTCTCGCAACTCCACACATGAGATGTACTGGGTCTCTGG

GGCAAAGAGCAACATCATAAAAAGTGTGTCCACCACAAGTCAGCTCCTCCTGGGACGCATGGATGGCCCCAGGAGGCCAGTG
 AAATATGAGGAGGATGTGAACCTCGGCTCGGGTACACGAGCTGTGGCAAGCTGTGCTGAGGCTCCTAACATGAAAATCATCG
 GCAGGCGCATTGAGAGAATCCGCAATGAACATGCAGAAACATGGTTTCTTGATGAAAACCAACCATACAGGACATGGGCCTAC
 CATGGGAGCTACGAAGCCCCACGCAAGGATCAGCGTCTTCCCTCGTGAACGGGGTTGTTAGACTCCTGTCAAAGCCTTGGGA
 CGTGGTGAAGTACAGGAATAGCCATGACTGACACCACACCATACGGCCAACAAAGAGTCTTCAAAGAAAAAGTGGAC
 ACCAGGGTGCCAGATCCCCAAGAAGGCACTCGCCAGGTAATGAACATAGTCTTCTTGGCTGTGGAAGGAGCTGGGGAAAC
 GCAAGCGGCCACGCGTCTGCACCAAAGAAGAGTTTATCAACAAGGTGCGCAGCAATGCAGCACTGGGAGCAATATTTGAAGA
 GGAAAAAGAATGGAAGACGGCTGTGGAAGCTGTGAATGATCCAAGGTTTTGGGCCCTAGTGGATAGGGAGAGAGAACACCA
 CCTGAGAGGAGAGTGTACAGCTGTGTGTACAACATGATGGGAAAAAGAGAAAAGAAGCAAGGAGAGTTCGGGAAAGCAA
 AAGGTAGCCGCGCCATCTGGTACATGTGGTTGGGAGCCAGATTCTTGGAGTTGAAGCCCTTGGATTCTTGAACGAGGACCAT
 TGGATGGGAAGAGAAAACTCAGGAGGTGGAGTCGAAGGGTTAGGATTGCAAAGACTTGGATACATTCTAGAAGAAATGAAT
 CGGGCACCAGGAGGAAAGATGTACGCAGATGACACTGCTGGCTGGGACACCCGCATTAGTAAGTTTGATCTGGAGAATGAAG
 CTCTGATTACCAACCAATGGAGGAAGGGCACAGAACTCTGGCGTTGGCCGTGATTAAATACACATACCAAAACAAAGTGGTG
 AAGGTTCTCAGACCAGCTGAAGGAGGAAAAACAGTTATGGACATCATTTCAAGACAAGACCAGAGAGGGAGTGGACAAGTT
 GTCACCTATGCTCTCAACACATTACCAACTTGGTGGTGCAGCTTATCCGGAACATGGAAGCTGAGGAAGTGTAGAGATGCA
 AGACTTATGGTTGTGAGGAAGCCAGAGAAAGTGACCAGATGGTTGCAGAGCAATGGATGGGATAGACTCAAACGAATGGC
 GGTCAGTGGAGATGACTGCGTTGTGAAGCCAATCGATGATAGGTTTGCACATGCCCTCAGGTTCTTGAATGACATGGGAAAA
 GTTAGGAAAGACACACAGGAGTGGAAACCCCTGACTGGATGGAGCAATGGGAAGAAGTCCCGTTCTGCTCCACCACTTCA
 ACAAGCTGTACCTCAAGGATGGGAGATCCATTGTGGTCCCTTGCCGCCACCAAGATGAACTGATTGGCCGAGCTCGCGTCTCA
 CCAGGGGGCAGGATGGAGCATCCGGGAGACTGCCTGTCTTCAAAATCATATGCGCAGATGTGGCAGCTCCTTTATTTCCACAG
 AAGAGACCTTCGACTGATGGCTAATGCCATTTGCTCGGCTGTGCCAGTTGACTGGGTACCACTGGGAGAACCACCTGTGCAA
 TCCATGGAAAAGGAGAATGGATGACCACTGAGGACATGCTCATGGTGTGGAATAGAGTGTGGATTGAGGAGAACCACCATA
 TGGAGGACAAGACTCCTGTAACAAAATGGACAGACATTCCCTATCTAGGAAAAAGGGAGGACTTATGGTGTGGATCCCTTATA
 GGGCACAGACCCCGCACCCTTGGGCTGAAAACATCAAAGACACAGTCAACATGGTGCGCAGGATCATAGGTGATGAAGAAA
 AGTACATGGACTATCTATCCACCAAGTCCGCTACTTGGGTGAGGAAGGGTCCACACCCGGAGTGTGTGAAGCACCAATTTA
 GTGTTGTGAGGCTGCTAGTCAGCCACAGTTTGGGGAAAGCTGTGCAGCCTGTAACCCCCCAGGAGAAGCTGGGAAACCAA
 GCTCATAGTCAGGCCGAGAACGCCATGGCACGGAAGAAGCCATGCTGCCTGTGAGCCCCCTCAGAGGACACTGAGTCAAAAA
 CCCACGCGCTTGGAAAGCGCAGGATGGGAAAAAGAAGGTGGCGACCTTCCCCACCTTCAATCTGGGGCCTGAACTGGAGACT
 AGCTGTGAATCTCCAGCAGAGGGACTAGTGGTTAGAGGAGACCCCCGGAAAAACGCAAAACAGCATATTGACGCTGGGAAA
 GACCAGAGACTCCATGAGTTTCCACCAGCTGGCCGCCAGGCACAGATCGCCGAACAGCGCGCGCGGTGTGGGGAATCCA
 TGGTTTCT

AY632535.2 NC_012532.1 Zika virus strain MR 766, Uganda, complete genome (SEQ ID NO: 12)

AGTTGTTGATCTGTGTGAGTCAGACTGCGACAGTTCGAGTCTGAAGCGAGAGCTAACAACAGTATCAACAGGTTTAATTTGGA
 TTTGGAACGAGAGTTTCTGGTCATGAAAAACCCAAAGAAGAAATCCGGAGGATCCGGATTGTCAATATGCTAAACGCGG
 AGTAGCCCGTGTAACCCCTTGGGAGGTTTGAAGAGGTTGCCAGCCGACTTCTGCTGGGTGATGGACCCATCAGAATGGTTT
 TGGCGATACTAGCCTTTTGAAGATTACAGCAATCAAGCCATCACTGGGCCTTATCAACAGATGGGGTCCGTGGGGAAAAAA
 GAGGCTATGGAAATAATAAAGAGTTCAAGAAAGATCTTGTGCTGATGTTGAGAATAATCAATGCTAGGAAAGAGAGGAAGA
 GACGTGGCGCAGACACCAGCATCGGAATCATTGGCCTCCTGCTGACTACAGCCATGGCAGCAGAGATCACTAGACGCGGGAG
 TGCATACTACATGTACTTGGATAGGAGCGATGCCGGGAAGGCCATTTCTGTTGCTACCACTTGGGAGTGAACAAGTGCCACG
 TACAGATCATGGACCTCGGGCACATGTGTGACGCCACCATGAGTTATGAGTGCCCTATGCTGGATGAGGGAGTGGAAACCAGA
 TGATGTGATTGCTGGTGAACACGACATCAACTTGGGTTGTGTACGGAACCTGTATCACAACAAAGGTGAGGACCGGCGAT
 CTAGAAGAGCCGTGACGCTCCCTTCTCACTCTACAAGGAAGTTGCAACGCGGTGCGAGACCTGTTAGAATCAAGAGAATAC

ACGAAGCACTTGATCAAGGTTGAAAACCTGGATATTAGGAACCCCGGGTTTGCCTAGTGCCGTTGCCATTGCCTGGCTTTT
 GGGGAAGCTCGACGAGCCAAAAAGTCATATACTTGGTCATGATACTGCTGATTGCCCGGCATACAGTATCAGGTGCATTGGAG
 TCAGCAATAGAGACTTCGTGGAGGGCATGTGAGGTGGGACCTGGGTTGATGTTGTCTTGGAACTGGAGGCTGCGTTACCGT
 GATGGCACAGGACAAGCCAACAGTCGACATAGAGTTGGTCACGACGACGGTTAGTAACATGGCCGAGGTAAGATCCTATTGC
 TACGAGGCATCGATATCGGACATGGCTTCGGACAGTCGTTGCCCAACACAAGGTGAAGCCTACCTTGACAAGCAATCAGACAC
 TCAATATGTCTGCAAAAGAACATTAGTGGACAGAGGTTGGGGAAACGGTTGTGGACTTTTGGCAAAGGGAGCTTGGTGACA
 TGTGCCAAGTTTACGTGTTCTAAGAAGATGACCGGGAAGAGCATTCAACCGGAAAATCTGGAGTATCGGATAATGCTATCAGT
 GCATGGCTCCCGCATAGCGGGATGATTGGATATGAAAACCTGACGAAGATAGAGCGAAAGTCGAGGTTACGCCCTAATTCACCA
 AGAGCGGAAGCAACCTTGGGAGGCTTTGGAACTTAGGACTTGACTGTGAACCAAGGACAGGCTTGACTTTTTCAGATCTGTA
 TTACCTGACCATGAACAATAAGCATTGGTTGGTGACAAAAGAGTGGTTTCATGACATCCCATTTGCCCTTGGCATGCTGGGGCAG
 ACACCGGAACTCCACTGGAACAACAAGAGGCTTGGTAGAATTCAGGATGCCACGCCAAGAGGCAAACCGTCGTCGT
 TCTGGGGAGCCAGGAAGGAGCCGTTACACGGCTCTCGCTGGAGCTCTAGAGGCTGAGATGGATGGTGCAAAAGGGAAAGGCT
 GTTCTCTGGCCATTGAAATGCCGCTAAAAATGGACAAGCTTAGATTGAAGGGCGTGTGCATATTCCTTGTGCACTGCGGCATT
 CACATTCACCAAGSTCCAGCTGAAACACTGCATGGAACAGTCACAGTGGAGGTGCAGTATGCAGGGACAGATGGACCCTGC
 AAGATCCAGTCCAGATGGCGGTGGACATGCAGACCCTGACCCAGTTGGAAGGCTGATAACCGCCAACCCCGTGATTACTGA
 AAGCACTGAGAACTCAAAGATGATGTTGGAGCTTGACCCACCATTTGGGGATTCTTACATTGTCATAGGAGTTGGGGACAAGA
 AAATCACCCACCCTGGCATAGGAGTGGTAGCACCATCGGAAAGGCATTGAGGCCACTGTGAGAGGCGCCAAAGAGAATGGC
 AGTCTGGGGGATACAGCCTGGGACTTCGGATCAGTCGGGGGTGTGTTCAACTCACTGGGTAAAGGGCATTACCCAGATTTTG
 GAGCAGCCTTCAAATCACTGTTTGGAGGAATGTCTGGTTCTCACAGATCCTCATAGGCACGCTGCTAGTGTGGTTAGGTTTGA
 ACACAAAGAAATGGATCTATCTCCCTCACATGCTTGGCCCTGGGGGGAGTGATGATCTTCTCTCCACGGCTGTTTCTGCTGACG
 TGGGGTGCTCAGTGGACTTCTCAAAAAGGAAACGAGATGTGGCACGGGGGTATTCTATATAATGATGTTGAAGCCTGGAG
 GGACCGGTACAAGTACCATCTGACTCCCCCGCAGATTGGCAGCAGCAGTCAAGCAGGCTGGGAAGAGGGGATCTGTGGG
 ATCTCATCCGTTTCAAGAATGGAACATCATGTGGAATCAGTAGAAGGGGAGCTCAATGCTATCCTAGAGGAGAATGGAG
 TTCAACTGACAGTTGTTGTGGATCTGTAAAAAACCCATGTGGAGAGGTCCACAAAGATTGCCAGTGCCTGTGAATGAGCTG
 CCCCATGGCTGGAAAGCCTGGGGGAAATCGTATTTGTTAGGGCGGCAAGACCAACAACAGTTTGTGTCGACGGTGACAC
 ACTGAAGGAATGTCCGCTTGAGCAGAGAGCATGGAATAGTTTCTTGTGGAGGATCACGGGTTTGGAGTCTTCCACACCAGTG
 TCTGGCTTAAGGTCAGAGAAGATTACTATTAGAATGTGACCCAGCCGTCATAGGAACAGCTGTTAAGGGAAGGGAGGCCGC
 GCACAGTGATCTGGGCTATTGGATTGAAAGTGAAAAGAATGACACATGGAGGCTGAAGAGGGGCCACCTGATTGAGATGAAA
 ACATGTGAATGGCCAAAGTCTCACACATTGTGACAGATGGAGTAGAAGAAAGTGATCTTATCATACCCAAGTCTTTAGCTGG
 TCCACTCAGCCACCACAACACCAGAGAGGGTTACAGAACCAAGTGAAAGGGCCATGGCACAGTGAAGAGCTTGAAATCCGG
 TTTGAGGAATGTCCAGGCACCAAGGTTACGTGGAGGAGACATGCGGAACTAGAGGACCATCTCTGAGATCAACTACTGCAA
 GTGGAAGGGTCATTGAGGAATGGTGCTGTAGGGAATGCACAATGCCCCACTATCGTTTCGAGCAAAAGACGGCTGCTGGTA
 TGGAATGGAGATAAGGCCAGGAAAGAACCAGAGAGCAACTTAGTGAGGTCAATGGTGACAGCGGGGTCAACCGATCATAT
 GGACCACTTCTCTTGGAGTGCTTGTGATTCTACTCATGGTGACAGGAGGGGTTGAAGAAGAGAATGACCACAAAGATCATCA
 TGAGCACATCAATGGCAGTGCTGGTAGTCATGATCTTGGGAGGATTTCAATGAGTGACCTGGCCAAGCTTGTGATCCTGATG
 GGTGCTACTTTTCGAGAAATGAACACTGGAGGAGATGTAGCTCACTTGGCATTGGTAGCGGCATTAAAGTCAGACCAGCCTT
 GCTGGTCTCCTTCAATTTTCAGAGCCAATTGGACACCCCGTGAGAGCATGCTGCTAGCCCTGGCTTCGTGTCTTCTGCAAACTGC
 GATCTCTGCTCTTGAAGGTGACTTGATGGTCCTCATTAAATGGATTGTCTTGGCCTGGTTGGCAATTCGAGCAATGGCCGTGCC
 ACGCACTGACAACATCGCTCTACCAATCTTGGCTGCTCTAACACCACTAGCTCGAGGCACACTGCTCGTGGCATGGAGAGCGG
 GCCTGGCTACTTGTGGAGGGATCATGCTCCTCTCCCTGAAAGGGAAAGGTAGTGTGAAGAAGAACCTGCCATTTGTGATGGCC
 CTGGGATTGACAGCTGTGAGGGTAGTAGACCTATTAATGTGGTAGGACTACTGTTACTCACAAGGAGTGGGAAGCGGAGCT
 GGCCCCCTAGTGAAGTTCTCACAGCCGTTGGCTGATATGTGCACTGGCCGGAGGGTTTGCCAAGGCAGACATTGAGATGGCT
 GGACCCATGGCTGCAGTAGGCTTGCTAATTGTGAGCTATGTGGTCTCGGGAAAGAGTGTGGACATGTACATTGAAAGAGCAG
 GTGACATCACATGGGAAAAGGACGCGGAAGTCACTGGAAACAGTCTCGGCTTGACGTGGCACTGGATGAGAGTGGTGACTT
 CTCCTTGGTAGAGGAAGATGGTCCACCCATGAGAGAGATCATACTCAAGGTGGTCTGATGGCATCTGTGGCATGAACCCAA
 TAGCTATACCTTTTGTGCGAGGAGCGTGGTATGTGTATGTGAAGACTGGGAAAAGGAGTGGCGCCCTCTGGGACGTGCCTGC

