

# SARS-CoV-2 Genomic Surveillance in Brazil

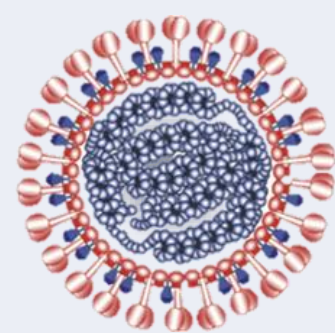
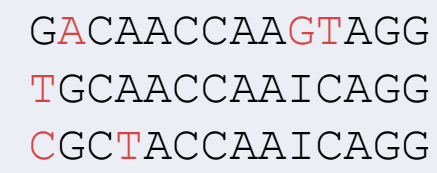
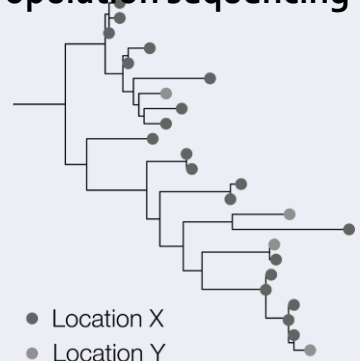
Jorge Kalil, MD, PhD, *Dr hc*, FRCP (LON)

Instituto Todos pela Saúde

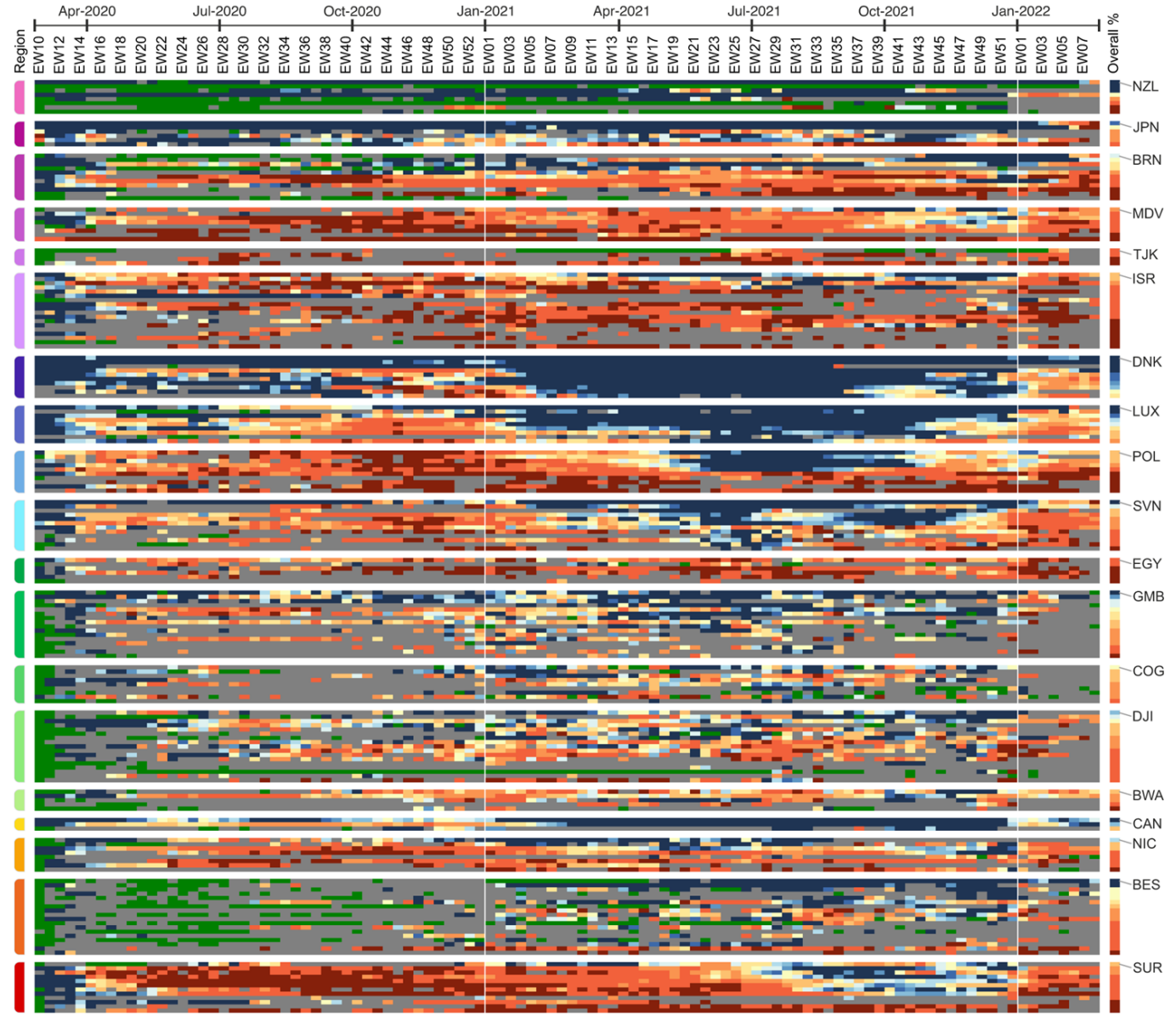
Faculdade de Medicina da USP

# Real-time virus genome sequencing: maximizing public health impact

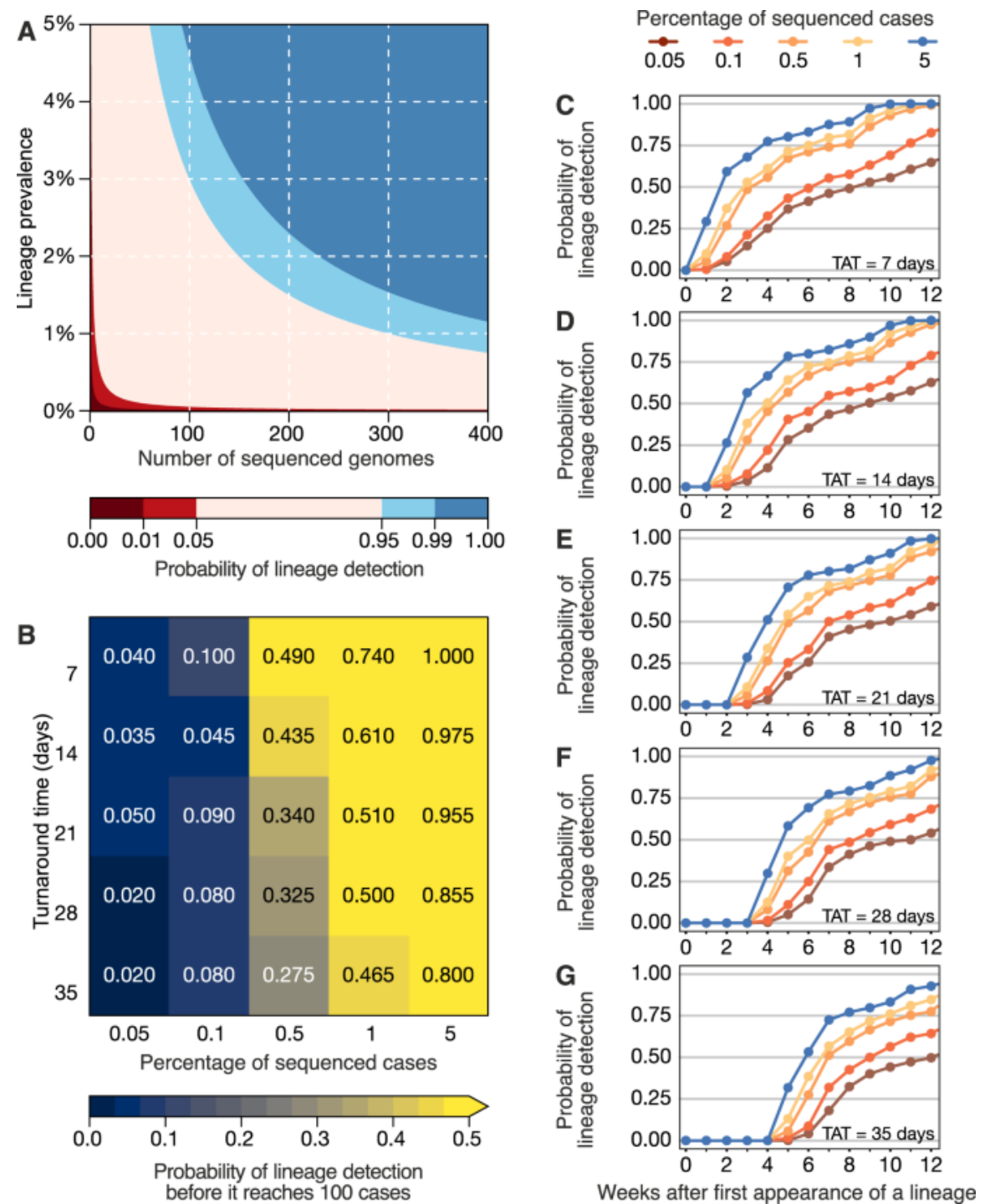
**Effective genomic surveillance requires** high quality samples and metadata **and** substantial investment in terms of staff, equipment, reagents, bioinformatic infrastructure, **and** effective collaboration between scientific community and stakeholders

