Abordagem genômica usada para vigilância genômica populacional e monitoramento ambiental das variantes de Sars-Cov-2

RCB0300-Biotecnologia III

wilsonjr@usp.br

JOHNS HOPKINS | **CORONAVIRUS RESOURCE CENTER**

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Tracking Home | Data Visualizations ∨ | **Global Map** | U.S. Map | Data in Motion | Tracking FAQ

COVID-19 Dashboard by the Center for Systems Science and Engineering (CSSE) at Johns Hopkins University (JHU)

Last Updated at (M/D/YYYY)
4/17/2022, 9:20 PM

Total Cases	Total Deaths	Total Vaccine Doses Administered
504,458,423	6,197,934	11,168,755,649

28-Day Cases	28-Day Deaths	28-Day Vaccine Doses Administered
34,608,972	123,036	397,113,437

Cases | Deaths by Country/Region/Sovereignty

Korea, South
28-Day: 6,932,106 | 8,664
Totals: 16,305,752 | 21,092

Germany
28-Day: 4,698,981 | 6,022
Totals: 23,416,663 | 132,942

France
28-Day: 3,632,313 | 3,228
Totals: 27,960,919 | 145,194

Vietnam
28-Day: 2,626,046 | 1,117
Totals: 10,432,547 | 42,944

Italy
28-Day: 1,859,656 | 3,910
Totals: 15,712,088 | 161,687

United Kingdom
28-Day: 1,673,021 | 7,915
Totals: 21,916,961 | 172,014

Australia
28-Day: 1,484,477 | 1,054
Totals: 5,404,102 | 6,782

Japan
28-Day: 1,271,490 | 1,942
Totals: 7,371,466 | 29,025

US
28-Day: 894,850 | 17,010
Totals: 80,627,545 | 988,617

Thailand
28-Day: 675,990 | 2,636
Totals: 4,029,959 | 26,882

Brazil
28-Day: 625,642 | 4,796
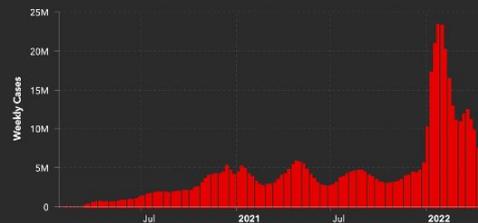Totals: 30,252,618 | 662,207

Admin0 | Admin1 | Admin2

28-Day | Totals | Incidence | Case-Fatality Ratio | Global Vaccinations | US Vaccinations | Terms of Use

Esri, FAO, NOAA

Powered by Esri

Weekly Cases

Weekly Deaths

Weekly Doses Administered

Weekly | 28-Day

Last Updated at (M/D/YYYY)
4/17/2022, 10:20 PM

Total Cases	Total Deaths	Total Vaccine Doses Administered
504,512,302	6,198,067	11,168,758,945

28-Day Cases	28-Day Deaths	28-Day Vaccine Doses Administered
34,608,972	123,036	397,113,437

Cases | Deaths by Country/Region/Sovereignty

Australia
28-Day: 1,484,477 | 1,054
Totals: 5,405,474 | 6,782

Japan
28-Day: 1,271,490 | 1,942
Totals: 7,371,466 | 29,025

US
28-Day: 894,850 | 17,010
Totals: 80,632,301 | 988,618

Thailand
28-Day: 675,990 | 2,636
Totals: 4,029,959 | 26,882

Brazil
28-Day: 625,642 | 4,796
Totals: 30,252,618 | 662,207

Austria
28-Day: 616,798 | 1,020
Totals: 4,053,217 | 16,420

China
28-Day: 566,648 | 3,460
Totals: 1,787,618 | 13,777

Netherlands
28-Day: 543,176 | 381
Totals: 8,194,946 | 22,780

Russia
28-Day: 503,922 | 8,962
Totals: 17,811,199 | 366,001

Greece
28-Day: 456,304 | 1,644
Totals: 3,238,169 | 28,588

Malaysia
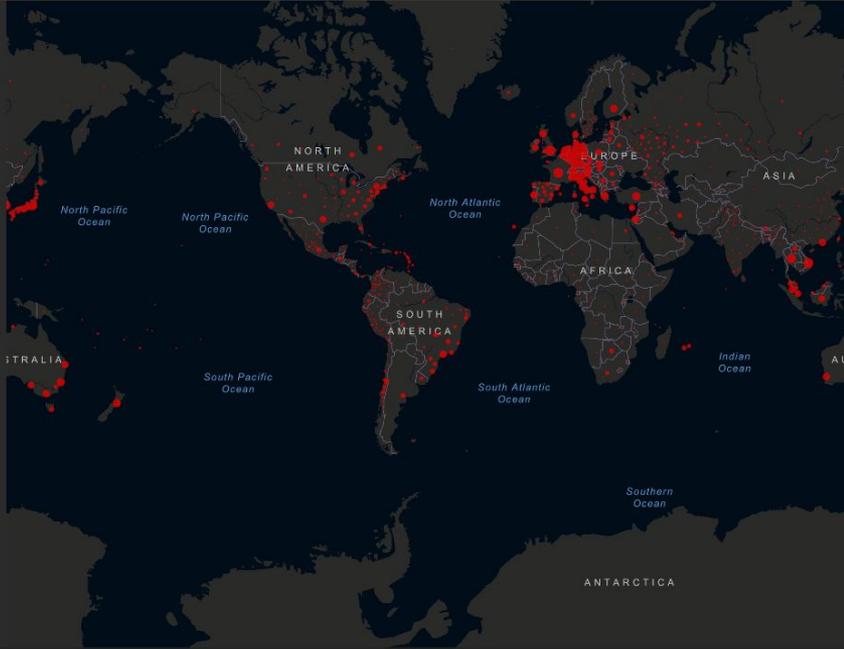28-Day: 408,383 | 1,080
Totals: 4,389,025 | 35,421

New Zealand
28-Day: 344,843 | 403
Totals: 828,808 | 554

Turkey
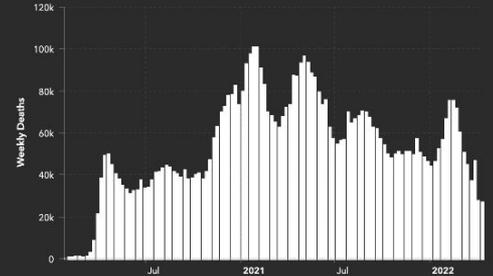28-Day: 310,833 | 1,369
Totals: 14,994,937 | 98,568

Admin0 Admin1 Admin2

NORTH AMERICA

North Pacific Ocean

North Pacific Ocean

North Atlantic Ocean

EUROPE

ASIA

AFRICA

AUSTRALIA

South Pacific Ocean

SOUTH AMERICA

South Atlantic Ocean

Indian Ocean

AUS

Southern Ocean

ANTARCTICA

Esri, FAO, NOAA

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28-Day Totals Incidence Case-Fatality Ratio Global Vaccinations US Vaccinations Terms of Use