TCCCAAAGAAGTGAAGAAAGGAGAGACCACAGATGGAGTGTACAGAGTGATGACTCGCAGACTGCTAGGTTCAACACAGGTT
 GGAGTGGGAGTCATGCAAGAGGGAGTCTTCCACACCATGTGGCAGGTTACAAAAGGAGCCGCACTGAGGAGCGGTGAGGGA
 AGACTTGATCCATACTGGGGGGATGTCAAGCAGGACTTGGTGTACATACTGTGGGCCTTGGAAAGTTGGATGCAGCTTGGGATG
 GACTCAGCGAGGTACAGCTTTTGGCCGTACCTCCCGGAGAGAGGGCCAGAAACATTAGACCCTGCCTGGAATATTCAAGACA
 AAGGACGGGGACATCGGAGCAGTTGCTCTGGACTACCCTGCAGGGACCTCAGGATCTCCGATCCTAGACAAATGTGGAAGAG
 TGATAGGACTCTATGGCAATGGGGTTGTGATCAAGAATGGAAGCTATGTTAGTGCTATAACCCAGGGAAAGAGGGAGGAGG
 AGACTCCGGTTGAATGTTTCGAACCTCGATGCTGAAGAAGAAGCAGCTAACTGCTTGGATCTGCATCCAGGAGCCGGAAAA
 ACCAGGAGAGTTCTTCTGAAATAGTCCGTGAAGCCATAAAAAAGAGACTCCGGACAGTGATCTTGGCACCAACTAGGGTTGT
 CGCTGCTGAGATGGAGGAGGCCCTTGAGAGGACTTCCGGTGCGTTACATGACAAAGCAGTCAACGTCACCCATTCTGGGACA
 GAAATCGTTGATTGATGTGCCATGCCACTTTCACCTCAGCCTTACTACAACCCATCAGAGTCCCTAATTACAATCTCAACATCAT
 GGATGAAGCCCACTTACAGACCCCTCAAGTATAGCTGCAAGAGGATACATATCAACAAGGGTTGAAATGGGCGAGGCGGCT
 GCCATTTTATGACTGCCACACCACAGGAACCCGTGATGCGTTTCTGACTCTAACTCACCATCATGGACACAGAAGTGGAA
 GTCCCAGAGAGAGCCTGGAGCTCAGGCTTGATTGGGTGACAGACCATTCTGGGAAAACAGTTTGGTTCCGTTCAAGCGTGA
 GAAACGGAAATGAAATCGCAGCCTGTCTGACAAAGGCTGGAAAGCGGGTCATACAGCTCAGCAGGAAGACTTTTGAGACAGA
 ATTTAGAAAACAAAAAATCAAGAGTGGGACTTTGTACAAACCTGACATCTCAGAGATGGGCGCAACTTCAAGGCTGACC
 GGGTCATAGACTCTAGGAGATGCCATAAACAGTCATACTTGATGGTGAGAGAGTCATCTTGGCTGGGCCATGCCCTGTACG
 CATGCTAGTGCTGCTCAGAGGAGAGGACGTATAGGCAGGAACCTAACAACTGGAGATGAGTACATGTATGGAGGTGGG
 TGTGCAGAGACTGATGAAGGCCATGCACACTGGCTGAAGCAAGATGCTTCTTGACAACATCTACCTCCAGGATGGCCTCAT
 AGCCTCGCTCTATCGGCCTGAGGCCGATAAGGTAGCCGCCATTGAGGGAGAGTTTAAGCTGAGGACAGAGCAAAGGAAGAC
 CTTCTGGAACCTCATGAAGAGAGGAGACCTTCCCGTCTGGCTAGCCTATCAGGTTGCATCTGCCGGAATAACTTACACAGACA
 GAAGATGGTGCTTTGATGGCACAACCAACAACACCATAATGGAAGACAGTGTAACAGCAGAGGTTTGGACAAAGTATGGAGA
 GAAGAGAGTGCTCAAACCGAGATGGATGGATGCTAGGGTCTGTTTACAGACCATGCGGCCCTGAAGTCTTCAAAGAATTGCCC
 GCTGGAAAAAGAGGAGCGGCTTTGGGAGTAATGGAGGCCCTGGGAACACTGCCAGGACACATGACAGAGAGGTTTCAGGAA
 GCCATTGACAACCTCGCCGTGCTCATGCGAGCAGAGACTGGAAGCAGGCCCTTATAAGGCAGCGGCAGCCCAACTGCCGGAGA
 CCTAGAGACCATTATGCTCTTAGGTTTGTGGGAACAGTTTCACTGGGGATCTTCTTCTGCTTGATGCGGAATAAGGGCATCG
 GGAAGATGGGCTTTGGAATGGTAACCTTGGGGCAGTGATGGCTCATGTGGCTTTCGGAAATTGAACAGCCAGAATTGC
 ATGTGCTCTCATTTGTTGTGTTTTATTACTGGTGGTGCTCATACCCGAGCCAGAGAAGCAAAGATCTCCCCAAGATAACCAGAT
 GGCAATTATCATCATGGTGGCAGTGGGCCTTCTAGGTTTGATAACTGCAACGAACTTGGATGGCTGGAAAGAACAAAAAT
 GACATAGCTCATCTAATGGGAAGGAGAGAAGAAGGAGCAACCATGGGATTCTCAATGGACATTGATCTGCGGCCAGCCTCCG
 CCTGGGCTATCTATGCCGATTGACAACCTCATCACCCAGCTGTCCAACATGCGGTAACCACTTATACAACAACCTACTCCTT
 AATGGCGATGGCCACACAAGCTGGAGTGCTGTTTGGCATGGGCAAGGGATGCCATTTATGCATGGGGACCTTGGAGTCCCG
 CTGCTAATGATGGGTGCTATTACAATTAACACCCCTGACTCTGATAGTAGCTATCATTCTGCTTGTGGCGCACTACATGTACT
 TGATCCAGGCCCTACAAGCGGCAGCAGCGCGTGCTGCCAGAAAAGGACAGCAGCTGGCATCATGAAGAATCCCGTTGTGGA
 TGGAATAGTGGTAACCTGACATTGACACAATGACAATAGACCCCCAGGTGGAGAAGAAGATGGGACAAGTGTACTCATAGCA
 GTAGCCATCTCCAGTGCTGTGCTGCTGCGGACCGCCTGGGGATGGGGGGAGGCTGGAGCTCTGATCACAGCAGCGACCTCCA
 CCTTGTGGGAAGGCTCTCCAAACAAATACTGGAACCTCTACAGCCACCTCACTGTGCAACATCTTACAGAGGAAGCTATCTGG
 CAGGAGCTTCCCTTATCTATACAGTGACGAGAAACGCTGGCCTGGTTAAGAGACGTGGAGGTGGGACGGGAGAGACTCTGG
 GAGAGAAGTGGAAAGCTCGTCTGAATCAGATGTGCGCCCTGGAGTTCTACTCTTATAAAAAGTCAGGTATCACTGAAGTGTGT
 AGAGAGGAGGCTCCCGTGCCCTCAAGGATGGAGTGGCCACAGGAGGACATGCCGTATCCCGGGGAAGTGCAAGATCAGA
 TGGTTGGAGGAGAGAGGATATCTGCAGCCCTATGGGAAGGTTGTTGACCTCGGATGTGGCAGAGGGGGCTGGAGCTATTAT
 GCCGCCACCATCCGCAAAGTGCAAGGAGTGAGAGGATACACAAAGGGAGGTCCCGGTATGAAGAACCATGCTGGTGCAA
 AGCTATGGGTGGAACATAGTTCGTCTCAAGAGTGGAGTGGACGCTTCCACATGGCGGCTGAGCCGTGTGACACTCTGCTGTG
 TGACATAGGTGAGTCATCATCTAGTCTGAAGTGGAAAGAGACACGAACACTCAGAGTGCTCTCTATGGTGGGGGACTGGCTT
 GAAAAAGACCAAGGGGCTTCTGTATAAAGGTGCTGTGCCCATACACCAGCACTATGATGGAAACCATGGAGCGACTGCAAC
 GTAGGCATGGGGGAGGATTAGTCAGAGTGCCATTGTGTCGCAACTCCACACATGAGATGACTGGGTCTCTGGGGCAAAGAG
 CAACATCATAAAAAGTGTGTCCACCACAAGTCAGCTCCTCTGGGACGCATGGATGGCCCCAGGAGGCCAGTGAATATGAG

GAGGATGTGAACCTCGGCTCGGGTACACGAGCTGTGGCAAGCTGTGCTGAGGCTCCTAACATGAAAATCATCGGCAGGCGCA
 TTGAGAGAATCCGCAATGAACATGCAGAAACATGGTTCTTGATGAAAACCAACCATACAGGACATGGGCTACCATGGGAGC
 TACGAAGCCCCACGCAAGGATCAGCGTCTTCCTCGTGAACGGGGTTGTTAGACTCCTGTCAAAGCCTTGGGACGTGGTGAC
 TGGAGTTACAGGAATAGCCATGACTGACACCACACCATACGGCCAACAAAGAGTCTTCAAAGAAAAAGTGGACACCAGGGTG
 CCAGATCCCCAAGAAGGCACTCGCCAGGTAATGAACATAGTCTTCTGCTGGCTGTGGAAGGAGCTGGGGAAACGCAAGCGGC
 CACGCGTCTGCACCAAGAAGAGTTTATCAACAAGGTGCGCAGCAATGCAGCACTGGGAGCAATATTGAAGAGGAAAAAGA
 ATGGAAGACGGCTGTGGAAGCTGTGAATGATCCAAGTTTTGGGCCCTAGTGGATAGGGAGAGAGAACACCACCTGAGAGG
 AGAGTGTACAGCTGTGTGTACAACATGATGGGAAAAAGAGAAAAGCAAGGAGAGTTCGGGAAAGCAAAAGGTAGCC
 GCGCCATCTGGTACATGTGGTTGGGAGCCAGATTCTGGAGTTTGAAGCCCTTGGATTCTTGAACGAGGACCATTGGATGGGA
 AGAGAAAACCTCAGGAGGTGGAGTCGAAGGGTTAGGATTGCAAAGACTTGGATACATTCTAGAAGAAATGAATCGGGCACCA
 GGAGGAAAGATGTACGCAGATGACACTGCTGGCTGGGACACCCGATTAGTAAGTTTGATCTGGAGAATGAAGCTCTGATTA
 CCAACCAAATGGAGGAAGGGACAGAACTCTGGCGTTGGCCGTGATTAAATACACATACCAAAAACAAAGTGGTGAAGTTCT
 CAGACCAGCTGAAGGAGGAAAAACAGTTATGGACATCATTTCAAGACAAGACCAGAGAGGGAGTGGACAAGTTGTCACTTAT
 GCTCTCAACACATTACCAACTTGGTGGTGACGCTTATCCGGAACATGGAAGCTGAGGAAGTGTAGAGATGCAAGACTTATG
 GTTGTGAGGAAGCCAGAGAAAGTGACCAGATGGTTGCAGAGCAATGGATGGGATAGACTCAAACGAATGGCGGTCACTGG
 AGATGACTGCGTTGTGAAGCCAATCGATGATAGGTTGCACATGCCCTCAGGTTCTTGAATGACATGGGAAAAGTTAGGAAAG
 ACACACAGGAGTGGAAACCCTCGACTGGATGGAGCAATTGGGAAGAAGTCCCGTTCTGCTCCCACTTCAACAAGCTGTAC
 CTCAAGGATGGGAGATCCATTGTGGTCCCTTGGCCGCCACCAAGATGAACTGATTGGCCGAGCTCGCGTCTCACCAGGGGCAG
 GATGGAGCATCCGGGAGACTGCCTGTCTGCAAAATCATATGCGCAGATGTGGCAGCTCCTTTATTTCCACAGAAGAGACCTT
 CGACTGATGGCTAATGCCATTTGCTCGGCTGTGCCAGTTGACTGGGTACCAACTGGGAGAACCACCTGGTCAATCCATGAAAA
 GGGAGAATGGATGACCACTGAGGACATGCTCATGGTGTGGAATAGAGTGTGGATTGAGGAGAACGACCATATGGAGGACAA
 GACTCTGTAAACAAATGGACAGACATTCCCTATCTAGGAAAAAGGGAGGACTTATGGTGTGGATCCCTTATAGGGCACAGAC
 CCCGCCACTTGGGCTGAAAACATCAAAGACACAGTCAACATGGTGGCAGGATCATAGGTGATGAAGAAAAGTACATGGA
 CTATCTATCCACCAAGTCCGCTACTTGGGTGAGGAAGGGTCCACACCCGGAGTGTGTAAGCACCAATTTAGTGTGTCAGG
 CCTGCTAGTCAGCCACAGTTTGGGGAAGCTGTGCAGCCTGTAACCCCCCAGGAGAAGCTGGGAAACCAAGCTCATAGTCA
 GGCCGAGAACGCCATGGCAGGGAAGGACCATGCTGCTGTGAGCCCTCAGAGGACACTGAGTCAAAAAACCCACGCGCT
 TGGAAGCGCAGGATGGGAAAAGAAGGTGGCGACCTCCCCACCTTCAATCTGGGGCCTGAAGTGGAGACTAGCTGTGAATC
 TCCAGCAGAGGGACTAGTGGTTAGAGGAGACCCCGGAAAACGCAAAACAGCATATTGACGTGGGAAAGACCAGAGACTC
 CATGAGTTTCCACCAGCTGGCCGCCAGGCACAGATCGCCGAACCTCGCGGCCGGTGTGGGGAATCCATGGTTCT

>Chimeric Asian ZIKV Sequence H/PF/2013 polyprotein flanked with consensus sequence from
 other strains (SEQ ID NO: 13)

GTTGTTGATCTGTGTGAATCAGACTGCGACAGTTCGAGTTTGAAGCGAAAGCTAGCAACAGTATCAACAGGTTTATTTGGAT
 TTGGAAACGAGAGTTTCTGGTCATGAAAAACCAAAAAAGAAATCCGGAGGATTCCGGATTGTCAATATGCTAAACGCGGA
 GTAGCCCGTGTGAGCCCTTTGGGGCTTGAAGAGGCTGCCAGCCGACTTCTGCTGGGTCATGGGCCCATCAGGATGGTCTT
 GGCGATTCTAGCCTTTTGAAGATTACGGCAATCAAGCCATCACTGGGTCTCATCAATAGATGGGGTTCAGTGGGGAAAAAG
 AGGCTATGGAATAATAAAGAAGTTCAAGAAAGATCTGGCTGCCATGCTGAGAATAATCAATGCTAGGAAGGAGAAGAAGA
 GACGAGGCGCAGATACTAGTGTGGAAITGTTGGCTCCTGCTGACCACAGCTATGGCAGCGGAGGTCACTAGACGTGGGAG
 TGCATACTATATGTAAGTGGACAGAAACGACGCTGGGGAGGCCATATCTTTCAACCACATTGGGGATGAATAAGTGTATAT
 ACAGATCATGGATCTTGGACACATGTGTGATGCCACCATGAGCTATGAATGCCCTATGCTGGATGAGGGGGTGGAAACAGAT
 GACGTCGATTGTTGGTGCAACACGACGTCAACTTGGGTTGTGTACGGAACCTGCCATCACAAAAAGGTGAAGCACGGAGAT
 CTAGAAGAGCTGTGACGCTCCCTCCCATTTCACTAGGAAGCTGCAACCGCGTCCGCAACCTGGTTGGAATCAAGAGAATAC
 ACAAAGCACTTGATTAGAGTCGAAAATTGGATATTCAGGAACCTGGCTTCGCGTAGCAGCAGCTGCCATCGCTTGGCTTTTG

GGAAGCTCAACGAGCCAAAAAGTCATATACTTGGTCATGATACTGCTGATTGCCCCGGCATAACAGCATCAGGTGCATAGGAGT
 CAGCAATAGGGACTTTGTGGAAGGTATGTCAGGTGGGACTTGGGTTGATGTTGCTTGGAAACATGGAGGTTGTGTACCCGTA
 ATGGCACAGGACAAACCGACTGTGACATAGAGCTGGTTACAACAACAGTCAGCAACATGGCGGAGGTAAGATCCTACTGCT
 ATGAGGCATCAATATCGGACATGGCTTCGGACAGCCGCTGCCAACACAAGGTGAAGCCTACCTTGACAAGCAATCAGACACT
 CAATATGTCTGCAAAAGAACGTTAGTGGACAGAGGCTGGGGAATGGATGTGGACTTTTGGCAAAGGGAGCCTGGTGACAT
 GCGCTAAGTTTGCATGCTCCAAGAAAATGACCGGGAAGAGCATCCAGCCAGAGAATCTGGAGTACCGGATAATGCTGTCACT
 TCATGGCTCCAGCACAGTGGGATGATCGTTAATGACACAGGACATGAAACTGATGAGAATAGAGCGAAGGTTGAGATAACG
 CCCAATTCACCAAGAGCCGAAGCCACCCTGGGGGGTTTGGGAAGCCTAGGACTTGATTGTGAACCGAGGACAGGCCTTGACTT
 TTCAGATTGTATTACTTGACTATGAATAACAAGCACTGGTTGGTTCACAAGGAGTGGTTCACGACATTCCATTACCTTGGCAC
 GCTGGGGCAGACACCGGAACCTCCACTGGAACAACAAAGAAGCACTGGTAGAGTTCAAGGACGCACATGCCAAAAGGCAA
 ACTGTCGTGGTTCTAGGGAGTCAAGAAGGAGCAGTTCACACGGCCCTTGCTGGAGCTCTGGAGGCTGAGATGGATGGTGCAA
 AGGGAAGGCTGTCTCTGGCCACTTGAAATGTCGCCTGAAATGGATAAATTAGATTGAAGGGCGTGCATACTCCTTGCTGT
 ACCGCAGCGTTCACATTACCAAGATCCCGGCTGAAACACTGCACGGGACAGTCACAGTGGAGGTACAGTACGCAGGGACAG
 ATGGACCTTGCAAGTTCCAGCTCAGATGGCGGTGGACATGCAAACTCTGACCCAGTTGGGAGGTTGATAACCGCTAACCCC
 GTAATCACTGAAAGCACTGAGAACTTAAGATGATGCTGGAACCTTGATCCACCATTGGGGACTCTTACATTGTCATAGGAGTC
 GGGGAGAAGAAGATCACCCACCACTGGCACAGGAGTGGCAGCACCATTGGAAAAGCATTGAAGCCACTGTGAGAGGTGCC
 AAGAGAATGGCAGTCTTGGGAGACACAGCCTGGGACTTTGGATCAGTTGGAGGCGCTCTCAACTCATTGGGCAAGGGCATCC
 ATCAAATTTTGGAGCAGCTTCAAATCATTGTTGGAGGAATGTCCTGGTTCTCAAAATTCTCATTGGAACGTTGCTGATGTG
 GTTGGGTCTGAACACAAAGAATGGATCTATTTCCCTTATGTGCTTGGCCTTAGGGGGAGTGTGATCTTCTTATCCACAGCTGT
 CTCTGCTGATGTGGGGTGTCTGGTGGACTTCTCAAAGAAGGAGACGAGATGCGGTACAGGGGTGTTCTGCTATAACGACGTT
 GAAGCCTGGAGGGACAGGTACAAGTACCCTCTGACTCCCCCGTAGATTGGCAGCAGCAGTCAAGCAAGCCTGGGAAGATG
 GTATCTGTGGGATCTCTCTGTTTCAAGAATGGAAAACATCATGTGGAGATCAGTAGAAGGGGAGCTCAACGCAATCTTGGA
 GAGAATGGAGTTCAACTGACGGTCTGTTGGGATCTGTAACCAACCCCATGTGGAGAGGTCCACAGAGATTGCCCGTGCCTG
 TGAACGAGCTGCCCCACGGCTGGAAGGCTTGGGGGAAATCGTACTTCGTGAGAGCAGCAAAGACAAATAACAGCTTTGTCGT
 GGATGGTGACACACTGAAGGAATGCCCACTCAAACATAGAGCATGGAACAGCTTCTTGTGGAGGATCATGGGTTCCGGGTA
 TTTCACTAGTGTCTGGCTCAAGGTTAGAGAAGATTATTATTAGAGTGTGATCCAGCCGTTATTGGAACAGCTGTTAAGGGA
 AAGGAGGCTGTACACAGTATCTAGGCTACTGGATTGAGAGTGAGAAGATGACACATGGAGGCTGAAGAGGGCCCATCTG
 ATCGAGATGAAAACATGTGAATGGCCAAAGTCCCACACATTGTGGACAGATGGAATAGAAGAGAGTGATCTGATCATACCCA
 AGTCTTTAGCTGGGCCACTCAGCCATCACAATACCAGAGAGGGCTACAGGACCCAAATGAAAGGGCCATGGCACAGTGAAGA
 GCTTGAAATTCGGTTTGAGGAATGCCAGGCACTAAGGTCCACGTGGAGGAAACATGTGGAACAAGAGGACCATCTCTGAGA
 TCAACCACTGCAAGCGGAAGGGTGATCGAGGAATGGTGTGAGGGAGTGCACAATCCCCCACTGTCTTCCGGGCTAAAG
 ATGGCTGTTGGTATGGAATGGAGATAAGGCCCAGGAAAGAACAGAAAGTAAGTAAAGTCAAGTGGTGAAGTGCAGGATC
 AACTGATCACATGGATCACTTCTCCCTTGGAGTGCTTGTGATTCTGCTCATGCTGAGGAAGGGCTGAAGAAGAGAATGACCA
 CAAAGATCATATAAGCACATCGATGGCAGTGTCTGGTAGCTATGATCCTGGGAGGATTTTCAATGAGTGACCTGGCTAAGCTT
 GCAATTTTGATGGGTGCCACCTTCGCGGAAATGAACACTGGAGGAGATGTAGCTCATCTGGCGCTGATAGCGGCATTCAAAGT
 CAGACCAGCGTTGCTGGTATCTTTCATCTCAGAGCTAATTGGACACCCCGTGAAAGCATGCTGCTGGCCTTGGCCTCGTGTCT
 TTTGCAAACTGCGATCTCCGCCTTGAAGGCGACCTGATGGTTCTCATCAATGGTTTTGCTTTGGCCTGGTTGGCAATACGAGC
 GATGGTTGTTCCACGCACTGATAACATCACCTTGGCAATCCTGGCTGCTCTGACACCACTGGCCCCGGGGCACACTGCTTGTGGC
 GTGGAGAGCAGGCCCTTGCTACTTGCGGGGGGTTTATGCTCCTCTCTGGAAGGGAAAAGGCAGTGTGAAGAAGAACTTACCA
 TTTGTCATGGCCCTGGGACTAACCGCTGTGAGGCTGGTCGACCCCATCAACGTGGTGGGACTGCTGTTGCTACAAGGAGTGG
 GAAGCGGAGCTGGCCCCCTAGCGAAGTACTCACAGCTGTTGGCCTGATATGCGCATTGGCTGGAGGGTTCCGCAAGGCAGAT
 ATAGAGATGGCTGGGCCATGGCCGCGTGGTCTGCTAATTGTGAGTTACGTGGTCTCAGGAAAGAGTGTGGACATGTACA
 TTGAAAGAGCAGGTGACATCACATGGGAAAAAGATGCGGAAGTCACTGGAACAGTCCCCGGCTCGATGTGGCGCTAGATGA
 GAGTGGTGATTCTCCCTGGTGGAGGATGACGGTCCCCCATGAGAGAGATCATACTCAAGGTGGTCTGATGACCATCTGTG
 GCATGAACCAATAGCCATACCTTTGCAGCTGGAGCGTGGTACGTATACGTGAAGACTGGAAAAGGAGTGGTGTCTCTATG
 GGATGTGCTGCTCCAAGGAAGTAAAAAGGGGGAGACCACAGATGGAGGTACAGAGTAATGACTCGTAGACTGCTAGG