	Untargeted sequencing	Targeted sequencing	Population sequencing
			
<b>Require</b>	Metagenomics human and non-human samples	Targeted sequencing of $\Delta 69-70$ , extensive experimental work	Random population (representativity) sequencing
<b>Goal</b>	Pathogen identification, understand origins of viral outbreaks	Design of diagnostics, therapeutics, phenotypic changes (e.g., Alpha, Omicron)	Large-scale patterns, drivers and assess detection (e.g., <i>R</i> , <i>pop size</i> , <i>dispersal patterns</i> )
		Investigate transmission clusters & complement epi (e.g., <i>outbreaks in hospitals, travelers</i> )	
		Non-random, dense cluster & community sequencing	

# Disparities in SARS-CoV-2 global genomic surveillance



Turn around time and number of sequences are important to detect new variants in real time



# ITpS (Instituto Todos pela Saúde)

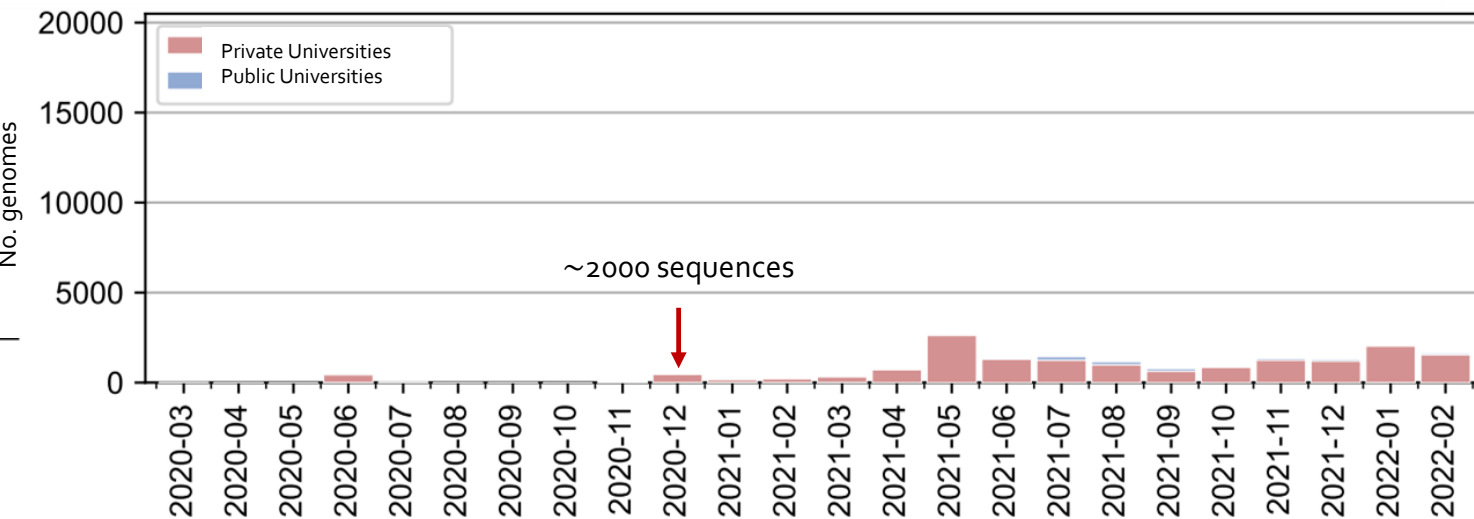
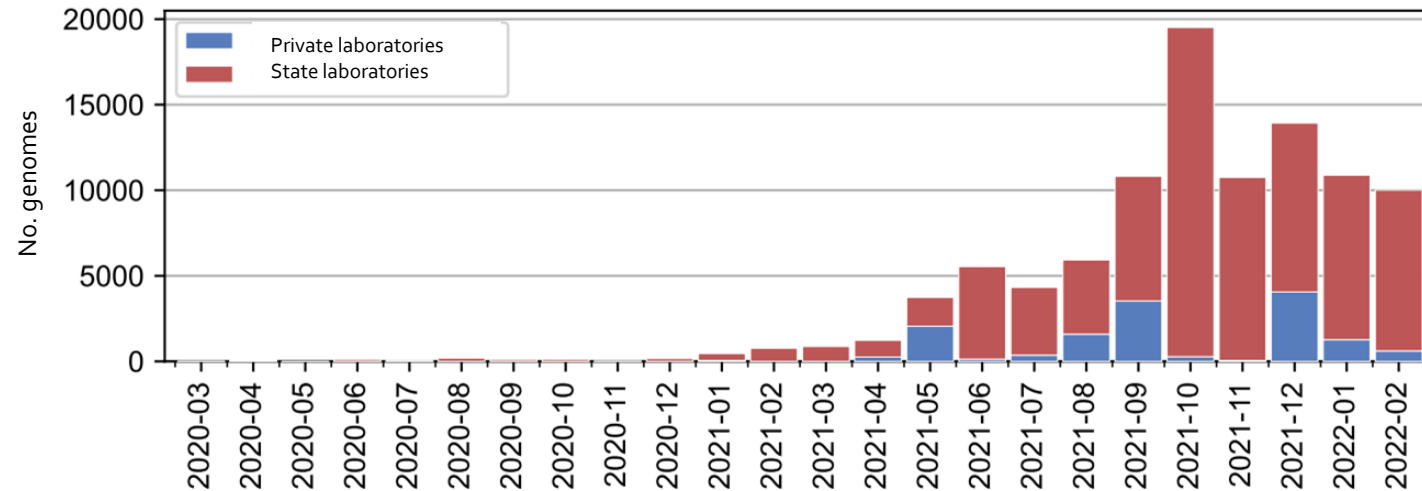
**Instituto Todos pela Saúde (ITpS)** is a non-profit organization created in Feb 2021 .

**Objective** – Collaborate in the development of an epidemiological surveillance system to prepare Brazil to face future outbreaks.

Articulate networks to obtain relevant scientific information to help the country in public health decision-making.



