UNIVERSIDADE FEDERAL DE MINAS GERAIS
INSTITUTO DE CIÊNCIAS BIOLÓGICAS
DEPARTAMENTO DE GENÉTICA, ECOLOGIA E EVOLUÇÃO
PROGRAMA DE PÓS-GRADUAÇÃO EM GENÉTICA

Hugo José Alves

VIGILÂNCIA GENÔMICA DO SARS-CoV-2 NO ESTADO DE MINAS GERAIS - BRASIL

Belo Horizonte – MG

2022

Hugo José Alves

Vigilância genômica de variantes de SARS-CoV-2 no estado de Minas Gerais – Brasil

Versão Final

Dissertação submetida ao Programa de Pós-Graduação em Genética da Universidade Federal de Minas Gerais como requisito parcial para obtenção do título de mestre em genética.

ORIENTADOR: Dr. Renato Santana Aguiar

COORIENTADOR: Dr. Renan Pedra de Souza

Belo Horizonte – MG

2022

043 Alves, Hugo José.
Vigilância genômica de variantes de SARS-CoV-2 no estado de Minas Gerais – Brasil [manuscrito] / Hugo José Alves. – 2022.
155 f. : il. ; 29,5 cm.

Orientador: Dr. Renato Santana Aguiar. Coorientador: Dr. Renan Pedra de Souza.
Dissertação (mestrado) – Universidade Federal de Minas Gerais, Instituto de Ciências Biológicas. Programa de Pós-Graduação em Genética.

1. Genômica. 2. Covid-19. 3. Vírus da SARS. I. Aguiar, Renato Santana. II. Souza, Renan Pedra de. III. Universidade Federal de Minas Gerais. Instituto de Ciências Biológicas. IV. Título.

CDU: 575

Ficha catalográfica elaborada pela bibliotecária Fabiane C M Reis – CRB 6 – 2680

UNIVERSIDADE FEDERAL DE MINAS GERAIS
Instituto de Ciências Biológicas
Programa de Pós-Graduação em Genética

ATA DE DEFESA DE DISSERTAÇÃO

ATA DA DEFESA DE DISSERTAÇÃO	**323/2022** **entrada** **1º/2020**
Hugo José Alves	**CPF: 604.922.043-30**

Às nove horas do dia **30 de maio de 2022**, reuniu-se, no Instituto de Ciências Biológicas da UFMG, a Comissão Examinadora de Dissertação, indicada pelo Colegiado do Programa, para julgar, em exame final, o trabalho intitulado: **" Vigilância Genômica do SARS-CoV-2 no estado de Minas Gerais - Brasil"**, requisito para obtenção do grau de Mestre em **Genética.** Abrindo a sessão, o Presidente da Comissão, **Renato Santana**, após dar a conhecer aos presentes o teor das Normas Regulamentares do Trabalho Final, passou a palavra ao candidato, para apresentação de seu trabalho. Seguiu-se a arguição pelos Examinadores, com a respectiva defesa do candidato. Logo após, a Comissão se reuniu, sem a presença do candidato e do público, para julgamento e expedição de resultado final. Foram atribuídas as seguintes indicações:

Prof./Pesq.	Instituição	CPF	Indicação
Renato Santana	UFMG	000.086.336-06	Aprovado
Eduardo Martin Tarazona Santos	UFMG	012.494.056-02	Aprovado
Betania Paiva Drumond	UFMG	031.309.156-05	Aprovado

Pelas indicações, o candidato foi considerado: **APROVADO**

O resultado final foi comunicado publicamente ao candidato pelo Presidente da Comissão. Nada mais havendo a tratar, o Presidente encerrou a reunião e lavrou a presente ATA, que será assinada por todos os membros participantes da Comissão Examinadora.

Belo Horizonte, 30 de maio de 2022.

Renato Santana
Eduardo Martin Tarazona Santos
Betania Paiva Drumond

Assinatura dos membros da banca examinadora:

Documento assinado eletronicamente por **Renato Santana de Aguiar**, **Professor do Magistério Superior**, em 30/05/2022, às 11:59, conforme horário oficial de Brasília, com fundamento no art. 5º do Decreto nº 10.543, de 13 de novembro de 2020.

Documento assinado eletronicamente por **Betania Paiva Drumond**, **Professora do Magistério Superior**, em 31/05/2022, às 19:17, conforme horário oficial de Brasília, com fundamento no art. 5º do Decreto nº 10.543, de 13 de novembro de 2020.

Documento assinado eletronicamente por **Eduardo Martin Tarazona Santos**, **Professor do Magistério Superior**, em 01/06/2022, às 09:12, conforme horário oficial de Brasília, com fundamento no art. 5º do Decreto nº 10.543, de 13 de novembro de 2020.

A autenticidade deste documento pode ser conferida no site https://sei.ufmg.br/sei/controlador_externo.php?acao=documento_conferir&id_orgao_acesso_externo=0, informando o código verificador **1483724** e o código CRC **290ED0E4**.

Referência: Processo nº 23072.230557/2022-49 SEI nº 1483724

UNIVERSIDADE FEDERAL DE MINAS GERAIS
Instituto de Ciências Biológicas
Programa de Pós-Graduação em Genética

FOLHA DE APROVAÇÃO

" Vigilância Genômica do SARS-CoV-2 no estado de Minas Gerais - Brasil"

Hugo José Alves

Dissertação aprovada pela banca examinadora constituída pelos Professores:

Renato Santana
UFMG

Eduardo Martin Tarazona Santos
UFMG

Betania Paiva Drumond
UFMG

Belo Horizonte, 30 de maio de 2022.

Documento assinado eletronicamente por **Renato Santana de Aguiar**, **Professor do Magistério Superior**, em 30/05/2022, às 12:00, conforme horário oficial de Brasília, com fundamento no art. 5º do Decreto nº 10.543, de 13 de novembro de 2020.

Documento assinado eletronicamente por **Betania Paiva Drumond**, **Professora do Magistério Superior**, em 31/05/2022, às 19:17, conforme horário oficial de Brasília, com fundamento no art. 5º do Decreto nº 10.543, de 13 de novembro de 2020.

Documento assinado eletronicamente por **Eduardo Martin Tarazona Santos, Professor do Magistério Superior**, em 01/06/2022, às 09:12, conforme horário oficial de Brasília, com fundamento no art. 5º do Decreto nº 10.543, de 13 de novembro de 2020.

A autenticidade deste documento pode ser conferida no site https://sei.ufmg.br/sei/controlador_externo.php?acao=documento_conferir&id_orgao_acesso_externo=0, informando o código verificador **1483770** e o código CRC **8462A868**.

Referência: Processo nº 23072.230557/2022-49 SEI nº 1483770

DEDICATÓRIA

Dedico à minha mãe, Maria José Alves, por tudo que me deu e ensinou até esse momento.

AGRADECIMENTOS

Gostaria de agradecer primeiramente a Deus, por ter me permitido a chegar até aqui, me dando forças para continuar sempre e nunca **desistir** e me ajudou a realizar um sonho, não só meu, mas de toda minha família, em especial, minha mãe.

À minha mãe, Maria José Alves, que é meu tudo e sem o apoio, sem o incentivo eu não teria chegado até aqui, na realização de mais um sonho. Obrigado por tudo, pelos ensinamentos, pelas bases que sem elas, não seria a pessoa que sou hoje. Te amo para sempre.

À família Alves que sempre foi meu apoio, meu alicerce. Em especial a minha madrinha, Maria do Socorro Alves, que sempre cuidou de mim como uma segunda mãe, sempre me ajudou quando precisava. Ao meu irmão, Higor. São tantos parentes que não vão caber aqui na escrita, mas saibam que agradeço cada um de vocês.

À família que escolhemos que são meus amigos:

- Ao meus amigos do melhor laboratório que pude fazer parte (LBI), e que me acolheram muito bem, me fizeram sentir em casa e me ajudaram muito nessa nova jornada em outro estado: Daniel Costa, Fernanda Souza, João Locke, Diego Menezes, Paula Camargos, Vitor Geddes, Rafael Marques, Wallyson Costa, Isabela Braga, Rillry Calixto, Luiza Guerra e Jorge Ferreira.

- De longa data do ensino médio Natália, Lulu, Adalberto, Franklin, Rômulo, as gêmeas Val e Van, Suellen, Eric que ainda estão comigo até hoje dividindo momentos felizes e tristes, apoiando, fazendo parte da vida um do outro e mesmo de longe, ainda me ajudando nesses momentos;

- Aos amigos de outro curso Pâmela, Letícia, Amanda, Jéssica, Karyne, Ariane obrigado pelas melhores festas e conversas malucas, pela amizade que vai durar para sempre, pelos incentivos para está escrevendo isto aqui agora.

Ao Laboratório de Biologia Integrativa (LBI) que me deu a estrutura necessária para tudo que aprendi até hoje, a ser um profissional melhor.

Aos meus orientadores Renato Santana de Aguiar e Renan Pedra de Souza pelo acolhimento, apoio, carinho e conversas serias que me ajudaram nessa caminhada até aqui.

“Todas as vitórias ocultam uma abdicação”.

(Simone de Beauvoir)

RESUMO

A doença do Coronavírus 2019 (COVID-19) é causada pelo vírus da *Severe Acute Respiratory Syndrome Coronavirus 2* (SARS-CoV-2). A COVID-19 foi primeiramente identificada em dezembro de 2019 na cidade de Wuhan, China, em um grupo de pacientes com pneumonia até então de causa desconhecida. No Brasil, o primeiro caso suspeito de COVID-19 foi reportado em 27 de janeiro de 2020 e o primeiro caso confirmado por membros do nosso grupo de pesquisa foi em 26 de fevereiro de 2020, em São Paulo, de um paciente que retornou da Itália. As manifestações clínicas da COVID-19 são diversas, indo de sintomas leves a quadros graves. A gravidade dos sintomas pode variar desde os sintomas clássicos febris respiratórios até uma pneumonia viral grave com insuficiência respiratória potencialmente fatal. Logo que a pandemia de COVID-19 mostrou altos números de contágios por todo mundo, começaram a ser desenvolvidas e testadas vacinas que pudessem erradicar a pandemia. O SARS-CoV-2 tem um genoma de RNA de fita positiva de aproximadamente 30.000 bases de comprimento. Sua estrutura genômica é compartilhada com outros β-coronavírus e possui seis janelas abertas de leitura funcionais (ORFs) que são organizadas em ordem de 5' a 3', respectivamente: replicase (ORF1a / ORF1b), spike (S), envelope (E), membrana (M) e nucleocapsídeo (N). A proteína spike (S) é responsável pela interação do envelope viral com o receptor celular ACE2 e o processo de entrada do vírus. Mutações nessa região podem alterar a transmissibilidade do vírus, bem como, a neutralização por anticorpos gerados pelos programas de vacinação. A vigilância genômica viral, pode ser usada por órgãos de saúde pública no controle e prevenção da transmissão, além de identificar regiões críticas para reforço de estruturas hospitalares e vacinação. Nesta dissertação, propomos avaliar a distribuição das linhagens de SARS-CoV-2 através de um programa de vigilância genômica viral e suas consequências no cenário epidemiológico da COVID-19 no estado de Minas Gerais. No capítulo I apresentamos o desenvolvimento e padronização de uma metodologia rápida e eficaz de identificação das variantes de SARS-CoV-2, através da genotipagem das mutações virais definidoras das principais linhagens por PCR em tempo real. Essa metodologia foi eficaz e sensível na identificação das variantes de SARS-CoV-2 confirmada pelo sequenciamento do genoma completo viral o que nos permitiu o estabelecimento do Observatório de Vigilância Genômica – OviGen coordenado pelo nosso grupo de pesquisa em parceria com a Secretaria de Saúde de MG (SES-MG), Prefeitura de Belo Horizonte (PBH) e Fundação Ezequiel Dias (FUNED). No capítulo II, apresentamos os resultados do OviGen através do estudo retrospectivo de base populacional para uma vigilância genômica de variantes do SARS-CoV-2 nas 28 Unidades Regionais de Saúde de MG, no período de março a abril de 2021, período de maior registro de números de casos e óbitos e aumento da prevalência de variantes como Alfa, Gama e Zeta. Também foi possível a identificação de outras variantes, com menor frequência de circulação, que foram classificadas como "outras" linhagens pela genotipagem e confirmadas como variantes B.1.35, B1.1.28, P.4, P.5 e P.7 pelo sequenciamento de genoma completo. Utilizando estratégias de filogenia e filogeografia demonstramos a introdução da VOC Gama no estado de MG na data 07 de janeiro de 2021 e sua dispersão no estado de MG a partir da região sudeste, fronteira com Rio de Janeiro, alcançando cerca de 100% dos casos de infecção por COVID-19 em 27 semanas (julho de 2021). Os nossos resultados demonstraram o aumento da carga viral média entre os pacientes infectados com a variante gama confirmando o impacto da introdução desta VOC e consequente aumento nas taxas de transmissão e severidade de casos de COVID-19, reforçando a importância dos estudos de vigilância genômica viral no controle e transmissão da pandemia.

Palavras Chave: COVID-19, Gama, Minas Gerais, SARS-CoV-2, Vigilância.

ABSTRACT

Coronavirus disease 2019 (COVID-19) is caused by the Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) virus. COVID-19 was first identified in December 2019 in the city of Wuhan, China, in a group of patients with previously unknown pneumonia. In Brazil, the first suspected case of COVID-19 was reported on January 27, 2020 and the first case confirmed by members of our research group was on February 26, 2020, in São Paulo, of a patient who had returned from Italy. The clinical manifestations of COVID-19 are diverse, ranging from mild to severe symptoms. The severity of symptoms can range from classic febrile respiratory symptoms to severe viral pneumonia with life-threatening respiratory failure. As soon as the COVID-19 pandemic showed high numbers of infections around the world, vaccine initiatives that could eradicate the pandemic began to be developed and tested. SARS-CoV-2 has a positive-stranded RNA genome approximately 30,000 bases in length. Its genomic structure is shared with other β-coronaviruses and has six functional open reading frames (ORFs) that are arranged in order from 5' to 3', respectively: replicase (ORF1a/ORF1b), spike (S), envelope (E), membrane (M) and nucleocapsid (N). The spike protein (S) is responsible for the interaction of the viral envelope with the cell receptor ACE2 and the process of virus entry. Mutations in this region can alter the transmissibility of the virus, as well as the neutralization by antibodies generated by vaccination programs. Viral genomic surveillance can be used by public health agencies to control and prevent transmission, in addition to identifying critical regions for strengthening hospital structures and vaccination. In this dissertation, we propose to evaluate the distribution of SARS-CoV-2 strains through a viral genomic surveillance program and its consequences in the epidemiological scenario of COVID-19 in the state of Minas Gerais. In Chapter I, we present the development and standardization of a rapid and effective methodology for identifying SARS-CoV-2 variants, by genotyping the defining viral mutations of the main lineages by real-time PCR. This methodology was effective and sensitive in the identification of SARS-CoV-2 variants confirmed by the sequencing of the complete viral genome, which allowed us to establish the Genomic Surveillance Observatory - OviGen coordinated by our research group in partnership with the Health Department of MG (SES-MG), Belo Horizonte City Hall (PBH) and Ezequiel Dias Foundation (FUNED). In Chapter II, we present the results of OviGen through a retrospective population-based study for a genomic surveillance of SARS-CoV-2 variants in the 28 Regional Health Units of MG, from March to April 2021, the period of greatest registration number of cases and deaths and an increase in the prevalence of variants such as Alpha, Gamma and Zeta. It was also possible to identify other variants, with a lower frequency of circulation, which were classified as “other” strains by genotyping and confirmed as variants B.1.35, B1.1.28, P.4, P.5 and P.7 by complete genome sequencing. Using phylogeny and phylogeographic strategies, we demonstrate the introduction of VOC Gamma in the state of MG on January 7, 2021 and its dispersion in the state of MG from the southeast region, bordering Rio de Janeiro, reaching about 100% of cases of COVID-19 infection on 27 weeks (July 2021). Our results demonstrated the increase in mean viral load among patients infected with the gamma variant, demonstrating the impact of the introduction of this VOC and the consequent increase in transmission rates and severity of COVID-19 cases, reinforcing the importance of viral genomic surveillance studies in the control and transmission of the pandemic.

Keywords: COVID-19, Gamma, Minas Gerais, SARS-CoV-2, Surveillance.

LISTA DE FIGURAS

LISTA DE TABELAS

LISTA DE ABREVIATURAS

2019-nCoV – 2019 Novo Coronavírus;

ACE2 – sigla para Enzima Conversora de Angiotensina 2;

CatB – catepsina B;

CatL – catepsina L;

CDC – Centro de Controle de Doenças;

COVID-19 – Doença do Crororonavírus 2019;

E – Envelope;

EUA – Estados Unidos da América;

FUNED – Fundação Ezequiel Dias

Ɣ-CoV - Gammacoronavírus;

HCoV-229E - Human Coronavirus 229E;

HCoV-HKU1 - Human Coronavirus HKU1;

HCoV-NL63 - Human Coroavirus NL63;

HCoV-OC43 - Human Coronavirus OC43;

IDT – Integrated DNA Technologies

M – Membrana;

MERS-CoV – Middle East Respiratory Syndrome Coronavirus;

MG – Minas Gerais

MS – Ministério da Saúde;

N – Nucleocapsídeo;

NUPAD – Núcleo de Ações e Pesquisas em Apoio Diagnóstico;

OMS - Organização Mundial de Saúde;

OMS – Organização Mundial da Saúde

ORF – Open Read Frame;

OviGen - Observatório de Vigilância Genômica;

OviGen - Observatório de Vigilância Genômica;

PBH – Prefeitura de Belo Horizonte

PCR - Reação em Cadeia da Polimerase;

RBD - Region Binding Domain (Região do Domínio de Ligação);

Rdrp – RNA polimerase dependente de RNA;

RT-PCR – Transcrição Reversa - Reação em Cadeia da Polimerase

S – Spike;

S1 – Subunidade 1 da Spike;

S2 – Subunidade 2 da Spike;

SARS-CoV – Severe Acute Respiratory Syndrome Coronavirus;

SARS-CoV-2 – Severe Acute Respiratory Syndrome Coronavirus 2;

SES-MG – Secretaria de Estado da Saúde de Minas Gerais

ssRNA – single strand RNA;

TMPRSS2 – sigla para Protease Transmembranar Serina 2;

UFMG - Universidade Federal de Minas Gerais;

VOC – Variant of Concern (Variante de Preocupação);

VOI – Variant of Interest (Variante de Interesse);

β-CoV - Betacoronavírus;

α-CoV - Alphacoronavírus;

δ-CoV - Deltacoronavírus;

SUMÁRIO

1. INTRODUÇÃO

1.1. COVID-19

A doença do Coronavírus 2019 (COVID-19) é causada pelo vírus da *Severe Acute Respiratory Syndrome Coronavirus 2* (SARS-CoV-2). Ela foi primeiramente identificada em dezembro de 2019 na cidade de Wuhan, China, em um grupo de pacientes com pneumonia até então de causa desconhecida (Figura 1). Esse Coronavírus recém-descoberto foi originalmente denominado 2019 Novo Coronavírus (2019-nCoV) pela Organização Mundial da Saúde (OMS) e posteriormente SARS-CoV-2. A partir da sua identificação, os casos de 2019-nCoV foram relatados na Tailândia, Japão, Coréia, Estados Unidos da América, Vietnã e Cingapura em um primeiro momento, até a dispersão mundial caracterizada pela pandemia. (WANG et al., 2020; WHO, 2020; ZHU et al., 2020).

No Brasil, o primeiro caso suspeito de COVID-19 foi reportado em 27 de janeiro de 2020 e colocou o país em alerta nível 2 (risco iminente) (CRODA et al., 2020). O primeiro caso confirmado de COVID-19 foi em 26 de fevereiro de 2020, em São Paulo, de um paciente que retornou da Itália, o qual o nosso grupo de pesquisa participou na sua identificação e sequenciamento (JESUS et al., 2020). A partir desse ponto, o número de casos aumentou rapidamente no país e no dia 13 de março o Ministério da Saúde (MS) anunciou recomendações para prevenção da disseminação da COVID-19 e declaração do Estado de Emergência em Saúde (MINISTÉRIO DA SAÚDE, 2020). Até 21 de março, a doença havia se espalhado para todas as unidades federais do Brasil e em 19 de junho de 2020, o país registrou seu milionésimo caso e quase 49.000 mortes (CHARNER, 2020; MINISTÉRIO DA SAÚDE, 2021).

A OMS declarou no dia 11 de março de 2020, a COVID-19 como pandemia e número oficial de casos refere-se ao número de pessoas que foram confirmadas como positivas por testes moleculares e ou sorológicos (WHO, 2020). As taxas de subnotificação de casos são altas, chegando a 86% das infecções por COVID-19 no início da pandemia (LI et al., 2020). Vários outros estudos usando diferentes estratégias estimam que o número de infecções em muitos países pode ser muito maior do que o número de casos relatados (LAU et al., 2020; FLAXMAN et al., 2020). Dentre as pessoas que contraíram COVID-19, mais de 80% se recuperaram. Em pacientes que desenvolveram casos graves o intervalo médio entre o início dos sintomas e o óbito é de 6 a 41 dias, (ROTHAN & BYRAREDDY, 2020).

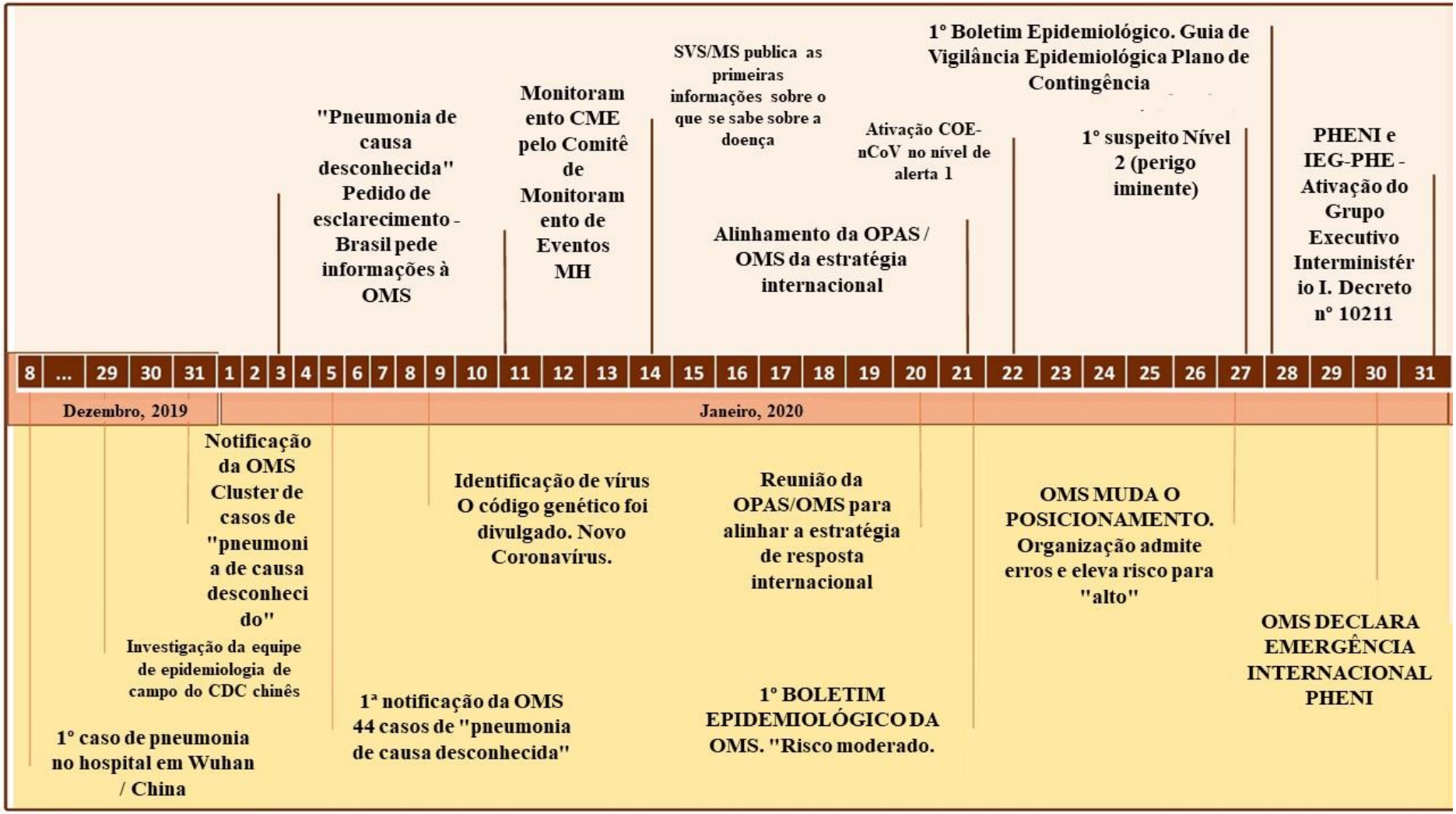

Figura 1 Evolução temporal da COVID-19 e ações das agências reguladoras internacionais e nacionais em resposta ao crescimento da pandemia. Adaptado de Croda et al., 2020.

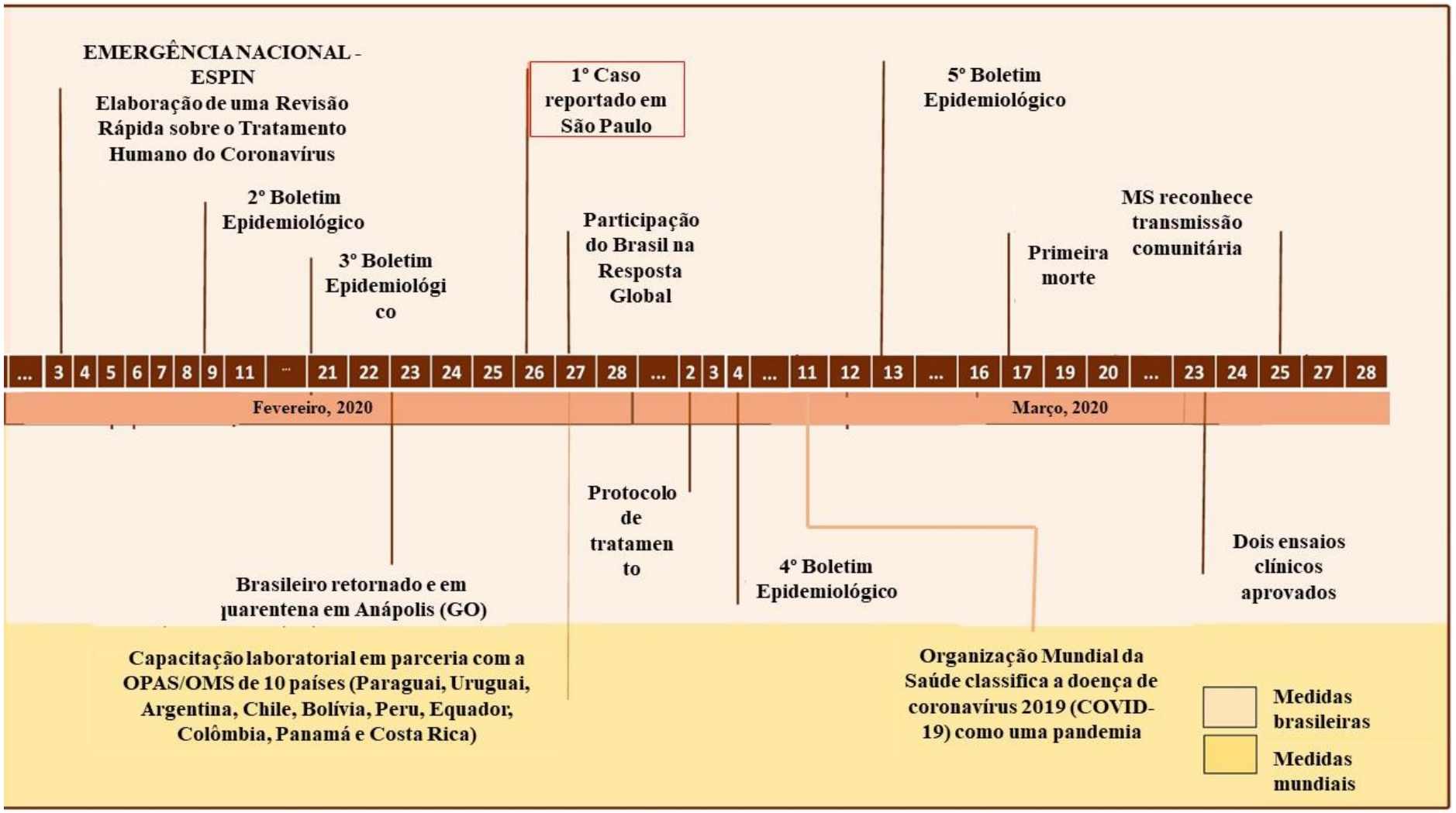

Figura 1. Continuação

Pessoas com maior risco de morte por COVID-19 são frequentemente aquelas com doenças subjacentes, como imunossuprimidos, problemas cardíacos ou pulmonares graves, obesidade grave ou idosos (YANEZ et al., 2020; CDC, 2021). A taxa geral de casos de óbitos de COVID-19 pelo mundo foi de 2,08% (4.495.014 mortes por 216.026.420 mortes), sendo que estes números variam por região (LAZZERINI & PUTOTO, 2020). A taxa de mortalidade estimada de COVID-19 relatada em 2020 é de 22,62% (IBRAHIM, 2020; KUPEK, 2021). Em 05 de maio de 2022, um total de 513.384.685 casos de COVI-19 foram confirmados em todo o mundo, resultando em 6.246.828 mortes (WHO, 2022).

No Brasil, de acordo com o Painel Coronavírus do Ministério da Saúde, o número de casos confirmados já passa dos 30 milhões. Desses, cerca de 29.609.064 se recuperaram da doença, porém, quando se fala em número de óbitos, o país se encontra no 3º colocado no ranking dos países com maior mortalidade contabilizada (663.896 óbitos confirmados) (MINISTÉRIO DA SAÚDE, 2022). Ainda segundo o Ministério da Saúde (2022), de acordo com os dados disponibilizados pelas Secretarias Estaduais de Saúde, a região Sudeste lidera o ranking com maior número de casos registrados (11.697.906) e óbitos (317.540), seguidos pelas regiões Nordeste, Sul, Centro-Oeste e Norte, respectivamente. Dentre os estados da região sudeste, Minas Gerais se encontra na 2ª posição em números de casos (3.360.000) e 3ª em número de óbitos (61.356) (MINISTÉRIO DA SAÚDE, 2022).

1.2 Manifestações clínicas

As manifestações clínicas da COVID-19 são diversas, indo de sintomas leves a quadros graves (GRANT et al., 2020; CDC,2021). Dentre os sintomas característicos temos alterações no olfato (anosmia) e paladar (ageusia), sendo considerados sinais confirmatórios (VAIARA et al., 2020). A gravidade dos sintomas pode variar desde semelhante a um sintoma gripal comum até pneumonia viral grave com insuficiência respiratória potencialmente fatal (BJM BEST PRATICE, 2020). Entre os indivíduos acometidos pela COVID-19, podemos ter os assintomáticos (casos de infeção que não se manifestam sintomas) e os sintomáticos, onde os sintomas mais comuns são febre, tosse e dificuldade em respirar (Figura 2) (CHEN et al., 2020). Entre outros possíveis sintomas menos frequentes estão garganta inflamada, corrimento nasal, espirros ou diarreia (Figura 2) (HUANG et al., 2020). Entre as possíveis complicações estão pneumonia grave, falência de vários órgãos e morte (HUI et al., 2020). Entre aqueles pacientes que desenvolvem sintomas, cerca de 81% apresentam sintomas leves a moderados (mesmo pneumonia leve), enquanto 14% manifestam sintomas graves, e 5% dos pacientes sofrem de sintomas críticos como alterações pulmonares visíveis através de radiografias de tórax e outras

técnicas de imagem, com anormalidades em vidro fosco, consolidação irregular, exsudatos alveolares e envolvimento interlobular, eventualmente indicando deterioração tecidual (CDC,2021).

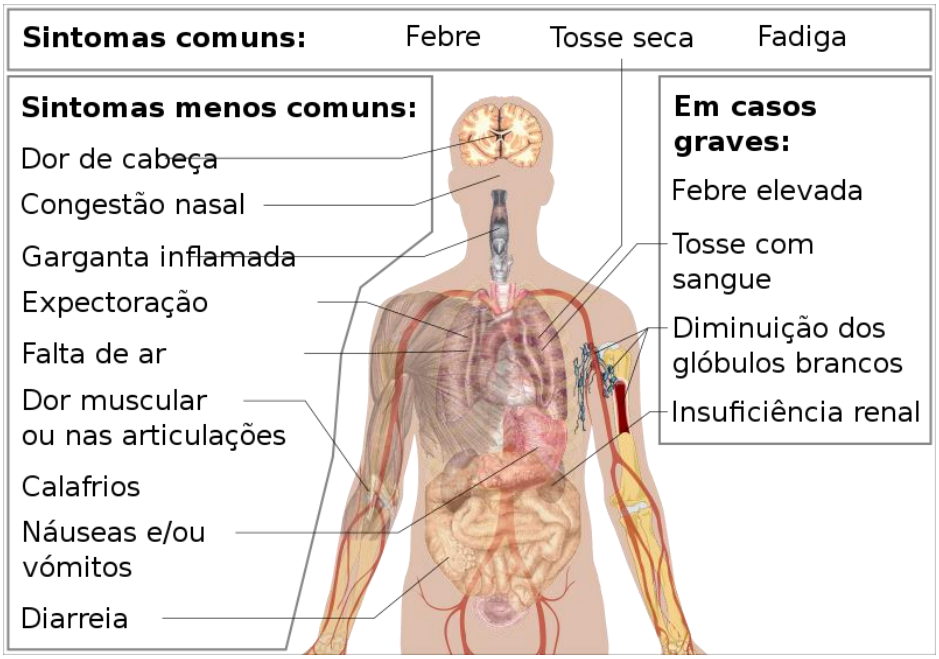

Figura 2. Descrição dos sintomas de COVID-19 de acordo com a gravidade. Por Mikael Häggström, M.D.- Author info- Reusing images- Conflicts of interest: NoneMikael Häggström - Obra do próprio, CC0, https://commons.wikimedia.org/w/index.php?curid=87644670

Pelo menos um terço das pessoas infectadas com o vírus não apresentam sintomas óbvios em nenhum momento da COVID-19 (PALMER, 2021; ORAN & TOPOL, 2021). Esses portadores assintomáticos geralmente não são testados e podem transmitir o vírus visto que apresentam cargas virais detectáveis (LAI et al.,2020; FURUKAWA, BROOKS, SOBEL, 2020). O intervalo médio entre o evento de infecção e a manifestação dos sintomas de COVID-19 é de quatro a cinco dias (GANDHI; LYCNH; DEL RIO, 2020). Na maioria dos casos os sintomas se resolvem cerca de 10-14 dias após o início dos sintomas. (WIERSINGA et al., 2020). A maioria das pessoas se recupera da fase aguda da doença (CDC, 2021).

Porém, a infecção pode progredir para doença grave com dispneia e sintomas torácicos graves correspondentes a pneumonia em aproximadamente 75% dos pacientes (GUAN et al., 2020). Como uma das principais manifestações graves, na segunda ou terceira semana de uma infecção sintomática, a pneumonia viral ocorre e os sinais proeminentes incluem diminuição da saturação de oxigênio, alterações pulmonares visíveis por meio de radiografias de tórax e outras técnicas de imagem, com anormalidades em vidro fosco, consolidação irregular, exsudatos alveolares e envolvimento interlobular, eventualmente indicando deterioração de tecido (VELAVAN; MEYER, 2020). A linfopenia parece ser comum e os marcadores inflamatórios (proteína C reativa e citocinas pró-inflamatórias) estão elevados (VELAVAN; MEYER, 2020).

1.3 Tratamento e Vacinas

Logo que a pandemia de COVID-19 mostrou altos números de contágios por todo mundo, vários laboratórios no mundo começaram a desenvolver e testar vacinas que pudessem ser usadas na prevenção de casos graves de COVID-19. No final de fevereiro de 2020, a OMS declarou que uma vacina contra o SARS-CoV-2, não deveria estar disponível nos próximos 18 meses (GRENFELL; DREW, 2020). Tentativas anteriores de desenvolver vacinas contra as doenças de coronavírus SARS e MERS acumularam conhecimento substancial sobre a estrutura e a função do coronavírus, o que acelerou o desenvolvimento de vacinas contra a COVID-19 em várias plataformas de tecnologia (DIAMOND; PIERSON, 2020).

Durante a pandemia, várias estratégias de tratamento da COVID-19 foram desenvolvidas e amplamente utilizadas na prática clínica incluindo corticosteroides, remdesivir, tocilizumabe e combinações de anticorpos monoclonais bamlanivimabe/etesevimabe e casirivimabe/imdevimabe, com ênfase em resultados clínicos, farmacologia, administração e potenciais interações medicamentosas (DDI) de relevância clínica (NHEAN et al., 2021; KUNDLAY et al., 2022). Antimaláricos e alguns antivirais (por exemplo, lopinavir e ritonavir) usados nos estágios iniciais da pandemia foram posteriormente considerados ineficazes e/ou associados a riscos à saúde do paciente (NHI - COVID-19 Treatment Guidelines, 2022). Em tal situação, a estratégia mais promissora para a superação da pandemia é a vacinação profilática de toda a população (KUNDLAY et al., 2022). As vacinas COVID-19 são classificadas em quatro categorias principais usando diferentes plataformas: (1) vacinas de vírus inativados ou atenuados, (2) vacinas à base de proteínas, (3) vacinas com vetores virais expressando imunógenos e (4) vacinas de ácido nucleico (NAGY; ALHATLANI, 2021). Na tabela 1 apresentamos um resumo de todas as vacinas que foram liberadas para uso emergencial durante a pandemia de COVID-19, descrevendo nome da vacina, situação atual, eficácia, país de origem, tecnologia utilizada e efeitos adversos.

Atualmente, cerca de 65.5% (4.68 bilhões de pessoas da população mundial está imunizada com pelo menos 1 dose dos diversos imunizantes aprovados para utilização contra COVID-19 (Figura 3) (OUR WORLD IN DATA, 2022). No Brasil, a primeira dose aplicada de vacina foi no dia 17 de janeiro de 2021, no estado de São Paulo, utilizando o imunizante Coronavac (TANRIOVER et al., 2021; ULHAQ et al., 2021). No país, atualmente, cerca de 77.5% (182.9 milhões) de pessoas estão vacinadas completamente (duas doses + reforço) (OUR WORLD IN DATA, 2022).

Tabela 1. Principais vacinas utilizadas no período da pandemia de COVID-19 em todo mundo.

Candidato vacinal (desenvolvedor/financiador)	Situação atual	Eficácia	País de origem	Tecnologia	Efeitos adversos	Referências e notas
Comirnaty ou Tozinameran ou BNT162b2 (Pfizer-BioNTech)	Liberada para uso emergencial, inclusive pela OMS para o programa Covax Facility	95%	Alemanha e Estados Unidos	RNA mensageiro	Comuns: fadiga e dor de cabeça Raros: reação alérgica moderada ou grave	POLACK et al., 2020
Moderna ou mRNA-1273 (Moderna, US National Institute of Allergy and Infectious Diseases e BARDA)	Liberada para uso emergencial	94,1%	Estados Unidos	RNA mensageiro	Comuns: dor no local a aplicação, podendo às vezes ocorrer vermelhidão e inchaço Raros: reação alérgica moderada ou grave	BADEN et al., 2021
Oxford-AstraZeneca ou ChAdOx1 ou Covishield ou AZD1222 (University of Oxford e AstraZeneca)	Liberada para uso emergencial, inclusive pela OMS para o Covax Facility	70,4%	Reino Unido	Vetor Viral não replicante expressando a proteína spike	Comuns: dor, sensação de calor e vermelhidão Incomuns: coceira, inchaço; hematoma (manchas roxas), caroço no local da aplicação, sensação de indisposição de forma geral, sensação de cansaço, calafrio,	PRECISION VACCINATIONS, 2022

					sensação febril, febre, dor de cabeça, enjoos (náusea), dor nas articulações, dor muscular	
Janssen Covid-19 ou Ad26.COV2.S ouJNJ-78436735 (Jannsen-Cilag)	Liberada para uso emergencial	66% de eficácia geral e 85% para prevenção de covid grave	Estados Unidos	Vetor Viral não replicante expressando a proteína spike		SADOFF et al., 2021
CanSino ou Ad5-nCoV CanSino Biologics, Institute of Biotechnology of the Academy of Military Medical Sciences)	Liberada para uso emergencial	65,7%	China	Vetor Viral não replicante expressando a proteína spike	Comuns: febre, dor e fadiga	ZHU et al., 2020 **Nota:** foi a primeira vacina a obter uma patente na China, em agosto de 2020.
CoronaVac ou Sinovac (Sinovac Biotech)	Liberada para uso emergencial	50,38%	China	Vírus inativado	Comuns: dor no local da aplicação, fadiga, febre, mialgia, diarreia, náusea e dor de cabeça	TANRIOVER et al., 2021; ULHAQ et al., 2021
Sinopharm-Pequim (Sinopharm)	Liberada para uso emergencial	79,3%	China	Vírus inativado		CNN BRASIL, 2020
Covaxin ou BBV152 (Bharat Biotech)	Liberada para uso emergencial	81%	Índia	Vírus inativado	Comuns: dor no local da injeção, dor de cabeça, fadiga e febre	ELLA et al., 2021 **Nota 1**: a vacina foi liberada na Índia antes dos dados da fase 2 dos testes

						Nota 2: no Brasil ela seria produzida em parceria com a Precisa Medicamentos
Sputnik V ou Gam-COVID-Vac (Instituto Gamaleya)	Liberada para uso emergencial	91,6%	Rússia	Vetor Viral não replicante expressando a proteína spike	Os eventos adversos, registrados por 94% dos participantes do estudo, mais comuns foram sensações parecidas com as causadas pela gripe, reações no local da injeção, dor de cabeça e astenia.	LOGUNOV et al., 2021 **Nota**: a vacina foi liberada antes do final dos testes da fase 3 como estratégia do governo russo para que ela fosse conhecida como a primeira registrada no mundo Nota 2: no Brasil ela será produzida em parceria com a União Química
EpiVacCorona (Novosibirsk Scientific Center Vector)	Liberada para uso emergencial	Desconhecida	Rússia	Subunidade de proteína		RYZHIKOV et al., 2021 **Nota:** como acontece com a vacina Sputnik V, faltam dados robustos e certificados internacionalmente sobre a vacina
BBIBP-CorV	Liberada para uso emergencial	78,1%	China	Vírus inativado		WANG et al., 2020; XIA et al., 2021
ZyCoV-D (Zydus Cadila)	Liberada para uso emergencial	66,6%	India	DNA		DEY et al., 2021; MOMIN et al., 2021
Medigen - Dynavax	Liberada para uso emergencial	Desconhecida	Taiwan	Subunidade de proteína		NG; LIU; MAHALINGAM,

						2020; CHAN et al., 2021
Abdala (Centro de Ingeniería Genética y Biotecnología (CIGB)	Liberada para uso emergencial	92.28%	Cuba	Subunidade de proteína		TAYLOR, 2021; HERNÁNDEZ et al., 2022 **NOTA:** Está sendo estudada a aplicação intramuscular e intranasal
Soberana 2 (**FINLAY-FR-2**)	Liberada para uso emergencial	62%	Cuba	Subunidade de proteína		REED, 2022
Soberana Plus (Instituto Finlay)	Liberada para uso emergencial	92% junto com a soberana 2.	Cuba	Subunidade de proteína		REED, 2022

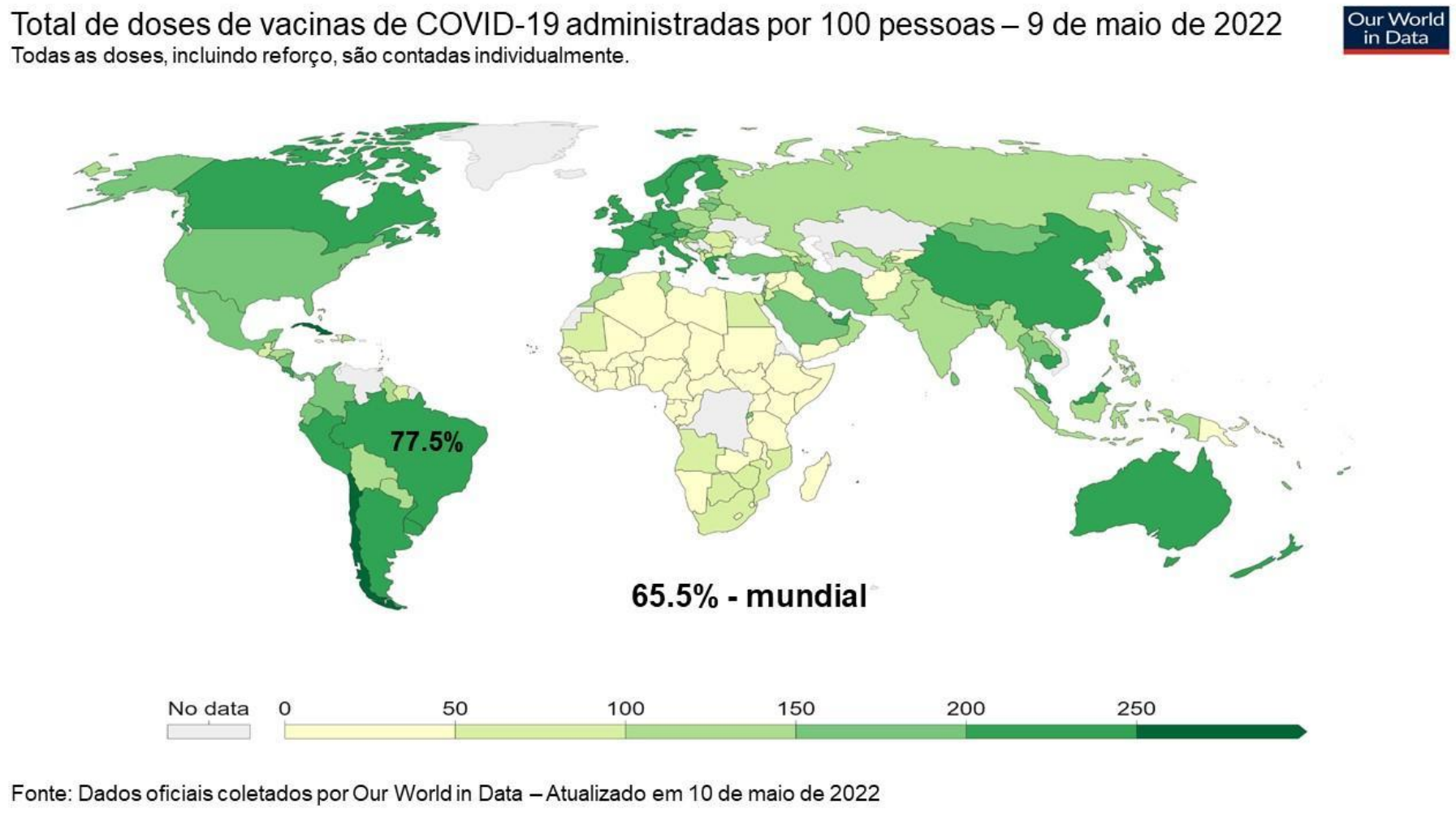

Figura 3. Representação mundial de doses aplicadas de vacinas contra COVID-19 atualizadas até o dia 10 de maio de 2022. Adaptado de Our World in Data, 2022 (Coronavírus COVID-19 Vaccinations - Our World in Data).