Weekly Cases
25M
20M
15M
10M
5M
0
Jul 2021 Jul 2022

Weekly Deaths
120k
100k
80k
60k
40k
20k
0
Jul 2021 Jul 2022

Weekly Doses Administered
350M
300M
250M
200M
150M
100M
50M
0
Jul 2021 Jul 2022

Weekly 28-Day

All Regions | Data Notes

WORLD COUNTRIES

BRAZIL

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OVERVIEW

| All Time | Past Day | Past Week | Past Month |

Confirmed Cases
30,250,077

Deaths
662,185

VACCINE TRACKER
Learn more about vaccines ›

Doses Administered
423,594,585

People Fully Vaccinated
162,490,311

% of Population Fully Vaccinated
76.99%

DATA TIMELINE

Explore the most vital information about how COVID-19 has affected your state since the pandemic first officially arrived in the United States in January 2020 – cases, deaths, test positivity, hospitalizations, and vaccinations.
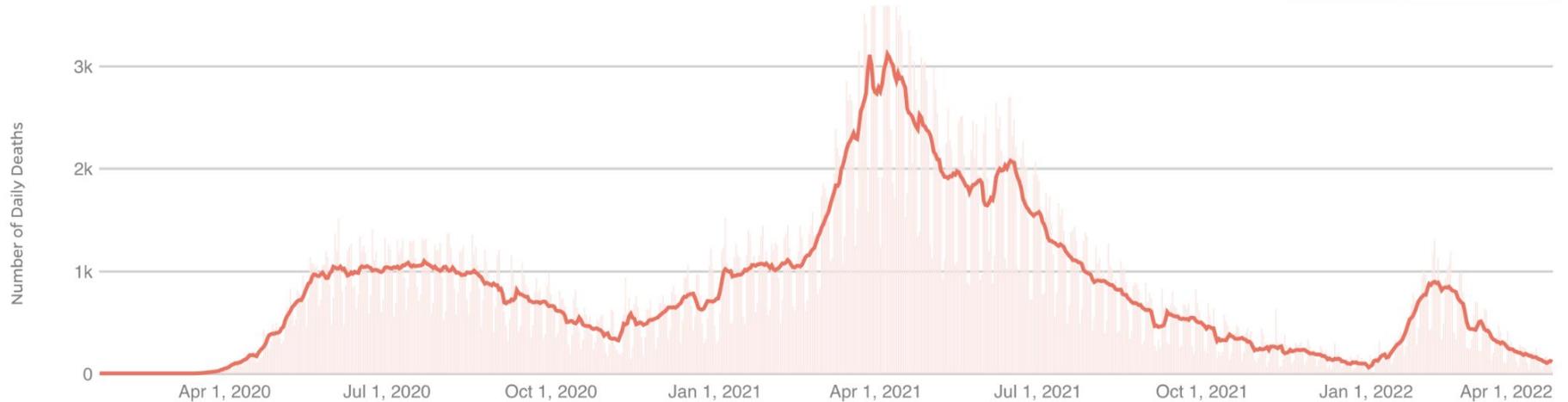
NEW Comparisons	Cases	Deaths

Number of Daily Cases

▫ Number of Daily Cases   — 7-Day Average of Daily Cases

All Time   Last 90 Days

Number of Daily Cases

150k

100k

50k

0

Apr 1, 2020   Jul 1, 2020   Oct 1, 2020   Jan 1, 2021   Apr 1, 2021   Jul 1, 2021   Oct 1, 2021   Jan 1, 2022   Apr 1, 2022
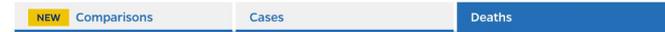
Data Sources: Cases and deaths data from JHU CSSE; testing and vaccine data from JHU CCI; and hospitalization data from the U.S. Department of Health and Human Services.
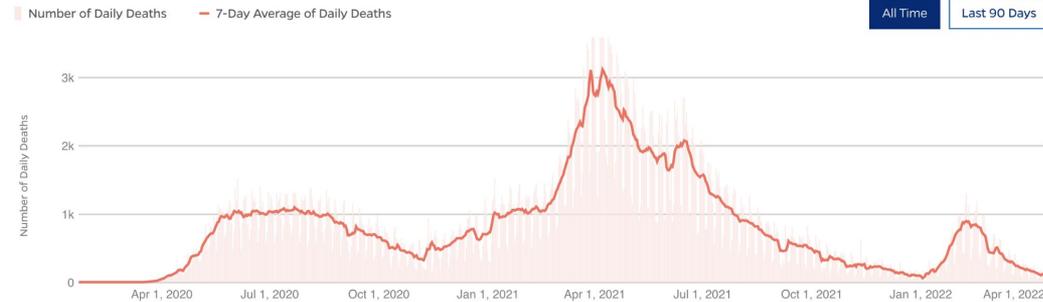
DATA TIMELINE

Explore the most vital information about how COVID-19 has affected your state since the pandemic first officially arrived in the United States in January 2020 – cases, deaths, test positivity, hospitalizations, and vaccinations.

NEW Comparisons	Cases	Deaths

Number of Daily Deaths

Number of Daily Deaths — 7-Day Average of Daily Deaths

All Time   Last 90 Days

Data Sources: Cases and deaths data from JHU CSSE; testing and vaccine data from JHU CCI; and hospitalization data from the U.S. Department of Health and Human Services.

DATA TIMELINE

Explore the most vital information about how COVID-19 has affected your state since the pandemic first officially arrived in the United States in January 2020 – cases, deaths, test positivity, hospitalizations, and vaccinations.

| NEW Comparisons | Cases | Deaths |

Number of Daily Cases

Number of Daily Cases   — 7-Day Average of Daily Cases

All Time | Last 90 Days

| NEW Comparisons | Cases | Deaths |

Number of Daily Deaths

Number of Daily Deaths   — 7-Day Average of Daily Deaths

All Time | Last 90 Days

Data Sources: Cases and deaths data from JHU CSSE; testing and vaccine data from JHU CCI; and hospitalization data from the U.S. Department of Health and Human Services.

Variants Of Concern (VOCs)?

Variant Of Interest (VOI)?

Currently circulating variants of concern (VOCs):

WHO label	Pango lineage•	GISAID clade	Nextstrain clade	Additional amino acid changes monitored°	Earliest documented samples	Date of designation
Delta	B.1.617.2	G/478K.V1	21A, 21I, 21J	+S:K417N +S:E484K	India, Oct-2020	VOI: 4-Apr-2021 VOC: 11-May-2021
Omicron*	B.1.1.529	GR/484A	21K, 21L, 21M	+S:R346K +S:L452R +S:F486V	Multiple countries, Nov-2021	VUM: 24-Nov-2021 VOC: 26-Nov-2021

Previously circulating VOCs:

WHO label	Pango lineage•	GISAID clade	Nextstrain clade	Earliest documented samples	Date of designation
Alpha	B.1.1.7	GRY	20I (V1)	United Kingdom, Sep-2020	VOC: 18-Dec-2020 Previous VOC: 09-Mar-2022
Beta	B.1.351	GH/501Y.V2	20H (V2)	South Africa, May-2020	VOC: 18-Dec-2020 Previous VOC: 09-Mar-2022
Gamma	P.1	GR/501Y.V3	20J (V3)	Brazil, Nov-2020	VOC: 11-Jan-2021 Previous VOC: 09-Mar-2022

There is no currently circulating variant of interest (VOI).

Previously circulating VOIs:

| WHO label	Pango lineage*	GISAID clade	Nextstrain clade	Earliest documented samples	Date of designation
Epsilon	B.1.427 B.1.429	GH/452R.V1	21C	United States of America, Mar-2020	VOI: 5-Mar-2021 Previous VOI: 6-Jul-2021
Zeta	P.2	GR/484K.V2	20B/S.484K	Brazil, Apr-2020	VOI: 17-Mar-2021 Previous VOI: 6-Jul-2021
Eta	B.1.525	G/484K.V3	21D	Multiple countries, Dec-2020	VOI: 17-Mar-2021 Previous VOI: 20-Sep-2021
Theta	P.3	GR/1092K.V1	21E	Philippines, Jan-2021	VOI: 24-Mar-2021 Previous VOI: 6-Jul-2021
Iota	B.1.526	GH/253G.V1	21F	United States of America, Nov-2020	VOI: 24-Mar-2021 Previous VOI: 20-Sep-2021
Kappa	B.1.617.1	G/452R.V3	21B	India, Oct-2020	VOI: 4-Aprl-2021 Previous VOI: 20-Sep-2021
Lambda	C.37	GR/452Q.V1	21G	Peru, Dec-2020	VOI: 14-Jun-2021 Previous VOI: 9-Mar-2022
Mu	B.1.621	GH	21H	Colombia, Jan-2021	VOI: 30-Aug-2021 Previous VOI: 9-Mar-2022

Informações e nível de risco relativo das variantes de preocupação de SARS-CoV-2; o vermelho representa risco muito alto, o laranja representa risco alto, o amarelo representa risco médio, o verde representa risco baixo e o cinza representa risco desconhecido (LEDFORD et al., 2021).