# Evolution of the number of SARS-CoV-2 genomes in Brazil



- Over 183,000 complete genome sequences (15 Oct'22)
- Over 34.6 million reported cases (0.53% sequenced)
- 54 days from sample collection to GISAID deposition

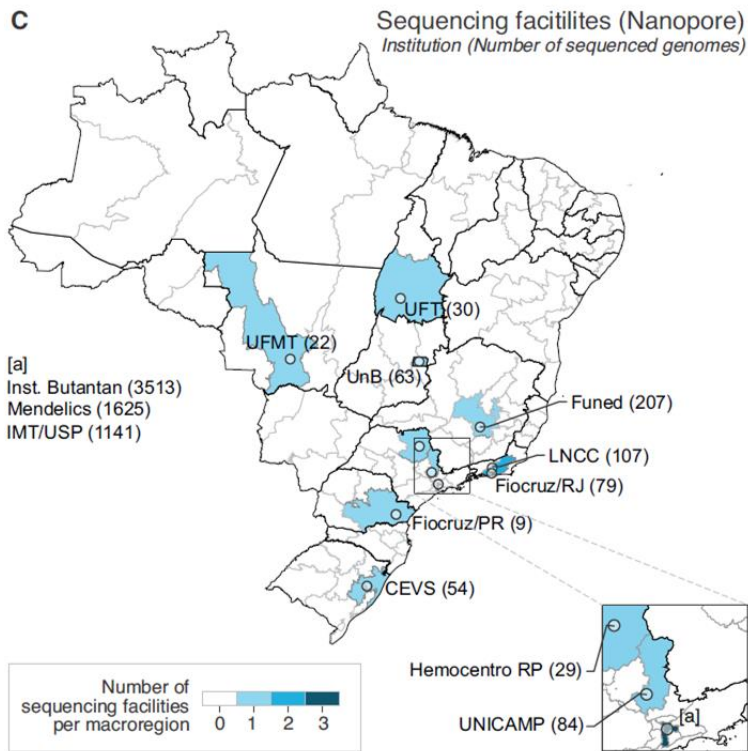
# Epidemic virus: Number of full-length genome from Brazil

Virus	No. Brazil Genomes in GenBank or GISAID
Yellow fever	195
Dengue 1-4	281
St. Louis encephalitis virus	1
West Nile	5
Zika	76
Mayaro virus	24
Venezuelan equine encephalitis virus	0
Chikungunya	78
Influenza	1182