1.4 SARS-CoV-2

O SARS-CoV-2 faz parte do grupo dos Coronavírus (Família *Coronaviridae*, Subfamília *Orthocoronaviridae*), composto por vírus envelopados de fita única de RNA com polaridade positiva e estão relacionados a infecções do trato respiratório, em humanos (ZHOU et al., 2020). O nome Coronavírus se deve a sua estrutura em formato de halo ou coroa (Figura 4) (CÂNDIDO et al., 2020). A subfamília *Orthocoronaviridae* divide-se em quatro gêneros: *Alphacoronavírus* (α-CoV), *Betacoronavírus* (β-CoV), *Gammacoronavírus* (ɣ-CoV) e *Deltacoronavírus* (δ-CoV) (GORBALENYA et al., 2020). Dentre os coronavírus que acometem os humanos temos o *Human Coronavirus OC43* (HCoV-OC43 - β-CoV), *Human Coronavirus HKU1* (HCoV-HKU1 - β-CoV), *Human Coronavirus 229E* (HCoV-229E - α-CoV) e *Human Coroavirus NL63* (HCoV-NL63 - α-CoV), os quais causam sintomas leves a moderados; e os que causam sintomas potencialmente severos como *Severe Acute Respiratory Syndrome Coronavirus* (SARS-CoV - β-CoV), *Middle East Respiratory Syndrome Coronavirus* (MERS-CoV - β-CoV) e, mais recente, *Severe Acute Respiratory Syndrome Coronavirus 2* (SARS-CoV-2 - β-CoV) (ARAÚJO et al., 2020). SARS-CoV-2 tem 79% de identidade de sequência do genoma com o SARS-CoV e 50% de identidade de sequência de genoma com o MERS-CoV (LU et al., 2020). O SARS-CoV-2 tem um genoma de RNA de fita positiva de aproximadamente 30.000 bases (Figura 4) (V'KOVSKI et al., 2020). O diâmetro de cada partícula do vírus é de 80-120 nanômetros (Figura 4) (CHEN, et al., 2020). Sua estrutura genômica é compartilhada com outros β-coronavírus e possui seis janelas abertas de leitura (ORFs) que são organizadas em ordem de 5' a 3', respectivamente: replicase (ORF1a / ORF1b), spike (S), envelope (E), membrana (M) e nucleocapsídeo (N) (Figura 4). Além disso, sete ORFs putativas que codificam proteínas acessórias são intercaladas entre genes estruturais (CHAN et al., 2020). No total são geradas 26 proteínas virais através de processos de "splicing diferencial" e processamento da poliproteína viral. Entre os quatro genes estruturais (S, E, M e N), a identidade de aminoácidos entre SARS-CoV-2 e SARS-CoV excede 90%, exceto pela diferença de transcrição no gene S (LU et al., 2020; ZHOU et al., 2020). O gene da replicase ou RNA polimerase dependente de RNA (RDRP) cobre dois terços do genoma 5' e codifica uma grande poliproteína que é clivada proteoliticamente em 16 proteínas conhecidas como Nsp 1-16 (Figura 4). A maioria dessas proteínas não estruturais de SARS-CoV-2 tem mais de 85% de identidade de sequência de aminoácidos com SARS-CoV (CHAN et al., 2020).

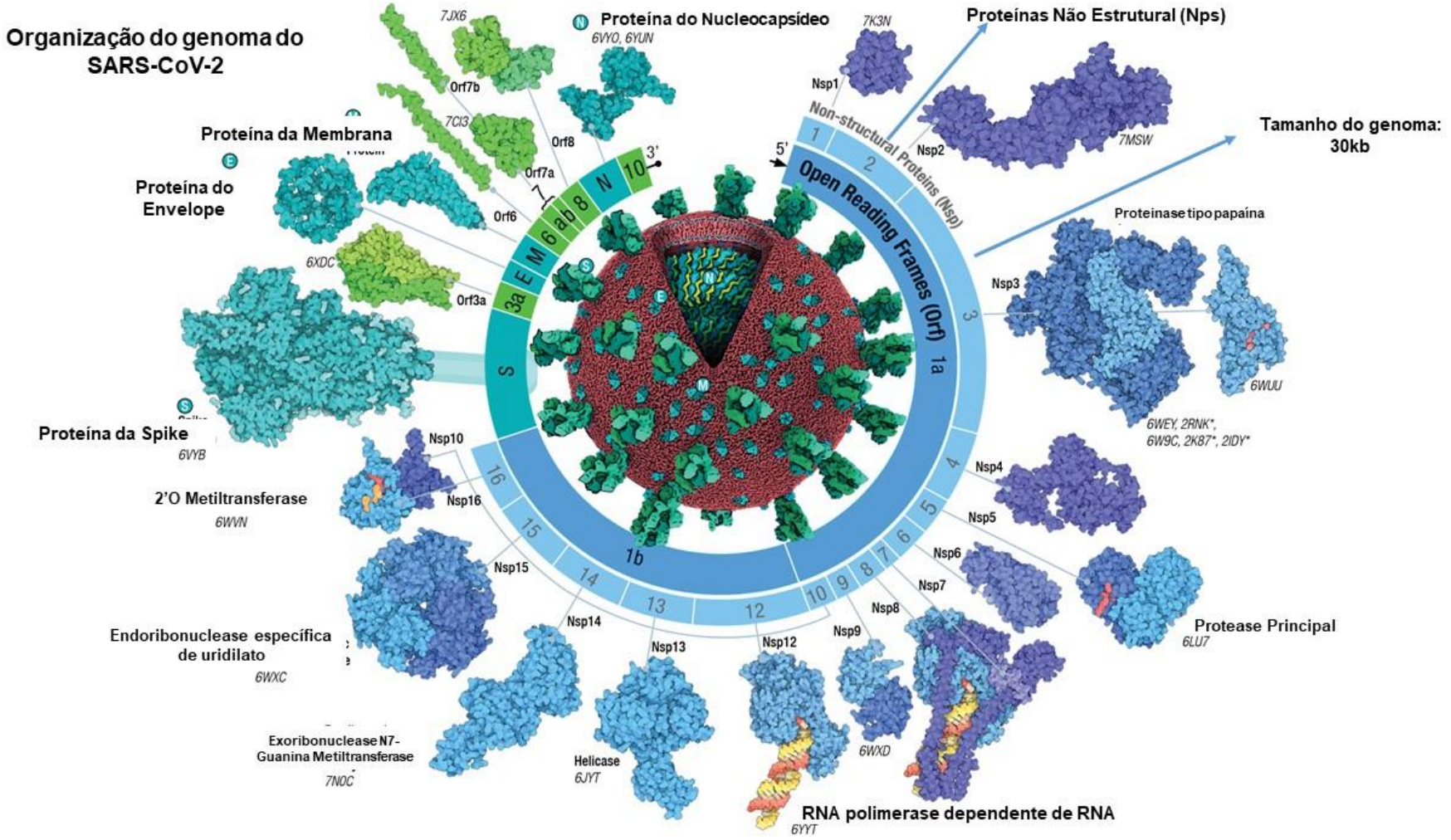

Figura 4. Representação esquemática da estrutura protéica e genoma do SARS-CoV-2. Esquema da estrutura proteica e organização genômica do SARS-CoV-2 mostrando a ordem dos genes virais e as proteínas codificadas. Adaptado de Galanopoulos et al., 2020.

No SARS-CoV-2, a proteína spike (S) é responsável pela interação do envelope viral com o receptor celular ACE2 e o processo de entrada do vírus (Figura 5). Logo após o surto de SARS-CoV em 2002-2003, o ACE2 foi identificado como um receptor funcional que permitia a infecção por este vírus (TANONAKA; MARUNOUCHI, 2003). A alta homologia genômica e estrutural (76% de identidade de aminoácidos) entre a proteína S de SARS-CoV e SARS-CoV-2 suportou a identificação de ACE2 como o receptor de superfície celular de SARS-CoV-2 (Figura 5) (ZHOU et al., 2020; LETKO; MARZI; MUNSTER, 2020; WALLS et al., 2020). O domínio de ligação ao receptor (RDB) da proteína spike é dividido em subunidades S1 e S2. O domínio S1 catalisa a ligação ao receptor celular ACE2 e a subunidade S2 é responsável pelo processo de fusão do envelope viral à membrana das células. Além da ligação ao receptor, a clivagem proteolítica da proteína S1 do coronavírus por proteases derivadas da célula hospedeira é essencial para permitir o processo de fusão entre o envelope viral e a membrana citoplasmática da célula (MATSUYAMA et al., 2010; GIERER et al., 2013). O SARS-CoV usa a serina protease de superfície celular (TMPRSS2 – Figura 5) para iniciação e entrada, embora as cisteína proteases endossômicas catepsina B (CatB) e catepsina L (CatL) também possam ajudar neste processo (OU et al., 2020). A afinidade da região RBD da proteína S de SARS-CoV-2 para ACE2 demonstrou ser semelhante à RBD de SARS-CoV ou ainda mais forte (WALLS et al., 2020; LAN et al., 2020; SHANG et al., 2020).

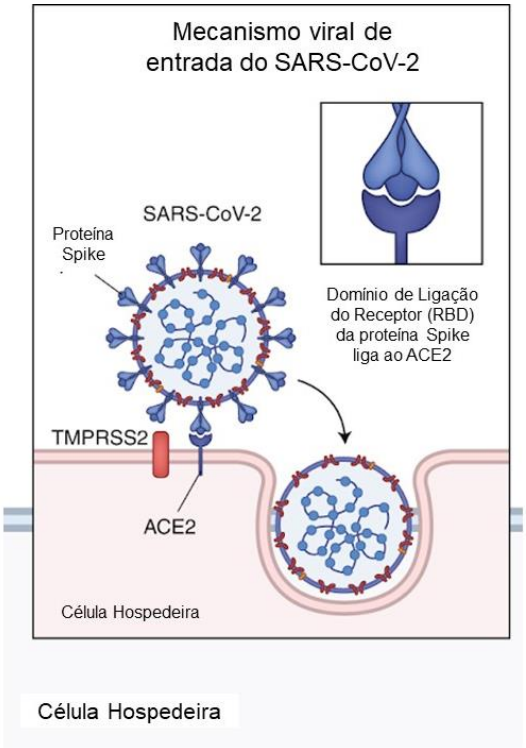

Figura 5. Representação do processo de entrada do SARS-CoV-2 na célula hospedeira através do sistema de receptores TMPRSS2 / ACE2. Após a S1 do RBD se ligar ao receptor ACE2, ocorre o

processo de proteólise dessa subunidade pela ação da TMPRSS2 e consequente entrada do vírus na célula pelo englobamento da partícula viral. Adaptado de Gupta et al., 2020.

As mutações são eventos naturais aleatórios no processo evolutivo dos vírus e desde a caracterização genômica inicial do SARS-CoV-2, esse vírus foi dividido em diferentes grupos genéticos ou clados (PAHO, 2021). Algumas mutações específicas definem os grupos genéticos virais (também chamados de linhagens). Essas linhagens estão circulando atualmente em todo o mundo e devido a vários processos de microevolução, geraram diferenças dentro de cada grupo genético pré-definidos. Estas diferenças podem gerar variantes virais dentro de cada linhagem ou clado gerando as variantes de SARS-CoV-2 (PAHO, 2021). A taxa média de mutação em vírus de RNA varia de 10^{-3} e 10^{-5} substituições de nucleotídeos por ano (HADFIELD et al., 2018). Apesar do SARS-CoV-2 possuir um dos maiores genomas entre vírus de RNA, foi descoberto que estes estão sofrendo mutações relativamente lenta em relação a outros vírus de RNA, apresentando taxa de aproximadamente $10^{-6}/10^{-7}$. (DE SOUZA et al., 2021; RANSKIN, 2021). Isso se deve ao fato deste vírus possuir uma enzima capaz de revisar e reparar mutações ao longo do genoma: RNA polimerase dependente de RNA (Rdrp) (RANSKIN, 2021). As mutações na proteína S do SARS-CoV-2, podem otimizar a ligação da partícula viral ao receptor celular ACE2 aumentando a entrada do vírus nas células e aumentar as taxas de transmissibilidade viral (LAURING; MALANI, 2021). Outras mutações podem fazer com que o SARS-CoV-2 seja menos responsivo aos tratamentos para COVID-19, ou até mesmo aos anticorpos neutralizantes estimulados pela vacina (LAURING; MALANI, 2021).

Desde dezembro de 2019, os primeiros genomas virais disponíveis foram obtidos a partir de pacientes de Wuhan e outras províncias da China sendo caracterizado como linhagem A (RAMBAUT et al., 2020). Com o avanço da pandemia em outros países e surgimento de novas mutações, a nova linhagem B foi identificada em países da Europa. O que diferencia ambas as linhagens é a ausência de dois nucleotídeos na linhagem B que estão presentes na linhagem A (posição 8782 na nsp4 da ORF1a e a posição 28144 na ORF8) (RAMBAUT et al., 2020). O tipo “B” evoluiu para outros tipos, incluindo B.1, que é o ancestral principal de variantes no mundo. Mais recentemente, a OMS criou uma nova classificação seguindo o alfabeto grego para as novas variantes Alfa, Beta, Gama e Delta identificadas em 2021 (RAMBAUT et al., 2020). Até 22 de março de 2021, mais de 845.000 sequências genômicas completas estavam disponíveis em bancos de dados acessíveis ao público como GISAID, Nextclade, entre outros (PAHO, 2021). Identificar mutações ou polimorfismos virais associados ao aumento nas taxas de transmissão, na virulência ou na diminuição da eficácia das

vacinas foi possível devido aos programas de vigilância genômica de SARS-CoV-2 implementados em diversos países, além do Brasil (PAHO, 2021).

Nos últimos meses da pandemia, variantes do vírus SARS-CoV-2 tem preocupado a comunidade científica devido à sua alta taxa de transmissão e associação com casos graves: Alfa, Beta, Gama, Delta e mais recente, Ômicron, inicialmente identificadas em pacientes infectados respectivamente no Reino Unido, na África do Sul, Manaus (Brasil), Índia e África do Sul, respectivamente (CDC, 2022; FARIA et al., 2021). Alguns dos países nas Américas relataram variantes como o Brasil, que relatou a variante Zeta (P.2), inicialmente descrita no Rio de Janeiro por Voloch et al (2021) em parceria com membros do nosso grupo de pesquisa e foi posteriormente associada ao aumento observado nas taxas de transmissão entre setembro de 2020 (0,7%) e fevereiro de 2021 (45%) (PAHO, 2021; WHO, 2021). Essa variante também foi relatada na Argentina, Chile, México, Sint Maarten, Uruguai e Venezuela (PAHO, 2021). A partir da contínua evolução do SARS-CoV-2 e características biológicas das variantes, estas são classificadas em Variantes de Preocupação (Variants of Concern – VOC's), Variantes de Interesse (Variants of Interest – VOI's) como mostrado na tabela 2 (CDC, 2022; WHO, 2022).

Tabela 2. Classificação das variantes do SARS-CoV-2 de acordo com Centro de Controle de Doenças - CDC (26 de abril de 2022).

CLASSIFICAÇÃO	CARACTERÍSTICAS	VARIANTES
Variante de Preocupação (Variant of Concern – VOC)	- Com alterações genéticas que são previstas ou conhecidas por afetarem as características do vírus, como transmissibilidade, gravidade da doença, escape imunológico, escape diagnóstico ou terapêutico; E - Identificado por causar transmissão comunitária significativa ou múltiplos aglomerados de COVID-19, em vários países com prevalência relativa crescente, juntamente com o aumento do número de casos ao longo do tempo, ou outros impactos epidemiológicos aparentes que sugerem um risco emergente para a saúde pública global.	Circulando atualmente: - Ômicron. Fora de circulação: - Alfa; - Beta; - Gama; - Delta;
Variante de Interesse (Variant of Interest – VOI)	- Aumento da transmissibilidade ou mudança prejudicial na epidemiologia do COVID-19, mas com transmissão limitada a regiões geográficas específicas ou países; OU - Aumento da virulência ou alteração na apresentação clínica da doença; OU - Diminuição da eficácia das medidas de saúde pública e sociais ou diagnósticos, vacinas, terapêuticas disponíveis.	Fora de circulação: - Epsilon; - Zeta; - Eta; - Theta; - Iota; - Kappa; - Lambda; - Mu.

A Figura 6 mostra as notificações das variantes de preocupação e interesse que ocorreram bem próximas, cronologicamente, bem com os países de origem: a Alfa em 14 de dezembro de 2020 (Reino Unido), a Beta em 18 de dezembro de 2020 (África do Sul); a Gama, descrita em novembro de 2020, no Brasil (Manaus - Amazonas) (FARIAS et al., 2021); a Delta foi descrita primeiramente na Índia, em outubro de 2020 e mais recentemente a Ômicron com primeiro caso relatado em novembro de 2021, na África (FLORES-VEJA et al., 2022). A variante Gama não está geneticamente relacionada às variantes SARS-CoV-2 Alfa (B.1.1.7) e Beta (B.1.351), porém, essa variante possui 12 mutações na proteína S, incluindo três mutações de interesse em comum com a B.1.351 (K417N/T, E484K e N501Y) que podem afetar a transmissibilidade e a resposta imune do hospedeiro (RIBAS et al., 2021). Foi demonstrado que mutações com a troca de aminoácido N501Y na região RBD da proteína S, possui 10X mais afinidade pelo receptor ACE2 que o aminoácido selvagem (LIU et al., 2021).

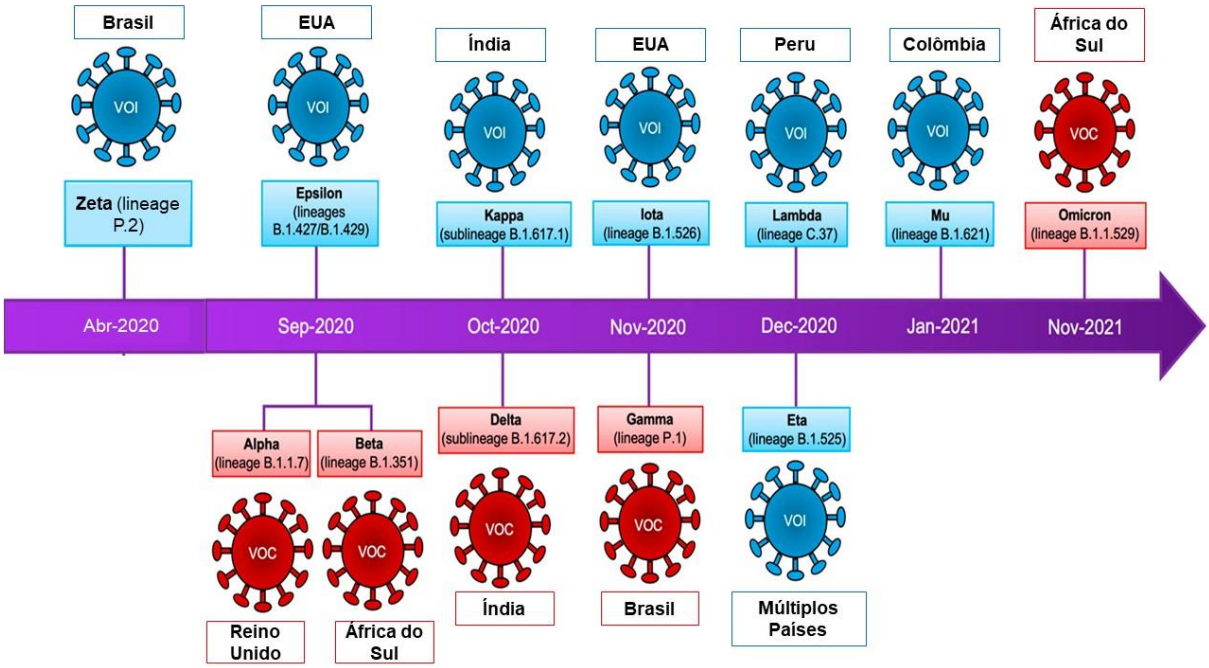

Figura 6. Descrição datada e com local de surgimento de variantes do SARS-CoV-2 ao longo do tempo. Adaptado de Flores-Vega et al., 2022.

1.5 Vigilância genômica

O sequenciamento do genoma total do vírus, traduzido na vigilância genômica viral, é de extrema importância no controle de epidemias com identificação e rastreamento de novas variantes virais. Além disso, a vigilância genômica viral é crucial para identificar padrões de transmissão viral através de modelos filogenéticos e filogeográficos na estimativa de introdução dos vírus e eventos de dispersão. A vigilância genômica viral, pode ser usada por órgãos de saúde pública no controle e prevenção da transmissão, além de identificar regiões críticas para

reforço de estruturas hospitalares e vacinação (CDC, 2021; WHO, 2021). Vigilância em epidemias virais podem ser feitas por meio da vigilância genômica, bem como pela detecção de sinais epidemiológicos e tendências inesperadas (WHO, 2021). Essas duas vertentes de evidência devem ser reunidas em tempo hábil para fornecer uma ampla compreensão da evolução viral e seu impacto potencial no controle de doenças, a fim de orientar a resposta da saúde pública (CDC, 2021).

1.5.1 Dinâmica das variantes no Brasil

No Brasil, a dinâmica das variantes de SARS-CoV-2 estão bem elucidadas: começando com a variante Beta, a qual tem relatos de casos em meio outubro de 2020 (SLAVOV et al., 2021); primeiro caso da variante Alfa foi em em dezembro de 2020, no estado de São Paulo (CLARO et al., 2020); a variante Zeta, em julho de 2020, no Rio de Janeiro (VOLOCH et al., 2021); a Gama apenas em dezembro de 2020, em Manaus (RIBAS et al., 2021); em junho de 2021 foi reportado a primeira transmissão comunitária da variante Delta no estado do Rio de Janeiro, Brasil (LAMARCA et al., 2021) e mais recente, a variante Ômicron, no fim de novembro de 2021 (ALCANTARA et al., 2022).

Estas variantes podem ser diferenciadas pelos seus perfis de mutações ao longo de todo seu genoma, onde as mais utilizadas são do gene S, como mostrado na Figura 7 (FLORES-VEJA et al., 2022). A variante Gama de SARS-CoV-2 foi descrita primeiramente em Manaus em dezembro de 2020 alcançando níveis de 91% entre as amostras positivas nos meses seguintes (RIBAS et al., 2021; FARIA et al., 2021). Identificada pela primeira vez em outubro de 2020, merece ser citada a linhagem brasileira Zeta (P.2), portadora da mutação E484K, pois já era a mais prevalente entre as linhagens sequenciadas de pacientes que desenvolveram sintomas em novembro no estado do Rio de Janeiro (VOLOCH et al., 2021). Foi verificado que desde o início da emergência das linhagens Gama (P.1) e Zeta (P.2), em outubro de 2020, em apenas 4 meses estas linhagens correspondiam juntas por 75% de todas as linhagens sequenciadas em todo o Brasil, a partir de dados analisando da Rede Genômica Fiocruz, que reúne pesquisadores de diversos institutos da Fundação Oswaldo Cruz (RIBAS et al., 2021). Na cidade de Manaus estas duas linhagens juntas corresponderam a 97,8% das amostras de vírus sequenciados em janeiro de 2021 (RIBAS et al., 2021; VOLOCH et al., 2021).

Como descrito anteriormente, a região Sudeste está sendo foco de maior incidência em número de casos de COVID-19, bem como a maior taxa de óbitos de todas as regiões do Brasil. Dentre os estados que fazem parte desta região, temos o estado de Minas Gerais com a segunda

colocação em número de casos e terceira em número de óbitos (11.697.906 e 317.540, respectivamente). Apesar de diversos estudos genômicos de COVID-19 terem sido conduzidos na região, um estudo populacional com cobertura estadual ainda não foi realizado. Nesse projeto visamos avaliar as linhagens de SARS-CoV-2 circulantes nas diversas unidades regionais que compõem o nosso estado de Minas Gerais através da implementação de uma nova estratégia capaz de identificar as variantes de SARS-CoV-2 de uma maneira rápida e com menores custos. Essa nova metodologia associada ao sequenciamento do genoma viral irá nos permitir o processamento de um número maior de amostras necessárias em um estado tão complexo como Minas Gerais, com cerca de 853 municípios e posição estratégica no território nacional, fazendo limite com diversos estados brasileiros de outras regiões.

Então, devido ao cenário epidemiológico que o Brasil se encontrava onde temos aumento no número de casos e mortes. Isso deve-se ao aumento dispersão da então nova variante (Gama - P.1) descrita em Manaus em novembro de 2020 e a notificação da introdução da mesma no estado de Minas Gerais. Devido a este fato, houve a necessidade de uma estratégia para montar um processo de vigilância genômica no estado com intuito de monitorar o perfil de variantes circulantes no período de março a abril de 2021. Pensando nesse cenário, foi desenvolvido e utilizado uma metodologia de genotipagem de variantes do SARS-CoV-2 que fossem mais rápidas e baratas que o sequenciamento de genoma completo e que pudesse ter uma cobertura estadual, além de regiões de fronteiras com estado. Este foi um projeto piloto, mais tarde nomeado de Observatório de Vigilância Genômica (OviGen), em parceria com Secretaria de Estado da Saúde, Fundação Ezequiel Dias (FUNED), Núcleo de Ações e Pesquisas em Apoio Diagnóstico da Universidade Federal de Minas Gerais (NUPAD/UFMG). Este projeto encontra-se operante até os dias atuais.

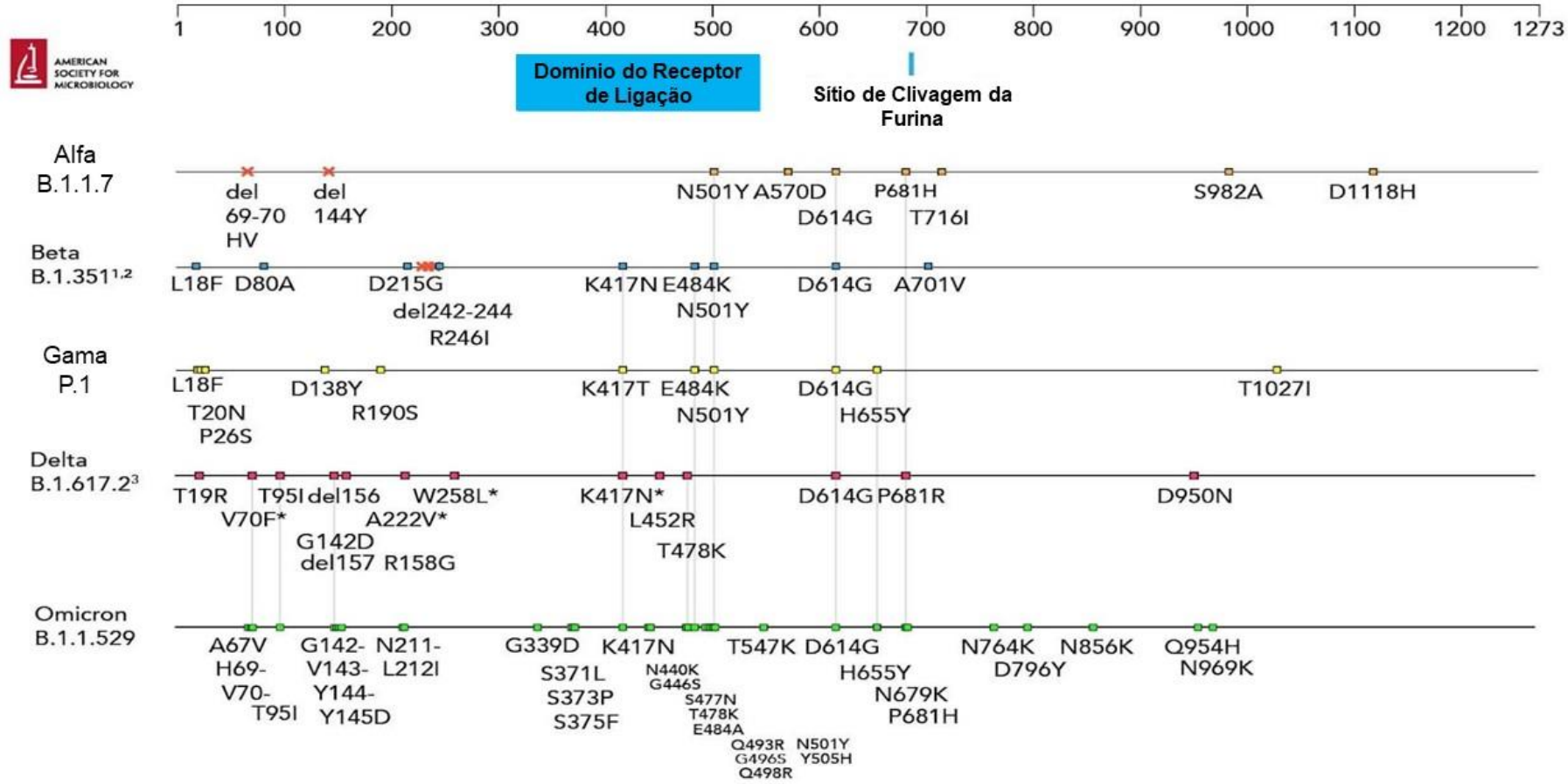

Figura 7. Comparativo de variantes de preocupação, mostrando pontos de deleções ou trocas de aminoácidos ao longo do gene spike (S) de SARS-CoV-2. Adaptado de Hagen, 2021.

2. OBJETIVOS

2.1 Objetivo Geral

Identificar e avaliar a frequência de variantes do SARS-CoV-2 no estado de Minas Gerais durante os meses de março a abril de 2021, período de aumento no número de casos e mortes por COVID-19.

2.2 Objetivos Específicos

- Desenvolver novas metodologias rápidas e de baixo custo para identificar as diferentes variantes do SARS-CoV-2;

- Verificar a ocorrência e distribuição de variantes do SARS-CoV-2 nas 28 unidades regionais do estado de Minas Gerais;

- Identificar possíveis novas variantes do SARS-CoV-2 por sequenciamento completo do genoma;

- Estimar datas de introdução, locais de entrada e dispersão das variantes de SARS-CoV-2 no estado de MG através de modelos filogenéticos e filogeográficos;

- Avaliar o impacto da introdução das variantes do SARS-CoV-2 nas taxas de transmissibilidade, aumento dos casos e severidade de COVID-19 através da integração entre metadados genômicos e epidemiológicos.

CAPÍTULO I

Neste primeiro capítulo, apresentamos o artigo intitulado "*Rapid and lowcost identification of SARS-CoV-2 variants through RT-qPCR genotyping*" submetido para a revista Current Protocols in Molecular Biology na data 25 de abril de 2022, onde desenvolvemos uma metodologia rápida, de baixo custo e com capacidade de identificação das variantes de SARS-CoV-2 em larga escala através da genotipagem por RT-PCR das principais mutações no gene spike definidoras das VOCs e VOIs circulantes no Brasil. Para isso iniciadores e sondas de genotipagem foram desenhados para as mutações K417T, E484K e N501Y do gene spike do SARS-CoV-2 capaz de definir as principais linhagens como Alfa, Gama e Zeta utilizando o sistema aberto de RT-PCR rhAmp (Integrated DNA Technologies – IDT). Para acelerar o processo de identificação de variantes de SARS-CoV-2 esse trabalho foi também publicado no biorrepositório de protocolos (https://dx.doi.org/10.17504/protocols.io.buf2ntqe) que tem sido usado por diferentes pesquisadores no mundo. No artigo submetido apresentamos a introdução com a justificativa de implementação do protocolo, assim como os materiais e métodos disponíveis incluindo as sequências de iniciadores, além dos resultados confirmados pelo sequenciamento do genoma completo. A sensibilidade do método foi avaliada a partir de misturas artificiais das diferentes linhagens de SARS-CoV-2 para validação da estratégia molecular.

RAPID AND LOWCOST IDENTIFICATION OF SARS-CoV-2 VARIANTS THROUGH RT-qPCR GENOTYPING

Victor Emmanuel Viana Geddes[1], Filipe Romero Rebello Moreira[3], Diego Menezes Bonfim[1], **Hugo José Alves[1]**, João Locke Ferreira de Araújo[1], Daniel Costa Queiroz[1], Rafael Marques de Souza[1], Rennan Garcias Moreira[4], Camila Zolini de Sá[2], Danielle Alves Gomes Zauli[4], Joice do Prado Silva[5], Aline Brito de Lima[5], Frederico Scott Varella Malta[5], Alessandro Clayton de Souza Ferreira[5], Victor Cavalcanti Pardini[5], Amilcar Tanuri[3], Renan Pedra Souza[1*] and Renato Santana Aguiar[1,5,6*].

[1] Laboratório de Biologia Integrativa, Departamento de Genética, Ecologia e Evolução, Instituto de Ciências Biológicas, Universidade Federal de Minas Gerais, Belo Horizonte, Brazil.

[2] Laboratório de Diversidade Genética Humana, Departamento de Genética, Ecologia e Evolução, Instituto de Ciências Biológicas, Universidade Federal de Minas Gerais, Belo Horizonte, Brazil.

[3] Departamento de Genética, Instituto de Biologia, Universidade Federal do Rio de Janeiro, Rio de Janeiro, Brazil.

[4] Centro de Laboratórios Multiusuários, Instituto de Ciências Biológicas, Universidade Federal de Minas Gerais, Belo Horizonte, Brazil.

[5] Instituto Hermes Pardini, Belo Horizonte, Brazil

[6] Instituto D'Or de Pesquisa e Ensino (IDOR), Rio de Janeiro, Brazil.

Keywords: SARS-CoV-2, variants, genotyping

Running title: GENOTYPING OF SARS-CoV-2 VARIANTS.

***Corresponding author:** Renato Santana Aguiar (santanarnt@ufmg.br) and Renan Pedra Souza (renanpedra@gmail.com).

Corresponding address: Renato S. Aguiar, Laboratório de Biologia Integrativa, G3-60. Instituto de Ciências Biológicas, UFMG. Av. Antônio Carlos 6627 Pampulha. 31270901 - Belo Horizonte, MG – Brasil.

Abstract

Brazil was largely affected by SARS-CoV-2 pandemic, both in number of cases and deaths reported. Furthermore, the appearance of new variants brought more concern to this scenario. We present here a fast, low cost genotyping method to identify Alpha, Gamma and Zeta, the three major variants currently circulating in Brazil, through RT-qPCR. This methodology uses allele-specific primers based on rhAmp technology for the Spike mutations K417T, E484K and N501Y to classify variants and can be implemented in any SARS-Cov-2 molecular diagnosis laboratory, taking up to 5 h from sample processing to variant identification. This methodology is suitable for epidemiological and viral surveillance studies, being faster and cheaper than deep-sequencing. However, as a limitation, the variant classification depends on the panel of primers used and the identification of new variants keep relying only on deep-sequencing methodologies. Besides, samples with low viral load (CT > 30) can be difficult to assess. The results expected are displayed as a cartesian allelic dot plot and can be easily interpreted using a logical key based on the combination of mutations found for the different Spike mutation sites.

Introduction

Brazil was one of the most affected countries during the SARS-CoV-2 pandemic, with more than 18 million cases and more than 500.000 deaths reported. Together with the increasing rate of cases, the emergence of new variants possessing mutations that affect immunogenicity and transmissibility (1-4) poses a concerning burden in the healthcare system.

In Brazil, three such lineages are currently circulating: Gamma (previously known as P.1), a lineage firstly described in Manaus (5), Zeta (previously known as P.2), firstly described in Rio de Janeiro (6), both already reported in other cities in the country (7), and Alpha (previously known as B.1.1.7), a lineage initially identified in England and recently associated to increasing mortality rates (8, 9, 10). In this scenario, it urges the necessity of a rapid assessment methodology for identification of variants that could contribute to a better

epidemiological surveillance and public healthcare administration decisions in dealing with the pandemic.

Although deep-sequencing is the only way to identify new variants and mutations, it is an expensive and time-consuming technique (11). Here, we describe a PCR genotyping approach to correctly assess the circulating emergent variants, Alpha, Gamma and Zeta in Brazil. Genotyping is a quicker methodology requiring only a real time PCR machine available in most of laboratories performing SARS-CoV-2 molecular diagnosis. We designed a pair of forward primers attached to the FAM or VIC dyes (Table 1) for each mutation site (i.e., K417T, E484K and N502Y); the primers for the wild-type (WT) allele are attached to the FAM dye and the primers for the mutant (Mut) alleles to the VIC dye. A reverse primer that does not discriminate the mutation is used for each specific site assessed.

Table 1. Oligonucleotides used in this study

Target	Sequence	Application
K417T	Forward 5' - /rhAmp-F/TCCAGGGCAAACTGGAAArGATTG/GT3/ (FAM) Forward 5' - /rhAmp-Y/CCAGGGCAAACTGGAACrGATTG/GT3/ (VIC) Reverse 5' - GCAGCTATAACGCAGCCTGTAAAATrCATCT/GT2/	rhAmp
E484K	Forward 5' - /rhAmp-F/TGTAAAGGAAAGTAACAATTAAAACCTTCrAACAC/GT3/ (FAM) Forward 5' - /rhAmp-Y/TGTAAAGGAAAGTAACAATTAAAACCTTTrAACAC/GT3/ (VIC) Reverse 5' - GCCCTGTATAGATTGTTTAGGAAGTCTAATrCTC AA/GT4/	rhAmp
N501Y	Forward 5' - /rhAmp-F/TCATATGGTTTCCAACCCACTArATGGT/GT2/ (FAM) Forward 5' - /rhAmp-Y/CATATGGTTTCCAACCCACTTrATGGT/GT2/ (VIC) Reverse 5' - GCGGTGCATGTAGAAGTTCAAAAGAArAGTAC/GT1/	rhAmp
N1	Forward 5' - GACCCCAAAATCAGCGAAAT Reverse 5' - TCTGGTTACTGCCAGTTGAATCTG Probe 5' – ACCCCGCATTACGTTTGGTGGACC (FAM)	RT-qPCR
N2	Forward 5' - TTACAAACATTGGCCGCAAA Reverse 5' - GCGCGACATTCCGAAGAA Probe 5' – ACAATTTGCCCCCAGCGCTTCAG (VIC)	RT-qPCR
RNaseP	Forward 5' - AGATTTGGACCTGCGAGCG Reverse 5' - GAGCGGCTGTCTCCACAAGT Probe 5' – TTCTGACCTGAAGGCTCTGCGCG (Cy5)	RT-qPCR

The SARS-CoV-2 swab samples can be extracted by any RNA extraction commercial kit available. The cDNA synthesis can also be performed by any retrotranscriptase kit available. As this protocol uses rhAmp technology (IDT Technologies) that depends of active RNAse H, cDNA synthesis must be performed separately, resulting in a longer protocol compared to one-step-based technologies. We recommend to run a RT-qPCR beforehand to assess the Cycle

Threshold (CT), as sample with low viral load (CT > 30) may not be genotyped. Using a logical key of the combination of the mutations found, the variant call can be simply done without further training. Nonetheless, samples that eventually does not fit in the classification provided should be sequenced as they could represent new variants. Although other protocols have been described (12, 13, 14), the genotyping strategy presented here is the first one to discriminate the variants of concern and interest (Alpha, Gamma, Zeta) using an open access technology that allow laboratories elsewhere to order primers and identify variants.

Material and Methods

The protocol described in this peer-reviewed article is published on protocols.io, https://dx.doi.org/10.17504/protocols.io.buf2ntqe and is included for printing as supporting information file 1 with this article.

Expected Results

We genotyped 81 SARS-CoV-2 positive samples and 10 negative samples (negative controls) comprehending 11 different states in Brazil: Amazonas, Bahia, Distrito Federal, Goiás, Espírito Santo, Minas Gerais, Mato Grosso, Paraná, Rio de Janeiro, Rio Grande do Sul and São Paulo. Samples were obtained through nasopharyngeal swabs from patients from Clementino Fraga Filho University Hospital, Rio de Janeiro (M3, M6 and M7, patients from Manaus hospitalized in Rio de Janeiro) and from Hermes Pardini Institute, a large diagnostic company widespread throughout the country with approval of ethical committee (4.165.442). Samples had CT ranging 12-31 and were collected between 11/06/2020 and 03/27/2021. The RNA extraction was performed using *Quick*-RNA Viral Kit (Zymo Research) according to manufacturer's instructions. The presence of SARS-CoV-2 was confirmed using primers from CDC (Centers for Disease Control and Prevention) for the N (nucleocapsid) gene (Table 1) and Luna® Universal Probe One-Step RT-qPCR Kit (New England Biolabs) in the ABI 7500

(Applied Biosystems) thermocycler. A typical expected genotyping result in a CFX Opus 96 platform using this protocol is depicted in Fig 1.

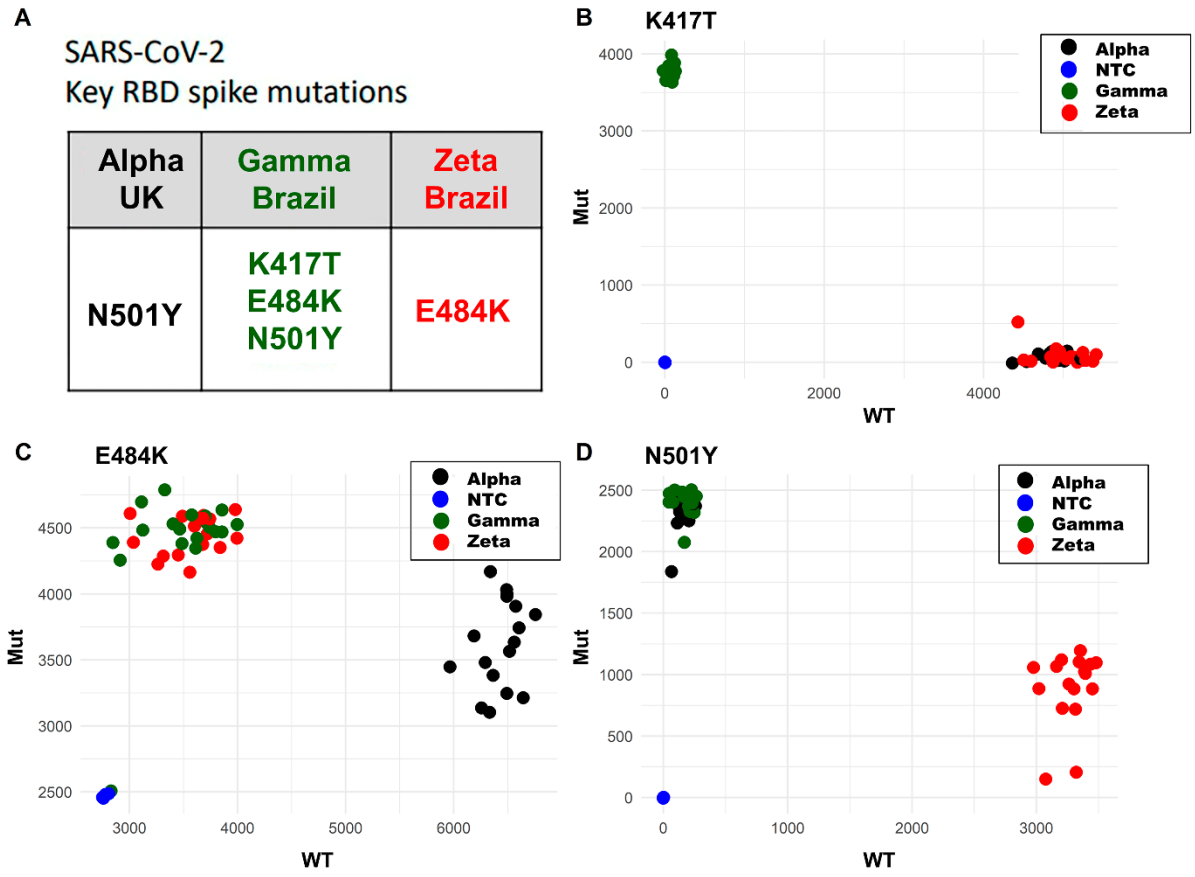

Figure 1. Allelic discrimination plots for mutations K417T, E484K and N501Y. (**A**) Summary of the distribution of the three mutation in the lineages Alpha, Gamma and Zeta. Allelic discrimination plot for K417T (**B**), E484K (**C**) and N501Y (**D**) mutations. Blue dots represent negative controls (NTC), black, green and red dots represent variant Alpha, Gamma and Zeta, respectively. X-axis and Y-axis are displayed in arbitrary Relative Fluorescent Units (RFUs) for FAM and HEX/VIC channels, respectively. WT – wild type; Mut – mutated.

Each dot represents one sample: samples with WT allele migrate along the x-axis, and samples with the Mut allele, along y-axis. Using the logical key in Fig 1 A, the resulting clusters from the allelic dot plot can be used to classify the variants: for example, the Alpha variant presents a mutation only in the position 501 of the aminoacidic chain (N□ Y), therefore, samples that are WT for K417T (Fig 1 B) and for E848K (Fig 1 C), but are mutants for N501Y (Fig 1 D) are classified as Alpha variants (black dots). The same remains true for the other

variants, as Zeta are mutated only in E484K (red dots) and Gamma variants are mutated in all three sites (green dots).

Moreover, this methodology has enough sensitivity to detect sub-represented viral populations as low as 10% of total viral RNA (Fig 2). We quantified the viral RNA using a standard curve and mixed artificially the RNAs from 2 variants at the proportions 10%:90%, 50%:50% and 90%:10%. The multicomponent curves demonstrate that even as 10% of the population, both WT (Fig 2 A-C) and Mut (Fig 2 D-F) alleles can be detected by this method.

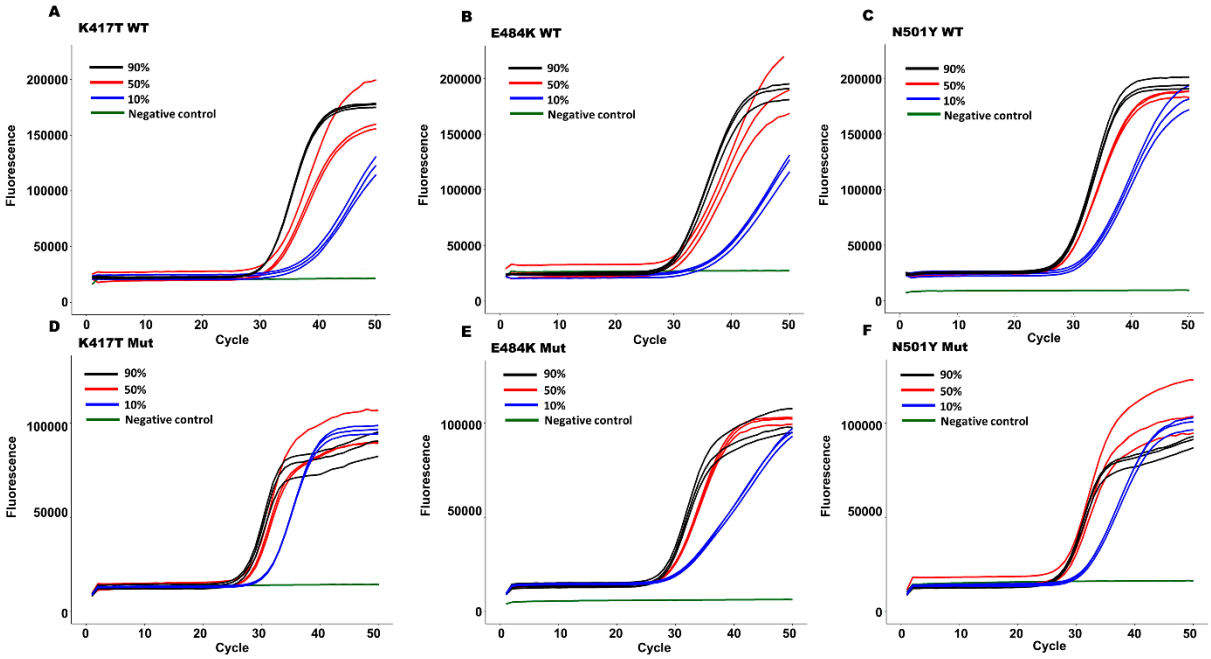

Figure 2. Multicomponent curves of mixtures for mutations K417T, E484K and N501Y. Curves of WT alleles for K417T (**A**), E484K (**B**) and N501Y (**C**), and mutant alleles for K417T (**D**), E484K(**E**) and N501Y(**F**) in artificially mixed populations. Black lines represent a 90% composition of the mixture for the WT (**A-C**) or mutant **(D-F**) allele. Red and blue represent a 50% and 10% composition of the population, respectively. Green lines represent negative controls. The viral concentration at each dilution point was 1.6 x 10^6 (10%), 8 x 10^6 (50%) and 1.44 x 10^7 (90%) viral RNA copies. Y-axis are displayed in arbitrary Relative Fluorescent Units (RFUs) and x-axis represents the cycle of threshold. Samples SEQ46 (Gamma), SEQ56 (Zeta) and SEQ29 (Alpha) were used as variants representatives: for K417T discrimination a mixture between SEQ46 and SEQ29 was done and for E484K and N501Y two mixtures between SEQ56 and SEQ29 were done. WT – wild type; Mut – mutant.

