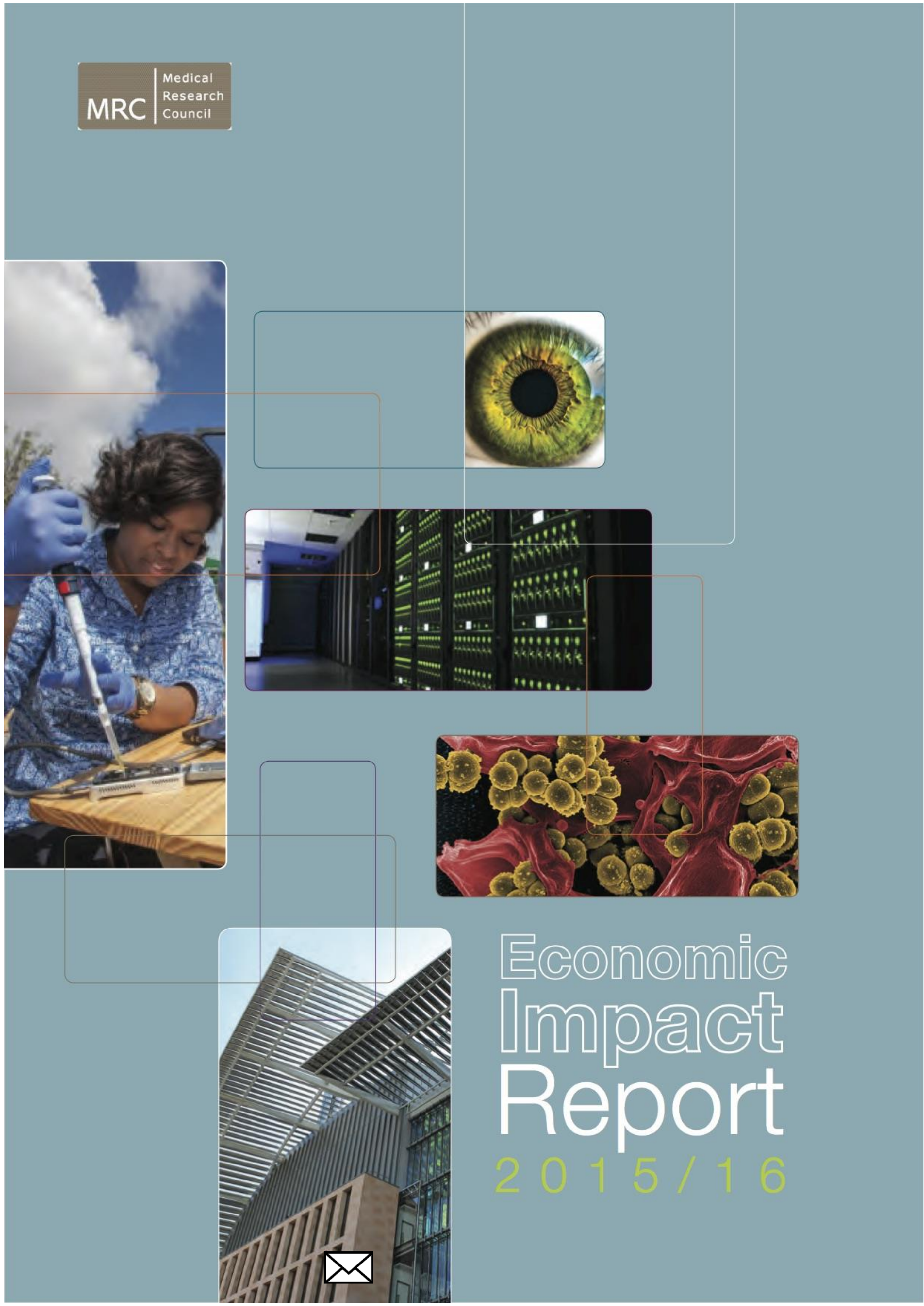
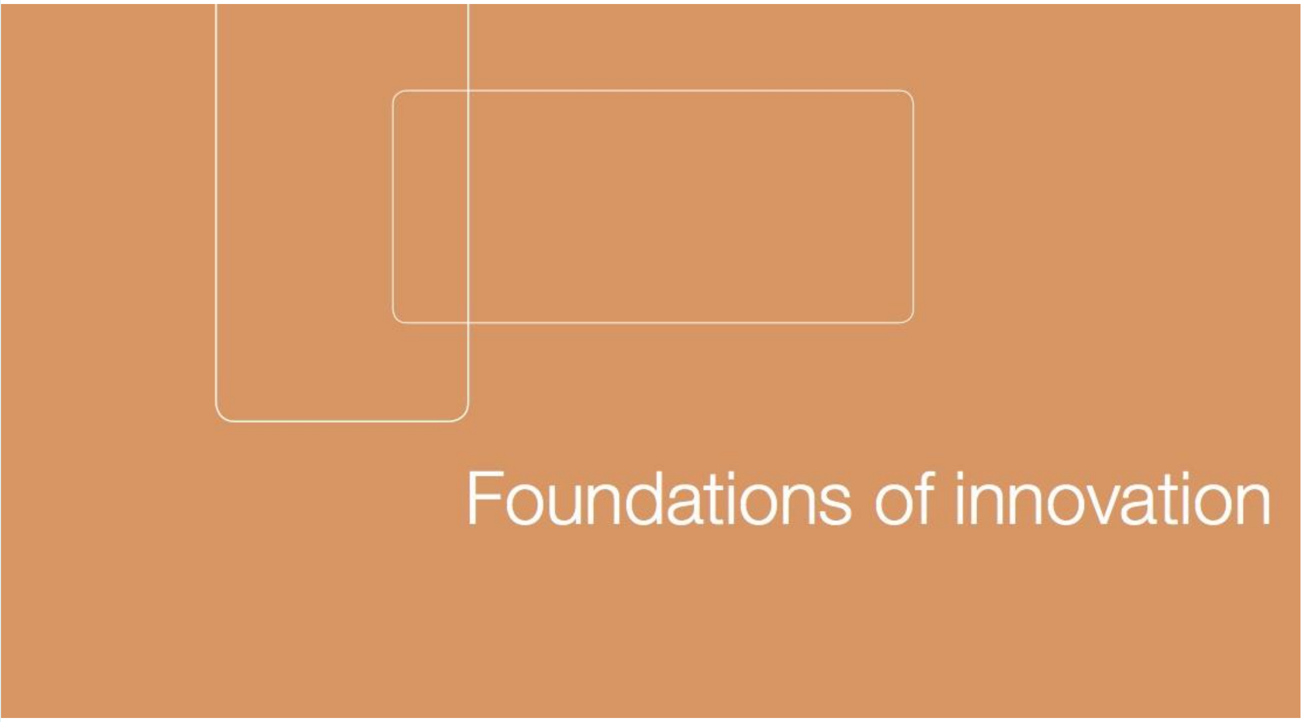


MRC Medical Research Council

Economic Impact Report 2015/16

WHO: *ZiBRA on the world Heath organisation radar*: http://www.who.int/csr/research-and-development/emerging-evidence/en/)

Financial Times: https://www.ft.com/content/e5137540-4064-11e7-9d56-25f963e998b2



Foundations of innovation

Luiz Carlos Alcantara

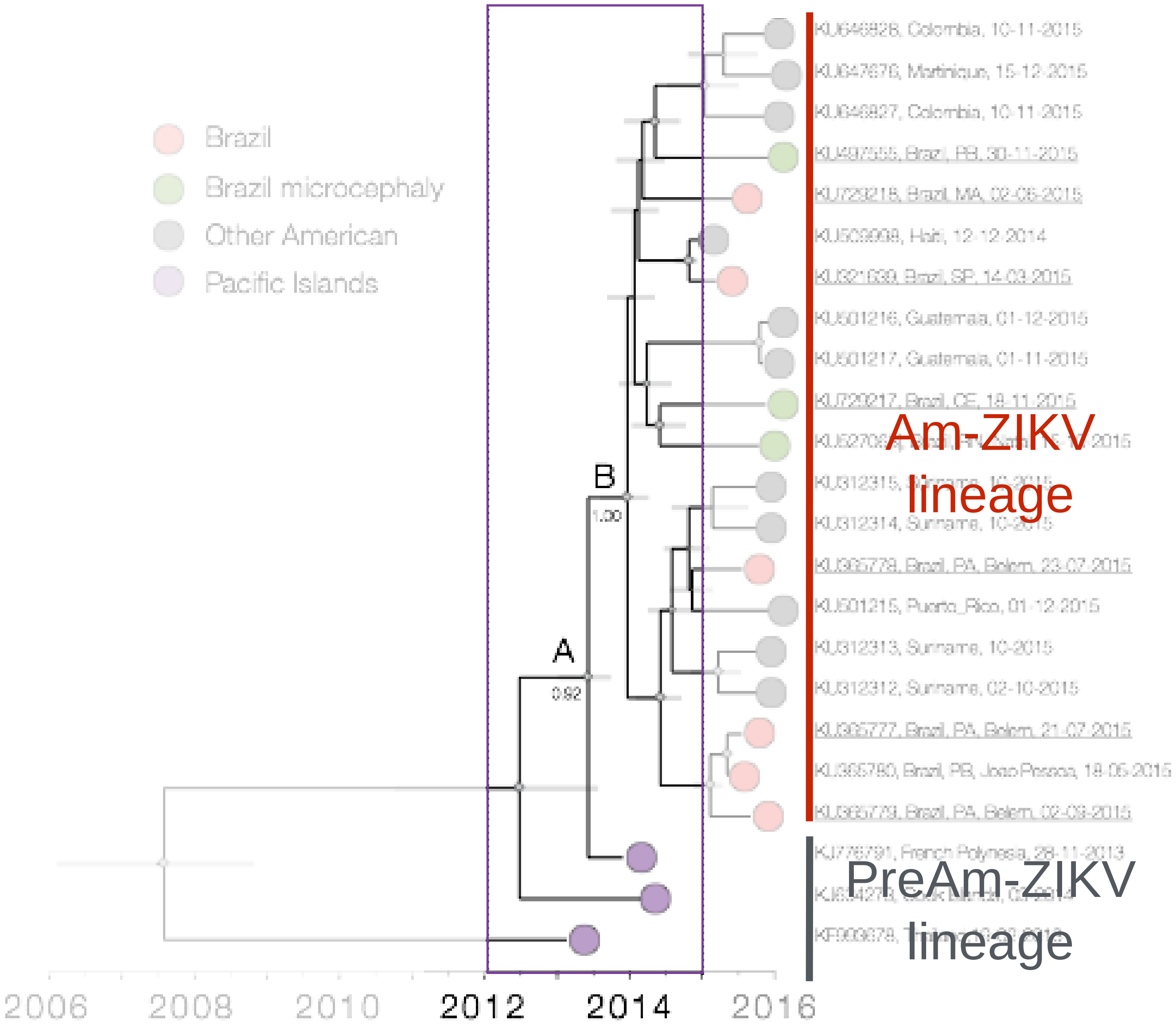
Fundação Oswaldo Cruz - Bahia

lalcan@bahia.fiocruz.br / alcantaraluiz42@gmail.com

Mobile real-time surveillance of arboviruses in Brazil

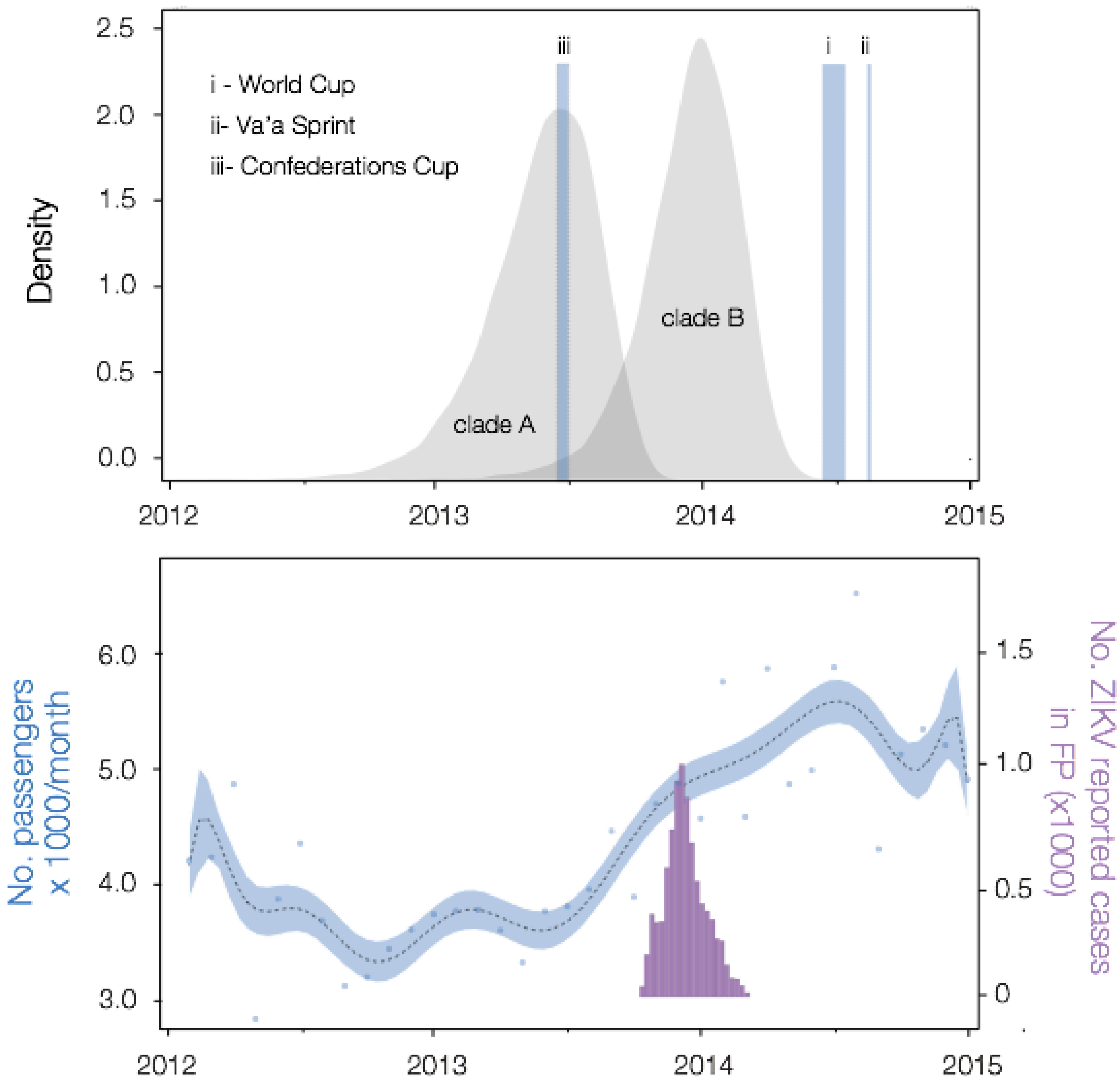
Emergence of ZIKV as a function of local transmission regime, viral pathogenesis and global mobility

ZIKV Asian genotype
molecular clock phylogeny



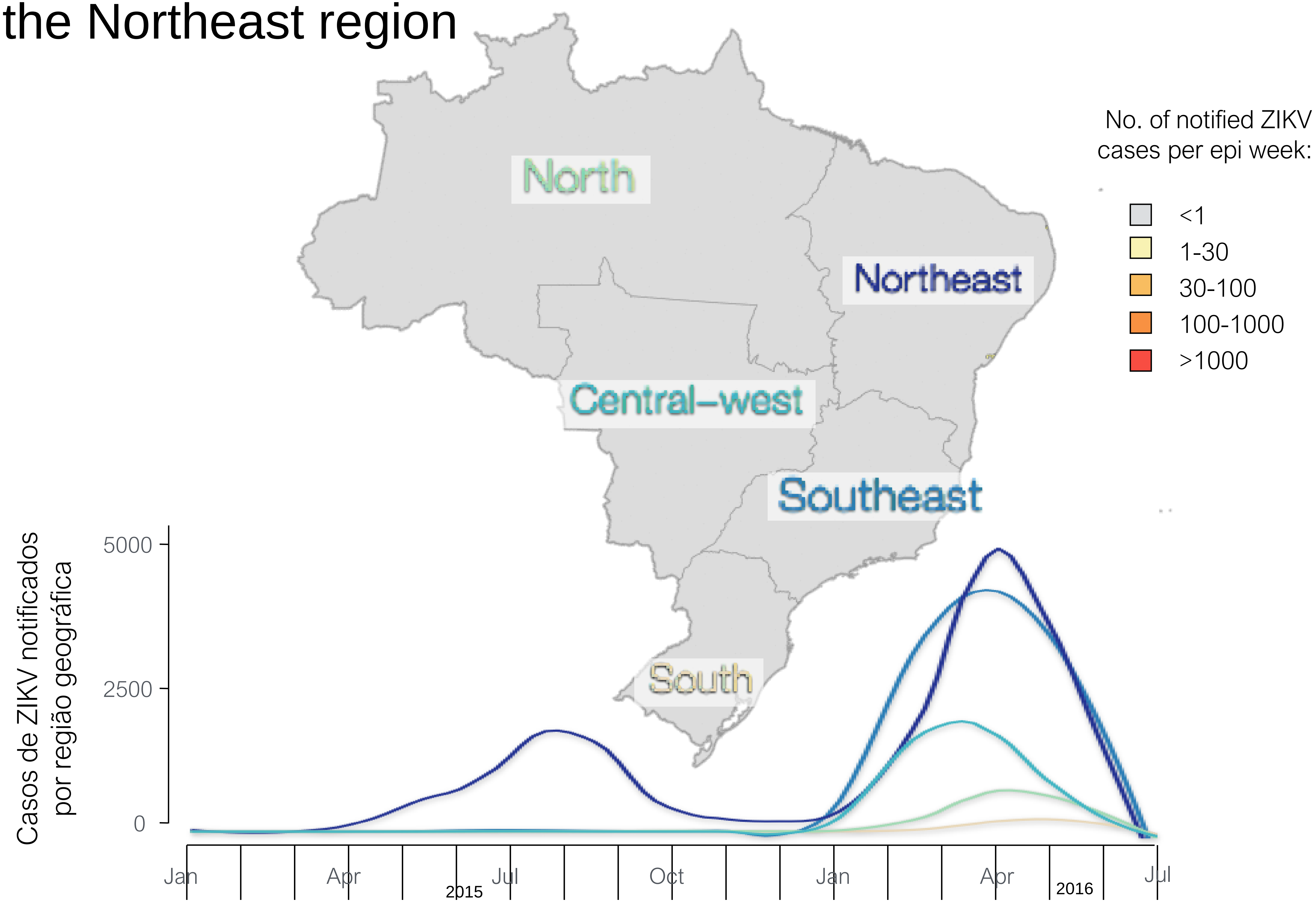
ZIKV has a high rate of evolutionary change (approx. 10^{-3}-10^{-4}s/s/y)