TTCAACACAAGTTGGAGTGGGAGTTATGCAAGAGGGGGTCTTTCACACTATGTGGCACGTACAAAAAGGATCCGCGCTGAGA
 AGCGGTGAAGGGAGACTTGATCCATACTGGGGAGATGTCAAGCAGGATCTGGTGTCTACTGTGGTCCATGGAAGCTAGATG
 CCGCCTGGGACGGGCACAGCGAGGTGCAGCTCTTGGCCGTGCCCCCGGAGAGAGAGCGAGGAACATCCAGACTCTGCCCCG
 GAATATTTAAGACAAAGGATGGGGACATTGGAGCGGTTGCGCTGGATTACCCAGCAGGAACCTCAGGATCTCCAATCCTAGA
 CAAGTGTGGGAGAGTGATAGGACTTTATGGCAATGGGGTCGTGATCAAAAATGGGAGTTATGTTAGTGCCATCACCCAAGGG
 AGGAGGGAGGAAGAGACTCCTGTTGAGTGCTTCGAGCCTTCGATGTGAAGAAGAAGCAGCTAACTGTCTTAGACTTGATC
 CTGGAGCTGGGAAAACCAGGAGAGTTCTTCTGAAATAGTCCGTGAAGCCATAAAAAACAAGACTCCGTACTGTGATCTTAGCT
 CCAACCAGGGTTGTGCTGCTGAAATGGAGGAAGCCCTTAGAGGGCTTCCAGTGCGTTATATGACAACAGCAGTCAATGTCAC
 CCACTCTGGAACAGAAATCGTCGACTTAATGTGCCATGCCACCTTCACTTCACGTCTACTACAGCCAATCAGAGTCCCCAACTAT
 AATCTGTATATTATGGATGAGGCCCACTTCACAGATCCCTCAAGTATAGCAGCAAGAGGATACATTTCAACAAGGGTTGAGAT
 GGGCGAGGCGGCTGCCATCTTCATGACCGCCACGCCACCAGGAACCGTGACGCATTTCCGGACTCCAACCTACCAATTATGG
 ACACCGAAGTGGAGTCCCAGAGAGAGCCTGGAGCTCAGGCTTTGATTGGGTGACGGATCATTCTGGAAAAACAGTTTGTT
 TGTTCAGCGTGAGGAACGGCAATGAGATCGCAGCTTGTCTGACAAAGGCTGGAAAACGGGTACACAGCTCAGCAGAAAG
 ACTTTTGAGACAGAGTTCCAGAAAACAAAACATCAAGAGTGGGACTTTGTCTGTGACAACTGACATTTAGAGATGGGCGCCAA
 CTTAAAGCTGACCGTGTATAGATTCCAGGAGATGCCAAAGCCGGTCATACTTGATGGCGAGAGAGTCATTCTGGCTGGAC
 CCATGCTGTACACATGCCAGCGCTGCCAGAGGAGGGGGCGCATAGGCAGGAATCCCAACAAACCTGGAGATGAGTATCT
 GTATGGAGGTGGGTGCGCAGAGACTGACGAAGACCATGCACACTGGCTTGAAGCAAGAATGCTCCTTGACAATATTTACCTCC
 AAGATGGCCTCATAGCCTCGCTCTATCGACCTGAGGCGGACAAAAGTAGCAGCCATTGAGGGAGAGTTCAAGCTTAGGACGGGA
 GCAAAGGAAGACCTTTGTGGAACCTCATGAAAAGAGGAGATCTTCTGTTTGGCTGGCCTATCAGGTTGCATCTGCCGAATAA
 CCTACACAGATAGAAGATGGTGTCTTGATGGCAGCACCAACAACACCATAATGGAAGACAGTGTGCCGGCAGAGGTGTGGAC
 CAGACACGGAGAGAAAAGAGTGTCTCAACCGAGGTGGATGGACGCCAGAGTTTGTTCAGATCATGCGGCCCTGAAGTCATTC
 AAGGAGTTTCCGCTGGGAAAAGAGGAGCGGCTTTTGGAGTGATGGAAGCCCTGGGAACACTGCCAGGACACATGACAGAG
 AGATTCCAGGAAGCCATTGACAACCTCGCTGTGCTCATGCGGGCAGAGACTGGAAGCAGGCCTTACAAAGCCGCGCGGGCCC
 AATTGCCGGAGACCCTAGAGACCATTATGCTTTTGGGGTTGCTGGGAACAGTCTCGCTGGGAATCTTTTCTGTTGATGAGG
 AACAGGGCATAGGGAAGATGGGCTTTGGAATGGTGACTCTTGGGGCCAGCGCATGGCTCATGTGGCTCTCGGAAATTGAGC
 CAGCCAGAATTGCATGTGTCTCATTTGTTGTGTTCTATTGCTGGTGGTGTCTATACCTGAGCCAGAAAAGCAAAGATCTCCCC
 AGGACAACCAATGGCAATCATCATGGTAGCAGTAGGTCTTCTGGGCTTGATTACCGCCAATGAACTCGGATGTTGGAG
 AGAACAAAGAGTGACCTAAGCCATCTAATGGGAAGGAGAGAGGAGGGGGCAACCATAGGATTCTCAATGGACATTGACCTG
 CGGCCAGCCTCAGCTTGGGCCATCTATGCTGCCCTTGACAACCTTTCATTACCCAGCCGTCACCATGCAGTGACCACTTCATACA
 ACAACTACTCCTTAATGGCGATGGCCACGCAAGCTGGAGTGTGTTTGGTATGGGCAAAGGGATGCCATTCTACGCATGGGAC
 TTTGGAGTCCCGCTGCTAATGATAGGTTGCTACTCACAAATTAACACCCCTGACCCTAATAGTGGCCATCATTTTGTCTGTGGCGC
 ACTACATGTACTTGATCCCAGGGCTGCAGGCAGCAGCTGCGCGTGTGCCCAGAAGAGAACGGCAGCTGGCATCATGAAGAA
 CCTGTTGTGGATGGAATAGTGGTGACTGACATTGACACAATGACAATTGACCCCAAGTGAGAGAAAAGATGGGACAGGTG
 CTACTCATAGCAGTAGCCGTCTCCAGCGCCATACTGTGCGGGACCGCTGGGGGTGGGGGGAGGCTGGGGCCCTGATCACAG
 CGGCAACTTCCACTTTGTGGGAAGGCTCTCCGAACAAGTACTGGAACCTCTACAGCCACTTCACTGTGTAACATTTTATGGG
 GAAGTTACTTGGCTGGAGCTTCTCTAATCTACACAGTAACAAGAAACGCTGGCTTGGTCAAGAGACGTGGGGGTGGAACAGG
 AGAGACCTGGGAGAGAAATGGAAGGCCCGCTTGAACAGATGTGCGCCCTGGAGTTCTACTCTACAAAAAGTCAGGCATC
 ACCGAGGTGTGCAGAGAAGAGGCCCCGCGCCCTCAAGGACGGTGTGGCAACGGGAGGCCATGTGTGTCCGAGGAAGT
 GCAAAGCTGAGATGTTTGGTGGAGCGGGGATACCTGCAGCCCTATGGAAGGTCATTGATCTTGGATGTGGCAGAGGGGGC
 TGGAGTTACTACGCCGCCACCATCCGCAAAGTTCAAGAAGTGAAAGGATACACAAAAGGAGGGCCCTGGTCATGAAGAACCCA
 TGTITGGTGCAAAGCTATGGGTGGAACATAGTCCGTCTTAAGAGTGGGGTGACGCTCTTTCATATGGCGGCTGAGCCGTGTGA
 CACGTTGCTGTGTGACATAGGTGAGTCATCATGTAGTCTGAAGTGAAGAAGCACGGACGCTCAGAGTCTCTCCATGGTGG
 GGGATTGGCTTGAAAAAGAGCAGGAGCCTTTGTATAAAAGTGTGTGCCATACACCAGCACTATGATGGAACCTTGAGG
 CGACTGCAGCGTAGGTATGGGGGAGGACTGGTCAGAGTGCCACTCTCCGCAACTCTACACATGAGATGTACTGGGTCTCTG
 GAGCGAAAAGCAACACCATAAAAAAGTGTGTCCACCACGAGCCAGCTCTTGGGGCGCATGGACGGGGCCAGGAGGCCAGT
 GAAATATGAGGAGGATGTGAATCTGGCTCTGGCACGCGGGCTGTGGTAAGCTGCGCTGAAGCTCCCAACATGAAGATCATT

PAT022-EP-PR

GGTAACCGCATTGAAAGGATCCGCAGTGAGCACGCGGAAACGTGGTTCTTTGACGAGAACCACCCATATAGGACATGGGCTT
ACCATGGAAGCTATGAGGCCCCACACAAGGGTCAGCGTCTCTCTAATAAACGGGGTTGTCAGGCTCTGTCAAAACCTGG
GATGTGGTGAAGTACAGGAATAGCCATGACCGACACACACCGTATGGTCAGCAAAGAGTTTCAAGGAAAAAGTGG
ACACTAGGGTGCCAGACCCCAAGAAGGCACTCGTCAGGTTATGAGCATGGTCTCTTCTGGTTGTGGAAAGAGCTAGGCAA
ACACAAACGGCCACGAGTCTGTACCAAAGAAGAGTTCATCAACAAGGTTCTGTAGCAATGCAGCATTAGGGGCAATATTTGAA
GAGGAAAAAGAGTGGAAAGACTGCAGTGGAAAGCTGTGAACGATCCAAGGTTCTGGGCTCTAGTGGACAAGGAAAGAGAGCAC
CACCTGAGAGGAGAGTGCCAGAGTTGTGTGTACAACATGATGGGAAAAAGAGAAAGAAACAAGGGGAATTTGGAAAGGCC
AAGGGCAGCCGCGCCATCTGGTATATGTGGCTAGGGGCTAGATTTCTAGAGTTCGAAGCCCTTGGATTCTTGAACGAGGATCA
CTGGATGGGGAGAGAGAACTCAGGAGGTGGTGTGAAGGGCTGGGATTACAAAGACTCGGATATGTCCTAGAAGAGATGAG
TCGCATACCAGGAGGAAGGATGTATGCAGATGACACTGCTGGCTGGGACACCCGCATCAGCAGTTTGATCTGGAGAATGAA
GCTCTAATCACCAACCAATGGAGAAAGGGCACAGGGCCTTGGCATTGGCCATAATCAAGTACACATACCAAAACAAGTGGT
AAAGGTCCTTAGACCAGCTGAAAAAGGGAAGACAGTTATGGACATTATTTGAGACAAGACCAAGGGGGAGCGGACAAGT
TGTCACITACGCTCTTAACACATTTACCAACCTAGTGGTGCAACTCATTCCGAATATGGAGGCTGAGGAAGTTCTAGAGATGCA
AGACTTGTGGCTGCTGCGGAGGTCAGAGAAAGTGACCAACTGGTTGCAGAGCAACGGATGGGATAGGCTCAAACGAATGGC
AGTCAGTGGAGATGATTGCGTTGTGAAGCCAATTGATGATAGGTTTGCACATGCCCTCAGGTTCTTGAATGATATGGGAAAAG
TTAGGAAGGACACACAAGAGTGGAAACCTCAACTGGATGGGACAACCTGGGAAGAAGTCCGTTTTGCTCCCACTTCAAC
AAGCTCCATCTCAAGGACGGGAGGTCCATTGTGGTTCCCTGCCGCCACCAAGATGAACTGATTGGCCGGGCCCCGCTCTCC
AGGGGCGGGATGGAGCATCCGGGAGACTGCTTGCTAGCAAAATCATATGCGCAAATGTGGCAGCTCCTTTATTTCCACAGAA
GGGACCTCCGACTGATGGCCAATGCCATTTGTCATCTGTGCCAGTTGACTGGGTCCAACTGGGAGAACTACCTGGTCAATCC
ATGGAAAGGGAGAATGGATGACCACTGAAGACATGCTTGTGGTGTGGAACAGAGTGTGGATTGAGGAGAACGACCACATGG
AAGACAAGACCCGATTACGAAATGGACAGACATTCCTATTTGGGAAAAAGGGAAGACTTGTGGTGTGGATCTCTCATAGG
GCACAGACCGCGCACCACCTGGGCTGAGAACATTAACCAACAGTCAACATGGTGCGCAGGATCATAGGTGATGAAGAAAAG
TACATGGACTACCTATCCACCCAAGTTCGCTACTTGGGTGAAGAAGGGTCTACACCTGGAGTGTGTGAAGCACCAATCTTAGTG
TTGTCAGGCCTGCTAGTCAGCCACAGCTTGGGGAAAGCTGTGCAGCCTGTGACCCCCCAGGAGAAGCTGGGAAACCAAGCC
TATAGTCAGGCCGAGAACGCCATGGCACGGAAGAAGCCATGCTGCTGTGAGCCCCCTCAGAGGACACTGAGTCAAAAACCC
CACGCGCTTGGAGGCGCAGGATGGGAAAAGAAGGTGGCGACCTTCCCCACCTTCAATCTGGGGCCTGAACTGGAGATCAGC
TGTGGATCTCCAGAAGAGGGACTAGTGGTTAGAGGAGACCCCCGAAAAACGCAAAACAGCATATTGACGCTGGGAAAGAC
CAGAGACTCCATGAGTTTCCACCACGCTGGCCGCCAGGCACAGATCGCCGAATAGCGCGCGCGGTGTGGGGAATCC

In some embodiments, the Zika virus has a RNA genome corresponding to the DNA sequence provided by the nucleic acid sequence of any one of SEQ ID NOs: 2-13. In some embodiments, the Zika virus has a variant genome that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5%, 99.6%, 99.7%, 99.8% or 99.9% identical to any one of SEQ ID NOs: 2-13.

Provided below are amino acid sequences of the E-proteins of Zika strains that may be used in the methods, compositions, and/or vaccines described herein.