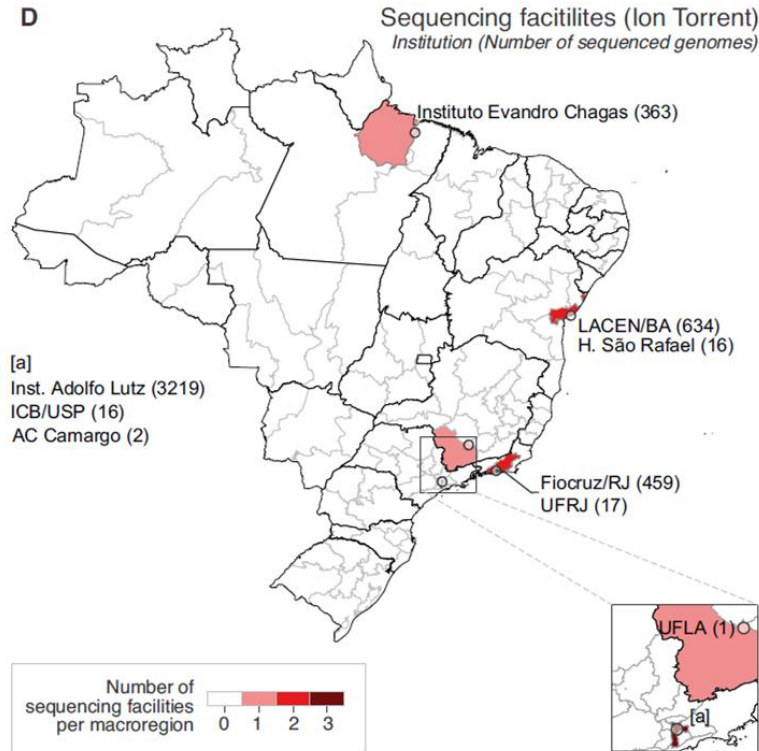


# Heterogeneity in sequencing platforms used

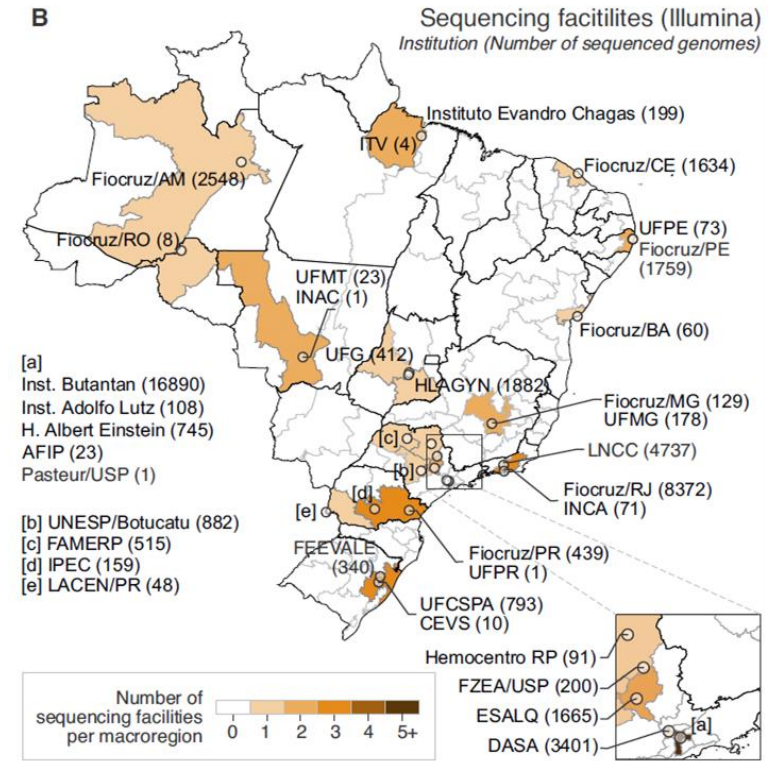
## ONT Nanopore



## Ion Torrent

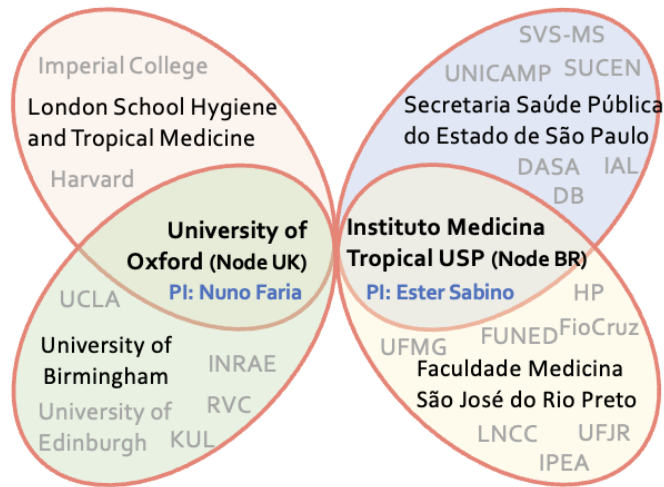


## Illumina





# (1) Brazil-UK CADDE Research Collaboration



## CORONAVIRUS

### Evolution and epidemic spread of SARS-CoV-2 in Brazil

Darlan S. Candido<sup>1,2,\*</sup>, Ingra M. Claro<sup>2,3,\*</sup>, Jaqueline G. de Jesus<sup>2,3,\*</sup>, William M. Souza<sup>4,\*</sup>, Filipe R. R. Moreira<sup>5,\*</sup>, Simon Dellicour<sup>6,7,\*</sup>, Thomas A. Mellan<sup>8,\*</sup>, Louis du Plessis<sup>1</sup>, Rafael H. M. Pereira<sup>9</sup>, Flavia C. S. Sales<sup>2,3</sup>, Erika R. Manuil<sup>2,3</sup>, Julien Théze<sup>10</sup>, Luiz Almeida<sup>11</sup>, Mariane T. Menezes<sup>5</sup>, Carolina M. Voloch<sup>5</sup>, Marcilio J. Fumagalli<sup>4</sup>, Thais M. Coletti<sup>2,3</sup>, Camila A. M. da Silva<sup>2,3</sup>, Mariana S. Ramundo<sup>2,3</sup>, Mariene R. Amorim<sup>12</sup>, Henrique H. Hoeltgebaum<sup>13</sup>, Swapnil Mishra<sup>3</sup>, Mandev S. Gill<sup>7</sup>, Luiz M. Carvalho<sup>14</sup>, Lewis F. Buss<sup>2</sup>, Carlos A. Prete Jr.<sup>15</sup>, Jordan Ashworth<sup>16</sup>, Helder I. Nakaya<sup>17</sup>, Pedro S. Peixoto<sup>18</sup>, Oliver J. Brady<sup>19,20</sup>, Samuel M. Nicholls<sup>21</sup>, Amílcar Tanuri<sup>5</sup>, Átila D. Rossi<sup>5</sup>, Carlos K. V. Braga<sup>9</sup>, Alexandra L. Gerber<sup>11</sup>, Ana Paula de C. Guimarães<sup>11</sup>, Nelson Gaburo Jr.<sup>22</sup>, Cecília Salete Alencar<sup>23</sup>, Alessandro C. S. Ferreira<sup>24</sup>, Cristiano X. Lima<sup>25,26</sup>, José Eduardo Levi<sup>27</sup>, Celso Granato<sup>28</sup>, Giulia M. Ferreira<sup>29</sup>, Ronaldo S. Francisco Jr.<sup>11</sup>, Fabiana Granja<sup>30,31</sup>, Marcia T. Garcia<sup>31</sup>, Maria Luiza Moretti<sup>32</sup>, Mauricio W. Perroud Jr.<sup>32</sup>, Terezinha M. P. P. Castilheiras<sup>33</sup>, Carolina S. Lazari<sup>34</sup>, Sarah C. Hill<sup>35</sup>, Andrea Aruska de Souza Santos<sup>36</sup>, Camila L. Simeoni<sup>37</sup>, Julia Forato<sup>37</sup>, Andrei C. Sposito<sup>37</sup>, Angelica Z. Schreiber<sup>38</sup>, Magnun N. N. Santos<sup>38</sup>, Camila Zolini de Sá<sup>39</sup>, Renan P. Souza<sup>39</sup>, Luciana C. Resende-Moreira<sup>40</sup>, Mauro M. Tebeira<sup>41</sup>, Josy Hubner<sup>42</sup>, Patricia A. F. Leme<sup>43</sup>, Renan G. Moreira<sup>44</sup>, Mauricio L. Nogueira<sup>45</sup>, Brazil-UK Centre for Arbovirus Discovery, Diagnosis, Genomics and Epidemiology (CADDE) Genomic Network, Neil M. Ferguson<sup>8</sup>, Silvia F. Costa<sup>2,3</sup>, José Luiz Proença-Modena<sup>12</sup>, Ana Tereza R. Vasconcelos<sup>11</sup>, Samir Bhatt<sup>4</sup>, Philippe Leme<sup>4</sup>, Chieh-Hsi Wu<sup>46</sup>, Andrew Rambaut<sup>47</sup>, Nick J. Loman<sup>21</sup>, Renato S. Aguiar<sup>39</sup>, Oliver G. Pybus<sup>4</sup>, Ester C. Sabino<sup>2,3</sup>, Nuno Rodrigues Faria<sup>1,2,8,†</sup>

Candido et al., *Science* **369**, 1255–1260 (2020) 4 September 2020 **Science**

## CORONAVIRUS

### Three-quarters attack rate of SARS-CoV-2 in the Brazilian Amazon during a largely unmitigated epidemic

Lewis F. Buss<sup>1,\*</sup>, Carlos A. Prete Jr.<sup>2,\*</sup>, Claudia M. M. Abraham<sup>3,\*</sup>, Alfredo Mendrone Jr.<sup>4,5,\*</sup>, Tassila Salomon<sup>6,7,\*</sup>, Cesar de Almeida-Neto<sup>4,5</sup>, Rafael F. O. França<sup>8</sup>, Maria C. Belotti<sup>2</sup>, Maria P. S. S. Carvalho<sup>3</sup>, Allyson G. Costa<sup>3</sup>, Myuki A. E. Crispim<sup>3</sup>, Suzete C. Ferreira<sup>4,5</sup>, Nelson A. Fraiji<sup>3</sup>, Susie Gurgenda<sup>9</sup>, Charles Whittaker<sup>10</sup>, Leonardo T. Kamaura<sup>11</sup>, Pedro L. Takecian<sup>11</sup>, Pedro da Silva Peixoto<sup>11</sup>, Marcio K. Oikawa<sup>12</sup>, Anna S. Nishiya<sup>4,5</sup>, Vanderson Rocha<sup>4,5</sup>, Nanci A. Salles<sup>4</sup>, Andreza Aruska de Souza Santos<sup>13</sup>, Martirene A. da Silva<sup>3</sup>, Brian Custer<sup>14,15</sup>, Kris V. Parag<sup>16</sup>, Manoel Barral-Netto<sup>17</sup>, Moritz U. G. Kraemer<sup>18</sup>, Rafael H. M. Pereira<sup>19</sup>, Oliver G. Pybus<sup>18</sup>, Michael P. Busch<sup>14,15</sup>, Márcia C. Castro<sup>9</sup>, Christopher Dye<sup>18</sup>, Vítor H. Nascimento<sup>2</sup>, Nuno R. Faria<sup>1,16,18,†</sup>, Ester C. Sabino<sup>†</sup>

Buss et al., *Science* **371**, 288–292 (2021) 15 January 2021

**Science**

## CORONAVIRUS

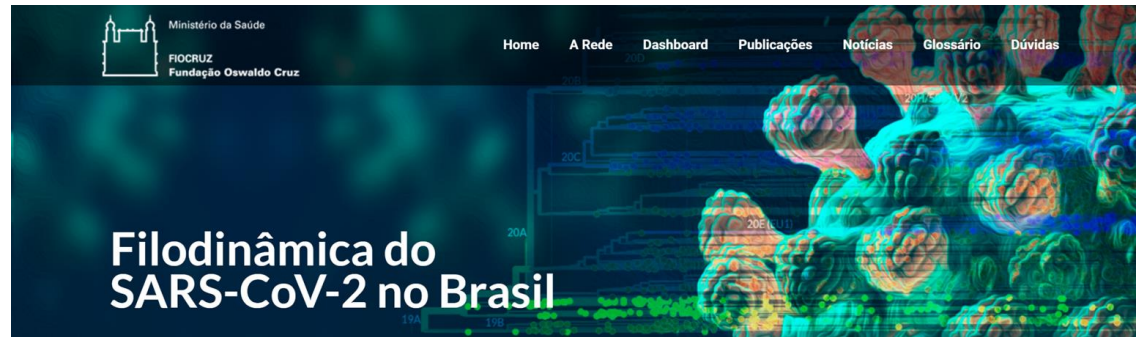
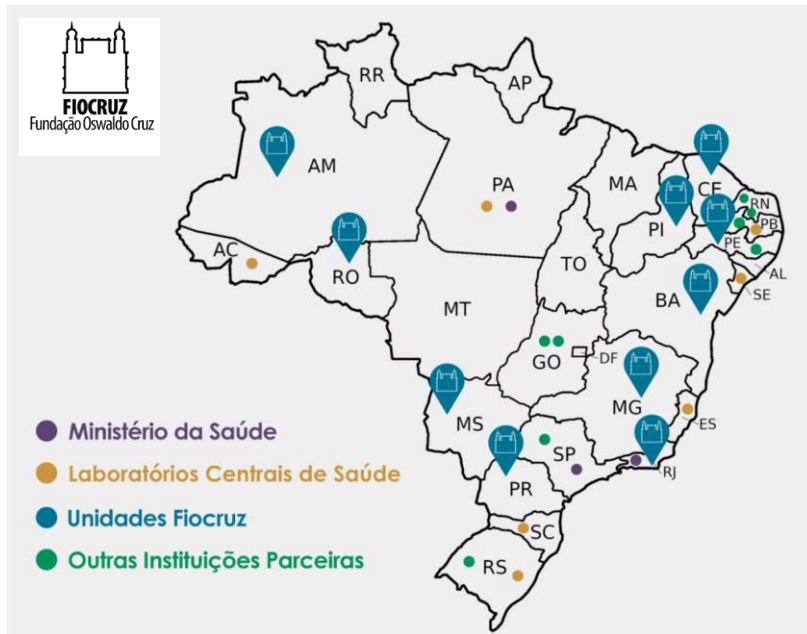
### Genomics and epidemiology of the P.1 SARS-CoV-2 lineage in Manaus, Brazil