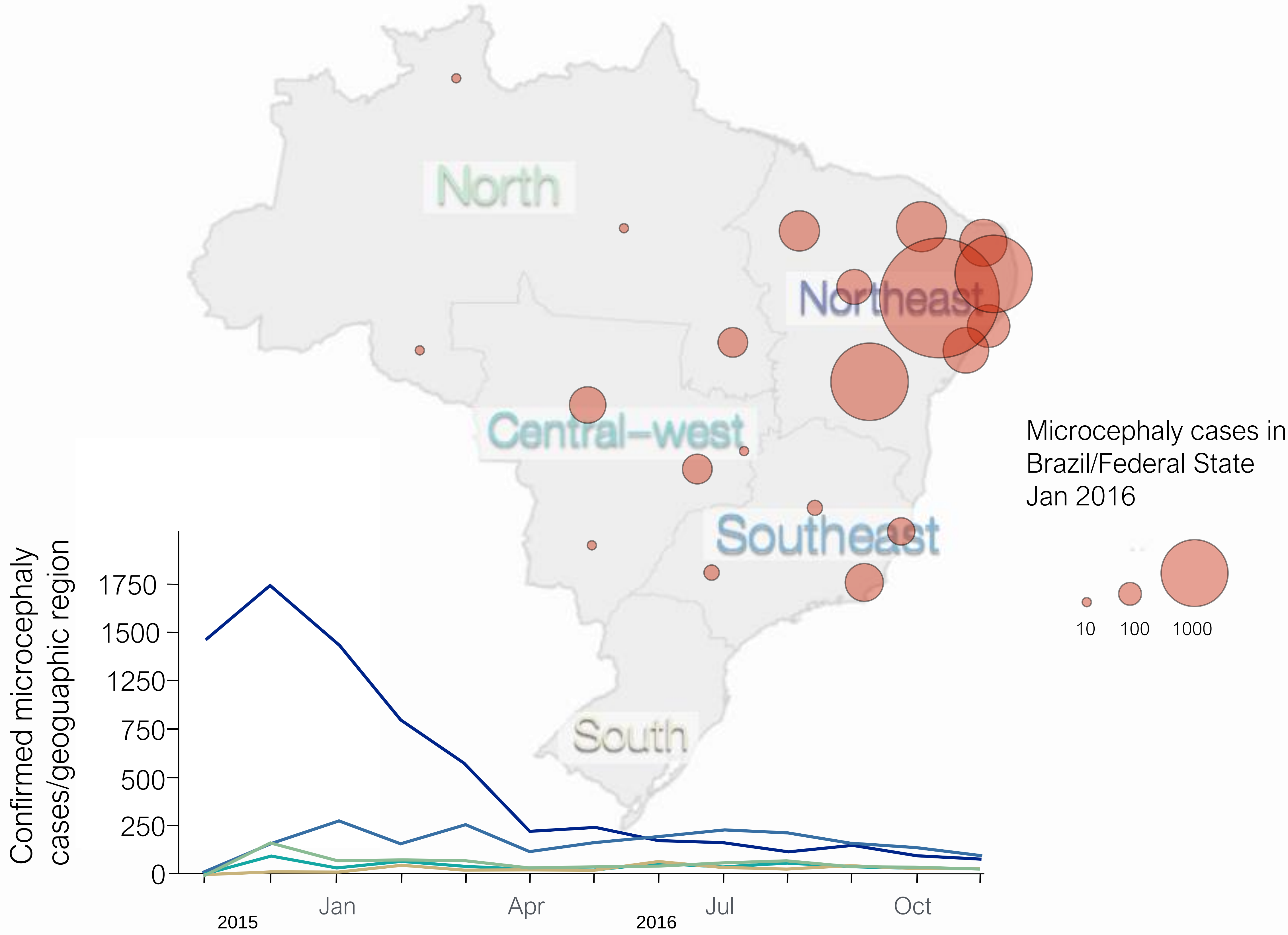
Combination of genetic
and flight data



Faria et al. *Science* March 2016

Earliest ZIKV cases were in the Northeast region

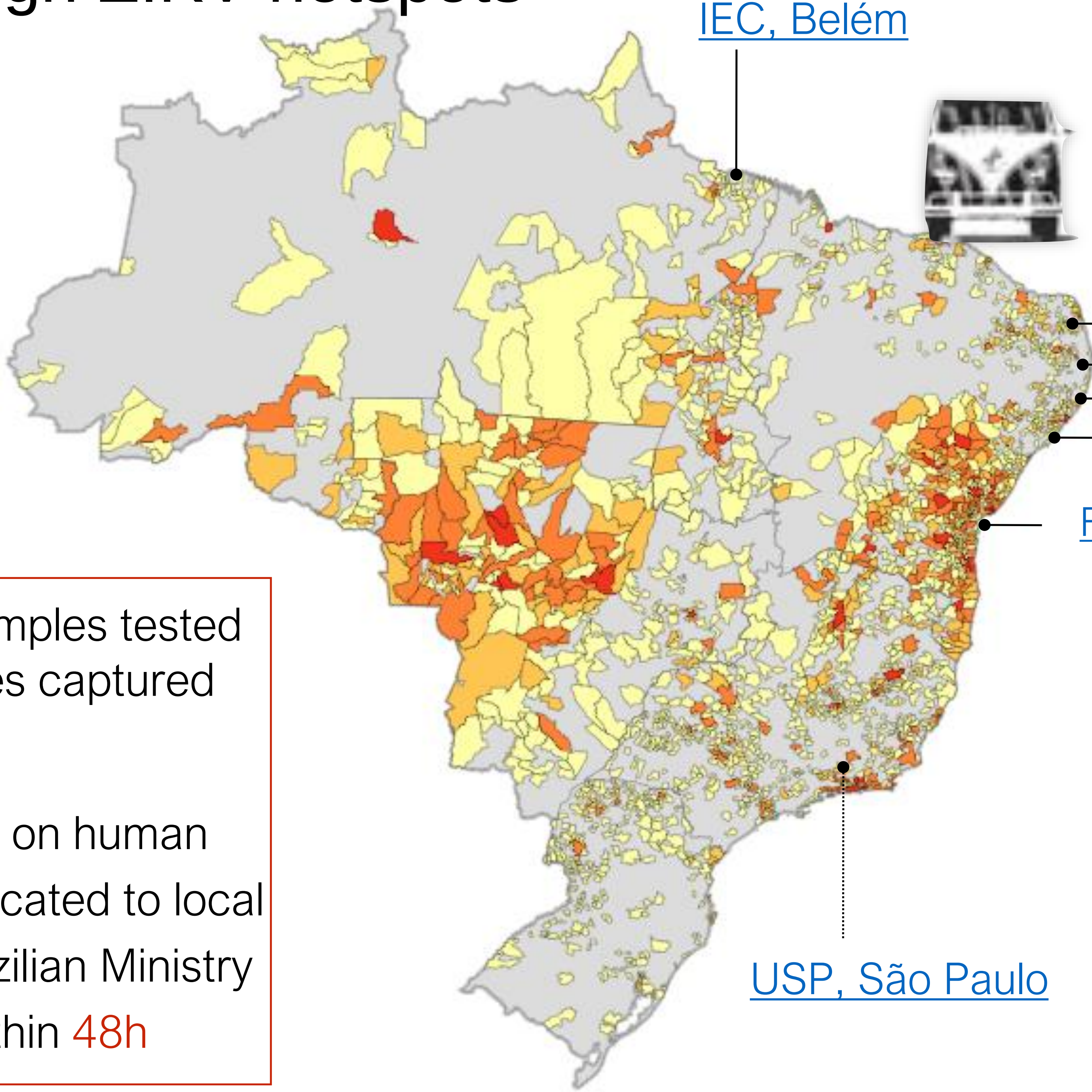




Microcephaly cases in
Brazil/Federal State
Jan 2016

Details can be found in zibraproject.github.io

The ZiBRA project, a sequencing journey through ZIKV hotspots



IEC, Belém

Natal

João Pessoa

Recife

Maceio

Fiocruz Bahia

USP, São Paulo

1401 human samples tested
838 mosquitoes captured

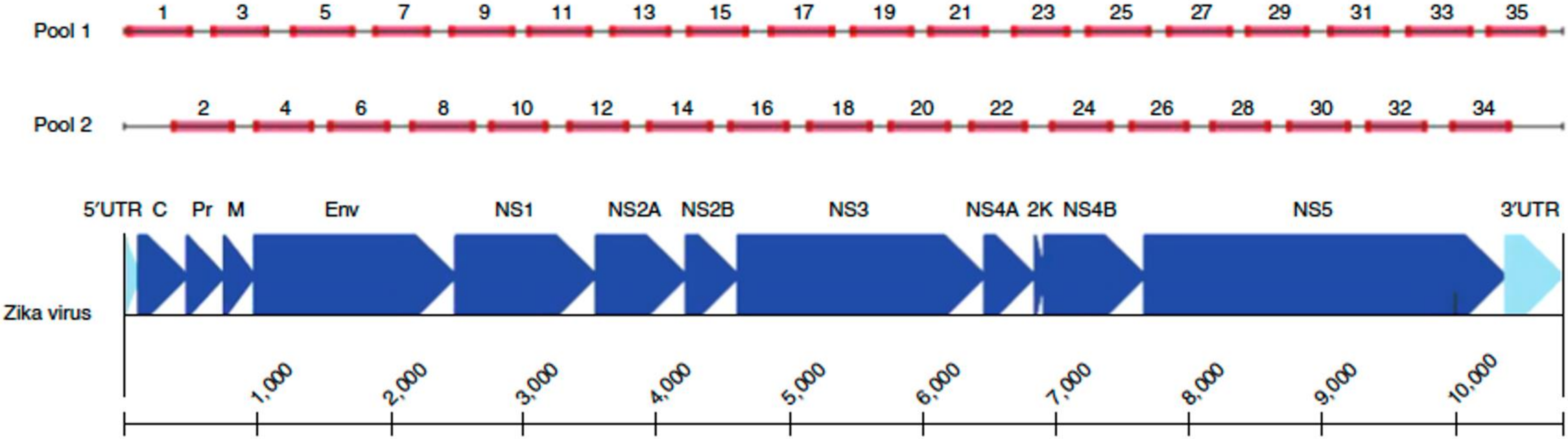
↓

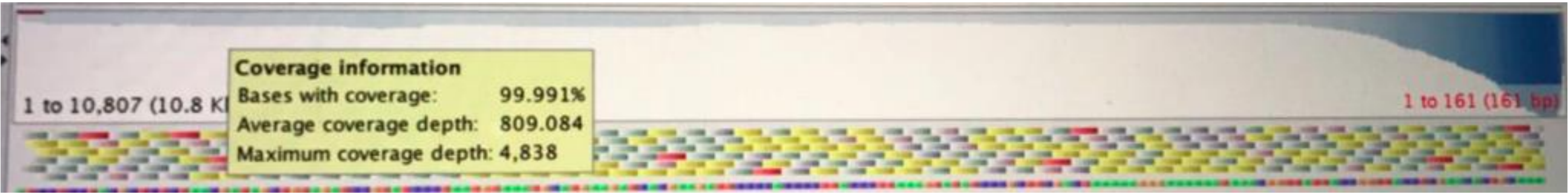
RT-PCR results on human samples communicated to local LACENs and Brazilian Ministry of Health within 48h

After the ZiBRA journey, molecular surveillance continued in SP and Bahia.


CIÊNCIA NA ESTRADA: EDUCAÇÃO
VOLARE W8

Zika virus sequencing protocoll





1 to 10,807 (10.8 K

Coverage information

Bases with coverage: 99.991%

Average coverage depth: 809.084

Maximum coverage depth: 4,838

1 to 161 (161 bp)

ZiBRA’s commitment to rapid data sharing

Improving the efficiency of global outbreak control and tracking of diseases

Pre-publication data sharing, in line with WHO Consultation Data Sharing in Emergencies (1-2 Sep 2015):

Research is essential in the context of public health emergencies. The primary purpose of such research is to advance public health, prevent illness and save lives. Researchers should always weigh the public health consequences of their actions in withholding and sharing results.[1]

Real-time data sharing:

Twitter: https://twitter.com/zibraproject

Website: zibraproject.github.io

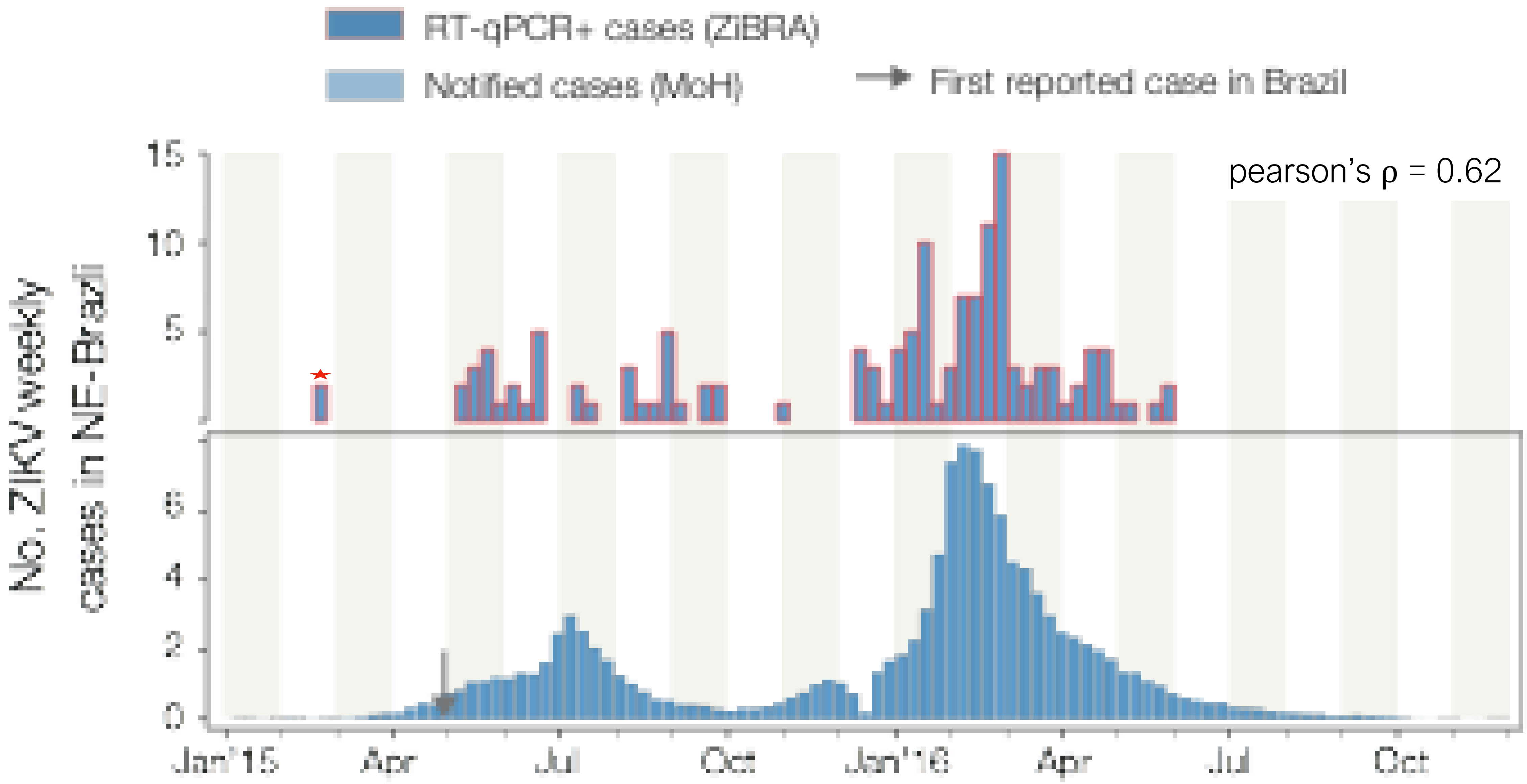
Github: https://github.com/zibraproject/