PAT022-EP-PR

isol-ARB15076.AHF49784.1.Central_African_Republic/291-788 Flavivirus envelope glycoprotein E. (SEQ ID NO: 14)

IRCIGVSNRDFVEGMSGGTWVDVVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDRLGWGNGCGLFGKGSVLTCAKFTCSKKMTGKSIQPENLEYRIMLSVHGSQHSQMIVNDENRAKVEVTPNSPRA
EATLGGFGSLGLDCEPRTGLDFSDLYLTMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQTVVVLGS
QEGAVHTALAGALEAEMDGAKGRFLSGHLKCRKMDKRLKGVSYSLCTAAFTFTKVPATLHGTVTVEVQYAGTDGPCKVPAQM
AVDMQTLTPVGRITANPVITESTENSKMMLELDPFPGDSYIVIGVGDKKITHHWHRSGSTIGKAFEATVRGAKRMAVLGDTAWDF
GSVGGVFNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLVWLGLNTKNGSISLTCLALGGVMIFLSTAVSA

isol-IbH_30656.AEN75265.1.Nigeria/291-788 Flavivirus envelope glycoprotein E. (SEQ ID NO: 15)

IRCIGVSNRDFVEGMSGGTWVDVVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDRLGWGNGCGLFGKGSVLTCAKFTCSKKMTGKSIQPENLEYRIMLSVHGSQHSQMIVNDENRAKVEVTPNSPRA
EATLGGFGSLGLDCEPRTGLDFSDLYLTMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQTVVVLGS
QEGAVHTALAGALEAEMDGAKGRFLSGHLKCRKMDKRLKGVSYSLCTAAFTFTKVPATLHGTVTVEVQYAGRDGPCKVPAQM
AVDMQTLTPVGRITANPVITESTENSKMMLELDPFPGDSYIVIGVGDKKITHHWHRSIGKAFEATVRGAKRMAVLGDTAWDF
GSVGGVFNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLVWLGLNTKNGSISLTCLALGGVMIFLSTAVSA

ArB1362.AHL43500.1.-/291-794 Flavivirus envelope glycoprotein E. (SEQ ID NO: 16)

IRCIGVSNRDFVEGMSGGTWVDVVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDRLGWGNGCGLFGKGSVLTCAKFTCSKKMTGKSIQPENLEYRIMLSVHGSQHSQMIVNDXXXXXXNRAEVEVT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLTMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRFLSGHLKCRKMDKRLKGVSYSLCTAAFTFTKVPATLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFPGDSYIVIGVGDKKITHHWHRSGSTIGKAFEATVRGAKRMAVLG
DTAWDFGSVGGVFNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLVWLGLNTKNGSISLTCLALGGVMIFLSTAVSA

ArD128000.AHL43502.1.-/291-794 Flavivirus envelope glycoprotein E. (SEQ ID NO: 17)

IRCIGVSNRDFVEGMSGGTWVDVVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDRLGWGNGCGLFGKGSVLTCAKFTCSKKMTGKSIQPENLEYRIMLSVHGSQHSQMIXXXXXGHETDENRAKVEVT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLTMNNKHRLVRKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRFLSGHLKCRKMDKRLKGVSYSLCTAAFTFTKVPATLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFPGDSYIVIGVGDKKITHHWLKKGSSIGKAFEATVRGAKRMAVLG
DTAWDFGSVGGVFNSLGKGVHQIFGAAFKSLFGGMSWFSQILIGTLLVWLGLNTKNGSISLTCLALGGVMIFLSTAVSA

ArD158095.AHL43505.1.-/291-794 Flavivirus envelope glycoprotein E. (SEQ ID NO: 18)

IRCIGVSNRDFVEGMSGGTWVDVVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDRLGWGNGCGLFGKGSVLTCAKFTCSKKMTGKSIQPENLEYRIMLSVHGSQHSQMIVNDIGHETDENRAKVEVT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLTMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRFLSGHLKCRKMDKRLKGVSYSLCTAAFTFTKVPATLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFPGDSYIVIGVGDKKITHHWHRSGSTIGKAFEATVRGAKRMAVLG
DTAWDFGSVGGVFNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLVWLGLNTKNGSISLTCLALGGVMIFLSTAVSA

ArD158084.AHL43504.1.-/291-794 Flavivirus envelope glycoprotein E. (SEQ ID NO: 19)

PAT022-EP-PR

IRCIGVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDRGWNGCGLFGKGSVLTCAKFTCSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIVNDIGHETDENRAKVEVT
PNSPRAEATLGGFGLDCEPRTGLDSDLYLTMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRLFSGHLKCRKMDKRLKGVSYSLCTAAFTFTKVP AETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFGDSYIVIGVGDKKITHHWRSGSTIGKAFEATVRGAKRMAVLG
DTAWDFGSVGGVFNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLVWLGLNTKNGSISLTCLALGGVMIFLSTAVSA

isol-ARB13565.AHF49783.1.Central_African_Republic/291-794 Flavivirus envelope glycoprotein E. (SEQ ID NO: 20)

IRCIGVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDRGWNGCGLFGKGSVLTCAKFTCSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIVNDIGHETDENRAKVEVT
PNSPRAEATLGGFGLDCEPRTGLDSDLYLTMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRLFSGHLKCRKMDKRLKGVSYSLCTAAFTFTKVP AETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFGDSYIVIGVGDKKITHHWRSGSTIGKAFEATVRGAKRMAVLG
DTAWDFGSVGGVFNSLGKGVHQIFGAAFKSLFGGMSWFSQILIGTLLVWLGLNTKNGSISLTCLALGGVMIFLSTAVSA

isol-ARB7701.AHF49785.1.Central_African_Republic/291-794 Flavivirus envelope glycoprotein E. (SEQ ID NO: 21)

IRCIGVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDRGWNGCGLFGKGSVLTCAKFTCSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIVNDIGHETDENRAKVEVT
PNSPRAEATLGGFGLDCEPRTGLDSDLYLTMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRLFSGHLKCRKMDKRLKGVSYSLCTAAFTFTKVP AETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFGDSYIVIGVGDKKITHHWRSGSTIGKAFEATVRGAKRMAVLG
DTAWDFGSVGGVFNSLGKGVHQIFGAAFKSLFGGMSWFSQILIGTLLVWLGLNTKNGSISLTCLALGGVMIFLSTAVSA

isol-ArD_41519.AEN75266.1.Senegal/291-794 Flavivirus envelope glycoprotein E. (SEQ ID NO: 22)

IRCIGVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDRGWNGCGLFGKGSVLTCAKFTCSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIVNDIGHETDENRAKVEVT
PNSPRAEATLGGFGLDCEPRTGLDSDLYLTMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRLFSGHLKCRKMDKRLKGVSYSLCTAAFTFTKVP AETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFGDSYIVIGVGDKKITHHWRSGSTIGKAFEATVRGAKRMAVLG
DTAWDFGSVGGVFNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLVWLGLNTKNGSISLTCLALGGVMIFLSTAVSA

MR766-NIID.BAP47441.1.Uganda/291-794 Flavivirus envelope glycoprotein E. (SEQ ID NO: 23)

IRCIGVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDRGWNGCGLFGKGSVLTCAKFTCSKKMTGKSIQPENLEYRIMLSVHGSQHSGMTVNDIGYETDENRAKVEVT
PNSPRAEATLGGFGLDCEPRTGLDSDLYLTMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGLFSGHLKCRKMDKRLKGVSYSLCTAAFTFTKVP AETLHGTVTVEVQYAGTDGPCK
IPVQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFGDSYIVIGVGDKKITHHWRSGSTIGKAFEATVRGAKRMAVLGD
TAWDFGSVGGVFNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLVWLGLNTKNGSISLTCLALGGVMIFLSTAVSA

PAT022-EP-PR

LC002520.1/326-829 Zika virus genomic RNA, strain: MR766-NIID, Uganda, Flavivirus envelope glycoprotein E. (SEQ ID NO: 24)

IRCIGVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWGNGCGLFGKGSVLTCAKFTCSKKMTGKSIQPENLEYRIMLSVHGSQHSGMTVNDIGYETDENRAKVEVT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLTMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGKLFSGHLKCRKMDKRLKGVSYSLCTAAFTFTKVP AETLHGTVTVEVQYAGTDGPCK
IPVQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFPGDSYIVIGVGDKKITHHWHRSGSTIGKA FEATVRGAKRMAVLGD
TAWDFGSVGGVFNSLGKGIHQIFGA AFKSLFGGMSWFSQILIGTLLVWLGLNTKNGSISLTCLALGGVMIFLSTAVSA

isol-MR_766.AEN75263.1.Uganda/291-794 Flavivirus envelope glycoprotein E. (SEQ ID NO: 25)

IRCIGVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWGNGCGLFGKGSVLTCAKFTCSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIVNDTG YETDENRAKVEVT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLTMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGKLFSGHLKCRKMDKRLKGVSYSLCTAAFTFTKVP AETLHGTVTVEVQYAGTDGPCK
IPVQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFPGDSYIVIGVGDKKITHHWHRSGSTIGKA FEATVRGAKRMAVLGD
TAWDFGSVGGVFNSLGKGIHQIFGA AFKSLFGGMSWFSQILIGTLLVWLGLNTKNGSISLTCLALGGVMIFLSTAVSA

ArD7117.AHL43501.1.-/291-794 Flavivirus envelope glycoprotein E. (SEQ ID NO: 26)

IRCIGVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWGNGCGLFGKGSVLTCAKFTCSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIVNDIGHETDENRAKVEVT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLTMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRLFSGHLKCRKMDKRLKGVSYSLCTAVCTAAKVP AETLHGTVTVEVQYAGTDGPC
KVPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFPGDSYIVIGVGDKKITHHWHRSGSTIGKA FEATVRGAKRMAVL
GDTAWDFGSVGGVFNSLGKGIHQIFGA AFKSLFGGMSWFSQILIGTLLVWLGLNTKNGSISLTCLALGGVMIFLSTAVSA

AY632535.2/326-825 NC_012532.1 Zika virus strain MR 766, Uganda, Flavivirus envelope glycoprotein E.
(SEQ ID NO: 27)

IRCIGVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWGNGCGLFGKGSVLTCAKFTCSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIGYETDEDR AKVEVT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLTMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRLFSGHLKCRKMDKRLKGVSYSLCTAAFTFTKVP AETLHGTVTVEVQYAGTDGPCK
IPVQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFPGDSYIVIGVGDKKITHHWHRSGSTIGKA FEATVRGAKRMAVL
GDTAWDFGSVGGVFNSLGKGIHQIFGA AFKSLFGGMSWFSQILIGTLLVWLGLNTKNGSISLTCLALGGVMIFLSTAVSA

MR_766.AAV34151.1.Uganda/291-790 Flavivirus envelope glycoprotein E. [Q32ZE1|Q32ZE1_9FL (SEQ ID
NO: 28)

IRCIGVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWGNGCGLFGKGSVLTCAKFTCSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIGYETDEDR AKVEVT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLTMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRLFSGHLKCRKMDKRLKGVSYSLCTAAFTFTKVP AETLHGTVTVEVQYAGTDGPCK
IPVQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFPGDSYIVIGVGDKKITHHWHRSGSTIGKA FEATVRGAKRMAVL
GDTAWDFGSVGGVFNSLGKGIHQIFGA AFKSLFGGMSWFSQILIGTLLVWLGLNTKNGSISLTCLALGGVMIFLSTAVSA

PAT022-EP-PR

MR_766.YP_009227198.1.Uganda/1-500 envelope protein E [Zika virus] (SEQ ID NO: 29)

IRCIQVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWGNGCGLFGKGSVLTCAKFTCSKKMTGKSIQPENLEYRIMLSVHGSQHSQSGMIGYETDEDRAKVEVTPNSPR
AEATLGGFGSLGLDCEPRTGLDFSDLYLTMMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQTVVVL
GSQEGAVHTALAGALEAEMDGAKGRLFSGHLKCRLLKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCKIPVQ
MAVDMQTLTPVGRUITANPVITESTENSKMMLELDPFGDSYIVIGVGDKKITHHWHRSSTIGKAFEATVRGAKRMAVLGDTAW
DFGSVGGVFNLSLKGKIHQIFGAAFKSLFGGMSWFSQILIGTLLVWLGLNTKNGSISLTCLALGGVMIFLSTAVSA

KU681081.3/308-811 Zika virus isolate Zika virus/H.sapiens-tc/THA/2014/SV0127- 14, Thailand, Flavivirus envelope glycoprotein E. (SEQ ID NO: 30)

IRCIQVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWGNGCGLFGKGSVLTCAKFAKSKMTGKSIQPENLEYRIMLSVHGSQHSQSGMIVNDTGHETDENRAKVEIT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLTMMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRLLSSGHLKCRLLKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRUITANPVITEGTENSKMMLELDPFGDSYIVIGVGKKITHHWHRSSTIGKAFEATVRGAKRMAVLG
DTAWDFGSVGGVNLNLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSA

isol-Zika_virus%*H.sapiens-tc*%THA%2014%SV0127- 14.AMD61710.1.Thailand/291-794 Flavivirus envelope glycoprotein E. (SEQ ID NO: 31)

IRCIQVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWGNGCGLFGKGSVLTCAKFAKSKMTGKSIQPENLEYRIMLSVHGSQHSQSGMIVNDTGHETDENRAKVEIT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLTMMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRLLSSGHLKCRLLKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRUITANPVITEGTENSKMMLELDPFGDSYIVIGVGKKITHHWHRSSTIGKAFEATVRGAKRMAVLG
DTAWDFGSVGGVNLNLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSA

CK-ISL_2014.AIC06934.1.Cook_Islands/1-504 Flavivirus envelope glycoprotein E. (Fragment) OS=Zika virus
GN=E PE=4 SV=1 (SEQ ID NO: 32)

IRCIQVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWGNGCGLFGKGSVLTCAKFAKSKMTGKSIQPENLEYRIMLSVHGSQHSQSGMIVNDTGHETDENRAKVEIT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLTMMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRLLSSGHLKCRLLKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRUITANPVITESTENSKMMLELDPFGDSYIVIGVGKKITHHWHRSSTIGKAFEATVRGAKRMAVLG
TAWDFGSVGGALNLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSA

Natal_RGN.AMB18850.1.Brazil:_Rio_Grande_do_Norte,_Natal/291-794 Flavivirus envelope glycoprotein E.]
(SEQ ID NO: 33)

IRCIQVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWGNGCGLFGKGSVLTCAKFAKSKMTGKSIQPENLEYRIMLSVHGSQHSQSGMIVNDTGHETDENRAKVEIT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLTMMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRLLSSGHLKCRLLKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK

PAT022-EP-PR

VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFPGDSYIVIGVGEKKITHHWHRSBSTIGKAFAEATVRGAKRMAVLGD
TAWDFGSGVGGALNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSA

isol-Si323.AMC37200.1.Colombia/1-504 Flavivirus envelope glycoprotein E. (SEQ ID NO: 34)

IRCIGVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDRCWGNGCGLFGKGSVLTCAKFACSKKMTGKSIQENLEYRIMLSVHGSQHSQSGMIVNDTGHETDENRAKVEIT
PNSPRAEATLGGFGLDCEPRTGLDFSDLYLTMNNKHWLVHKEWFHDIPLPWHAGADTGTTPHWNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRLSSGHLKCRKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFPGDSYIVIGVGEKKITHHWHRSBSTIGKAFAEATVRGAKRMAVLGD
TAWDFGSGVGGALNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSA

KU707826.1/317-820 Zika virus isolate SSABR1, Brazil, Flavivirus envelope glycoprotein E. (SEQ ID NO: 35)

IRCIGVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDRCWGNGCGLFGKGSVLTCAKFACSKKMTGKSIQENLEYRIMLSVHGSQHSQSGMIVNDTGHETDENRAKVEIT
PNSPRAEATLGGFGLDCEPRTGLDFSDLYLTMNNKHWLVHKEWFHDIPLPWHAGADTGTTPHWNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRLSSGHLKCRKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFPGDSYIVIGVGEKKITHHWHRSBSTIGKAFAEATVRGAKRMAVLGD
TAWDFGSGVGGALNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSA

KU509998.1/326-829 Zika virus strain Haiti/1225/2014, Haiti, Flavivirus envelope glycoprotein E. (SEQ ID NO: 36)

IRCIGVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDRCWGNGCGLFGKGSVLTCAKFACSKKMTGKSIQENLEYRIMLSVHGSQHSQSGMIVNDTGHETDENRAKVEIT
PNSPRAEATLGGFGLDCEPRTGLDFSDLYLTMNNKHWLVHKEWFHDIPLPWHAGADTGTTPHWNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRLSSGHLKCRKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFPGDSYIVIGVGEKKITHHWHRSBSTIGKAFAEATVRGAKRMAVLGD
TAWDFGSGVGGALNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSA

isol-GDZ16001.AML82110.1.China/291-794 Flavivirus envelope glycoprotein E. (SEQ ID NO: 37)

IRCIGVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDRCWGNGCGLFGKGSVLTCAKFACSKKMTGKSIQENLEYRIMLSVHGSQHSQSGMIVNDTGHETDENRAKVEIT
PNSPRAEATLGGFGLDCEPRTGLDFSDLYLTMNNKHWLVHKEWFHDIPLPWHAGADTGTTPHWNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRLSSGHLKCRKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFPGDSYIVIGVGEKKITHHWHRSBSTIGKAFAEATVRGAKRMAVLGD
TAWDFGSGVGGALNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSA

BeH819015.AMA12085.1.Brazil/291-794 Flavivirus envelope glycoprotein E. (SEQ ID NO: 38)

IRCIGVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDRCWGNGCGLFGKGSVLTCAKFACSKKMTGKSIQENLEYRIMLSVHGSQHSQSGMIVNDTGHETDENRAKVEIT
PNSPRAEATLGGFGLDCEPRTGLDFSDLYLTMNNKHWLVHKEWFHDIPLPWHAGADTGTTPHWNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRLSSGHLKCRKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFPGDSYIVIGVGEKKITHHWHRSBSTIGKAFAEATVRGAKRMAVLGD
TAWDFGSGVGGALNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSA

PAT022-EP-PR

MRS_OPY_Martinique_PaRi_2015.AMC33116.1.Martinique/291-794 Flavivirus envelope glycoprotein E. (SEQ ID NO: 39)

IRCIGVSNRDFVEGMSGGTWVDVVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDRGWNGCGLFGKGSVLTCAKFACSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIVNDTGHETDENRAKVEIT
PNSPRAEATLGGFGLDCEPRTGLDFSDLYYLTMMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRLSSGHLKCRLLKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRUITANPVITESTENSKMMLELDPFPGDSYIVIGVGEKKITHHWHRSBSTIGKAFAEATVRGAKRMAVLGD
TAWDFGSGVGALNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSA

KU501215.1/308-811 Zika virus strain PRVABC59, Puerto Rico, Flavivirus envelope glycoprotein E. (SEQ ID NO: 40)