Nuno R. Faria<sup>1,2,3,4,\*</sup>, Thomas A. Mellan<sup>1,2,†</sup>, Charles Whittaker<sup>1,2,†</sup>, Ingra M. Claro<sup>3,5,†</sup>, Darlan da S. Candido<sup>3,4,†</sup>, Swapnil Mishra<sup>1,2,†</sup>, Myuki A. E. Crispim<sup>6,7</sup>, Flavia C. S. Sales<sup>3,5</sup>, Ivona Hawryluk<sup>1,2</sup>, John T. McCrone<sup>8</sup>, Ruben J. G. Hulswit<sup>9</sup>, Lucas A. M. Franco<sup>3,5</sup>, Mariana S. Ramundo<sup>3,5</sup>, Jaqueline G. de Jesus<sup>3,5</sup>, Pamela S. Andrade<sup>10</sup>, Thais M. Coletti<sup>3,5</sup>, Giulia M. Ferreira<sup>11</sup>, Camila A. M. Silva<sup>3,5</sup>, Erika R. Manuil<sup>3,5</sup>, Rafael H. M. Pereira<sup>12</sup>, Pedro S. Peixoto<sup>13</sup>, Moritz U. G. Kraemer<sup>14</sup>, Nelson Gaburo Jr.<sup>14</sup>, Cecilia da C. Camilo<sup>14</sup>, Henrique Hoeltgebaum<sup>15</sup>, William M. Souza<sup>16</sup>, Esmeria C. Rocha<sup>3,5</sup>, Leandro M. de Souza<sup>3,5</sup>, Mariana C. de Pinho<sup>3,5</sup>, Leonardo J. T. Araujo<sup>17</sup>, Frederico S. V. Malta<sup>18</sup>, Aline B. de Lima<sup>18</sup>, Joice do P. Silva<sup>18</sup>, Danielle A. G. Zauli<sup>18</sup>, Alessandro C. de S. Ferreira<sup>19</sup>, Ricardo P. Schneckenberg<sup>19</sup>, Daniel J. Laydon<sup>1,2</sup>, Patrick G. T. Walker<sup>1,2</sup>, Hannah M. Schlüter<sup>15</sup>, Ana L. P. dos Santos<sup>20</sup>, Maria S. Vidal<sup>20</sup>, Valentina S. Del Caro<sup>20</sup>, Rosinaldo M. F. Filho<sup>20</sup>, Helem M. dos Santos<sup>20</sup>, Renato S. Aguiar<sup>21</sup>, José L. Proença-Modena<sup>22</sup>, Bruce Nelson<sup>23</sup>, James A. Hay<sup>24,25</sup>, Mélodie Monod<sup>15</sup>, Xenia Miscouridou<sup>15</sup>, Helen Coupland<sup>1,2</sup>, Raphael Sonabend<sup>1,2</sup>, Michaela Vollmer<sup>1,2</sup>, Axel Gandy<sup>15</sup>, Carlos A. Prete Jr.<sup>26</sup>, Vítor H. Nascimento<sup>26</sup>, Marc A. Suchard<sup>27</sup>, Thomas A. Bowden<sup>9</sup>, Sergei L. K. Pond<sup>28</sup>, Chieh-Hsi Wu<sup>29</sup>, Oliver Ratmann<sup>15</sup>, Neil M. Ferguson<sup>1,2</sup>, Christopher Dye<sup>4</sup>, Nick J. Loman<sup>30</sup>, Philippe Leme<sup>21</sup>, Andrew Rambaut<sup>4</sup>, Nelson A. Fraiji<sup>3,32</sup>, Maria do P. S. S. Carvalho<sup>6,33</sup>, Oliver G. Pybus<sup>4,34,†</sup>, Seth Flaxman<sup>35</sup>, Samir Bhatt<sup>1,2,35,†</sup>, Ester C. Sabino<sup>3,5,†</sup>

Faria et al., *Science* **372**, 815–821 (2021) 21 May 2021

**Science**

# (2) FioCruz Genomic Network



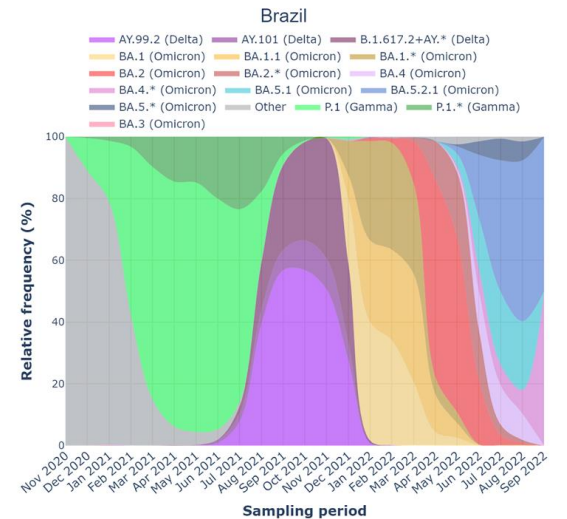
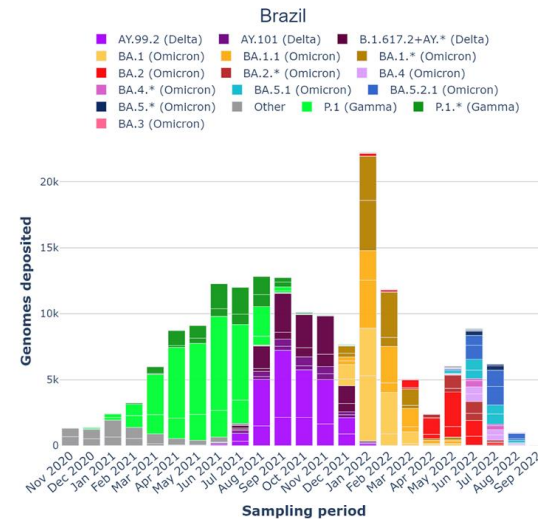
Genomes generated from samples collected in Brazil and deposited on GISAID by the FioCruz Genomic Network or other institutions

Genomes sequenced (total)	Genomes sequenced/100K cases	Most important genomes <sup>1</sup> in Aug/2022
<b>179,510</b>	<b>517.2</b>	BA.5.2.1 (Omicron): 523 genomes (52.1%)
		BA.5.1 (Omicron): 223 genomes (22.2%)
		BA.4 (Omicron): 85 genomes (8.5%)

<sup>1</sup>The ratios shown here do not necessarily represent the true ratios. Sample biases may have been introduced due to investigations of unusual cases, contact tracing, or sample selection due to inference protocols for detection of VOCs by RT-PCR

## COVID-19 in Amazonas, Brazil, was driven by the persistence of endemic lineages and P.1 emergence

Felipe Gomes Naveca<sup>1,2</sup>, Valdinete Nascimento<sup>1</sup>, Victor Costa de Souza<sup>1</sup>, André de Lima Corado<sup>1</sup>, Fernanda Nascimento<sup>1</sup>, George Silva<sup>1</sup>, Ágatha Costa<sup>1</sup>, Débora Duarte<sup>1</sup>, Karina Pessoa<sup>1</sup>, Matilde Mejía<sup>1</sup>, Maria Júlia Brandão<sup>1</sup>, Michele Jesus<sup>2</sup>, Luciana Gonçalves<sup>3</sup>, Cristiano Fernandes da Costa<sup>3</sup>, Vanderson Sampaio<sup>3</sup>, Daniel Barros<sup>3</sup>, Marneide Silva<sup>4</sup>, Tirza Mattos<sup>4</sup>, Gemilson Pontes<sup>5</sup>, Ligia Abdalla<sup>6</sup>, João Hugo Santos<sup>7</sup>, Ighor Arantes<sup>8</sup>, Filipe Zimmer Dezordi<sup>9</sup>, Marilda Mendonça Siqueira<sup>10</sup>, Gabriel Luz Wallau<sup>9</sup>, Paola Cristina Resende<sup>10</sup>, Edson Delatorre<sup>11</sup>, Tiago Gräf<sup>12</sup> and Gonzalo Bello<sup>8</sup>