Furthermore, we confirmed the variants genotypes using deep-sequencing with QIAseq® SARS-CoV-2 Primer Panel and QIAseq FX DNA Library kits (Qiagen) on the MiSeq platform (Illumina). All consensus genome sequences were screened with PANGOLIN

software (https://github.com/cov-lineages/pangolin), which confirmed all samples belonged to either variants Alpha, Gamma or Zeta, with only two exceptions: samples BH30 and BH35, which were WT for all three genotyped sites and were classified as B.1.1.28 variant by the sequencing, corroborating the absence of mutations on those sites. The sample data used here are summarized in Table 2.

Table 2. Summary of samples used in this study

Sample	City	State	Date	rhAmp Genotype	Sequencing Genotype	RT-qPCR CTs
						N
M3	Manaus	AM	02/03/2021	Gamma	Gamma	17
M6	Manaus	AM	02/03/2021	Gamma	Gamma	15
M7	Manaus	AM	02/03/2021	Gamma	Gamma	16
SEQ46	Campos dos Goytazes	RJ	12/17/2020	Gamma	Gamma	17
SEQ51	Belo Horizonte	MG	11/06/2020	Zeta	Zeta	19
SEQ52	Belo Horizonte	MG	11/06/2020	Zeta	Zeta	25
SEQ54	Belo Horizonte	MG	01/19/2021	Zeta	Zeta	25
SEQ55	Belo Horizonte	MG	01/22/2021	Zeta	Zeta	27
SEQ56	Belo Horizonte	MG	01/25/2021	Zeta	Zeta	18
SEQ57	Belo Horizonte	MG	01/27/2021	Zeta	Zeta	18
SEQ58	Belo Horizonte	MG	01/28/2021	Zeta	Zeta	22
SEQ1	Belo Horizonte	MG	01/12/2021	Alpha	Alpha	20
SEQ2	Belo Horizonte	MG	01/13/2021	Alpha	Alpha	23
SEQ11	Belo Horizonte	MG	01/07/2021	Alpha	Alpha	26
SEQ25	Cuiabá	MT	01/24/2021	Alpha	Alpha	17
SEQ28	Belo Horizonte	MG	01/09/2021	Alpha	Alpha	23
SEQ29	Belo Horizonte	MG	01/09/2021	Alpha	Alpha	16
SEQ48	Barbacena	MG	01/15/2021	Alpha	Alpha	26
AM01	Belo Horizonte	MG	01/12/2021	Alpha	Alpha	15
AM02	Belo Horizonte	MG	01/13/2021	Alpha	Alpha	19
AM03	Belo Horizonte	MG	01/14/2021	Alpha	Alpha	13
AM04	Valinhos	SP	01/12/2021	Alpha	Alpha	23
AM07	Araxá	MG	01/04/2021	Alpha	Alpha	12

AM09	Belo Horizonte	MG	01/08/2021	Alpha	Alpha	21
AM10	Curitiba	PR	01/07/2021	Alpha	Alpha	16
AM11	Belo Horizonte	MG	01/07/2021	Alpha	Alpha	21
AM18	Belo Horizonte	MG	01/09/2021	Alpha	Alpha	18
AM19	Belo Horizonte	MG	01/09/2021	Alpha	Alpha	14
AM23	Rio de Janeiro	RJ	01/11/2021	Alpha	Alpha	19
AM24	Americana	SP	01/08/2021	Alpha	Alpha	20
AM25	Aracaju	SE	01/08/2021	Alpha	Alpha	16
AM26	Campos dos Goytacazes	RJ	01/11/2021	Alpha	Alpha	18
AM28	São Sebastião do Passe	BA	01/18/2021	Alpha	Alpha	20
AM29	Primavera do Leste	MT	01/14/2021	Alpha	Alpha	22
AM30	Porto Alegre	RS	01/18/2021	Undetermined	B.1.1.28	31
AM31	Betim	MG	01/21/2021	Alpha	Alpha	18
AM34	Barra de São Francisco	ES	01/12/2021	Alpha	Alpha	12
AM36	Manaus	AM	01/11/2021	Gamma	Gamma	14
AM38	Barbacena	MG	01/15/2021	Alpha	Alpha	23
BH2	Belo Horizonte	MG	02/26/2021	Zeta	Zeta	12
BH7	Belo Horizonte	MG	02/27/2021	Gamma	Gamma	14
BH8	Belo Horizonte	MG	02/27/2021	Gamma	Gamma	22
BH10	Belo Horizonte	MG	02/27/2021	Zeta	Zeta	19
BH11	Belo Horizonte	MG	02/27/2021	Gamma	Gamma	19
BH12	Belo Horizonte	MG	02/27/2021	Zeta	Zeta	14
BH13	Belo Horizonte	MG	02/27/2021	Zeta	Zeta	16
BH15	Belo Horizonte	MG	02/27/2021	Zeta	Zeta	16
BH16	Belo Horizonte	MG	02/27/2021	Gamma	Gamma	28
BH17	Belo Horizonte	MG	02/27/2021	Gamma	Gamma	16
BH20	Belo Horizonte	MG	02/27/2021	Zeta	Zeta	16
BH21	Belo Horizonte	MG	02/27/2021	Zeta	Zeta	12
BH22	Belo Horizonte	MG	02/27/2021	Zeta	Zeta	17
BH23	Belo Horizonte	MG	02/27/2021	Gamma	Gamma	13

BH24	Belo Horizonte	MG	02/27/2021	Zeta	Zeta	17
BH25	Belo Horizonte	MG	02/27/2021	Zeta	Zeta	20
BH26	Belo Horizonte	MG	02/27/2021	Zeta	Zeta	29
BH27	Belo Horizonte	MG	02/27/2021	Zeta	Zeta	15
BH28	Belo Horizonte	MG	02/27/2021	Zeta	Zeta	27
BH30	Belo Horizonte	MG	02/27/2021	Undetermined	B.1.1.28	20
BH31	Belo Horizonte	MG	02/27/2021	Gamma	Gamma	17
BH32	Contagem	MG	02/27/2021	Zeta	Zeta	12
BH33	Belo Horizonte	MG	02/26/2021	Zeta	Zeta	18
BH34	Belo Horizonte	MG	02/27/2021	Gamma	Gamma	15
BH35	Belo Horizonte	MG	02/27/2021	Undetermined	B.1.1.28	30
BH36	Belo Horizonte	MG	02/27/2021	Zeta	Zeta	15
BH39	Belo Horizonte	MG	03/03/2021	Alpha	Alpha	12
BH40	Belo Horizonte	MG	03/03/2021	Zeta	Zeta	16
BH41	Belo Horizonte	MG	03/03/2021	Gamma	Gamma	13
BH42	Belo Horizonte	MG	03/02/2021	Gamma	Gamma	17
BH43	Belo Horizonte	MG	03/03/2021	Gamma	Gamma	15
BH47	Belo Horizonte	MG	03/03/2021	Zeta	Zeta	15
BH49	Belo Horizonte	MG	03/03/2021	Alpha	Alpha	14
BH54	Belo Horizonte	MG	03/02/2021	Gamma	Gamma	16
BH55	Belo Horizonte	MG	03/03/2021	Gamma	Gamma	14
BH57	Belo Horizonte	MG	03/03/2021	Gamma	Gamma	17
BH58	Belo Horizonte	MG	03/02/2021	Gamma	Gamma	16
BH59	Belo Horizonte	MG	03/02/2021	Gamma	Gamma	15
BH60	Belo Horizonte	MG	03/01/2021	Gamma	Gamma	15
BH61	Belo Horizonte	MG	03/03/2021	Gamma	Gamma	17
BH62	Belo Horizonte	MG	03/03/2021	Gamma	Gamma	16
BH63	Belo Horizonte	MG	03/03/2021	Zeta	Zeta	15
55-2910266	Brasilia	DF	03/26/2021	NC	NC	NA
56-9685480	Brasilia	DF	03/27/2021	NC	NC	NA
56-9680768	Brasilia	DF	03/26/2021	NC	NC	NA

58-2379598	São Jose dos Campos	SP	03/27/2021	NC	NC	NA
56-9681179	Brasilia	DF	03/26/2021	NC	NC	NA
56-9682218	Brasilia	DF	03/26/2021	NC	NC	NA
52-1893914	Morrinhos	GO	03/27/2021	NC	NC	NA
159-5019414	Morrinhos	GO	03/27/2021	NC	NC	NA
52-1893928	Morrinhos	GO	03/27/2021	NC	NC	NA
159-5019418	Morrinhos	GO	03/27/2021	NC	NC	NA

NC – negative control, NA – not appliable, AM – Amazonas, BA – Bahia, DF – Distrito Federal, ES – Espírito Santo, GO – Goiás, MG – Minas Gerais, MT – Mato Grosso, PR – Paraná, RJ – Rio de Janeiro, RS – Rio Grande d Sul, SE – Sergige, SP – São Paulo.

Supporting Information

S1: Step-by-step protocol, also available on protocols.io.

Acknowledgements

We acknowledge support from the Rede Corona-ômica BR MCTI/FINEP affiliated to RedeVírus/MCTI (FINEP 01.20.0029.000462/20, CNPq 404096/2020-4). This project was also supported by CNPq (R.S.A.: 312688/2017-2 and 439119/2018-9; R.P.S.: 310627/2018-4), MEC/CAPES (14/2020 - 23072.211119/2020-10), FINEP (0494/20 01.20.0026.00), FAPEMIG (R.P.S.: APQ-00475-20) and FAPERJ (C.M.V.: 26/010.002278/2019) and by CADDE/FAPESP (MR/S0195/1 and FAPESP 18/14389-0) (N.R.F.).

Authors' contribution

Conceptualization, R.P.S. and R.S.A.; Methodology, V.E.V.G., F.R.R.M., D.M.B., H.J.A., J.L.F.A., D.C.Q., R.M.S., R.G.M., J.P.S.; Validation, V.E.V.G., F.R.R.M., D.M.B., H.J.A., J.L.F.A., D.C.Q., R.M.S., R.G.M., J.P.S. ; Resources, C.Z.S., D.A.G.Z., A.B.L., F.S.V.M., A.C.S.F., V.C.P., A.T., R.P.S. and R.S.A.; Writing – Original Draft, V.E.V.G., R.P.S. and R.S.A.; Writing – Review & Editing, V.E.V.G, R.P.S. and R.S.A.; Visualization, R.P.S. and R.S.A.; Supervision, R.P.S. and R.S.A.; Project Administration, R.P.S. and R.S.A.; Funding Acquisition, R.P.S. and R.S.A..

References

1. Greaney, A.J., Loes, A.N., Crawford, K.H.D., Starr, T.N., Malone, K.D., Chu, H.Y., and Bloom, J.D. (2021). Comprehensive mapping of mutations to the SARS-CoV-2 receptor-binding domain that affect recognition by polyclonal human serum antibodies. BioRxiv 2020.12.31.425021.
2. Starr, T.N., Greaney, A.J., Hilton, S.K., Ellis, D., Crawford, K.H.D., Dingens, A.S., Navarro, M.J., Bowen, J.E., Tortorici, M.A., Walls, A.C., et al. (2020). Deep Mutational Scanning of SARS-CoV-2 Receptor Binding Domain Reveals Constraints on Folding and ACE2 Binding. Cell 182, 1295-1310.e20.
3. Wang, Z., Schmidt, F., Weisblum, Y., Muecksch, F., Barnes, C.O., Finkin, S., Schaefer-Babajew, D., Cipolla, M., Gaebler, C., Lieberman, J.A., et al. (2021). mRNA vaccine-elicited antibodies to SARS-CoV-2 and circulating variants. BioRxiv 2021.01.15.426911.
4. Weisblum, Y., Schmidt, F., Zhang, F., DaSilva, J., Poston, D., Lorenzi, J.C.C., Muecksch, F., Rutkowska, M., Hoffmann, H.-H., Michailidis, E., et al. (2020). Escape from neutralizing antibodies by SARS-CoV-2 spike protein variants. Elife 9, e61312.
5. Faria, N.R., Mellan, T.A., Whittaker, C., Claro, I.M., Candido, D. da S., Mishra, S., Crispim, M.A.E., Sales, F.C., Hawryluk, I., McCrone, J.T., et al. (2021). Genomics and epidemiology of a novel SARS-CoV-2 lineage in Manaus, Brazil. MedRxiv 2021.02.26.21252554.
6. Voloch, C.M., Silva F, R. da, de Almeida, L.G.P., Cardoso, C.C., Brustolini, O.J., Gerber, A.L., Guimarães, A.P. de C., Mariani, D., Costa, R.M. da, Ferreira, O.C., et al. (2020). Genomic characterization of a novel SARS-CoV-2 lineage from Rio de Janeiro, Brazil. MedRxiv 2020.12.23.20248598.
7. Francisco Jr, R. da S., Benites, L.F., Lamarca, A.P., de Almeida, L.G.P., Hansen, A.W., Gularte, J.S., Demoliner, M., Gerber, A.L., de C Guimarães, A.P., Antunes, A.K.E., et al. (2021). Pervasive transmission of E484K and emergence of VUI-NP13L with evidence of SARS-CoV-2 co-infection events by two different lineages in Rio Grande do Sul, Brazil. Virus Res. *296*, 198345.
8. Volz, E., Mishra, S., Chand, M., Barrett, J.C., Johnson, R., Geidelberg, L., Hinsley, W.R., Laydon, D.J., Dabrera, G., O'Toole, Á., et al. (2021). Transmission of SARS-CoV-2 Lineage B.1.1.7 in England: Insights from linking epidemiological and genetic data. MedRxiv 2020.12.30.20249034.
9. Claro, I.M., da Silva Sales, F.C., Ramundo, M.S., Candido, D.S., Silva, C.A.M., de Jesus, J.G., Manuli, E.R., de Oliveira, C.M., Scarpelli, L., Campana, G., et al. (2021). Local Transmission of SARS-CoV-2 Lineage B.1.1.7, Brazil, December 2020. Emerg. Infect. Dis. *27*, 970–972.
10. Davies, N.G., Jarvis, C.I., Edmunds, W.J., Jewell, N.P., Diaz-Ordaz, K., and Keogh, R.H. (2021). Increased mortality in community-tested cases of SARS-CoV-2 lineage B.1.1.7. Nature.
11. Weisblum, Y., Schmidt, F., Zhang, F., DaSilva, J., Poston, D., Lorenzi, J.C.C., Muecksch, F., Rutkowska, M., Hoffmann, H.-H., Michailidis, E., et al. (2020). Escape from neutralizing antibodies by SARS-CoV-2 spike protein variants. Elife 9, e61312.
12. Vogels, C.B.F., Breban, M., Alpert, T., Petrone, M.E., Watkins, A.E., Hodcroft, E.B., Mason, C.E., Khullar, G., Metti, J., Dudley, J.T., et al. (2021). PCR assay to enhance

global surveillance for SARS-CoV-2 variants of concern. MedRxiv 2021.01.28.21250486.

13. Graber, T.E., Mercier, É., D'Aoust, P.M., Hoang, H.-D., Tian, X., Tasneem, S., Bhatnagar, K., and Delatolla, R. (2021). An allele-specific primer extension assay to quantify the proportion of B.1.1.7-specific SARS-CoV-2 RNA in wastewater. MedRxiv 2021.02.22.21252041.
14. Haim-Boukobza, S., Roquebert, B., Trombert-Paolantoni, S., Lecorche, E., Verdurme, L., Foulongne, V., Selinger, C., Michalakis, Y., Sofonea, M.T., and Alizon, S. (2021). Rapid SARS-CoV-2 variants spread detected in France using specific RT-PCR testing. MedRxiv 2021.02.20.21251927.

CAPÍTULO II

Neste capítulo apresentamos o manuscrito em preparação intitulado "*Monitoring the establishment of VOC Gamma in Minas Gerais, Brazil: a retrospective study of epidemiological and genomic surveillance"* que será submetido à revista Frontiers in Microbiology. Neste trabalho apresentamos o programa de vigilância genômica de SARS-CoV-2 a nível estadual em Minas Gerais, onde conseguimos cobrir todo território dividido em 28 Unidades Regionais de Saúde (URS). Para isso, foi feito um cálculo amostral que representasse toda a população do estado e no total foram coletadas 1240 amostras cobrindo cerca de 305 munícipios (35.8%) das 28 URS. Uma das principais e inovadoras metodologias utilizada neste trabalho foi uma genotipagem de variantes de SARS-CoV-2 baseada em qPCR (PCR em Tempo Real), a qual foi desenvolvida e validada por nosso grupo de pesquisa (dados no Capítulo I), e que se mostrou eficiente, mais barata e ao mesmo tempo, rápida para obtenção de resultados. Esse trabalho serviu de piloto para um programa de monitoramento de variantes que se estendeu ao longo de 2021 até os dias atuais, o qual continuou com o objetivo de monitoramento da circulação de variantes no estado: o Observatório de Vigilância Genômica (OviGen), em parceria com a a UFMG, Secretaria de Saúde do Estado (SES), Prefeitura de Belo Horizonte, Fundação Ezequiel Dias e o Grupo Hermes Pardini.

TITLE: Monitoring the establishment of VOC Gamma in Minas Gerais, Brazil: a retrospective study of epidemiological and genomic surveillance

Running Title: SARS-CoV-2 VOC Gamma establishment

Authors: Hugo José Alves[1]*, João Locke Ferreira de Araújo[1]*, Paula Luize Camargos Fonseca[1]*, Filipe Romero Rebello Moreira[2]*, Diego Menezes Bonfim[1], Daniel Costa Queiroz[1], Lucyene Miguita Luiz[3], Rafael Marques de Souza[1], Victor Emmanuel Viana Geddes[1], Walyson C. Costa[1], Jaqueline Silva de Oliveira[4], Eva L. A. Medeiros[4], Carolina L. A. de Souza[5], Juliana W. Saliba[5], André Luiz de Menezes[6], Eneida Santos de Oliveira[6], Felipe C. de M. Iani[7], Talita E. R. Adelino[7], Rennan Garcias Moreira[8], Danielle Alves Gomes Zauli[9], Joice do Prado Silva[9], Frederico Scott Varella Malta[9], Alessandro Clayton de Souza Ferreira[1], Victor Cavalcanti Pardini[9], Ana Valesca Fernandes Gilson Silva[10], Adriano de Paula Sabino[11], Natália Virtude Carobin[11], Karine L. Lourenço[12], Santuza M. R. Teixeira[12], Ana Paula S. M. Fernandes[12], Flavio G. da Fonseca[12], Jônatas Santos Abrahão[13], Rodrigo Araújo Lima Rodrigues[13], Renan Pedra de Souza[1‡], Renato Santana Aguiar [1,14 ‡]

Affiliation:

1- Laboratório de Biologia Integrativa, Departamento de Genética, Ecologia e Evolução, Instituto de Ciências Biológicas, Universidade Federal de Minas Gerais, Belo Horizonte, Brazil.

2- Laboratório de Virologia Molecular, Departamento de Genética, Instituto de Biologia, Universidade Federal do Rio de Janeiro, Rio de Janeiro, Brazil.

3 - Departamento de Patologia, Instituto de Ciências Biológicas, Universidade Federal de Minas Gerais, Belo Horizonte, Brazil.

4 - Subsecretaria de Vigilância em Saúde, Secretaria de Estado de Saúde de Minas Gerais, Belo Horizonte, Minas Gerais, Brazil.

5 - Pan American Health Organization - PAHO, Brasilia, Brazil.

6 - Secretaria Municipal de Saúde, Prefeitura de Belo Horizonte, Belo Horizonte, Brazil.

7 - Fundação Ezequiel Dias, Belo Horizonte, Brazil.

8 - Centro de Laboratórios Multiusuários, Instituto de Ciências Biológicas, Universidade Federal de Minas Gerais, Belo Horizonte, Brazil.

9 - Instituto Hermes Pardini, Belo Horizonte, Brazil.

10 - Escola de Saúde Pública de Betim, Secretaria Municipal de Saúde, Prefeitura de Betim, Betim, Brazil.

11 - Faculdade de Farmácia, Universidade Federal de Minas Gerais, Belo Horizonte, Brazil.

12 - Centro de Tecnologia de Vacinas, Universidade Federal de Minas Gerais, Belo Horizonte, Minas Gerais, Brazil.
13 – Laboratório de Vírus, Departamento de Microbiologia, Instituto de Ciências Biológicas, Universidade Federal de Minas Gerais, Brazil.
14 - Instituto D'Or de Pesquisa e Ensino (IDOR), Rio de Janeiro, Brasil.
* These authors have contributed equally to this work and share the first authorship.
‡ These authors have contributed equally to this work and are corresponding authors.

Correspondence should be addressed to:
Renan Pedra de Souza (renanpedra@gmail.com) and Renato S Aguiar (santanarnt@gmail.com).

Address for correspondence: Laboratório de Biologia Integrativa, G3-60. Instituto de Ciências Biológicas, UFMG. Av. Antônio Carlos 6627, Pampulha. 31270-901 - Belo Horizonte, MG – Brasil.

Abstract

The emergence of new SARS-CoV-2 variants of concern (VOC) poses striking difficulties in controlling the COVID-19 pandemic worldwide. The Gamma variant was associated with increased infection and transmission rates in Brazil. Most of the data suggest an increasing number of hospitalization and death cases concurrent with the emergence of the Gamma variant in Brazil. Here, we followed 1,240 positive patients for COVID-19, covering a total of 305 (35.8%) municipalities distributed in 28 Regional Health Units (RHU) and evaluating the genomic and clinical results of the virus representative of the state of Minas Gerais (MG), Brazil, during the biggest peak of pandemic and establishment of VOC Gamma. Data collection includes *Ct* values, virus genomic information, symptoms, clinical course and comorbidities. Over the period studied, there was an increase in cases of VOC Gamma (71.2%) in the 28 RHU's in MG. In addition to some patients with the Zeta lineage (12.4%) in the state, some isolated clusters of VOC Alpha (9.6%) could be found in specific regions of the state. Other less frequent lineages (6.8%) such as B.1.1, B.1.1.28, P.4, P.5 and P.7 were also identified circulating through the state. With our genomic characterization approach, we estimated the introduction of Gamma on January 7, 2021 at RHU Belo Horizonte. Three months after its introduction, the frequency of Gamma cases reached almost 100% in the state of MG. In addition, we identified SARS-CoV-2 strains sharing spike mutations with other

variants. We did not observe differences in mortality among patients infected with the variants described in this work.

INTRODUCTION

The emergence of a novel Betacoronavirus infecting humans in late 2019 led the world to this century's most challenging global health crisis. The Coronavirus Disease 2019 (COVID-19) pandemic, caused by Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2), resulted in more than 468.202 million cases and 6.074 million deaths worldwide by the end of March 2022 (WHO, 2022). The pandemic caused collapses in health systems worldwide, especially in locations where effective measures to control viral spread were not practiced or available (Brizzi et al., 2022).

Among the numerous lineages of SARS-CoV-2 described so far, some have called the attention of public health authorities given their association with higher rates of viral transmission, disease severity, and resistance to the neutralizing antibodies elicited by prophylactic vaccines (Li et al., 2020; Gidari et al., 2021). These lineages were defined as Variants of Concern (VOCs) and are responsible for the increase in disease incidence and transmission waves (WHO, 2022). These VOCs were initially identified in the United Kingdom (UK) (Alpha), South Africa (Beta), Brazil (Gamma), and India (Delta) (Naveca et al., 2021; Cherian et al., 2021; Faria et al., 2021; Tegally et al., 2021; Volz et al., 2021). These variants quickly spread to other countries, enhancing the difficulty of controlling the pandemic (WHO, 2022). More recently, the VOC Omicron emerged with up to 46 new mutations in the SARS-CoV-2 genome (initially described in South Africa), which has spread rapidly, creating new COVID-19 waves in several countries including Brazil (Kannan et al., 2022).

Since the beginning of the COVID-19 pandemic in Brazil, genomic surveillance studies showed replacement of SARS-CoV-2 lineages over time (Claro et al., 2021; Slavov et al., 2021; Voloch et al., 2021a). Most of the early COVID-19 cases were caused by the introduction of B.1.1.28 and B.1.1.33 lineages, followed by the Zeta (P.2) variant in the southeast region of Brazil in July 2020, concurrent with the progressive decline of the number of cases. Despite the international introduction of VOC Alpha at the end of 2020, the number of cases associated with this variant never reached the same proportion of the UK or other countries in the northern hemisphere (Torres et al., 2021; Paulo et al., 2022). The VOC Gamma, first named P.1, emerged in Manaus, possibly in mid-November 2020, resulting in a new wave of infections and causing the local public health system to collapse (Castro et al., 2021). Until 2020, the country had registered around 7,6 million cases and 195,000 deaths (OPAS., 2021). Four

months later, another wave of infection occurred, reaching a 7-days moving average of 77,000 new cases and 3,000 deaths per day (OPAS., 2021). The progression of the disease was observed in all states of the country. In Minas Gerais (MG), the fourth largest state in area and second most populous in the country, there was an increase of approximately 240% in the moving average of cases and 470% of deaths from January 1st to the peak of the disease in mid-April 2021 (OPAS., 2021).

With the approval of safe and effective vaccines to prevent the disease by the end of 2020, there has been a substantial decrease in the number of cases and deaths from COVID-19 (Brüssow and Zuber, 2022). Since the beginning of vaccination programs, the number of severe cases and deaths have dramatically declined in Brazil. Until the beginning of April 2021, during VOC Gamma establishment, 13.6% population (28,696,332 doses) were vaccinated in all Brazilian territories, in which 1.1% (2,294,840 doses) corresponded to the MG state population (OPAS., 2021).

The emergence and dissemination of VOCs throughout Brazil highlighted the necessity and importance of genomic surveillance as a fundamental strategy in the context of public health. Notwithstanding, previous studies suggested increasing the number of hospitalization and death cases with the emergence of VOC Gamma, but not at the patient level. Most of the studies compared the mortality rates in pre and post periods of Gamma introduction (Faria et al., 2021; Gidari et al., 2021; Gräf et al., 2021; Brizzi et al., 2022). Herein, we conducted a retrospective epidemiological study conducted during March and April 2021, covering all regions from MG State (southwest of Brazil), combining epidemiological, genomic, and clinical outcome data to understand the distribution of the SARS-CoV-2 variants throughout the state in up to 1,240 positive COVID-19 patients.

METHODS

Study design

In this population-based retrospective study, we primarily aimed to identify the frequency of distinct SARS-CoV-2 VOCs in the state of Minas Gerais (MG) from March 01st to April 27th, 2021, the period of a higher increase in the number of cases and fatalities due to COVID-19 (OPAS., 2021). SARS-CoV-2 variants were identified by PCR-genotyping and genome sequencing (see methods below) in 1,240 human nasopharyngeal swabs positive for SARS-CoV-2 by RT-PCR with samples presenting *Ct*<30 distributed throughout the state (Figure 1 and Supplementary Table 1). Minas Gerais (MG) is the fourth largest state in Brazil, with a 586,528 km² area, and is divided into 28 Regional Health units (RHUs) with different

population densities (Supplementary Figure 1). For the distribution of the samples, we considered that 56% should be allocated proportionally to all RHUs and the remaining 44% proportionally to the population density of each unit (Supplementary Table 2). Samples from all RHUs were randomly selected considering the intended evaluation period and the sample size for each RHU. Samples were collected in 11 laboratories *Laboratório de Biologia Integrativa* (LBI/UFMG), *Laboratório de Vírus* (LabVirus/UFMG), *Laboratório Institucional de Pesquisa em Biomarcadores* (LINBIO/UFMG), *Núcleo de Ações e Pesquisa em Apoio Diagnóstico* (NUPAD), *CT Vacinas - Universidade Federal de Minas Gerais* (UFMG), *Universidade Federal de Viçosa* (UFV), *Universidade Federal dos Vales do Jequitinhonha e Mucurí* (UFVJM), *Laboratório de Referência da Prefeitura Municipal de Belo Horizonte* (PBH), *Secretaria de Saúde de Estado de Minas Gerais*, *Fundação Ezequiel Dias* (FUNED) and *Instituto Hermes Pardini*, representing public and private institutions of COVID-19 diagnosis in the state. A Research Ethics Committee approved our study under protocol CAAE 33202820.7.1001.5348.

Epidemiological data and clinical outcome analysis

To explore the epidemiological scenario in the MG state, before and after the introduction of VOC Gamma, we retrieved public data to evaluate the number of cases and deaths per epidemiological week (EW) distributed by each RHU. The EW 45 to 49 (2020) and 01 - 13 (2021) were evaluated (https://coronavirus.saude.mg.gov.br/dadosabertos). Vaccination data were accessed for the same period (saude.gov.br) (Figure 1 and Supplementary Table 3).

Moreover, to explore the transmissibility of SARS-CoV-2 lineages in MG, we investigated the RT-qPCR Cycle threshold (*Ct*) values during the EW 45 - 13 (November 2020 to March 2021). In total, 115,621 positive samples for SARS-CoV-2 collected by *Instituto Hermes Pardini* laboratory covering 343 (40.1%) municipalities and all the RHUs from MG were used to explore the distribution of *Cts* during the study period. The *Cts* were obtained from the diagnosis of SARS-CoV-2 using the TaqPath COVID-19 CE-IVD RT-PCR kit (ThermoFisher Scientific, USA) (Supplementary Table 4). The median for the genes MS2 (extraction control) and viral Nucleocapsid (N gene) were calculated per epidemiological week and a curve was plotted using the ggplot package from R program (Wickham et al., 2022).

Epidemiological data related to comorbidities, symptomatology and clinical outcome of the samples with SARS-CoV-2 variant identification were also explored. Data was retrieved from *Sistema de Informações de Vigilância Epidemiológica* (SIVEP) and e-SUS databases,

respecting patient protection laws. Comorbidity data were available only for 91 hospitalized patients. Information on symptomatology was obtained for 657 patients, and 587 patients presented information available for the clinical outcome (Supplementary Table 3). Logistic regression models were generated to evaluate the difference between the VOCs Gamma and Alpha frequencies and between the frequencies of deaths by the VOC Gamma and Zeta variant. The analysis was performed in the R program (R Core Team, 2021).

Heatmaps were generated using data from epidemiological weeks (EW) 45 e 49 (2020), 01, 05, 09 e 13 (2021) to explore the evolution of the number of cases and deaths throughout the MG state. All analyses were performed in Rstudio version 4.2.3, using the packages Rlang (Lionel et al., 2022), geobr (Almeida et al., 2020), ggplot2 (Wickham et al., 2022), and ggaluvial (Jason et al., 2020).

cDNA synthesis and rhAmp genotyping assay

The 1,240 SARS-CoV-2 positive samples collected in our study were genotyped using specific primers and probes to detect defining variant mutations (Figure 1). First, the samples were used to synthesize cDNA using the High-Capacity cDNA Reverse Transcription Kit (Thermo Fisher Scientific) according to the manufacturer's instructions (final volume of 20 µl with 14.2 µl of total RNA). The cDNA was used as input in an RT-qPCR reaction using the rhAmp SNP Genotyping System technology (Integrated DNA Technology - IDT, CA, USA) as described previously (Geddes et al., 2021). The concentration of each solution and final volume used for each genotyping reaction was: rhAmp Genotyping Master Mix (1X), rhAmp Reporter Mix (1.12X) and Specific SNP Primer (1.5X) were used in one final volume of 10 µL and following these cycling conditions: 95ºC for 10 minutes followed by 60 cycles with 95ºC for 15 seconds, 57ºC for 1 minute and 68ºC for 30. In total, three viral polymorphisms in the spike gene were evaluated: K417T (A22812C), E484K (G23012A) and N501Y (A23063T) (Supplementary Table 5). Samples mutated only at position 501 were classified as VOC Alpha (B.1.1.7 lineage), while samples mutated only at position 484 were classified as Zeta variant (also named as P.2). Samples mutated for the three positions (417, 484 and 501) were classified as VOC Gamma (P.1 lineage and sublineages). Spatio-temporal heatmaps were constructed considering the PCR-genotyping results. Samples with mutation profiles different from expected variants were considered "others" in our analyses and sequenced. Data analysis was carried out in R software (version 4.1.1) (R Core Team, 2021) using the packages geobr (Almeida et al., 2020), sf (Sumner et al., 2022), and ggplot2 (Wickham et al., 2022) packages.

Library preparation and genome sequencing

In total, 240 samples were sequenced in our study. Sixty-two samples from October 28th, 2020 and February 28th, 2021. Another 167 positive samples collected between March 01st, 2021 and March 31th, 2021 classified by the genotyping method as "other" lineages (*n* = 24) or randomly selected (*n* = 143) and 11 samples were selected after the genotyping sampling period (first week of May). All samples sequences presented *Ct*<30 (Figure 1).

Sequencing libraries were prepared using the QIAseq FX DNA Library Prep kit (QIAGEN, Germany) and sequenced on the Illumina MiSeq platform (Illumina, USA) with v3 (600 cycles) cartridges, following all manufacturer's instructions. Negative controls were used in each round of sample processing steps (cDNA synthesis, viral genome amplification and library preparation).

SARS-CoV-2 genome assembly and lineage classification

Sequencing data were processed following a previously described pipeline (Romero et al., 2021). Briefly, raw reads were filtered with fastp v0.20.1 (Chen et al., 2018) to remove short and low-quality reads (Phred score <30) and adapter sequences. The remaining reads were aligned against the SARS-CoV-2 reference genome (NC_045512.2) with Bowtie2 v2.4.2 (Langmead and Salzberg, 2012). Mapping files were then indexed and sorted with SAMtools v1.12(Li, 2011), and BCFtools v2.30.0 (Li, 2011) was used to infer the consensus genome sequences. Finally, BEDtools (Quinlan and Hall, 2010) was used to mask low depth sites (<10x coverage). Sequences with less than 70% genome coverage were removed from downstream analysis. The consensus sequences generated in our study were classified using the Pangolin tool v.3.1.14 and the NextClade web application v.1.7.0 (Hadfield et al., 2018). Mutations associated with possible novel lineages have been manually verified in raw sequencing data. All consensus sequences were deposited on the GISAID EpiCOV database.

Phylogenetic and Phylodynamic analysis of VOCs in Minas Gerais

A comprehensive reference dataset (*n* = 6,110) was created with public genomes available on the GISAID EpiCOV database to confirm the lineage classification and contextualize the novel genomes. This dataset comprehends all Brazilian sequences, plus one international sequence per country per epidemiological week since the first reported SARS-CoV-2 genome (Available on GISAID 2022, April 11th), plus the ten sequences closely related to each genome generated in our study. The dataset was aligned with minimap v (Li, 2018),

and a maximum likelihood phylogeny was inferred with IQ-tree v2.0.3 (Minh et al., 2020) under the GTR+F+I+G4 model (Tavare, 1986; Yang, 1994).

To further contextualize the dynamics of introduction and spread of SARS-CoV-2 VOC Gamma into MG, we assembled one additional dataset to perform the time-scaled phylogeographic reconstruction. Brazilian sequences from all states assembled the dataset. The number of sequences included is proportional to each federal unit (*n* = 1,610, considering approximately 20 sequences for each of the 27 federative units of Brazil during the months of January - May 2021). Given the size of obtained datasets, an efficient maximum-likelihood based method - Tree Time v (Sagulenko et al., 2018) - was used to scale branch lengths in time and reconstruct phylogeographic history. The molecular clock analysis was performed using a fixed evolutionary rate (1e-3), and a discrete symmetric model was used to estimate transitions among ancestral locations in the trees. The model comprehended six discrete categories, MG (*n*=115) and five Brazilian politically defined regions: North (*n*=376), Northeast (*n*=583), CentreWest (*n*=154), Southeast (except MG; *n*=182), South (*n*=200). The tree was rooted in the divergence between P.1 and the clade P.1-like I (Gräf et al., 2021). Migration models were applied to infer the number of import and export cases to MG.

RESULTS

Epidemiological data and clinical aspects of SARS-CoV-2 in MG state

Here, we investigated the dynamics of cases and deaths in the MG state before introducing the VOC Gama. The first genome sequenced of VOC Gamma in MG was identified in EW 5 of 2021 (accessed on the GISAID EPICoV database - 30 Jan 2021). The number of cases and deaths was lower during the EWs 45 - 53 (2020) in contrast with increasing death rates observed by SES-MG during the first 13 EWs of 2021, after Gamma introduction (Figure 2A and Supplementary Table 3). In EW 45 (2020), 9,637 positive cases and 189 deaths were confirmed. During the entire period evaluated in 2020, 189,630 cases and 3,008 deaths were confirmed (for every 63 cases of COVID-19, one patient died). However, only in EW 8 (three weeks after Gamma first described in MG state), 37,578 cases and 837 deaths were confirmed (for every 44 cases of COVID-19, one patient died). The increasing rates in mortality were observed until the last EW evaluated (EW 13), in which 59,987 cases and 2,174 deaths were confirmed (one died out of 28 cases). The epidemiological data suggest increasing rates of transmission and fatality after Gamma introduction in the state of MG (Figure 2A and Supplementary Table 3).

Gamma introduction in MG happened in a scenario where the vaccination process was starting only to populations classified as risk groups (healthy workers or individuals with age superior to 80 years). Vaccination against COVID-19 in the MG state started during EW 4 (2021) and continued to increase during the consecutive weeks. In total, 2,297,840 doses were distributed in the state during the entire period of our analysis (equivalent to almost 11% of the population of MG) (Figure 2B and Supplementary Table 3). Increasing transmission rates also followed gamma introduction in MG in the state. Analysis from 115,621 RT-PCR confirmed cases showed a significant decrease in *Cts* values from the N gene with no corresponding variation in endogenous cellular control (MS2 gene) (Figure 2C). We observed a difference in medians between the EWs for the *Cts* referring to the N gene amplification ($p<0.0001$; $df = 4$), and the EWs 5 and 13 were below the general median (*Ct* = 18.34). The overall median *Ct* value was 25.78, fluctuating over the period (Supplementary Table 4).

Moreover, our analysis showed an oscillation in the number of confirmed cases across the state during the time interval of this study (22 EWs) (Figure 3A). The RHU Belo Horizonte, which corresponds to the capital from MG, and presents a superior population density, maintained higher positivity rates, reaching 21,028 cases in the EW 12, pos-Gamma introduction. The RHU Uberlândia also showed a considerable increase in the number of cases in the first weeks, reaching 5,289 cases in EW 9. Nevertheless, there was a decrease in the number of positive cases after the EW 10 (Figure 3A and Supplementary Table 4). At the end of the EW 17, the RHUs Belo Horizonte and Uberlândia (Central-West and West regions) had the highest positive cases in the state, 204,005 and 66,567 positive cases, respectively. The RHU Januária (North region) presented the lowest number of cases at the end of the study (6,135) and Pirapora on the opposite side of the MG state corresponding to the northeast region (4,643) (Supplementary Table 4). The total number of cases recorded over time was reflected in the state's mortality (Figure 3B). The RHU Belo Horizonte maintained the higher numbers of deaths over the 17 weeks evaluated, with a peak at EW 15, counting 610 deaths. The RHU Uberlândia had a rise in EW 10 (266 deaths) followed by a decrease, reaching 113 deaths in EW 17. The RHUs Januária and Pirapora also had the total number of cases reflected in mortality, representing 96 and 86 deaths, respectively. These results suggest a possible introduction of Gamma from the central-west region of MG (RHU Uberlandia) coming from the north Brazilian area (Manaus, Amazon state), where Gamma was first described.

Circulation of SARS-CoV-2 variants in MG state

In order to evaluate whether the increasing number of cases and deaths observed in MG was associated with VOC Gamma introduction, we performed a population random based study across the state. A total of 1,240 samples distributed in 28 RHUs were genotyped for three lineage defining mutations in the S gene (K417T, E484K and N501Y), respecting the population density in each region. We observed that the majority of the samples were classified as VOC Gamma (71.2%) (Figure 4A), followed by the VOI Zeta (12.4%) (Figure 4B). The VOC Alpha was also identified circulating in the state, but with a lower frequency (9.6%) (Figure 2C). Other genotypes presenting different combinations of lineage defining mutations in the S gene (K417T, E484K and N501Y) were classified as "others" (6.8%) and targeted for whole genome sequencing (Figure 4D).

The VOI Zeta was present in 54.5% of the total samples from RHU Pedra Azul (northeast region) and 41.4% in RHU Ubá (south area) (Figure 4B and Supplementary Table 6). On the other hand, the VOC Alpha represented 53.2% of the total samples from RHU Coronel Fabriciano (southeast region) and 44.8% from RHU Teófilo Otoni (northeast region), which suggest a cluster of transmission in these regions (Figure 4C). There is no pattern of dispersion for the "other lineage" group with the lowest general frequencies in the state. However, they significantly participated in the genotyping results in the north and southwest regions (RHUs Pirapora and Alfenas), showing frequencies of 21.4% and 17.1%, respectively (Supplementary Table 6).

Although the VOC Gamma had a frequency of 71.2% throughout the state, it represented 100% of the genotyping performed for the RHUs located in the central-west regions (RHUs Patos de Minas and Uberlândia), except for Juiz de Fora, border from Rio de Janeiro, and southeast part of MG (Figure 4A). The RHUs in the northeast of MG (Pedra Azul and Teófilo Otoni) had the lowest relative frequencies for the VOC Gamma, 30.3% and 24.1%, respectively (Figure 4A). The VOC Gamma was the only one identified in all RHUs.

For the samples classified as VOCs and VOIs, information related to symptoms, comorbidities and clinical outcomes for each of them were obtained from SES-MG (Supplementary Table 3). The subjects participating in the study observed comorbidities such as asthma, heart disease, diabetes, immunosuppression, neurological disorders, obesity, pneumonia, and kidney disease (Figure 4E). All comorbidities were observed in only patients infected with VOC Gamma. Heart disease, diabetes and obesity were most frequent in patients infected with the VOC Gamma (42.2%, 25.7% and 10.8%, respectively). For VOC Alpha, just heart disease, diabetes, immunosuppressed and pneumonia were observed in patients infected with this VOC. And heart disease was the most frequent comorbidity, present in 60% of the

samples with VOC Alpha (Supplementary Table 3). For both Zeta and “other” lineages were described with heart disease, diabetes and obesity only, which heart disease was most frequent with 50% in both patients infected with those lineage (Supplementary Table 3).

The symptoms of cough, coryza, fever, headache, sore throat, dyspnea, anosmia, and ageusia were observed in patients participating in the study (Figure 4F). All symptoms were frequent in patients infected with VOC Gamma and Alpha or Zeta e “other” lineages. In all patients infected with all lineages described here, cough and headache were the most reported (Figure 4F). When comparing deaths between the different lineages, no differences were observed between patients infected by VOC Gamma versus Alpha VOC (p= 0.335; OR: 0.69; 95%CI: 0.31 – 1.38), nor when comparing deaths by VOC Gamma against Zeta lineage (p=0.408; OR: 1.44; 95%CI: 0.61 – 3.61).

Prevalence of Gamma VOC in MG

Three lineages (Alpha, Gamma and Zeta) were identified circulating in the state through genotyping of critical mutations in the spike gene. Samples with different profiles of mutations and misclassified were further sequenced. Representative samples previously characterized as Gama, Alpha and Zeta by genotyping were also sequenced to confirm our genotyping strategy. A subset of 240 novel SARS-CoV-2 genomes was generated in our study with an average genome coverage of 97.84% and a mean depth of 585X. Complete whole-genome sequencing metrics are available in Supplementary Table 7.

According to the Pango lineages classification, up to 40% of the samples were identified as Gamma (48.75%; 87/240) or other three sublineages (P.1 - 87, P.1.1 - 3, P.1.14 - 10, P.1.15 – 15, P.1.17 - 1). Other lineages were also found; however, with lower frequency: VOC Alpha (12.5%; 30/240), B.1.1.28 (3.33%; 8/240), Zeta (29.16%; 70/240), P.4 (2.08%; 5/240), B.1.1 (2.5%; 6/240), B.1.1.33 (0.41%; 1/240) and P.7 (0.41%; 1/240) (Supplementary Table 7). Therefore, sequencing confirms the genotyping results and reinforces the prevalence of VOC Gamma in MG co-circulating with other lineages (Figure 5).

Circulation of other SARS-CoV-2 lineages in MG

Despite the prevalence of Gamma VOC in MG, our genotyping strategy accelerates the possible identification of novel SARS-CoV-2 genomes. According to our genotyping approach, 84 samples were classified as "Other" lineages with different combinations of defining VOCs and VOIs Spike mutations, from which 21 were sequenced. Sixteen (76.19%) sequences were classified as other lineages by the Pangolin tool. One sequence (LBI412) in the

phylogenetic analysis was close to the P.5 lineage clade as an ancestral group. However, these sequences do not present the same mutation profile as the identified sequences (S: Q14K, T95I, G142D, N501Y, S640F, Q677H, D936G, V1176F), suggesting a novel genome lineage. Moreover, five sequences (LBI311, LBI312, LBI313, LBI401 and LBI406) were characterized as the P.4 lineage. The primary mutation that characterizes this variant is the L452R and I720V in the Spike gene. Another sample also has the mutation L452R but was classified as B.1.1 (LBI318 and LBI314). Our dataset also identified a sample classified as P.7 (LBI402) (Figure 5). Unlike the other variants identified in this study that have many mutations in the Spike gene, the P.7 variant has only three: T21835C, A23403G/D614G and G25088T/V1176F. Moreover, ten sequences were classified as B.1.1.28 (LBI315, LBI316, LBI321, LBI404, LBI405, LBI422, LBI423 and LBI424), and two genomes (LBI215 and LBI218) near the B.1.1.28 clade presented the unique mutations E484Q and N501T forming a novel sub-cluster of B.1. In our phylogenetic analyses, five samples (LBI322, LBI325, LBI375, LBI378 and LBI379) classified as Gamma presented the unique E484K and N501T, being considered P.1-*like* genomes. All these results reinforce the importance of our strategy of genotyping/sequencing to screen large scale samples increasing the chance of identifying novel SARS-CoV-2 genomes with higher frequencies of 2.5% in the population. All low-frequency lineages identified in our study had at least 100x depth and coverage greater than 70%.