Preliminary Results: virological.org

Virus diversity: nextstrain.org

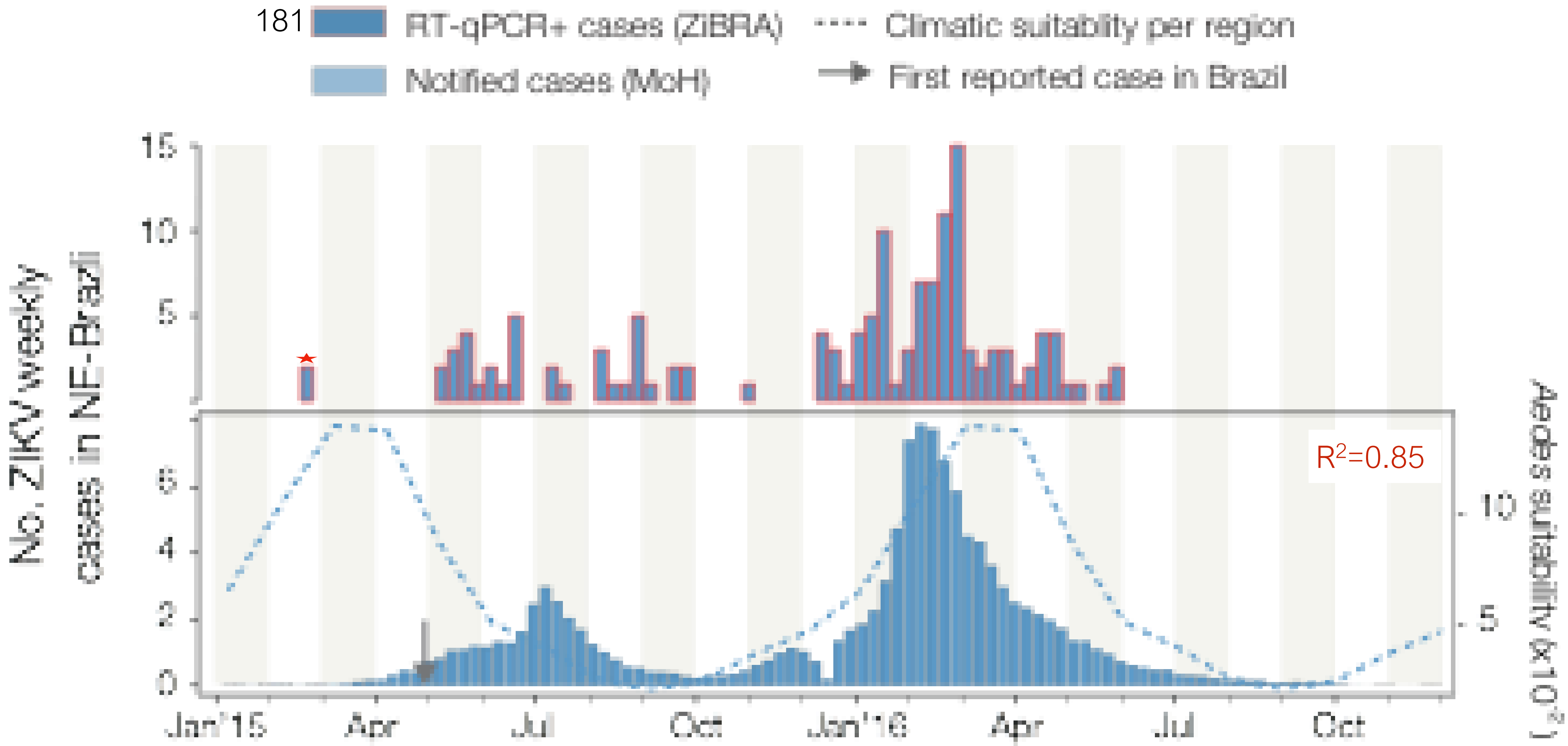
[1] Aarestrup and Koopmans, Cell 2016

Zika virus MoH notified cases is positively associated with Zika RT-qPCR+ cases

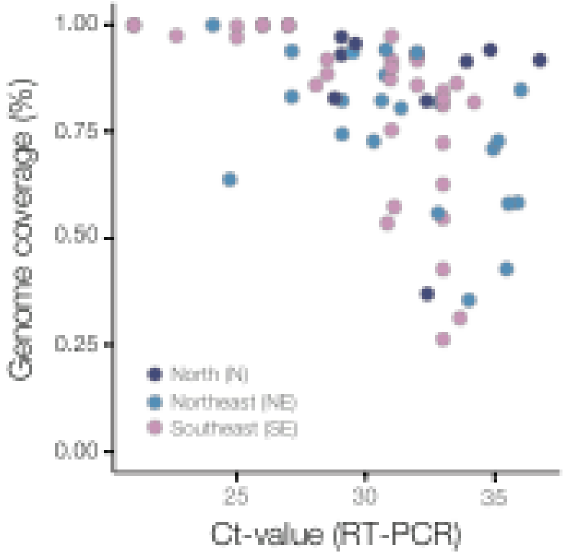


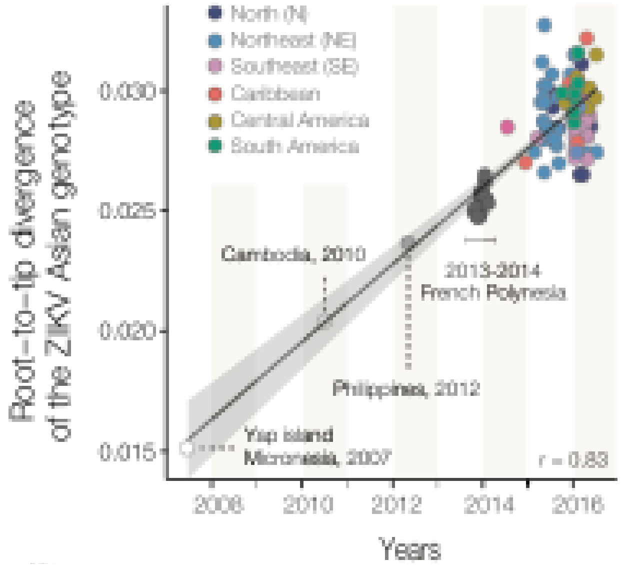
ZiBRA RT-qPCR+ data represents well the 2015-16 epidemic in NE Brazil

Zika virus MoH notified cases is positively associated with Zika RT-qPCR+ cases and climatic suitability



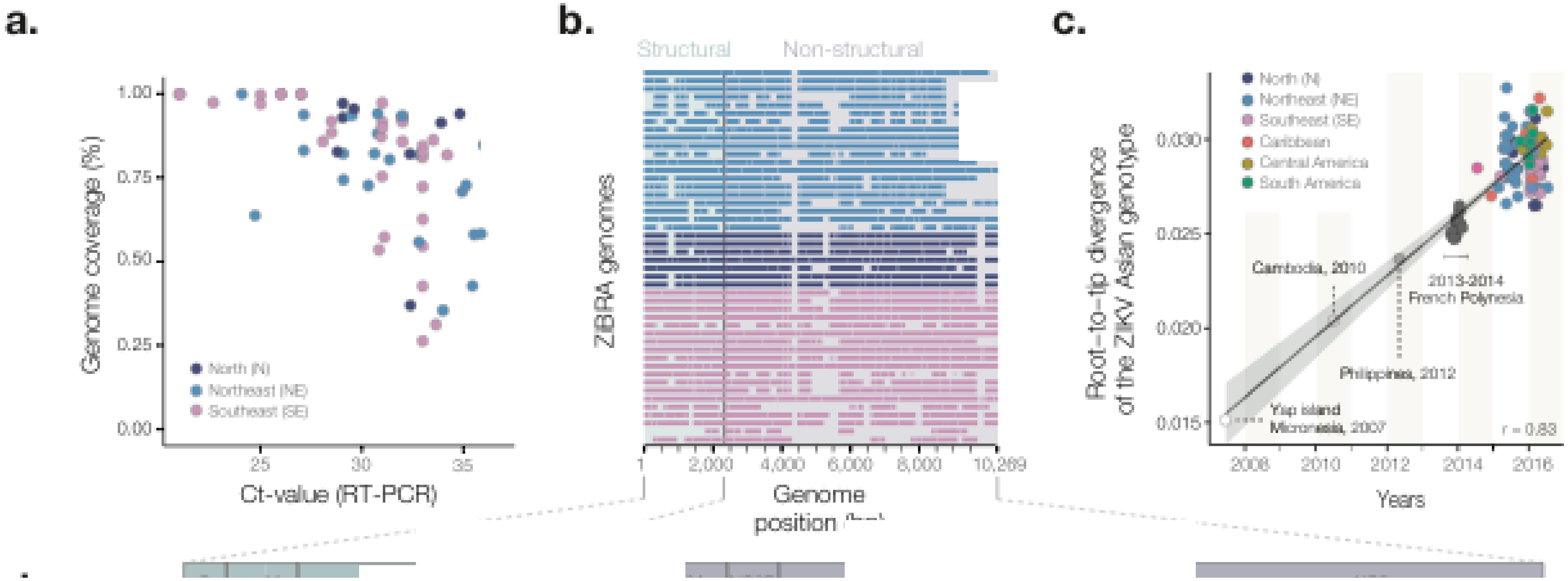
Genomic diversity of PreAm-ZIKV and Am-ZIKV lineages



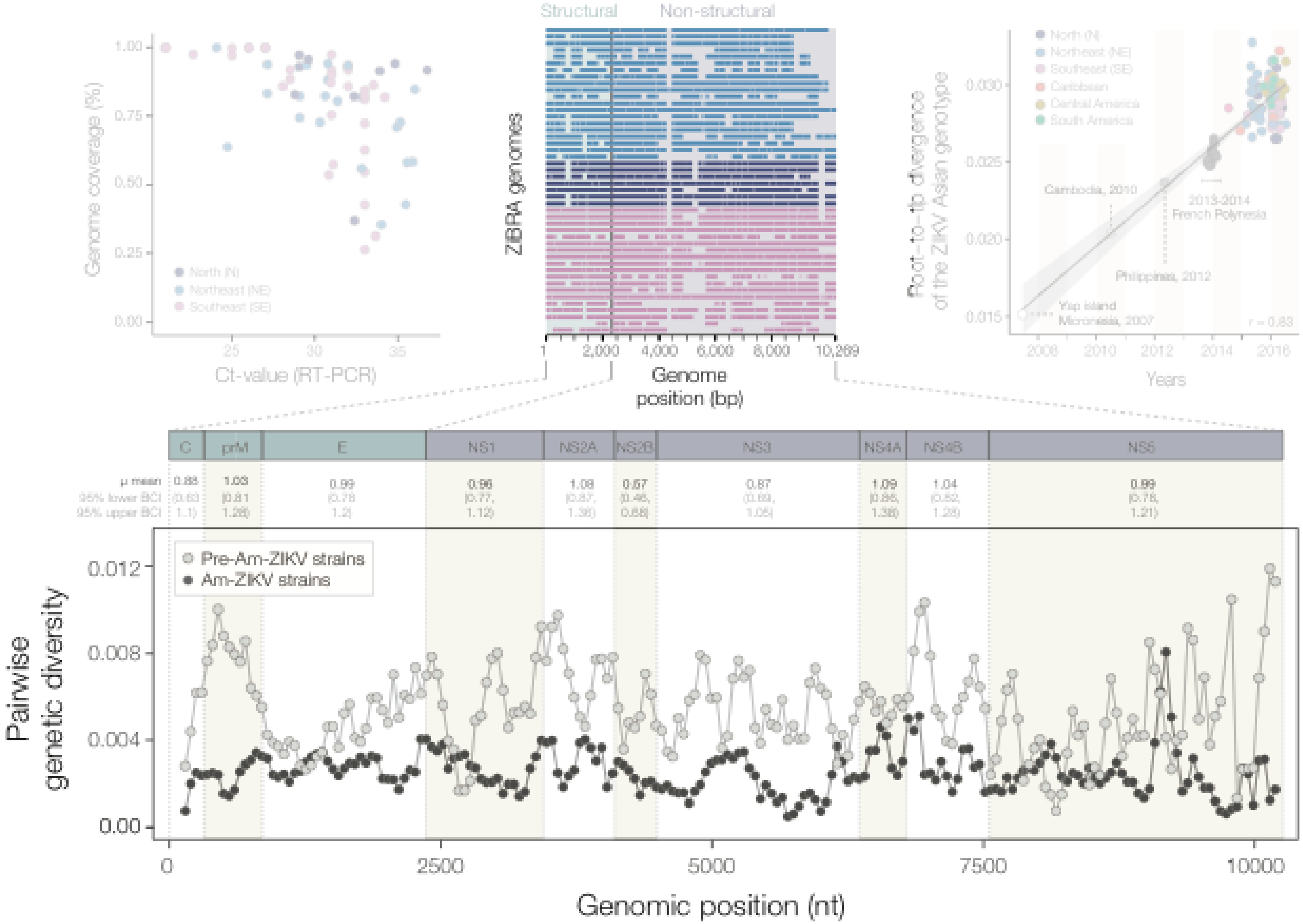


Genomic diversity of PreAm-ZIKV and Am-ZIKV lineages

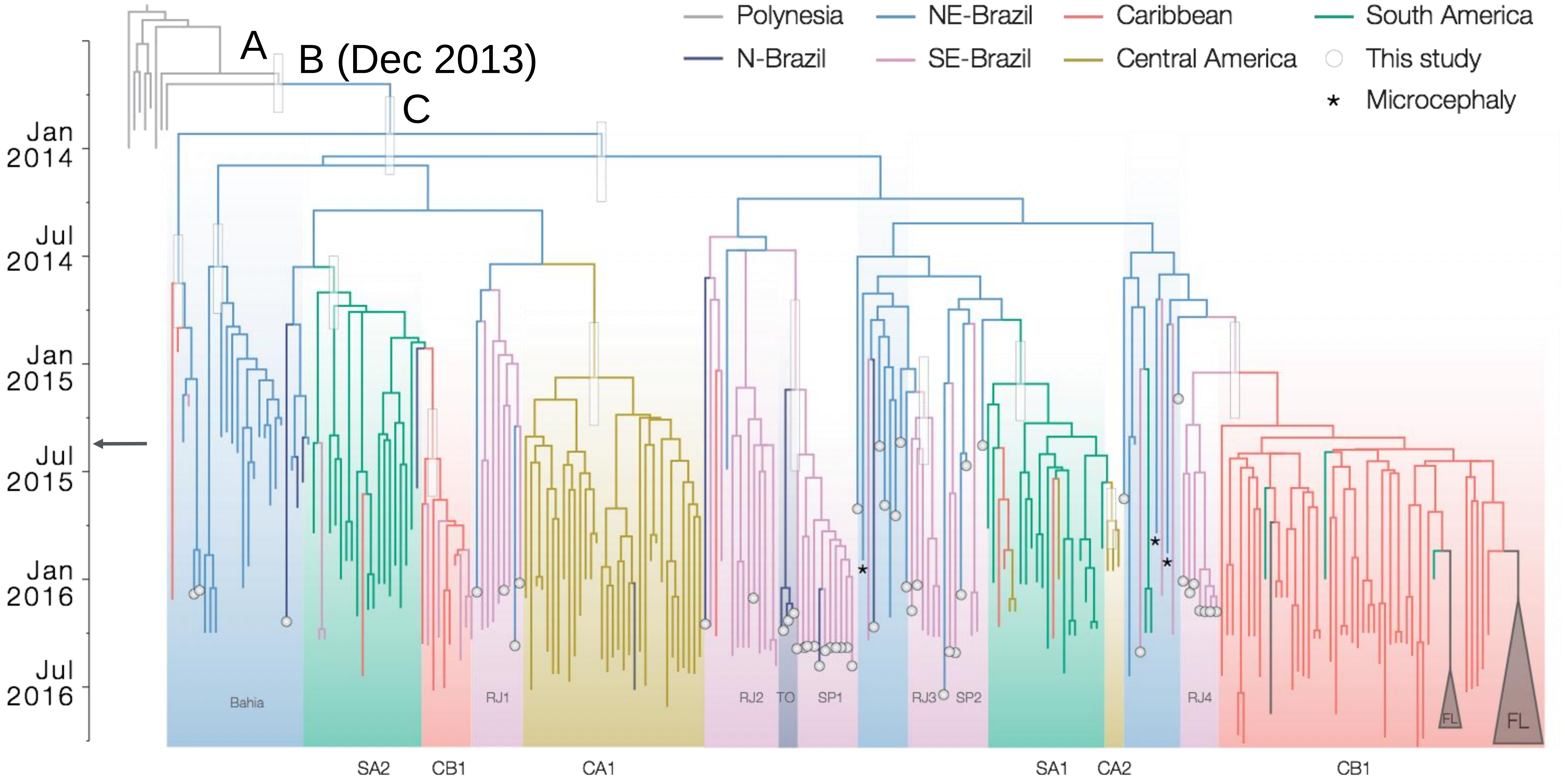
Zika vírus genetic diversity and sequencing statistics



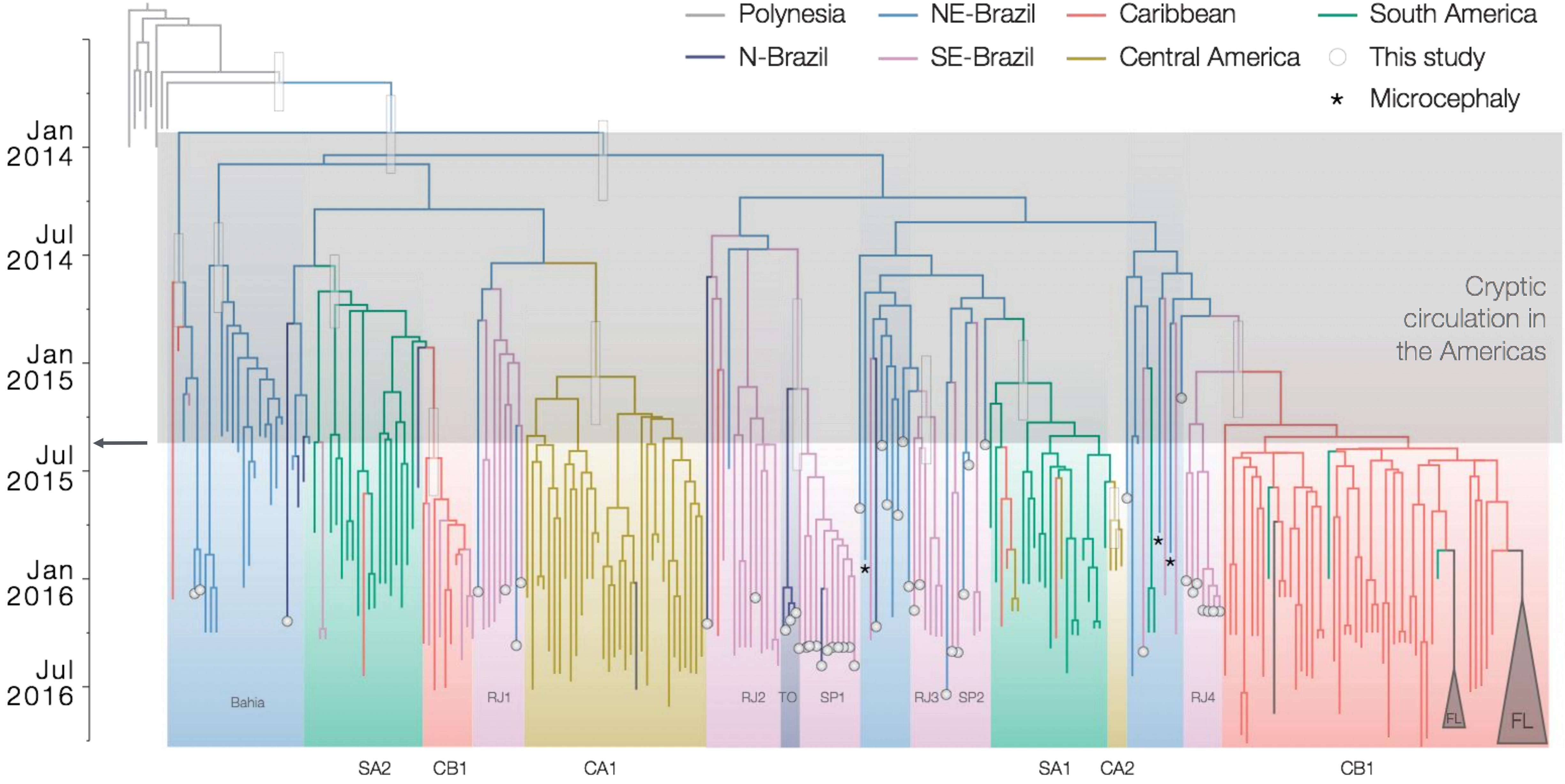
Genomic diversity of PreAm-ZIKV and Am-ZIKV lineages