Identificação			Emersão			Mudanças e estatísticas				Neutralização da atividade do anticorpo	
Nomenclatura	Linhagem	País do primeiro surto	Primeira amostra	Data da designação para VOC	Principais mutações	Transmissibilidade	Hospitalização	Mortalidade		Por infecção natural	Por vacinação
Delta	B.1.617.2	Índia	10/20	06/05/21	L452R, T478K, P681R	>76-117%	>39-147%	>50-230%		Ocorreram reinfecções	Redução da eficácia para os casos não graves
Alfa	B.1.1.7	Reino Unido	20/09/20	18/12/20	69–70del, N501Y, P681H	>24-33%	>47-57%	>44-74%		Redução mínima	Redução mínima
	B.1.1.7 com E484K		26/01/21	05/02/21	E484K, 69–70del, N501Y, P681H					Consideravelmente reduzido	Consideravelmente reduzido
Gama	P.1	Brasil/Japão	11/20	15/01/21	K417T, E484K, N501Y	>29-48%	Possivelmente aumentado	>20-90%		Pouco reduzido	Retido
Beta	B.1.351	África do Sul	05/20	14/01/21	K417N, E484K, N501Y	>20-30%	Sob estudo	Possivelmente aumentado		Parcialmente reduzido, resposta de células T ainda eficazes	Reduzido contra casos sintomáticos não graves, retido para casos graves
Ômicron	B.1.1.529	África do Sul	09/11/21	26/11/21	P681H, N440K, N501Y, S477N, muitas outras	Possivelmente aumentado	<37-45% em relação à variante Delta	Sob estudo		Aumento da taxa de reinfecção	Redução da eficácia contra doença sintomática, dados desconhecidos para o estágio grave

Proposta de 2020

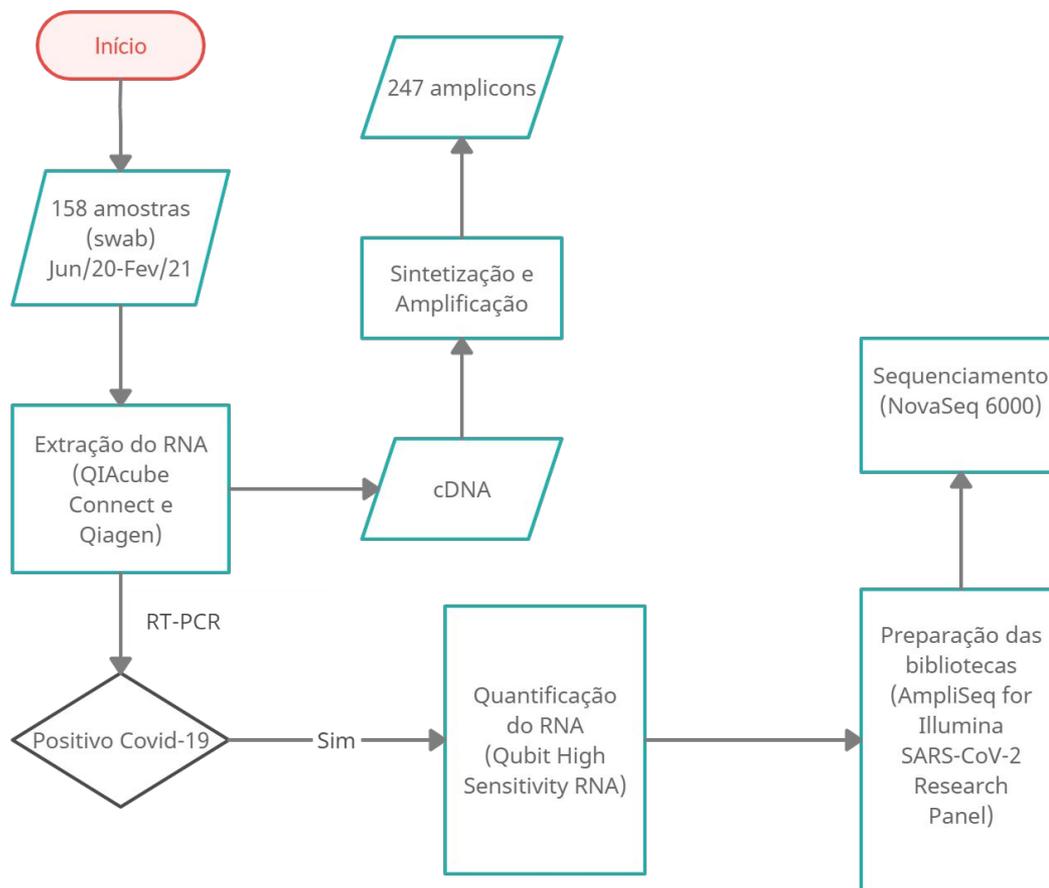# Abordagem genômica para investigar variações genéticas do Sars-CoV-2 e no hospedeiro humano