IRCIGVSNRDFVEGMSGGTWVDVVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDRGWNGCGLFGKGSVLTCAKFACSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIVNDTGHETDENRAKVEIT
PNSPRAEATLGGFGLDCEPRTGLDFSDLYYLTMMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRLSSGHLKCRLLKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRUITANPVITESTENSKMMLELDPFPGDSYIVIGVGEKKITHHWHRSBSTIGKAFAEATVRGAKRMAVLGD
TAWDFGSGVGALNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSA

Haiti%1225%2014.AMB37295.1.Haiti/291-794 Flavivirus envelope glycoprotein E. (SEQ ID NO: 41)

IRCIGVSNRDFVEGMSGGTWVDVVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDRGWNGCGLFGKGSVLTCAKFACSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIVNDTGHETDENRAKVEIT
PNSPRAEATLGGFGLDCEPRTGLDFSDLYYLTMMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRLSSGHLKCRLLKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRUITANPVITESTENSKMMLELDPFPGDSYIVIGVGEKKITHHWHRSBSTIGKAFAEATVRGAKRMAVLGD
TAWDFGSGVGALNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSA

KU527068.1/308-811 Zika virus strain Natal RGN, Brazil: Rio Grande do Norte, Natal, Flavivirus envelope glycoprotein E. (SEQ ID NO: 42)

IRCIGVSNRDFVEGMSGGTWVDVVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDRGWNGCGLFGKGSVLTCAKFACSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIVNDTGHETDENRAKVEIT
PNSPRAEATLGGFGLDCEPRTGLDFSDLYYLTMMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRLSSGHLKCRLLKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRUITANPVITESTENSKMMLELDPFPGDSYIVIGVGEKKITHHWHRSBSTIGKAFAEATVRGAKRMAVLGD
TAWDFGSGVGALNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSA

isol-Z1106027.ALX35662.1.Suriname/5-508 Flavivirus envelope glycoprotein E. (SEQ ID NO: 43)

IRCIGVSNRDFVEGMSGGTWVDVVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDRGWNGCGLFGKGSVLTCAKFACSKKMTGKSIQPENLEYRIMLSVHGSQHSGMIVNDTGHETDENRAKVEIT
PNSPRAEATLGGFGLDCEPRTGLDFSDLYYLTMMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRLSSGHLKCRLLKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRUITANPVITESTENSKMMLELDPFPGDSYIVIGVGEKKITHHWHRSBSTIGKAFAEATVRGAKRMAVLGD
TAWDFGSGVGALNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSA

PAT022-EP-PR

isol-FLR.AMM39804.1.Colombia:_Barranquilla/291-794 Flavivirus envelope glycoprotein E. (SEQ ID NO: 44)

IRCIGVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDRGWNGCGLFGKGSVLTCAKFACSKKMTGKSIQPENLEYRIMLSVHGSQHSQSGMIVNDTGHETDENRAKVEIT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYYLTMMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRLSSGHLKCRMKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFPGDSYIVIGVGEKKITHHWHRSGSTIGKAFEATVRGAKRMAVLGD
TAWDFGSGVGGALNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSA

PLCal_ZV_isol-From_Vero_E6_cells.AHL37808.1.Canada/254-757 Flavivirus envelope glycoprotein E. (SEQ ID NO: 45)

IRCIGVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDRGWNGCGLFGKGSVLTCAKFACSKKMTGKSIQPENLEYRIMLSVHGSQHSQSGMIVNDTGHETDENRAKVEIT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYYLTMMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRLSSGHLKCRMKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFPGDSYIVIGVGEKKITHHWHRSGSTIGKAFEATVRGAKRMAVLGD
TAWDFGSGVGGALNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSA

BeH818995.AMA12084.1.Brazil/291-794 Flavivirus envelope glycoprotein E. [Zika virus].

IRCIGVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDRGWNGCGLFGKGSVLTCAKFACSKKMTGKSIQPENLEYRIMLSVHGSQHSQSGMIVNDTGHETDENRAKVEIT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYYLTMMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRLSSGHLKCRMKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFPGDSYIVIGVGEKKITHHWHRSGSTIGKAFEATVRGAKRMAVLGD
TAWDFGSGVGGALNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSA

H/PF/2013.AHZ13508.1.French_Polynesia/291-794 Flavivirus envelope glycoprotein E. (SEQ ID NO: 47)

IRCIGVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDRGWNGCGLFGKGSVLTCAKFACSKKMTGKSIQPENLEYRIMLSVHGSQHSQSGMIVNDTGHETDENRAKVEIT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYYLTMMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRLSSGHLKCRMKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFPGDSYIVIGVGEKKITHHWHRSGSTIGKAFEATVRGAKRMAVLGD
TAWDFGSGVGGALNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSA

PRVABC59.AMC13911.1.Puerto_Rico/291-794 Flavivirus envelope glycoprotein E. (SEQ ID NO: 48)

IRCIGVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDRGWNGCGLFGKGSVLTCAKFACSKKMTGKSIQPENLEYRIMLSVHGSQHSQSGMIVNDTGHETDENRAKVEIT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYYLTMMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRLSSGHLKCRMKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFPGDSYIVIGVGEKKITHHWHRSGSTIGKAFEATVRGAKRMAVLGD
TAWDFGSGVGGALNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSA

KU321639.1/326-829 Zika virus strain ZikaSPH2015, Brazil, Flavivirus envelope glycoprotein E. (SEQ ID NO: 49)

PAT022-EP-PR

IRCIGVSNRDFVEGMSGGTWVDIVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTYVCKRTLVDRLGWNGCGLFGKGSVLTCAKFAKSKMTGKSIQPENLEYRIMLSVHGSQHSQSGMIVNDTGHETDENRAKVEIT
PNSPRAEATLGGFGLDCEPRTGLDSDLYLTMNNKHWLVHKEWFHDIPLPWHAGADTGTTPHWNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRLSSGHLKCRKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFPGDSYIVIGVGEKKITHHWHRSGSTIGKAFEATVRGAKRMAVLGD
TAWDFGSVGGALNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSA

ZikaSPH2015.ALU33341.1.Brazil/291-794 Flavivirus envelope glycoprotein E. (SEQ ID NO: 50)

IRCIGVSNRDFVEGMSGGTWVDIVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTYVCKRTLVDRLGWNGCGLFGKGSVLTCAKFAKSKMTGKSIQPENLEYRIMLSVHGSQHSQSGMIVNDTGHETDENRAKVEIT
PNSPRAEATLGGFGLDCEPRTGLDSDLYLTMNNKHWLVHKEWFHDIPLPWHAGADTGTTPHWNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRLSSGHLKCRKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFPGDSYIVIGVGEKKITHHWHRSGSTIGKAFEATVRGAKRMAVLGD
TAWDFGSVGGALNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSA

103344.AMC13912.1.Guatemala/291-794 polyprotein [Zika virus]. 103344.AMC13912.1.Guatemala
Flavivirus envelope glycoprotein E. (SEQ ID NO: 51)

IRCIGVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTYVCKRTLVDRLGWNGCGLFGKGSVLTCAKFAKSKMTGKSIQPENLEYRIMLSVHGSQHSQSGMIVNDTGHETDENRAKVEIT
PNSPRAEATLGGFGLDCEPRTGLDSDLYLTMNNKHWLVHKEWFHDIPLPWHAGADTGTTPHWNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRLSSGHLKCRKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFPGDSYIVIGVGEKKITHHWHRSGSTIGKAFEATVRGAKRMAVLGD
TAWDFGSVGGALNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSA

isol-Brazil-ZKV2015.AMD16557.1.Brazil/291-794 Flavivirus envelope glycoprotein E. (SEQ ID NO: 52)

IRCIGVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTYVCKRTLVDRLGWNGCGLFGKGSVLTCAKFAKSKMTGKSIQPENLEYRIMLSVHGSQHSQSGMIVNDTGHETDENRAKVEIT
PNSPRAEATLGGFGLDCEPRTGLDSDLYLTMNNKHWLVHKEWFHDIPLPWHAGADTGTTPHWNKEALVEFKDAHAKRQT
VVVLGTQEGAVHTALAGALEAEMDGAKGRLSSGHLKCRKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFPGDSYIVIGVGEKKITHHWHRSGSTIGKAFEATVRGAKRMAVLGD
TAWDFGSVGGALNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSA

KU497555.1/308-811 Zika virus isolate Brazil-ZKV2015, Flavivirus envelope glycoprotein E. (SEQ ID NO: 53)

IRCIGVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTYVCKRTLVDRLGWNGCGLFGKGSVLTCAKFAKSKMTGKSIQPENLEYRIMLSVHGSQHSQSGMIVNDTGHETDENRAKVEIT
PNSPRAEATLGGFGLDCEPRTGLDSDLYLTMNNKHWLVHKEWFHDIPLPWHAGADTGTTPHWNKEALVEFKDAHAKRQT
VVVLGTQEGAVHTALAGALEAEMDGAKGRLSSGHLKCRKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFPGDSYIVIGVGEKKITHHWHRSGSTIGKAFEATVRGAKRMAVLGD
TAWDFGSVGGALNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSA

isol-ZJ03.AMM39806.1.China/291-794 Flavivirus envelope glycoprotein E. (SEQ ID NO: 54)

IRCIGVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTYVCKRTLVDRLGWNGCGLFGKGSVLTCAKFAKSKMTGKSIQPENLEYRIMLSVHGSQHSQSGMIVNDTGHETDENRAKVEIT

PAT022-EP-PR

PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYYLTMMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRLSSGHLKCRKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFGDSYIVIGVGEKKITHHWHRSGSTIGKAFEATVRGARRMAVLG
DTAWDFGSGVGGALNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSA

isol-F5513025.AFD30972.1.Cambodia/291-794 Flavivirus envelope glycoprotein E. (SEQ ID NO: 55)

IRCIGVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDRLGWGNGCGLFGKGSVLTCAKFAKSKMTGKSIQPENLEYRIMLSVHGSQHSQSGMIVNDTGHETDENRAKVEIT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYYLTMMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRLSSGHLKCRKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFGDSYIVIGVGEKKITHHWHRSGSTIGKAFEATVRGAKRMAVLGD
TAWDFGSGVGGALNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSA

isol-Z1106032.ALX35660.1.Suriname/291-794 Flavivirus envelope glycoprotein E. [Zika virus] (SEQ ID NO: 56)

IRCIGVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDRLGWGNGCGLFGKGSVLTCAKFAKSKMTGKSIQPENLEYRIMLSVHGSQHSQSGMIVNDTGHETDENRAKVEIT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYYLTMMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRLSSGHLKCRKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFGDSYIVIGVGEKKITHHWHRSGSTIGKAFEATVRGAKRMAVLGD
TAWDFGSGVGGALNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLMWLGLNNAKNGSISLMCLALGGVLIFLSTAVSA

isol-Z1106033.ALX35659.1.Suriname/291-794 Flavivirus envelope glycoprotein E. [Zika virus] (SEQ ID NO: 57)

IRCIGVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDRLGWGNGCGLFGKGSVLTCAKFAKSKMTGKSIQPENLEYRIMLSVHGSQHSQSGMIVNDTGHETDENRAKVEIT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYYLTMMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRLSSGHLKCRKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFGDSYIVIGVGEKKITHHWHRSGSTIGKAFEATVRGAKRMAVLGD
TAWDFGSGVGGALNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLMWLGLNNAKNGSISLMCLALGGVLIFLSTAVSA

isol-BeH828305.AMK49165.1.Brazil/291-794 Flavivirus envelope glycoprotein E. (SEQ ID NO: 58)

IRCIGVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDRLGWGNGCGLFGKGSVLTCAKFAKSKMTGKSIQPENLEYRIMLSVHGSQHSQSGMIVNDTGHETDENRAKVEIT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYYLTMMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRLSSGHLKCRKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFGDSYIVIGVGEKKITHHWHRSGSTIGKAFEATVRGAKRMAVLGD
TAWDFGSGVGGALNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSA

isol-GD01.AMK79468.1.China/291-794 Flavivirus envelope glycoprotein E. (SEQ ID NO: 59)

IRCIGVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDRLGWGNGCGLFGKGSVLTCAKFAKSKMTGKSIQPENLEYRIMLSVHGSQHSQSGMIVNDTGHETDENRAKVEIT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYYLTMMNNKHWLVHKEWFHDIPLPWHAGADTGTPHWNNKEALVEFKDAHAKRQT

PAT022-EP-PR

VVVLGSQEGAVHTALAGALEAEMDGAKGRLSSGHLKCRKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFPGDSYIVIGVGEKKITHHWHRSSTIGKAFEATVRGAKRMAVLGD
TAWDFGSVGGALNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSA

isol-Z1106031.ALX35661.1.Suriname/291-794 Flavivirus envelope glycoprotein E. (SEQ ID NO: 60)

IRCIGVSNRDFVEGMSGGTWVDVVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWGNGCGLFGKGSVLTCAKFAKSKKMTGKSIQPENLEYRIMLSVHGSQHSQMIVNDTGHETDENRAKVEIT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLTMNNKHVLVHKEWFHDIPLPHWAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRLSSGHLKCRKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VLAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFPGDSYIVIGVGEKKITHHWHRSSTIGKAFEATVRGAKRMAVLGD
TAWDFGSVGGALNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSA

ACD75819.1.Micronesia/291-794 Flavivirus envelope glycoprotein E. (SEQ ID NO: 61)

IRCIGVSNRDFVEGMSGGTWVDVVLEHGGCVTVMAQDKPAVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWGNGCGLFGKGSVLTCAKFAKSKKMTGKSIQPENLEYRIMLSVHGSQHSQMIVNDTGHETDENRAKVEIT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLTMNNKHVLVHKEWFHDIPLPHWAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRLSSGHLKCRKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFPGDSYIVIGVGEKKITHHWHRSSTIGKAFEATVRGAKRMAVLGD
TAWDFGSVGGALNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLVWLGLNTKNGSISLTCLALGGVLIFLSTAVSA

KU681082.3/308-811 Zika virus isolate Zika virus/H.sapiens-tc/PHL/2012/CPC-0740, Philippines, Flavivirus
envelope glycoprotein E. (SEQ ID NO: 62)

IRCIGVSNRDFVEGMSGGTWVDVVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWGNGCGLFGKGSVLTCAKFAKSKKMTGKSIQPENLEYRIMLSVHGSQHSQMIVNDTGHETDENRAKVEIT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLTMNNKHVLVHKEWFHDIPLPHWAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRLSSGHLKCRKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFPGDSYIVIGVGEKKITHHWHRSSTIGKAFEATVRGAKRMAVLGD
TAWDFGSVGGALNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLVWLGLNTKNGSISLTCLALGGVLIFLSTAVSA

isol-Zika_virus%*H.sapiens-tc*/PHL%2012%CPC-0740.AMD61711.1.Philippines/291-794 Flavivirus envelope
glycoprotein E. (SEQ ID NO: 63)

IRCIGVSNRDFVEGMSGGTWVDVVLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDGRWGNGCGLFGKGSVLTCAKFAKSKKMTGKSIQPENLEYRIMLSVHGSQHSQMIVNDTGHETDENRAKVEIT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLTMNNKHVLVHKEWFHDIPLPHWAGADTGTPHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRLSSGHLKCRKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFPGDSYIVIGVGEKKITHHWHRSSTIGKAFEATVRGAKRMAVLGD
TAWDFGSVGGALNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLVWLGLNTKNGSISLTCLALGGVLIFLSTAVSA

isol-BeH823339.AMK49164.2.Brazil/291-794 Flavivirus envelope glycoprotein E. (SEQ ID NO: 64)

IRCIGVSNRDFVEGMSGGTWVDVVLEHGGCVTVMAQDKPTVDIELVSTTVSNMAEVRSYCYEATISDIASDSRCPTQGEAYLDKQ
DTQYVCKRTLVDGRWGNGCGLFGKGSVLTCAKFAKSKKMTGKSIQPENLEYRIMLSVHGSQHSQMIVNDTGHETDENRAKVEIT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYLTMNNKHVLVHKEWFHDIPLPHWAGADTGTPHWNNKEALVEFKDAHAKRQT
AVVLGSQEGAVHTALAGALEAEMDGAKGRLSSGHLKCRKMDKRLKGVSYSLCTAAFTFTKIPAETLHGTVTVEVQYAGTDGPCK

PAT022-EP-PR

VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFPGDSYIVIGVGEKKITHHWHRSGSTIGKAFEATVRGAKRMAVLGD
TAWDFGSVGGALNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSA

isol-P6-740.AEN75264.1.Malaysia/291-794 Flavivirus envelope glycoprotein E. (SEQ ID NO: 65)

IRCI GVS NRDFVEGMSGGTWVDV VLEHGGCVTVMAQDKPTVDIELVTTTVSNMAEVR SYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVD RGVNGCGLF GKGSLVTC AKFACSKKMTGKSIQ PENLEYRIMLSVHGSQHSGMIVNDXGHETDENRAKVEIT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYYLT MN NKHWLVHKEWFHDIPLPWHAGADTGT PHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRLSSGHLKCR LKMDKLR LKGVSYSLCTAAFTFTKIP AETLHGT VTVVEVQYAGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFPGDSYIVIGVGD K KITHHWXRSGSTIGKAFEATVRGAKRMAVLG
DTAWDFGSVGGALNSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLVWLGLNTKNGSISLTCLALGGVLIFLSTAVSA

KU744693.1/326-829 Zika virus isolate VE_Ganxian, China, Flavivirus envelope glycoprotein E. (SEQ ID NO: 66)

IRCI GVS NRDFVEGMSGGTWVDV VLEHGGCVTAMAQDKPTVDIELVTTTVSNMAEVR SYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVD RGVNGCGLF GKGSLVTC AKFACSKKMTGKSIQ PENLEYRIMLSVHGSQHSGMLVNDTG HETDENRAKVEIT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYYLT MN NKHWLAHKEWFHDIPLPWHAGAATGT PHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRLSSGHLKCR LKMDKLR LKGVSYSLCTAAFTFTKIP AETVDGT VTVVEGQYGGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFPGDSYIVIGVGEKKITHHWHRSGSTIGKAFEATVRGAKRMAVLGD
TAWDFGSVGGALNSLGKGIHQIIGA AFKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSG

isol-VE_Ganxian.AMK79469.1.China/291-794 Flavivirus envelope glycoprotein E. (SEQ ID NO: 67)