# (3) CoronaOmica Network



1. Universidade Feevale – RS
2. Universidade Federal de Santa Maria – RS
3. Instituto para Pesquisa do Câncer de Guarapuava – PR
4. Universidade de São Paulo – SP
5. Faculdade de Medicina de São José do Rio Preto – SP
6. Universidade Estadual de Campinas – SP
7. Universidade Estadual Paulista – SP
8. Hospital Israelita Albert Einstein – SP
9. Universidade Federal do Rio de Janeiro – RJ
10. Laboratório Nacional de Computação Científica – RJ
11. Fundação Oswaldo Cruz – RJ
12. Universidade Federal de Minas Gerais – MG
13. Universidade de Brasília – DF
14. Universidade Federal do Tocantins – UFT
15. Universidade Federal do Oeste da Bahia – BA
16. Universidade Federal de Pernambuco – PE
17. Instituto Nacional de Pesquisas da Amazônia – AM



Virus Evolution, 2021, 7(2), 1–12  
 DOI: <https://doi.org/10.1093/ve/veab087>  
 Advance access publication date: 1 October 2021  
 Research Article

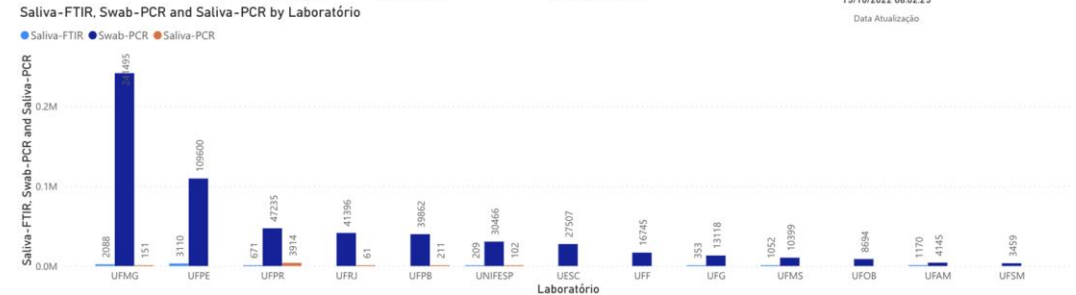
## Epidemiological dynamics of SARS-CoV-2 VOC Gamma in Rio de Janeiro, Brazil

Filipe Romero Rebelo Moreira,<sup>1,4,8</sup> Mirela D'arc,<sup>2,4</sup> Diana Mariani,<sup>1</sup> Alice Laschuk Herlinger,<sup>1</sup> Francine Bittencourt Schiffer,<sup>2</sup> Atila Duque Rossi,<sup>2</sup> Isabela de Carvalho Leitão,<sup>3</sup> Thamiris dos Santos Miranda,<sup>2</sup> Mathheus Augusto Calvano Cosentino,<sup>2</sup> Marcelo Calado de Paula Torres,<sup>1</sup> Raissa Mirella dos Santos Cunha da Costa,<sup>1</sup> Cássia Cristina Alves Gonçalves,<sup>1</sup> Débora Souza Faffe,<sup>3</sup> Rafael Mello Galliez,<sup>4</sup> Orlando da Costa Ferreira Junior,<sup>1</sup> Renato Santana Aguiar,<sup>5,6,7</sup> André Felipe Andrade dos Santos,<sup>2</sup> Carolina Moreira Voloch,<sup>1,11</sup> Terezinha Marta Pereira Pinto Castiñeiras,<sup>4,8</sup> and Amilcar Tanuri<sup>1,11</sup> on behalf of the COVID-19-UFRJ Workgroup

13
58
613.77K

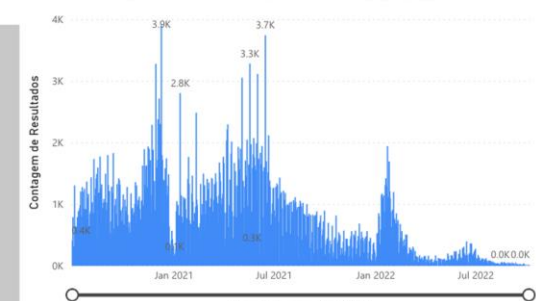
Laboratórios      Local Coleta      Testes Realizados

15/10/2022 08:02:25  
 Data Atualização



13
58
613.77K

Laboratórios      Locais de coleta      Testes Realizados



Resultados por dia SWAB

Estado	Testes Realizados	Local Coleta
MG	241643	5
PE	112533	1
RJ	58220	17
PR	51234	7
PB	39939	3
BA	37099	19
SP	30963	1
GO	15578	3
RS	12013	1
MS	10400	2
<b>Total</b>	<b>613767</b>	<b>58</b>

# (4) Butantan Network

Weekly Reports starting in May 2021

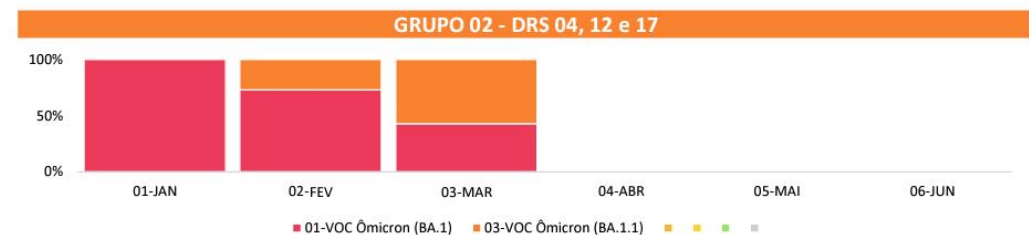
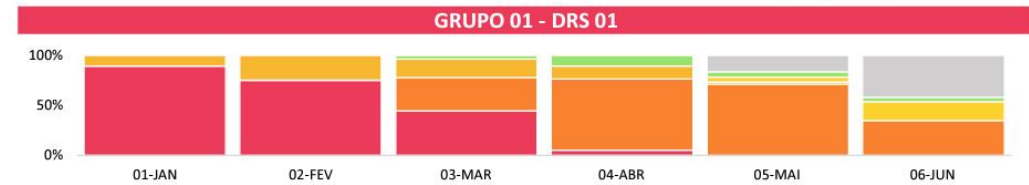


Lab Móvel do Butantan reinicia diagnósticos de Covid-19 e sequenciamento de variantes em Bauru

## Genomic epidemiology of the SARS-CoV-2 epidemic in Brazil

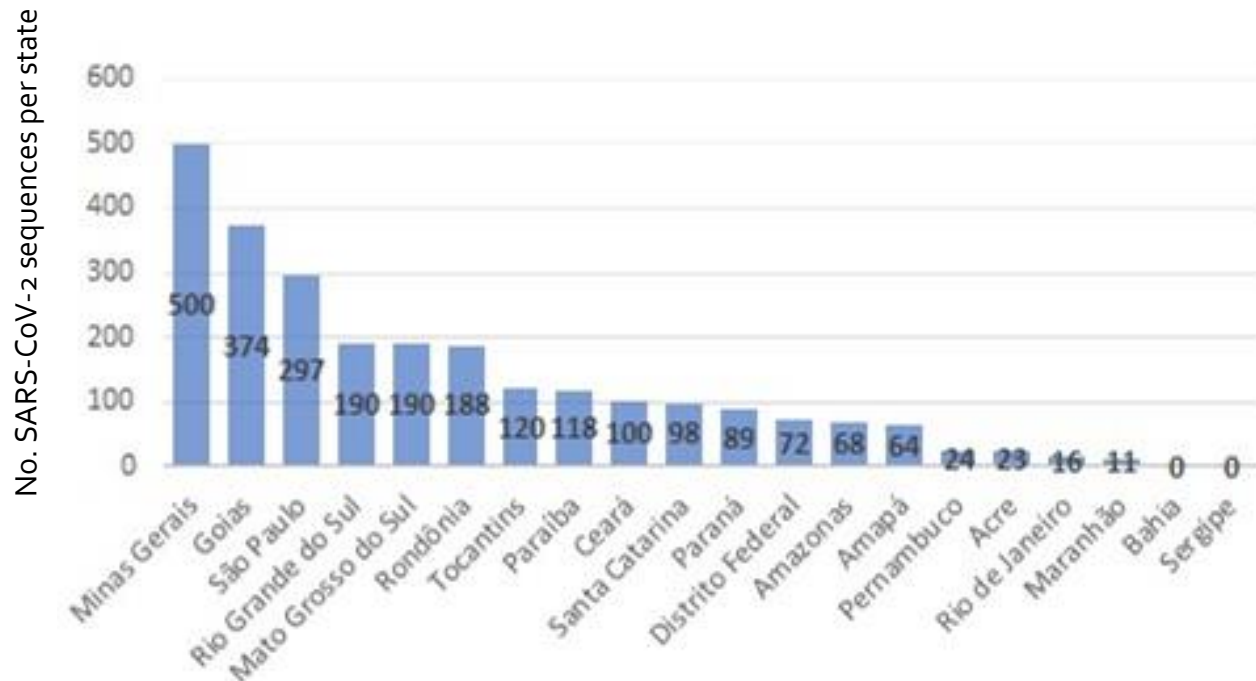
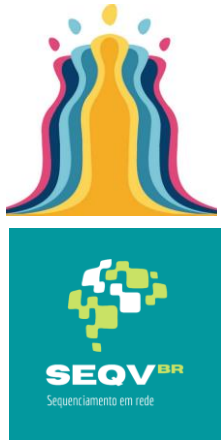
nature  
microbiology