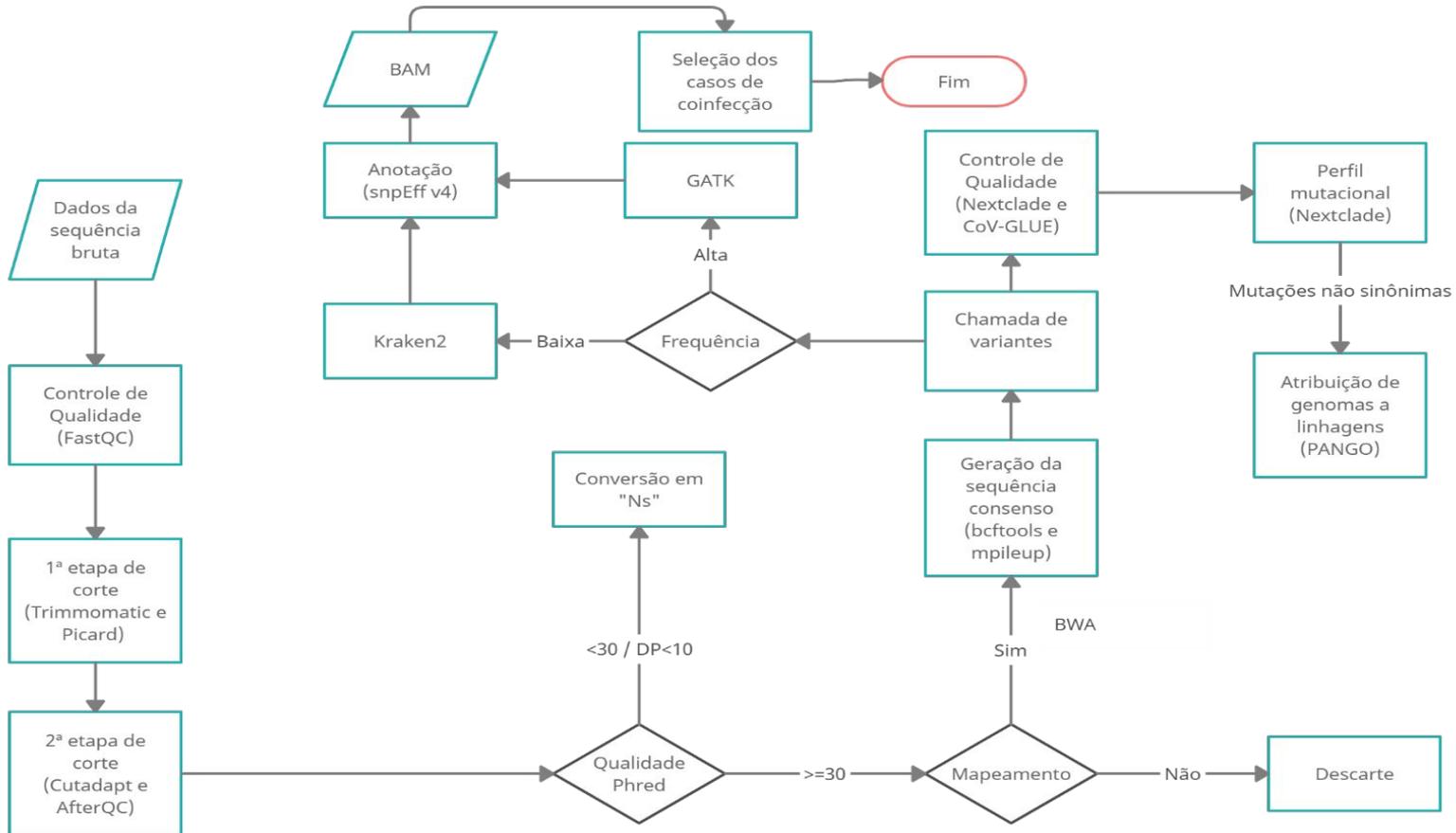## Correlação genética com a evolução clínica dos indivíduos positivos para o Sars-CoV-2
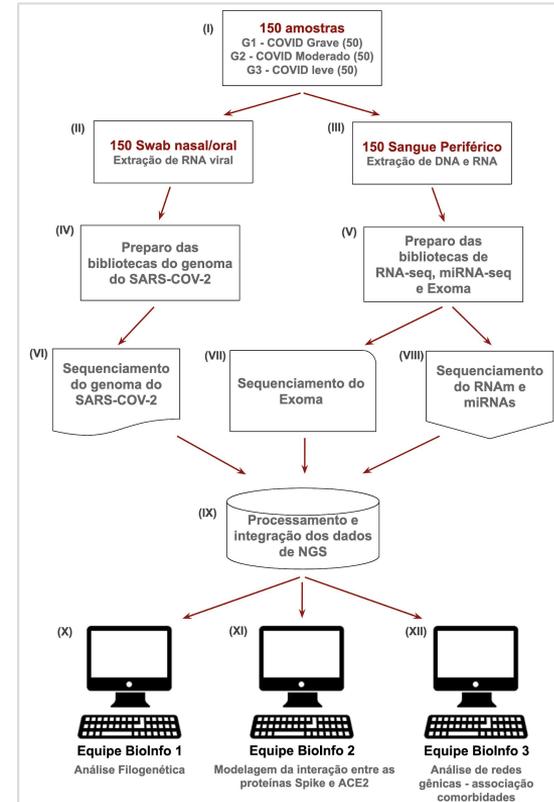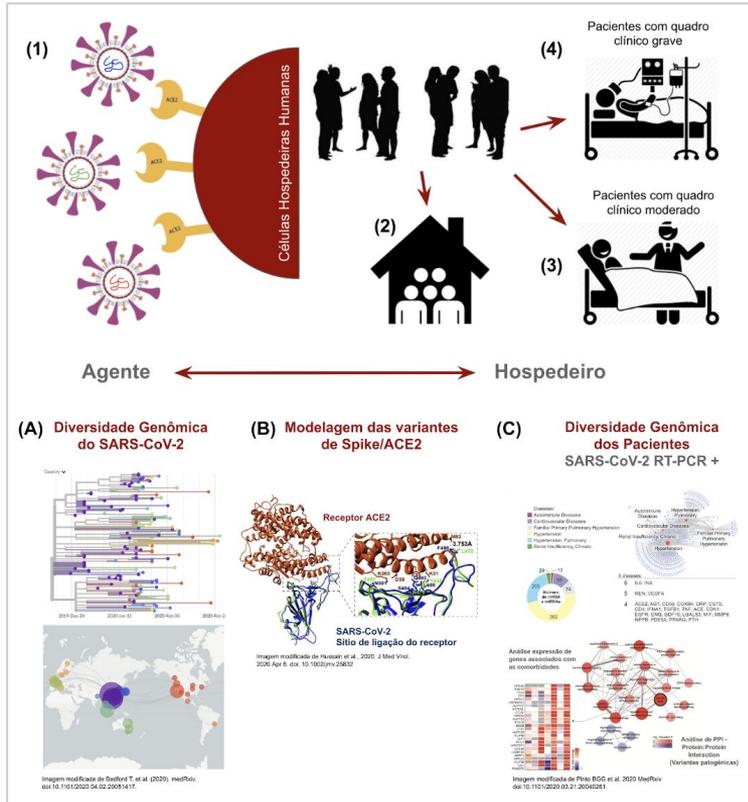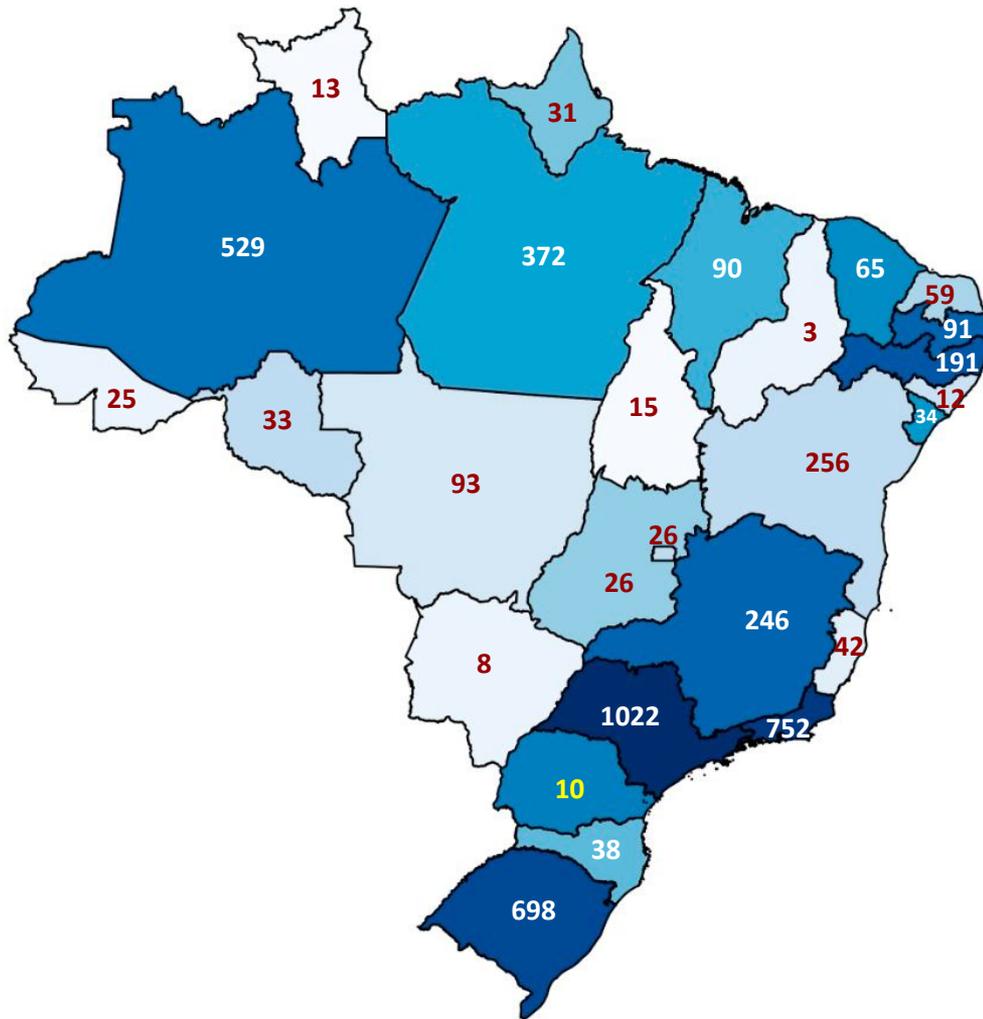
Estados	No. Genomas Sequênciados
São Paulo (SP)	1022
Rio de Janeiro (RJ)	752
Rio Grande do Sul (RS)	696
Amazonas (AM)	529
Pará (PA)	372
Bahia (BA)	256
Minas Gerais (MG)	246
Pernambuco (PE)	191
Paraná (PR)	105
Mato Grosso (MT)	93
Paraíba (PB)	91
Maranhão (MA)	90
Ceará (CE)	65
Goiás (GO)	64
Rio Grande do Norte (RN)	59
Espírito Santo (ES)	42
Santa Catarina (SC)	38
Sergipe (SE)	34
Rondônia (RO)	33
Amapá (AP)	31
Tocantins (TO)	26
Distrito Federal (DF)	26
Acre (AC)	25
Roraima (RR)	13
Alagoas (AL)	12
Mato Grosso do Sul (MS)	8
Piauí (PI)	3