IRCI GVS NRDFVEGMSGGTWVDV VLEHGGCVTAMAQDKPTVDIELVTTTVSNMAEVR SYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVD RGVNGCGLF GKGSLVTC AKFACSKKMTGKSIQ PENLEYRIMLSVHGSQHSGMLVNDTG HETDENRAKVEIT
PNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYYLT MN NKHWLAHKEWFHDIPLPWHAGAATGT PHWNNKEALVEFKDAHAKRQT
VVVLGSQEGAVHTALAGALEAEMDGAKGRLSSGHLKCR LKMDKLR LKGVSYSLCTAAFTFTKIP AETVDGT VTVVEGQYGGTDGPCK
VPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFPGDSYIVIGVGEKKITHHWHRSGSTIGKAFEATVRGAKRMAVLGD
TAWDFGSVGGALNSLGKGIHQIIGA AFKSLFGGMSWFSQILIGTLLMWLGLNTKNGSISLMCLALGGVLIFLSTAVSG

ArD157995.AHL43503.1./291-794 Flavivirus envelope glycoprotein E. (SEQ ID NO: 68)

ISCIGVSNRDLVEGMSGGTWVDV VLEHGGCVTEMAQDKPTVDIELVTMTVSNMAEVR SYCYEASISDMASASRCPTQGEPSLDK
QSDTQSVCKRTLGD RGVNGCGIF GKGSLVTC SKFTCKKMPGKSIQ PENLEYRIMLPVHGSQHSGMIVNDIG HETDENRAKVEV
TPNSPRAEATLGGFGSLGLDCEPRTGLDFSDLYYLT MN NKHWLVHKEWFHDIPLPWHAGADTGT PHWNNKEALVEFKDAHAKRO
TVVVLGSQEGAVHTALAGALEAEMDGAKGRLSFGHLKCR LKMDKLR LKGVSYSLCTAAFTFTKIP AETLHGT VTVVEVQSAGTDGPC
KVPAQMAVDMQTLTPVGRITANPVITESTENSKMMLELDPFPGDSYIVIGVGD K KITHHWHRSGSTIGKAFEATVRGAKRMAVL
GDTAWDFGSVGGVFNLSLGKGIHQIFGAAFKSLFGGMSWFSQILIGTLLVWLGLNTKNGSISLTCLALGGVMIFLSTAVSA

MR_766.ABI54475.1.Uganda/291-788 Flavivirus envelope glycoprotein E. (SEQ ID NO: 69)

PAT022-EP-PR

IRCIQVSNRDFVEGMSGGTWVDVLEHGGCVTVMAQDKPTVDIELVTTTNSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQ
SDTQYVCKRTLVDRGWGNGCGLFGKGSVLTCAKFTCSKKMTGKSIQPENLEYRIMLSVHG5QH5GMIVNDENRAKVEVTPNSPRA
EATLGGFGSLGLDCEPRTGLDFSDLYLTMNNKHWLVHKEWFHDIPLWHAGADTGTPHWNNKEALVEFKDAHAKRQTVVVLGS
QEGAVHTALAGALEAEMDGAKGRLFSGHLKCRKMDKLRKLGVSYSLCTAAFTFTKPAETLHGTVTVEVQYAGTDGPCKVPAQM
AVDMQTLTPVGRITANPVITESTENSKMMLELDPFPGDSYIVIGVGDKKITHHWHRSGSTIGKAFEATVRGAKRMAVLGDTAWDF
GSVGGVFNSLKGKIHQIFGAAFKSLFGGMSWFSQJLIGTLLVWLGLNTKNGSISLTCLALGGVMIFLSTAVSA

In some embodiments, the Zika virus has polyprotein, including an envelope (E) protein, with an amino acid sequence provided by any one of SEQ ID NO: 14-70. In some embodiments, the polyprotein or E protein sequence is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5%, 99.6%, 99.7%, 99.8% or 99.9% identical to any one of SEQ ID NOs: 2-69.

The terms "identical" or percent "identity" in the context of two or more nucleic acids or amino acid sequences refer to two or more sequences or subsequences that are the same. Two sequences are "substantially identical" if two sequences have a specified percentage of amino acid residues or nucleotides that are the same (e.g., at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity) over a specified region or over the entire sequence, when compared and aligned for maximum correspondence over a comparison window, or designated region as measured using one of the following sequence comparison algorithms or by manual alignment and visual inspection. Optionally, the identity exists over a region that is at least about 50 nucleotides (or 10 amino acids) in length, or more preferably over a region that is 100 to 500 or 1000 or more nucleotides (or 20, 50, 200 or more amino acids) in length. In some embodiments, the identity exists over the length of a protein, such as the E protein.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. Methods of alignment of sequences for comparison are well known in the art. See, e.g., by the local homology algorithm of Smith and Waterman (1970) Adv. Appl. Math. 2:482c, by the homology alignment algorithm of Needleman and Wunsch, J. Mol. Biol. 48:443, 1970, by the search for similarity method of Pearson and Lipman. Proc. Natl. Acad. Sci. USA 85:2444, 1988, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, Jalview and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Or., Madison, WI), by multi sequence alignment implementation using e.g. CLUSTALW (Larkin et al., (2007). Bioinformatics, 23,

2947-2948.) or MAFFT (Kato & Toh 2008 Briefings in Bioinformatics 9:286-298), or by manual alignment and visual inspection (see. e.g., Brent et al., Current Protocols in Molecular Biology, John Wiley & Sons, Inc. (Ringbou ed., 2003)). Two examples of algorithms that are suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al., Nuc. Acids Res. 25:3389-3402, 1977; and Altschul et al., J. Mol. Biol. 215:403-410, 1990, respectively.

EXAMPLES

Example 1: Development of a purification process for live attenuated Chikungunya virus vaccine produced in Vero cells

A downstream process was developed for the purification of infectious Chikungunya virus particles whereby non-infectious virus particles and aggregates are removed by the addition of protamine sulphate. The unexpected and novel purification properties of protamine sulphate (PS) were evaluated in purification processes for Chikungunya Virus (ChikV) as follows:

A downstream purification process for the attenuated Chikungunya virus mutant "Δ5nsP3" (as described by Hallengård et al., 2014, *supra*) produced under standard cell culture conditions in Vero cells was developed. Briefly, the downstream process consists of crude harvest filtration followed by concentration and diafiltration on a tangential flow filtration (TFF) system. DNA and host cell proteins were reduced by precipitation with protamine sulphate and by batch adsorption, respectively. Sucrose density gradient centrifugation was done as a final polishing step. Out of 16 roller bottles 1×10^{12} total PFU were purified with an overall DSP process yield of 10 - 15 % (~1 log₁₀ TCID₅₀ loss). Sucrose gradient pool samples were characterized with regard to product-related impurities, such as hcDNA, HCP and endotoxins and met safety criteria.

Harvest of Vero cell culture medium containing ChikV Δ5nsP3

ChikV Δ5nsP3 was grown on Vero cells in roller bottles. A first harvest was performed after 24 hours post infection (hpi; day 1 harvest) and stored at 2-8°C until further processing. After the first harvest, fresh medium was added and the roller bottles were returned to the incubator. A second harvest was done after 48 hours post infection (day 2 harvest) and stored at 2-8 °C.

Filtration of crude cell culture harvest

At both harvest timepoints the crude harvest was immediately filtered using a 0.2 µm filter capsule (GE ULTA™ CG, 2 inch). The filtered harvest after 48 hpi was pooled together with the 24 hpi harvest and the pooled filtered harvest material was immediately further processed by ultrafiltration.

Purification of ChikV Δ5nsP3 by tangential flow filtration (TFF)

The pooled filtered harvest material was further processed by tangential flow filtration (TFF) in order to concentrate the harvest, reduce host cell proteins and replace the depleted cell culture medium with a defined buffer system (buffer exchange). A Millipore TFF system (Millipore Pellicon II mini membrane holder) equipped with a 100 kDa cutoff PES membrane module (Pellicon2 Biomax, 1000 cm²) was used for concentration and buffer exchange. A Pellicon2 Biomax membrane module was mounted on the Pellicon II mini filter holder and the device was connected to a peristaltic pump. The system was first rinsed with ultra-pure water and then sanitized by recirculation of 0.1 M NaOH for 60 min. In case the system was not used immediately, it was stored in 0.1 M NaOH until use. Prior to use the system was rinsed with 1 L of RO-water followed by buffer A until the permeate pH value was constant at pH 7.4 ± 0.2.

Adjustment of the ChikV Δ5nsP3 harvest (pH, salt)

The pooled filtered harvest material was adjusted to a final concentration of 25 mM Tris and 150 mM NaCl using stock solutions of both components (see Table 1). This adjustment was done to increase buffering capacity and to reduce unspecific adsorption to the membrane. The necessary volumes of stock solutions D (1 M Tris, pH 7.4) and E (4.5 M NaCl) were calculated as follows:

Volume of stock solution D (1 M Tris, pH 7.4) added to pooled harvest = Volume of pooled filtered harvest / 40

Volume of stock solution E (4.5 M NaCl) added to pooled harvest = Volume of pooled filtered harvest / 30

Example: 4 L harvest obtained from 20 RB (850cm²) would require addition of 100 mL stock solution D (1 M Tris, pH 7.4) and 133 mL stock solution E (4.5 M NaCl).

The calculated volumes of stock solution D and Buffer E were added to the pooled filtered harvest under gentle stirring. The adjusted harvest was then stirred using a magnetic stirrer for 5 minutes at room temperature.

Concentration and diafiltration of the ChikV Δ 5nsP3 harvest by TFF

In a first step the adjusted harvest material was concentrated approximately 10 fold. The feed flowrate was approximately 220 mL/min. The transmembrane flux at a transmembrane pressure of approximately 0.6 bar was in the range of 90 ± 5 mL/min per 1000 cm² membrane. After concentration, the cell culture medium was exchanged against 25 mM Tris, 150 mM NaCl, pH 7.5 by continuous diafiltration with 6 volume exchanges. The diafiltration buffer was supplied to the feed vessel from a measuring cylinder by a second peristaltic pump set to a flowrate of approximately 90 mL/min. Minor flowrate adjustments of the second peristaltic pump in the range of ± 10 mL/min were done manually to ensure a constant volume of harvest in the feed vessel. After 6 volume exchanges, diafiltration was stopped. The liquid remaining in the membrane module was recovered by pumping the module empty with air.

Sucrose addition to diafiltrated ChikV Δ 5nsP3 material

After diafiltration, sucrose stock solution H (50% (w/w) sucrose solution) was added to the diafiltrated material to achieve a final sucrose concentration of 10% (w/w). The volume of buffer H was calculated as follows:

Volume of stock solution H added (mL) = Volume (mL) of diafiltrated ChikV material $\times$ 0.25
(dilution factor = 1:4) (i.e., final sucrose concentration is 10%)

Example: 400mL diafiltrated ChikV solution would require addition of 100mL stock solution H (50% sucrose).

The calculated volume of solution H was added to the diafiltrated ChikV Δ 5nsP3 material under gentle stirring and the solution was then stirred using a magnetic stirrer for a further 5 minutes at room temperature. (At this stage of the process the material can be either immediately further processed or stored frozen ($< -65^{\circ}\text{C}$, hold step).)

DNA reduction by protamine sulphate precipitation

A DNA precipitation step using protamine sulphate (PS) was performed to reduce hcDNA. Protamine sulphate stock solution L (50 mg/mL PS in PBS) was added to the diafiltrated ChikV Δ5nsP3 material to a final nominal concentration of ~1.6 mg/mL. The necessary volume of stock solution L was calculated as follows:

Volume of stock solution L (50 mg/mL PS) added = Volume of diafiltrated ChikV Δ5nsP3 material in 10% sucrose / 31

Example: 500 mL diafiltrated ChikV Δ5nsP3 solution in 10% sucrose would require addition of 16 mL stock solution L (50 mg/mL PS in PBS).

The protamine sulphate stock solution was added while stirring the ChikV Δ5nsP3 material using a magnetic stirrer followed by incubation at 2-8°C for 30 minutes. After incubation, the DNA precipitate was not removed. The material was immediately further processed by batch adsorption with Capto™ Core 700 chromatography media.

Batch adsorption with Capto™ Core 700

To reduce HCPs, a batch adsorption step with Capto™ Core 700 (CC700) chromatography medium was performed after DNA precipitation. CC700 slurry (50% slurry in buffer A) was added directly to the protamine sulphate treated material. The required slurry volume was determined based on the volume of ChikV harvest material (d1+d2) and was calculated as follows:

Volume of CC700 slurry added to PS-treated concentrated harvest (mL) = Volume of ChikV Δ5nsP3 harvest material (mL) × 0.02 (dilution factor = 1:50) (i.e., final concentration of CC700 is 1%)

After slurry addition, the material was incubated at 4°C for 15 minutes under constant agitation using a magnetic stirrer. After incubation, the CC700 solid matter was allowed to settle by gravity for 10 minutes. The ChikV Δ5nsP3 material was then removed from the top of the solution in order to avoid blocking of the filter by the CaptoCore particles. The remaining CaptoCore particles and the DNA precipitate were then removed from the solution by filtration using a 0.2 μm Mini Kleenpak EKV filter capsule (Pall). The resulting filtrate was further processed by sucrose density gradient centrifugation.

Sucrose density gradient centrifugation

Sucrose density gradient centrifugation (SGC) was used for final concentration and polishing of the ChikV $\Delta 5nsP3$ material. The ChikV material was loaded on top of a solution consisting of three layers of sucrose with different densities. The three sucrose layers were selected based on a preliminary study which showed the formation of a linear sucrose gradient and good separation of the virus particles from residual contaminants. The optimal volumes of the sucrose solutions were determined empirically. The volumes of individual layers for a centrifugation at 500 mL scale are shown in Table 3.

Table 3. Sucrose concentrations and volumes (500 mL scale).

Solution	Volume (mL)
Harvest with 10% sucrose	360
15% sucrose	40
35% sucrose	40
50% sucrose	60
Total volume	500

Preparation of the sucrose gradient

The sucrose gradient bottles (500 mL) were prepared by underlaying the individual sucrose layers. A 3.5 mm ID plastic tube was attached to 60 cm of peristaltic pump tubing. The plastic tube was mounted on a laboratory stand using a clamp and placed into the centrifuge bottle. The nozzle of the plastic tube was touching the bottom of the bottle. Using a peristaltic pump set to a flow rate of 25 mL per minute, the ChikV $\Delta 5nsP3$ material and the sucrose solutions were pumped into the cylinder. A measuring cylinder was used as a feed vessel. The first solution pumped was the ChikV $\Delta 5nsP3$ material as it had the lowest density (10% sucrose (w/w)). Following the addition of the ChikV $\Delta 5nsP3$ material, the sucrose solutions were pumped in ascending order starting with the lowest (15%), followed by the 35% sucrose solution and finishing with the highest density sucrose solution (50%). After all sucrose solutions were transferred, the plastic tubing was carefully removed in order not to disturb the layers.

Centrifugation

Prior to centrifugation a Beckman Avanti JXN-26 centrifuge equipped with rotor Beckman 10.500 was pre-cooled to 4°C. The prepared SG bottles were carefully transferred into the pre-cooled (4°C) rotor so as to not to disturb the sucrose layers. The bottles were centrifuged at 10,000 rpm (~18,500 rcf) at 4°C for 17-20 hours. (In case a different centrifuge system with a different rotor would be used, the necessary speed and centrifugation times would need to be calculated based on the k-factor in order to achieve comparable centrifugation efficiency.)

Sucrose gradient harvest

Harvesting of the sucrose gradient was done manually using a peristaltic pump. A 3.5 mm ID plastic tube attached to 60 cm of peristaltic pump tubing was used for harvesting the sucrose gradient. The 500 mL bottle containing the centrifuged gradient was mounted onto a laboratory stand in a tilted position (~12°) using a clamp. The plastic tubing was then placed into the bottle touching the bottom edge of the bottle and was fastened in position using a clamp. This resulted in a small gap of 1-2 mm between the tubing inlet and the bottom of the bottle. Using a peristaltic pump set to a flow rate of 60 mL per minute, the gradient was harvested and manually split into 5 mL fractions. A third of the bottle volume was harvested and the rest was discarded. The fractions were immediately tested by measuring UV absorbance in a plate reader as described below.

Analysis of fractions by UV absorbance and SEC-HPLC

UV absorbance measurement was used as primary method for analysis of the sucrose gradient fractions. Absorbance at 214, 280 and 260 nm was tested immediately after fractionation was completed. Briefly, a 100 µL sample of each fraction was transferred into a 96 well plate and absorbance at 214, 260 and 280 nm was measured using a plate reader. The absorbance values were plotted against the fraction number. A representative profile is shown in Fig. 4A. The ChikV Δ5nsP3 containing fractions were indicated by a peak in all three measured wavelengths (Fig. 4A, grey shaded area). The presence of impurities was indicated by an increase of the UV214 signal after the main peak. The fractions comprising the main peak were

pooled from the peak start to the valley of the 214 nm curve. This method can be used as single method for pooling ChikV $\Delta 5nsP3$ fractions.

After identification of the virus containing fractions, the respective fractions were pooled. Pooling criteria for SGC fractions were based on UV 260 nm data, e.g. start of pooling at ~10% of peak maximum, end of pooling at ~30% of peak maximum. (Final pooling criteria at a manufacturing scale may need to be determined empirically.) The sucrose gradient pool was either stored at $< -65^{\circ}\text{C}$ or immediately further formulated to drug substance (DS).

Size exclusion chromatography

The final pooled SGC fractions containing purified infectious ChikV $\Delta 5nsP3$ virus particles were analyzed for purity by SEC-HPLC. In brief, SEC was performed as follows: a Superose 6 10/300 Increase column (GE Healthcare) equilibrated with PBS + 250 mM NaCl, pH 7.4 at 1 ml/min and 25°C , was used to detect ChikV particles at 214 nm detection wavelength in the pooled samples. SEC-HPLC is a semi-quantitative (relative yield) and qualitative (purity) method that separates intact virus particles from virus aggregates and host cell proteins (HCPs). The method cannot distinguish between infectious and non-infectious virus particles due to their identical retention time.