Phylodynamics of VOC introduction into MG

Time-scaled phylogeographic reconstruction has been performed with a comprehensive dataset to explore the temporal and spatial dynamics of VOC Gamma introduction into the MG state (Figure 6). Analysis of the dataset estimated the origins of VOC Gamma on October 19nd 2020 (90% CI: September 07th 2020 - November 11th 2020), with the earliest introduction in MG occurring by the beginning of 2021 (January 07th 2021; 90% CI: December 25th 2020 - January 25th 2021). The model suggests more than 100 distinct introduction events in Brazil (102 events), culminating in diverse clades, revealing autochthonous transmission chains. The Southeast region is mainly responsible for importation cases in the state of MG (with almost 60 introduction events), followed by the Northeast and South regions (each region with 19 and 17 introduction events). These events led to the emergence of different 14 clades from MG, while others are represented by single sequences (singletons) (Figure 6). The time for the most recent common ancestor (tMRCA) for MG clades was May 02nd 2021. Our time-scaled phylogeographic reconstructions coincide with the first confirmed case of infection by the Gamma variant in the state of MG identified in mid-January 2021. Since then, the number of

cases identified by the Gamma variant has been increasing, reaching the highest number of cases in March and April. Following the dominance of Gamma VOC in the MG state, new genomes were identified with lower frequencies (13.71%; 17/124) but presented new signatures such as K417T, synA23380T and A845S mutations in the spike gene, suggesting diversification of this variant.

DISCUSSION

Since the identification of VOC Gamma in the city of Manaus - Amazonas (Brazil), several studies have reported the spread of this variant associated with increasing numbers of cases and deaths of COVID-19, leading to a public health collapse in the country (Romero et al., 2021; Brizzi et al., 2022). In this study, using PCR-genotyping to define the main VOCs and VOIs, whole-genome sequencing and epidemiological data, we identified the main variants and strains circulating in the state of MG during the first months of 2021 and their impact on COVID-19 lethality. According to the data collected from SES-MG, the number of cases and deaths before establishing VOC Gamma was lower than in the first two months of 2021 in MG. Metadata analysis of 119,507 RT-PCR positive cases of COVID-19 covering the whole state of MG showed the Gamma introduction was associated with higher viral load in RT-PCR exams (lower *Cts* values) potentializing the virus transmission rates. Our results suggest a change in the epidemiological scenario after describing the first VOC Gamma genome in MG (January 30th 2021), just one month after its identification in Manaus (Farias et al., 2021; Naveca et al., 2021).

After the description of the first case of Gamma in MG, the occurrence of cases increased substantially in MG. At the end of our study (March - 2021), the prevalence of Gamma cases was 71.2%. According to previous studies, the Gamma reached 100% prevalence in the capital of MG at the end of April 2021 (Silva et al., 2022). Moreover, since the identification of Gamma, this variant became the most prevalent in all Brazilian states during the first months of 2021. This variant was also responsible for the second wave of COVID-19 in Brazil (Brizzi et al., 2022).

Studies involving Gamma showed that this variant presents a higher spread rate and chances of developing severe cases and deaths related to different mutations in the spike gene (Faria et al., 2021; Romero et al., 2021). The N501Y mutation, first described in VOC Alpha, is responsible for the increased affinity of the S viral protein to the human ACE2 receptor (Volz et al., 2021). The presence of the K417T mutation and the N501Y in Gamma intensified this affinity between the virus protein and the cell receptor (Castro et al., 2021). This process

contributed to an increase in patients' viral load and, consequently, severe clinical outcomes (Faria et al., 2021). The considerable heterogeneity of symptoms seen in COVID-19 varied greatly throughout the pandemic (Carrillo-Larco and Altez-Fernandez, 2020; Izcovich et al., 2020; Oran and Topol, 2021). Many of the described comorbidities associated with severe COVID-19 were evaluated in our study. Heart diseases were reported in almost half of these patients, reinforcing the risk of cardiac comorbidities to develop severe cases of COVID-19. Heart disease comprises a large part of the risk groups for severe COVID-19 (Wang, 2020; Gao et al., 2021) as well as diabetes and hypertension (Gasmi et al., 2021).

Patients diagnosed with diabetes were observed with considerable frequency in the sample. According to published data, chronic exposure to an abnormal metabolic environment can lead to disturbances in innate and adaptive immunity, cytokine storm release, and an increase in viral infection (Gao et al., 2021; Zhou et al., 2021). Together, all these factors can increase the risk of a severe prognosis for COVID-19 (Izcovich et al., 2020; Gao et al., 2021).

Moreover, the period of this study coincides with the beginning of vaccination in Brazil, which started in January 2021. Nevertheless, the vaccination process did not prevent the spread of Gamma and the occurrence of the second peak of COVID-19 infection, with daily death reaching over 4,000 records during the months of our study (OPAS 2021). According to the data collected through SES-MG, a small portion of the population had received the first dose, and an even smaller part had received the second dose. During our study scenario, the vaccines available were Oxford-AstraZeneca (ChAdOx1) and CoronaVac (Sinovac Biotech), the latter being responsible for more than 80% of applications, according to data from the Brazilian Health Ministry. However, it is expected that with the increase in vaccination, a reduction in the number of cases and deaths and an improvement in patient prognosis will occur (Wiersinga et al., 2020; Gidari et al., 2021). To corroborate the results found in our PCR-genotyping strategy, we selected 240 samples to be sequenced. Sequencing and phylogenetic analyses confirmed all samples characterized by PCR-genotyping as Alpha, Gamma, or Zeta. However, other lineages were also found in circulation with a much lower frequency, suggesting that they were not fixed in the state epidemiological scenario during our study. For example, the P.4 lineage described as the second most prevalent in the state of SP (behind only Gamma) was found with low frequency (only five samples) in MG. P.4 lineage had 15 amino-acid mutations (six occurring in the spike gene, such as L452R and I720V), and after its description in Porto Ferreira city, it was described circulating in other 29 cities within SP state (southeast region) (Bittar et al., 2021). This lineage was also found in other Brazilian regions (northeast) but with a low frequency (Bittar et al., 2021). Another case is the P.5 lineage, described for the first time

in the states of SP and RJ (Francisco Junior et al., 2021) and only three samples were found in our study (Francisco Junior et al., 2021). The P.5 presents 12 nonsynonymous mutations, of which five are in the Spike gene (F2L, Q14K, T95I, E484Q, and N501T). The P.7 lineage also was described for the first time in the SP state and harbored a cluster of nonsynonymous mutations specific to this clade. Nevertheless, different from the other two lineages described with low frequency in our study, P.7 presents only two mutations in the Spike gene (D614G and V1176F) and in other positions on the genome N:P13L, ORF3a: T151I and ORF9b P10S (Sant'Anna et al., 2021). In the GISAID EpiCoV database (search on May 17th 2022), are available 267 sequences classified as P.4, 60 classified as P.5, and 315 genomes classified as P.7. All P.4 and P.5 genomes available are from Brazil. More than 65% (207 genomes) of P.7 genomes also were identified in our country. These three lineages emerged in the first semester of 2021 in Brazilian states and descended from the lineage B.1.1.28 (Bittar et al., 2021; Francisco Junior et al., 2021; Sant'Anna et al., 2021). Despite emerging from Brazilian regions, this lineage was not found in high frequency in other Brazilian regions, and therefore, they are not considered a variant of interest or concern.

The VOC Alpha was first described in the state along with VOC Gamma. Still, despite that, it ended up not prevailing, growing in frequency only in some points in the state, perhaps because these described regions are immigration hotspots to the USA, where Alpha dominated the population at the time of this study (Mitchell et al., 2021; Washington et al., 2021). In contrast, besides being more frequent in MG, the VOC Gamma was also possible to identify other sub lineages. In our study, the sub lineages of Gamma P.1.1, P.1.14, P.1.15 and P.1.17 were reported by whole-genome sequencing. These sub lineages can also be called P.1-*like* genomes and present additional mutations that were not identified in the first description of the VOC Gamma (Paulo, 2021; Romero et al., 2021). The presence of Gamma sub lineages suggests an accumulation of mutations during the evolution of this variant.

After the dominance period of Gamma, the VOC Delta replaced the Gamma cases in MG state. This variant has been described as more transmissible and associated with symptom severity (Geovanetti et al., 2022). However, its introduction in Brazil and MG did not lead to a third wave of infection, as expected. Possible explanations may consider the advance of vaccination in the state during the growth period of the Delta variant, in addition to other factors, such as the genetic background of the Brazilian population, in addition to environmental factors such as hospital structure and stronger preventive behavior (Geovanetti et al., 2022). Currently, the Omicron variant, first confirmed in the state in November 2021, reaching 100% of state infections in the fourth epidemiological week (January 2022).

Currently, the Omicron variant, including its sub variants (BA.2, BA.3, BA.4 and BA.5), represent 100% of infections in the country. (Secretaria de Saúde do estado de Minas Gerais, 2022). The high rate of transmissibility, the vaccine escape that this variant has and the relaxation of preventive measures may explain the increase in the number of symptomatic cases (Chenchula et al., 2022).

Nevertheless, it is essential to point out that the circulation of multiple lineages can interfere with the epidemiological scenario and increase the chance of new lineages and/or variants. Our results reinforce the combination of genotyping and whole-genome sequencing as an effective strategy to improve and accelerate large-scale genome surveillance programs to detect and track the expansion of circulating lineages through the territory. With this strategy, a more significant number of samples can be classified in less time, allowing a more accurate report of the state's real-time epidemiological scenario.

Since we observed that Gamma was the dominant in MG, we performed a time-scaled phylogenetic inference to estimate the probable date of introduction. Our results suggest that VOC Gamma emerged between October-November 2020 in the Brazilian North region, as described by previous studies (Faria et al., 2021; Ramundo et al., 2021). According to our data, the first introduction event came from the Belo Horizonte RHU (90% CI January 07th 2021; 90% CI: December 25th 2020 - January 25th 2021) and after that, through multiple locations, being the Southeast region responsible for most of the introduction events (56). The results found in our phylogeny evidence a widespread transmission of Gamma variant in MG and the presence of multiple clusters of transmission. The rapid spread of Gamma was also reported e in other Brazilian states, such as Amazonas (North region) and Rio de Janeiro (Southeast region) (Romero et al., 2021; Brizzi et al., 2022). Studies suggest that the Gamma is more transmissible than other lineages, such as the previous Zeta and B.1.1.28, with higher viral loads on human samples (Romero et al., 2021; Torres et al., 2021; Brizzi et al., 2022). Our study observed a reduction in *Ct* value for the Nucleoprotein (N) gene, corroborating the previous studies indicating that Gamma presents higher viral loads than the other lineages circulating in the same period in the MG state.

Overall, our study reports a genomic surveillance analysis based on PCR-genotyping and whole-genome sequencing that highlighted the epidemiological dynamics of the introduction of VOC Gamma in MG. Despite the increase in viral load observed in the study, symptomatology and clinical outcome data suggest no difference between the previous variants. Despite this, studies show an association between the introduction of Gamma in the state and an increase in severe cases, with rates varying between states (Brizzi et al., 2022).

Other lineages were also found in low frequency circulating. From the phylogenetic reconstruction analysis, it was possible to establish that the southeast region was responsible for the state's most significant number of introductions. Finally, the description of the dynamics of dispersion and dominance of the VOC Gamma in the state is essential for understanding the evolutionary dynamics of the virus so that this knowledge can contribute to future epidemiological interventions.

Data sharing

All consensus genome sequences characterized in this study have been deposited on GISAID and are publicly available (Supplementary Table 7).

Conflict of interests

We declare no conflicts of interest.

Funding

We acknowledge support from the Rede Corona-ômica BR MCTI/FINEP affiliated to 116 RedeVírus/MCTI (FINEP 01.20.0029.000462/20, CNPq 404096/2020-4). This project was also supported by CNPq (R.S.A.: 312688/2017-2 and 439119/2018-9; R.P.S.: 310627/2018-4), MEC/CAPES 118 (14/2020 - 23072.211119/2020-10), FINEP (0494/20 01.20.0026.00), UFMG-NB3, FINEP nº 1139/20 (RSA), FAPEMIG (R.P.S.: APQ-00475-20) and FAPERJ (R.S.A 202.922/2018).

Reference

Almeida, R., Arruda, D., Nascimento, I., Santiago, B., Silva, W., Andrade, P. R., et al. (2020). Package ‘ geobr ’ R topics documented :

Bittar, C., Possebon, F. S., Ullmann, L. S., Geraldini, D. B., da Costa, V. G., de Almeida, L. G. P., et al. (2021). The Emergence of the New P.4 Lineage of SARS-CoV-2 With Spike L452R Mutation in Brazil. *Front. public Heal.* 9, 745310. doi:10.3389/fpubh.2021.745310.

Brizzi, A., Whittaker, C., Servo, L. M. S., Hawryluk, I., Prete, C. A. J., de Souza, W. M., et al. (2022). Spatial and temporal fluctuations in COVID-19 fatality rates in Brazilian hospitals. *Nat. Med.* doi:10.1038/s41591-022-01807-1.

Brüssow, H., and Zuber, S. (2022). Can a combination of vaccination and face mask wearing contain the COVID-19 pandemic? *Microb. Biotechnol.* 15, 721–737. doi:10.1111/1751-7915.13997.

Carrillo-Larco, R. M., and Altez-Fernandez, C. (2020). Anosmia and dysgeusia in COVID-19: A systematic review. *Wellcome open Res.* 5, 94. doi:10.12688/wellcomeopenres.15917.1.

Castro, M. C., Kim, S., Barberia, L., Ribeiro, A. F., Gurzenda, S., Ribeiro, K. B., et al. (2021). Spatiotemporal pattern of COVID-19 spread in Brazil. *Science (80-.).* 372, 821–826. doi:10.1126/science.abh1558.

Chen, S., Zhou, Y., Chen, Y., and Gu, J. (2018). fastp : an ultra-fast all-in-one FASTQ preprocessor. 884–890. doi:10.1093/bioinformatics/bty560.

Cherian, S., Potdar, V., Jadhav, S., Yadav, P., Gupta, N., Das, M., et al. (2021). SARS-CoV-2 Spike Mutations, L452R, T478K, E484Q and P681R, in the Second Wave of COVID-19 in Maharashtra, India. *Microorganisms* 9. doi:10.3390/microorganisms9071542.

Claro, I. M., da Silva Sales, F. C., Ramundo, M. S., Candido, D. S., Silva, C. A. M., de Jesus, J. G., et al. (2021). Local Transmission of SARS-CoV-2 Lineage B.1.1.7, Brazil, December 2020. *Emerg. Infect. Dis.* 27, 970–972. doi:10.3201/eid2703.210038.

Wickham H (2016). *ggplot2: Elegant Graphics for Data Analysis*. Springer-Verlag New York. ISBN 978-3-319-24277-4, https://ggplot2.tidyverse.org.

Emmanuel, V., Geddes, V., Moreira, F., Bonfim, D. M., Alves, H. J., Locke, J., et al. (2021). A novel RT-qPCR assay for detection of SARS-CoV-2 variants based on RhAmp technology (IDT technologies). 1–3.

Faria, N. R., Mellan, T. A., Whittaker, C., Claro, I. M., Candido, D. da S., Mishra, S., et al. (2021). Genomics and epidemiology of the P.1 SARS-CoV-2 lineage in Manaus, Brazil.

Science 372, 815–821. doi:10.1126/science.abh2644.

Francisco Junior, R. da S., Lamarca, A. P., de Almeida, L. G. P., Cavalcante, L., Machado, D. T., Martins, Y., et al. (2021). Turnover of SARS-CoV-2 lineages shaped the pandemic and enabled the emergence of new variants in the state of Rio de Janeiro, Brazil. *Viruses* 13, 1–13. doi:10.3390/v13102013.

Gao, Y.-D., Ding, M., Dong, X., Zhang, J.-J., Kursat Azkur, A., Azkur, D., et al. (2021). Risk factors for severe and critically ill COVID-19 patients: A review. *Allergy* 76, 428–455. doi:10.1111/all.14657.

Gasmi, A., Peana, M., Pivina, L., Srinath, S., Gasmi Benahmed, A., Semenova, Y., et al. (2021). Interrelations between COVID-19 and other disorders. *Clin. Immunol.* 224, 108651. doi:10.1016/j.clim.2020.108651.

Gidari, A., Sabbatini, S., Bastianelli, S., Pierucci, S., Busti, C., Monari, C., et al. (2021). Cross-neutralization of SARS-CoV-2 B.1.1.7 and P.1 variants in vaccinated, convalescent and P.1 infected. *J. Infect.* 83, 467–472. doi:10.1016/j.jinf.2021.07.019.

Gräf, T., Bello, G., Venas, T. M. M., Pereira, E. C., Paixão, A. C. D., Appolinario, L. R., et al. (2021). Identification of a novel SARS-CoV-2 P.1 sub-lineage in Brazil provides new insights about the mechanisms of emergence of variants of concern. *Virus Evol.* 7, veab091. doi:10.1093/ve/veab091.

Hadfield, J., Megill, C., Bell, S. M., Huddleston, J., Potter, B., Callender, C., et al. (2018). Nextstrain: real-time tracking of pathogen evolution. *Bioinformatics* 34, 4121–4123. doi:10.1093/bioinformatics/bty407.

Izcovich, A., Ragusa, M. A., Tortosa, F., Lavena Marzio, M. A., Agnoletti, C., Bengolea, A., et al. (2020). Prognostic factors for severity and mortality in patients infected with COVID-19: A systematic review. *PLoS One* 15, e0241955. doi:10.1371/journal.pone.0241955.

Jason, A., Brunson, C., and Read, Q. D. (2020). *Package ' ggalluvial . '* doi:10.1007/0-387-28695-0>.

Kannan, S. R., Spratt, A. N., Sharma, K., Chand, H. S., Byrareddy, S. N., and Singh, K. (2022). Omicron SARS-CoV-2 variant: Unique features and their impact on pre-existing antibodies. *J. Autoimmun.* 126, 102779. doi:10.1016/j.jaut.2021.102779.

Langmead, B., and Salzberg, S. L. (2012). Fast gapped-read alignment with Bowtie 2. *Nat. Methods* 9, 357–359. doi:10.1038/nmeth.1923.

Li, H. (2011). A statistical framework for SNP calling , mutation discovery , association mapping and population genetical parameter estimation from sequencing data. 27,

2987–2993. doi:10.1093/bioinformatics/btr509.

Li, H. (2018). Minimap2 : pairwise alignment for nucleotide sequences. 34, 3094–3100. doi:10.1093/bioinformatics/bty191.

Li, Q., Wu, J., Nie, J., Zhang, L., Hao, H., Liu, S., et al. (2020). The Impact of Mutations in SARS-CoV-2 Spike on Viral Infectivity and Antigenicity. *Cell* 182, 1284-1294.e9. doi:10.1016/j.cell.2020.07.012.

Lionel, A., Wickham, H., and Henry, M. L. (2022). Package ‘ rlang .’

Minh, B. Q., Schmidt, H. A., Chernomor, O., Schrempf, D., Woodhams, M. D., von Haeseler, A., et al. (2020). IQ-TREE 2: New Models and Efficient Methods for Phylogenetic Inference in the Genomic Era. *Mol. Biol. Evol.* 37, 1530–1534. doi:10.1093/molbev/msaa015.

Mitchell, P. K., Martins, M., Reilly, T., Caserta, L. C., Anderson, R. R., Cronk, B. D., et al. (2021). SARS-CoV-2 B.1.1.7 Variant Infection in Malayan Tigers, Virginia, USA. *Emerg. Infect. Dis.* 27, 3171–3173. doi:10.3201/eid2712.211234.

OPAS, O. P. A. DE S. Alerta Epidemiológico COVID-19: Aumento de hospitalizações e mortes entre pacientes com menos de 60 anos de idade. 26 de abril de 2021.

Oran, D. P., and Topol, E. J. (2021). The Proportion of SARS-CoV-2 Infections That Are Asymptomatic : A Systematic Review. *Ann. Intern. Med.* 174, 655–662. doi:10.7326/M20-6976.

Paulo, C.-S. (2021). SARS-CoV-2 variants in severely symptomatic and deceased persons who had been vaccinated against. 1–5.

Paulo, S., Nanev, S., Bezerra, S., Strazza, E., Vieira, E., Serrano, J., et al. (2022). Genomic monitoring of the SARS-CoV-2 B1 . 1 . 7 (WHO VOC Alpha) in the. 308. doi:10.1016/j.virusres.2021.198643.

Quinlan, A. R., and Hall, I. M. (2010). BEDTools : a flexible suite of utilities for comparing genomic features. 26, 841–842. doi:10.1093/bioinformatics/btq033.

Ramundo, M. S., Jesus, J. G. De, Andrade, P. S., and Coletti, T. M. (2021). Genomics and epidemiology of the P.1 SARS-CoV-2 lineage in Manaus, Brazil. 821, 815–821.

Romero, F., Moreira, R., Mirela, D., Mariani, D., Herlinger, A. L., Schiffler, F. B., et al. (2021). Epidemiological dynamics of SARS-CoV-2 VOC Gamma in Rio de Janeiro , Brazil. 7.

Sagulenko, P., Puller, V., and Neher, R. (2018). TreeTime: Maximum-likelihood phylodynamic analysis. *Virus Evol.* 4, vex042. doi:10.1093/ve/vex042.

Sant’Anna, F. H., Muterle Varela, A. P., Prichula, J., Comerlato, J., Comerlato, C. B., Roglio, V. S., et al. (2021). Emergence of the novel SARS-CoV-2 lineage VUI-NP13L and

massive spread of P.2 in South Brazil. *Emerg. Microbes Infect.* 10, 1431–1440. doi:10.1080/22221751.2021.1949948.

Silva, J. P., Lima, A. B. De, Alvim, L. B., Mendonça, C. P. T. B., Fonseca, P. L. C., Moreira, F. R. R., et al. (2022). Delta Variant of SARS-CoV-2 Replacement in Brazil : A National Epidemiologic Surveillance Program.

Slavov, S. N., Giovanetti, M., Dos Santos Bezerra, R., Fonseca, V., Santos, E. V., Rodrigues, E. S., et al. (2021). Molecular surveillance of the on-going SARS-COV-2 epidemic in Ribeirao Preto City, Brazil. *Infect. Genet. Evol. J. Mol. Epidemiol. Evol. Genet. Infect. Dis.* 93, 104976. doi:10.1016/j.meegid.2021.104976.

Sumner, M., Cook, I., and Baston, D. (2022). Package ‘ sf .’

Tavare, S. (1986). Some probabilistic and statistical problems in the analysis of DNA sequences. *Some Math. Quest. Biol. / DNA Seq. Anal. Ed. by Robert M. Miura*.

Tegally, H., Wilkinson, E., Giovanetti, M., Iranzadeh, A., Fonseca, V., Giandhari, J., et al. (2021). Detection of a SARS-CoV-2 variant of concern in South Africa. *Nature* 592, 438–443. doi:10.1038/s41586-021-03402-9.

Torres, C., Mojsiejczuk, L., Acuña, D., Alexay, S., Amadio, A., Aulicino, P., et al. (2021). Cost-Effective Method to Perform SARS-CoV-2 Variant Surveillance : Detection of Alpha , Gamma , Lambda , Delta , Epsilon , and Zeta in Argentina. 8, 1–10. doi:10.3389/fmed.2021.755463.

Voloch, C. M., da Silva Francisco, R., de Almeida, L. G. P., Cardoso, C. C., Brustolini, O. J., Gerber, A. L., et al. (2021a). Genomic Characterization of a Novel SARS-CoV-2 Lineage from Rio de Janeiro, Brazil. *J. Virol.* 95, 1–5. doi:10.1128/jvi.00119-21.

Voloch, C. M., da Silva Francisco, R. J., de Almeida, L. G. P., Cardoso, C. C., Brustolini, O. J., Gerber, A. L., et al. (2021b). Genomic characterization of a novel SARS-CoV-2 lineage from Rio de Janeiro, Brazil. *J. Virol.* 95. doi:10.1128/JVI.00119-21.

Volz, E., Mishra, S., Chand, M., Barrett, J. C., Johnson, R., Geidelberg, L., et al. (2021). Assessing transmissibility of SARS-CoV-2 lineage B.1.1.7 in England. *Nature* 593, 266–269. doi:10.1038/s41586-021-03470-x.

Wang, B. X. (2020). Susceptibility and prognosis of COVID-19 patients with cardiovascular disease. *Open Hear.* 7, 7–9. doi:10.1136/openhrt-2020-001310.

Washington, N. L., Gangavarapu, K., Zeller, M., Bolze, A., Cirulli, E. T., Schiabor Barrett, K. M., et al. (2021). Emergence and rapid transmission of SARS-CoV-2 B.1.1.7 in the United States. *Cell* 184, 2587-2594.e7. doi:10.1016/j.cell.2021.03.052.

WHO (2022). COVID-19 weekly epidemiological update. *World Heal. Organ.*, 1–23.

Available at: https://www.who.int/publications/m/item/covid-19-weekly-epidemiological-update.

Wiersinga, W. J., Rhodes, A., Cheng, A. C., Peacock, S. J., and Prescott, H. C. (2020). Pathophysiology, Transmission, Diagnosis, and Treatment of Coronavirus Disease 2019 (COVID-19): A Review. *JAMA* 324, 782–793. doi:10.1001/jama.2020.12839.

Yang, Z. (1994). Maximum likelihood phylogenetic estimation from DNA sequences with variable rates over sites: approximate methods. *J. Mol. Evol.* 39, 306–314. doi:10.1007/BF00160154.

Zhou, Y., Chi, J., Lv, W., and Wang, Y. (2021). Obesity and diabetes as high-risk factors for severe coronavirus disease 2019 (Covid-19). *Diabetes. Metab. Res. Rev.* 37, e3377. doi:10.1002/dmrr.3377.

TABLE AND FIGURE LEGENDS

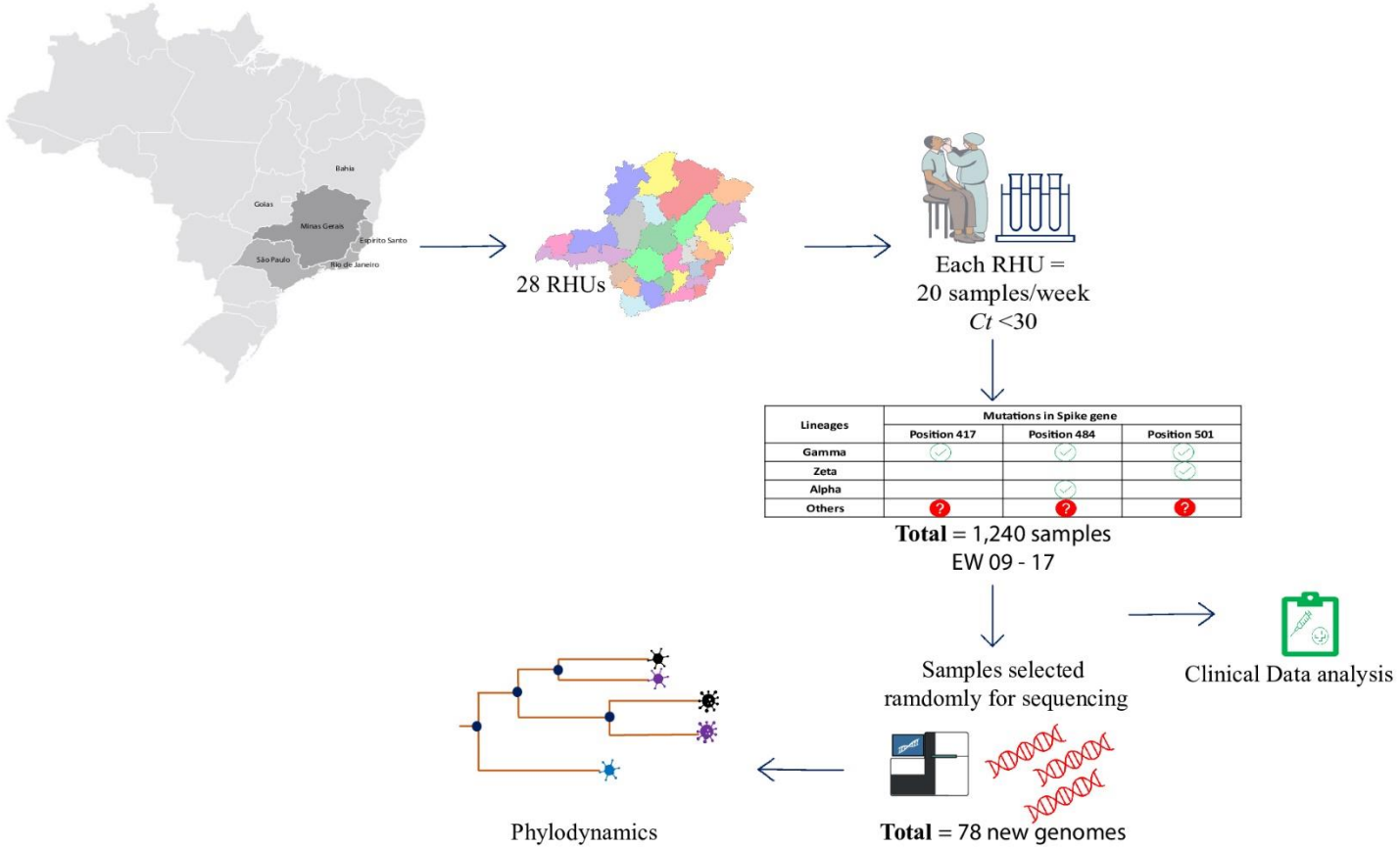

Figure 1. Graphic representation of the methodological process used in this work. Samples were collected from 28 Regional Health Units (RHU) in the state of Minas Gerais, totaling 1240 nasopharyngeal swab samples. All samples were submitted to rhAmp genotyping metodology to profile K417T, E484K and N501Y mutations and 78 genomes were sequenced for phylogeny and phylogeography analysis. Available clinical data from the collected samples were annotated and epidemiological data from the entire state were collected such as Ct values, number of confirmed cases and number of deaths.

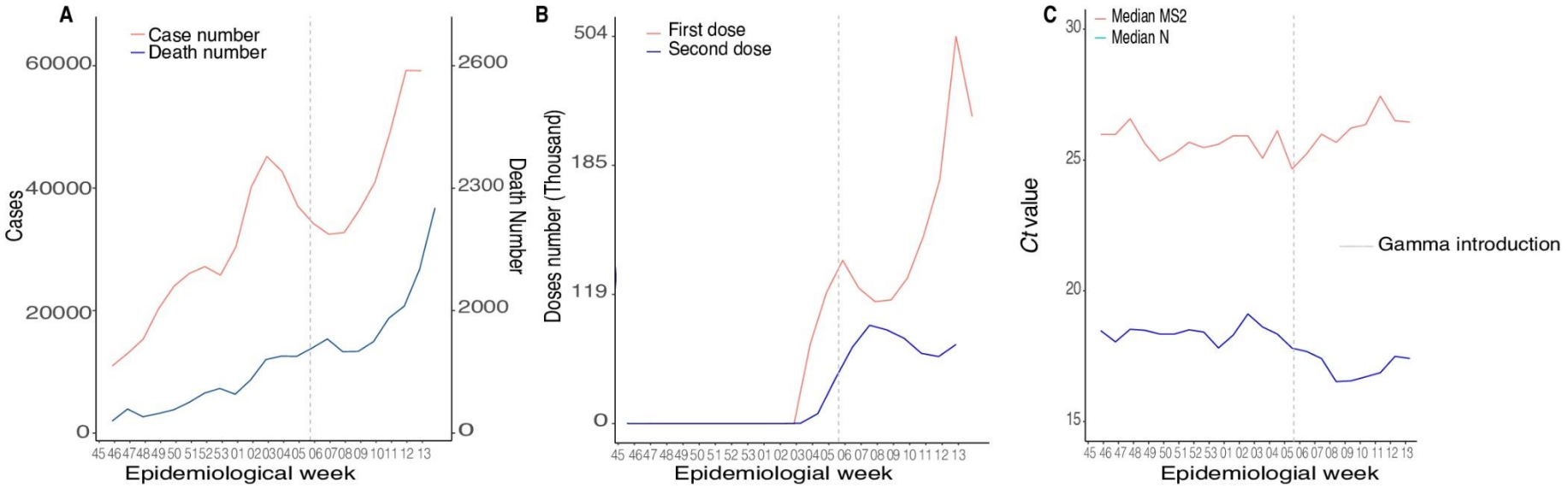

Figure 2. Temporal distribution of epidemiological data between Epidemiological Weeks 45/2020 - 13/2021. **(A)** Distribution of the number of positive SARS-CoV-2 cases and deaths in Brazil. **(B)** Number of 1st and 2nd vaccine doses distributed in the country. **(C)** Distribution of Ct's from samples diagnosed in the country by the RT-PCR methodology for SARS-CoV-2 N gene and MS2 (intern control gene).

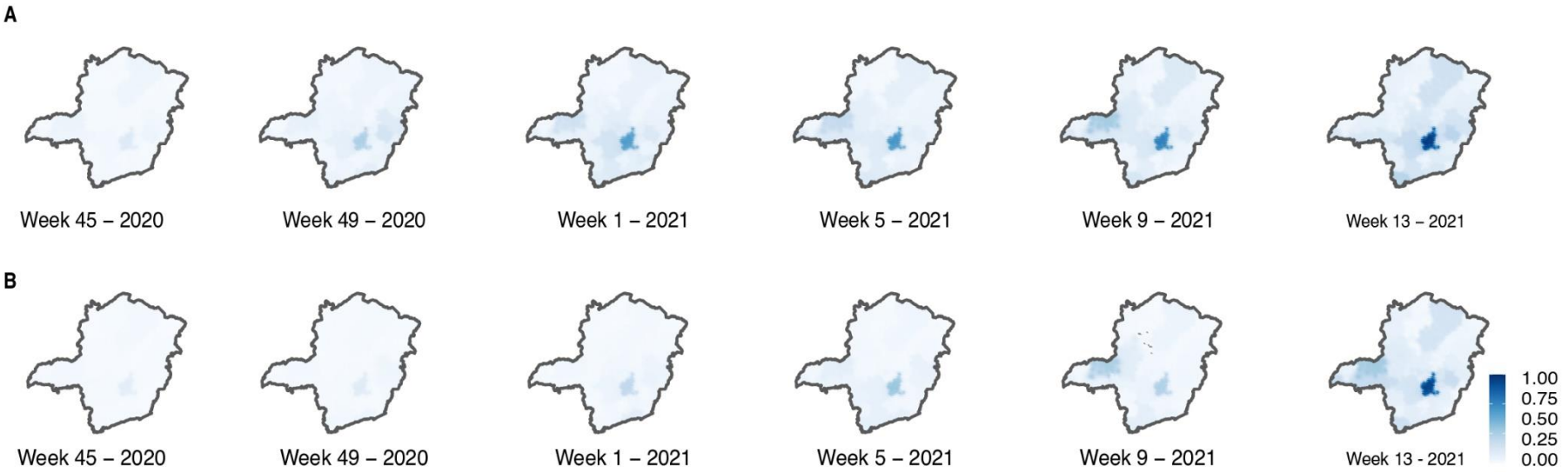

Figure 3. Spatio-temporal distribution of epidemiological data between Epidemiological Weeks 45/2020 - 13/2021. **(D)** Distribution of the number of positive cases for SARS-CoV-2 in the state of Minas Gerais. **(E)** Distribution of the number of deaths in the state of Minas Gerais.

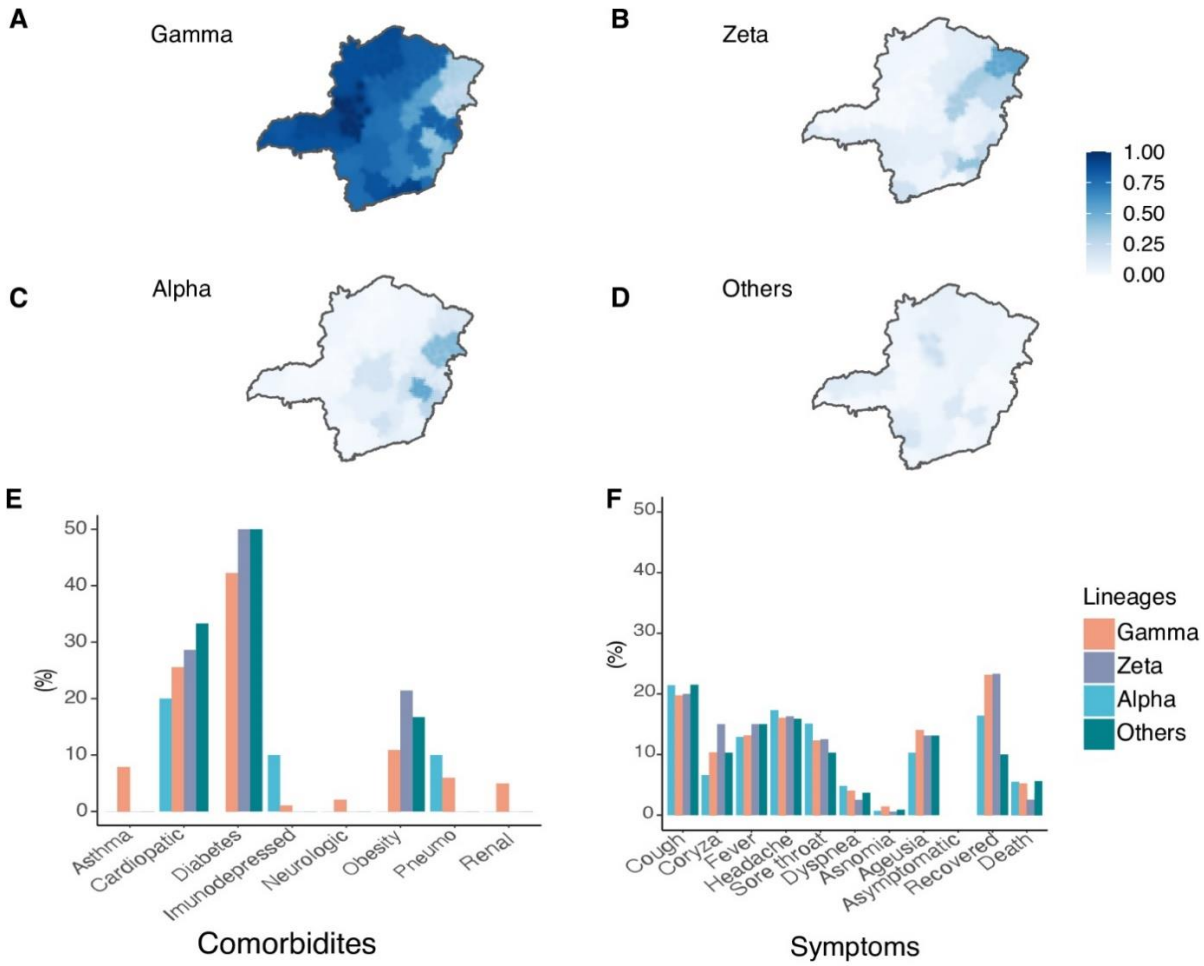

Figure 4. Distribution of SARS-CoV-2 lineages in the state of Minas Gerais and clinical data from the samples collected. **(A)** Spatial distribution of samples genotyped as VOC Gamma. **(B)** Spatial distribution of samples genotyped as Zeta lineage. (C) Spatial distribution of samples genotyped as VOC Alpha. **(D)** Spatial distribution of samples genotyped as "Other" lineages. **(E)** Relationship among reported comorbidities and SARS-CoV-2 variants found in the samples. **(F)** Relationship between reported outcomes and SARS-CoV-2 lineages found in the samples from our study.

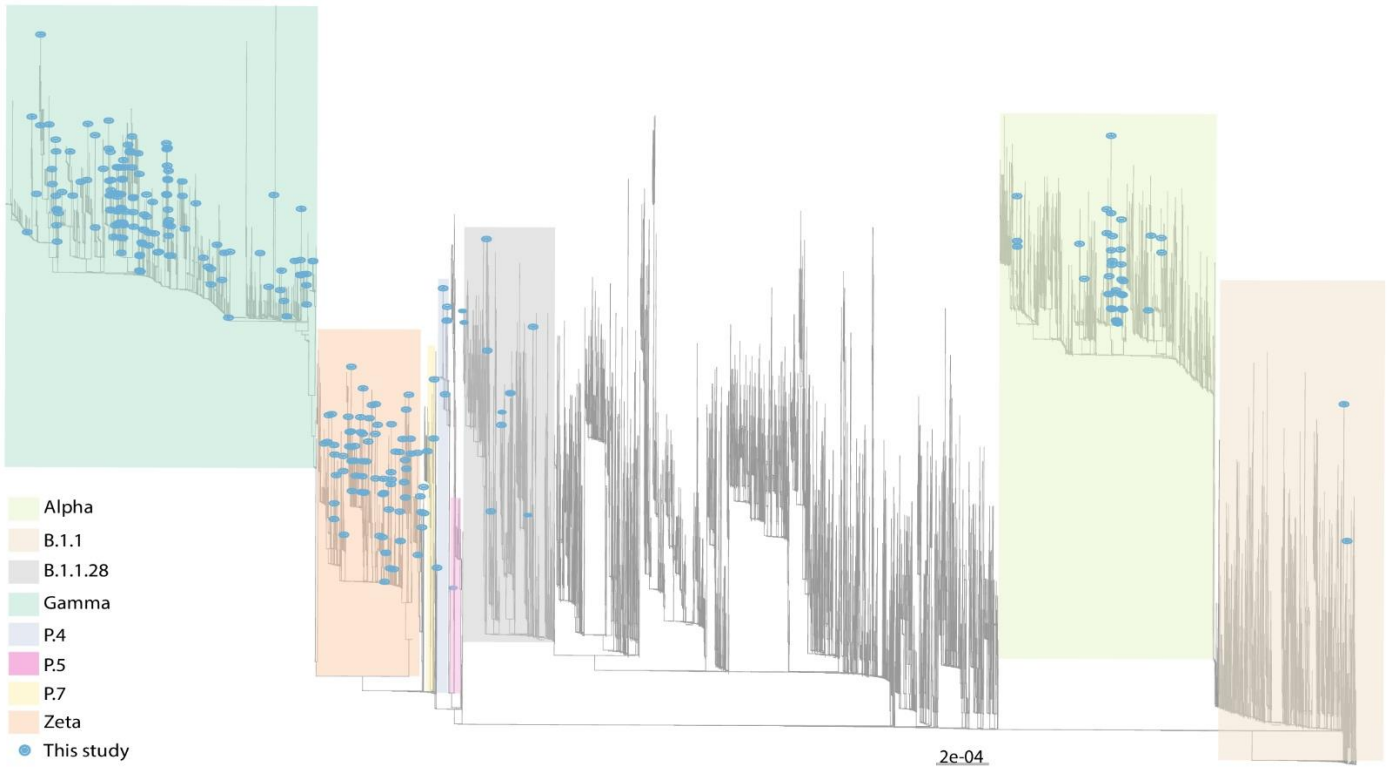

Figure 5. Maximum likelihood inference phylogeny to corroborate the lineage classification using a global reference dataset (see material and methods section). The genomes generated in our study (n=240) are represented by blue circles. Lineages Alpha, Gamma and Zeta are represented by the colors. Samples genotyped as "Others" were sequenced as Lineages B.1.1, B.1.1.28, P4, P5 and P7, represented by the colors.

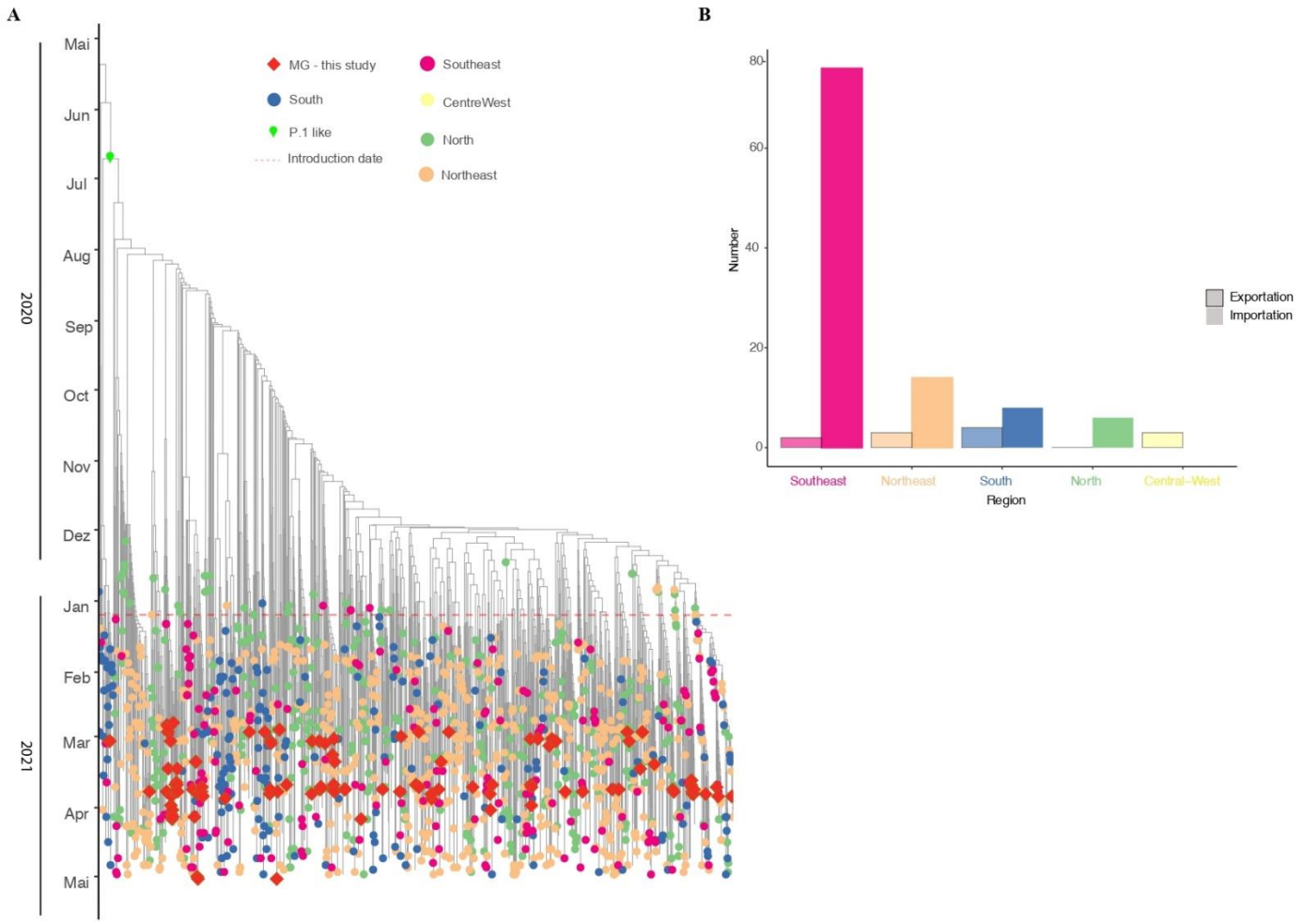

Figure 6. Molecular clock of novel Gamma genomes with a comprehensive Brazilian dataset (see material and methods). Time scaled phytogeographic estimated with TreeTime under a fixed evolutionary rate (10-3 s/s/y) and a six-states symmetric discrete model (North, Northeast, Southeast, South, Central-West in MG.