Amostragem, extração do RNA e sequenciamento
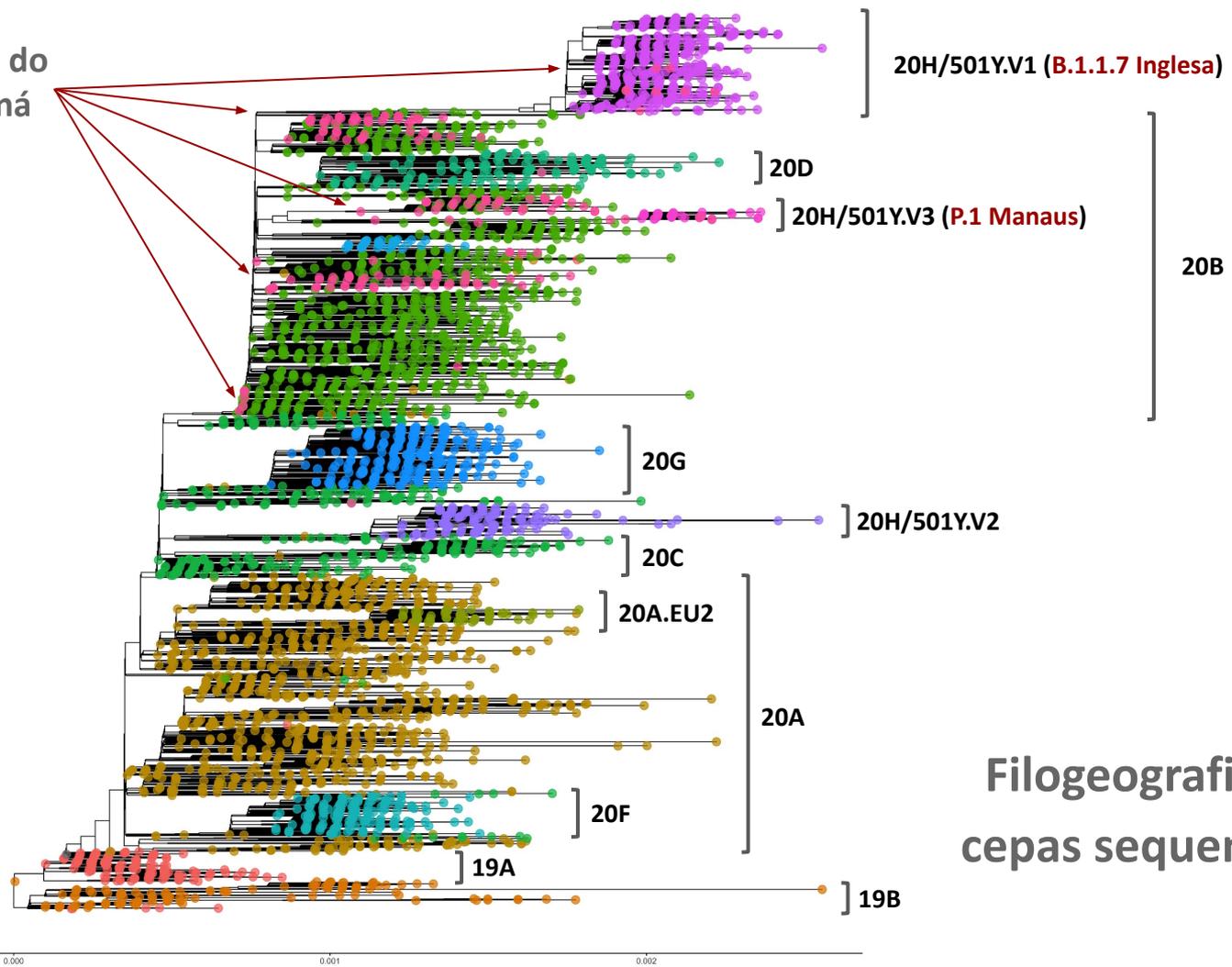
Análise de Bioinformática

Distribuição das Cepas

B.1
1.3%

B.1.1
7.6%

P.2
18.4%

P.1
2.5%

N.9
0.6%

N.5
0.6%

C.36
0.6%

B.1.362
0.6%

B.1.1.7
3.8%

B.1.1.28
32.9%

B.1.1.33
31.0%
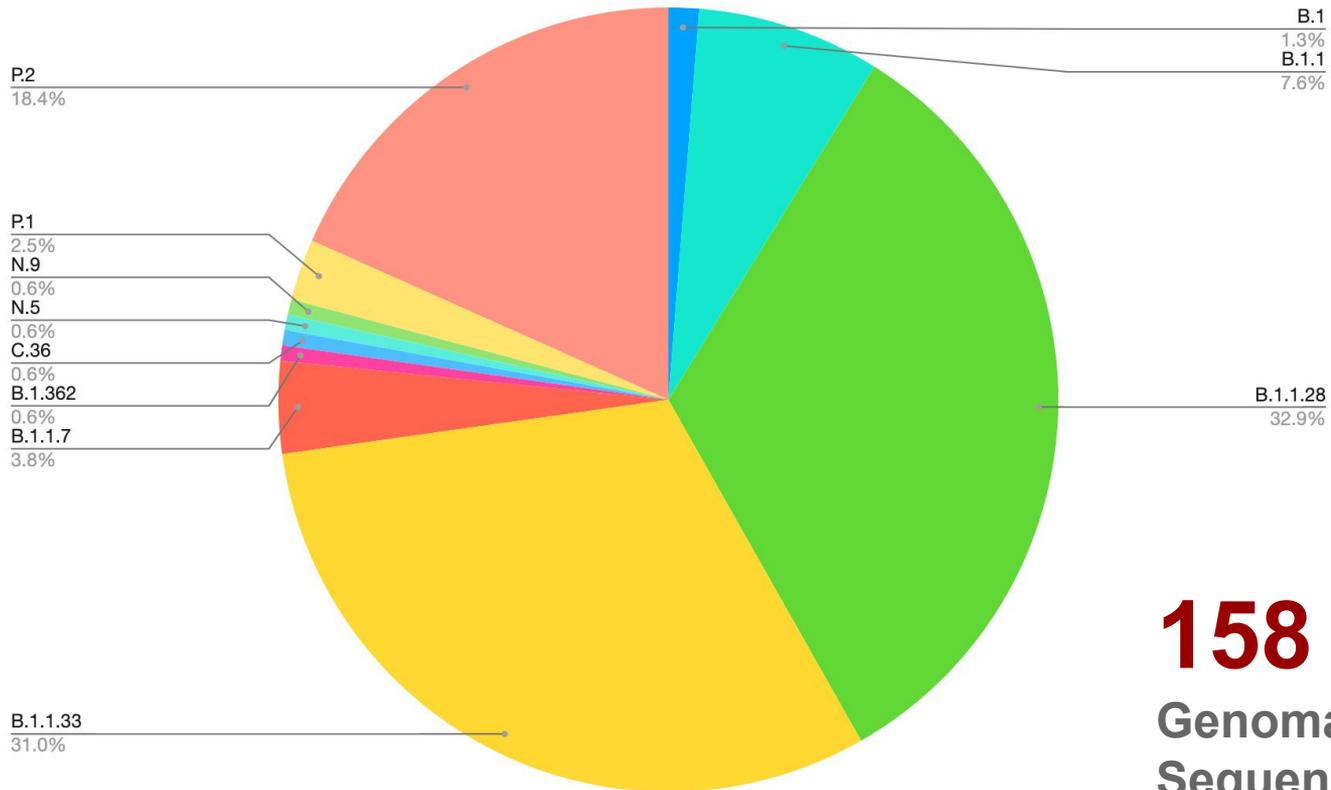
158

Genomas
Sequenciados
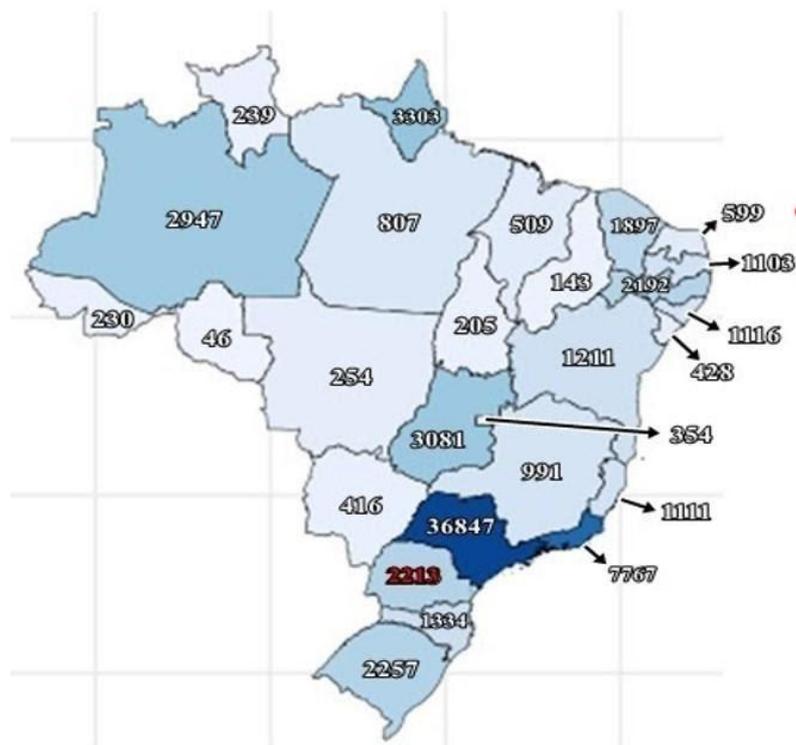
Estados	Nº de Genomas Sequenciados
São Paulo – SP	36847
Rio de Janeiro – RJ	7767
Amapá – AP	3303
Goiás – GO	3081
Amazonas – AM	2947
Rio Grande do Sul –RS	2257
Paraná – PR	2213
Pernambuco – PE	2192
Ceará – CE	1897
Santa Catarina – SC	1334
Bahia – BA	1211
Alagoas – AL	1116
Espírito Santo – ES	1111
Paraíba – PB	1103
Minas Gerais – MG	991
Pará – PA	807
Rio Grande do Norte – RN	599
Maranhão – MA	509
Sergipe – SE	428
Mato Grosso do Sul – MS	416
Distrito Federal – DF	354
Mato Grosso – MT	254
Roraima – RR	239
Acre – AC	230
Tocantins – TO	205
Piauí – PI	143
Rondônia – RO	46