Origins of ZIKV-AL in Northeastern Brazil

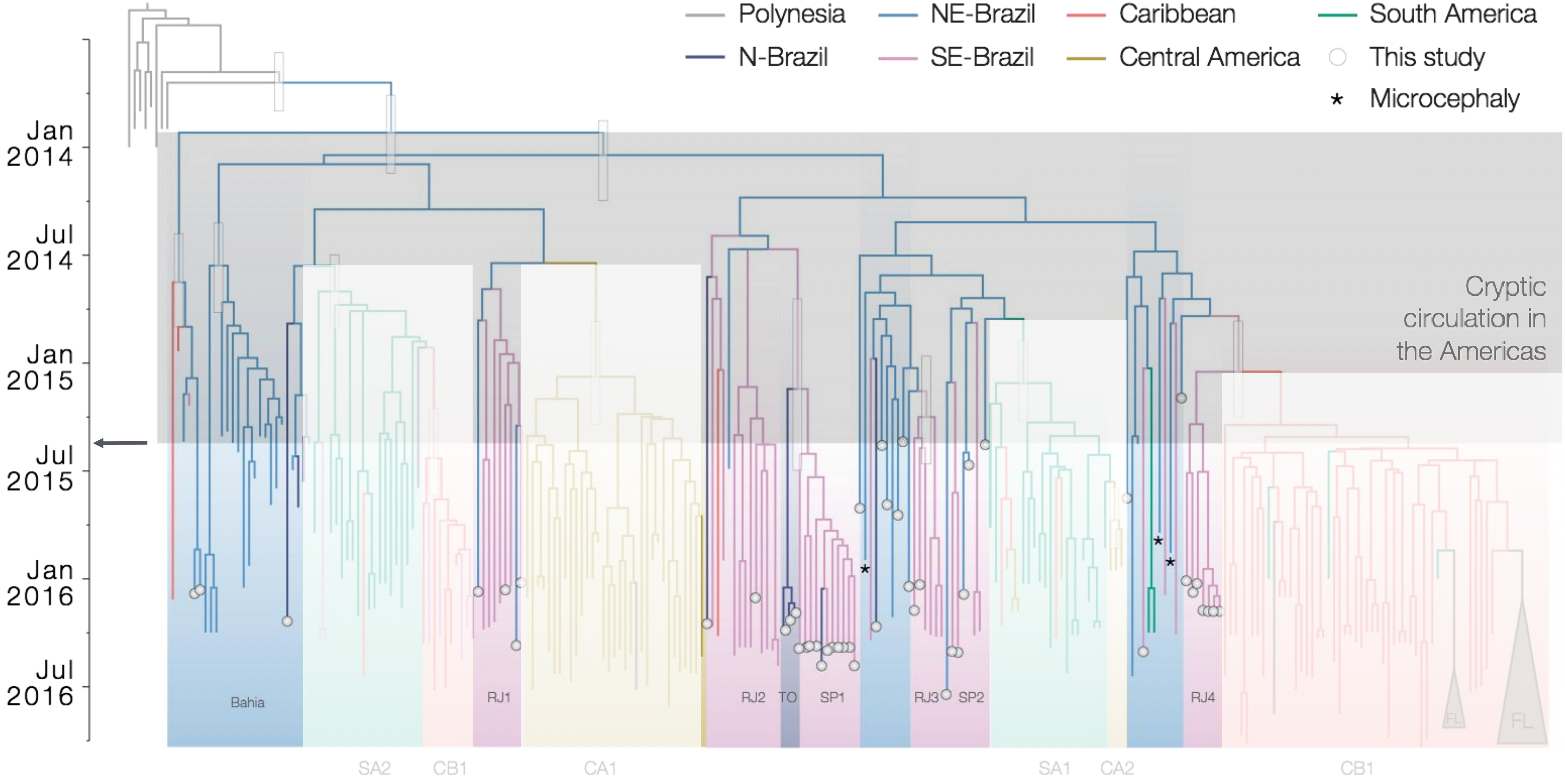

A
B (Dec 2013)
C

One year of cryptic transmission of ZIKV-AL



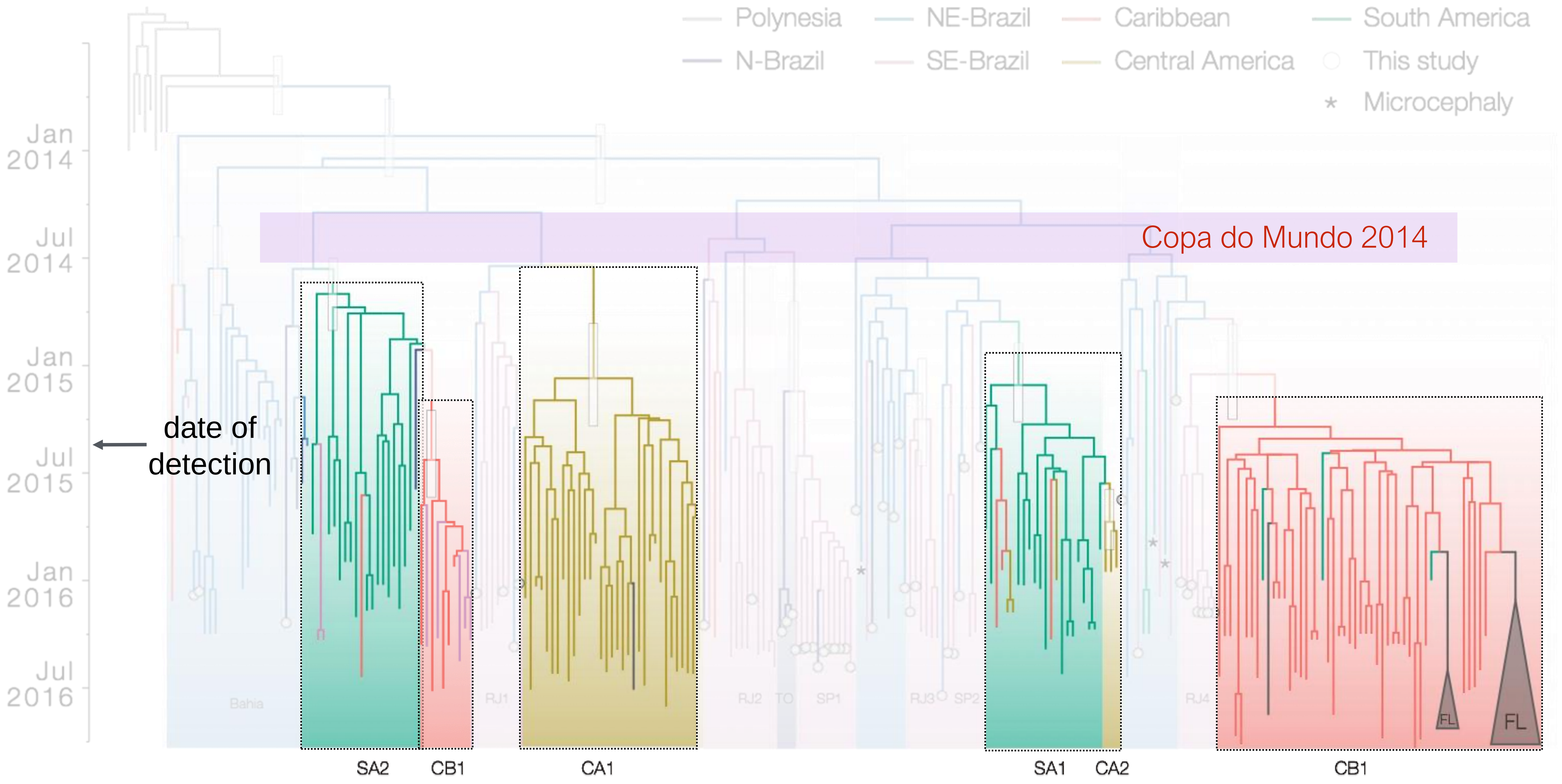
One year of cryptic transmission of ZIKV-AL

Within Brazilian geographic regions



One year of cryptic transmission of ZIKV-AL

Spread to other regions in the Americas



Thomas Jaenisch

Sarah Scotland

Luciano Chaves Franco Filho

Eduardo

Bruno Luís Sena do Nascimento

nature

THE INTERNATIONAL WEEKLY JOURNAL OF SCIENCE

ZIKA MAPPED

Genome sequences reveal origin and spread of the virus in the Americas

PAGES 355, 401, 406 & 411

HISTORY

VENICE TIME MACHINE

Digitized archive to reveal 1,000 years of Venetian life

PAGE 341

POLICY

UNDER THE GUN

Why firearms research must not be muzzled

PAGE 345

PHYSICS

TRANSFER OF POWER

Wire-free charging goes mobile

PAGES 354 & 307

NATURE.COM/NATURE

Giselle Barbosa-Lima

Cynthia Loo

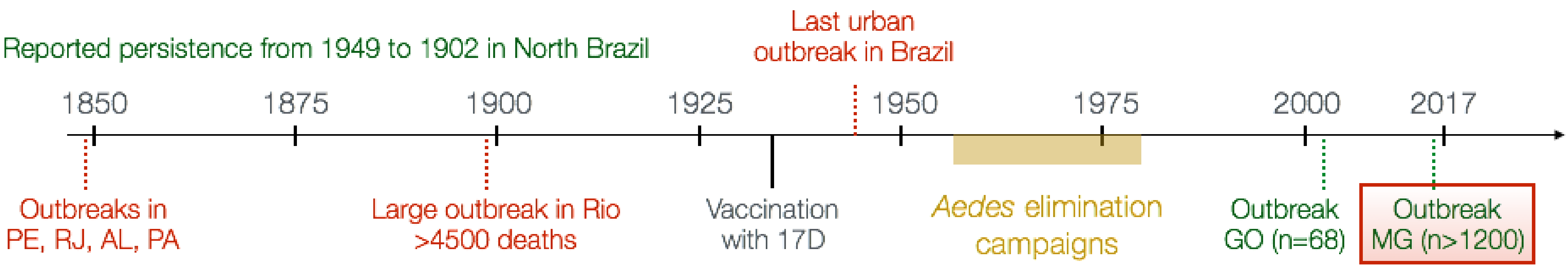
Charles Chiu

Pardis Sabeti

ZIBRA^2

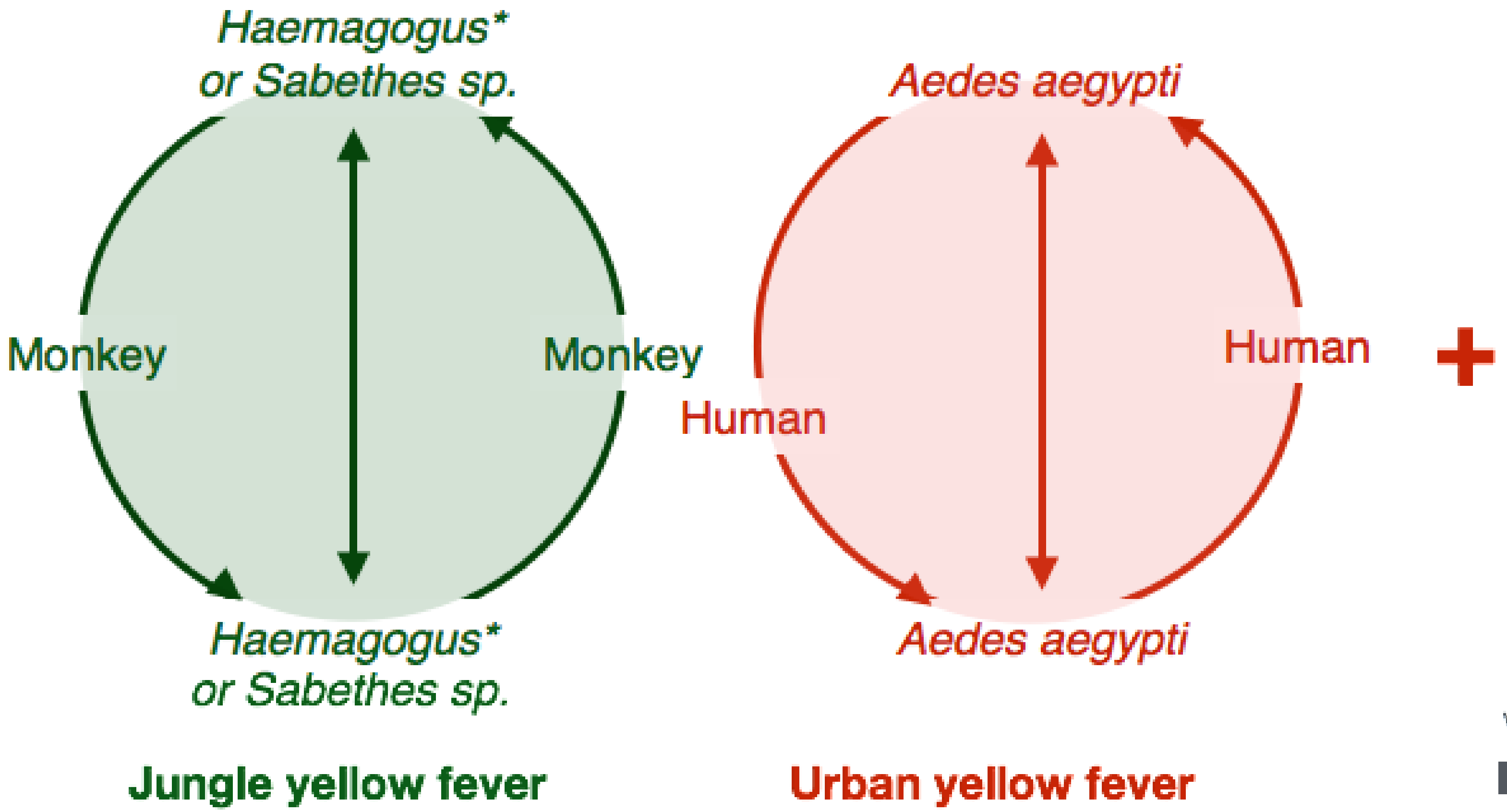
ZIKA IN BRAZIL REAL TIME ANALYSIS^2

Yellow Fever Outbreak in Minas Gerais, 2016-2017(?)

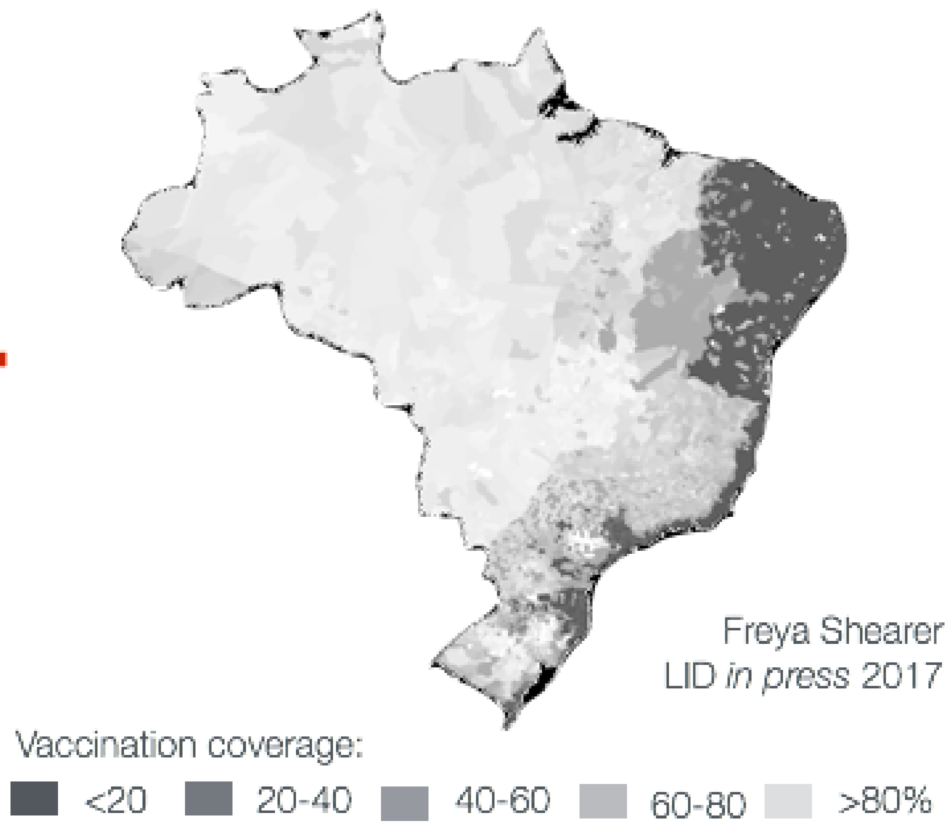


Vainio & Cutts, WHO 1981

Transmission cycles in South America



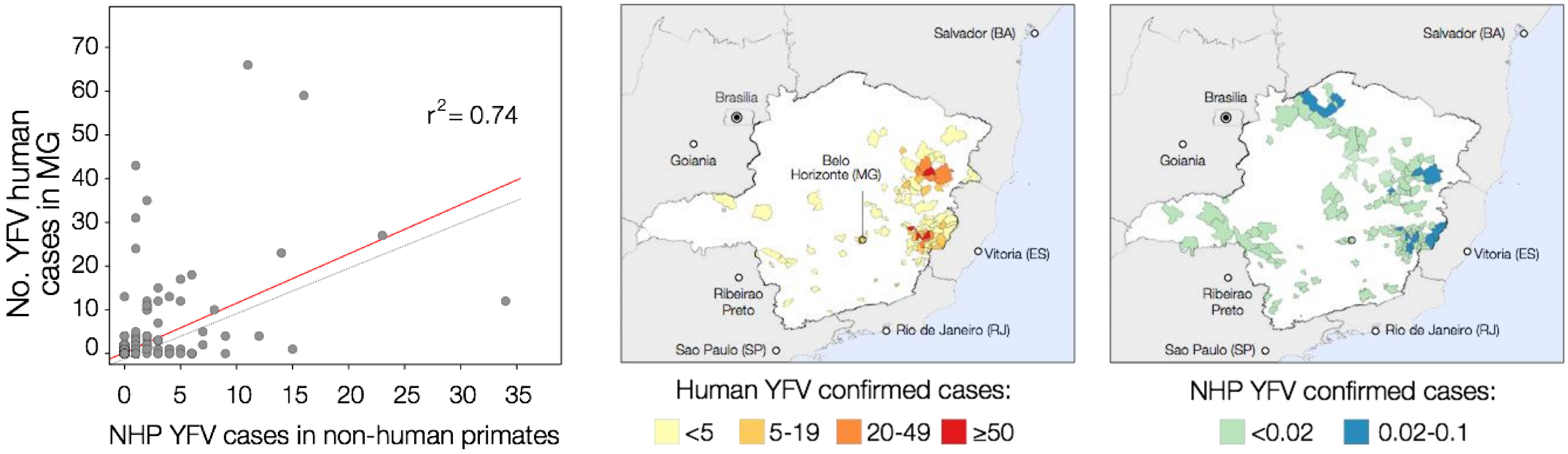
Yellow Fever vaccination coverage Brazil 2016