Supplementary Figure 1. Representation of the 28 Regional Health Units in the state of Minas Gerais.

Supplementary Table 1. Information about the sample used in this work. Description of the 1240 samples on the regional health units obtained, collection date, municipality of origin and result of genotyping.

CODE	DATE OF COLLECTION	CITY	RHU	DIAGNOSTIC KIT	LINEAGE
MG01	2021/03/01	MONTE CARMELO	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG02	2021/03/01	BELO HORIZONTE	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG03	2021/03/01	BELO HORIZONTE	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG04	2021/03/01	BELO HORIZONTE	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG05	2021/03/01	BELO HORIZONTE	UBERLANDIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG06	2021/03/01	N.I.	UBERLANDIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG07	2021/03/01	BELO HORIZONTE	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG08	2021/03/01	BELO HORIZONTE	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG09	2021/03/01	MURIAE	UBA	CDC KIT	ZETA
MG10	2021/03/01	MURIAE	UBA	CDC KIT	OTHERS
MG11	2021/03/01	RIO CASCA	PONTE NOVA	CDC KIT	GAMMA
MG12	2021/03/01	RIO CASCA	PONTE NOVA	CDC KIT	GAMMA
MG13	2021/03/01	RIO CASCA	PONTE NOVA	CDC KIT	GAMMA
MG14	2021/03/01	AIMORES	GOVERNADOR VALADARES	CDC KIT	GAMMA
MG15	2021/03/01	RESPLENDOR	GOVERNADOR VALADARES	CDC KIT	ZETA
MG16	2021/03/01	RIO CASCA	PONTE NOVA	CDC KIT	GAMMA
MG17	2021/03/01	VARZEA DA PALMA	PIRAPORA	CDC KIT	GAMMA
MG18	2021/03/02	CONTAGEM	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG19	2021/03/02	CONTAGEM	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG20	2021/03/02	CONTAGEM	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG21	2021/03/02	CONTAGEM	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG22	2021/03/02	MONTALVANIA	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG23	2021/03/02	BELO HORIZONTE	JANUARIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG24	2021/03/02	N.I.	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG25	2021/03/02	ALVORADA DE MINAS	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA

MG26	2021/03/02	ARACUAI	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG27	2021/03/02	ARACUAI	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG28	2021/03/02	CAPELINHA	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG29	2021/03/02	CAPELINHA	PATOS DE MINAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG30	2021/03/02	SÃO GONÇALO DO ABAETÉ	UBERLANDIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG31	2021/03/03	SARZEDO	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG32	2021/03/03	PADRE PARAISO	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG33	2021/03/03	TEOFILO OTONI	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG34	2021/03/03	BELO HORIZONTE	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG35	2021/03/03	BELO HORIZONTE	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG36	2021/03/03	BELO HORIZONTE	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG37	2021/03/03	BELO HORIZONTE	TEOFILO OTONI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG38	2021/03/03	BELO HORIZONTE	TEOFILO OTONI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG39	2021/03/03	BELO HORIZONTE	UBERLANDIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG40	2021/03/03	BELO HORIZONTE	UBERLANDIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG41	2021/03/03	N.I.	UBERLANDIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG42	2021/03/03	N.I.	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG43	2021/03/03	N.I.	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG44	2021/03/03	COLUNA	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG45	2021/03/04	CATAGUASES	LEOPOLDINA	CDC KIT	GAMMA
MG46	2021/03/04	ALEM PARAIBA	LEOPOLDINA	CDC KIT	GAMMA
MG47	2021/03/04	CAMPO FLORIDO	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG48	2021/03/04	CAMPO FLORIDO	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG49	2021/03/04	CAMPO FLORIDO	UBERABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG50	2021/03/04	CAMPO FLORIDO	UBERABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG51	2021/03/04	BELO HORIZONTE	UBERABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG52	2021/03/04	BELO HORIZONTE	UBERABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG53	2021/03/04	BELO HORIZONTE	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA

MG54	2021/03/04	BELO HORIZONTE	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG55	2021/03/04	GOVERNADOR VALADARES	GOVERNADOR VALADARES	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG56	2021/03/04	COLUNA	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG57	2021/03/05	VARZEA DA PALMA	PIRAPORA	CDC KIT	GAMMA
MG58	2021/03/05	SANTO ANTONIO DO MONTE	DIVINOPOLIS	CDC KIT	GAMMA
MG59	2021/03/05	AUGUSTO DE LIMA	SETE LAGOAS	CDC KIT	GAMMA
MG60	2021/03/05	PARACATU	UNAI	CDC KIT	GAMMA
MG61	2021/03/05	PARACATU	UNAI	CDC KIT	GAMMA
MG62	2021/03/05	PARACATU	UNAI	CDC KIT	GAMMA
MG63	2021/03/05	PARACATU	PONTE NOVA	CDC KIT	ZETA
MG64	2021/03/05	ALVINOPOLIS	SETE LAGOAS	CDC KIT	GAMMA
MG65	2021/03/05	FELIXLANDIA	MONTES CLAROS	CDC KIT	GAMMA
MG66	2021/03/05	MONTES CLAROS	UBA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG67	2021/03/05	DIVINESIA	UBA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG68	2021/03/05	UBA	UBA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG69	2021/03/05	UBA	UBA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG70	2021/03/05	UBA	UBA	CDC KIT	GAMMA
MG71	2021/03/05	UBA	UBA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG72	2021/03/05	UBA	UBA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG73	2021/03/05	UBA	UBA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG74	2021/03/05	UBA	UBA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG75	2021/03/05	UBA	UBA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG76	2021/03/05	UBA	CORONEL FABRICIANO	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG77	2021/03/05	CORONEL FABRICIANO	PONTE NOVA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG78	2021/03/05	RIO CASCA	PONTE NOVA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG79	2021/03/05	RIO CASCA	ITABIRA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG80	2021/03/05	RIO PIRACICABA	SETE LAGOAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG81	2021/03/05	SETE LAGOAS	SETE LAGOAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA

MG82	2021/03/05	ARACAI	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG83	2021/03/05	MATOZINHOS	BARBACENA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG84	2021/03/05	JECEABA	DIVINOPOLIS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG85	2021/03/05	CAMPO BELO	BARBACENA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG86	2021/03/05	CIPOTANEA	UBA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG87	2021/03/05	TOCANTINS	UBA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG88	2021/03/05	TOCANTINS	UBA	CDC KIT	GAMMA
MG89	2021/03/05	TOCANTINS	SAO JOAO DEL REI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG90	2021/03/05	BOM SUCESSO	VARGINHA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG91	2021/03/05	CAXAMBU	VARGINHA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG92	2021/03/05	CAXAMBU	VARGINHA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG93	2021/03/05	CAXAMBU	POUSO ALEGRE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG94	2021/03/05	CAMBUI	POUSO ALEGRE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG95	2021/03/05	CAMBUI	POUSO ALEGRE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG96	2021/03/05	CAMBUI	BARBACENA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG97	2021/03/05	SAO BRAS DO SUACUI	ALFENAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG98	2021/03/05	MUZAMBINHO	SETE LAGOAS	CDC KIT	ALPHA
MG99	2021/03/05	TRES MARIAS	VARGINHA	CDC KIT	GAMMA
MG100	2021/03/05	CARVALHOS	UBA	CDC KIT	GAMMA
MG101	2021/03/05	RIO POMBA	POUSO ALEGRE	CDC KIT	GAMMA
MG102	2021/03/05	BUENO BRANDAO	VARGINHA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG103	2021/03/05	AIURUOCA	POUSO ALEGRE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG104	2021/03/05	BUENO BRANDAO	VARGINHA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG105	2021/03/05	CARVALHOS	DIVINOPOLIS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG106	2021/03/05	SANTO ANTONIO DO MONTE	VARGINHA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG107	2021/03/05	SERITINGA	UBA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG108	2021/03/05	RIO POMBA	UBA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG109	2021/03/05	RIO POMBA	UBA	CDC KIT	GAMMA

MG110	2021/03/05	RIO POMBA	UBA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG111	2021/03/05	RIO POMBA	POUSO ALEGRE	CDC KIT	ZETA
MG112	2021/03/05	ANDRADAS	POUSO ALEGRE	CDC KIT	ZETA
MG113	2021/03/05	ANDRADAS	POUSO ALEGRE	CDC KIT	ZETA
MG114	2021/03/05	ANDRADAS	POUSO ALEGRE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG115	2021/03/05	ANDRADAS	POUSO ALEGRE	CDC KIT	GAMMA
MG116	2021/03/05	ANDRADAS	POUSO ALEGRE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG117	2021/03/05	ANDRADAS	UBA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG118	2021/03/05	ERVALIA	UBA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG119	2021/03/05	ERVALIA	PONTE NOVA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG120	2021/03/05	SAO PEDRO DOS FERROS	UBA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG121	2021/03/05	MURIAE	UBA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG122	2021/03/05	MURIAE	UBA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG123	2021/03/05	MURIAE	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG124	2021/03/05	BRUMADINHO	DIVINOPOLIS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG125	2021/03/05	FORMIGA	PONTE NOVA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG126	2021/03/05	VICOSA	VARGINHA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG127	2021/03/05	SAO SEBASTIAO DO RIO VERDE	VARGINHA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG128	2021/03/05	SAO LOURENCO	VARGINHA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG129	2021/03/05	ITANHANDU	VARGINHA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG130	2021/03/05	ITANHANDU	ITABIRA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG131	2021/03/05	SANTA BARBARA	TEOFILO OTONI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG132	2021/03/05	NANUQUE	TEOFILO OTONI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG133	2021/03/05	CARAI	TEOFILO OTONI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG134	2021/03/05	CARLOS CHAGAS	TEOFILO OTONI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG135	2021/03/05	SANTA HELENA DE MINAS	TEOFILO OTONI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG136	2021/03/05	PADRE PARAISO	TEOFILO OTONI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG137	2021/03/05	ITAMBACURI	UBERLANDIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA

MG138	2021/03/05	CAMPO BELO	PASSOS	CDC KIT	GAMMA
MG139	2021/03/05	MOEDA	UNAI	CDC KIT	OTHERS
MG140	2021/03/05	VARZEA DA PALMA	DIVINOPOLIS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG141	2021/03/05	CAPELINHA	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG142	2021/03/05	MARIO CAMPOS	PIRAPORA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG143	2021/03/05	N.I.	DIAMANTINA	CDC KIT	OTHERS
MG144	2021/03/05	PIUMHI	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG145	2021/03/06	SAO SEBASTIAO DO PARAISO	PASSOS	CDC KIT	GAMMA
MG146	2021/03/06	PARACATU	UNAI	CDC KIT	GAMMA
MG147	2021/03/06	PARACATU	UNAI	CDC KIT	ZETA
MG148	2021/03/06	PARACATU	UNAI	CDC KIT	GAMMA
MG149	2021/03/06	JENIPAPO DE MINAS	DIAMANTINA	CDC KIT	ZETA
MG150	2021/03/06	UBERABA	UBERABA	CDC KIT	GAMMA
MG151	2021/03/06	FRUTAL	UBERABA	CDC KIT	GAMMA
MG152	2021/03/06	FRUTAL	UBERABA	CDC KIT	GAMMA
MG153	2021/03/06	ITURAMA	UBERABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG154	2021/03/06	ITURAMA	UBERABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG155	2021/03/06	FRONTEIRA	UBERABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG156	2021/03/06	FRONTEIRA	UBERABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG157	2021/03/06	VERISSIMO	UBERABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG158	2021/03/06	VERISSIMO	UBERABA	CDC KIT	ZETA
MG159	2021/03/06	PIRAJUBA	UBERABA	CDC KIT	GAMMA
MG160	2021/03/06	PIRAJUBA	UBERABA	CDC KIT	GAMMA
MG161	2021/03/06	ARAXA	UBERABA	CDC KIT	ZETA
MG162	2021/03/06	PIRACEMA	DIVINOPOLIS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG163	2021/03/06	BETIM	BELO HORIZONTE	CDC KIT	GAMMA
MG164	2021/03/06	BETIM	BELO HORIZONTE	CDC KIT	ZETA
MG165	2021/03/06	LAGOA SANTA	BELO HORIZONTE	CDC KIT	GAMMA

MG166	2021/03/06	SANTANA DO MANHUACU	MANHUAÇU	CDC KIT	ALPHA
MG167	2021/03/06	COIMBRA	UBA	CDC KIT	ZETA
MG168	2021/03/07	PARACATU	UNAI	CDC KIT	GAMMA
MG169	2021/03/07	PARACATU	UNAI	CDC KIT	GAMMA
MG170	2021/03/07	PARACATU	UNAI	CDC KIT	GAMMA
MG171	2021/03/07	FELIXLANDIA	SETE LAGOAS	CDC KIT	GAMMA
MG172	2021/03/07	IPATINGA	CORONEL FABRICIANO	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG173	2021/03/07	OLIVEIRA	DIVINOPOLIS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG174	2021/03/07	COLUNA	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG175	2021/03/08	MONTES CLAROS	MONTES CLAROS	CDC KIT	GAMMA
MG176	2021/03/08	MONTES CLAROS	MONTES CLAROS	CDC KIT	GAMMA
MG177	2021/03/08	MONTES CLAROS	MONTES CLAROS	CDC KIT	GAMMA
MG178	2021/03/08	MONTES CLAROS	MONTES CLAROS	CDC KIT	GAMMA
MG179	2021/03/08	MONTES CLAROS	MONTES CLAROS	CDC KIT	GAMMA
MG180	2021/03/08	MONTES CLAROS	MONTES CLAROS	CDC KIT	ZETA
MG181	2021/03/08	MONTES CLAROS	MONTES CLAROS	CDC KIT	GAMMA
MG182	2021/03/08	MONTES CLAROS	MONTES CLAROS	CDC KIT	GAMMA
MG183	2021/03/08	MONTES CLAROS	MONTES CLAROS	CDC KIT	GAMMA
MG184	2021/03/08	MONTES CLAROS	MONTES CLAROS	CDC KIT	GAMMA
MG185	2021/03/08	MONTES CLAROS	MONTES CLAROS	CDC KIT	OTHERS
MG186	2021/03/08	MONTES CLAROS	MONTES CLAROS	CDC KIT	ZETA
MG187	2021/03/08	MONTES CLAROS	MONTES CLAROS	CDC KIT	GAMMA
MG188	2021/03/08	MONTES CLAROS	MONTES CLAROS	CDC KIT	GAMMA
MG189	2021/03/08	MONTES CLAROS	MONTES CLAROS	CDC KIT	GAMMA
MG190	2021/03/08	MONTES CLAROS	MONTES CLAROS	CDC KIT	GAMMA
MG191	2021/03/08	MONTES CLAROS	MONTES CLAROS	CDC KIT	GAMMA
MG192	2021/03/08	MONTES CLAROS	MONTES CLAROS	CDC KIT	GAMMA
MG193	2021/03/08	MONTES CLAROS	MONTES CLAROS	CDC KIT	GAMMA

MG194	2021/03/08	MONTES CLAROS	MONTES CLAROS	CDC KIT	GAMMA
MG195	2021/03/08	MONTES CLAROS	MONTES CLAROS	CDC KIT	GAMMA
MG196	2021/03/08	MONTES CLAROS	MONTES CLAROS	CDC KIT	GAMMA
MG197	2021/03/08	MONTES CLAROS	MONTES CLAROS	CDC KIT	GAMMA
MG198	2021/03/08	MONTES CLAROS	MONTES CLAROS	CDC KIT	GAMMA
MG199	2021/03/08	MONTES CLAROS	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG200	2021/03/08	MONTES CLAROS	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG201	2021/03/08	SAO JOSE DO DIVINO	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG202	2021/03/08	IPATINGA	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG203	2021/03/08	IPATINGA	TEOFILO OTONI	CDC KIT	ALPHA
MG204	2021/03/08	ITAMBACURI	CORONEL FABRICIANO	CDC KIT	ALPHA
MG205	2021/03/08	PAVAO	CORONEL FABRICIANO	CDC KIT	GAMMA
MG206	2021/03/08	BELO HORIZONTE	TEOFILO OTONI	CDC KIT	ALPHA
MG207	2021/03/08	BELO HORIZONTE	TEOFILO OTONI	CDC KIT	ALPHA
MG208	2021/03/08	BELO HORIZONTE	UBERLANDIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG209	2021/03/08	BELO HORIZONTE	UBERLANDIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG210	2021/03/08	N.I.	UBERLANDIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG211	2021/03/08	N.I.	UBERLANDIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG212	2021/03/08	N.I.	UBERLANDIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG213	2021/03/08	N.I.	UBERLANDIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG214	2021/03/08	N.I.	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG215	2021/03/08	N.I.	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG216	2021/03/08	N.I.	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG217	2021/03/08	COLUNA	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG218	2021/03/08	COUTO DE MAGALHAES DE MINAS	MONTES CLAROS	CDC KIT	OTHERS
MG219	2021/03/08	COUTO DE MAGALHAES DE MINAS	MONTES CLAROS	CDC KIT	OTHERS
MG220	2021/03/08	COUTO DE MAGALHAES DE MINAS	UBERLANDIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG221	2021/03/09	CARNEIRINHO	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA

MG222	2021/03/09	PLANURA	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG223	2021/03/09	VERISSIMO	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG224	2021/03/09	CONQUISTA	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG225	2021/03/09	LAGOA SANTA	UBERABA	CDC KIT	ZETA
MG226	2021/03/09	DIVINOPOLIS	UBERABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG227	2021/03/09	BELO HORIZONTE	UBERABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG228	2021/03/09	BELO HORIZONTE	UBERABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG229	2021/03/09	BELO HORIZONTE	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG230	2021/03/09	BELO HORIZONTE	DIVINOPOLIS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG231	2021/03/09	BELO HORIZONTE	UBERLANDIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG232	2021/03/09	N.I.	UBA	CDC KIT	ZETA
MG233	2021/03/09	UBA	BELO HORIZONTE	CDC KIT	GAMMA
MG234	2021/03/09	PEDRO LEOPOLDO	BELO HORIZONTE	CDC KIT	GAMMA
MG235	2021/03/09	BELO HORIZONTE	BELO HORIZONTE	CDC KIT	GAMMA
MG236	2021/03/09	IGARAPE	BELO HORIZONTE	CDC KIT	GAMMA
MG237	2021/03/09	IGARAPE	BELO HORIZONTE	CDC KIT	ZETA
MG238	2021/03/09	IGARAPE	BELO HORIZONTE	CDC KIT	OTHERS
MG239	2021/03/09	IGARAPE	PATOS DE MINAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG240	2021/03/09	SÃO GONÇALO DO ABAETÉ	PATOS DE MINAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG241	2021/03/09	CRUZEIRO DA FORTALEZA	PATOS DE MINAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG242	2021/03/09	CARMO DO PARANAÍBA	PATOS DE MINAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG243	2021/03/09	LAGOA GRANDE	PATOS DE MINAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG244	2021/03/09	CARMO DO PARANAÍBA	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG245	2021/03/10	CATAGUASES	LEOPOLDINA	CDC KIT	GAMMA
MG246	2021/03/10	ARACUAI	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG247	2021/03/10	ARACUAI	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG248	2021/03/10	ARACUAI	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG249	2021/03/10	ARACUAI	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA

MG250	2021/03/10	ARACUAI	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG251	2021/03/10	VAZANTE	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG252	2021/03/10	ITAOBIM	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG253	2021/03/10	BELO HORIZONTE	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG254	2021/03/10	BELO HORIZONTE	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG255	2021/03/10	BELO HORIZONTE	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG256	2021/03/10	BELO HORIZONTE	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG257	2021/03/10	BELO HORIZONTE	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG258	2021/03/10	BELO HORIZONTE	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG259	2021/03/10	BELO HORIZONTE	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG260	2021/03/10	BELO HORIZONTE	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG261	2021/03/10	BELO HORIZONTE	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG262	2021/03/10	BELO HORIZONTE	PATOS DE MINAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG263	2021/03/10	BELO HORIZONTE	PEDRA AZUL	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG264	2021/03/10	BELO HORIZONTE	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG265	2021/03/11	CORINTO	SETE LAGOAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG266	2021/03/11	IBIRITE	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG267	2021/03/11	ITABIRA	ITABIRA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG268	2021/03/11	DATAS	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG269	2021/03/11	DATAS	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG270	2021/03/11	DATAS	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG271	2021/03/12	FELIXLANDIA	SETE LAGOAS	CDC KIT	GAMMA
MG272	2021/03/12	SANTO ANTONIO DO MONTE	DIVINOPOLIS	CDC KIT	GAMMA
MG273	2021/03/12	SANTO ANTONIO DO MONTE	DIVINOPOLIS	CDC KIT	GAMMA
MG274	2021/03/12	SANTANA DE PIRAPAMA	SETE LAGOAS	CDC KIT	ZETA
MG275	2021/03/12	TOMBOS	MANHUAÇU	CDC KIT	GAMMA
MG276	2021/03/12	FERVEDOURO	MANHUAÇU	CDC KIT	GAMMA
MG277	2021/03/12	SABINOPOLIS	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA

MG278	2021/03/12	SABINOPOLIS	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG279	2021/03/12	SABINOPOLIS	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG280	2021/03/12	AGUA COMPRIDA	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG281	2021/03/12	COMENDADOR GOMES	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG282	2021/03/12	COMENDADOR GOMES	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG283	2021/03/12	SAO FRANCISCO DE SALES	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG284	2021/03/12	CARNEIRINHO	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG285	2021/03/12	PRATA	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG286	2021/03/12	PRATA	UBERABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG287	2021/03/12	ATALEIA	UBERABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG288	2021/03/12	BELO HORIZONTE	UBERABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG289	2021/03/12	BELO HORIZONTE	UBERABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG290	2021/03/12	BELO HORIZONTE	UBERABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG291	2021/03/12	BELO HORIZONTE	UBERLANDIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG292	2021/03/12	BELO HORIZONTE	UBERLANDIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG293	2021/03/12	BELO HORIZONTE	TEOFILO OTONI	CDC KIT	ZETA
MG294	2021/03/12	BELO HORIZONTE	UBERLANDIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG295	2021/03/12	N.I.	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG296	2021/03/12	BELO HORIZONTE	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG297	2021/03/13	FELIXLANDIA	SETE LAGOAS	CDC KIT	GAMMA
MG298	2021/03/13	FELIXLANDIA	SETE LAGOAS	CDC KIT	GAMMA
MG299	2021/03/13	ITANHOMI	GOVERNADOR VALADARES	CDC KIT	ZETA
MG300	2021/03/13	MATHIAS LOBATO	GOVERNADOR VALADARES	CDC KIT	GAMMA
MG301	2021/03/13	MATHIAS LOBATO	GOVERNADOR VALADARES	CDC KIT	GAMMA
MG302	2021/03/13	ANDRADAS	POUSO ALEGRE	CDC KIT	ZETA
MG303	2021/03/13	ESPERA FELIZ	MANHUAÇU	CDC KIT	ALPHA
MG304	2021/03/13	SAO LOURENCO	VARGINHA	CDC KIT	GAMMA
MG305	2021/03/13	AGUA COMPRIDA	UBERABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA

MG306	2021/03/13	LIMEIRA DO OESTE	UBERABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG307	2021/03/13	PRATA	UBERLANDIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG308	2021/03/13	CAMPINA VERDE	ITUIUTABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG309	2021/03/13	SAO SEBASTIAO DO PARAISO	PASSOS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG310	2021/03/13	POCOS DE CALDAS	POUSO ALEGRE	CDC KIT	GAMMA
MG311	2021/03/14	FELIXLANDIA	SETE LAGOAS	CDC KIT	GAMMA
MG312	2021/03/14	ANDRADAS	POUSO ALEGRE	CDC KIT	ZETA
MG313	2021/03/14	PRADOS	SAO JOAO DEL REI	CDC KIT	GAMMA
MG314	2021/03/14	ITUIUTABA	ITUIUTABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG315	2021/03/14	ITUIUTABA	ITUIUTABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG316	2021/03/14	ITUIUTABA	ITUIUTABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG317	2021/03/14	SANTA VITORIA	ITUIUTABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG318	2021/03/14	ACUCENA	CORONEL FABRICIANO	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG319	2021/03/14	CATAS ALTAS	ITABIRA	CDC KIT	GAMMA
MG320	2021/03/15	RESPLENDOR	GOVERNADOR VALADARES	CDC KIT	GAMMA
MG321	2021/03/15	RESPLENDOR	GOVERNADOR VALADARES	CDC KIT	GAMMA
MG322	2021/03/15	RESPLENDOR	GOVERNADOR VALADARES	CDC KIT	GAMMA
MG323	2021/03/15	RESPLENDOR	GOVERNADOR VALADARES	CDC KIT	GAMMA
MG324	2021/03/15	SANTO ANTONIO DO MONTE	DIVINOPOLIS	CDC KIT	GAMMA
MG325	2021/03/15	SANTO ANTONIO DO MONTE	VARGINHA	CDC KIT	GAMMA
MG326	2021/03/15	ITANHANDU	VARGINHA	CDC KIT	GAMMA
MG327	2021/03/15	SAO LOURENCO	VARGINHA	CDC KIT	GAMMA
MG328	2021/03/15	SAO LOURENCO	VARGINHA	CDC KIT	GAMMA
MG329	2021/03/15	SAO LOURENCO	VARGINHA	CDC KIT	GAMMA
MG330	2021/03/15	SAO LOURENCO	SAO JOAO DEL REI	CDC KIT	GAMMA
MG331	2021/03/15	SAO LOURENCO	LEOPOLDINA	CDC KIT	GAMMA
MG332	2021/03/15	PRADOS	CORONEL FABRICIANO	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG333	2021/03/15	ALEM PARAIBA	CORONEL FABRICIANO	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA

MG334	2021/03/15	CARATINGA	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG335	2021/03/15	BELO ORIENTE	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG336	2021/03/15	VIRGEM DA LAPA	ITUIUTABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG337	2021/03/15	TURMALINA	ITUIUTABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG338	2021/03/15	CAMPINA VERDE	ITUIUTABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG339	2021/03/15	CAMPINA VERDE	ITUIUTABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG340	2021/03/15	CAMPINA VERDE	ITUIUTABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG341	2021/03/15	CAMPINA VERDE	PEDRA AZUL	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG342	2021/03/15	CAMPINA VERDE	PEDRA AZUL	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG343	2021/03/15	ITINGA	PEDRA AZUL	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG344	2021/03/15	ITAOBIM	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG345	2021/03/15	ITAOBIM	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG346	2021/03/15	BELO HORIZONTE	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG347	2021/03/15	BELO HORIZONTE	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG348	2021/03/15	BELO HORIZONTE	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG349	2021/03/15	BELO HORIZONTE	UBERLANDIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG350	2021/03/15	BELO HORIZONTE	UNAI	CDC KIT	GAMMA
MG351	2021/03/15	BELO HORIZONTE	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG352	2021/03/15	N.I.	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG353	2021/03/15	BURITIS	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG354	2021/03/15	BELO HORIZONTE	DIVINOPOLIS	CDC KIT	OTHERS
MG355	2021/03/15	BELO HORIZONTE	VARGINHA	CDC KIT	OTHERS
MG356	2021/03/15	DIAMANTINA	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG357	2021/03/16	ALEM PARAIBA	LEOPOLDINA	CDC KIT	GAMMA
MG358	2021/03/16	ALEM PARAIBA	LEOPOLDINA	CDC KIT	GAMMA
MG359	2021/03/16	CARATINGA	CORONEL FABRICIANO	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG360	2021/03/16	CARATINGA	CORONEL FABRICIANO	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG361	2021/03/16	CARATINGA	CORONEL FABRICIANO	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA

MG362	2021/03/16	CARATINGA	CORONEL FABRICIANO	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG363	2021/03/16	CARATINGA	CORONEL FABRICIANO	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG364	2021/03/16	BELO ORIENTE	CORONEL FABRICIANO	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG365	2021/03/16	NAQUE	CORONEL FABRICIANO	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG366	2021/03/16	NAQUE	CORONEL FABRICIANO	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG367	2021/03/16	ENTRE FOLHAS	CORONEL FABRICIANO	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG368	2021/03/16	ARACUAI	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG369	2021/03/16	ARACUAI	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG370	2021/03/16	ARACUAI	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG371	2021/03/16	ARACUAI	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG372	2021/03/16	ARACUAI	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG373	2021/03/16	TURMALINA	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG374	2021/03/16	TURMALINA	PEDRA AZUL	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG375	2021/03/16	JACINTO	PEDRA AZUL	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG376	2021/03/16	JACINTO	PEDRA AZUL	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG377	2021/03/16	JACINTO	PEDRA AZUL	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG378	2021/03/16	COMERCINHO	PEDRA AZUL	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG379	2021/03/16	ALMENARA	PEDRA AZUL	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG380	2021/03/16	COMERCINHO	PEDRA AZUL	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG381	2021/03/16	ITAOBIM	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG382	2021/03/16	BETIM	UBERABA	CDC KIT	GAMMA
MG383	2021/03/16	COMENDADOR GOMES	UBERABA	CDC KIT	GAMMA
MG384	2021/03/16	PERDIZES	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG385	2021/03/16	BELO HORIZONTE	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG386	2021/03/16	DIAMANTINA	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG387	2021/03/17	ALEM PARAIBA	LEOPOLDINA	CDC KIT	GAMMA
MG388	2021/03/17	ALEM PARAIBA	LEOPOLDINA	CDC KIT	GAMMA
MG389	2021/03/17	ALEM PARAIBA	LEOPOLDINA	CDC KIT	GAMMA

MG390	2021/03/17	CATAGUASES	LEOPOLDINA	CDC KIT	ZETA
MG391	2021/03/17	MUZAMBINHO	ALFENAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG392	2021/03/17	MUZAMBINHO	ALFENAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG393	2021/03/17	MUZAMBINHO	ALFENAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG394	2021/03/17	MUZAMBINHO	ALFENAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG395	2021/03/17	MUZAMBINHO	ALFENAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG396	2021/03/17	MUZAMBINHO	ALFENAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG397	2021/03/17	MUZAMBINHO	ALFENAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG398	2021/03/17	CARATINGA	CORONEL FABRICIANO	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG399	2021/03/17	CARATINGA	CORONEL FABRICIANO	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG400	2021/03/17	CORONEL FABRICIANO	CORONEL FABRICIANO	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG401	2021/03/17	IMBE DE MINAS	CORONEL FABRICIANO	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG402	2021/03/17	IAPU	CORONEL FABRICIANO	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG403	2021/03/17	IAPU	CORONEL FABRICIANO	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG404	2021/03/17	UBAPORANGA	CORONEL FABRICIANO	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG405	2021/03/17	INHAPIM	CORONEL FABRICIANO	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG406	2021/03/17	CARATINGA	CORONEL FABRICIANO	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG407	2021/03/17	SABINOPOLIS	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG408	2021/03/17	SABINOPOLIS	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG409	2021/03/17	SABINOPOLIS	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG410	2021/03/17	SABINOPOLIS	JANUARIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG411	2021/03/17	VARZELANDIA	PASSOS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG412	2021/03/17	ITAU DE MINAS	PEDRA AZUL	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG413	2021/03/17	MONTE FORMOSO	UNAI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG414	2021/03/17	BURITIS	UNAI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG415	2021/03/17	BURITIS	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG416	2021/03/17	BETIM	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG417	2021/03/17	CRISOLITA	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA

MG418	2021/03/17	MINAS NOVAS	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG419	2021/03/17	BELO HORIZONTE	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG420	2021/03/17	BELO HORIZONTE	BELO HORIZONTE	CDC KIT	GAMMA
MG421	2021/03/17	BELO HORIZONTE	TEOFILO OTONI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG422	2021/03/17	BELO HORIZONTE	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG423	2021/03/17	BELO HORIZONTE	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG424	2021/03/17	BELO HORIZONTE	PONTE NOVA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG425	2021/03/17	BELO HORIZONTE	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG426	2021/03/17	PONTE NOVA	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG427	2021/03/17	DIAMANTINA	PATOS DE MINAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG428	2021/03/17	FELICIO DOS SANTOS	PATOS DE MINAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG429	2021/03/17	JOÃO PINHEIRO	PATOS DE MINAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG430	2021/03/17	JOÃO PINHEIRO	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG431	2021/03/17	JOÃO PINHEIRO	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG432	2021/03/18	ALEM PARAIBA	LEOPOLDINA	CDC KIT	GAMMA
MG433	2021/03/18	ALEM PARAIBA	LEOPOLDINA	CDC KIT	GAMMA
MG434	2021/03/18	ALEM PARAIBA	LEOPOLDINA	CDC KIT	GAMMA
MG435	2021/03/18	MUZAMBINHO	ALFENAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG436	2021/03/18	MUZAMBINHO	ALFENAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG437	2021/03/18	GUARANESIA	ALFENAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG438	2021/03/18	CARATINGA	CORONEL FABRICIANO	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG439	2021/03/18	IBIRACATU	JANUARIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG440	2021/03/18	VARZELANDIA	JANUARIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG441	2021/03/18	VARZELANDIA	JANUARIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG442	2021/03/18	VARZELANDIA	JANUARIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG443	2021/03/18	VARZELANDIA	JANUARIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG444	2021/03/18	VARZELANDIA	JANUARIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG445	2021/03/18	VARZELANDIA	JANUARIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA

MG446	2021/03/18	MANGA	JANUARIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG447	2021/03/18	MATO VERDE	MONTES CLAROS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG448	2021/03/18	MATO VERDE	MONTES CLAROS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG449	2021/03/18	MATO VERDE	MONTES CLAROS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG450	2021/03/18	MONTE SANTO DE MINAS	PASSOS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG451	2021/03/18	MONTE SANTO DE MINAS	PASSOS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG452	2021/03/18	MONTES CLAROS	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG453	2021/03/18	MONTES CLAROS	MONTES CLAROS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG454	2021/03/18	MONTES CLAROS	MONTES CLAROS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG455	2021/03/18	MONTES CLAROS	MONTES CLAROS	CDC KIT	GAMMA
MG456	2021/03/18	MONTES CLAROS	MONTES CLAROS	CDC KIT	GAMMA
MG457	2021/03/18	MONTES CLAROS	MONTES CLAROS	CDC KIT	GAMMA
MG458	2021/03/18	SAO JOAO DA LAGOA	MONTES CLAROS	CDC KIT	GAMMA
MG459	2021/03/18	MONTES CLAROS	MONTES CLAROS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG460	2021/03/18	MONTES CLAROS	MONTES CLAROS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG461	2021/03/18	MONTES CLAROS	MONTES CLAROS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG462	2021/03/18	MONTES CLAROS	MONTES CLAROS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG463	2021/03/18	MONTES CLAROS	MONTES CLAROS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG464	2021/03/18	MONTES CLAROS	MONTES CLAROS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG465	2021/03/18	MONTES CLAROS	MONTES CLAROS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG466	2021/03/18	MONTES CLAROS	MONTES CLAROS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG467	2021/03/18	MONTES CLAROS	MONTES CLAROS	CDC KIT	GAMMA
MG468	2021/03/18	MONTES CLAROS	MONTES CLAROS	CDC KIT	GAMMA
MG469	2021/03/18	MONTES CLAROS	MONTES CLAROS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG470	2021/03/18	CURVELO	MONTES CLAROS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG471	2021/03/18	CARMESIA	SETE LAGOAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG472	2021/03/18	MONJOLOS	ITABIRA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG473	2021/03/18	VICOSA	SETE LAGOAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA

MG474	2021/03/18	VICOSA	PONTE NOVA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG475	2021/03/18	VICOSA	PONTE NOVA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG476	2021/03/18	VICOSA	PONTE NOVA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG477	2021/03/18	CORDISBURGO	PONTE NOVA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG478	2021/03/18	AUGUSTO DE LIMA	SETE LAGOAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG479	2021/03/18	PARACATU	SETE LAGOAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG480	2021/03/18	PARACATU	UNAI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG481	2021/03/18	PARACATU	UNAI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG482	2021/03/18	CORREGO DANTA	UNAI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG483	2021/03/18	CAMPINA VERDE	DIVINOPOLIS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG484	2021/03/18	CAMPINA VERDE	ITUIUTABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG485	2021/03/18	BELO HORIZONTE	ITUIUTABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG486	2021/03/18	BELO HORIZONTE	UBERLANDIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG487	2021/03/18	BELO HORIZONTE	UBERLANDIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG488	2021/03/18	N.I.	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG489	2021/03/18	N.I.	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG490	2021/03/18	BELO HORIZONTE	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG491	2021/03/18	BELO HORIZONTE	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG492	2021/03/18	FELICIO DOS SANTOS	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG493	2021/03/19	RIO CASCA	PONTE NOVA	CDC KIT	GAMMA
MG494	2021/03/19	RIO CASCA	DIVINOPOLIS	CDC KIT	GAMMA
MG495	2021/03/19	AMPARO DA SERRA	ALFENAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG496	2021/03/19	SANTO ANTONIO DO MONTE	CORONEL FABRICIANO	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG497	2021/03/19	GUARANESIA	CORONEL FABRICIANO	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG498	2021/03/19	CARATINGA	PASSOS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG499	2021/03/19	CARATINGA	PEDRA AZUL	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG500	2021/03/19	MONTE SANTO DE MINAS	PEDRA AZUL	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG501	2021/03/19	COMERCINHO	PEDRA AZUL	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA

MG502	2021/03/19	COMERCINHO	PEDRA AZUL	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG503	2021/03/19	DIVISOPOLIS	PEDRA AZUL	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG504	2021/03/19	PEDRA AZUL	PEDRA AZUL	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG505	2021/03/19	DIVISOPOLIS	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG506	2021/03/19	ALMENARA	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG507	2021/03/19	IPATINGA	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG508	2021/03/19	CATUJI	CORONEL FABRICIANO	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG509	2021/03/19	ITABIRITO	TEOFILO OTONI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG510	2021/03/19	BELO HORIZONTE	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG511	2021/03/19	BELO HORIZONTE	UBERLANDIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG512	2021/03/19	BELO HORIZONTE	UBERLANDIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG513	2021/03/19	BELO HORIZONTE	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG514	2021/03/19	BELO HORIZONTE	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG515	2021/03/19	N.I.	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG516	2021/03/19	N.I.	PONTE NOVA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG517	2021/03/19	BELO HORIZONTE	PONTE NOVA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG518	2021/03/19	BELO HORIZONTE	PONTE NOVA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG519	2021/03/19	BELO HORIZONTE	PONTE NOVA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG520	2021/03/19	VICOSA	DIVINOPOLIS	CDC KIT	GAMMA
MG521	2021/03/19	PONTE NOVA	DIVINOPOLIS	CDC KIT	GAMMA
MG522	2021/03/19	PONTE NOVA	PONTE NOVA	CDC KIT	OTHERS
MG523	2021/03/19	PONTE NOVA	PONTE NOVA	CDC KIT	OTHERS
MG524	2021/03/19	ITAUNA	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG525	2021/03/19	ITAUNA	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG526	2021/03/20	SANTO ANTONIO DO MONTE	DIVINOPOLIS	CDC KIT	GAMMA
MG527	2021/03/20	PARACATU	UNAI	CDC KIT	GAMMA
MG528	2021/03/20	PARACATU	UNAI	CDC KIT	GAMMA
MG529	2021/03/20	RESPLENDOR	GOVERNADOR VALADARES	CDC KIT	GAMMA

MG530	2021/03/20	GUAXUPE	ALFENAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG531	2021/03/20	GUAXUPE	ALFENAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG532	2021/03/20	CAPINOPOLIS	ITUIUTABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG533	2021/03/20	VARZEA DA PALMA	PIRAPORA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG534	2021/03/20	LIMEIRA DO OESTE	UBERABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG535	2021/03/20	CONQUISTA	UBERABA	CDC KIT	GAMMA
MG536	2021/03/20	COMENDADOR GOMES	UBERABA	CDC KIT	GAMMA
MG537	2021/03/20	UNIAO DE MINAS	UBERABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG538	2021/03/20	UNIAO DE MINAS	UBERABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG539	2021/03/20	CONQUISTA	UBERABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG540	2021/03/20	VERISSIMO	UBERABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG541	2021/03/20	SANTA LUZIA	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG542	2021/03/20	AUGUSTO DE LIMA	SETE LAGOAS	CDC KIT	ALPHA
MG543	2021/03/21	MANGA	JANUARIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG544	2021/03/21	MANGA	JANUARIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG545	2021/03/21	MANGA	JANUARIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG546	2021/03/21	MANGA	JANUARIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG547	2021/03/21	MANGA	JANUARIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG548	2021/03/21	MANGA	JANUARIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG549	2021/03/21	MONTALVANIA	JANUARIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG550	2021/03/21	MONTALVANIA	JANUARIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG551	2021/03/21	MONTALVANIA	JANUARIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG552	2021/03/21	MONTALVANIA	JANUARIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG553	2021/03/21	JANUARIA	MONTES CLAROS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG554	2021/03/21	MIRABELA	PIRAPORA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG555	2021/03/21	PIRAPORA	PIRAPORA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG556	2021/03/21	PIRAPORA	PIRAPORA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG557	2021/03/21	PIRAPORA	PIRAPORA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA

MG558	2021/03/21	PIRAPORA	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG559	2021/03/21	CONCEICAO DO MATO DENTRO	CORONEL FABRICIANO	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG560	2021/03/21	TIMOTEO	ITABIRA	CDC KIT	GAMMA
MG561	2021/03/21	JOAO MONLEVADE	ITABIRA	CDC KIT	GAMMA
MG562	2021/03/21	JOAO MONLEVADE	PONTE NOVA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG563	2021/03/21	PONTE NOVA	UBA	CDC KIT	GAMMA
MG564	2021/03/21	MURIAE	UBA	CDC KIT	ZETA
MG565	2021/03/21	MURIAE	DIVINOPOLIS	CDC KIT	GAMMA
MG566	2021/03/21	ITAUNA	DIVINOPOLIS	CDC KIT	GAMMA
MG567	2021/03/21	PIRACEMA	DIVINOPOLIS	CDC KIT	GAMMA
MG568	2021/03/21	ITAUNA	JANUARIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG569	2021/03/22	TRES MARIAS	SETE LAGOAS	CDC KIT	ALPHA
MG570	2021/03/22	TRES MARIAS	SETE LAGOAS	CDC KIT	GAMMA
MG571	2021/03/22	TRES MARIAS	SETE LAGOAS	CDC KIT	ZETA
MG572	2021/03/22	TRES MARIAS	SETE LAGOAS	CDC KIT	GAMMA
MG573	2021/03/22	RESPLENDOR	GOVERNADOR VALADARES	CDC KIT	GAMMA
MG574	2021/03/22	LAMIM	BARBACENA	CDC KIT	GAMMA
MG575	2021/03/22	LAMIM	BARBACENA	CDC KIT	GAMMA
MG576	2021/03/22	SAO BRAS DO SUACUI	BARBACENA	CDC KIT	GAMMA
MG577	2021/03/22	SAO BRAS DO SUACUI	BARBACENA	CDC KIT	ALPHA
MG578	2021/03/22	SAO BRAS DO SUACUI	BARBACENA	CDC KIT	GAMMA
MG579	2021/03/22	SAO BRAS DO SUACUI	BARBACENA	CDC KIT	GAMMA
MG580	2021/03/22	PARAGUACU	ALFENAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG581	2021/03/22	CORONEL FABRICIANO	CORONEL FABRICIANO	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG582	2021/03/22	CORONEL FABRICIANO	CORONEL FABRICIANO	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG583	2021/03/22	CAMPINA VERDE	ITUIUTABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG584	2021/03/22	CAMPINA VERDE	ITUIUTABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG585	2021/03/22	CAMPINA VERDE	ITUIUTABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA

MG586	2021/03/22	CAMPINA VERDE	ITUIUTABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG587	2021/03/22	CAMPINA VERDE	ITUIUTABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG588	2021/03/22	CAPINOPOLIS	ITUIUTABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG589	2021/03/22	JANUARIA	JANUARIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG590	2021/03/22	JANUARIA	JANUARIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG591	2021/03/22	ESPINOSA	MONTES CLAROS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG592	2021/03/22	PIMENTA	PASSOS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG593	2021/03/22	PIMENTA	PASSOS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG594	2021/03/22	CAPITOLIO	PASSOS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG595	2021/03/22	MONTE SANTO DE MINAS	PASSOS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG596	2021/03/22	DIVISOPOLIS	PEDRA AZUL	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG597	2021/03/22	DIVISOPOLIS	PEDRA AZUL	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG598	2021/03/22	MEDINA	PEDRA AZUL	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG599	2021/03/22	PIRAPORA	PIRAPORA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG600	2021/03/22	IBIAI	PIRAPORA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG601	2021/03/22	IBIAI	PIRAPORA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG602	2021/03/22	IBIAI	PIRAPORA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG603	2021/03/22	IBIAI	PIRAPORA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG604	2021/03/22	IBIAI	PIRAPORA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG605	2021/03/22	BURITIZEIRO	PIRAPORA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG606	2021/03/22	SERRA DOS AIMORES	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG607	2021/03/22	LADAINHA	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG608	2021/03/22	NOVO CRUZEIRO	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG609	2021/03/22	BELO HORIZONTE	TEOFILO OTONI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG610	2021/03/22	BELO HORIZONTE	TEOFILO OTONI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG611	2021/03/22	BELO HORIZONTE	TEOFILO OTONI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG612	2021/03/22	BELO HORIZONTE	UBERLANDIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG613	2021/03/22	BELO HORIZONTE	ITABIRA	CDC KIT	ALPHA

MG614	2021/03/22	N.I.	ITABIRA	CDC KIT	GAMMA
MG615	2021/03/22	NOVA ERA	ITABIRA	CDC KIT	GAMMA
MG616	2021/03/22	JOAO MONLEVADE	PONTE NOVA	CDC KIT	GAMMA
MG617	2021/03/22	JOAO MONLEVADE	ITABIRA	CDC KIT	ALPHA
MG618	2021/03/22	BARRA LONGA	ITABIRA	CDC KIT	ALPHA
MG619	2021/03/22	JOAO MONLEVADE	ITABIRA	CDC KIT	GAMMA
MG620	2021/03/22	BARAO DE COCAIS	ITABIRA	CDC KIT	GAMMA
MG621	2021/03/22	NOVA ERA	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG622	2021/03/22	NOVA ERA	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG623	2021/03/22	FELICIO DOS SANTOS	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG624	2021/03/22	FELICIO DOS SANTOS	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG625	2021/03/22	GOUVEA	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG626	2021/03/22	GOUVEA	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG627	2021/03/22	GOUVEA	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG628	2021/03/22	ITAMARANDIBA	DIVINOPOLIS	CDC KIT	GAMMA
MG629	2021/03/22	ITAMARANDIBA	DIVINOPOLIS	CDC KIT	GAMMA
MG630	2021/03/22	SANTANA DO JACARE	DIVINOPOLIS	CDC KIT	GAMMA
MG631	2021/03/22	CONCEICAO DO PARA	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG632	2021/03/22	BAMBUI	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG633	2021/03/23	ALVINOPOLIS	SAO JOAO DEL REI	CDC KIT	ALPHA
MG634	2021/03/23	ALVINOPOLIS	SAO JOAO DEL REI	CDC KIT	ALPHA
MG635	2021/03/23	ALVINOPOLIS	SAO JOAO DEL REI	CDC KIT	ALPHA
MG636	2021/03/23	BOM SUCESSO	SAO JOAO DEL REI	CDC KIT	ALPHA
MG637	2021/03/23	BOM SUCESSO	SAO JOAO DEL REI	CDC KIT	ALPHA
MG638	2021/03/23	BOM SUCESSO	BARBACENA	CDC KIT	GAMMA
MG639	2021/03/23	BOM SUCESSO	GOVERNADOR VALADARES	CDC KIT	GAMMA
MG640	2021/03/23	BOM SUCESSO	GOVERNADOR VALADARES	CDC KIT	GAMMA
MG641	2021/03/23	SAO BRAS DO SUACUI	GOVERNADOR VALADARES	CDC KIT	GAMMA