Cepas do Paraná

20H/501Y.V1 (B.1.1.7 Inglesa)

20D

20H/501Y.V3 (P.1 Manaus)
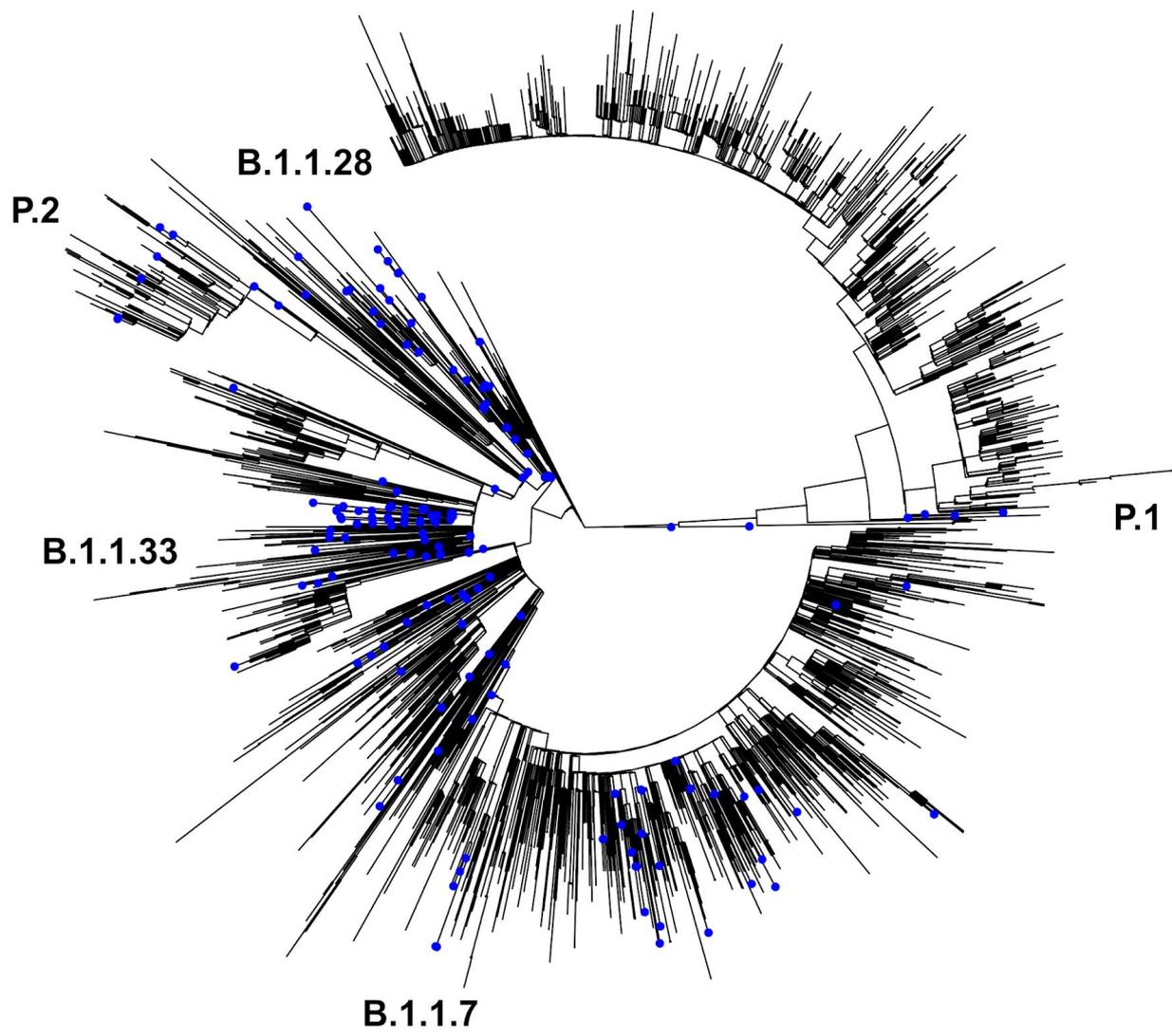
20B

20G

20H/501Y.V2

20C

20A.EU2

20A

20F

19A

19B

Nextstrain_clade

- 19A
- 19B
- 20A
- 20A.EU2
- 20B
- 20C
- 20D
- 20E (EU1)
- 20F
- 20G
- 20H/501Y.V2
- 20I/501Y.V1
- 20J/501Y.V3

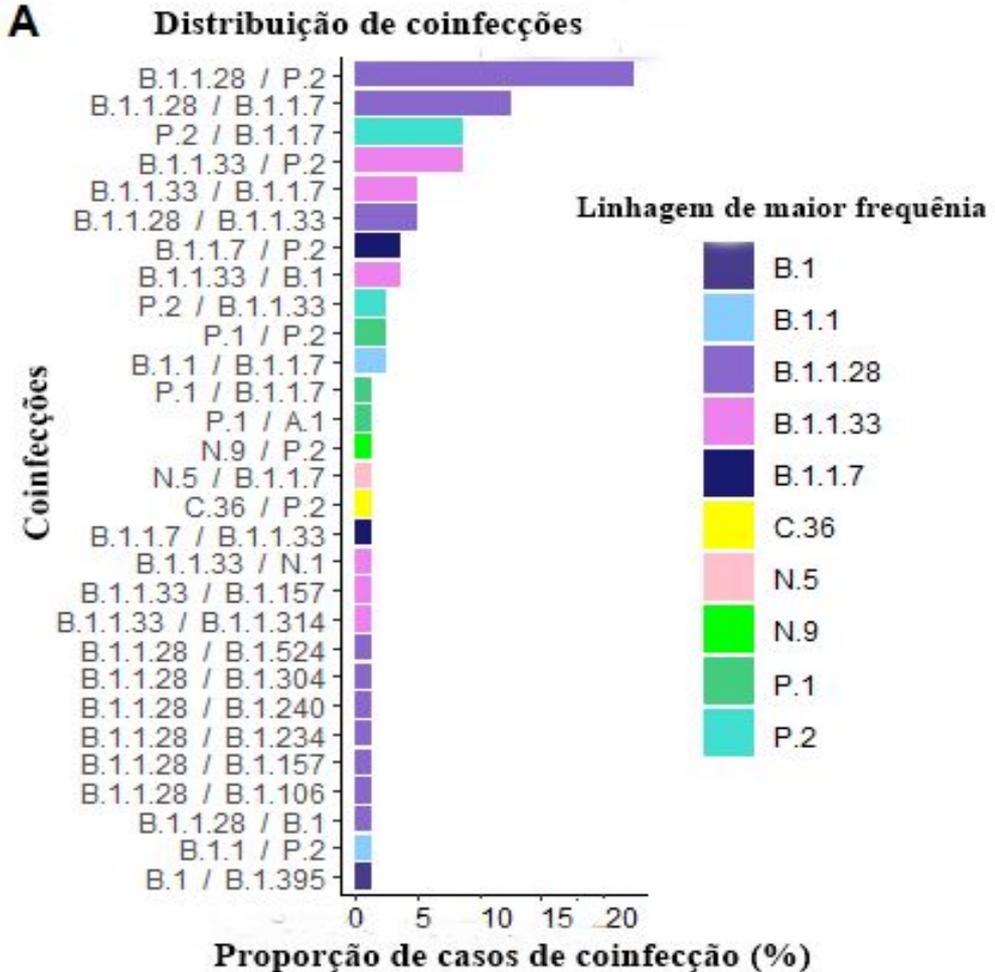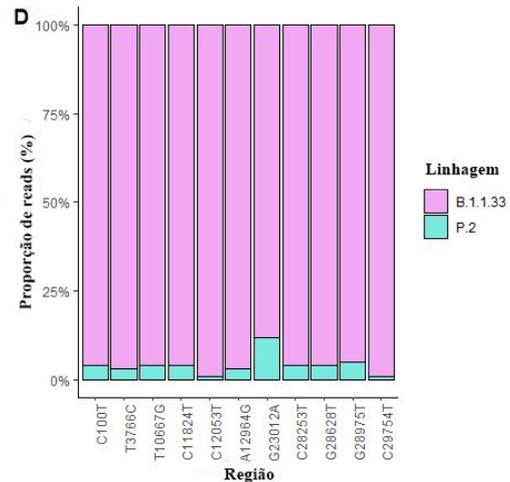Filogeografia das **4.922** cepas sequenciadas no Brasil