Freya Shearer
LID *in press* 2017

Spatial association between human e primates cases

Suspected and confirmed cases in MG (ELISA e RT-qPCR)

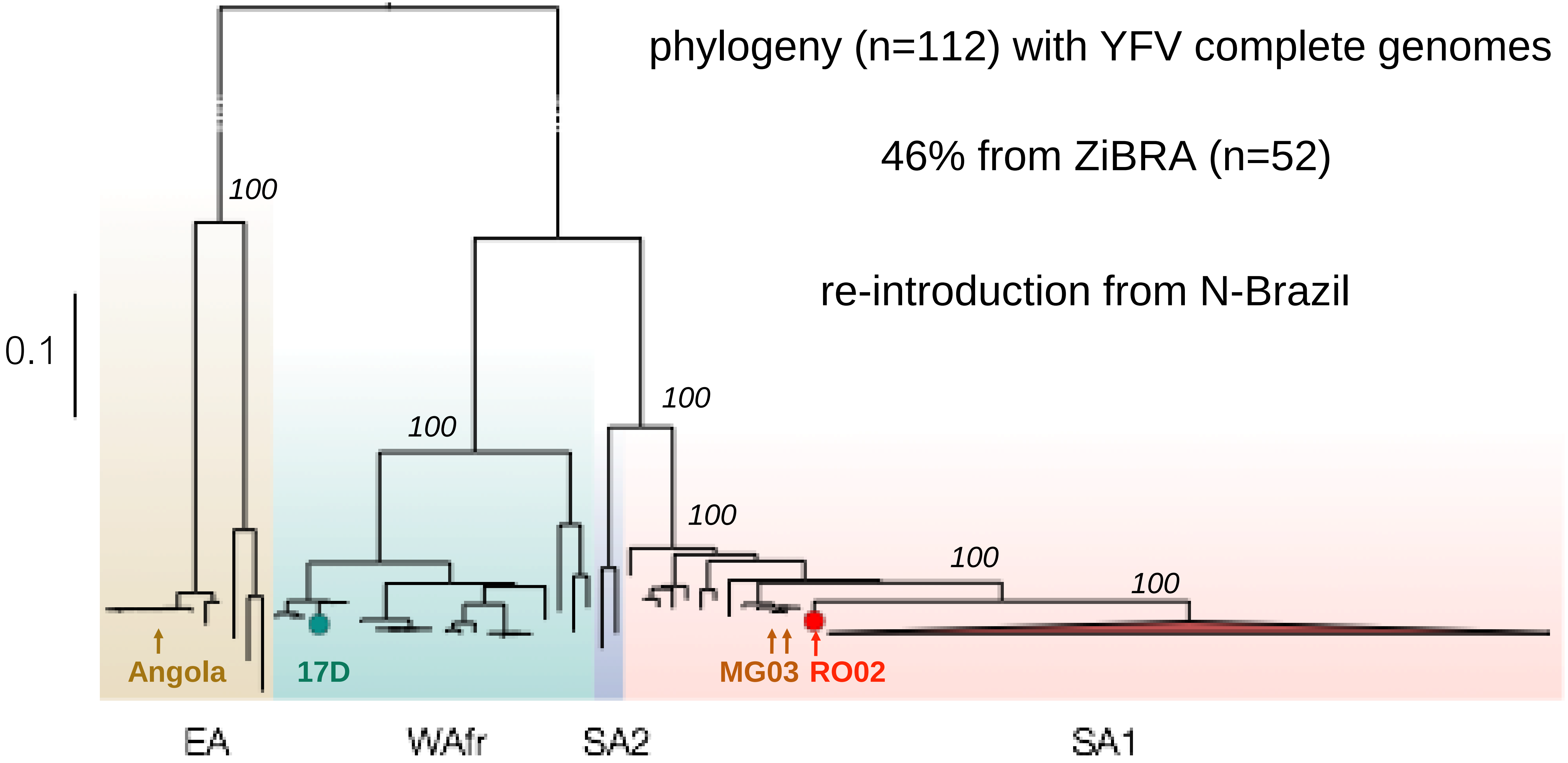


Genomic surveilance of YFV outbreak in SE-Brazil

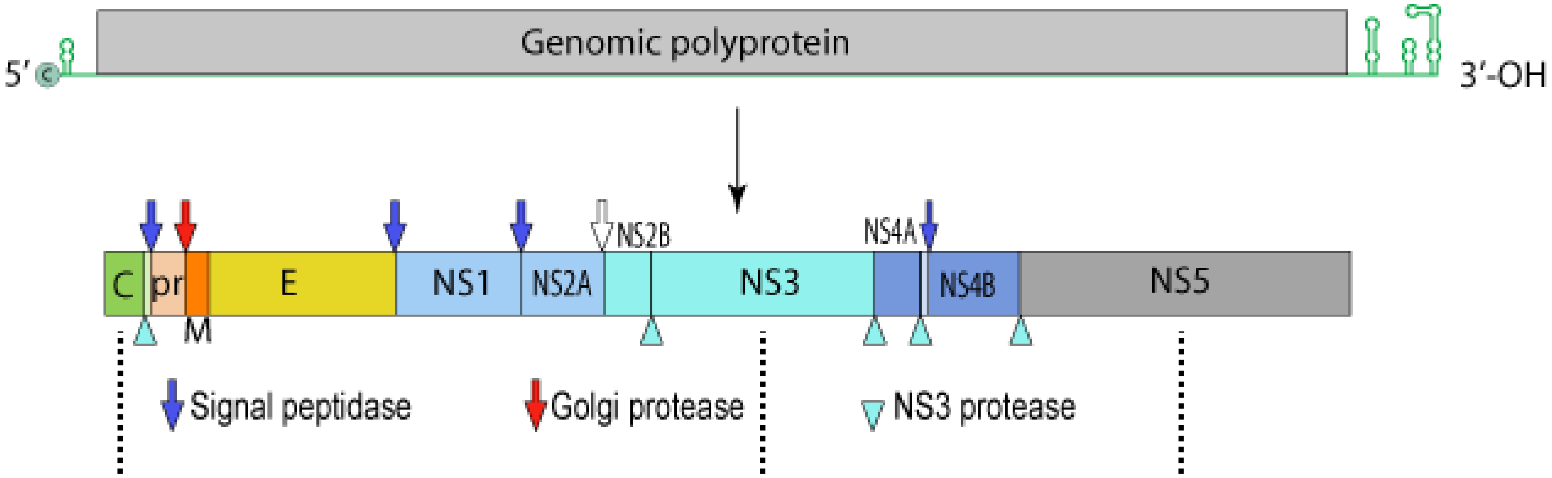
phylogeny (n=112) with YFV complete genomes

46% from ZiBRA (n=52)