As shown in Fig. 4B, there were identified two defined peaks by SEC: the ChikV $\Delta 5nsP3$ peak and a peak corresponding to buffer components. The SGC step yield based on SEC-HPLC data for pooled fractions F6-F11 was estimated at ~70 %. The final purity of the ChikV $\Delta 5nsP3$ SGC pool, based on SEC-HPLC analysis, was estimated at >95%.

SDS-PAGE and silver stain

SDS-PAGE silver stain was performed in order to qualitatively assess sample purity throughout the purification process from the first crude harvest through SGC. Briefly, ChikV process samples analyzed by SDS-PAGE/silver stain were diluted 1:1.33 with LDS buffer and were heated to 70°C for 5 minutes. The samples were loaded onto 4-12 % Bis-Tris Gels (NuPAGE). Silver staining was done using the Silver Express staining kit (Invitrogen).

A silver-stained gel of a representative ChikV Δ 5nsP3 purification is shown in Fig. 4C. The viral proteins E1, E2 and C are marked on the right-hand side of the gel. The final SGC pool (fraction 7-fraction 11) is shown in lane 12. Note that a defined HCP band migrating between ChikV protein E2 and C still appears after CaptoCore700 treatment that has been identified as a single band in SDS-PAGE. This impurity is removed by sucrose gradient centrifugation, but can still be seen in fractions 13 and 14 (corresponding to lanes 14 and 15 of Fig. 4C).

Enrichment of infectious ChikV Δ 5nsP3 particles by PS treatment

Although generally used as a method of removing contaminating hcDNA, it was observed in the course of the present invention that PS treatment also removes virus aggregates and HCPs. Size exclusion chromatography (SEC-HPLC, as described above) was used throughout the purification process to determine the purity of the ChikV virus relative to impurities which also generate UV absorption.

As can be seen in Fig. 5A, treatment with PS reduces not only host cell proteins and low molecular weight contaminants of the ChikV Δ 5nsP3 preparation, but also reduces the SEC area corresponding to virus products, including aggregates as indicated. A surprising finding, however, was that even a reduction of the total SEC area by 86% (in a representative experiment shown in Fig. 5B, grey portion of bars) did not result in a concomitant reduction in infectious virus particles as measured by TCID₅₀ (left axis). Instead, even though a large percentage of virus particles were removed by PS treatment, the infectious particles were not. This observation indicates that PS treatment selectively enriches infectious virus particles from a larger pool of total virus particles present in the crude harvest.

TCID₅₀ was performed to quantify infectious virus particles during the course of the purification process and to assign an active virus titer to final drug substance and drug product samples. Briefly, Vero cells were seeded at 2×10^4 cells per well in 100 μ L medium (EMEM with 2 mM L-Glutamine + 5 % FBS (+ 1 % antibiotic/antimycotic) in 96-well TC-treated flat-bottom plates and incubated overnight at 35°C / 5% CO₂. On day two, Vero cell monolayers were infected by adding 100 μ L of 1:10 serial dilutions of test samples to each of quintuplicate wells seeded with Vero cells and incubated at 35°C / 5% CO₂. On day seven, plaques were counted by

visualization under a microscope. The TCID₅₀ was calculated according to the Reed & Münch endpoint calculation method (Reed, L.J.; Muench, H. (1938) A simple method of estimating fifty percent endpoints" The American Journal of Hygiene 27: 493–497).

Furthermore, electron microscopy of ChikV samples before and after PS treatment showed that not only large aggregates but also smaller non-infectious virus-like particles (basically not fully assembled particles without RNA genome) are effectively removed by PS (Fig. 6).

Furthermore, this enrichment of infectious virus particles could also be observed when analyzing day one and day two crude harvests separately. As presented in Table 3, the SEC area (total virus particles) of the day 1 harvest remains roughly the same after PS treatment; whereas a large decrease in virus peak area is seen for the day 2 harvest. This observation was confirmed by MALLS analysis of the virus preparation, wherein it was seen that a higher percentage of virus particles were of the correct size following PS treatment. Similarly to the results shown in Fig. 5, day 1 and day 2 harvests showed no reduction in infectious particles as measured by TCID₅₀ following PS treatment, indicating that mainly non-infectious, immature and/or aggregated virus particles are removed during the PS treatment and infectious particles are enriched in the preparation.

Table 3. Overview of the process of ChikV Δ5nsP3 purification as described in Example 1. SEC-MALLS analysis of harvests before and after PS treatment shows the removal of larger virus particles (aggregates), an effect that is particularly pronounced for day 2 harvests.

	SEC	MALLS		Infectious particles
	Area [mAU*min]	Total particles/mL	% correct size (20-40 nm)	TCID ₅₀ log ₁₀
Harvest 1 (H1)	57	1.17E+11	49%	10.2
Harvest 1 + PS	53	1.33E+11	81%	10.0
Harvest 2 (H2)	36	4.60E+09	3%	7.9
H2 + protamine sulphate	2	8.80E+09	59%	7.9
Combined Harvests (C)	67	2.60E+10	14%	9.9
C + protamine sulphate	24	8.00E+10	72%	10.1

Finally, an overview of the relative amounts of ChikV particles and other components as measured by SEC-HPLC at various steps throughout the entire virus purification process from crude harvest (a) to the final SGC purified pool can be seen in Fig. 7. In sum, not only are the vast majority of contaminants and undesired products removed by the process, ChikV particles are highly purified. As shown by the previously presented data, the final preparation is a highly enriched preparation of infectious ChikV particles.

Drug Substance (DS) Formulation

The pooled SGC fractions are diluted with DS formulation buffer M (10 mM Tris, 5% Sucrose (w/w), 1% (10 mg/mL) rHSA, pH 7.4 ± 0.2). The final target volume of DS should be in the range of approximately 2 L. Based on current data the estimated range of the dilution factor might be 1:20 to 1:50.

Final DS sterile filtration

The final DS was filtered under aseptic conditions in a laminar flow hood using a sterility grade 0.2 µm syringe filter (e.g. 0.2 µm Mini Kleenpak EKV filter capsule with 220 cm² filter surface, Pall).

Quantification of host cell DNA (hcdNA) host cell protein (HCP) and endotoxin

The residual host cell DNA content of the sucrose gradient pool samples was determined by using the qPCR based assay. The DNA content in SGC pool was determined to be ≤ 0.002 ng/mL. The presence of residual host cell protein (HCP) from Vero cells was determined by ELISA. Residual host cell proteins present in the sucrose gradient pool samples were quantified using the Vero Cell HCP ELISA kit (Cygnus, F500). The residual host cell protein content in SGC pool was determined to be ≤ 200 ng/mL.

Endotoxin content of the SGC pool and DS was measured by Endosafe®-PTS™ system (Charles River). The system uses LAL reagents by a kinetic chromogenic methodology to measure color intensity directly related to the endotoxin content in a sample. Each cartridge contains precise amounts of a licensed LAL reagent, chromogenic substrate and an endotoxin

control standard. Samples were diluted 1:100 in WFI. The SGC Pool F7-F11 was determined to be < 5.00 EU/mL; likewise, the Drug Substance was also determined to have < 5.00 EU/mL.

The following specifications for impurities in final Drug product were proposed: hcDNA < 10 ng/dose; Endotoxins < 50 EU/dose; HCP < 200 ng/dose. These residual specifications would already be met in the highly concentrated SGC pool (~10 log TCID₅₀/mL), which provides a high margin of safety considering the high dilution factor of SGC pool to final DP of > 1:1000.

Example 2: Development of a purification process for inactivated Zika virus vaccine produced in Vero cells

A downstream process was developed for the purification of infectious Zika virus particles whereby host cell nucleic acids, non-infectious virus particles and aggregates are removed by the addition of protamine sulphate. On overview of an exemplary Zika vaccine downstream purification process from the crude harvest to formulation of the drug substance is shown in Figure 8. The unexpected and novel purification properties of protamine sulphate (PS) were evaluated in purification processes for Zika Virus (Zika) similarly as found above. Again non-infectious virus particle aggregates, HCP and other LMW impurities were removed by PS precipitation as shown by removal of aggregate shoulder in SEC-HPLC and no loss of infectious virus titer by PS treatment (Figure 10). Infectious particles were measured in the plaque assay (Table 4).

Effect of PS treatment on virus recovery

Samples of individual 30x concentrated harvests day 2, 3, 5 and 7 were analysed before and after PS treatment by SEC-HPLC and plaque assay. SEC-HPLC was used for determination of relative total ZikaV content (active + inactive) expressed as peak area, whereas the rel. ZikaV peak purity is given as relative content of virus monomer population to total virus peak. Plaque assay states the content of total active virus particles in each sample. Experimental results are summarized in Table 4. The virus peak recovery by SEC. HPLC was only between 12 to 36% with peak purity after PS treatment in the range of >90% (no virus aggregates detected). The recovery of active virus particles by plaque assay was all > 100% (130-700%, range within the

variability of the assay) showing that no active virus particles were lost during PS treatment. These results show that during PS treatment only non-infective (immature and/or aggregated virus) particles were removed.

Table 4: ZikaV Recovery by SEC-HPLC and Plaque assay before and after PS treatment.

SEC-HPLC

	Peak area mAU*min			
Harvest day	30x conc	30x +PS	SEC Recovery (%)	rel. virus monomer content after PS (%)
Day 2	101.36	18.63	18	89%
Day 3	144.51	17.48	12	90%
Day 5	19.97	5.92	30	96%
Day 7	68.80	24.43	36	99%

Plaque Assay

	PFU/mL		
Harvest day	30x conc	30x +PS	Plaque Recovery (%)
Day 2	3E+08	5E+08	179
Day 3	2E+08	4E+08	193
Day 5	1E+08	9E+08	700
Day 7	3E+08	4E+08	132

Example 3: Development of a purification process for Yellow Fever virus vaccine produced in Vero cells

A downstream process was developed for the purification of infectious yellow fever virus particles whereby host cell nucleic acids, non-infectious virus particles and aggregates are removed by the addition of protamine sulphate. The unexpected and novel purification

PAT022-EP-PR

properties of protamine sulphate (PS) were evaluated in purification processes for yellow fever (YF) as follows:

As before the treatment of YF-harvest with PS significantly reduces the amount of aggregates as seen with SEC for two vaccine strains currently in development (Figure 9).

What is claimed is:

CLAIMS

1. Use of protamine, preferably a protamine salt, to separate infectious and non-infectious virus particles, host cell proteins and/or undefined low molecular weight materials.
2. A process of purification of infectious virus particles, comprising the steps of:
 - (a) providing a crude harvest (a) comprising virus particles and impurities, wherein the impurities are generated from growing said virus particles on a cell substrate;
 - (b) reducing impurities from the crude harvest (a) by precipitation with an agent comprising protamine, preferably a protamine salt, more preferably a protamine sulphate, even more preferably a recombinant protamine sulphate, to obtain a virus preparation (b), wherein the enrichment of infectious virus particles in the virus preparation (b) relative to total virus products in the crude harvest (a) is in the range from at least 50% to 95%, preferably at least 80%.
3. The use of claim 1 or the process of claim 2, wherein the virus particles are selected from the group consisting of flaviviruses, e.g. yellow fever virus or Zika virus and alphaviruses, e.g. Chikungunya.
4. A process of purification of infectious virus particles, comprising the steps of:
 - (a) providing a crude harvest (a) comprising virus particles and impurities, wherein the impurities are generated from growing said virus particles on a cell substrate;
 - (b) reducing impurities from the crude harvest (a) by precipitation with an agent comprising protamine, preferably a protamine salt, more preferably a protamine sulphate, even more preferably a recombinant protamine sulphate, to obtain a virus preparation (b);
 - (c) further purifying the virus preparation (b) by one or more size exclusion methods such as (i) a sucrose density gradient centrifugation, (ii) a solid-phase matrix packed in a column comprising a ligand-activated core and an inactive shell comprising pores,

wherein the molecular weight cut off of the pores excludes the virus particles from entering the ligand-activated core, and wherein a molecule smaller than the molecular weight cutoff of the pores can enter the ligand-activated core and collecting the virus particles, and/or (iii) size exclusion chromatography to obtain a virus preparation (c) comprising the infectious virus particles, wherein the residual host cell DNA of the virus preparation (c) is less than 100 ng/mL and the residual host cell protein and the residual aggregates of infectious virus particles of the final virus preparation (c) is less than 1 µg/mL.

5. The process of claim 4, wherein the residual host cell DNA of the virus preparation (c) is less than 10 ng/mL and the residual host cell protein of the final virus preparation (c) is less than 100 ng/mL.
6. The process of any of claims 2 to 5, wherein the crude harvest (a) comprising virus particles and impurities is subjected to one or more pre-purification step(s) prior to step (b).
7. The process of claim 6, wherein the one or more pre-purification step(s) comprises
 - (a) filtration using a filter having a pore size equal to or less than 0.2 µm; and/or
 - (b) digestion of host cell genomic DNA by enzymatic treatment; and/or
 - (c) ultra/diafiltration using a hollow fiber membrane having a pore size equal to or greater than 300 kDa, preferably equal to or greater than 100 kDa.
8. The process of any one of claims 2 to 7, wherein the concentration of protamine sulphate is 0.5 to 3 mg/ml, more preferably 1 to 2 mg/ml, more preferably 1.2 to 1.8 mg/ml, more preferably 1.4 to 1.6 mg/ml, most preferably 1.6 mg/ml.
9. The process of any one of claims 2 to 8, wherein the enrichment of infectious virus particles in the virus preparation (c) or any final virus preparation relative to total virus products in the crude harvest (a) is in the range from at least 50% to 95%, preferably at least 80%.

10. The process of any one of claims 6 to 9, wherein the one or more pre-purification step(s) prior to step (b) of any of claims 6 to 9 is performed using a filter having a pore size equal to or less than 1 μm , preferably 0.2 μm .
11. The process of any one of claims 2 to 10, wherein the residual impurity of the virus preparation (c) is less than 10%.
12. The process of any one of claims 2 to 11, wherein the virus is propagated in a cell line selected from the group consisting of an EB66 cell line, a Vero cell line, a Vero- α His cell line, a HeLa cell line, a HeLa-S3 cell line, a 293 cell line, a PC12 cell line, a CHO cell line, a 3T3 cell line, a PerC6 cell line, a MDSK cell line, a chicken embryonic fibroblast cell line, a duck cell line, and a diploid avian cell line.
13. The process of claim 12, wherein said cell line is a Vero cell line.
14. The process of any one of claims 2 to 13, wherein the Zika virus is a live virus, an attenuated live virus, a chimeric virus, a modified live virus, or a recombinant live virus.
15. The process of any one of claims 2 to 14, wherein the Zika virus is a Zika virus strain of the Asian lineage or an immunogenic variant thereof.
16. The process of any one of claims 2 to 15, wherein said process resulting in final virus preparation (c) is followed by an inactivation step, wherein the virus is inactivated preferably by formaldehyde.
17. Use of the process according to any one of claims 1 to 16 for manufacturing a composition for immunization against a virus infection.

18. The use according to claim 18, wherein the composition for immunization against a virus infection is an infection caused by a group of viruses consisting of yellow fever virus, Chikungunya virus and Zika virus.
19. A composition comprising the virus particles obtainable or obtained by the process of any one of claims 2 to 16 for treating and/or preventing an infection.

PAT022-EP-PR

ABSTRACT

Described herein are processes for purifying infectious virus particles and uses of protamine in such processes.