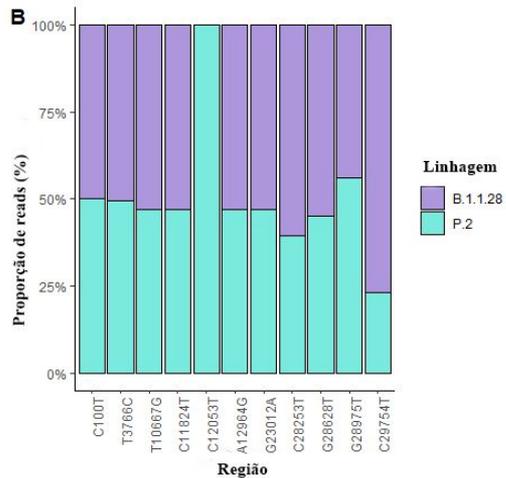0.000   0.001   0.002

Co-infecção ou Variação Intra-host

Total: 158 amostras
Coinfecções: 82 amostras (52%)
Únicas: 76 amostras

A Distribuição de coinfecções
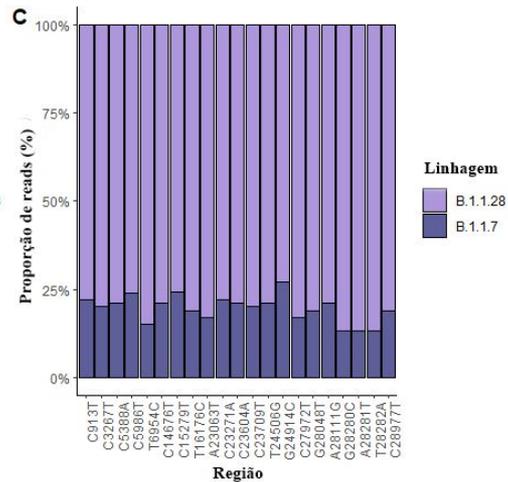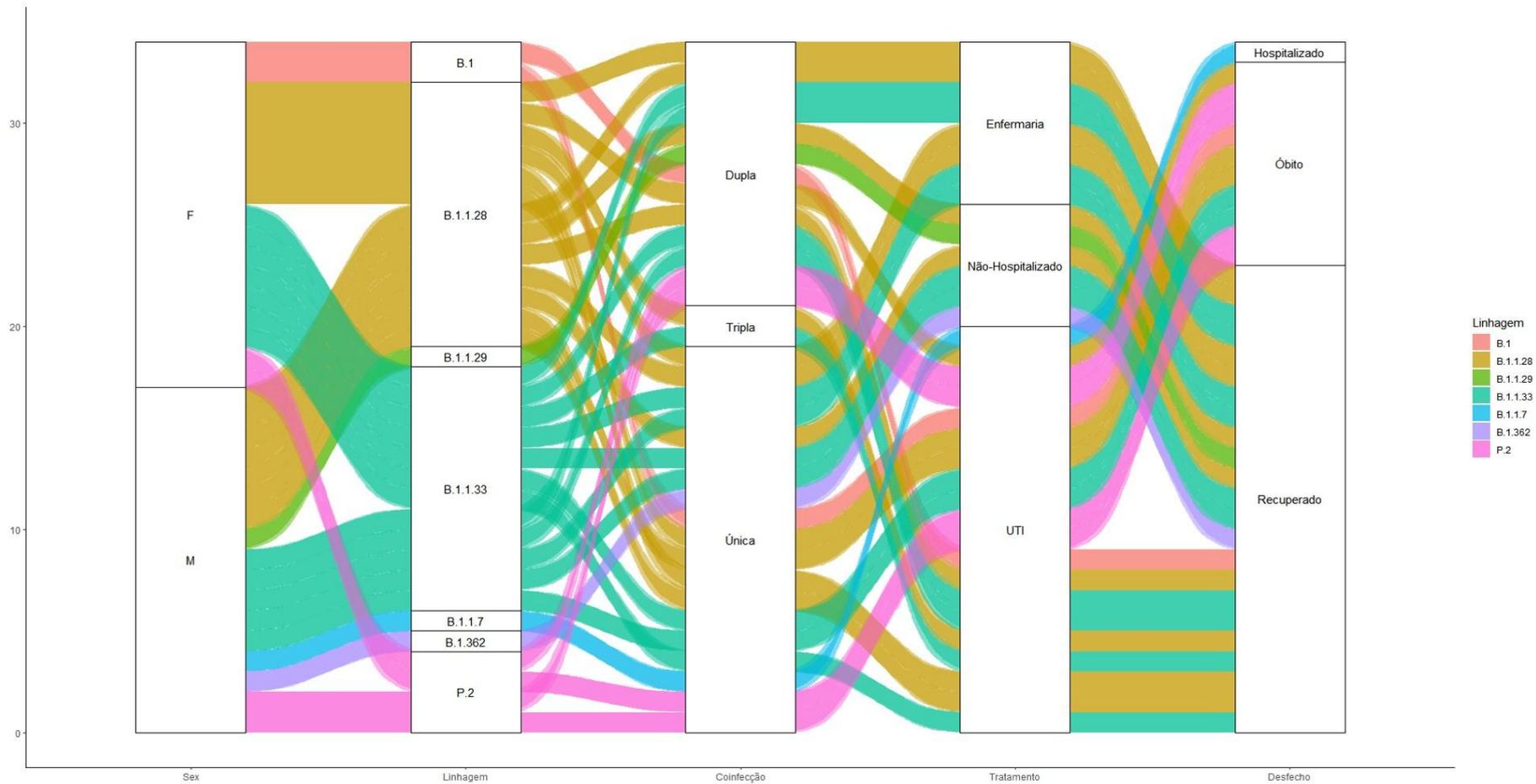
Monitoramento genômico ambiental das variantes de SARS-CoV-2 circulantes no Brasil