re-introduction from N-Brazil



** SNP 2016-2017

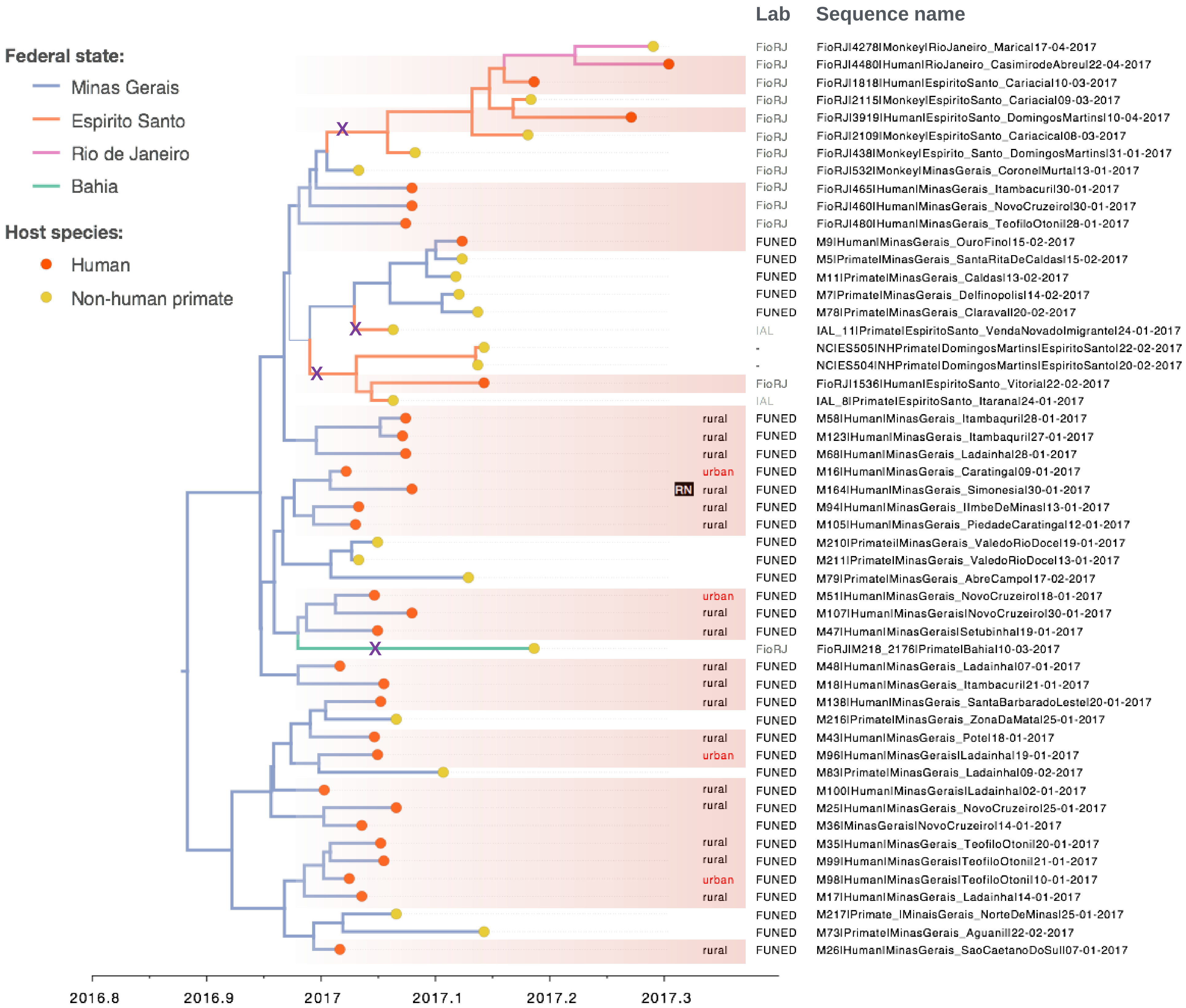


V108I

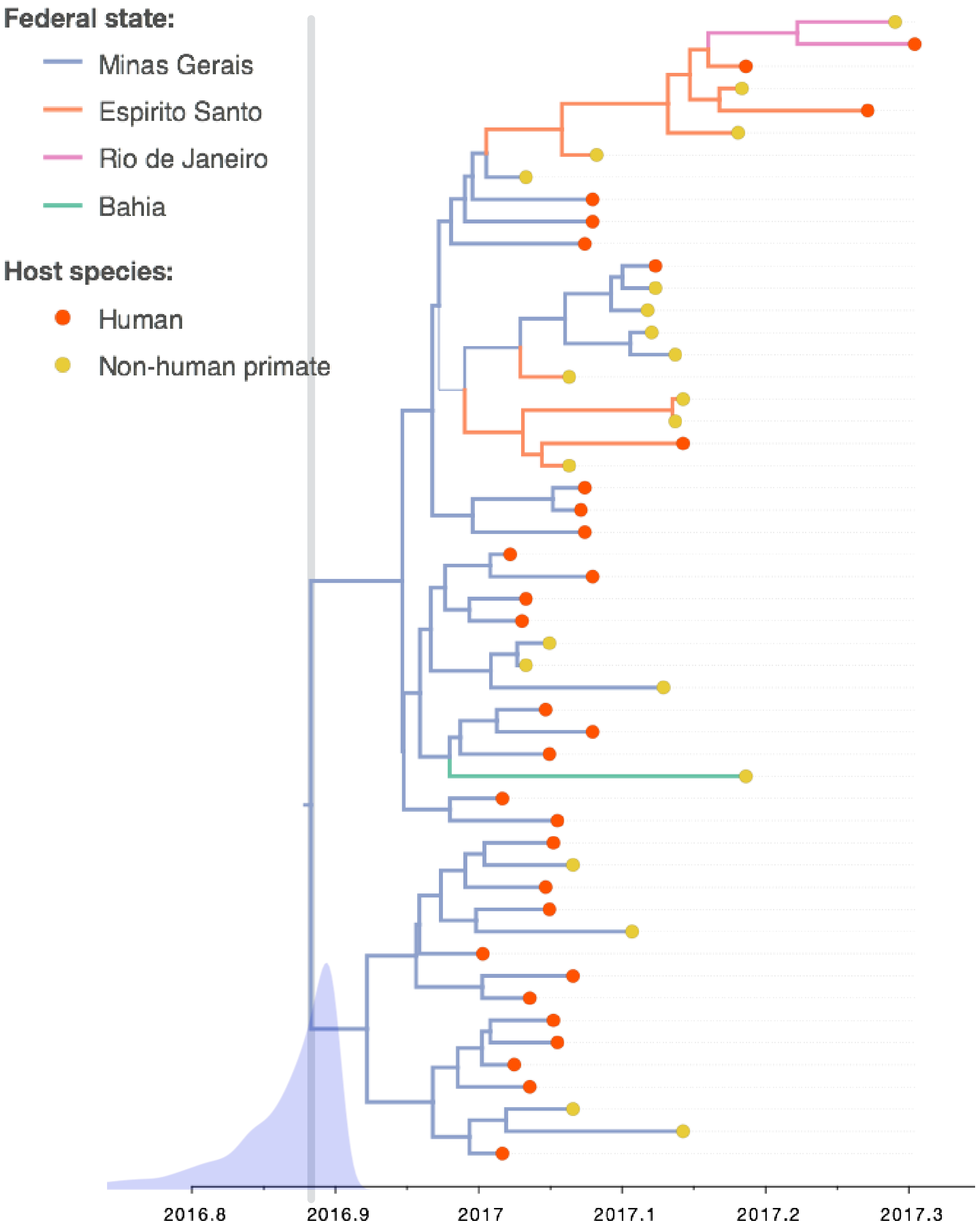
E1572D
K1605R

K2607Q
V2644I
G2679S
A2736T
N2803S
V3149A
N3215S

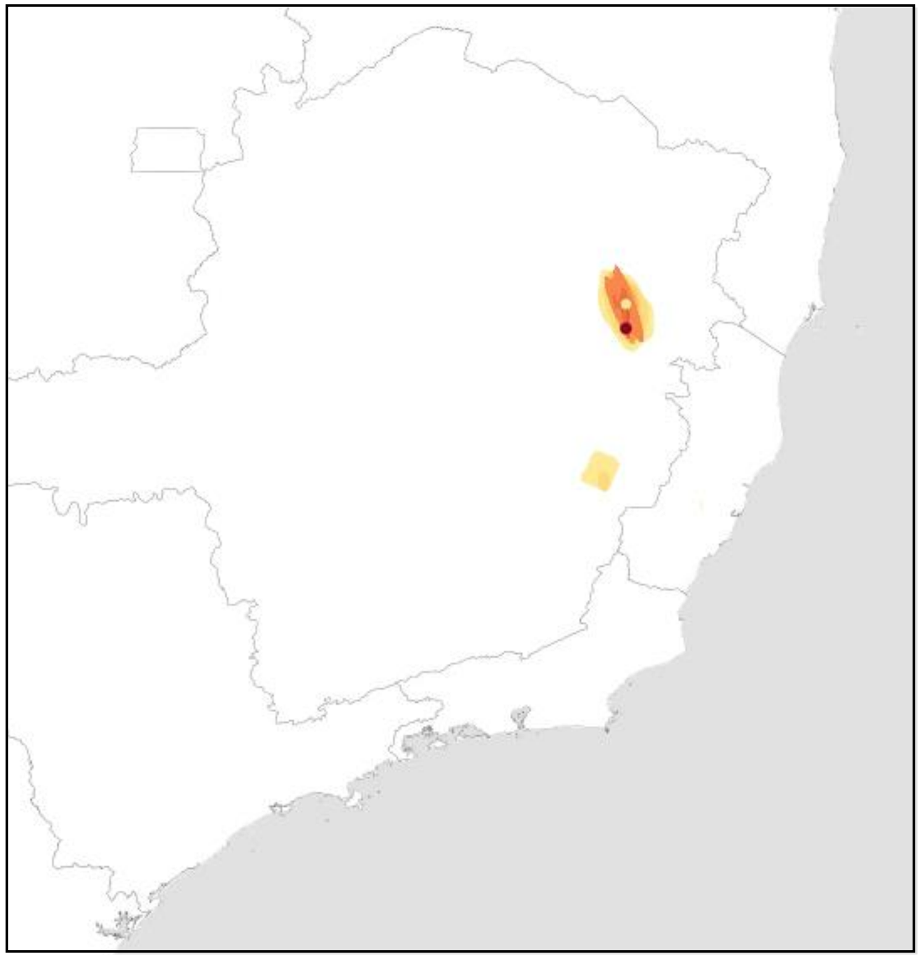
Origen and evolution of the outbreak



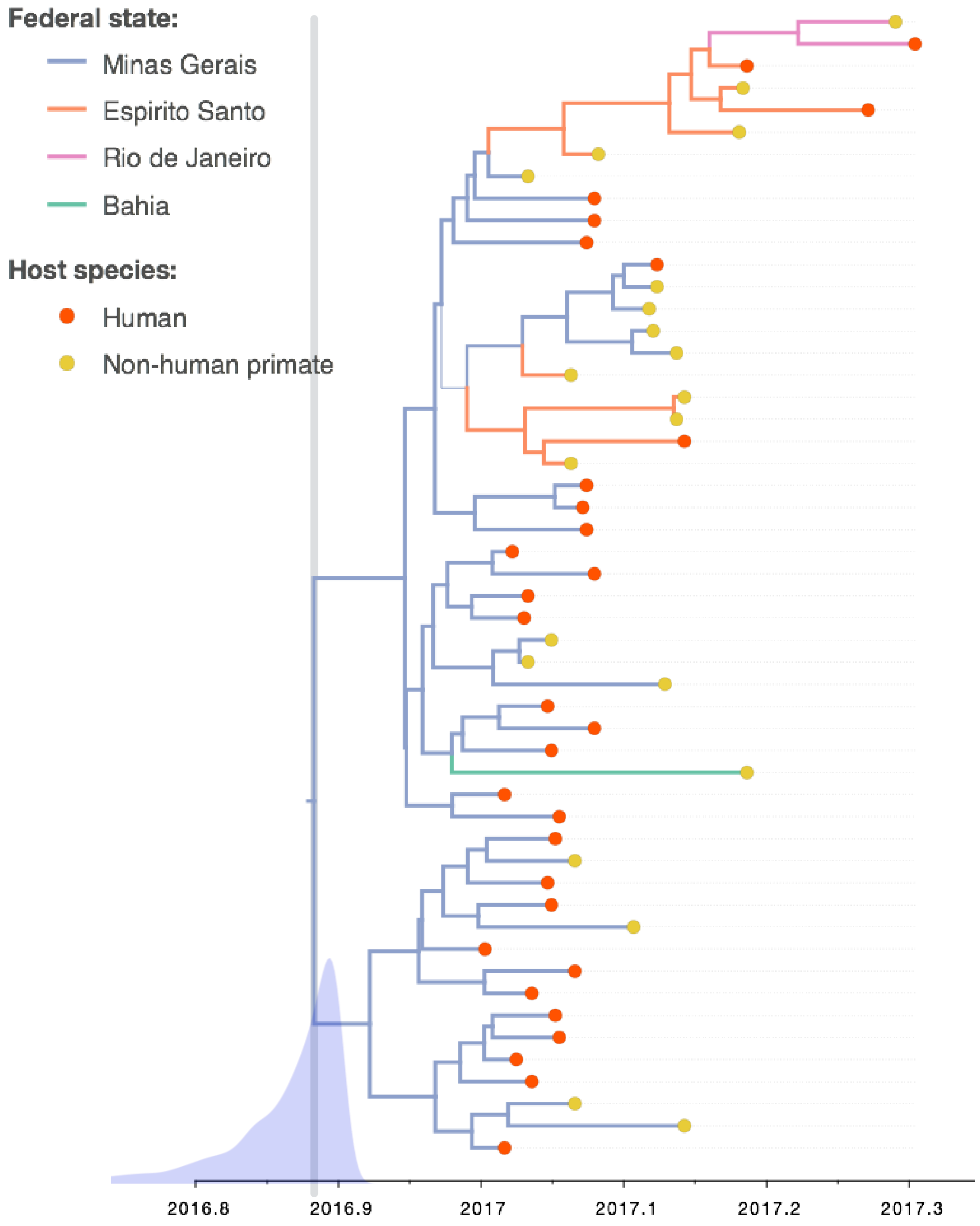
Wave of spread towards the SE-Brazil



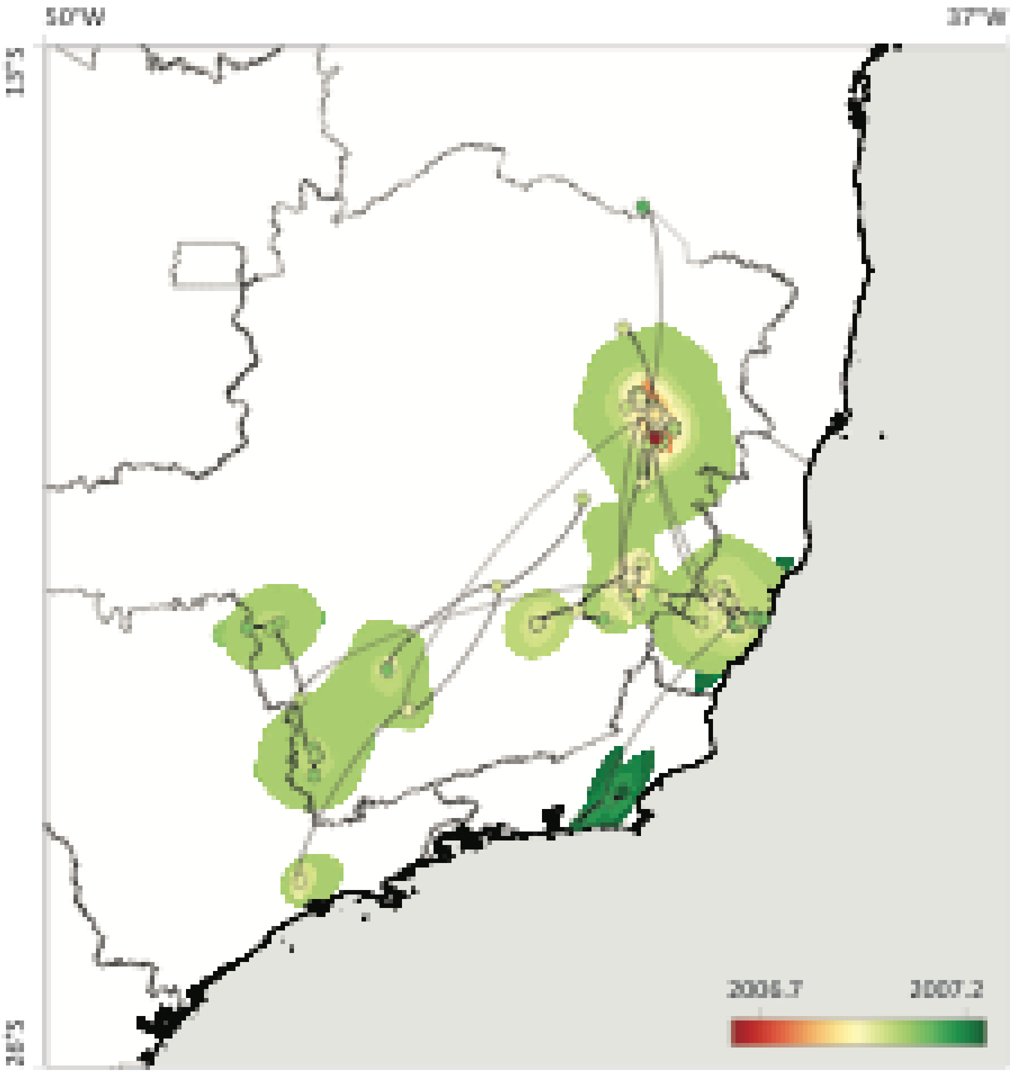
Spread of YFV



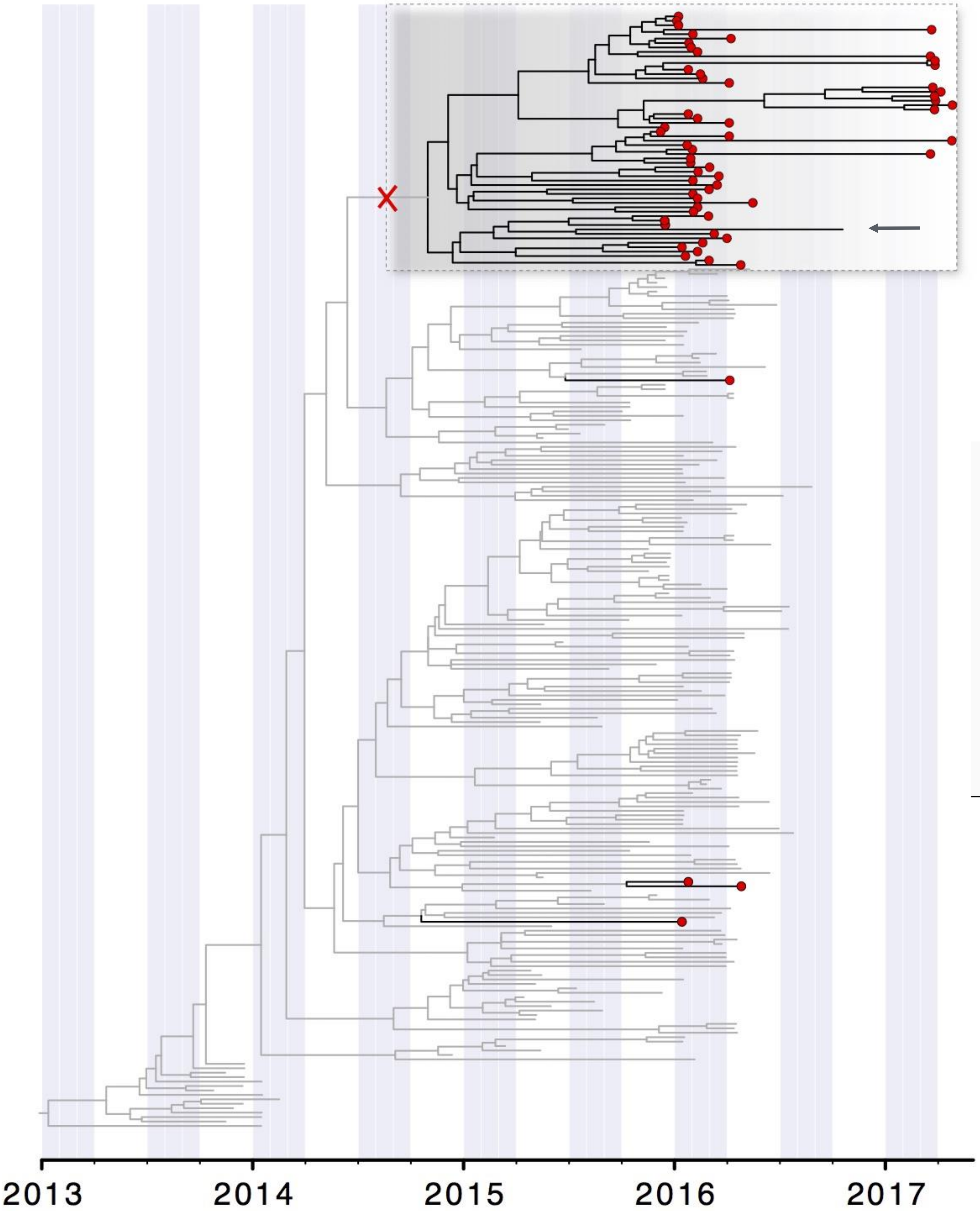
(branch velocity: 48-94 km/month)