MG642	2021/03/23	GOVERNADOR VALADARES	GOVERNADOR VALADARES	CDC KIT	GAMMA
MG643	2021/03/23	GOVERNADOR VALADARES	GOVERNADOR VALADARES	CDC KIT	GAMMA
MG644	2021/03/23	GOVERNADOR VALADARES	GOVERNADOR VALADARES	CDC KIT	GAMMA
MG645	2021/03/23	GOVERNADOR VALADARES	GOVERNADOR VALADARES	CDC KIT	GAMMA
MG646	2021/03/23	GOVERNADOR VALADARES	ALFENAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG647	2021/03/23	GOVERNADOR VALADARES	ALFENAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG648	2021/03/23	GOVERNADOR VALADARES	CORONEL FABRICIANO	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG649	2021/03/23	CABO VERDE	CORONEL FABRICIANO	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG650	2021/03/23	CABO VERDE	CORONEL FABRICIANO	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG651	2021/03/23	SANTANA DO PARAISO	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG652	2021/03/23	CARATINGA	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG653	2021/03/23	CARATINGA	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG654	2021/03/23	FRANCISCO BADARO	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG655	2021/03/23	FRANCISCO BADARO	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG656	2021/03/23	FRANCISCO BADARO	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG657	2021/03/23	FRANCISCO BADARO	JANUARIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG658	2021/03/23	FRANCISCO BADARO	JANUARIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG659	2021/03/23	MINAS NOVAS	MONTES CLAROS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG660	2021/03/23	ITUIUTABA	MONTES CLAROS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG661	2021/03/23	JANUARIA	MONTES CLAROS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG662	2021/03/23	JANUARIA	MONTES CLAROS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG663	2021/03/23	CLARO DOS POCOES	MONTES CLAROS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG664	2021/03/23	SAO JOAO DO PACUI	MONTES CLAROS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG665	2021/03/23	OLHOS-D"AGUA	MONTES CLAROS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG666	2021/03/23	MATO VERDE	PASSOS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG667	2021/03/23	CATUTI	PASSOS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG668	2021/03/23	ESPINOSA	PASSOS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG669	2021/03/23	FRUTA DE LEITE	PASSOS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA

MG670	2021/03/23	CASSIA	PASSOS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG671	2021/03/23	CASSIA	PASSOS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG672	2021/03/23	MONTE SANTO DE MINAS	PEDRA AZUL	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG673	2021/03/23	MONTE SANTO DE MINAS	PEDRA AZUL	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG674	2021/03/23	PASSOS	PEDRA AZUL	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG675	2021/03/23	PASSOS	PEDRA AZUL	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG676	2021/03/23	DIVISOPOLIS	PEDRA AZUL	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG677	2021/03/23	COMERCINHO	PEDRA AZUL	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG678	2021/03/23	JACINTO	PEDRA AZUL	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG679	2021/03/23	JACINTO	PIRAPORA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG680	2021/03/23	JORDANIA	PIRAPORA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG681	2021/03/23	JORDANIA	PIRAPORA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG682	2021/03/23	ITAOBIM	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG683	2021/03/23	PIRAPORA	UBERABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG684	2021/03/23	PIRAPORA	UBERABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG685	2021/03/23	VARZEA DA PALMA	DIVINOPOLIS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG686	2021/03/23	VARZEA DA PALMA	UBERLANDIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG687	2021/03/23	PIRAPORA	UBERLANDIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG688	2021/03/23	PIRAPORA	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG689	2021/03/23	SABARA	PONTE NOVA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG690	2021/03/23	UNIAO DE MINAS	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG691	2021/03/23	ARAXA	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG692	2021/03/23	LUZ	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG693	2021/03/23	N.I.	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG694	2021/03/23	N.I.	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG695	2021/03/23	BELO HORIZONTE	PONTE NOVA	CDC KIT	OTHERS
MG696	2021/03/23	VICOSA	PONTE NOVA	CDC KIT	OTHERS
MG697	2021/03/23	GOUVEA	PONTE NOVA	CDC KIT	OTHERS

MG698	2021/03/23	ITAMARANDIBA	ITUIUTABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG699	2021/03/23	ITAMARANDIBA	PIRAPORA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG700	2021/03/23	PRESIDENTE KUBITSCHEK	PIRAPORA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG701	2021/03/23	PRESIDENTE KUBITSCHEK	PIRAPORA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG702	2021/03/24	CABO VERDE	ALFENAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG703	2021/03/24	CABO VERDE	ALFENAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG704	2021/03/24	CABO VERDE	ALFENAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG705	2021/03/24	MUZAMBINHO	ALFENAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG706	2021/03/24	MUZAMBINHO	ALFENAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG707	2021/03/24	MUZAMBINHO	ALFENAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG708	2021/03/24	MUZAMBINHO	ALFENAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG709	2021/03/24	MUZAMBINHO	ALFENAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG710	2021/03/24	MUZAMBINHO	ALFENAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG711	2021/03/24	MUZAMBINHO	CORONEL FABRICIANO	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG712	2021/03/24	MUZAMBINHO	CORONEL FABRICIANO	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG713	2021/03/24	SANTANA DO PARAISO	JANUARIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG714	2021/03/24	CARATINGA	JANUARIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG715	2021/03/24	SAO JOAO DAS MISSOES	PASSOS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG716	2021/03/24	JANUARIA	PASSOS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG717	2021/03/24	PIMENTA	PEDRA AZUL	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG718	2021/03/24	PIMENTA	PEDRA AZUL	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG719	2021/03/24	JOAIMA	PEDRA AZUL	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG720	2021/03/24	PEDRA AZUL	PEDRA AZUL	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG721	2021/03/24	ITINGA	PIRAPORA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG722	2021/03/24	ITINGA	PIRAPORA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG723	2021/03/24	PIRAPORA	PIRAPORA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG724	2021/03/24	PIRAPORA	PIRAPORA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG725	2021/03/24	PIRAPORA	UNAI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA

MG726	2021/03/24	PIRAPORA	UNAI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG727	2021/03/24	PIRAPORA	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG728	2021/03/24	UNAI	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG729	2021/03/24	BURITIS	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG730	2021/03/24	JUATUBA	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG731	2021/03/24	SANTA LUZIA	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG732	2021/03/24	CAMPANARIO	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG733	2021/03/24	MALACACHETA	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG734	2021/03/24	LADAINHA	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG735	2021/03/24	NOVO ORIENTE DE MINAS	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG736	2021/03/24	FRONTEIRA DOS VALES	TEOFILO OTONI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG737	2021/03/24	FRONTEIRA DOS VALES	TEOFILO OTONI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG738	2021/03/24	AGUAS FORMOSAS	TEOFILO OTONI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG739	2021/03/24	POCOS DE CALDAS	TEOFILO OTONI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG740	2021/03/24	POCOS DE CALDAS	TEOFILO OTONI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG741	2021/03/24	POCOS DE CALDAS	TEOFILO OTONI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG742	2021/03/24	POCOS DE CALDAS	TEOFILO OTONI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG743	2021/03/24	POCOS DE CALDAS	UBERLANDIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG744	2021/03/24	POCOS DE CALDAS	UBERLANDIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG745	2021/03/24	POCOS DE CALDAS	UBERLANDIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG746	2021/03/24	POCOS DE CALDAS	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG747	2021/03/24	POCOS DE CALDAS	SAO JOAO DEL REI	CDC KIT	GAMMA
MG748	2021/03/24	POCOS DE CALDAS	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG749	2021/03/24	POCOS DE CALDAS	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG750	2021/03/24	ITAJUBA	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG751	2021/03/24	ITAJUBA	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG752	2021/03/24	ITAJUBA	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG753	2021/03/24	BELO HORIZONTE	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA

MG754	2021/03/24	BELO HORIZONTE	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG755	2021/03/24	BELO HORIZONTE	POUSO ALEGRE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG756	2021/03/24	BELO HORIZONTE	POUSO ALEGRE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG757	2021/03/24	BELO HORIZONTE	POUSO ALEGRE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG758	2021/03/24	BELO HORIZONTE	POUSO ALEGRE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG759	2021/03/24	BELO HORIZONTE	POUSO ALEGRE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG760	2021/03/24	BELO HORIZONTE	POUSO ALEGRE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG761	2021/03/24	N.I.	POUSO ALEGRE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG762	2021/03/24	N.I.	POUSO ALEGRE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG763	2021/03/24	N.I.	POUSO ALEGRE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG764	2021/03/24	N.I.	POUSO ALEGRE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG765	2021/03/24	BELO HORIZONTE	POUSO ALEGRE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG766	2021/03/24	BOM SUCESSO	POUSO ALEGRE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG767	2021/03/24	PRESIDENTE KUBITSCHEK	POUSO ALEGRE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG768	2021/03/24	SAO GONCALO DO RIO PRETO	POUSO ALEGRE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG769	2021/03/24	SAO GONCALO DO RIO PRETO	ALFENAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG770	2021/03/24	SAO GONCALO DO RIO PRETO	ALFENAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG771	2021/03/24	SAO GONCALO DO RIO PRETO	PIRAPORA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG772	2021/03/24	SABINOPOLIS	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG773	2021/03/24	SANTO ANTONIO DO ITAMBE	UBERLANDIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG774	2021/03/25	GUAXUPE	ALFENAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG775	2021/03/25	GUAXUPE	ALFENAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG776	2021/03/25	MUZAMBINHO	ALFENAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG777	2021/03/25	MUZAMBINHO	ALFENAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG778	2021/03/25	MUZAMBINHO	ALFENAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG779	2021/03/25	MUZAMBINHO	ALFENAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG780	2021/03/25	CARATINGA	CORONEL FABRICIANO	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG781	2021/03/25	JOANESIA	CORONEL FABRICIANO	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA

MG782	2021/03/25	CARATINGA	CORONEL FABRICIANO	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG783	2021/03/25	CARATINGA	CORONEL FABRICIANO	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG784	2021/03/25	ITUIUTABA	ITUIUTABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG785	2021/03/25	VARZELANDIA	JANUARIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG786	2021/03/25	VARZELANDIA	JANUARIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG787	2021/03/25	VARZELANDIA	JANUARIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG788	2021/03/25	MONTALVANIA	JANUARIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG789	2021/03/25	MONTALVANIA	JANUARIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG790	2021/03/25	ITACARAMBI	JANUARIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG791	2021/03/25	MANGA	JANUARIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG792	2021/03/25	SAO JOAO DA PONTE	JANUARIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG793	2021/03/25	SAO JOAO DA PONTE	JANUARIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG794	2021/03/25	MANGA	JANUARIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG795	2021/03/25	MANGA	JANUARIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG796	2021/03/25	JANUARIA	JANUARIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG797	2021/03/25	SAO JOAO DO PACUI	MONTES CLAROS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG798	2021/03/25	SAO JOAO DO PACUI	MONTES CLAROS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG799	2021/03/25	PADRE CARVALHO	MONTES CLAROS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG800	2021/03/25	CLARO DOS POCOES	PASSOS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG801	2021/03/25	MONTE SANTO DE MINAS	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG802	2021/03/25	FELIXLANDIA	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG803	2021/03/25	CAETE	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG804	2021/03/25	CAETE	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG805	2021/03/25	SAO JOAQUIM DE BICAS	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG806	2021/03/25	INIMUTABA	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG807	2021/03/25	PAINEIRAS	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG808	2021/03/25	SANTO HIPOLITO	SETE LAGOAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG809	2021/03/25	PARA DE MINAS	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA

MG810	2021/03/25	PARA DE MINAS	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG811	2021/03/25	LAGOA SANTA	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG812	2021/03/25	AMPARO DO SERRA	SETE LAGOAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG813	2021/03/25	CAMPO BELO	SETE LAGOAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG814	2021/03/25	CAMPO BELO	SETE LAGOAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG815	2021/03/25	SANTA CRUZ DO ESCALVADO	DIVINOPOLIS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG816	2021/03/25	SANTA CRUZ DO ESCALVADO	DIVINOPOLIS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG817	2021/03/25	SAO JOSE DA LAPA	BELO HORIZONTE	CDC KIT	GAMMA
MG818	2021/03/25	NOVA UNIAO	PONTE NOVA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG819	2021/03/25	SAO SEBASTIAO DO OESTE	DIVINOPOLIS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG820	2021/03/25	SAO SEBASTIAO DO OESTE	DIVINOPOLIS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG821	2021/03/25	IGARAPE	PONTE NOVA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG822	2021/03/25	JABOTICATUBAS	PONTE NOVA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG823	2021/03/25	CARANGOLA	BELO HORIZONTE	CDC KIT	GAMMA
MG824	2021/03/25	CARANGOLA	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG825	2021/03/25	CARANGOLA	DIVINOPOLIS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG826	2021/03/25	DIVINO	DIVINOPOLIS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG827	2021/03/25	DIVINO	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG828	2021/03/25	DIVINO	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG829	2021/03/25	DIVINO	MANHUAÇU	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG830	2021/03/25	CARANGOLA	MANHUAÇU	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG831	2021/03/25	CARANGOLA	MANHUAÇU	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG832	2021/03/25	FERVEDOURO	MANHUAÇU	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG833	2021/03/25	TOMBOS	MANHUAÇU	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG834	2021/03/25	TOMBOS	MANHUAÇU	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG835	2021/03/25	ESPERA FELIZ	MANHUAÇU	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG836	2021/03/25	ESPERA FELIZ	MANHUAÇU	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG837	2021/03/25	ESPERA FELIZ	MANHUAÇU	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA

MG838	2021/03/25	SABARA	MANHUAÇU	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG839	2021/03/25	SERITINGA	MANHUAÇU	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG840	2021/03/25	BOM JESUS DO AMPARO	MANHUAÇU	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG841	2021/03/25	BOM JESUS DO AMPARO	MANHUAÇU	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG842	2021/03/25	BOM JESUS DO AMPARO	MANHUAÇU	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG843	2021/03/25	JECEABA	MANHUAÇU	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG844	2021/03/25	MATEUS LEME	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG845	2021/03/25	CHALE	VARGINHA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG846	2021/03/25	CHALE	ITABIRA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG847	2021/03/25	CHALE	ITABIRA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG848	2021/03/25	CONCEICAO DE IPANEMA	ITABIRA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG849	2021/03/25	DURANDE	BARBACENA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG850	2021/03/25	DURANDE	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG851	2021/03/25	DURANDE	MANHUAÇU	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG852	2021/03/25	SIMONESIA	MANHUAÇU	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG853	2021/03/25	SIMONESIA	MANHUAÇU	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG854	2021/03/25	SANTA BARBARA DO TUGURIO	MANHUAÇU	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG855	2021/03/25	GUANHAES	MANHUAÇU	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG856	2021/03/25	GUANHAES	MANHUAÇU	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG857	2021/03/25	GUANHAES	MANHUAÇU	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG858	2021/03/25	GUANHAES	MANHUAÇU	CDC KIT	GAMMA
MG859	2021/03/25	GUANHAES	MANHUAÇU	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG860	2021/03/25	GUANHAES	BARBACENA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG861	2021/03/25	DIOGO DE VASCONCELOS	ITABIRA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG862	2021/03/25	SANTANA DO RIACHO	ITABIRA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG863	2021/03/25	ITAUNA	ITABIRA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG864	2021/03/25	ITAUNA	ITABIRA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG865	2021/03/25	ITAUNA	ITABIRA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA

MG866	2021/03/25	ITAUNA	ITABIRA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG867	2021/03/25	ITAUNA	PONTE NOVA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG868	2021/03/25	ITAUNA	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG869	2021/03/25	SANTA BARBARA	DIVINOPOLIS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG870	2021/03/25	SANTA BARBARA	DIVINOPOLIS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG871	2021/03/25	FERROS	DIVINOPOLIS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG872	2021/03/25	FERROS	DIVINOPOLIS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG873	2021/03/25	FERROS	DIVINOPOLIS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG874	2021/03/25	TAQUARACU DE MINAS	DIVINOPOLIS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG875	2021/03/25	BOTELHOS	ITABIRA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG876	2021/03/25	PRUDENTE DE MORAIS	ITABIRA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG877	2021/03/25	CLAUDIO	ITABIRA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG878	2021/03/25	CLAUDIO	ITABIRA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG879	2021/03/25	CLAUDIO	ITABIRA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG880	2021/03/25	CLAUDIO	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG881	2021/03/25	TIMOTEO	ALFENAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG882	2021/03/25	DOM SILVERIO	SETE LAGOAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG883	2021/03/25	POMPEU	DIVINOPOLIS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG884	2021/03/25	BOA ESPERANCA	DIVINOPOLIS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG885	2021/03/25	BOA ESPERANCA	DIVINOPOLIS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG886	2021/03/25	BOA ESPERANCA	DIVINOPOLIS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG887	2021/03/25	VARGINHA	CORONEL FABRICIANO	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG888	2021/03/25	VARGINHA	PONTE NOVA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG889	2021/03/25	PRADOS	SETE LAGOAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG890	2021/03/25	RAPOSOS	VARGINHA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG891	2021/03/25	ITAMBE DO MATO DENTRO	VARGINHA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG892	2021/03/25	PRADOS	VARGINHA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG893	2021/03/25	PRADOS	VARGINHA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA

MG894	2021/03/25	PRADOS	VARGINHA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG895	2021/03/25	GUARACIABA	SAO JOAO DEL REI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG896	2021/03/25	CONGONHAS	BELO HORIZONTE	CDC KIT	GAMMA
MG897	2021/03/25	CONGONHAS	ITABIRA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG898	2021/03/25	CONGONHAS	SAO JOAO DEL REI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG899	2021/03/25	CONGONHAS	SAO JOAO DEL REI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG900	2021/03/25	CONGONHAS	SAO JOAO DEL REI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG901	2021/03/25	CONGONHAS	PONTE NOVA	CDC KIT	GAMMA
MG902	2021/03/25	CONGONHAS	BARBACENA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG903	2021/03/25	ELOI MENDES	BARBACENA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG904	2021/03/25	ELOI MENDES	BARBACENA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG905	2021/03/25	ITINGA	BARBACENA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG906	2021/03/25	ARACUAI	BARBACENA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG907	2021/03/25	ARACUAI	BARBACENA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG908	2021/03/25	PAPAGAIOS	BARBACENA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG909	2021/03/25	TRES CORACOES	VARGINHA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG910	2021/03/25	TRES CORACOES	VARGINHA	CDC KIT	GAMMA
MG911	2021/03/25	CAPIM BRANCO	PEDRA AZUL	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG912	2021/03/25	JOAO MONLEVADE	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG913	2021/03/25	JOAO MONLEVADE	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG914	2021/03/25	JOAO MONLEVADE	SETE LAGOAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG915	2021/03/25	JOAO MONLEVADE	VARGINHA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG916	2021/03/25	JOAO MONLEVADE	VARGINHA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG917	2021/03/25	JOAO MONLEVADE	SETE LAGOAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG918	2021/03/25	MANHUACU	ITABIRA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG919	2021/03/25	REDUTO	ITABIRA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG920	2021/03/25	MANHUACU	ITABIRA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG921	2021/03/25	MANHUACU	ITABIRA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA

MG922	2021/03/25	ALTO JEQUITIBA	ITABIRA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG923	2021/03/25	ALTO JEQUITIBA	ITABIRA	CDC KIT	GAMMA
MG924	2021/03/25	CONSELHEIRO LAFAIETE	MANHUAÇU	CDC KIT	ALPHA
MG925	2021/03/25	CONSELHEIRO LAFAIETE	MANHUAÇU	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG926	2021/03/25	CONSELHEIRO LAFAIETE	MANHUAÇU	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG927	2021/03/25	CONSELHEIRO LAFAIETE	MANHUAÇU	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG928	2021/03/25	CONSELHEIRO LAFAIETE	MANHUAÇU	CDC KIT	ALPHA
MG929	2021/03/25	SANTANA DO RIACHO	MANHUAÇU	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG930	2021/03/25	RIO MANSO	BARBACENA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG931	2021/03/25	POCOS DE CALDAS	BARBACENA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG932	2021/03/25	POCOS DE CALDAS	BARBACENA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG933	2021/03/25	POCOS DE CALDAS	BARBACENA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG934	2021/03/25	POCOS DE CALDAS	BARBACENA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG935	2021/03/25	POCOS DE CALDAS	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG936	2021/03/25	POCOS DE CALDAS	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG937	2021/03/25	POCOS DE CALDAS	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG938	2021/03/25	POCOS DE CALDAS	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG939	2021/03/25	POCOS DE CALDAS	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG940	2021/03/25	POCOS DE CALDAS	POUSO ALEGRE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG941	2021/03/25	POCOS DE CALDAS	POUSO ALEGRE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG942	2021/03/25	POCOS DE CALDAS	POUSO ALEGRE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG943	2021/03/25	POCOS DE CALDAS	POUSO ALEGRE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG944	2021/03/25	POCOS DE CALDAS	POUSO ALEGRE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG945	2021/03/25	POCOS DE CALDAS	POUSO ALEGRE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG946	2021/03/25	POCOS DE CALDAS	POUSO ALEGRE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG947	2021/03/25	ITAJUBA	POUSO ALEGRE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG948	2021/03/25	BELO HORIZONTE	POUSO ALEGRE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG949	2021/03/25	BELO HORIZONTE	POUSO ALEGRE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA

MG950	2021/03/25	BELO HORIZONTE	POUSO ALEGRE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG951	2021/03/25	BELO HORIZONTE	POUSO ALEGRE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG952	2021/03/25	BELO HORIZONTE	POUSO ALEGRE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG953	2021/03/25	BELO HORIZONTE	POUSO ALEGRE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG954	2021/03/25	BELO HORIZONTE	POUSO ALEGRE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG955	2021/03/25	SABINOPOLIS	POUSO ALEGRE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG956	2021/03/25	SABINOPOLIS	POUSO ALEGRE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG957	2021/03/25	SERRA AZUL DE MINAS	MONTES CLAROS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG958	2021/03/25	SERRO	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG959	2021/03/25	SERRO	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG960	2021/03/26	NOVA SERRANA	DIVINOPOLIS	CDC KIT	GAMMA
MG961	2021/03/26	SAO JOAO DEL REI	SAO JOAO DEL REI	CDC KIT	GAMMA
MG962	2021/03/26	RIO CASCA	PONTE NOVA	CDC KIT	GAMMA
MG963	2021/03/26	RIO CASCA	PONTE NOVA	CDC KIT	GAMMA
MG964	2021/03/26	CONSELHEIRO LAFAIETE	BARBACENA	CDC KIT	GAMMA
MG965	2021/03/26	CONSELHEIRO LAFAIETE	BARBACENA	CDC KIT	ZETA
MG966	2021/03/26	CONSELHEIRO LAFAIETE	BARBACENA	CDC KIT	ALPHA
MG967	2021/03/26	CONSELHEIRO LAFAIETE	BARBACENA	CDC KIT	GAMMA
MG968	2021/03/26	CONSELHEIRO LAFAIETE	BARBACENA	CDC KIT	ZETA
MG969	2021/03/26	COMENDADOR GOMES	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG970	2021/03/26	VESPASIANO	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG971	2021/03/26	BRUMADINHO	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG972	2021/03/26	PESCADOR	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG973	2021/03/26	FRANCISCOPOLIS	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG974	2021/03/26	POTE	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG975	2021/03/26	NOVA MODICA	UBERABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG976	2021/03/26	ITAJUBA	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG977	2021/03/26	ITAJUBA	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA

MG978	2021/03/26	ITAJUBA	TEOFILO OTONI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG979	2021/03/26	ITAJUBA	TEOFILO OTONI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG980	2021/03/26	ITAJUBA	TEOFILO OTONI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG981	2021/03/26	ITAJUBA	TEOFILO OTONI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG982	2021/03/26	ITAJUBA	UBERLANDIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG983	2021/03/26	ITAJUBA	PONTE NOVA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG984	2021/03/26	ITAJUBA	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG985	2021/03/26	ENTRE RIOS DE MINAS	PATOS DE MINAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG986	2021/03/26	BELO HORIZONTE	PATOS DE MINAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG987	2021/03/26	BELO HORIZONTE	POUSO ALEGRE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG988	2021/03/26	BELO HORIZONTE	POUSO ALEGRE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG989	2021/03/26	BELO HORIZONTE	POUSO ALEGRE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG990	2021/03/26	BELO HORIZONTE	POUSO ALEGRE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG991	2021/03/26	BELO HORIZONTE	POUSO ALEGRE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG992	2021/03/26	BELO HORIZONTE	POUSO ALEGRE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG993	2021/03/26	N.I.	POUSO ALEGRE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG994	2021/03/26	VICOSA	POUSO ALEGRE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG995	2021/03/26	SERRO	POUSO ALEGRE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG996	2021/03/26	PATOS DE MINAS	SAO JOAO DEL REI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG997	2021/03/26	PATOS DE MINAS	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG998	2021/03/27	JOAO MONLEVADE	ITABIRA	CDC KIT	GAMMA
MG999	2021/03/27	MONTES CLAROS	MONTES CLAROS	CDC KIT	GAMMA
MG1000	2021/03/27	BETIM	BELO HORIZONTE	CDC KIT	GAMMA
MG1001	2021/03/27	MANHUACU	MANHUAÇU	CDC KIT	ALPHA
MG1002	2021/03/27	BELO HORIZONTE	BELO HORIZONTE	CDC KIT	GAMMA
MG1003	2021/03/27	TIMOTEO	CORONEL FABRICIANO	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG1004	2021/03/27	NAQUE	CORONEL FABRICIANO	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1005	2021/03/27	ACUCENA	CORONEL FABRICIANO	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA

MG1006	2021/03/27	SANTANA DO PARAISO	CORONEL FABRICIANO	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG1007	2021/03/27	CONCEICAO DAS ALAGOAS	UBERABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1008	2021/03/27	CONCEICAO DAS ALAGOAS	UBERABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1009	2021/03/27	SANTA JULIANA	UBERABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1010	2021/03/27	CAMPOS ALTOS	UBERABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1011	2021/03/27	LIMEIRA DO OESTE	UBERABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1012	2021/03/27	SANTA VITORIA	ITUIUTABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1013	2021/03/27	SANTA VITORIA	ITUIUTABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1014	2021/03/27	CAMPOS ALTOS	UBERABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG1015	2021/03/27	SAO JOAO DEL REI	MANHUAÇU	CDC KIT	GAMMA
MG1016	2021/03/27	SAO JOAO DEL REI	MANHUAÇU	CDC KIT	ALPHA
MG1017	2021/03/27	SAO JOAO DEL REI	MANHUAÇU	CDC KIT	GAMMA
MG1018	2021/03/27	ESPERA FELIZ	MANHUAÇU	CDC KIT	ZETA
MG1019	2021/03/27	ESPERA FELIZ	SAO JOAO DEL REI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1020	2021/03/27	ESPERA FELIZ	SAO JOAO DEL REI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1021	2021/03/27	ESPERA FELIZ	SAO JOAO DEL REI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG1022	2021/03/28	LAGOA DA PRATA	DIVINOPOLIS	CDC KIT	GAMMA
MG1023	2021/03/28	BETIM	CORONEL FABRICIANO	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1024	2021/03/28	CARATINGA	PATOS DE MINAS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1025	2021/03/28	TIRADENTES	SAO JOAO DEL REI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1026	2021/03/28	SAO JOAO DEL REI	SAO JOAO DEL REI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1027	2021/03/28	SANTA CRUZ DE MINAS	SAO JOAO DEL REI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1028	2021/03/28	SANTA CRUZ DE MINAS	SAO JOAO DEL REI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1029	2021/03/28	PATOS DE MINAS	BELO HORIZONTE	CDC KIT	OTHERS
MG1030	2021/03/29	MONTES CLAROS	MONTES CLAROS	CDC KIT	GAMMA
MG1031	2021/03/29	FORTUNA DE MINAS	SETE LAGOAS	CDC KIT	GAMMA
MG1032	2021/03/29	PIRANGA	BARBACENA	CDC KIT	GAMMA
MG1033	2021/03/29	FELIXLANDIA	SETE LAGOAS	CDC KIT	GAMMA

MG1034	2021/03/29	FELIXLANDIA	GOVERNADOR VALADARES	CDC KIT	ALPHA
MG1035	2021/03/29	AIMORES	GOVERNADOR VALADARES	CDC KIT	GAMMA
MG1036	2021/03/29	SAO JOAO EVANGELISTA	GOVERNADOR VALADARES	CDC KIT	GAMMA
MG1037	2021/03/29	SAO JOAO EVANGELISTA	GOVERNADOR VALADARES	CDC KIT	GAMMA
MG1038	2021/03/29	SAO JOAO EVANGELISTA	GOVERNADOR VALADARES	CDC KIT	GAMMA
MG1039	2021/03/29	SAO JOAO EVANGELISTA	BELO HORIZONTE	CDC KIT	GAMMA
MG1040	2021/03/29	JABOTICATUBAS	ITABIRA	CDC KIT	ALPHA
MG1041	2021/03/29	JABOTICATUBAS	PONTE NOVA	CDC KIT	ZETA
MG1042	2021/03/29	BELA VISTA DE MINAS	SETE LAGOAS	CDC KIT	GAMMA
MG1043	2021/03/29	RIO DOCE	LEOPOLDINA	CDC KIT	GAMMA
MG1044	2021/03/29	RIO DOCE	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1045	2021/03/29	PRUDENTE DE MORAIS	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1046	2021/03/29	PRUDENTE DE MORAIS	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1047	2021/03/29	CATAGUASES	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1048	2021/03/29	OURO VERDE DE MINAS	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1049	2021/03/29	ITAUNA	TEOFILO OTONI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG1050	2021/03/29	SAO JOAO DEL REI	DIVINOPOLIS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ZETA
MG1051	2021/03/29	SAO JOAO DEL REI	UBERLANDIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1052	2021/03/29	SANTA CRUZ DE MINAS	SAO JOAO DEL REI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1053	2021/03/29	SAO JOAO DEL REI	SAO JOAO DEL REI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1054	2021/03/29	PIUMHI	SAO JOAO DEL REI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1055	2021/03/29	PIUMHI	SAO JOAO DEL REI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1056	2021/03/29	MONTE SANTO DE MINAS	PASSOS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1057	2021/03/29	MONTE SANTO DE MINAS	PASSOS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1058	2021/03/29	CAMPINA VERDE	PASSOS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1059	2021/03/29	CAMPINA VERDE	PASSOS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1060	2021/03/29	ENTRE RIOS DE MINAS	ITUIUTABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1061	2021/03/29	CAMPINA VERDE	ITUIUTABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA

MG1062	2021/03/29	BELO HORIZONTE	SETE LAGOAS	CDC KIT	OTHERS
MG1063	2021/03/29	BELO HORIZONTE	BELO HORIZONTE	CDC KIT	OTHERS
MG1064	2021/03/29	BELO HORIZONTE	PONTE NOVA	CDC KIT	OTHERS
MG1065	2021/03/29	BELO HORIZONTE	SETE LAGOAS	CDC KIT	OTHERS
MG1066	2021/03/29	BELO HORIZONTE	SAO JOAO DEL REI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG1067	2021/03/29	N.I.	ITUIUTABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG1068	2021/03/30	JUIZ DE FORA	JUIZ DE FORA	CDC KIT	GAMMA
MG1069	2021/03/30	JUIZ DE FORA	JUIZ DE FORA	CDC KIT	GAMMA
MG1070	2021/03/30	JUIZ DE FORA	JUIZ DE FORA	CDC KIT	GAMMA
MG1071	2021/03/30	JUIZ DE FORA	JUIZ DE FORA	CDC KIT	GAMMA
MG1072	2021/03/30	JUIZ DE FORA	JUIZ DE FORA	CDC KIT	GAMMA
MG1073	2021/03/30	JUIZ DE FORA	JUIZ DE FORA	CDC KIT	GAMMA
MG1074	2021/03/30	JUIZ DE FORA	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1075	2021/03/30	PEDRO LEOPOLDO	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1076	2021/03/30	NOVA LIMA	BARBACENA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1077	2021/03/30	BARBACENA	UBERABA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1078	2021/03/30	VERISSIMO	PONTE NOVA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1079	2021/03/30	SAO JOAO DEL REI	PONTE NOVA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1080	2021/03/30	SAO JOAO DEL REI	PONTE NOVA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1081	2021/03/30	SANTA CRUZ DE MINAS	SAO JOAO DEL REI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1082	2021/03/30	PONTE NOVA	SAO JOAO DEL REI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1083	2021/03/30	VICOSA	SAO JOAO DEL REI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1084	2021/03/31	VICOSA	UBERLANDIA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1085	2021/03/31	N.I.	PIRAPORA	CDC KIT	GAMMA
MG1086	2021/03/31	VARZEA DA PALMA	PIRAPORA	CDC KIT	GAMMA
MG1087	2021/04/01	VARZEA DA PALMA	PASSOS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1088	2021/04/01	MONTE SANTO DE MINAS	PASSOS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1089	2021/04/01	MONTE SANTO DE MINAS	PASSOS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS

MG1090	2021/04/01	MONTE SANTO DE MINAS	PASSOS	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG1091	2021/04/02	MONTE SANTO DE MINAS	POUSO ALEGRE	CDC KIT	GAMMA
MG1092	2021/04/02	CAMBUI	POUSO ALEGRE	CDC KIT	GAMMA
MG1093	2021/04/02	POCOS DE CALDAS	POUSO ALEGRE	CDC KIT	GAMMA
MG1094	2021/04/02	POCOS DE CALDAS	POUSO ALEGRE	CDC KIT	GAMMA
MG1095	2021/04/02	POCOS DE CALDAS	POUSO ALEGRE	CDC KIT	GAMMA
MG1096	2021/04/02	POCOS DE CALDAS	POUSO ALEGRE	CDC KIT	GAMMA
MG1097	2021/04/02	POCOS DE CALDAS	POUSO ALEGRE	CDC KIT	GAMMA
MG1098	2021/04/02	POCOS DE CALDAS	POUSO ALEGRE	CDC KIT	GAMMA
MG1099	2021/04/02	POCOS DE CALDAS	POUSO ALEGRE	CDC KIT	GAMMA
MG1100	2021/04/02	POCOS DE CALDAS	POUSO ALEGRE	CDC KIT	GAMMA
MG1101	2021/04/02	POCOS DE CALDAS	POUSO ALEGRE	CDC KIT	GAMMA
MG1102	2021/04/03	POCOS DE CALDAS	POUSO ALEGRE	CDC KIT	GAMMA
MG1103	2021/04/03	CAMBUI	POUSO ALEGRE	CDC KIT	GAMMA
MG1104	2021/04/03	SANTA RITA DO SAPUCAI	POUSO ALEGRE	CDC KIT	GAMMA
MG1105	2021/04/03	POCOS DE CALDAS	POUSO ALEGRE	CDC KIT	GAMMA
MG1106	2021/04/03	POCOS DE CALDAS	SETE LAGOAS	CDC KIT	GAMMA
MG1107	2021/04/03	FELIXLANDIA	SETE LAGOAS	CDC KIT	GAMMA
MG1108	2021/04/03	FELIXLANDIA	VARGINHA	CDC KIT	GAMMA
MG1109	2021/04/04	COQUEIRAL	SETE LAGOAS	CDC KIT	ALPHA
MG1110	2021/04/04	FELIXLANDIA	SETE LAGOAS	CDC KIT	GAMMA
MG1111	2021/04/04	FELIXLANDIA	LEOPOLDINA	CDC KIT	GAMMA
MG1112	2021/04/04	RECREIO	LEOPOLDINA	CDC KIT	GAMMA
MG1113	2021/04/04	CATAGUASES	LEOPOLDINA	CDC KIT	ZETA
MG1114	2021/04/04	ALEM PARAIBA	PONTE NOVA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1115	2021/04/04	ALEM PARAIBA	LEOPOLDINA	CDC KIT	OTHERS
MG1116	2021/04/05	PONTE NOVA	VARGINHA	CDC KIT	GAMMA
MG1117	2021/04/05	SAO LOURENCO	VARGINHA	CDC KIT	GAMMA

MG1118	2021/04/05	SAO LOURENCO	VARGINHA	CDC KIT	GAMMA
MG1119	2021/04/05	SAO LOURENCO	VARGINHA	CDC KIT	GAMMA
MG1120	2021/04/05	SAO LOURENCO	VARGINHA	CDC KIT	GAMMA
MG1121	2021/04/05	SAO LOURENCO	VARGINHA	CDC KIT	GAMMA
MG1122	2021/04/05	SAO LOURENCO	VARGINHA	CDC KIT	GAMMA
MG1123	2021/04/05	SAO LOURENCO	VARGINHA	CDC KIT	GAMMA
MG1124	2021/04/05	SAO LOURENCO	VARGINHA	CDC KIT	GAMMA
MG1125	2021/04/05	SAO LOURENCO	VARGINHA	CDC KIT	GAMMA
MG1126	2021/04/05	SAO LOURENCO	VARGINHA	CDC KIT	GAMMA
MG1127	2021/04/05	SAO LOURENCO	VARGINHA	CDC KIT	GAMMA
MG1128	2021/04/05	SAO LOURENCO	VARGINHA	CDC KIT	GAMMA
MG1129	2021/04/05	SAO LOURENCO	VARGINHA	CDC KIT	GAMMA
MG1130	2021/04/05	ITANHANDU	VARGINHA	CDC KIT	GAMMA
MG1131	2021/04/05	ITANHANDU	PONTE NOVA	CDC KIT	GAMMA
MG1132	2021/04/05	RAUL SOARES	MANHUAÇU	CDC KIT	ZETA
MG1133	2021/04/05	MANHUACU	SETE LAGOAS	CDC KIT	ALPHA
MG1134	2021/04/05	FELIXLANDIA	SETE LAGOAS	CDC KIT	GAMMA
MG1135	2021/04/05	FELIXLANDIA	SETE LAGOAS	CDC KIT	GAMMA
MG1136	2021/04/05	FELIXLANDIA	SETE LAGOAS	CDC KIT	GAMMA
MG1137	2021/04/05	FELIXLANDIA	SETE LAGOAS	CDC KIT	GAMMA
MG1138	2021/04/05	FELIXLANDIA	SETE LAGOAS	CDC KIT	GAMMA
MG1139	2021/04/05	FELIXLANDIA	GOVERNADOR VALADARES	CDC KIT	GAMMA
MG1140	2021/04/05	GOVERNADOR VALADARES	LEOPOLDINA	CDC KIT	GAMMA
MG1141	2021/04/05	LEOPOLDINA	JUIZ DE FORA	CDC KIT	ALPHA
MG1142	2021/04/05	JUIZ DE FORA	JUIZ DE FORA	CDC KIT	GAMMA
MG1143	2021/04/05	JUIZ DE FORA	JUIZ DE FORA	CDC KIT	GAMMA
MG1144	2021/04/05	JUIZ DE FORA	JUIZ DE FORA	CDC KIT	GAMMA
MG1145	2021/04/05	JUIZ DE FORA	LEOPOLDINA	CDC KIT	ALPHA

MG1146	2021/04/05	ALEM PARAIBA	LEOPOLDINA	CDC KIT	ZETA
MG1147	2021/04/05	CATAGUASES	JUIZ DE FORA	CDC KIT	GAMMA
MG1148	2021/04/05	JUIZ DE FORA	JUIZ DE FORA	CDC KIT	GAMMA
MG1149	2021/04/05	JUIZ DE FORA	JUIZ DE FORA	CDC KIT	GAMMA
MG1150	2021/04/05	JUIZ DE FORA	JUIZ DE FORA	CDC KIT	GAMMA
MG1151	2021/04/05	JUIZ DE FORA	JUIZ DE FORA	CDC KIT	GAMMA
MG1152	2021/04/05	BETIM	BELO HORIZONTE	CDC KIT	GAMMA
MG1153	2021/04/05	BETIM	BELO HORIZONTE	CDC KIT	GAMMA
MG1154	2021/04/05	BETIM	BELO HORIZONTE	CDC KIT	GAMMA
MG1155	2021/04/05	BETIM	BELO HORIZONTE	CDC KIT	GAMMA
MG1156	2021/04/05	BETIM	BELO HORIZONTE	CDC KIT	GAMMA
MG1157	2021/04/05	BETIM	BELO HORIZONTE	CDC KIT	GAMMA
MG1158	2021/04/05	BETIM	BELO HORIZONTE	CDC KIT	GAMMA
MG1159	2021/04/05	BETIM	BELO HORIZONTE	CDC KIT	GAMMA
MG1160	2021/04/05	FUNILANDIA	SETE LAGOAS	CDC KIT	GAMMA
MG1161	2021/04/05	CONSELHEIRO LAFAIETE	BARBACENA	CDC KIT	GAMMA
MG1162	2021/04/05	CONSELHEIRO LAFAIETE	BARBACENA	CDC KIT	GAMMA
MG1163	2021/04/05	CONSELHEIRO LAFAIETE	BARBACENA	CDC KIT	GAMMA
MG1164	2021/04/05	COQUEIRAL	VARGINHA	CDC KIT	ALPHA
MG1165	2021/04/05	COQUEIRAL	VARGINHA	CDC KIT	GAMMA
MG1166	2021/04/06	MONTES CLAROS	MONTES CLAROS	CDC KIT	GAMMA
MG1167	2021/04/06	BELO HORIZONTE	VARGINHA	CDC KIT	GAMMA
MG1168	2021/04/06	SAO LOURENCO	MONTES CLAROS	CDC KIT	GAMMA
MG1169	2021/04/06	MONTES CLAROS	MONTES CLAROS	CDC KIT	GAMMA
MG1170	2021/04/06	MONTES CLAROS	MONTES CLAROS	CDC KIT	GAMMA
MG1171	2021/04/06	MONTES CLAROS	MONTES CLAROS	CDC KIT	GAMMA
MG1172	2021/04/06	MONTES CLAROS	MONTES CLAROS	CDC KIT	GAMMA
MG1173	2021/04/06	MONTES CLAROS	MONTES CLAROS	CDC KIT	GAMMA

MG1174	2021/04/06	MONTES CLAROS	MONTES CLAROS	CDC KIT	GAMMA
MG1175	2021/04/06	MONTES CLAROS	MONTES CLAROS	CDC KIT	GAMMA
MG1176	2021/04/06	MONTES CLAROS	MONTES CLAROS	CDC KIT	GAMMA
MG1177	2021/04/06	MONTES CLAROS	MONTES CLAROS	CDC KIT	GAMMA
MG1178	2021/04/06	MONTES CLAROS	MONTES CLAROS	CDC KIT	GAMMA
MG1179	2021/04/06	MONTES CLAROS	MONTES CLAROS	CDC KIT	GAMMA
MG1180	2021/04/06	MONTES CLAROS	MONTES CLAROS	CDC KIT	GAMMA
MG1181	2021/04/06	MONTES CLAROS	GOVERNADOR VALADARES	CDC KIT	GAMMA
MG1182	2021/04/06	GOVERNADOR VALADARES	GOVERNADOR VALADARES	CDC KIT	GAMMA
MG1183	2021/04/06	GOVERNADOR VALADARES	GOVERNADOR VALADARES	CDC KIT	GAMMA
MG1184	2021/04/06	GOVERNADOR VALADARES	GOVERNADOR VALADARES	CDC KIT	GAMMA
MG1185	2021/04/06	GOVERNADOR VALADARES	GOVERNADOR VALADARES	CDC KIT	GAMMA
MG1186	2021/04/06	GOVERNADOR VALADARES	GOVERNADOR VALADARES	CDC KIT	GAMMA
MG1187	2021/04/06	GOVERNADOR VALADARES	GOVERNADOR VALADARES	CDC KIT	GAMMA
MG1188	2021/04/06	GOVERNADOR VALADARES	GOVERNADOR VALADARES	CDC KIT	GAMMA
MG1189	2021/04/06	GOVERNADOR VALADARES	GOVERNADOR VALADARES	CDC KIT	ZETA
MG1190	2021/04/06	GOVERNADOR VALADARES	GOVERNADOR VALADARES	CDC KIT	GAMMA
MG1191	2021/04/06	GOVERNADOR VALADARES	GOVERNADOR VALADARES	CDC KIT	GAMMA
MG1192	2021/04/06	GOVERNADOR VALADARES	GOVERNADOR VALADARES	CDC KIT	ALPHA
MG1193	2021/04/06	GOVERNADOR VALADARES	GOVERNADOR VALADARES	CDC KIT	ALPHA
MG1194	2021/04/06	GOVERNADOR VALADARES	DIVINOPOLIS	CDC KIT	GAMMA
MG1195	2021/04/06	DIVINOPOLIS	GOVERNADOR VALADARES	CDC KIT	GAMMA
MG1196	2021/04/06	GOVERNADOR VALADARES	PONTE NOVA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1197	2021/04/06	PONTE NOVA	BELO HORIZONTE	CDC KIT	OTHERS
MG1198	2021/04/07	VICOSA	PONTE NOVA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1199	2021/04/07	PONTE NOVA	PONTE NOVA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1200	2021/04/08	VICOSA	PONTE NOVA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1201	2021/04/08	VICOSA	PONTE NOVA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA

MG1202	2021/04/08	VICOSA	PONTE NOVA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1203	2021/04/09	CAETE	ITABIRA	CDC KIT	GAMMA
MG1204	2021/04/09	FERROS	DIVINOPOLIS	CDC KIT	GAMMA
MG1205	2021/04/09	MARTINHO CAMPOS	SETE LAGOAS	CDC KIT	GAMMA
MG1206	2021/04/09	SETE LAGOAS	SETE LAGOAS	CDC KIT	GAMMA
MG1207	2021/04/09	SETE LAGOAS	SETE LAGOAS	CDC KIT	GAMMA
MG1208	2021/04/09	SETE LAGOAS	SETE LAGOAS	CDC KIT	GAMMA
MG1209	2021/04/09	SETE LAGOAS	SETE LAGOAS	CDC KIT	GAMMA
MG1210	2021/04/09	SETE LAGOAS	BELO HORIZONTE	CDC KIT	OTHERS
MG1211	2021/04/10	BELO HORIZONTE	BELO HORIZONTE	CDC KIT	GAMMA
MG1212	2021/04/10	SETE LAGOAS	SETE LAGOAS	CDC KIT	GAMMA
MG1213	2021/04/10	JENIPAPO DE MINAS	DIAMANTINA	CDC KIT	GAMMA
MG1214	2021/04/10	JENIPAPO DE MINAS	DIAMANTINA	CDC KIT	GAMMA
MG1215	2021/04/10	JENIPAPO DE MINAS	DIAMANTINA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG1216	2021/04/11	MARTINHO CAMPOS	DIVINOPOLIS	CDC KIT	GAMMA
MG1217	2021/04/11	SETE LAGOAS	SETE LAGOAS	CDC KIT	GAMMA
MG1218	2021/04/11	SAO PEDRO DOS FERROS	PONTE NOVA	CDC KIT	GAMMA
MG1219	2021/04/11	SAO PEDRO DOS FERROS	PONTE NOVA	CDC KIT	GAMMA
MG1220	2021/04/11	SAO PEDRO DOS FERROS	PONTE NOVA	CDC KIT	GAMMA
MG1221	2021/04/11	SAO PEDRO DOS FERROS	PONTE NOVA	CDC KIT	GAMMA
MG1222	2021/04/11	SAO PEDRO DOS FERROS	PONTE NOVA	CDC KIT	GAMMA
MG1223	2021/04/12	ARACAI	SETE LAGOAS	CDC KIT	GAMMA
MG1224	2021/04/12	CAETE	BELO HORIZONTE	CDC KIT	GAMMA
MG1225	2021/04/12	CAETE	SETE LAGOAS	CDC KIT	GAMMA
MG1226	2021/04/12	FORTUNA DE MINAS	SETE LAGOAS	CDC KIT	GAMMA
MG1227	2021/04/12	FORTUNA DE MINAS	PONTE NOVA	CDC KIT	GAMMA
MG1228	2021/04/12	SAO PEDRO DOS FERROS	PONTE NOVA	CDC KIT	GAMMA
MG1229	2021/04/12	SAO PEDRO DOS FERROS	PONTE NOVA	CDC KIT	GAMMA

MG1230	2021/04/12	SAO PEDRO DOS FERROS	DIVINOPOLIS	CDC KIT	ALPHA
MG1231	2021/04/12	SAO PEDRO DOS FERROS	PONTE NOVA	CDC KIT	GAMMA
MG1232	2021/04/12	CARMO DA MATA	BELO HORIZONTE	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG1233	2021/04/12	TEIXEIRAS	PONTE NOVA	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	OTHERS
MG1234	2021/04/26	PARACATU	UNAI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	ALPHA
MG1235	2021/04/26	PARACATU	UNAI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1236	2021/04/27	PARACATU	UNAI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1237	2021/04/27	PARACATU	UNAI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1238	2021/04/27	PARACATU	UNAI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1239	2021/04/27	PARACATU	UNAI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA
MG1240	2021/04/27	PARACATU	UNAI	TaqPath™ COVID-19 CE-IVD RT-PCR Kit	GAMMA

Supplementary Table 2. Calculation of sample size for each of the 28 Regional Health Unit, Minas Gerais - Brazil.