Resultados Preliminares
Dec - 2021

Graphical abstract

- 60 Cities
- 4,728 Samples
- 8 Trillion bases
- 31 Core Taxa
- Drug Resistance
- 748 Bacteria
- Regional Signatures
- 10,928 Viruses
- 838,532 CRISPR Arrays
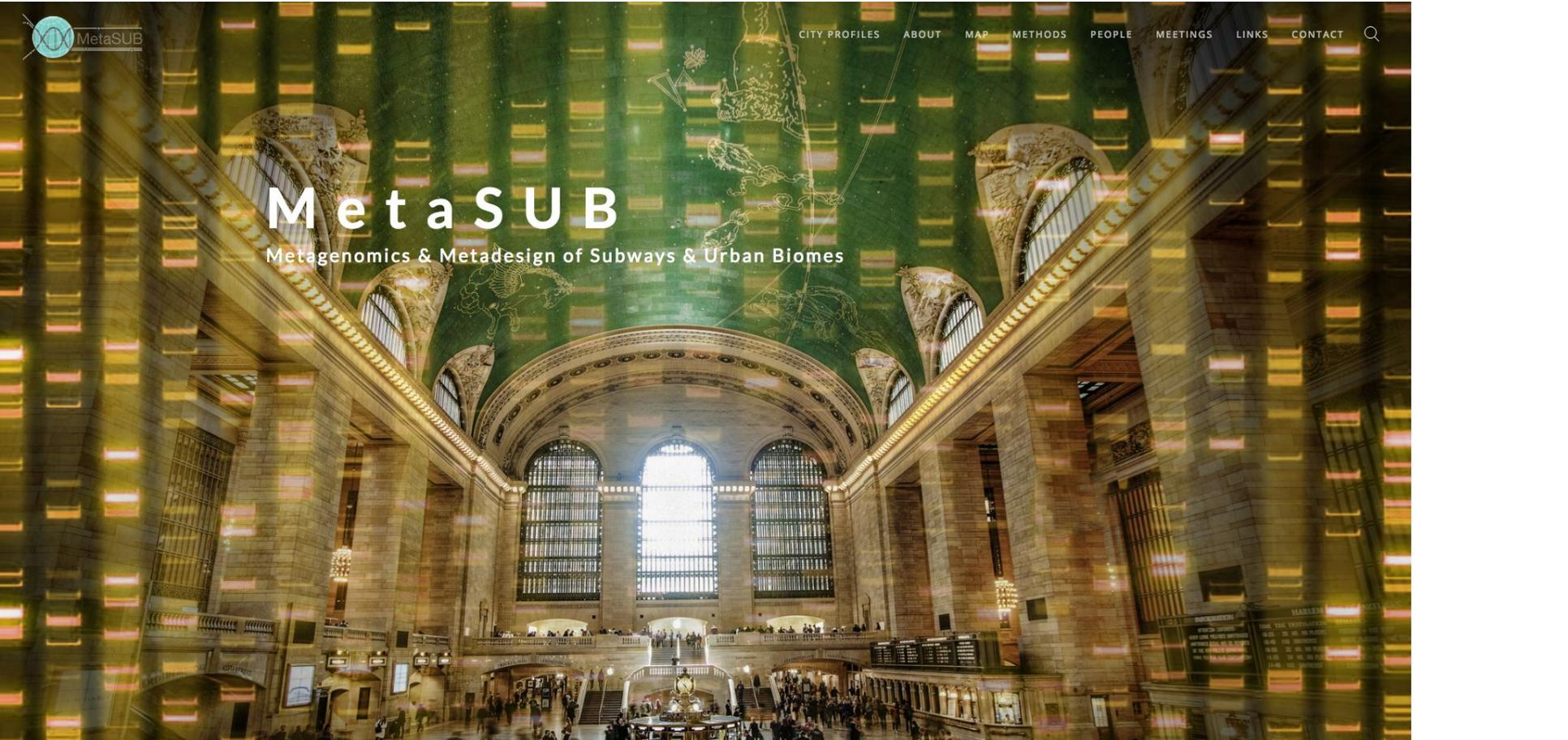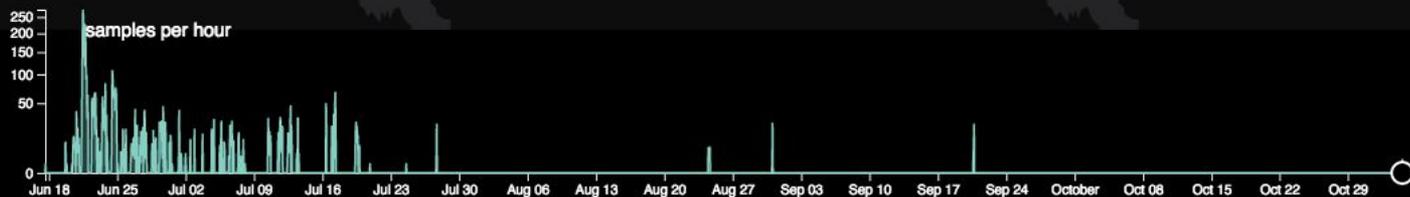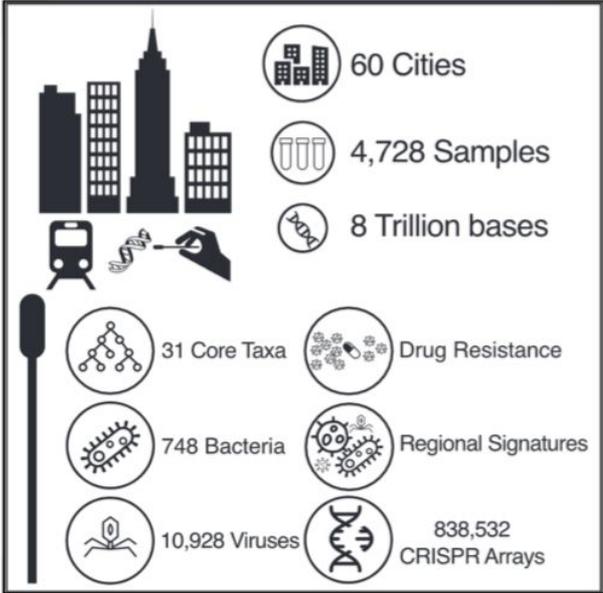
Since 2016, ongoing

Cell

Article

A global metagenomic map of urban microbiomes and antimicrobial resistance

David Danko,[1,2,68] Daniela Bezdan,[1,2,38,39,68] Evan E. Afshin,[1,2] Sofia Ahsanuddin,[3] Chandrima Bhattacharya,[1,2] Daniel J. Butler,[1,2] Kern Rei Chng,[4] Daisy Donnellan,[1,2] Jochen Hecht,[5] Katelyn Jackson,[1,2] Katerina Kuchin,[1,2] Mikhail Karasikov,[6,64,65] Abigail Lyons,[1,2] Lauren Mak,[1,2] Dmitry Meleshko,[1,2] Harun Mustafa,[6,64,65] Beth Mutai,[5,8] Russell Y. Neches,[7] Amanda Ng,[4] Olga Nikolayeva,[9] Tatyana Nikolayeva,[9] Eileen Png,[4] Krista A. Ryon,[1,2] Jorge L. Sanchez,[1,2] Heba Shaaban,[1,2] Maria A. Sierra,[1,2] Dominique Thomas,[1,2] Ben Young,[1,2] Omar O. Abudayyeh,[10] Josue Alicea,[1,2] Malay Bhattacharyya,[11,12] Ran Blekhman,[13] Eduardo Castro-Nallar,[14] Ana M. Cañas,[1,2] Aspassia D. Chatziefthimiou,[1,2] Robert W. Crawford,[15] Francesca De Filippis,[16,17] Youping Deng,[18] Christelle Desnues,[19] Emmanuel Dias-Neto,[20] Marius Dybwad,[21] Eran Elhaik,[22] Danilo Ercolini,[16,17] Alina Frolova,[23,62] Dennis Gankin,[10] Jonathan S. Gootenberg,[10] Alexandra B. Graf,[24] David C. Green,[25] Iman Hajirasouliha,[1,2] Jaden J.A. Hastings,[1,2]

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[2]The Bin Talal Bin Abdulaziz Alsaud Institute for Computational Biomedicine, New York, NY, USA

Brazil

Serrana

Ribeirão Preto

Guarulhos

São Paulo City

Londrina

Guarapuava

Curitiba

São José do Rio Preto
Barretos
Franco
Araçatuba
Ribeirão Preto
Presidente Prudente
Araraquara
Bauru
Campinas
Marília
Sorocaba
São Paulo
São José dos Campos
Itapeva
Registro
Santos

Pirapora do Bom Jesus
Franco da Rocha
Caieiras
Mairiporã
Santa Isabel
Cajamar
Araraquara
Santana de Parnaíba
Guarulhos
Arujá
Guararema
Barueri
Jandira
Osasco
Itaquaquecetuba
Itapevi
Carapicuíba
Taboão da Serra
São Paulo
Poá
Ferraz de Vasconcelos
Mogi das Cruzes
Salesópolis
Vargem Grande Paulista
Cotia
Embu das Artes
Diadema
São Caetano do Sul
Santo André
Mauá
Suzano
Biritiba Mirim
Itapecerica da Serra
São Lourenço da Serra
Embu-Guaçu
São Bernardo do Campo
Ribeirão Pires
Rio Grande da Serra
Juquitiba

Paranavaí
Maringá
Cornélio Procópio
Jacarezinho
Umuarama
Apucarana
Londrina
Campo Mourão
Ivaiporã
Toledo
Ponta Grossa
Cascavel
Laranjeiras do Sul
Guarapuava
Irati
Curitiba
Francisco Beltrão
Paranaguá
Pato Branco
União da Vitória

A

a.1 — Metas definidas para elaboração da proposta

Plano para elaboração e desenvolvimento do Projeto

Definição das cidades e locais de coleta nas cidades selecionadas

Definição das equipes e empresas parceiras

a.2

Coletas das amostras

Metagenômica do Sars-Cov-2

a.3

Pré-processamento dos dados de sequenciamento

Análise estatística das cepas de Sars-Cov-2

a.4 — Conclusão do Projeto Piloto

Elaboração do relatório final e rascunho da publicação

Metas definidas para os dois meses de projeto

B

b.1 — Segunda/Terça-feira

Coleta em 3 cidades dos Estados do Paraná e São Paulo

Coleta entre 3 e 5 locais por cidade

b.3 — Quinta/Sexta-feira

Sequenciamento das bibliotecas genômicas de Sars-Cov-2

b.5 — Segunda-feira

Avaliação dos resultados de coleta e análise de dados

Plano Semanal

Coleta e envio das amostras

Extração de RNA e início do preparo das bibliotecas

Sequenciamento das amostras

Análise de Bioinformática

Relatório semanal com resultado das análises

Procedimento padronizado e executado pelo laboratório responsável de cada Estado

b.2 — Quarta-feira

Aplicação de algoritmos para avaliar a qualidade de dados, mapeamento e anotação das cepas de Sars-Cov-2

b.4 — Sábado/Domingo

Resultados em Processamento