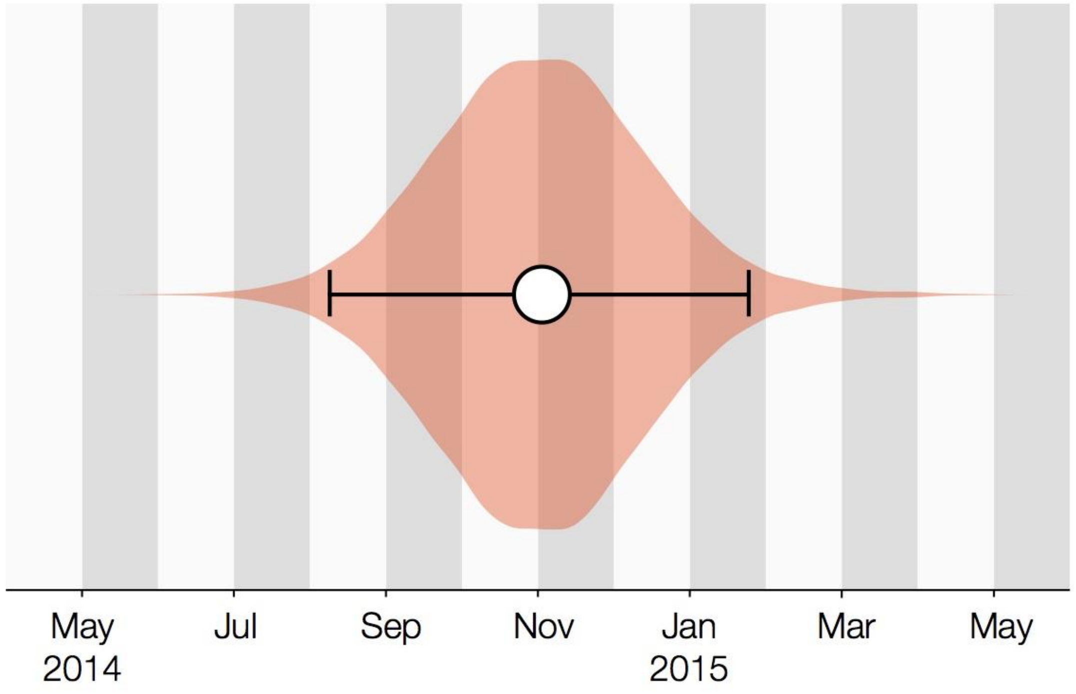


Spread of YFV



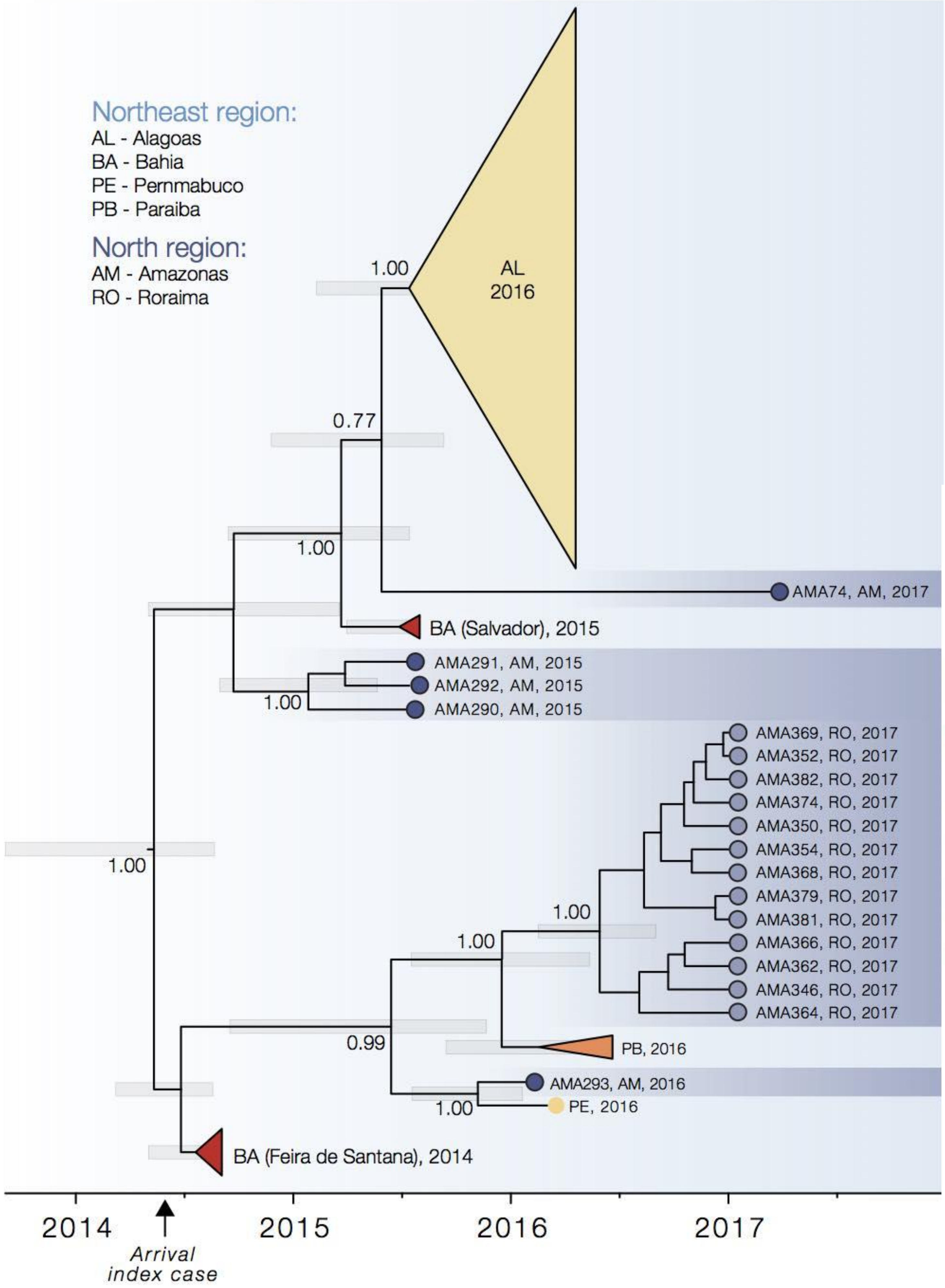
ZIBRA-2 (ZIKV) results in N-Brazil

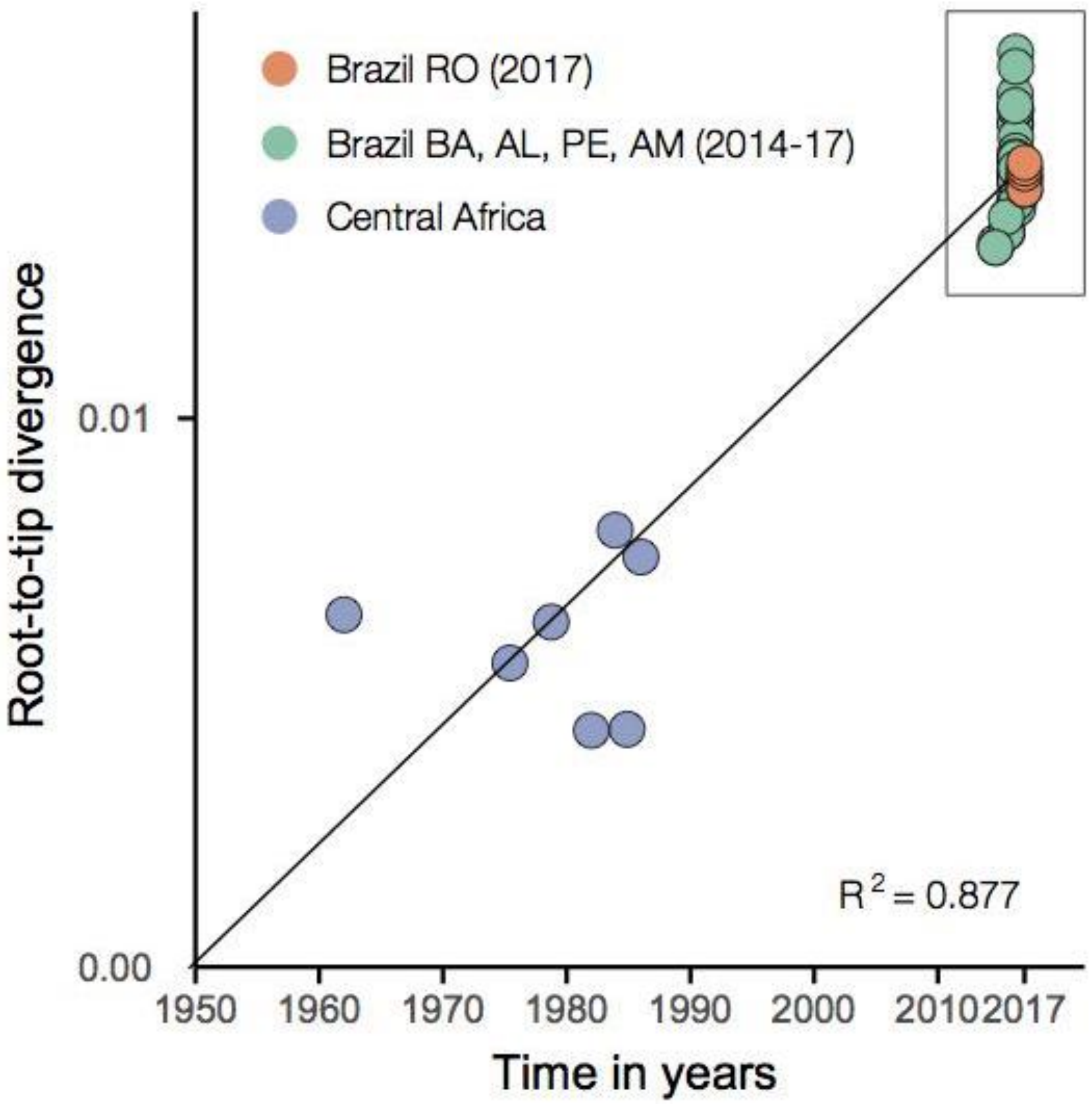


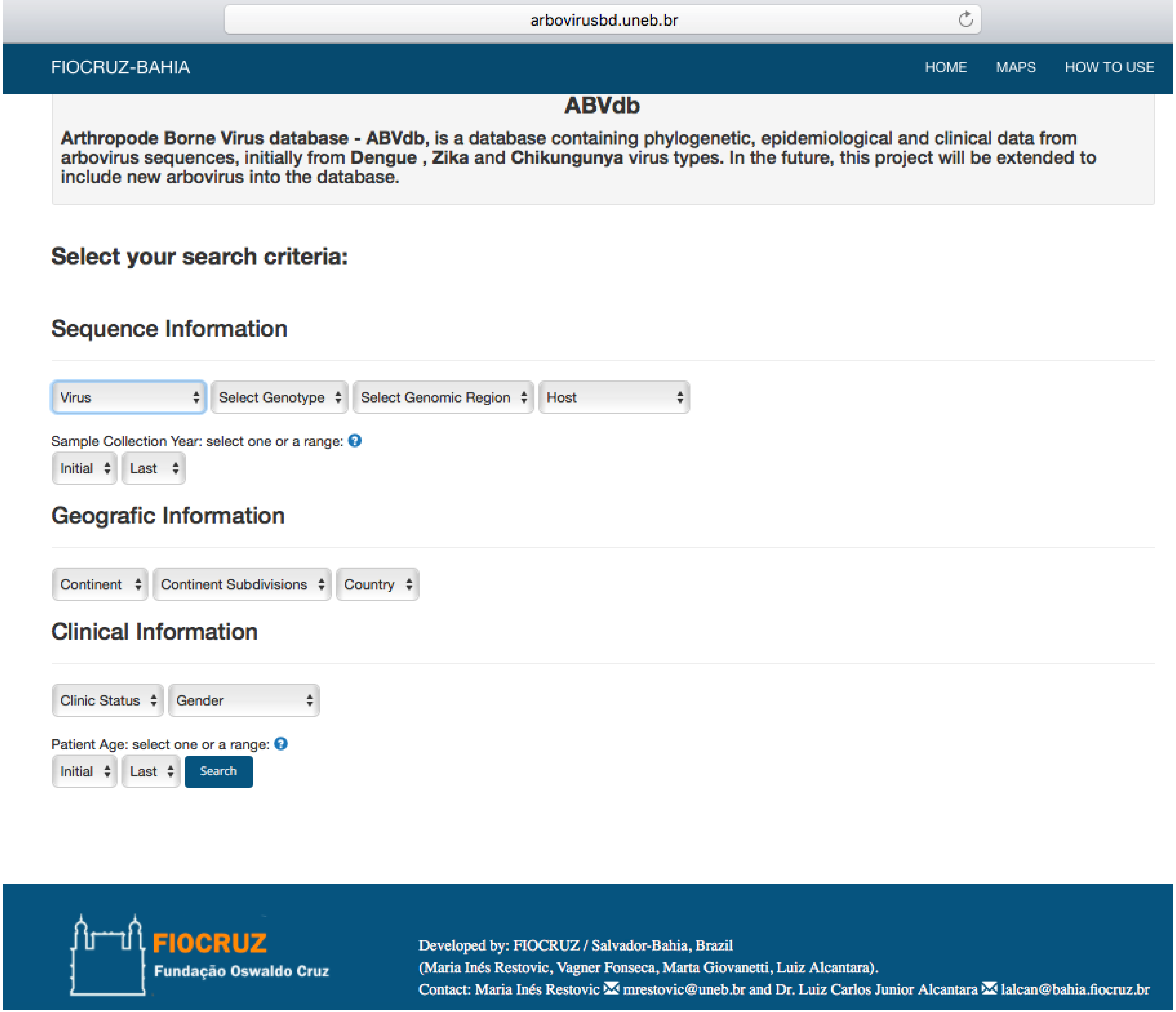


Posterior TMRCA ZIKV-Manaus

ZIBRA-2 (CHIKV) results in N-Brazil







ABVdb

Arthropode Borne Virus database - ABVdb, is a database containing phylogenetic, epidemiological and clinical data from arbovirus sequences, initially from **Dengue** , **Zika** and **Chikungunya** virus types. In the future, this project will be extended to include new arbovirus into the database.

Select your search criteria:

Sequence Information

Sample Collection Year: select one or a range:

Geografic Information

Clinical Information

Patient Age: select one or a range:

Developed by: FIOCRUZ / Salvador-Bahia, Brazil
(Maria Inés Restovic, Vagner Fonseca, Marta Giovanetti, Luiz Alcantara).
Contact: Maria Inés Restovic ✉ mrestovic@uneb.br and Dr. Luiz Carlos Junior Alcantara ✉ lalcan@bahia.fiocruz.br

Zika Virus: Data displayed by Country,Continent Subdivisions and Continent

🔵 Less than 20 sequences 🟢 Between 20 and 40 sequences 🟡 Between 41 and 80 sequences 🔴 More than 80 sequences

Developed by: FIOCRUZ / Salvador-Bahia, Brazil
(Maria Inés Restovic, Vagner Fonseca, Marta Giovanetti, Luiz Alcantara).
Contact: Maria Inés Restovic ✉ mrestovic@uneb.br and Dr. Luiz Carlos Junior Alcantara ✉ lalcan@bahia.fiocruz.br

Bioinformatic Tools

http://genomedetective.com/vis/typingtool/virus/

Pan-viral Typing Tool *Version 0.0*

Pan-Viral NGS Typing Tool Version Beta 1

The pan-viral typing tool is an easy to use, accurate and fast method to identify all virus species in the submitted input files. After the viruses have been identified at the species level, you can click through to one of the phylogenetic subtyping tools to further analyse the identified viruses. Currently subtyping tools for 10 viruses are installed.

The tool works with assembled FASTA input as well as with raw NGS data from FASTQ files.

The tool can currently assemble genomes for 7298 viral species. The process uses Blast (fasta seqs) and/or DIAMOND (fastq) in order to identify a virus species from the ICTV master list and the RefSeq database. The tool also use SPADes to contruct de-novo assemblies of viral genomes in order to provide assembled genomes in fasta and bam formats. Our tool accepts pair-ended FASTQ files (no limit on the number of reads) and FASTA files with up to 2000 sequences.

NGS: upload FASTQ reads

File type ● Pair end read ○ Single end read ○ Contigs

Supported formats: fastq or compressed fastq (zip, gz)

Paired end 1: nenhum arquivo selecionado

Paired end 2: nenhum arquivo selecionado

Or let the server download the files for you.

Enter the Run Number and Download SRA file. Example: ERR233413

Download srr file:

Classical: upload FASTA

You may either:

A. Paste one or more sequences in FASTA format in the input field.
B. Upload a FASTA file.
C. Upload FASTQ files.
D. Revisit results of a previous run

A) Paste nucleotide sequence(s) in FASTA format:

```
>2I.AF100469.1992_dengue
TCCAGGCTTTACCATAATGGCCGCAATCCTGGCATACACCATAGGAACGACGCATTTCCAAAGAGTCC
TGATATTCATCCTACTGACAGCCATCGCTCCTTCAATGACAATGCGCTGCATAGGAATATCAAATAGG
GACTTTGTGGAAGGAGTGTCAGGAGGGAGTTGGGTTGACATAGTTTTAGAACATGGAAGTTGTGTGAC
GACGATGGCAAAAAATAAACCAACACTGGACTTTGAACTGATAAAAACAGAAGCCAAACAACCCGCCA
CCTTAAGGAAGTACTGTATAGAGGCTAAACTGACCAACACGACAACAGACTCGCGCTGCCCAACACAA
GGGGAACCCACCCTGAATGAAGAGCAGGACAAAAGGTTTGTCTGCAAACATTCTATGGTAGACAGAGG
ATGGGGAAATGGATGTGGATTGTTTGGAAAAGGAGGCATCGTGACCTGTGCTATGTTCACATGCAAAA
AGAACATGGAAGGGAAAATTGTGCAGCCAGAAAACCTGGAATACACTGTCGTGATAACACCTCATTCA
GGGGAAGAACATGCAGTCGGAAATGACACAGGAAAACATGGTAAAGAAGTCAAGATAACACCACAGAG
CTCCATCACAGAGGCGGAACTGACAGGCTATGGCACTGTTACGATGGAGTGCTCTCCAAGAACGGGCC
TCGACTTCAATGAGATGGTGTTGCTGCAAATGGAAGACAAAGCTTGGCTGGTGCACAGACAATGGTTC
CTAGACCTACCGTTGCCATGGCTGCCCGGAGCAGACACACAAGGATCAAATTGGATACAGAAAGAGAC
ATTGGTCACCTTCAAAAATCCCCATGCGAAAAAACAGGATGTTGTTGTCTTAGGATCCCAAGAAGGGG
CCATGCACACAGCACTCACAGGGGCCACGGAAATCCAAATGTCATCAGGAAACCTGCTGTTCACAGGA
```

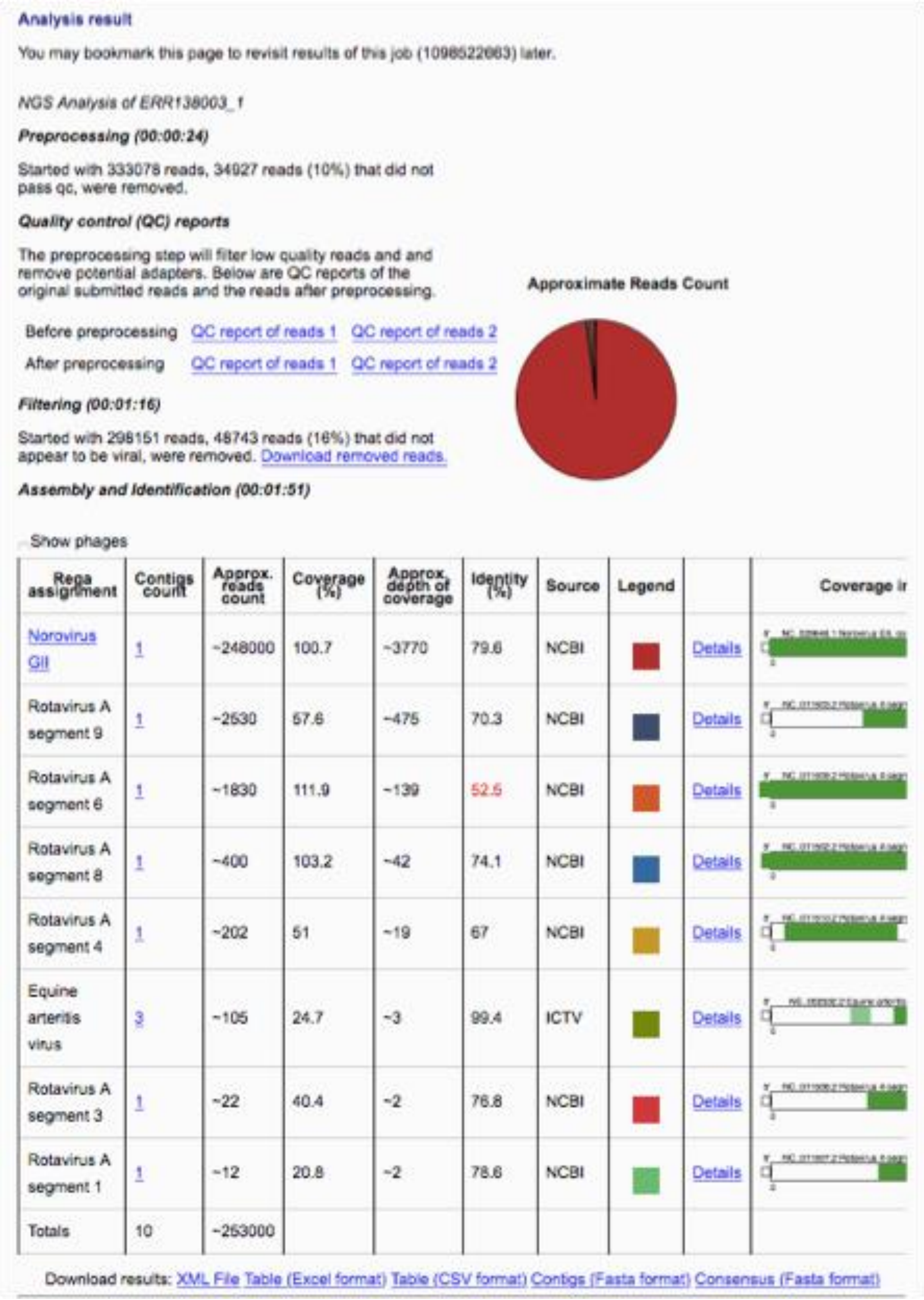
B) Or, upload a FASTA with nucleotide sequences:

nenhum arquivo selecionado

C) Or, revisit results from a previous run:

De novo assemblages from raw reads of metagenomics or amplicom sequencing using NGS methods

http://genomedetective.com/vis/typingtool/virus/



Analysis result

You may bookmark this page to revisit results of this job (1098522063) later.

NGS Analysis of ERR138003_1

Preprocessing (00:00:24)

Started with 333078 reads, 34927 reads (10%) that did not pass qc, were removed.

Quality control (QC) reports

The preprocessing step will filter low quality reads and and remove potential adapters. Below are QC reports of the original submitted reads and the reads after preprocessing.

Before preprocessing	QC report of reads 1	QC report of reads 2
After preprocessing	QC report of reads 1	QC report of reads 2

Filtering (00:01:16)

Started with 298151 reads, 48743 reads (16%) that did not appear to be viral, were removed. Download removed reads.