RHU	Estimated population - people [2020]	Proportionality factor by population	Sample n = 1000 with 56% uniform allocation + 44% proportional	Sample for n = 1000 with 56% uniform allocation + rounding	real weight factor	uniform allocation	total sample	sample weight
ALFENAS	539145	0.02532069	11.1411037	11	0.025	20	31	0.030357143
BARBACENA	506450	0.023785185	10.4654814	10	0.022727273	20	30	0.029220779
BELO HORIZONTE	4458065	0.209370917	92.12320336	92	0.209090909	20	112	0.122402597
CORONEL FABRICIANO	1043624	0.049013308	21.56585559	22	0.05	20	42	0.042857143
DIAMANTINA	375731	0.017646029	7.764252724	8	0.018181818	20	28	0.026948052
DIVINÓPOLIS	1099116	0.051619464	22.71256403	23	0.052272727	20	43	0.043993506
GOVERNADOR VALADARES	1083297	0.050876532	22.38567402	22	0.05	20	42	0.042857143
ITABIRA	459055	0.021559301	9.486092535	9	0.020454545	20	29	0.028084416
ITUIUTABA	196747	0.00924013	4.065657161	4	0.009090909	20	24	0.022402597
JANUÁRIA	609261	0.028613655	12.59000822	13	0.029545455	20	33	0.03262987
JUIZ DE FORA	527882	0.024791729	10.90836065	11	0.025	20	31	0.030357143
LEOPOLDINA	239440	0.011245186	4.947882055	5	0.011363636	20	25	0.023538961
MANHUAÇU	780738	0.036666991	16.13347619	16	0.036363636	20	36	0.036038961
MONTES CLAROS	1483405	0.069667415	30.65366263	31	0.070454545	20	51	0.053084416
PASSOS	265310	0.012460159	5.48246988	5	0.011363636	20	25	0.023538961
PATOS DE MINAS	398873	0.018732882	8.242468087	8	0.018181818	20	28	0.026948052
PEDRA AZUL	319031	0.01498314	6.59258169	7	0.015909091	20	27	0.025811688
PIRAPORA	89460	0.004201447	1.848636521	2	0.004545455	20	22	0.02012987
PONTE NOVA	404200	0.018983062	8.352547304	8	0.018181818	20	28	0.026948052
POUSO ALEGRE	1845090	0.08665378	38.1276633	38	0.086363636	20	58	0.061038961
SÃO JOÃO DEL REI	219654	0.010315946	4.539016392	5	0.011363636	20	25	0.023538961
SETE LAGOAS	700912	0.032918001	14.48392043	14	0.031818182	20	34	0.033766234
TEÓFILO OTONI	613149	0.028796253	12.67035138	13	0.029545455	20	33	0.03262987
UBÁ	506180	0.023772505	10.45990202	10	0.022727273	20	30	0.029220779
UBERABA	1381535	0.064883139	28.548581	29	0.065909091	20	49	0.050811688
UBERLÂNDIA	419846	0.019717869	8.675862384	9	0.020454545	20	29	0.028084416
UNAÍ	131672	0.006183913	2.720921842	3	0.006818182	20	23	0.021266234
VARGINHA	595798	0.027981372	12.31180351	12	0.027272727	20	32	0.031493506

Supplementary Table 3. Clinical and epidemiological data. **(3A)** Distribution of positive cases in the state of Minas Gerais over the Epidemiological Weeks (EW) 45/2020 - 13/2021. **(3B)** Distribution of vaccine doses applied in Minas Gerais, throughout EW 45/2020 - 13/2021. **(3C)** Clinical data collected from comorbidities, observed symptoms, and clinical outcomes.

Table 3A. Distribution of positive cases in the state of Minas Gerais over the weeks 45/2020 - 13/2021.					
DATE		**EW**	**GENOTYPED SAMPLES**	**TOTAL POSITIVE CASES**	**TOTAL DEATH**
2020/11/01	2020/11/07	45		9637	189
2020/11/08	2020/11/14	46		12285	300
2020/11/15	2020/11/21	47		14220	228
2020/11/22	2020/11/28	48		17459	258
2020/11/29	2020/12/05	49		25307	293
2020/12/06	2020/12/12	50		25701	362
2020/12/13	2020/12/19	51		29993	448
2020/12/20	2020/12/26	52		28138	492
2020/12/27	2021/01/02	53		26880	438
2021/01/03	2021/01/09	1		38453	571
2021/01/10	2021/01/16	2		48837	761
2021/01/17	2021/01/23	3		49452	793
2021/01/24	2021/01/30	4		43280	791
2021/01/31	2021/02/06	5		36889	868
2021/02/07	2021/02/13	6		36989	953
2021/02/14	2021/02/20	7		32967	834
2021/02/21	2021/02/27	8		37578	837
2021/02/28	2021/03/06	9	167	41318	928
2021/03/07	2021/03/13	10	143	47684	1147
2021/03/14	2021/03/20	11	232	60080	1258
2021/03/21	2021/03/27	12	479	69570	1602
2021/03/28	2021/04/03	13	88	59987	2174
2021/04/04	2021/04/10	14	106		
2021/04/11	2021/04/17	15	18		
2021/04/18	2021/04/24	16	0		
2021/04/25	2021/05/01	17	7		
TOTAL			1240	603084	13517

Table 3B. Distribution of vaccine doses applied in Minas Gerais, throughout EW 45/2020 - 13/2021.					
DATE		**EW**	TOTAL VACCINES IN MG	TOTAL 1st DOSE IN MG	TOTAL 2nd DOSE IN MG
2020/11/01	2020/11/07	45	0	0	0
2020/11/08	2020/11/14	46	0	0	0
2020/11/15	2020/11/21	47	0	0	0
2020/11/22	2020/11/28	48	0	0	0
2020/11/29	2020/12/05	49	0	0	0
2020/12/06	2020/12/12	50	0	0	0
2020/12/13	2020/12/19	51	0	0	0
2020/12/20	2020/12/26	52	0	0	0
2020/12/27	2021/01/02	53	0	0	0
2021/01/03	2021/01/09	1	0	0	0
2021/01/10	2021/01/16	2	0	0	0
2021/01/17	2021/01/23	3	0	0	0
2021/01/24	2021/01/30	4	185906	185111	795
2021/01/31	2021/02/06	5	141448	119203	22245
2021/02/07	2021/02/13	6	154775	74906	79869
2021/02/14	2021/02/20	7	195850	120708	75142
2021/02/21	2021/02/27	8	161347	87808	73539
2021/02/28	2021/03/06	9	147910	78933	68977
2021/03/07	2021/03/13	10	227155	171507	55648
2021/03/14	2021/03/20	11	224469	185895	38574
2021/03/21	2021/03/27	12	271275	209628	61647
2021/03/28	2021/04/03	13	587705	504051	83654
2021/04/04	2021/04/10	14	0	0	0
2021/04/11	2021/04/17	15	0	0	0
2021/04/18	2021/04/24	16	0	0	0
2021/04/25	2021/05/01	17	0	0	0
TOTAL			2297840	1737750	560090

Table 3C. Clinical data collected from comorbidities, observed symptoms, and clinical outcomes.					
CLINICAL DATA		**LINEAGE**			
		ALPHA	**GAMMA**	**ZETA**	**OTHERS**
COMORBITIES	DIABETES	20.0%	25.5%	28.6%	33.3%
	HEART DISEASE	60.0%	42.2%	50.0%	50.0%
	IMMUNOSUPPRESSED	10.0%	1.0%	0.0%	0.0%
	OBESITY	0.0%	10.8%	21.4%	16.7%
	PNEUMONIA	10.0%	5.9%	0.0%	0.0%
	ASTHMA	0.0%	7.8%	0.0%	0.0%
	RENAL	0.0%	4.9%	0.0%	0.0%
	NEUROLOGICAL	0.0%	2.0%	0.0%	0.0%
SYMPTOMS	FEVER	12.9%	13.1%	15.0%	15.0%
	SORE THROAT	15.1%	12.3%	12.5%	10.3%
	COUGH	21.4%	19.7%	20.0%	21.5%
	ASYMPTOMATIC	0.7%	1.4%	0.6%	0.9%
	HEADACHE	17.3%	16.0%	16.3%	15.9%
	OTHERS	10.3%	14.0%	13.1%	13.1%
	DYSPNEA	4.8%	4.0%	2.5%	3.7%
	CORYZA	6.6%	10.3%	15.0%	10.3%
	ANOSMIA	5.2%	3.9%	2.5%	5.6%
	AUGESY	5.5%	5.2%	2.5%	3.7%
OUTCOME	RECOVERED	83.6%	76.9%	76.7%	90.0%
	DEATH	16.4%	23.1%	23.3%	10.0%

Supplementary Table 4. Ct data.

Table is available at the link: https://drive.google.com/drive/folders/1rhWZu_dQiOq3GpeUHZrdxg5MnSyZFatk?usp=sharing

Supplementary Table 5. Primers and probes used to determinate SARS-CoV-2 lineages.

Target	Sequence	Application	Lineages		
			Alpha	Zeta	Gama
K417T	Forward 5’ - /rhAmp-F/TCCAGGGCAAACTGGAA**A**rGATTG/GT3/ (FAM) Forward 5’ - /rhAmp-Y/CCAGGGCAAACTGGAA**C**rGATTG/GT3/ (VIC) Reverse 5’ - GCAGCTATAACGCAGCCTGTAAAATrCATCT/GT2/	rhAmp	WT	WT	MUT
E484K	Forward 5’ - /rhAmp-F/TGTAAAGGAAAGTAACAATTAAAACCTT**C**rAACAC/GT3/ (FAM) Forward 5’ - /rhAmp-Y/TGTAAAGGAAAGTAACAATTAAAACCTT**T**rAACAC/GT3/ (VIC) Reverse 5’ - GCCCTGTATAGATTGTTTAGGAAGTCTAATrCTC AA/GT4/	rhAmp	WT	MUT	MUT
N501Y	Forward 5’ - /rhAmp-F/TCATATGGTTTCCAACCCACT**A**rATGGT/GT2/ (FAM) Forward 5’ - /rhAmp-Y/CATATGGTTTCCAACCCACT**T**rATGGT/GT2/ (VIC) Reverse 5’ - GCGGTGCATGTAGAAGTTCAAAAGAArAGTAC/GT1/	rhAmp	MUT	WT	MUT

WT: Wild Type; MUT: Mutant

Supplementary Table 6. Frequency comparison between SARS-CoV-2 lineages by RHU in MG state.

RHU	TOTAL MG (%)	DISTRIBUTION OF VARIANTS BY RHU			
		TOTAL GAMMA (%)	TOTAL ZETA (%)	TOTAL ALPHA (%)	TOTAL "OTHERS" (%)
ALFENAS	35 (2.8%)	27 (77.1%)	2 (5.7%)	0 (0.0%)	6 (17.1%)
BARBACENA	34 (2.7%)	23 (67.6%)	7 (20.6%)	4 (11.8%)	0 (0.0%)
BELO HORIZONTE	174 (14.0%)	120 (69.0%)	15 (8.6%)	14 (8.0%)	25 (14.4%)
CORONEL FABRICIANO	47 (3.8%)	18 (38.3%)	3 (6.4%)	25 (53.2%)	1 (2.1%)
DIAMANTINA	81 (6.5%)	44 (54.3%)	29 (35.8%)	3 (3.7%)	5 (6.2%)
DIVINOPOLIS	47 (3.8%)	37 (78.7%)	4 (8.5%)	4 (8.5%)	2 (4.3%)
GOVERNADOR VALADARES	39 (3.1%)	32 (82.1%)	3 (7.7%)	4 (10.3%)	0 (0.0%)
ITABIRA	38 (3.1%)	30 (78.9%)	1 (2.6%)	7 (18.4%)	0 (0.0%)
ITUIUTABA	26 (2.1%)	22 (84.6%)	0 (0.0%)	1 (3.8%)	3 (11.5%)
JANUARIA	39 (3.1%)	35 (89.7%)	1 (2.6%)	0 (0.0%)	3 (7.7%)
JUIZ DE FORA	15 (1.2%)	14 (93.3%)	0 (0.0%)	1 (6.7%)	0 (0.0%)
LEOPOLDINA	21 (1.7%)	16 (76.2%)	3 (14.3%)	1 (4.8%)	1 (4.8%)
MANHUACU	40 (3.2%)	18 (45.0%)	10 (25.0%)	11 (27.5%)	1 (2.5%)
MONTES CLAROS	77 (6.2%)	63 (81.8%)	8 (10.4%)	2 (2.6%)	4 (5.2%)
PASSOS	28 (2.3%)	21 (75.0%)	3 (10.7%)	1 (3.6%)	3 (10.7%)
PATOS DE MINAS	13 (1.0%)	13 (100.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)
PEDRA AZUL	33 (2.7%)	10 (30.3%)	18 (54.5%)	4 (12.1%)	1 (3.0%)
PIRAPORA	28 (2.3%)	22 (78.6%)	0 (0.0%)	0 (0.0%)	6 (21.4%)
PONTE NOVA	59 (4.8%)	45 (76.3%)	3 (5.1%)	3 (5.1%)	8 (13.6%)
POUSO ALEGRE	69 (5.6%)	53 (76.8%)	13 (18.8%)	1 (1.4%)	2 (2.9%)
SAO JOAO DEL REI	30 (2.4%)	21 (70%)	1 (3.3%)	6 (20.0%)	2 (6.7%)
SETE LAGOAS	55 (4.4%)	41 (74.5%)	2 (3.6%)	10 (18.2%)	2 (3.6%)
TEOFILO OTONI	29 (2.3%)	7 (24.1%)	8 (27.6%)	13 (44.8%)	1 (3.4%)
UBA	29 (2.3%)	15 (51.7%)	12 (41.4%)	1 (3.4%)	1 (3.4%)

UBERABA	46 (3.7%)	40 (87.0%)	5 (10.9%)	1 (2.2%)	0 (0.0%)
UBERLANDIA	34 (2.7%)	31 (91.2%)	0 (0.0%)	0 (0.0%)	3 (8.8%)
UNAI	27 (2.2%)	24 (88.9%)	1 (3.7%)	1 (3.7%)	1 (3.7%)
VARGINHA	47 (3.8%)	41 (87.2%)	2 (4.3%)	1 (2.1%)	3 (6.4%)
		TOTAL FREQUENCY OF EACH VARIANT IN EVERY STATE OF MG.			
TOTAL	1240 (100%)	883 (71.2%)	154 (12.4%)	119 (9.6%)	84 (6.8%)

Supplementary Table 7. Whole genome sequencing data from the samples in this study.

Lab_code_number	Colect_date (AAAA-MM-DD)	number_of_raw_reads	number_of_paired_filtered_reads	number_of_unpaired_filtered_reads	number_of_mapped_reads	efficiency	average_depth	coverage_10x	coverage_100x	coverage_1000x	genome_coverage	VARIANT	Pango_Lineages	Accesion_Number_GISAID
LBI311	25/03/2021	896278	856262	7448	844962	0.942745	3283.33	0.997325	0.943116	0.684413	0.997559	-	P.4	EPI_ISL_6508495
LBI312	25/03/2021	157094	151498	1142	148886	0.947751	601,229	0.995352	0.956426	0.115741	0.995352	-	P.4	EPI_ISL_6508496
LBI313	25/03/2021	107896	103272	1002	102427	0.949312	431,565	0.977527	0.876902	0.0635722	0.978664	-	P.4	EPI_ISL_6508560
LBI314	27/03/2021	417752	389190	5549	187514	0.448864	766,841	0.936461	0.609136	0.185165	0.939471	-	B.1.1	EPI_ISL_6508522
LBI315	12/03/2021	325154	307812	4944	306191	0.94168	1238.65	0.990503	0.97221	0.526034	0.991138	-	B.1.1.28	EPI_ISL_6508498
LBI316	23/03/2021	427410	412906	3647	398772	0.932996	1725.85	0.988229	0.907534	0.524362	0.98853	-	B.1.1.28	EPI_ISL_6508491
LBI318	22/03/2021	469760	453950	4172	450505	0.959011	1905.51	0.997626	0.982978	0.654316	0.997659	-	B.1.1	EPI_ISL_6508487
LBI321	01/03/2021	255210	247482	2156	245742	0.962901	1097.67	0.991272	0.935491	0.424539	0.991773	-	B.1.1.28	EPI_ISL_6508478
LBI322	27/03/2021	871812	842046	8577	840810	0.96444	3730.11	0.997592	0.962746	0.753035	0.997592	Gamma	P.1.15	EPI_ISL_6508494
LBI323	23/03/2021	807136	785108	5863	781917	0.968755	3433.09	0.997659	0.982811	0.790222	0.997659	Alpha	B.1.1.7	EPI_ISL_6508538
LBI324	29/03/2021	375910	362218	2916	359627	0.956684	1545.77	0.997559	0.957998	0.646958	0.997559	Gamma	P.1.15	EPI_ISL_6508499
LBI325	02/04/2021	716120	670908	4328	663949	0.927148	2538.69	0.990269	0.925058	0.581146	0.991506	Gamma	P.1.15	EPI_ISL_6508497
LBI375	02/04/2021	278442	266708	2651	264034	0.948255	1105.86	0.975019	0.820453	0.411698	0.97833	Gamma	P.1.15	EPI_ISL_6508561
LBI376	05/04/2021	286110	273310	3191	267423	0.934686	1153.27	0.987961	0.887871	0.499281	0.990402	Gamma	P.1.14	EPI_ISL_6508500
LBI377	05/04/2021	342606	333800	2341	333160	0.972429	1469.68	0.991673	0.97221	0.691101	0.991673	-	P.2	EPI_ISL_6508492
LBI378	05/04/2021	288444	279786	2050	279422	0.968722	1201.16	0.996857	0.968431	0.470287	0.997224	Gamma	P.1.17	EPI_ISL_6508489
LBI379	06/04/2021	371652	346472	3415	343474	0.924182	1254.48	0.953149	0.83413	0.405578	0.955322	Gamma	P.1.15	EPI_ISL_6508575
LBI380	06/04/2021	582360	554114	5899	545421	0.93657	2243.28	0.968866	0.915092	0.583988	0.969435	Gamma	P.1.15	EPI_ISL_6508566
LBI381	24/03/2021	377822	368404	2576	367224	0.97195	1625.23	0.99368	0.969501	0.654316	0.994215	Alpha	B.1.1.7	EPI_ISL_6508547
LBI382	22/03/2021	331972	322174	1886	320597	0.965735	1337.05	0.989667	0.9589	0.559141	0.991138	Alpha	B.1.1.7	EPI_ISL_6508544
LBI383	10/03/2021	426382	411354	3861	409734	0.960955	1740.01	0.997659	0.973949	0.733806	0.997659	-	P.2	EPI_ISL_6508477
LBI384	16/03/2021	315176	308354	1709	307885	0.976867	1382.75	0.996522	0.975554	0.633582	0.997224	Alpha	B.1.1.7	EPI_ISL_6508548

LBI385	23/03/2021	327874	315356	3881	315099	0.961037	1382.13	0.985921	0.903889	0.550145	0.986256	Alpha	B.1.1.7	EPI_ISL_6508553
LBI387	20/03/2021	344376	327630	5080	193973	0.563259	853,333	0.929138	0.620807	0.244056	0.936461	Alpha	B.1.1.7	EPI_ISL_6508523
LBI389	22/03/2021	465096	454060	2734	454140	0.976444	1982.8	0.997626	0.991707	0.796542	0.997693	Alpha	B.1.1.7	EPI_ISL_6508535
LBI390	23/03/2021	420942	406254	2950	404740	0.96151	1673.37	0.99806	0.983246	0.726817	0.99806	Alpha	B.1.1.7	EPI_ISL_6508533
LBI391	16/03/2021	390746	380220	3250	381305	0.975839	1712.54	0.997525	0.981607	0.727185	0.997525	Alpha	B.1.1.7	EPI_ISL_6508540
LBI392	24/03/2021	407844	399932	1951	399702	0.980036	1790.91	0.998161	0.9896	0.789085	0.998395	Alpha	B.1.1.7	EPI_ISL_6508537
LBI401	26/03/2021	394416	382108	4054	384482	0.974813	1707.41	0.997659	0.989867	0.756613	0.997659	-	P.4	EPI_ISL_6508476
LBI402	05/03/2021	385334	372770	4209	374583	0.9721	1681.77	0.990034	0.963047	0.62793	0.990034	-	P.7	EPI_ISL_6508503
LBI403	12/03/2021	361808	353948	2289	354290	0.979221	1608.47	0.934321	0.837909	0.558773	0.939203	Gamma	P.1.14	EPI_ISL_6508521
LBI404	13/03/2021	367966	360438	2092	359726	0.977607	1607.82	0.997927	0.997392	0.772565	0.99796	-	B.1.1.28	EPI_ISL_6508490
LBI405	17/03/2021	533644	522538	3204	522825	0.979726	2366.22	0.998395	0.997525	0.830519	0.998428	-	B.1.1.28	EPI_ISL_6508501
LBI406	25/03/2021	476650	460714	4656	461096	0.967368	1934.33	0.985754	0.911213	0.571448	0.987025	-	P.4	EPI_ISL_6508551
LBI411	08/03/2021	486510	475466	3243	475130	0.976609	2117.84	0.993914	0.985119	0.736883	0.994482	Alpha	B.1.1.7	EPI_ISL_6508545
LBI412	25/03/2021	566914	555150	3315	553722	0.97673	2521.87	0.997659	0.987459	0.806775	0.997659	-	None	EPI_ISL_6508549
LBI413	25/03/2021	365304	358148	2120	356158	0.974963	1635.2	0.925492	0.839715	0.561449	0.931345	Alpha	B.1.1.7	EPI_ISL_6508526
LBI414	16/03/2021	357846	346378	2447	346655	0.968727	1465.08	0.99582	0.91663	0.603719	0.996589	Alpha	B.1.1.7	EPI_ISL_6508543
LBI415	15/03/2021	401860	394432	2052	393665	0.979607	1778.26	0.950273	0.859111	0.586162	0.953282	Alpha	B.1.1.7	EPI_ISL_6508580
LBI416	17/03/2021	324212	316644	2688	316870	0.977354	1452.82	0.998662	0.982142	0.680567	0.998729	Alpha	B.1.1.7	EPI_ISL_6508534
LBI417	16/03/2021	394450	385870	1897	385106	0.976311	1682.97	0.994014	0.967595	0.718088	0.994817	Alpha	B.1.1.7	EPI_ISL_6508546
LBI418	17/03/2021	407924	397246	3182	398342	0.97651	1762.61	0.997759	0.997124	0.770424	0.997759	Alpha	B.1.1.7	EPI_ISL_6508539
LBI419	17/03/2021	442574	432380	3249	433195	0.978808	1941.22	0.997559	0.997124	0.830853	0.997592	Alpha	B.1.1.7	EPI_ISL_6508536
LBI422	25/03/2021	546656	527420	4306	509110	0.931317	2200.27	0.848142	0.72481	0.380965	0.851821	-	B.1.1.28	EPI_ISL_6508512
LBI423	12/03/2021	399840	382220	6018	230716	0.577021	1063.13	0.71762	0.565662	0.332308	0.729124	-	B.1.1.28	EPI_ISL_6508516
LBI424	25/03/2021	374120	362450	3341	348445	0.931372	1556.25	0.844531	0.714209	0.393639	0.857339	-	B.1.1.28	EPI_ISL_6508510
LBI425	15/03/2021	343744	331856	4126	331328	0.96388	1486.72	0.904759	0.777848	0.487041	0.911915	Gamma	P.1	EPI_ISL_6508531
LBI426	25/03/2021	488872	477392	2967	476004	0.973678	2083.12	0.98572	0.915661	0.764472	0.987493	Gamma	P.1	EPI_ISL_6508552
LBI427	26/03/2021	418518	407762	3376	407829	0.97446	1833.15	0.949905	0.824666	0.615089	0.954352	-	P.2	EPI_ISL_6508578
LBI428	29/03/2021	343348	335856	2305	335764	0.977912	1514.53	0.904558	0.783199	0.479049	0.908069	Alpha	B.1.1.7	EPI_ISL_6508530
LBI432	16/03/2021	871474	849420	6475	849922	0.975269	3768.36	0.985654	0.903722	0.747216	0.986055	-	P.2	EPI_ISL_6508554
LBI433	25/03/2021	725414	701502	6856	700631	0.965836	3065.96	0.936829	0.829716	0.648363	0.940976	Alpha	B.1.1.7	EPI_ISL_6508519
LBI434	24/03/2021	381832	373622	2265	353689	0.926295	1569.77	0.960171	0.860616	0.647962	0.963549	Alpha	B.1.1.7	EPI_ISL_6508573
LBI435	19/03/2021	752312	736108	4693	736550	0.979049	3276.27	0.998294	0.953416	0.830887	0.998361	-	P.2	EPI_ISL_6508488
LBI436	10/03/2021	449222	440006	2310	439444	0.978233	1942.08	0.992543	0.919573	0.720898	0.992977	Alpha	B.1.1.7	EPI_ISL_6508541
LBI437	12/03/2021	300292	294620	1618	290454	0.967239	1308.53	0.957663	0.842959	0.555998	0.962111	Gamma	P.1	EPI_ISL_6508574
LBI484	22/03/2021	131262	127180	1528	127205	0.969092	796,544	0.935425	0.802996	0.313748	0.935993	Gamma	P.1	EPI_ISL6508520
LBI511	31/03/2021	348156	331894	4592	322962	0.927636	1955.75	0.975855	0.900244	0.487242	0.975989	Gamma	P.1.15	EPI_ISL_6508555
LBI514	25/03/2021	288348	277434	3900	275853	0.956667	1775.11	0.997559	0.996422	0.751965	0.997559	Gamma	P.1.15	EPI_ISL_6508493

LBI515	05/03/2021	318790	303744	4020	253384	0.79483	1522.21	0.859512	0.582784	0.253252	0.869746	-	P.2	EPI_ISL_6508508
LBI530	04/03/2021	259864	252974	2577	253137	0.974113	1624.65	0.997559	0.9793	0.676588	0.997726	Gamma	P.1.15	EPI_ISL_6508502
LBI531	25/03/2021	259864	252974	2577	253137	0.974113	1624.65	0.997559	0.9793	0.676588	0.997726	Gamma	P.1.14	EPI_ISL_6508507
LBI532	24/03/2021	259864	252974	2577	253137	0.974113	1624.65	0.997559	0.9793	0.676588	0.997726	Gamma	P.1	EPI_ISL_6508514
LBI597	04/04/2021	171928	164908	2258	164801	0.958547	979,619	0.974718	0.872521	0.42668	0.976792	Gamma	P.1.15	EPI_ISL6508524
LBI598	11/03/2021	202736	196200	2292	195975	0.966651	1189.35	0.930174	0.752132	0.41658	0.936796	Alpha	B.1.1.7	EPI_ISL_9983271
LBI606	01/03/2021	264870	250190	2990	247613	0.934847	1385.94	0.94024	0.75046	0.409089	0.944487	Gamma	P.1	EPI_ISL6508617
LBI607	02/03/2021	197408	188226	3729	189274	0.958796	1370.59	0.989299	0.941979	0.579507	0.989466	Gamma	P.1	EPI_ISL6508482
LBI608	03/03/2021	252930	244768	2610	243790	0.963864	1374.98	0.937498	0.771561	0.483463	0.943216	Gamma	P.1	EPI_ISL6508518
LBI672	15/03/2021	292378	281594	2710	280309	0.958721	1408.87	0.993445	0.938066	0.616694	0.994817	Gamma	P.1.15	EPI_ISL6508483
LBI673	17/03/2021	316242	304438	2213	302914	0.957855	1269.27	0.981908	0.915995	0.568906	0.987225	Gamma	P.1	EPI_ISL6508550
LBI674	17/03/2021	229964	221898	2568	222628	0.968099	1354.56	0.980671	0.914156	0.607698	0.984583	Gamma	P.1	EPI_ISL6508556
LBI675	24/03/2021	286276	274176	2431	272995	0.953608	1276.24	0.996823	0.936428	0.608869	0.996857	Gamma	P.1	EPI_ISL6508484
LBI676	24/03/2021	271688	262140	1878	261219	0.961467	1262.5	0.994181	0.929673	0.559041	0.994248	Alpha	B.1.1.7	EPI_ISL6508542
LBI677	25/03/2021	218206	210584	1542	208347	0.954818	916,633	0.979801	0.864796	0.360867	0.980571	Gamma	P.1.15	EPI_ISL6508558
LBI678	25/03/2021	321778	309894	2163	306718	0.953198	1300.88	0.74133	0.56904	0.271143	0.757048	Gamma	P.1	EPI_ISL6508515
LBI679	29/03/2021	274052	263332	2151	261980	0.95595	1235.42	0.995452	0.94753	0.555764	0.996455	Gamma	P.1.15	EPI_ISL6508485
LBI680	29/03/2021	246624	237354	1395	234888	0.952413	960,223	0.987426	0.940207	0.381601	0.990235	Gamma	P.1.15	EPI_ISL6508486
LBI698	17/03/2021	271796	263292	2928	262264	0.96493	1516.06	0.97007	0.867873	0.615089	0.972912	Gamma	P.1.15	EPI_ISL6508565
LBI280	11/03/2021	1191760	1138330	10903	648864	0.544459	2688.12	0.984951	0.857439	0.460455	0.990269	Zeta	P.2	EPI_ISL_3155947
LBI373	31/03/2021	97924	87282	4941	91318	0.93254	432,386	0.955623	0.841521	0.0727017	0.957295	Gamma	P.1	EPI_ISL_3155987
LBI408	01/05/2021	376572	364532	2917	364071	0.966803	1615.25	0.968498	0.948768	0.640437	0.974484	Gamma	P.1.14	EPI_ISL_9983351
LBI409	02/05/2021	361686	350920	2314	350748	0.969758	1490.29	0.964853	0.928602	0.609303	0.965789	Gamma	P.1	EPI_ISL_9983366
LBI410	02/05/2021	774372	756874	4891	757358	0.978029	3410.22	0.973347	0.933585	0.690366	0.974417	Gamma	P.1.14	EPI_ISL_9983338
LBI429	24/02/2021	317686	310132	2296	307133	0.966782	1392	0.996923	0.941243	0.598669	0.996923	Zeta	P.2	EPI_ISL_6508479
LBI430	15/03/2021	412636	401980	3489	400562	0.970739	1791.93	0.997759	0.95044	0.724342	0.997759	Zeta	P.2	EPI_ISL_6508480
LBI431	16/03/2021	485770	474760	3408	473092	0.973901	2118.49	0.998696	0.95977	0.754105	0.998729	Zeta	P.2	EPI_ISL_6508481
FUNED-LBI-BC1	26/03/2021											Zeta	P.2	EPI_ISL_6508513
FUNED-LBI-BC2	26/03/2021											Gamma	P.1	EPI_ISL_6508504
FUNED-LBI-BC3	24/03/2021											Zeta	P.2	EPI_ISL_6508509
FUNED-LBI-BC4	22/03/2021											-	B.1.1	EPI_ISL_6513968
FUNED-LBI-BC5	25/03/2021											Zeta	P.2	EPI_ISL_6508511
FUNED-LBI-BC6	27/03/2021											Gamma	P.1	EPI_ISL_6513957
FUNED-LBI-BC7	22/03/2021											Gamma	P.1	EPI_ISL_6514068
FUNED-LBI-BC8	25/03/2021											Gamma	P.1.1	EPI_ISL_6513981
FUNED-LBI-BC9	24/03/2021											Gamma	P.1	EPI_ISL_6514233
FUNED-LBI-BC10	24/03/2021											Gamma	P.1	EPI_ISL_6508568

FUNED-LBI-BC11	24/03/2021											Gamma	P.1	EPI_ISL_6514216
FUNED-LBI-BC12	24/03/2021											Gamma	P.1	EPI_ISL_6514013
FUNED-LBI-BC13	22/03/2021											Gamma	P.1	EPI_ISL_6514172
FUNED-LBI-BC14	20/03/2021											Gamma	P.1	EPI_ISL_6508570
FUNED-LBI-BC15	25/03/2021											Gamma	P.1	EPI_ISL_6514265
FUNED-LBI-BC16	25/03/2021											Alpha	B.1.1.7	EPI_ISL_6508576
FUNED-LBI-BC17	24/03/2021											Gamma	P.1.14	EPI_ISL_6514157
FUNED-LBI-BC18	26/03/2021											Gamma	P.1	EPI_ISL_6514132
FUNED-LBI-BC20	24/03/2021											Gamma	P.1	EPI_ISL_6508569
FUNED-LBI-BC21	25/03/2021											Gamma	P.1.14	EPI_ISL_6514276
FUNED-LBI-BC22	24/03/2021											Gamma	P.1	EPI_ISL_6513944
FUNED-LBI-BC23	24/03/2021											Gamma	P.1	EPI_ISL_6514021
FUNED-LBI-BC24	25/03/2021											Gamma	P.1	EPI_ISL_6514053
FUNED-LBI-BC25	26/03/2021											Gamma	P.1	EPI_ISL_6514223
FUNED-LBI-BC26	26/03/2021											Gamma	P.1	EPI_ISL_6514239
FUNED-LBI-BC27	28/03/2021											Gamma	P.1	EPI_ISL_6514062
FUNED-LBI-BC28	22/03/2021											Gamma	P.1	EPI_ISL_6514086
FUNED-LBI-BC29	26/03/2021											Zeta	P.2	EPI_ISL_6508506
FUNED-LBI-BC30	26/03/2021											Zeta	P.2	EPI_ISL_6508571
FUNED-LBI-BC31	29/03/2021											Zeta	P.2	EPI_ISL_6513964
FUNED-LBI-BC32	24/03/2021											Gamma	P.1	EPI_ISL_6514199
FUNED-LBI-BC33	24/03/2021											Gamma	P.1	EPI_ISL_6508525
FUNED-LBI-BC34	27/03/2021											Alpha	B.1.1.7	EPI_ISL_6508505
FUNED-LBI-BC35	25/03/2021											Gamma	P.1	EPI_ISL_6513950
FUNED-LBI-BC36	27/03/2021											Gamma	P.1	EPI_ISL_6513995
FUNED-LBI-BC37	26/03/2021											Gamma	P.1	EPI_ISL_6514185
FUNED-LBI-BC38	23/03/2021											Gamma	P.1.14	EPI_ISL_6513935
FUNED-LBI-BC39	23/03/2021											Gamma	P.1	EPI_ISL_6514031
FUNED-LBI-BC40	27/03/2021											-	B.1.1.332	EPI_ISL_6508528
FUNED-LBI-BC41	23/03/2021											Gamma	P.1	EPI_ISL_6514008
FUNED-LBI-BC42	26/03/2021											Gamma	P.1	EPI_ISL_6513971
FUNED-LBI-BC43	23/03/2021											Gamma	P.1	EPI_ISL_6508527
FUNED-LBI-BC44	25/03/2021											Zeta	P.2	EPI_ISL_6508529
FUNED-LBI-BC45	26/03/2021											Gamma	P.1.14	EPI_ISL_6514058
FUNED-LBI-BC46	26/03/2021											Zeta	P.2	EPI_ISL_6508579
FUNED-LBI-BC47	28/03/2021											Gamma	P.1	EPI_ISL_6514001
FUNED-LBI-BC48	13/03/2021											Gamma	P.1	EPI_ISL_6508564

FUNED-LBI-BC49	15/03/2021											Alpha	B.1.1.7	EPI_ISL_6513927
FUNED-LBI-BC50	23/03/2021											Gamma	P.1.7	EPI_ISL_6514016
FUNED-LBI-BC51	24/03/2021											Gamma	P.1	EPI_ISL_6514047
FUNED-LBI-BC52	26/03/2021											Zeta	P.2	EPI_ISL_6508577
FUNED-LBI-BC53	26/03/2021											Gamma	P.1	EPI_ISL_6514217
FUNED-LBI-BC54	26/03/2021											Zeta	P.2	EPI_ISL_6508567
FUNED-LBI-BC55	25/03/2021											Gamma	P.1	EPI_ISL_6514259
FUNED-LBI-BC56	25/03/2021											Gamma	P.1	EPI_ISL_6514074
FUNED-LBI-BC57	26/03/2021											Zeta	P.2	EPI_ISL_6508581
FUNED-LBI-BC58	26/03/2021											Gamma	P.1	EPI_ISL_6514038
FUNED-LBI-BC59	24/03/2021											Gamma	P.1	EPI_ISL_6508562
FUNED-LBI-BC60	24/03/2021											Gamma	P.1	EPI_ISL_6508563
FUNED-LBI-BC61	24/03/2021											Gamma	P.1	EPI_ISL_6514279
FUNED-LBI-BC62	27/03/2021											Gamma	P.1.14	EPI_ISL_6514178
FUNED-LBI-BC64	26/02/2021											Zeta	P.2	EPI_ISL_6514148
FUNED-LBI-BC65	26/02/2021											Zeta	P.2	EPI_ISL_6514100
FUNED-LBI-BC66	26/02/2021											Zeta	P.2	EPI_ISL_6513921
FUNED-LBI-BC67	22/03/2021											Gamma	P.1	EPI_ISL_6513987
FUNED-LBI-BC68	22/03/2021											Gamma	P.1	EPI_ISL_6508557
FUNED-LBI-BC69	22/03/2021											Gamma	P.1	EPI_ISL_6514291
FUNED-LBI-BC70	22/03/2021											Gamma	P.1	EPI_ISL_6514167
LBI51/2020	17/12/2020											Zeta	P.2	EPI_ISL_1494960
LBI52/2020	06/11/2020											Zeta	P.2	EPI_ISL_1494961
LBI54	19/01/2021											Zeta	P.2	EPI_ISL_1494962
LBI55	22/01/2021											Zeta	P.2	EPI_ISL_1494963
LBI56	25/01/2021											Zeta	P.2	EPI_ISL_1494964
LBI57	27/01/2021											Zeta	P.2	EPI_ISL_1494965
LBI58	28/01/2021											Zeta	P.2	EPI_ISL_1494966
LBI143/2020	28/10/2020	966156	218994	332798	540659	0.559598	2911.86	29864	29830	0.998696	0.99893	Zeta	P.2	EPI_ISL_1494967
LBI144/2020	03/12/2020	836708	39580	338695	370899	0.443284	1477.9	29846	29095	0.998228	0.999967	Zeta	P.2	EPI_ISL_1494968
LBI145	08/01/2021	1353514	109762	549662	619013	0.457338	2733.92	29663	28158	0.992576	0.998729	Zeta	P.2	EPI_ISL_1494969
LBI146/2020	11/12/2020	530984	40006	215581	248809	0.468581	1075.19	29834	29360	0.997693	0.99883		B.1.1	EPI_ISL_1494970
LBI147	07/01/2021	3625050	359630	1491629	1829398	0.504655	8503.22	29858	29833	0.998595	0.999699	Zeta	P.2	EPI_ISL_1494971
LBI150/2020	26/11/2020	2425828	398358	939729	1292591	0.532845	6684.87	28249	24845	0.951376	0.998027		B.1.1	EPI_ISL_1494972
LBI151/2020	17/11/2020	2318156	246672	884883	1038493	0.447982	4795.73	29106	25858	0.973615	0.994248	Zeta	P.2	EPI_ISL_1494973
LBI153	09/02/2021	89518	15554	29990	38918	0.434751	201,474	29400	19955	0.98338	0.997693	Zeta	P.2	EPI_ISL_1494974
LBI154	09/02/2021	220472	30588	83127	111779	0.506999	532.74	29593	25625	0.9897	0.997793	Zeta	P.2	EPI_ISL_1494975

LBI172	22/02/2021	476484	78092	182234	256360	0.538024	1290.23	29861	29824	0.998629	0.999666	Zeta	P.2	EPI_ISL_1494976
LBI173	26/02/2021	652734	102382	255128	349768	0.535851	1782.79	29859	29200	0.998529	0.99893	Gamma	P.1	EPI_ISL_1494977
LBI174	26/02/2021	135280	28536	48752	75820	0.560467	402,523	29306	27627	0.980504	0.998662	Gamma	P.1	EPI_ISL_1494978
LBI176	23/02/2021	60616	10456	22848	32384	0.534248	165.48	29625	20171	0.992208	0.998361	Alpha	B.1.1.7	EPI_ISL_1494979
LBI177	23/02/2021	142982	32512	50036	80405	0.562344	437,317	29732	27300	0.995385	0.997893	Zeta	P.2	EPI_ISL_1494980
LBI178	24/02/2021	95616	17164	34852	50957	0.532934	258,289	29618	25195	0.992743	0.997693	Zeta	P.2	EPI_ISL_1494981
LBI179	24/02/2021	301586	27286	120526	144891	0.48043	646,644	29151	28067	0.975822	0.997392	Gamma	P.1	EPI_ISL_1494982
LBI180	24/02/2021	229738	73996	72550	144625	0.629521	848,085	29749	29196	0.995285	0.998161	Zeta	P.2	EPI_ISL_1494983
LBI181	26/02/2021	88530	13056	33257	45685	0.51604	226,287	29424	20845	0.987593	0.99786	Zeta	P.2	EPI_ISL_1494984
LBI185	26/02/2021	2520854	284614	1037402	1291309	0.512251	6111.86	29871	29830	0.998963	0.999632	Zeta	P.2	EPI_ISL_1494985
LBI190	27/02/2021	274978	48446	102554	149005	0.54188	754,096	29786	28348	0.996489	0.998629	Gamma	P.1	EPI_ISL_1494986
LBI191	27/02/2021	571096	215966	166564	375110	0.656825	2298.1	27710	23905	0.928602	0.998395	Gamma	P.1	EPI_ISL_1494987
LBI193	27/02/2021	199156	80142	53506	131515	0.660362	808,067	29834	29488	0.997726	0.999131	Zeta	P.2	EPI_ISL_1494988
LBI194	27/02/2021	204776	81558	56988	135778	0.663056	833,419	29735	28541	0.995151	0.99883	Gamma	P.1	EPI_ISL_1494989
LBI195	27/02/2021	351080	40546	147030	183785	0.523485	899,147	29855	29692	0.998395	0.999866	Zeta	P.2	EPI_ISL_1494990
LBI196	27/02/2021	213688	22610	90619	111485	0.521719	538,753	29831	29122	0.997592	0.99883	Zeta	P.2	EPI_ISL_1494991
LBI198	27/02/2021	2427184	825998	735076	1529133	0.630003	9063.77	29861	29833	0.998595	0.999465	Zeta	P.2	EPI_ISL_1494992
LBI199	27/02/2021	396966	190326	95579	247136	0.622562	1595.12	23139	18933	0.779587	0.936863	Gamma	P.1	EPI_ISL_1494993
LBI200	27/02/2021	1945968	636606	608760	1221471	0.627693	7208.75	29870	29836	0.998963	0.999632	Gamma	P.1	EPI_ISL_1494994
LBI203	27/02/2021	1326172	352262	454530	794021	0.598732	4430.53	29861	29801	0.998595	0.999833	Zeta	P.2	EPI_ISL_1494995
LBI204	27/02/2021	1433322	229146	573413	792303	0.552774	4112.58	29859	29830	0.998562	0.999833	Zeta	P.2	EPI_ISL_1494996
LBI205	27/02/2021	1190820	594296	277857	860877	0.722928	5546.81	29865	29835	0.998729	0.9999	Zeta	P.2	EPI_ISL_1494997
LBI206	27/02/2021	2177784	312180	881311	1168325	0.536474	5881.18	29855	29801	0.998495	0.999498	Gamma	P.1	EPI_ISL_1494998
LBI207	27/02/2021	986720	321008	311136	616395	0.624691	3647.36	29845	29834	0.998094	1	Zeta	P.2	EPI_ISL_1494999
LBI208	27/02/2021	709606	178840	250870	419140	0.590666	2385.63	29834	29331	0.997726	0.998294	Zeta	P.2	EPI_ISL_1495000
LBI209	27/02/2021	115946	57050	27654	80970	0.698342	527,849	23326	16565	0.792262	0.918871	Zeta	P.2	EPI_ISL_1495001
LBI210	27/02/2021	233218	29064	96439	121469	0.520839	596,048	29831	29626	0.997592	0.999599	Zeta	P.2	EPI_ISL_1495002
LBI211	27/02/2021	302108	122920	72341	173405	0.573983	1131.61	21580	16232	0.729793	0.873926	Zeta	P.2	EPI_ISL_1495003
LBI213	27/02/2021	181396	78826	49120	125741	0.693185	798,361	29781	28983	0.996054	0.999264	-	B.1.1	EPI_ISL_1495004
LBI214	27/02/2021	1558444	809508	362001	1156265	0.741936	7616.34	29843	29817	0.997994	0.999565	Gamma	P.1	EPI_ISL_1495005
LBI216	26/02/2021	294958	149370	69942	216446	0.73382	1418.68	29836	29536	0.997759	0.999231	Zeta	P.2	EPI_ISL_1495006
LBI217	27/02/2021	93164	21934	33317	54271	0.582532	297,485	29320	25502	0.980805	0.996355	Gamma	P.1	EPI_ISL_1495007
LBI219	27/02/2021	54092	5388	22764	26888	0.497079	127,303	29495	16525	0.989031	0.997559	Zeta	P.2	EPI_ISL_1495008
LBI220	01/03/2021	1574472	162596	643543	785673	0.499007	3631.37	29859	29831	0.998595	0.998896	Zeta	P.2	EPI_ISL_1495009
LBI221	03/03/2021	577046	64180	243275	298938	0.518049	1448.59	29670	28922	0.993646	0.998194	Gamma	P.1	EPI_ISL_1495010
LBI222	05/03/2021	737208	86776	305750	386591	0.524399	1883.01	29822	28989	0.997525	0.998261	Gamma	P.1	EPI_ISL_1495011
LBI223	03/03/2021	1240066	719316	250201	962269	0.775982	6451.02	29150	28419	0.975153	0.994215	Gamma	P.1	EPI_ISL_1495012