FIGURE 1

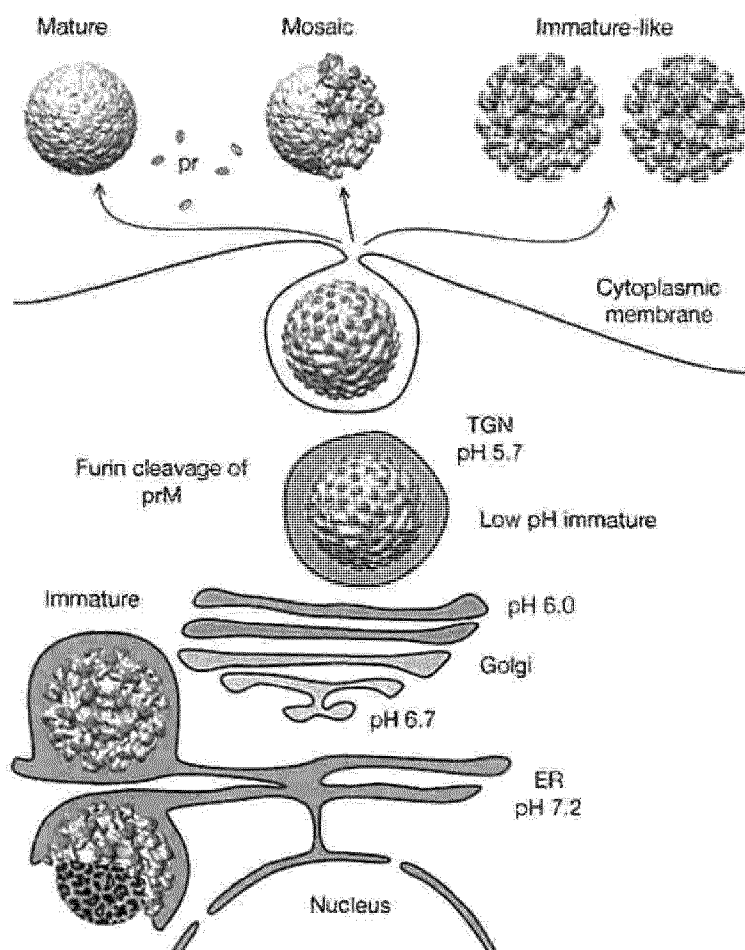


FIGURE 2

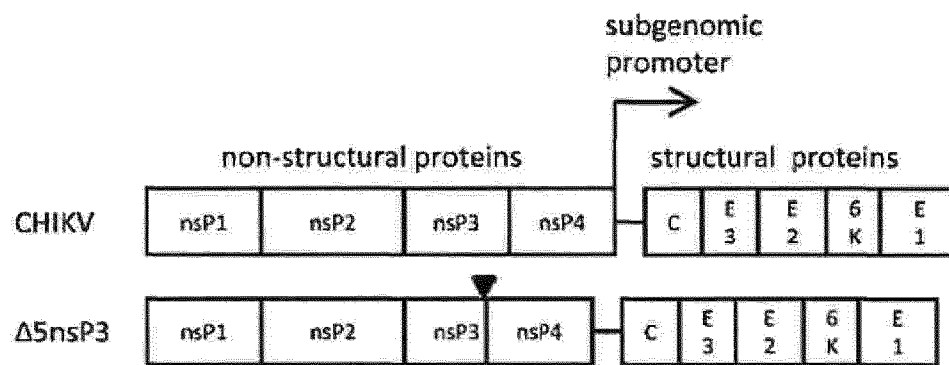


FIGURE 3

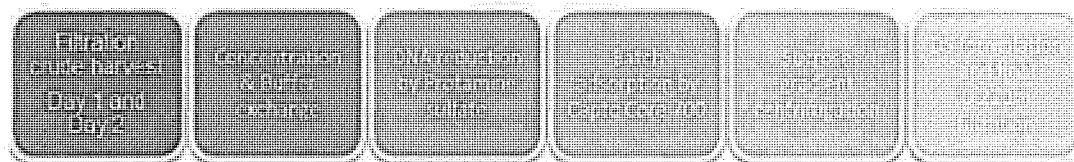


FIGURE 4A

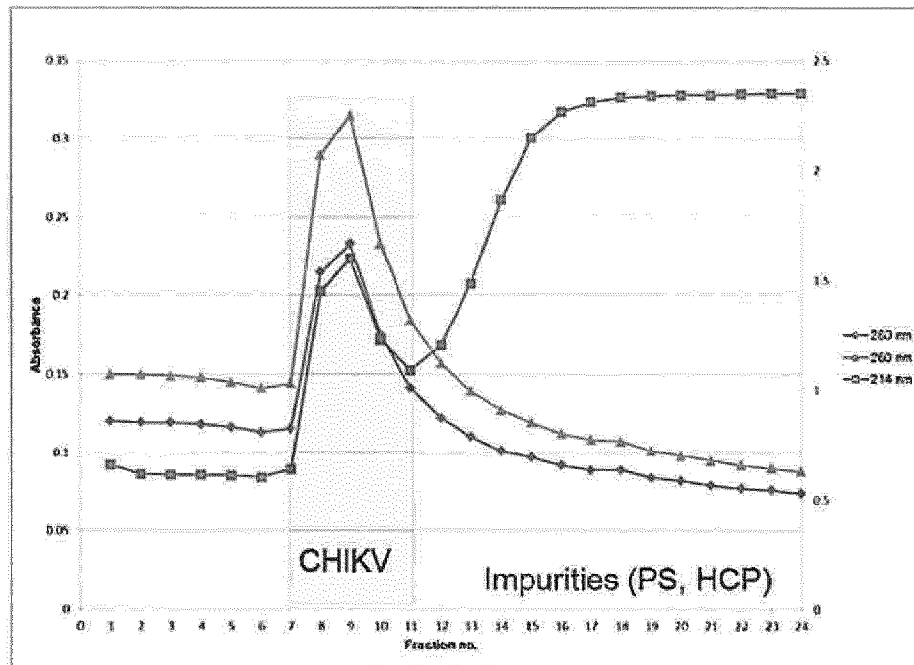


FIGURE 4B

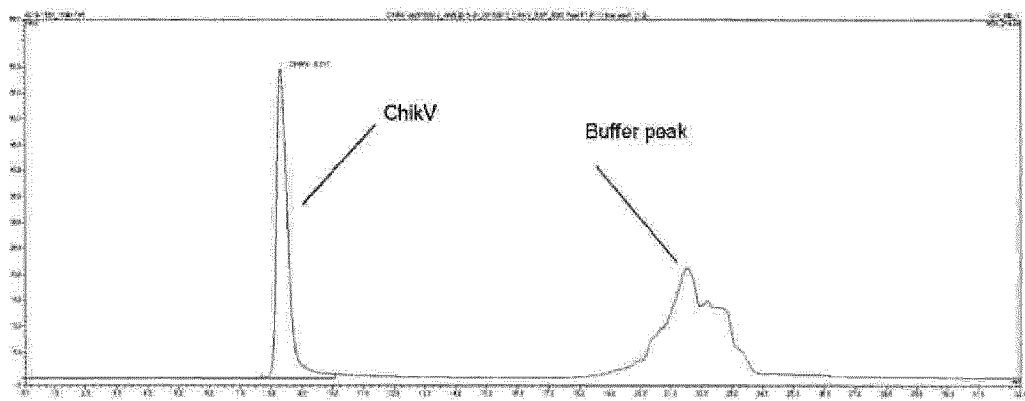
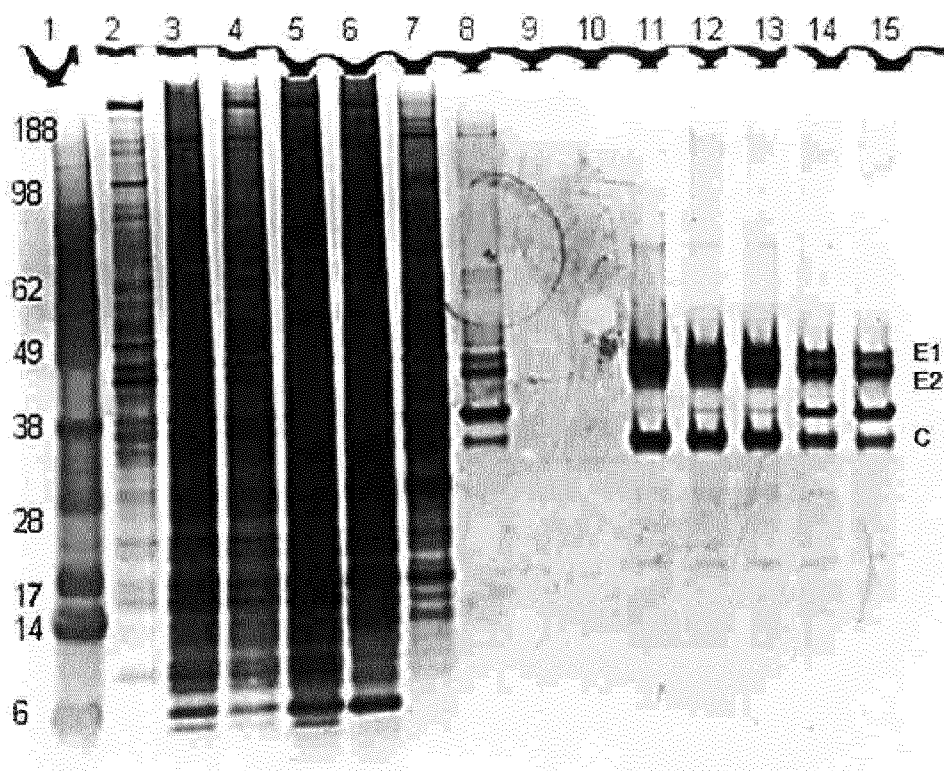


FIGURE 4C



Lane	Sample
1	Marker Seeblueplus2
2	CHIKV lot20150812_WV82015-01_Filtered harvest 0.2 μ _24hpi
3	CHIKV lot20150812_WV82015-01_Filtered harvest 0.2 μ _48hpi
4	20150813_CHIKV_DSP_UF/DF_Load
5	20150813_CHIKV_DSP_UF/DF_conc. 10x
6	20150813_CHIKV_DSP_UF/DF_conc.&dia. 11x
7	20150813_CHIKV_DSP_PStreatment
8	20150813_CHIKV_DSP_PS&CC700treatment
9	20150813_CHIKV_DSP_SGCFrac F5
10	20150813_CHIKV_DSP_SGCFrac F6
11	20150813_CHIKV_DSP_SGCPool F7-F10
12	20150813_CHIKV_DSP_SGCPool F7-F11 (final pool)
13	20150813_CHIKV_DSP_SGCPool F7-F12
14	20150813_CHIKV_DSP_SGCFrac F13
15	20150813_CHIKV_DSP_SGCFrac F14

FIGURE 5A

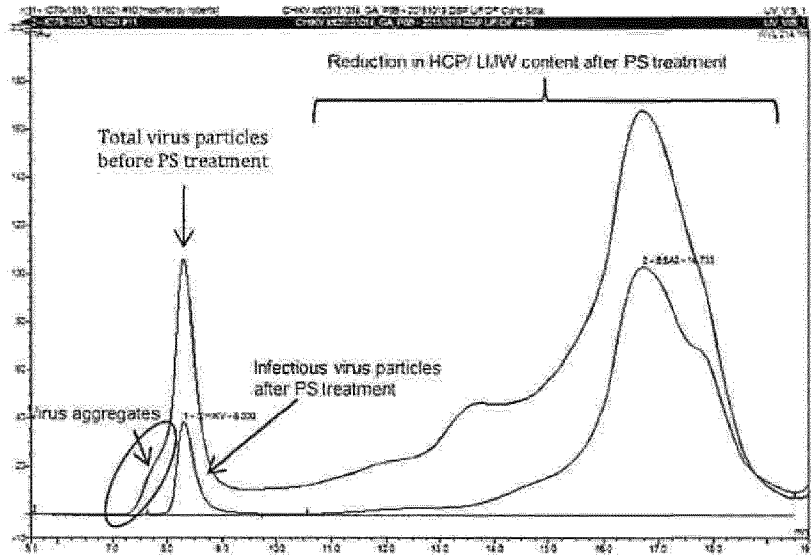


FIGURE 5B

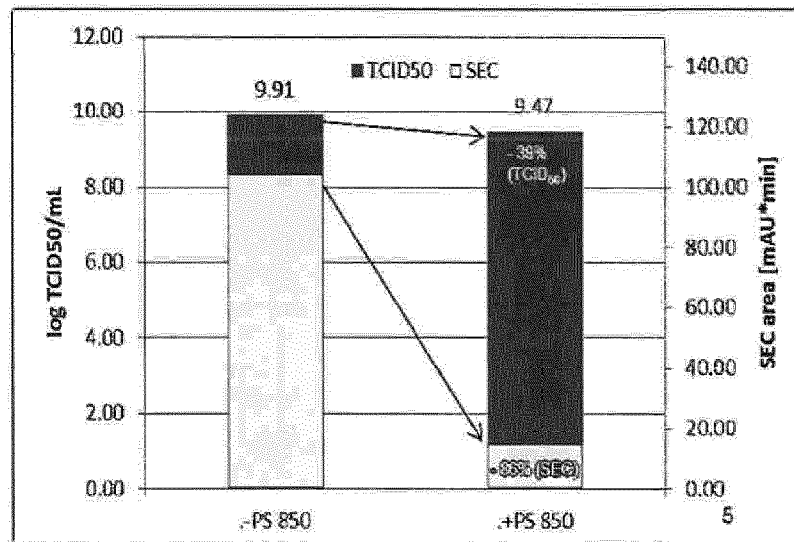


FIGURE 6

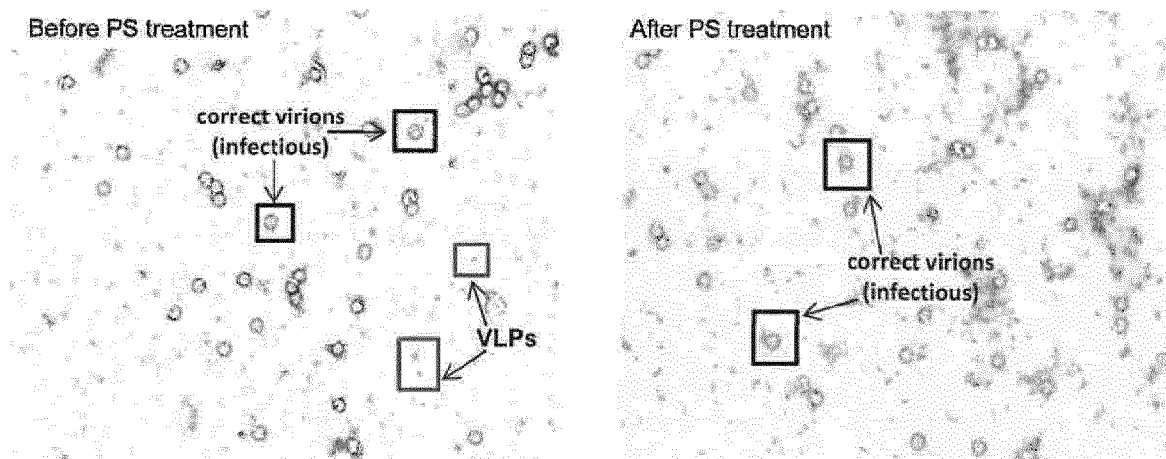


FIGURE 7

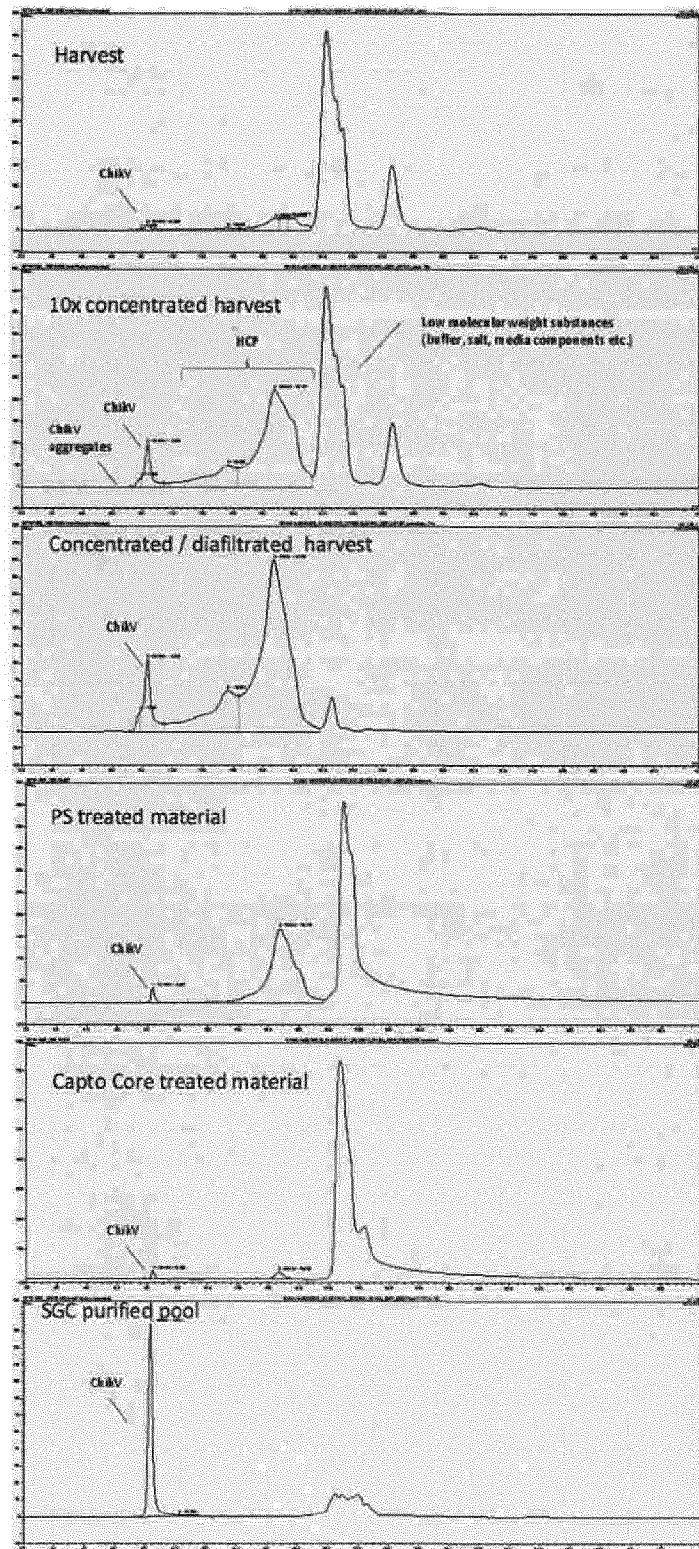


FIGURE 8

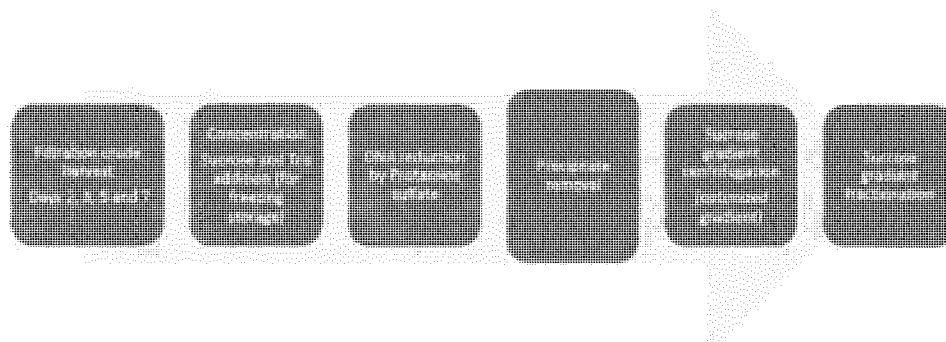


Figure 9

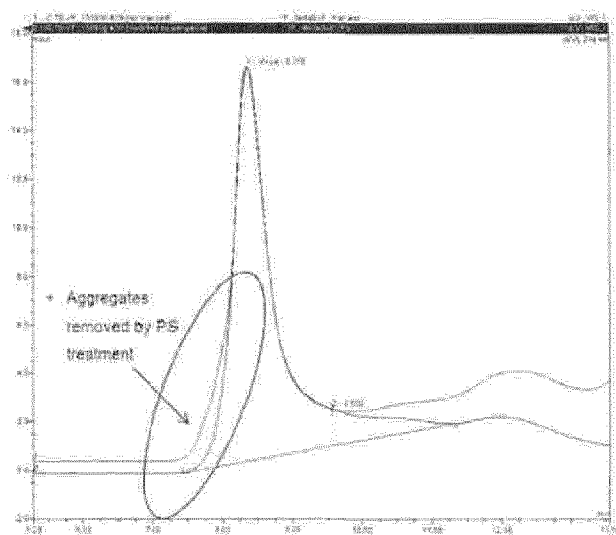


Figure 10