Assembly and Identification (00:01:51)

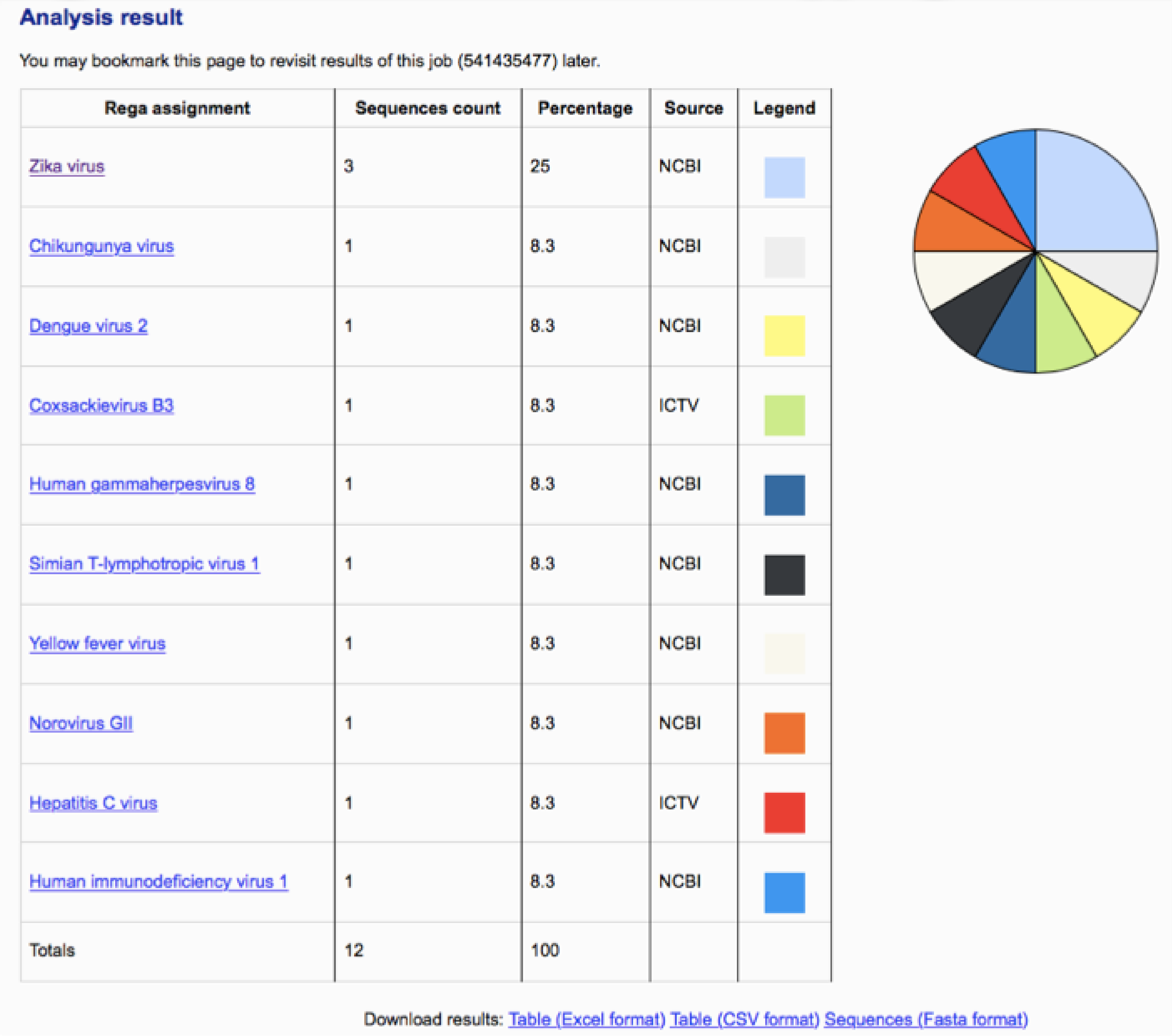
Show phages

Rega assignment	Contigs count	Approx. reads count	Coverage (%)	Approx. depth of coverage	Identity (%)	Source	Legend		Coverage ir
Norovirus GII	1	~248000	100.7	~3770	79.6	NCBI	🟥	Details	
Rotavirus A segment 9	1	~2530	57.6	~475	70.3	NCBI	🟦	Details	
Rotavirus A segment 6	1	~1830	111.9	~139	52.5	NCBI	🟧	Details	
Rotavirus A segment 8	1	~400	103.2	~42	74.1	NCBI	🟦	Details	
Rotavirus A segment 4	1	~202	51	~19	67	NCBI	🟨	Details	
Equine arteritis virus	3	~105	24.7	~3	99.4	ICTV	🟩	Details	
Rotavirus A segment 3	1	~22	40.4	~2	76.8	NCBI	🟥	Details	
Rotavirus A segment 1	1	~12	20.8	~2	78.6	NCBI	🟩	Details	
Totals	10	~253000							

Download results: XML File Table (Excel format) Table (CSV format) Contigs (Fasta format) Consensus (Fasta format)

Typing Tools

http://genomedetective.com/vis/typingtool/virus/



Analysis result

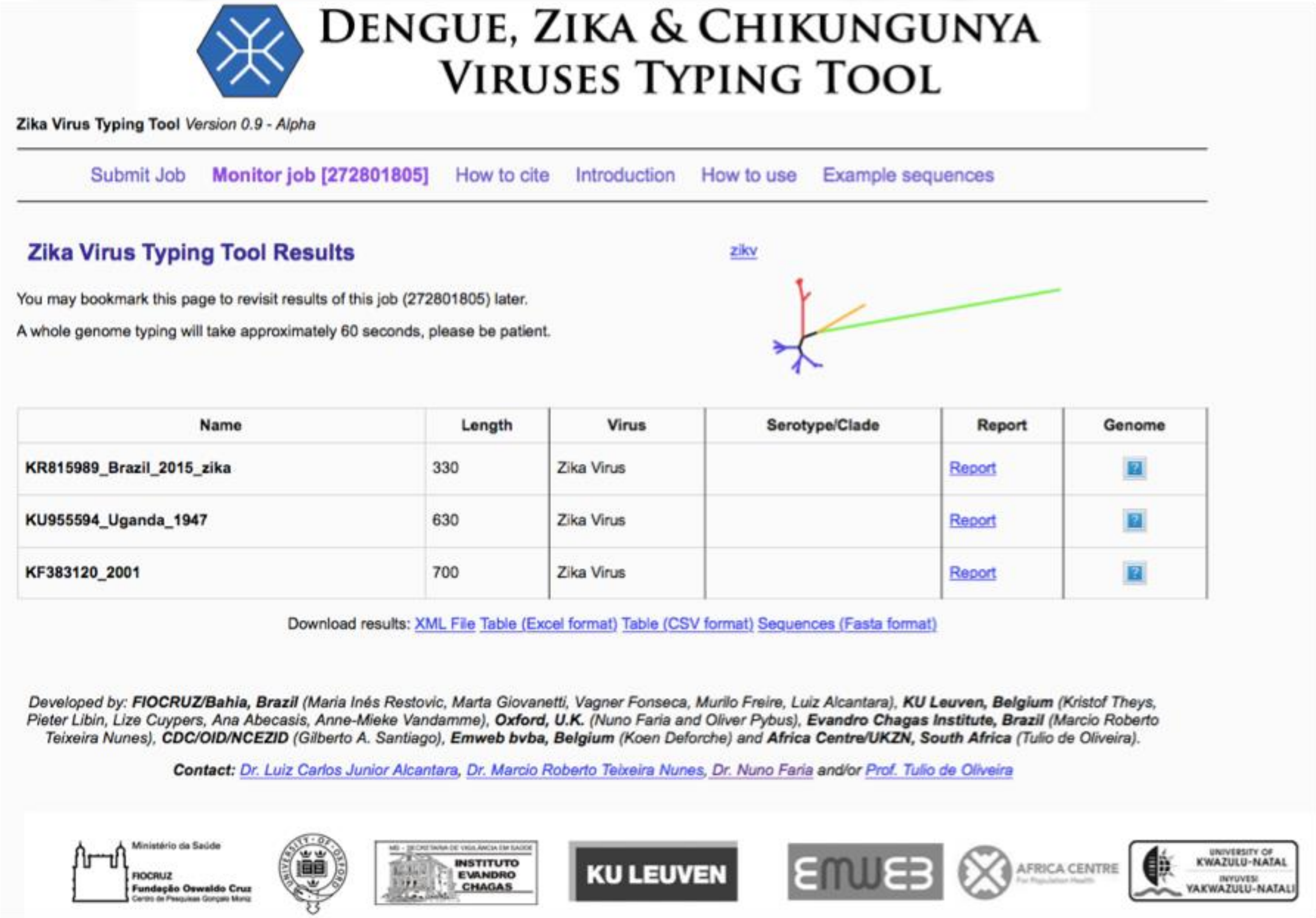
You may bookmark this page to revisit results of this job (541435477) later.

Rega assignment	Sequences count	Percentage	Source	Legend
Zika virus	3	25	NCBI	🟦
Chikungunya virus	1	8.3	NCBI	⬜
Dengue virus 2	1	8.3	NCBI	🟨
Coxsackievirus B3	1	8.3	ICTV	🟩
Human gammaherpesvirus 8	1	8.3	NCBI	🟦
Simian T-lymphotropic virus 1	1	8.3	NCBI	⬛
Yellow fever virus	1	8.3	NCBI	⬜
Norovirus GII	1	8.3	NCBI	🟧
Hepatitis C virus	1	8.3	ICTV	🟥
Human immunodeficiency virus 1	1	8.3	NCBI	🟦
Totals	12	100		

Download results: Table (Excel format) Table (CSV format) Sequences (Fasta format)

Subtyping Tools

http://genomedetective.com/vis/typingtool/virus/



Zika Virus Typing Tool *Version 0.9 - Alpha*

Zika Virus Typing Tool Results

You may bookmark this page to revisit results of this job (272801805) later.

A whole genome typing will take approximately 60 seconds, please be patient.

Name	Length	Virus	Serotype/Clade	Report	Genome
KR815989_Brazil_2015_zika	330	Zika Virus		Report	?
KU955594_Uganda_1947	630	Zika Virus		Report	?
KF383120_2001	700	Zika Virus		Report	?

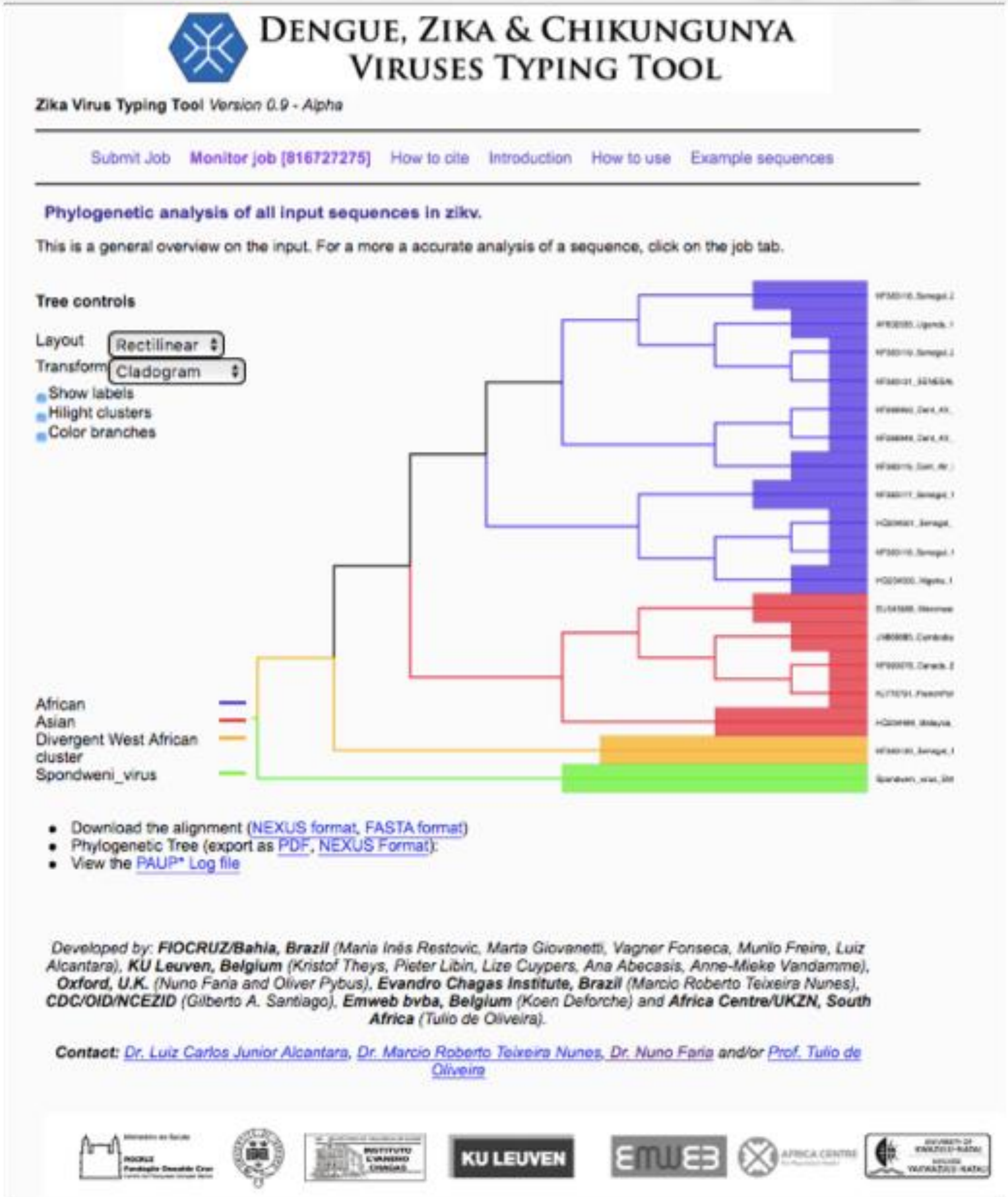
Download results: XML File Table (Excel format) Table (CSV format) Sequences (Fasta format)

Developed by: ***FIOCRUZ/Bahia, Brazil*** *(Maria Inés Restovic, Marta Giovanetti, Vagner Fonseca, Murilo Freire, Luiz Alcantara),* ***KU Leuven, Belgium*** *(Kristof Theys, Pieter Libin, Lize Cuypers, Ana Abecasis, Anne-Mieke Vandamme),* ***Oxford, U.K.*** *(Nuno Faria and Oliver Pybus),* ***Evandro Chagas Institute, Brazil*** *(Marcio Roberto Teixeira Nunes),* ***CDC/OID/NCEZID*** *(Gilberto A. Santiago),* ***Emweb bvba, Belgium*** *(Koen Deforche) and* ***Africa Centre/UKZN, South Africa*** *(Tulio de Oliveira).*

Contact: *Dr. Luiz Carlos Junior Alcantara, Dr. Marcio Roberto Teixeira Nunes, Dr. Nuno Faria and/or Prof. Tulio de Oliveira*

Subtyping Tools

http://genomedetective.com/vis/typingtool/virus/



Zika Virus Typing Tool *Version 0.9 - Alpha*

Phylogenetic analysis of all input sequences in zikv.

This is a general overview on the input. For a more a accurate analysis of a sequence, click on the job tab.

Tree controls

Layout: Rectilinear

Transform: Cladogram

- Download the alignment (NEXUS format, FASTA format)
- Phylogenetic Tree (export as PDF, NEXUS Format):
- View the PAUP* Log file

Developed by: **FIOCRUZ/Bahia, Brazil** *(Maria Inês Restovic, Marta Giovanetti, Vagner Fonseca, Murilo Freire, Luiz Alcantara),* **KU Leuven, Belgium** *(Kristof Theys, Pieter Libin, Lize Cuypers, Ana Abecasis, Anne-Mieke Vandamme),* **Oxford, U.K.** *(Nuno Faria and Oliver Pybus),* **Evandro Chagas Institute, Brazil** *(Marcio Roberto Teixeira Nunes),* **CDC/OID/NCEZID** *(Gilberto A. Santiago),* **Emweb bvba, Belgium** *(Koen Deforche) and* **Africa Centre/UKZN, South Africa** *(Tulio de Oliveira).*

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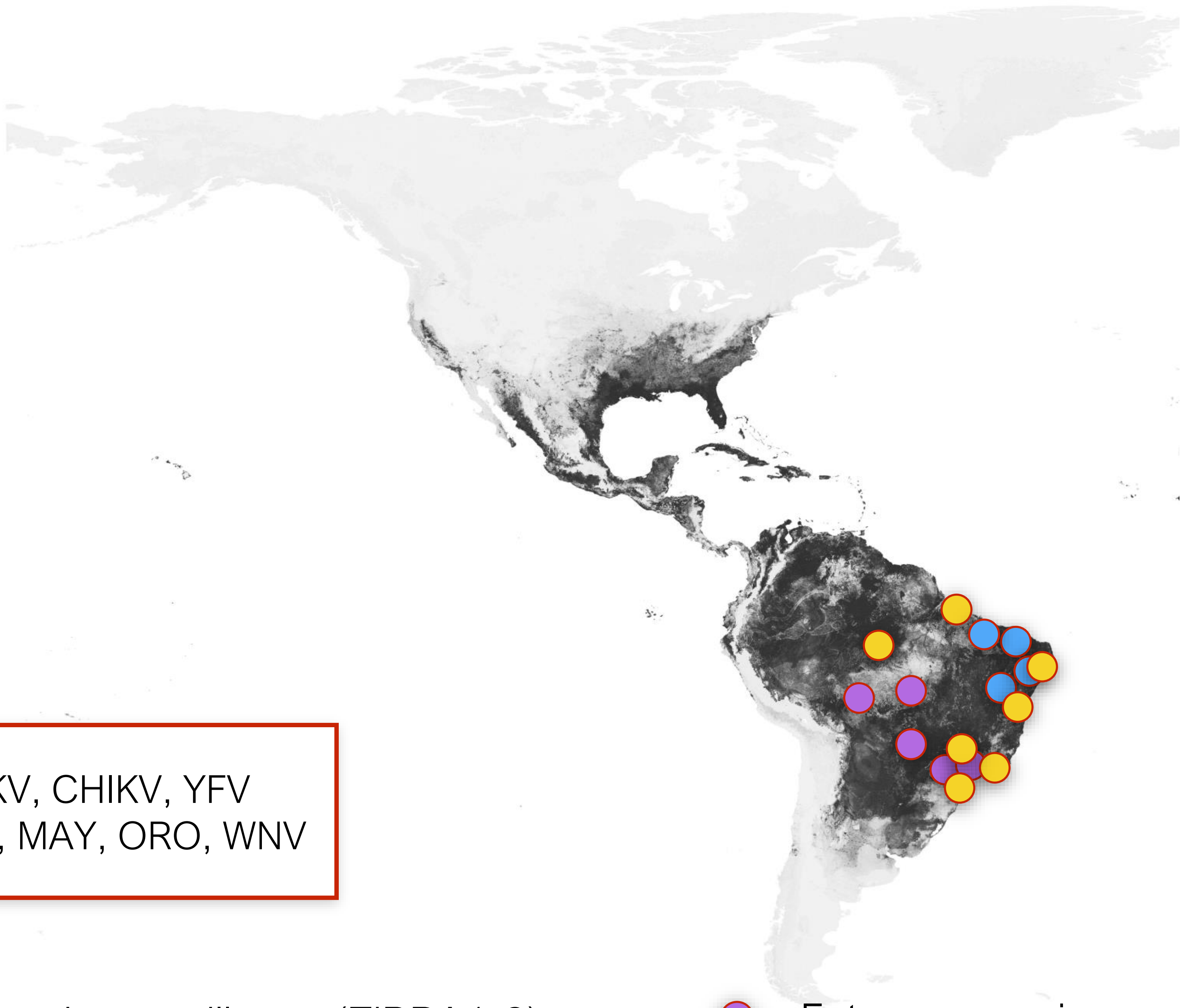
Genomic surveillance on the ground



ZIKV, CHIKV, YFV
DENV, MAY, ORO, WNV

● Ongoing genomic surveillance (ZiBRA1-2)

● Past genomic surveillance (ZiBRA1 project)

● Future genomic surveillance (ZiBRA2 project)

ZIBRA

ZIKA IN BRAZIL REAL TIME ANALYSIS

http://zibraproject.github.io/
https://twitter.com/zibraproject

UNIVERSITY OF BIRMINGHAM

UNIVERSITY OF OXFORD

MRC Medical Research Council

Ministério da Saúde CGLAB
SVS Secretaria de Vigilância em Saúde

Universidade de São Paulo

IEC
INSTITUTO EVANDRO CHAGAS

Ministério da Saúde
FIOCRUZ
Fundação Oswaldo Cruz
Centro de Pesquisas Gonçalo Moniz

Oxford NANOPORE Technologies

QIAGEN

FERPEL
COMÉRCIO E REPRESENTAÇÃO

ZIBRA 2

ZIKA IN BRAZIL REAL TIME ANALYSIS

THANK YOU!