LBI224	03/03/2021	1233348	623444	293530	908213	0.73638	5933.12	29849	29685	0.998194	0.999632	Zeta	P.2	EPI_ISL_1495013
LBI226	03/03/2021	768004	196468	272207	454859	0.592261	2582.87	29844	29208	0.998027	0.999465	Gamma	P.1	EPI_ISL_1495014
LBI228	02/03/2021	345626	143794	94988	235131	0.680305	1472.48	29838	29389	0.997826	0.999398	Gamma	P.1	EPI_ISL_1495015
LBI229	03/03/2021	464382	252470	98926	346602	0.746373	2284.04	29737	29322	0.994449	0.999231	Gamma	P.1	EPI_ISL_1495016
LBI233	03/03/2021	555388	288346	124650	407639	0.733972	2668.46	29871	29832	0.998997	0.999565	Zeta	P.2	EPI_ISL_1495017
LBI235	03/03/2021	298662	159886	63834	219937	0.736408	1450.73	29845	29667	0.998127	1	Alpha	B.1.1.7	EPI_ISL_1495018
LBI240	02/03/2021	98254	46806	22779	68359	0.695738	440,802	29832	28553	0.997626	0.998395	Gamma	P.1	EPI_ISL_1495019
LBI241	03/03/2021	363692	215152	67424	280859	0.772244	1899.16	29792	29590	0.996355	0.999565	Gamma	P.1	EPI_ISL_1495020
LBI243	03/03/2021	251322	150770	45536	194318	0.773183	1317.79	29802	29080	0.996622	0.999298	Gamma	P.1	EPI_ISL_1495021
LBI244	02/03/2021	2236746	1279670	435676	1702898	0.761328	11487.4	29849	29788	0.998294	1	Gamma	P.1	EPI_ISL_1495022
LBI245	02/03/2021	130036	55928	34136	88594	0.681304	557,718	29831	28678	0.997659	0.999465	Gamma	P.1	EPI_ISL_1495023
LBI246	01/03/2021	265386	139600	57105	194994	0.734756	1294.23	29802	29026	0.996622	0.999565	Gamma	P.1	EPI_ISL_1495024
LBI247	03/03/2021	230474	140760	41270	180243	0.782054	1229.34	29788	29178	0.996154	0.997325	Gamma	P.1	EPI_ISL_1495025
LBI248	03/03/2021	83324	48094	16296	63897	0.76685	432,801	29779	25602	0.995987	0.998194	Gamma	P.1	EPI_ISL_1495026
LBI249	03/03/2021	141778	75128	30671	104880	0.739748	696,181	29802	28743	0.996622	0.99883	Zeta	P.2	EPI_ISL_1495027
LBI257	11/03/2021	245930	139410	49486	187894	0.764014	1251.37	21699	15384	0.7319	0.89787	Zeta	P.2	EPI_ISL_1495028
LBI261	03/03/2021	78570	34340	21052	54577	0.694629	344.9	29798	28355	0.996522	0.998529	Alpha	B.1.1.7	EPI_ISL_1495029
LBI262	03/03/2021	298962	143470	71085	211258	0.706638	1360.01	29839	28646	0.99786	0.999833	Zeta	P.2	EPI_ISL_1495030
LBI263	03/03/2021	32342	18632	6448	24817	0.76733	165,834	29691	18994	0.994348	0.999231	Gamma	P.1	EPI_ISL_1495031
LBI266	25/02/2021	105710	52258	25138	76656	0.725154	496,567	28930	24719	0.97104	0.998161	Gamma	P.1	EPI_ISL_1495032
LBI267	24/02/2021	163172	81162	38826	118224	0.724536	768,735	28743	20905	0.964184	0.99786	Zeta	P.2	EPI_ISL_1495033
LBI268	17/02/2021	280066	126258	73706	197177	0.704038	1261.97	29839	29503	0.997927	0.998896	Zeta	P.2	EPI_ISL_1495034
LBI270	15/03/2021	524674	288882	111939	396780	0.756241	2636.57	29837	28926	0.997793	0.998228	Gamma	P.1	EPI_ISL_1495035
LBI271	12/03/2021	141066	72658	32230	102343	0.725497	672,579	29330	27195	0.984884	0.998662	Gamma	P.1	EPI_ISL_1495036
LBI272	09/03/2021	408426	214858	87978	296540	0.726056	1953.95	28930	24755	0.97104	0.997893	Gamma	P.1	EPI_ISL_1495037
LBI273	04/03/2021	269332	146176	58271	202176	0.750657	1338.01	29825	29174	0.997458	0.99903	Gamma	P.1	EPI_ISL_1495038
LBI279	13/01/2021	162654	84464	35671	112679	0.692753	739,629	23387	17181	0.794837	0.889376	Zeta	P.2	EPI_ISL_1495039
LBI281	12/02/2021	836792	388098	208329	536598	0.641256	3458.02	27971	22960	0.938802	0.988864	Zeta	P.2	EPI_ISL_1495040
LBI282	01/02/2021	155324	77396	36682	112481	0.72417	731,019	29842	29434	0.997994	0.999431	Zeta	P.2	EPI_ISL_1495041
LBI283	22/02/2021	325292	193890	62390	254442	0.782196	1712.22	29815	29422	0.997057	0.99903	Zeta	P.2	EPI_ISL_1495042
LBI215	27/02/2021	655762	64136	274912	328183	0.500461	1532.93	29848	29327	0.998228	1	-	P.5	EPI_ISL_1497548
LBI218	28/02/2021	120104	67012	24587	89420	0.744521	595,506	22787	17182	0.764706	0.91128	-	P.5	EPI_ISL_1497549

3. DISCUSSÃO

A pandemia do COVID-19 tem sido um marco na história da humanidade. Devido à falta de informações sobre o SARS-CoV-2 e ao seu rápido surgimento e dispersão pelo mundo, surgiu a necessidade de desenvolver tecnologias que nos dessem informações necessárias sobre métodos de combate e erradicação desse vírus. Neste trabalho, desenvolvemos e aplicamos uma nova metodologia de genotipagem de variantes do SARS-CoV-2, bem como o estudo da dinâmica de variantes em circulação no estado de Minas Gerais, no período de março a abril de 2021. Como proposto no capítulo I, desenvolvemos e validamos uma metodologia de genotipagem de variantes de SARS-CoV-2, o qual foi utilizado para diferenciação entre 3 variantes específicas em circulação no país, no início de 2021: Alfa, Gama e Zeta. Além disso, esta metodologia tem a facilidade de ser estendida para diversas variantes através de desenhos de iniciadores específicos para as variantes de interesse. Foi uma metodologia pioneira nessa área de genotipagem de variantes muito antes dos kits de genotipagem da Thermo (Taq Path) entre outras e foi adotado até mesmo pela OMS para acelerar o processo de identificação de variantes e por empresa privada (Hermes Pardini) no estado de Minas Gerais que faz tem vários pontos no Brasil todo e processa essas amostras aqui na sede. O CooLabs, um programa de cooperativa de laboratórios da UFMG, também aderiu a essa metodologia para rotina durante a pandemia. Outra vantagem dessa metodologia é a não necessidade de equipamentos mega sofisticados, onde laboratórios de biologia molecular tendo estrutura básica como uma máquina de qPCR consegue aplicar o processo para detecção dessas variantes. Algumas desvantagens da metodologia é a limitação para utilização na detecção de variantes novas, pois como tem a necessidade do sequenciamento para descrição das novas mutações, é preciso também destas mesmas informações para o desenho de novos iniciadores para adaptação da genotipagem para novas variantes. Métodos de vigilância amplos e baratos são necessários para rastrear variantes de interesse do SARS-CoV-2 globalmente, embora o sequenciamento seja o padrão-ouro para de variantes circulantes, a vigilância genômica de rotina não está disponível em muitos lugares devido à falta de recursos e experiência (VOGELS et al., 2021).

No capítulo II, com o auxílio dessa metodologia, contribuímos com o processo de vigilância genômica aplicado no estado de Minas Gerais em um período da pandemia onde houve um aumento significativo de número de casos e mortes tanto no país, quanto no estado devido ao surgimento e rápida dispersão de uma nova variante altamente transmissível e, na maior parte dos casos, com desfecho grave ou óbitos. Isso nos permitiu um mapeamento mais rápido e satisfatório sobre a situação do estado e, adicionando a metodologia de sequenciamento

de genoma completo, conseguimos descrever uma breve história sobre a introdução da variante Gama no estado.

A rápida dispersão do SARS-CoV-2 pelo mundo teve influência de fatores climáticos ambientais como temperatura e umidade, os quais afetaram a taxa de mortalidade (MA et al. 2020; SAJADI et al. 2020; WANG et al. 2020). Estudo de Sabarathinam et al. (2022) demonstrou que nos países os quais tiveram os primeiros casos noticiados de dispersão do SARS-CoV-2 (Coreia do Sul, China, Malásia, Cingapura, Índia, Kuwait, Itália, Espanha, França, Alemanha, Reino Unido e Estados Unidos da América) tiveram uma influência de fatores climáticos ambientais (temperatura, umidade relativa, ponto de orvalho, velocidade do vento e precipitação).

Com a dispersão do vírus ao longo do globo, viu-se a necessidade de ferramentas de monitoramento das variantes em circulação e possíveis novas, e como resultado, muitos países aumentaram sua capacidade de sequenciamento de genoma completo do SARS-CoV-2 (recomendado pela OMS 10% do total de amostras positivas), mas infelizmente, o sequenciamento de genoma completo é mais lento que o teste de PCR e, portanto, não é adequado para rastreamento de contatos para limitar a propagação do vírus (CABECINHAS et al., 2021; VOGELS et al., 2021). Alternativas mais simples foram desenvolvidas para detecção rápida de VOC's e rastreamento de contatos, como ensaios de triagem baseados em RT-PCR, produzindo resultados em poucas horas (KAMI et al., 2021; VEJA-MAGAÑA et al., 2021). Um trabalho realizado na França, de Bal et al. (2021), utilizou as técnicas baseadas em qPCR (TaqPath kit) para detecção de VOC's, as quais utilizam alvos para regiões do gene Orf1ab, S (ΔH69/ΔV70) e N. Já Migueres et al. (2021) conduziram um trabalho de comparação com kit TaqPath e o ensaio de ID tríplex, onde este último conseguia detectar e diferenciar variantes B1.1.7 de B1.1.35/P1, obtendo ótimos resultados.

Diferente da nossa metodologia, o kit TaqPath não foi desenvolvido para serviços de vigilância genômica de variantes de SARS-CoV-2 e possui várias limitações (VOGELS et al., 2021). Por exemplo, o kit consegue identificar a variante B1.1.7 (Alfa), mas devido ao compartilhamento de genoma da mutação ΔH69/ΔV70 com outras variantes circulantes (B1.258 e B1.375), não era possível a confirmação das mesmas (LARSEN; WOROBEY, 2020; MORENO et al., 2021). Em contrapartida, nossa metodologia nos permite a detecção de variantes de interesse devido ao fato de podermos desenhar iniciadores para regiões específicas, podendo assim, detectar e diferenciar diferentes variantes em circulação em uma mesma área

geográfica, de forma mais rápida que o sequenciamento de genoma completo e tão eficiente quanto.

Mais tarde, outros kits de detecção de variantes de SARS-CoV-2 foram desenvolvidos para variantes específicas (VOGELS et al., 2021), porém, ainda caros quando comparados ao sistema de genotipagem por rhAmp (IDT). Com a preocupação de desenvolver estratégias para conter a disseminação do SARS-CoV-2 e, ao mesmo tempo, obter informações sobre situação das variantes em circulação e possíveis novas emergentes, as metodologias de genotipagem foram sendo aperfeiçoadas para estudos de monitoramento dessas variantes (YANIV et al., 2021). A vigilância genômica do SARS-CoV-2 se tornou uma ferramenta indispensável para o monitoramento das variantes que estavam em circulação no mundo desde então. Isso permitia às autoridades competentes de saúde nas suas tomadas de decisões sobre estratégias que poderiam ser utilizadas para evitar ou minimizar os danos causados pela dispersão descontrolada do vírus. Embora o início da pandemia variou em cada país, o intervalo entre o primeiro caso e o período de *lockdown* desempenhou um papel significativo na disseminação (SABARATHINAM et al., 2022).

No Brasil, até o período do presente estudo, foi marcado por duas ondas de epidemia: primeira data por volta de fevereiro a março de 2020, caracterizado por variantes de SARS-CoV-2 como B.1.1.28 e B.1.1.33 (GIOVANETTI et al., 2021). A segunda por volta de outubro de 2020 até julho de 2021, com circulação de variantes como Zeta (P.2), Alfa (B.1.1.7) nova em ascensão, Gama (P.1), a qual já se encontrava espalha por todo país em janeiro de 2021 e dominou por 8 meses consecutivos (GIOVANETTI et al., 2022). A variante Alfa foi detectada no período, mas não manteve frequência acima de 2% na população (OPAS/OMS 2021). A variante Zeta (P.2) dominou amplamente a primeira onda epidêmica que persistiu até março de 2021, quando foi substituída por Gamma (GIOVANETTI et al., 2022). Aqui no Brasil, a Gama tornou-se dominante no Amazonas apenas três semanas após sua detecção e pouco tempo após, pelo país todo, o que foi refletido no aumento do número de casos e óbitos registrados (FARIAS et al., 2021; MARTINS et al., 2021). Porém, essa rápida dispersão causou impactos na população devido a fatores como a estrutura hospitalar, um estudo com 462.366 pacientes, realizado no Brasil em 17 estados, demonstrou que 20% teve desfecho fatal (BRIZZI et al., 2022). Apesar do período de vacinação coincidir com o momento de aumento da frequência da Gama no país, não foi observado uma diminuição no número de casos diários e mortes até abril de 2021 (GIOVANETTI et al., 2022). Quando comparado a variante Delta no país, esta foi introduzida por volta de julho de 2021 e teve uma maior taxa de dispersão e alta frequência,

substituindo a Gama já em agosto de 2021 (GANYANI et al., 2020; GIOVANETTI et al., 2022). Apesar de ter taxa de transmissão maior que a Gama, não foi observado um aumento do número de casos e óbitos relativos à variante Delta, o que pode ser explicado pela taxa de vacinação está em mais de 50%, associado a imunidade adquirida por infecção de variantes anteriores (Alfa, Beta, Gama) (GIOVANETTI et al., 2022).

No mundo, vários trabalhos relatam a importância que tiveram os processos de vigilância genômica do vírus. Aqui no Brasil, tivemos alguns trabalhos que monitoram essas variantes, porém, em menor escala quando comparado ao mundo como Bezerra et al. (2021), o qual trabalhou com amostras de pacientes da região norte (Amazonas) e nordeste (Pernambuco), utilizando a metodologia de sequenciamento de genoma completo. Outro trabalho temos de Voloch et al. (2021), o qual conseguiu caracterizar a então nova variante Zeta no estado do Rio de Janeiro, a partir do sequenciamento de 180 genomas. Um diferencial do nosso trabalho é que podemos chamar a atenção para o tamanho amostral utilizado aqui, que teve uma escala de estado inteiro, diferente de outros trabalhos que só amostravam parte da população, principalmente das capitais. Outro ponto que podemos discutir são as regiões onde houveram mais estudos de vigilância, que são as regiões sul e sudeste. Isso se dá muito devido ao tamanho populacional encontrado nessas regiões e também por vias de transição de pessoas tanto brasileiras quanto estrangeiras.

Nosso estudo acompanha um momento onde observamos a entrada da Gama no estado de Minas Gerais, seu crescimento e sobreposição as outras variantes em co-circulação naquele momento (Alfa e Zeta), além da detecção de outras linhagens menos frequentes como a B.1.1, B.1.1.28, B.1.1.33, P4, P5 e P7, as quais foram classificadas como “outras” linhagens pela nossa metodologia de genotipagem. Nesse ponto, teriam maior interesse as regiões sudeste e sul, pois diversas das variantes em circulação (Ômicron, Delta) ou que já circularam (Alfa, Beta, Gama e Zeta) no país tiveram pontos de introdução advindas de brasileiros chegando do exterior (BEZERRA et al., 2021; VOLOCH et al., 2021). Com isso, nosso trabalho conseguiu alcançar o objetivo de fazer uma vigilância genômica do SARS-CoV-2 em todo o estado de Minas Gerais e foi possível a determinação da introdução da Gama no estado.

4. CONCLUSÃO

Foi desenvolvido uma metodologia mais barata e rápida que o sequenciamento de genoma completo para detecção de variantes de SARS-CoV-2: genotipagem rhAmp, metodologia que posteriormente foi recomendada pela OMS como ferramenta de vigilância em outras localidades, além de aderida na rotina de serviço por outras instituições como Hermes Pardini para esse mesmo propósito.

Foi possível identificar a frequência e distribuição de variantes de SARS-CoV-2 no estado de Minas Gerais, que é dividido em 28 URS, durante período de crescimento de número de casos e mortes no estado devido a inserção e dispersão de uma nova variante de preocupação: Gama. Além disso, conseguimos observar o processo de chegada, dispersão e predominância dessa variante no estado e em cada uma das 28 URS.

Foi identificado a presença de variantes com menor frequência em circulação no estado, e, a partir de dados de sequenciamento de parte dessas amostras, foi possível determinar suas linhagens. Também, a partir de dados de sequenciamento, conseguimos predizer a data de inserção da Gama no estado, além do possível local de origem.

O desenvolvimento de diferentes tecnologias para aplicação na saúde pública em cenários como o atual mostrou-se de grande valia para se obter novas informações sobre o SARS-CoV-2 e elaborar diferentes estratégias para o combate da pandemia de COVID-19. A importância da vigilância genômica em momentos como esse da pandemia se mostrou eficiente para obtenção de uma resposta rápida, em tempo real, sobre a situação das variantes em circulação no estado de Minas Gerais e também, serviu como apoio informativo sobre medidas que o governo do estado, junto com o governo federal poderia atuar para evitar ou, pelo menos, diminuir o número de casos e óbitos ocasionados pela pandemia.

REFERÊNCIAS

ALCANTARA, L. C. J. et al. SARS-CoV-2 epidemic in Brazil: how the displacement of variants has driven distinct epidemic waves. **Virus Research**, v. 315, n. March, p. 198785, jul. 2022.

ARAUJO, D. B. et al. SARS-CoV-2 isolation from the first reported patients in Brazil and establishment of a coordinated task network. **Memórias do Instituto Oswaldo Cruz**, v. 115, n. 12, p. 1–8, 2020.

BADEN, L. R. et al. Efficacy and Safety of the mRNA-1273 SARS-CoV-2 Vaccine. **New England Journal of Medicine**, v. 384, n. 5, p. 403–416, 4 fev. 2021.

BAL, A. et al. Two-step strategy for the identification of SARS-CoV-2 variant of concern 202012/01 and other variants with spike deletion H69–V70, France, August to December 2020. **Eurosurveillance**, v. 26, n. 3, p. 1–5, 21 jan. 2021.

BATTY, C. J. et al. Vaccine formulations in clinical development for the prevention of severe acute respiratory syndrome coronavirus 2 infection. **Advanced Drug Delivery Reviews**, v. 169, p. 168–189, fev. 2021.

BBC NEWS. Coronavírus: a eficácia da CoronaVac e demais vacinas explicada em 4 gráficos. *In*: BBC NEWS. **Coronavírus: a eficácia da CoronaVac e demais vacinas explicada em 4 gráficos**. [*S. l.*], 14 jan. 2021. Disponível em: https://www.bbc.com/portuguese/brasil-55655588. Acesso em: 29 abr. 2022.

BEZERRA, M. F. et al. A Sanger-based approach for scaling up screening of SARS-CoV-2 variants of interest and concern. **Infection, Genetics and Evolution**, v. 92, n. January, p. 104910, ago. 2021.

BJM BEST PRATICE. Coronavirus disease 2019 (COVID-19). *In*: BJM BEST PRATICE. **Coronavirus disease 2019 (COVID-19)**. [*S. l.*], 7 abr. 2022. Disponível em: https://bestpractice.bmj.com/topics/en-gb/3000201#important-update. Acesso em: 29 abr. 2022.

BRIZZI, A. et al. Spatial and temporal fluctuations in COVID-19 fatality rates in Brazilian hospitals. **Nature Medicine**, 10 maio 2022.

CANDIDO, D. S. et al. Evolution and epidemic spread of SARS-CoV-2 in Brazil. **Science**, v. 369, n. 6508, p. 1255–1260, 4 set. 2020.

CENTERS FOR DISEASES CONTROL AND PREVETION. Centers for Diseases Control and Prevetion. Symptoms of COVID-19. **Your Health**, [*S. l.*], p. SN, 22 fev. 2021. Disponível em: https://www.cdc.gov/coronavirus/2019-NCov/symptoms-testing/symptoms.html. Acesso em: 20 ago. 2021.

CENTERS FOR DISEASES CONTROL AND PREVETION. Centers for Diseases Control and Prevetion. Interim Clinical GuidaNCe for Management of Patients with Confirmed Coronavirus Disease (COVID-19). **Interim Clinical GuidaNCe for Management of Patients with Confirmed Coronavirus Disease (COVID-19)**, [*S. l.*], p. SN, 16 fev. 2021. Disponível em: https://www.cdc.gov/coronavirus/2019-NCov/hcp/clinical-guidaNCe-management-patients.html. Acesso em: 20 ago. 2021.

CENTERS FOR DISEASES CONTROL AND PREVETION. Centers for Diseases Control and Prevetion. Post-COVID Conditions. *In*: **Post-COVID Conditions**. [*S. l.*], 12 jul. 2021.

Disponível em: https://www.cdc.gov/coronavirus/2019-NCov/long-term-effects.html. Acesso em: 20 ago. 2021.

CENTERS FOR DISEASES CONTROL AND PREVETION. Centers for Diseases Control and Prevetion. SARS-CoV-2 Variant Classifications and Definitions. **SARS-CoV-2 Variant Classifications and Definitions**, [*S. l.*], p. SN, 24 ago. 2021. Disponível em: https://www.cdc.gov/coronavirus/2019-NCov/variants/variant-info.html#CoNCern. Acesso em: 23 ago. 2021.

CENTERS FOR DISEASES CONTROL AND PREVETION. People with Certain Medical Conditions. In: **People with Certain Medical Conditions.** [S. l.], 20 ago. 2021. Disponível em: https://www.cdc.gov/coronavirus/2019-NCov/need-extra-precautions/people-with-medical-conditions.html. Acesso em: 20 ago. 2021.

CHAN, J. F.-W. et al. Genomic characterization of the 2019 novel human-pathogenic coronavirus isolated from a patient with atypical pneumonia after visiting Wuhan. **Emerging Microbes & Infections**, v. 9, n. 1, p. 221–236, 1 jan. 2020.

CHAN, K. F. et al. COVID-19 vaccines and global stock markets. **Finance Research Letters**, n. March, p. 102774, mar. 2022.

CHARNER, Flora. Brazil tops 1 million Covid-19 cases. It may pass the US next, becoming the worst-hit country on the planet. **NCN**, [*S. l.*], p. SN, 19 jun. 2020. Disponível em: https://edition.ncn.com/2020/06/19/americas/brazil-one-million-coronavirus-jair-bolsonaro-cases-intl/index.html. Acesso em: 20 ago. 2021.

CHEN, N. et al. Epidemiological and clinical characteristics of 99 cases of 2019 novel coronavirus pneumonia in Wuhan, China: a descriptive study. **LaNCet (London, England)**, v. 395, n. 10223, p. 507–513, 2020.

CLARO, I. M. et al. Local Transmission of SARS-CoV-2 Lineage B.1.1.7, Brazil, December 2020. **Emerging Infectious Diseases**, v. 27, n. 3, p. 970–972, mar. 2021.

CNN BRASIL. China aprova vacina da Sinopharm contra a Covid-19 para uso geral. *In*: CNN BRASIL. **China aprova vacina da Sinopharm contra a Covid-19 para uso geral**. [*S. l.*], 31 dez. 2020. Disponível em: https://www.cnnbrasil.com.br/saude/china-aprova-vacina-da-sinopharm-contra-a-covid-19-para-uso-geral/. Acesso em: 29 abr. 2022.

CRODA, J. et al. COVID-19 in Brazil: advantages of a socialized unified health system and preparation to contain cases. **Revista da Sociedade Brasileira de Medicina Tropical**, v. 53, n. April, p. 2–7, 2020.

DE SOUZA, U. J. B. et al. High Rate of Mutational Events in SARS-CoV-2 Genomes across Brazilian Geographical Regions, February 2020 to June 2021. **Viruses**, v. 13, n. 9, p. 1806, 10 set. 2021.

DEY, A. et al. Immunogenic potential of DNA vaccine candidate, ZyCoV-D against SARS-CoV-2 in animal models. **Vaccine**, v. 39, n. 30, p. 4108–4116, jul. 2021.

ELLA, R. et al. Safety and immunogenicity of an inactivated SARS-CoV-2 vaccine, BBV152: a double-blind, randomised, phase 1 trial. **The Lancet Infectious Diseases**, v. 21, n. 5, p. 637–646, maio 2021.

FARIA, Nuno R. *et al*. Genomic characterisation of an emergent SARS-CoV-2 lineage in Manaus: preliminary findings. **SARS-CoV-2 Variant Classifications and Definitions**, [*S. l.*],

p. SN, 12 jan. 2021. Disponível em: https://virological.org/t/genomic-characterisation-of-an-emergent-sars-cov-2-lineage-in-manaus-preliminary-findings/586. Acesso em: 23 ago. 2021.

FLAXMAN, S. et al. Estimating the effects of non-pharmaceutical interventions on COVID-19 in Europe. **Nature**, v. 584, n. 7820, p. 257–261, 13 ago. 2020.

FLORES-VEGA, V. R. et al. SARS-CoV-2: Evolution and Emergence of New Viral Variants. **Viruses**, v. 14, n. 4, p. 653, 22 mar. 2022.

FURUKAWA, N. W.; BROOKS, J. T.; SOBEL, J. EvideNCe Supporting Transmission of Severe Acute Respiratory Syndrome Coronavirus 2 While Presymptomatic or Asymptomatic. **Emerging Infectious Diseases**, v. 26, n. 7, p. E1–E6, jul. 2020.

GANDHI, R. T.; LYNCH, J. B.; DEL RIO, C. Mild or Moderate Covid-19. **New England Journal of Medicine**, v. 383, n. 18, p. 1757–1766, 29 out. 2020.

GANYANI, T. et al. Estimating the generation interval for coronavirus disease (COVID-19) based on symptom onset data, March 2020. **Eurosurveillance**, v. 25, n. 17, 30 abr. 2020.

GIERER, S. et al. The Spike Protein of the Emerging Betacoronavirus EMC Uses a Novel Coronavirus Receptor for Entry, Can Be Activated by TMPRSS2, and Is Targeted by Neutralizing Antibodies. **Journal of Virology**, v. 87, n. 10, p. 5502–5511, 15 maio 2013.

GIOVANETTI, M. et al. SARS-CoV-2 shifting transmission dynamics and hidden reservoirs potentially limit efficacy of public health interventions in Italy. **Communications Biology**, v. 4, n. 1, p. 489, 21 dez. 2021.

GONCALVES CABECINHAS, A. R. et al. SARS-CoV-2 N501Y Introductions and Transmissions in Switzerland from Beginning of October 2020 to February 2021—Implementation of Swiss-Wide Diagnostic Screening and Whole Genome Sequencing. **Microorganisms**, v. 9, n. 4, p. 677, 25 mar. 2021.

GRANT, M. C. et al. The prevaleNCe of symptoms in 24,410 adults infected by the novel coronavirus (SARS-CoV-2; COVID-19): A systematic review and meta-analysis of 148 studies from 9 countries. **PLOS ONE**, v. 15, n. 6, p. e0234765, 23 jun. 2020.

GUAN, W. et al. Clinical Characteristics of Coronavirus Disease 2019 in China. **New England Journal of Medicine**, v. 382, n. 18, p. 1708–1720, 30 abr. 2020.

GUPTA, A. et al. Extrapulmonary manifestations of COVID-19. **Nature Medicine**, v. 26, n. 7, p. 1017–1032, 10 jul. 2020.

HADFIELD, J. et al. Nextstrain: real-time tracking of pathogen evolution. **Bioinformatics**, v. 34, n. 23, p. 4121–4123, 1 dez. 2018.

HAGEN, ASHLEY. Culpable Mutations of Omicron. *In*: AMERICAN SOCIETY FOR MICROBIOLOGY (org.). **How Ominous Is the Omicron Variant (B.1.1.529)?**. [*S. l.*], 16 dez. 2021. Disponível em: https://asm.org/Articles/2021/December/How-Ominous-is-the-Omicron-Variant-B-1-1-529. Acesso em: 29 abr. 2022.

HERNÁNDEZ-BERNAL, F. et al. Safety, tolerability, and immunogenicity of a SARS-CoV-2 recombinant spike RBD protein vaccine: A randomised, double-blind, placebo-controlled, phase 1-2 clinical trial (ABDALA Study). **eClinicalMedicine**, v. 46, p. 101383, abr. 2022.

HUANG, C. et al. Clinical features of patients infected with 2019 novel coronavirus in Wuhan, China. **The Lancet**, v. 395, n. 10223, p. 497–506, fev. 2020.

HUI, D. S. et al. The continuing 2019-nCoV epidemic threat of novel coronaviruses to global health — The latest 2019 novel coronavirus outbreak in Wuhan, China. **International Journal of Infectious Diseases**, v. 91, p. 264–266, fev. 2020.

IBRAHIM, N. K. Epidemiologic surveillaNCe for controlling Covid-19 pandemic: types, challenges and implications. **Journal of Infection and Public Health**, v. 13, n. 11, p. 1630–1638, nov. 2020.

ISTOÉ DINHEIRO (BRASIL). Brasil aplica a primeira vacina contra a covid-19 após aprovação da Anvisa. *In*: ISTOÉ (BRASIL). **Brasil aplica a primeira vacina contra a covid-19 após aprovação da Anvisa**. [*S. l.*], 17 jan. 2021. Disponível em: https://www.istoedinheiro.com.br/brasil-aplica-a-primeira-vacina-contra-a-covid-19-apos-aprovacao-da-anvisa/. Acesso em: 10 maio 2022.

KAMI, W. et al. Rapid and simultaneous identification of three mutations by the Novaplex™ SARS-CoV-2 variants I assay kit. **Journal of Clinical Virology**, v. 141, n. May, p. 104877, ago. 2021.

KUDLAY, D.; SVISTUNOV, A. COVID-19 Vaccines: An Overview of Different Platforms. **Bioengineering**, v. 9, n. 2, p. 72, 12 fev. 2022.

KUPEK, E. How many more? Under-reporting of the COVID-19 deaths in Brazil in 2020. **Tropical Medicine & International Health**, v. 00, n. 00, p. tmi.13628, 6 jun. 2021.

LAI, C.-C. et al. Asymptomatic carrier state, acute respiratory disease, and pneumonia due to severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2): Facts and myths. **Journal of Microbiology, Immunology and Infection**, v. 53, n. 3, p. 404–412, jun. 2020.

LAMARCA, A. P. et al. Genomic surveillance of SARS-CoV-2 tracks early interstate transmission of P.1 lineage and diversification within P.2 clade in Brazil. **PLOS Neglected Tropical Diseases**, v. 15, n. 10, p. e0009835, 13 out. 2021.

LAN, J. et al. Structure of the SARS-CoV-2 spike receptor-binding domain bound to the ACE2 receptor. **Nature**, v. 581, n. 7807, p. 215–220, 14 maio 2020.

LARSEN, Brendan B.; WOROBEY, Michael. Phylogenetic evidence that B.1.1.7 has been circulating in the United States since early- to mid-November. **Virologycal.org**, [*S. l.*], p. 1-7, 1 jan. 2021. Disponível em: https://virological.org/t/phylogenetic-evidence-that-b-1-1-7-has-been-circulating-in-the-united-states-since-early-to-mid-november/598. Acesso em: 29 abr. 2022.

LAU, H. et al. Internationally lost COVID-19 cases. **Journal of Microbiology, Immunology and Infection**, v. 53, n. 3, p. 454–458, jun. 2020.

LAURING, A. S.; MALANI, P. N. Variants of SARS-CoV-2. **JAMA**, p. 2021, 13 ago. 2021.

LAZZERINI, M.; PUTOTO, G. COVID-19 in Italy: momentous decisions and many uNCertainties. **The LaNCet Global Health**, v. 8, n. 5, p. e641–e642, maio 2020.

LETKO, M.; MARZI, A.; MUNSTER, V. FuNCtional assessment of cell entry and receptor usage for SARS-CoV-2 and other lineage B betacoronaviruses. **Nature Microbiology**, v. 5, n. 4, p. 562–569, 24 abr. 2020.

LI, R. et al. Substantial undocumented infection facilitates the rapid dissemination of novel coronavirus (SARS-CoV-2). **ScieNCe**, v. 368, n. 6490, p. 489–493, 1 maio 2020.

LIU, H. et al. The basis of a more contagious 501Y.V1 variant of SARS-CoV-2. **Cell Research**, v. 31, n. 6, p. 720–722, 23 jun. 2021.

LOGUNOV, D. Y. et al. Safety and efficacy of an rAd26 and rAd5 vector-based heterologous prime-boost COVID-19 vaccine: an interim analysis of a randomised controlled phase 3 trial in Russia. **The Lancet**, v. 397, n. 10275, p. 671–681, fev. 2021.

LU, R. et al. Genomic characterisation and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding. **The LaNCet**, v. 395, n. 10224, p. 565–574, fev. 2020.

MA, Y. et al. Effects of temperature variation and humidity on the death of COVID-19 in Wuhan, China. **Science of The Total Environment**, v. 724, p. 138226, jul. 2020.

MATSUYAMA, S. et al. Efficient Activation of the Severe Acute Respiratory Syndrome Coronavirus Spike Protein by the Transmembrane Protease TMPRSS2. **Journal of Virology**, v. 84, n. 24, p. 12658–12664, 15 dez. 2010.

MIGUERES, M. et al. Evaluation of two RT-PCR screening assays for identifying SARS-CoV-2 variants. **Journal of Clinical Virology**, v. 143, n. January, p. 104969, out. 2021.

MINISTÉRIO DA SAÚDE (Brasil). Brazil tops 1 million Covid-19 cases. It may pass the US next, becoming the worst-hit country on the planet. *In*: **Painel Coronavírus**. [*S. l.*], 28 ago. 2021. Disponível em: https://covid.saude.gov.br/. Acesso em: 05 maio 2022.

MINISTÉRIO DA SAÚDE (Brasil). Saúde anuncia orientações para evitar a disseminação do coronavírus. Available from: https://www.saude.gov.br/noticias/agencia-saude/46540-saude-anuncia-orientacoes-para-evitar-a-disseminacao-do-coronavirus. Accessed March 27, 2020.

MOMIN, T. et al. Safety and Immunogenicity of a DNA SARS-CoV-2 vaccine (ZyCoV-D): Results of an open-label, non-randomized phase I part of phase I/II clinical study by intradermal route in healthy subjects in India. **EClinicalMedicine**, v. 38, p. 101020, ago. 2021.

MORENO, Gage; BRAUN, Katarina; LARSEN, Brendan B.; ALPERT, Tara; WOROBEY, Michael; GRUBAUGH, Nathan; FRIEDRICH, Thomas; O'CONNOR, David; FAUVER, Joseph; BRITO, Anderson. Detection of non-B.1.1.7 Spike Δ69/70 sequences (B.1.375) in the United States. **Virologycal.org**, [*S. l.*], p. 1-7, 2 jan. 2021. Disponível em: https://virological.org/t/detection-of-non-b-1-1-7-spike-69-70-sequences-b-1-375-in-the-united-states/587. Acesso em: 29 abr. 2022.

NAGY, A.; ALHATLANI, B. An overview of current COVID-19 vaccine platforms. **Computational and Structural Biotechnology Journal**, v. 19, p. 2508–2517, 2021.

NG, W. H.; LIU, X.; MAHALINGAM, S. Development of vaccines for SARS-CoV-2. **F1000Research**, v. 9, p. 991, 17 ago. 2020.

NHEAN, S. et al. COVID-19: A Review of Potential Treatments (Corticosteroids, Remdesivir, Tocilizumab, Bamlanivimab/Etesevimab, and Casirivimab/Imdevimab) and Pharmacological Considerations. **Journal of Pharmacy Practice**, p. 089719002110481, 1 out. 2021.

NHI. Antiviral Therapy. *In*: NHI. **COVID-19 Treatment Guidelines**. [*S. l.*], 7 abr. 2022. Disponível em: https://www.covid19treatmentguidelines.nih.gov/therapies/antiviral-therapy/. Acesso em: 29 abr. 2022.

ORAN, D. P.; TOPOL, E. J. The Proportion of SARS-CoV-2 Infections That Are Asymptomatic. **Annals of Internal Medicine**, v. 174, n. 5, p. 655–662, maio 2021.

OU, X. et al. Characterization of spike glycoprotein of SARS-CoV-2 on virus entry and its immune cross-reactivity with SARS-CoV. **Nature Communications**, v. 11, n. 1, p. 1620, 27 dez. 2020.

OUR WORLD IN DATA (Oxford). Coronavirus (COVID-19) Vaccinations. *In*: OUR WORLD IN DATA (Oxford). **Coronavirus (COVID-19) Vaccinations**. [*S. l.*], 10 maio 2022. Disponível em: https://ourworldindata.org/covid-vaccinations?country=OWID_WRL. Acesso em: 10 maio 2022

PALMER, T. News in focus. **Practice Management**, v. 31, n. 5, p. 8–16, 2 maio 2021.

PAN AMERICAN HEALTH ORGANIZATION. Epidemiological update : Variants of SARS-CoV-2 in the Americas Genomic characterization of SARS-CoV-2. n. March, p. 1–8, 2021.

POLACK, F. P. et al. Safety and Efficacy of the BNT162b2 mRNA Covid-19 Vaccine. **New England Journal of Medicine**, v. 383, n. 27, p. 2603–2615, 31 dez. 2020.

PRECISION VACCINATIONS. Vaxzevria COVID-19 Vaccine (AstraZeneca). *In*: PRECISION VACCINATIONS. **Vaxzevria COVID-19 Vaccine (AstraZeneca)**. [*S. l.*], 20 mar. 2022. Disponível em: https://www.precisionvaccinations.com/vaccines/vaxzevria-covid-19-vaccine-astrazeneca. Acesso em: 29 abr. 2022.

RAMBAUT, A. et al. A dynamic nomeNClature proposal for SARS-CoV-2 lineages to assist genomic epidemiology. **Nature Microbiology**, v. 5, n. 11, p. 1403–1407, 15 nov. 2020.

RASKIN, S. Genetics of COVID-19. **Jornal de Pediatria**, v. 97, n. 4, p. 378–386, jul. 2021.

REED, G. Cuban COVID-19 Vaccines for Children: Rinaldo Puga MD MS Principal Investigator, Pediatric Clinical Trials for Soberana 02 and Soberana Plus. **MEDICC Review**, v. 24, n. 1, p. 14, 31 jan. 2022.

RIBAS FREITAS, A. R.; GIOVANETTI, M.; ALCANTARA, L. C. J. Variantes emergentes do SARS-CoV-2 e suas implicações na saúde coletiva. **InterAmerican Journal of Medicine and Health**, v. 4, 8 fev. 2021.

ROTHAN, H. A.; BYRAREDDY, S. N. The epidemiology and pathogenesis of coronavirus disease (COVID-19) outbreak. **Journal of Autoimmunity**, v. 109, n. January, p. 102433, maio 2020.

RYZHIKOV, A. B. et al. A single blind, placebo-controlled randomized study of the safety, reactogenicity and immunogenicity of the “EpiVacCorona” Vaccine for the prevention of COVID-19, in volunteers aged 18–60 years (phase I–II). **Russian Journal of Infection and Immunity**, v. 11, n. 2, p. 283–296, 24 mar. 2021.

RYZHIKOV, A. B. et al. Immunogenicity and protectivity of the peptide vaccine against SARS-CoV-2. **Annals of the Russian academy of medical sciences**, v. 76, n. 1, p. 5–19, 12 abr. 2021.

SABARATHINAM, C. et al. SARS-CoV-2 phase I transmission and mutability linked to the interplay of climatic variables: a global observation on the pandemic spread. **Environmental Science and Pollution Research**, n. 0123456789, 14 jan. 2022.

SADOFF, J. et al. Interim Results of a Phase 1–2a Trial of Ad26.COV2.S Covid-19 Vaccine. **New England Journal of Medicine**, v. 384, n. 19, p. 1824–1835, 13 maio 2021.

SAJADI, M. M. et al. Temperature and Latitude Analysis to Predict Potential Spread and Seasonality for COVID-19. **SSRN Electronic Journal**, p. 6–7, 2020.

SHANG, J. et al. Cell entry mechanisms of SARS-CoV-2. **Proceedings of the National Academy of ScieNCes**, v. 117, n. 21, p. 11727–11734, 26 maio 2020.

SHANG, J. et al. Structural basis of receptor recognition by SARS-CoV-2. **Nature**, v. 581, n. 7807, p. 221–224, 14 maio 2020.

SLAVOV, S. N. et al. Genomic monitoring unveil the early detection of the SARS-CoV-2 B.1.351 (beta) variant (20H/501Y.V2) in Brazil. **Journal of Medical Virology**, v. 93, n. 12, p. 6782–6787, 19 dez. 2021.

TANONAKA, K.; MARUNOUCHI, T. Angiotensin-converting enzyme 2 is a fuNCtional receptor for the SARS coronavirus. **Nature**, v. 426, p. 450–454, 2003.

TANRIOVER, M. D. et al. Efficacy and safety of an inactivated whole-virion SARS-CoV-2 vaccine (CoronaVac): interim results of a double-blind, randomised, placebo-controlled, phase 3 trial in Turkey. **The Lancet**, v. 398, n. 10296, p. 213–222, jul. 2021.

TAYLOR, L. Why Cuba developed its own covid vaccine—and what happened next. **BMJ**, v. 374, n. August, p. n1912, 5 ago. 2021.

ULHAQ, Z. S.; SORAYA, G. V.; INDRIANA, K. Breakthrough COVID-19 case after full-dose administration of CoronaVac vaccine. **Indian Journal of Medical Microbiology**, v. 39, n. 4, p. 562–563, out. 2021.

V'KOVSKI, P. et al. Coronavirus biology and replication: implications for SARS-CoV-2. **Nature Reviews Microbiology**, v. 19, n. 3, p. 155–170, 28 mar. 2021.

VAIRA, L. A. et al. Anosmia and Ageusia: Common Findings in COVID-19 Patients. **The Laryngoscope**, v. 130, n. 7, p. 1787–1787, 15 jul. 2020.

VEGA-MAGAÑA, N. et al. RT-qPCR Assays for Rapid Detection of the N501Y, 69-70del, K417N, and E484K SARS-CoV-2 Mutations: A Screening Strategy to Identify Variants With Clinical Impact. **Frontiers in Cellular and Infection Microbiology**, v. 11, n. May, p. 1–11, 20 maio 2021.

VELAVAN, T. P.; MEYER, C. G. The COVID-19 epidemic. **Tropical Medicine and International Health**, v. 25, n. 3, p. 278–280, 2020.

VOGELS, C. B. F. et al. Multiplex qPCR discriminates variants of concern to enhance global surveillance of SARS-CoV-2. **PLOS Biology**, v. 19, n. 5, p. e3001236, 7 maio 2021.

VOLOCH, C. M. et al. Genomic Characterization of a Novel SARS-CoV-2 Lineage from Rio de Janeiro, Brazil. **Journal of Virology**, v. 95, n. 10, p. 1–5, 26 abr. 2021.

WALLS, A. C. et al. Structure, FuNCtion, and Antigenicity of the SARS-CoV-2 Spike Glycoprotein. **Cell**, v. 181, n. 2, p. 281- 292.e6, abr. 2020.

WANG, C. et al. A novel coronavirus outbreak of global health concern. **The Lancet**, v. 395, n. 10223, p. 470–473, fev. 2020.

WANG, Y. et al. Unique epidemiological and clinical features of the emerging 2019 novel coronavirus pneumonia (COVID-19) implicate special control measures. **Journal of Medical Virology**, v. 92, n. 6, p. 568–576, 29 jun. 2020.

WIERSINGA, W. J. et al. Pathophysiology, Transmission, Diagnosis, and Treatment of Coronavirus Disease 2019 (COVID-19). **JAMA**, v. 324, n. 8, p. 782, 25 ago. 2020.

WORLD HEALTH ORGANIZATION (Geneva, Switzerland). Statement on the first meeting of the International Health Regulations (2005) **EmergeNCy Committee regarding the outbreak of novel coronavirus (2019-NCoV)**. Statement, Geneva, Switzerland, p. SN, 23 jan. 2020. Disponível em: https://www.who.int/news/item/23-01-2020-statement-on-the-meeting-of-the-international-health-regulations-(2005)-emergeNCy-committee-regarding-the-outbreak-of-novel-coronavirus-(2019-NCov). Acesso em: 20 ago. 2021.

WORLD HEALTH ORGANIZATION et al. Laboratory testing for coronavirus disease (COVID-19) in suspected human cases. Interim guidaNCe, [S. l.], p. 1 - 7, 19 mar. 2020. Disponível em: https://www.who.int/publications/i/item/10665-331501. Acesso em: 20 ago. 2021.

WORLD HEALTH ORGANIZATION. Coronavirus Disease (COVID-19) Dashboard|**WHO Coronavirus Disease (COVID-19) Dashboard**. 2020. Disponível em: URL: https://covid19.who.int/ Acesso em: 20 de março de 2021.

WORLD HEALTH ORGANIZATION. Novel coronavirus – Thailand (ex-China). Geneva: World Health Organization, Jan 14, 2020. https://www.who.int/csr/don/14-january-2020-novel-coronavirus-thailand/en/. Acesso em 20 de agosto de 2020.

WORLD HEALTH ORGANIZATION. Weekly epidemiological update. Publicado em 23 de março de 2021. Disponível em: https://bit.ly/3v6e0Mi. Acesso em: 20 de agosto de 2021.

WU, C. et al. Analysis of therapeutic targets for SARS-CoV-2 and discovery of potential drugs by computational methods. **Acta Pharmaceutica Sinica B**, v. 10, n. 5, p. 766–788, maio 2020.

YANEZ, N. D. et al. COVID-19 mortality risk for older men and women. **BMC Public Health**, v. 20, n. 1, p. 1742, 19 dez. 2020.

YANIV, K. et al. Direct RT-qPCR assay for SARS-CoV-2 variants of concern (Alpha, B.1.1.7 and Beta, B.1.351) detection and quantification in wastewater. **Environmental Research**, v. 201, n. May, p. 111653, 2021.

ZHOU, P. et al. A pneumonia outbreak associated with a new coronavirus of probable bat origin. **Nature**, v. 579, n. 7798, p. 270–273, 12 mar. 2020.

ZHU, F.-C. et al. Safety, tolerability, and immunogenicity of a recombinant adenovirus type-5 vectored COVID-19 vaccine: a dose-escalation, open-label, non-randomised, first-in-human trial. **The Lancet**, v. 395, n. 10240, p. 1845–1854, jun. 2020.

ZHU, N. et al. A Novel Coronavirus from Patients with Pneumonia in China, 2019. **New England Journal of Medicine**, v. 382, n. 8, p. 727–733, 20 fev. 2020.