The high numbers of COVID-19 cases and deaths in Brazil have made Latin America an epicentre of the pandemic. SARS-CoV-2 established sustained transmission in Brazil early in the pandemic, but important gaps remain in our understanding of virus transmission dynamics at a national scale. We use 17,135 near-complete genomes sampled from 27 Brazilian states and bordering country Paraguay. From March to November 2020, we detected co-circulation of multiple viral lineages that were linked to multiple importations (predominantly from Europe). After November 2020, we detected large, local transmission clusters within the country. In the absence of effective restriction measures, the epidemic progressed, and in January 2021 there was emergence and onward spread, both within and abroad, of variants of concern and variants under monitoring, including Gamma (P.1) and Zeta (P.2). We also characterized a genomic overview of the epidemic in Paraguay and detected evidence of importation of SARS-CoV-2 ancestor lineages and variants of concern from Brazil. Our findings show that genomic surveillance in Brazil enabled assessment of the real-time spread of emerging SARS-CoV-2 variants.

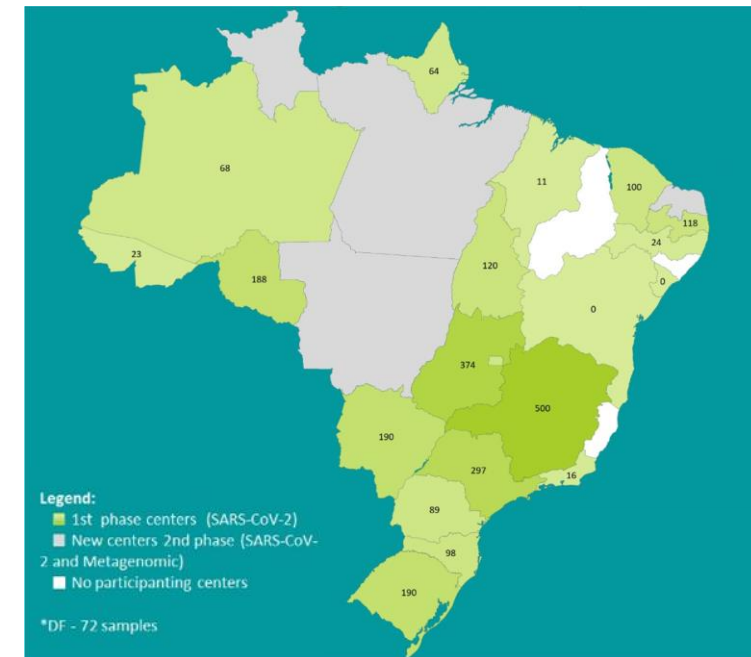


# (5) Seq-BR – Magalu & Mulheres do Brasil

- Designed in May 2021
- First Phase: Training between March and September 2022
- Second Phase (ongoing): 100 seq/month/Brazilian State Capital performed locally
- Third Phase: wastewater sewage genomic surveillance



Participating states, no. sequences



## (6) Genov Network



- Convenient residual diagnostic samples from large private laboratory network

Brazilian Region	No. (GISAID, 15 Sep 2022)	% cases
SOUTH	2,912	16.8
SOUTHEAST	3,463	20.0
MID-WEST	2,461	14.2
NORTHEAST	1,884	10.9
NORTH	147	0.8
SÃO PAULO CITY	3,716	21.4
RIO DE JANEIRO CITY	2,763	15.9
<b>TOTAL</b>	<b>17,346</b>	<b>100</b>

### Dynamics of SARS-CoV-2 Variants of Concern in Brazil, Early 2021

*José Eduardo Levi<sup>1,2\*</sup>, Cristina Mendes Oliveira<sup>1</sup>, Bianca Della Croce<sup>1</sup>, Paulo Telles<sup>1,3</sup>, Annelise Correa Wengerkievicz Lopes<sup>1</sup>, Camila Malta Romano<sup>2,4</sup>, Diego Bezerra Lira<sup>1</sup>, Anna Claudia Mello de Resende<sup>1</sup>, Flávia Paiva Lopes<sup>1</sup>, André Arroyo Ruiz<sup>1</sup> and Gustavo Campana<sup>1</sup>*





# (7) ITpS (Instituto Todos pela Saúde)



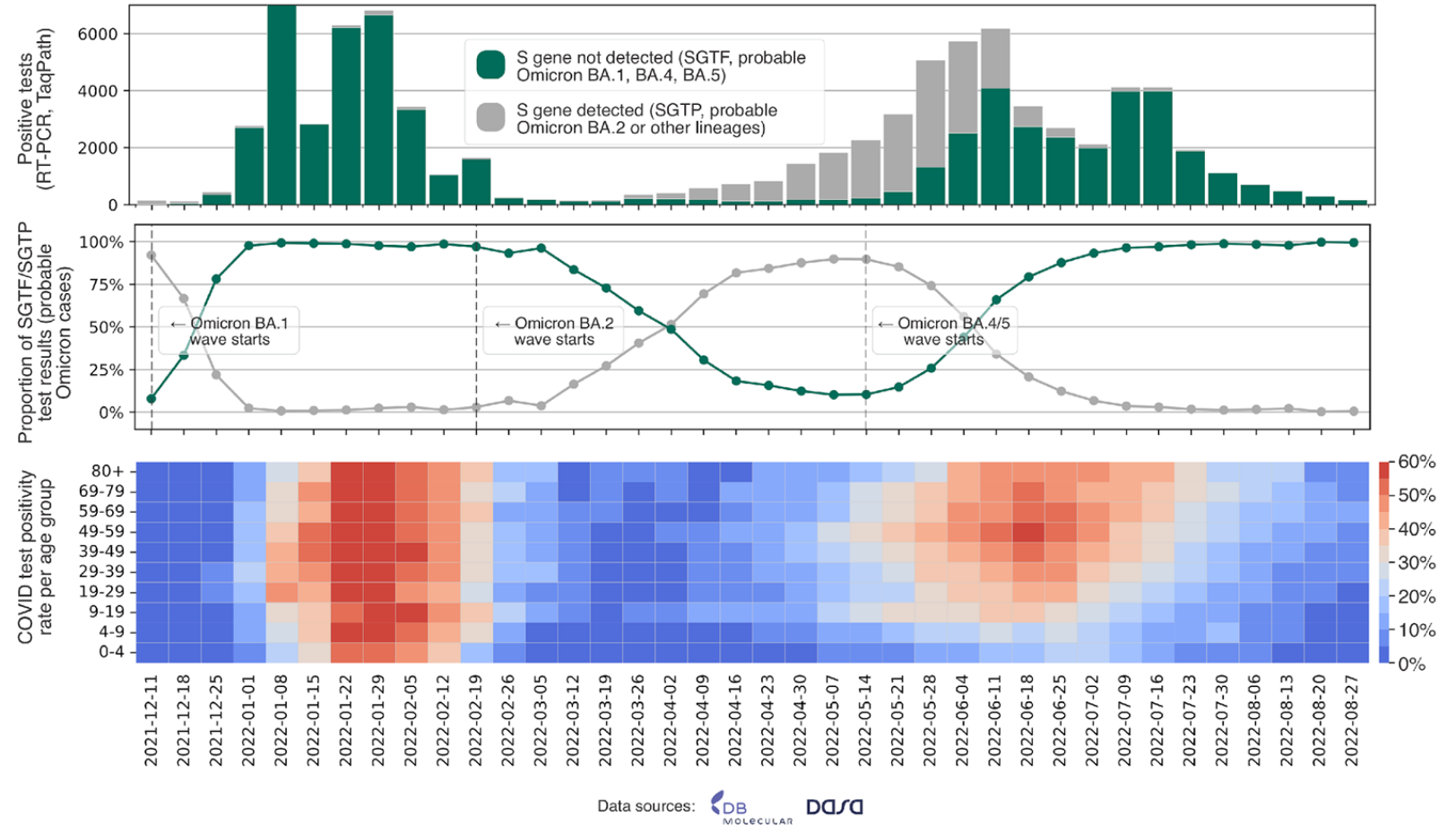
How to improve turn around time?

Data from private laboratories

Turn around time: 7 days

Data from ThermoFischer PCR:  
SGTFvs SGTP

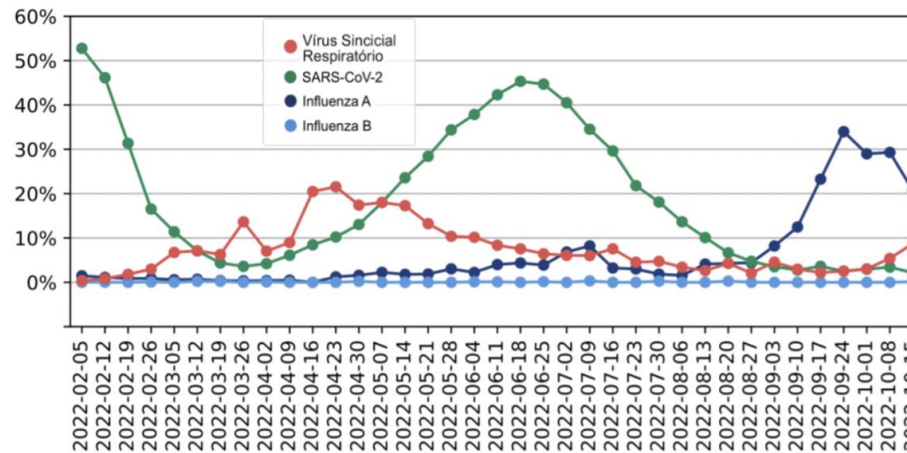
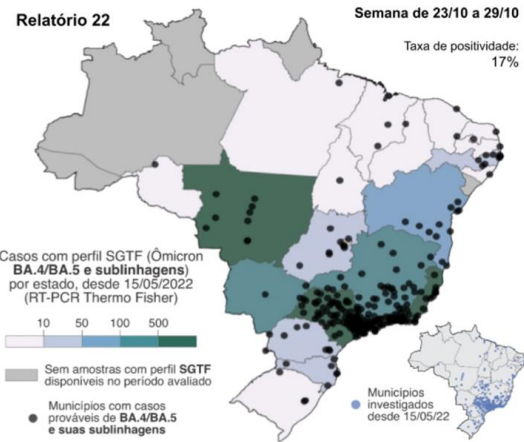
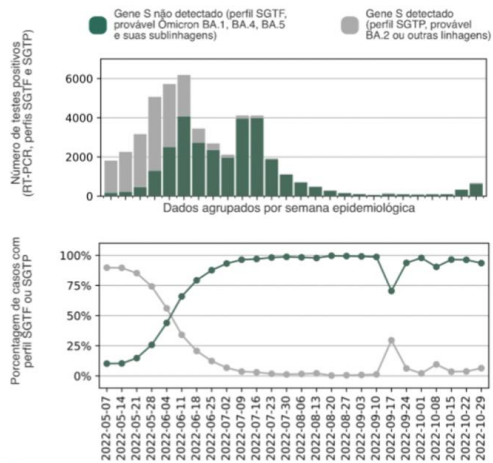
Data from all results: PCR+ rate





# ITpS (Instituto Todos pela Saúde)

## Monitoramento da variante Ômicron (de 01/05/2022 a 29/10/2022)



@todospelaude

Fonte dos dados: DB MOLECULAR DCSA

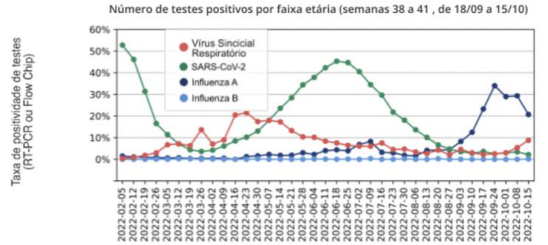
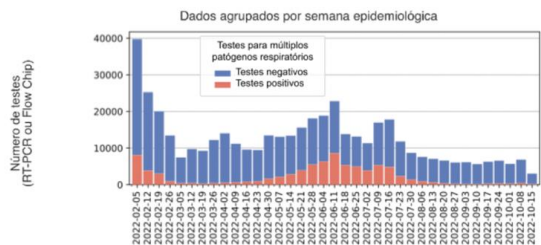
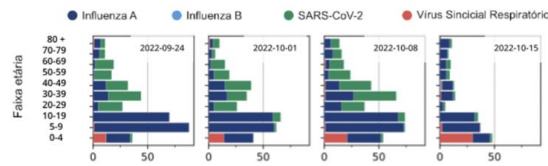
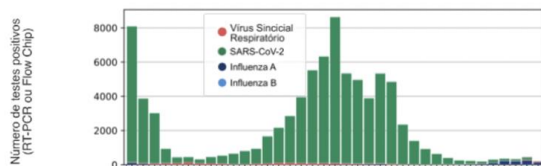


## Positividade de testes para COVID-19 (de 01/05/2022 a 29/10/2022)

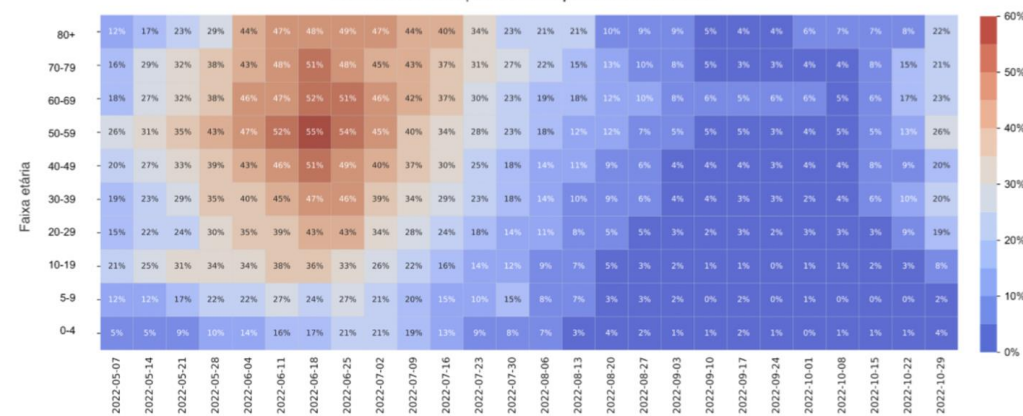


## Monitoramento de patógenos respiratórios (de 01/02/2022 a 15/10/2022)

@todospelaude



Positividade de testes para COVID-19 por faixa etária no Brasil



@todospelaude

Fonte dos dados: DB MOLECULAR HLAGym DCSA

@todospelaude

Fonte dos dados: DB MOLECULAR HLAGym DCSA

Website: <https://www.itps.org.br> | Coordinator: Jorge Kalil | Initial Funding: Itau Bank

# Conclusions

- Brazil has dramatically expanded the capacity to perform SARS-CoV-2 full-length genome sequencing across the country through state and private funding initiatives.
- Genomic diversity of other epidemic viruses remains poorly understood
- Median: 54 days - date of collection to submission to GISAID.
- Still a long delay between sample collection, sequence and information to the public for SARS-CoV-2, but even longer for other viruses.
- Need to organize the several initiatives to improve cost/effectiveness and sustainability of targeted and untargeted (metagenomic) virus sequencing.