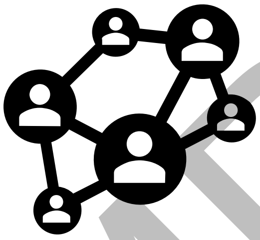
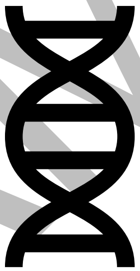
Alaska COVID Genomic Surveillance

Situation Report

24 February 2021





Prepared by the Alaska Sequencing Consortium, including Devin M. Drown[1], Jayme Parker[2], Lisa Smith[2], Eric Bortz[3], Jack Chen[1,2]

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Executive Summary: Sequence Analysis of COVID-19 in Alaska

- **403 cases of COVID-19 in Alaska sequenced** and released in a protected public database repository (GISAID: https://www.gisaid.org/).
- **Two variants of concern (VOC) identified**: B.1.1.7 (2 cases) and P.1 (1 case), identified in Anchorage/Mat-Su region.
- **Two variants of interest identified**: B.1.429 variant (6 groups of cases, statewide), and P.2 (one case in Southwest Alaska).
- **Phylogenetics: diverse lineages of SARS-CoV-2 are currently co-circulating in Alaska**, dominated by clades 20B, 20C, and 20G (lineage B.1 and others).

Genomic Sequencing Effort in Alaska

	Samples	Change from Previous Report
Genomes released on GISAID	403	+120
Genomes with sufficient phylogenetic information	389	+125

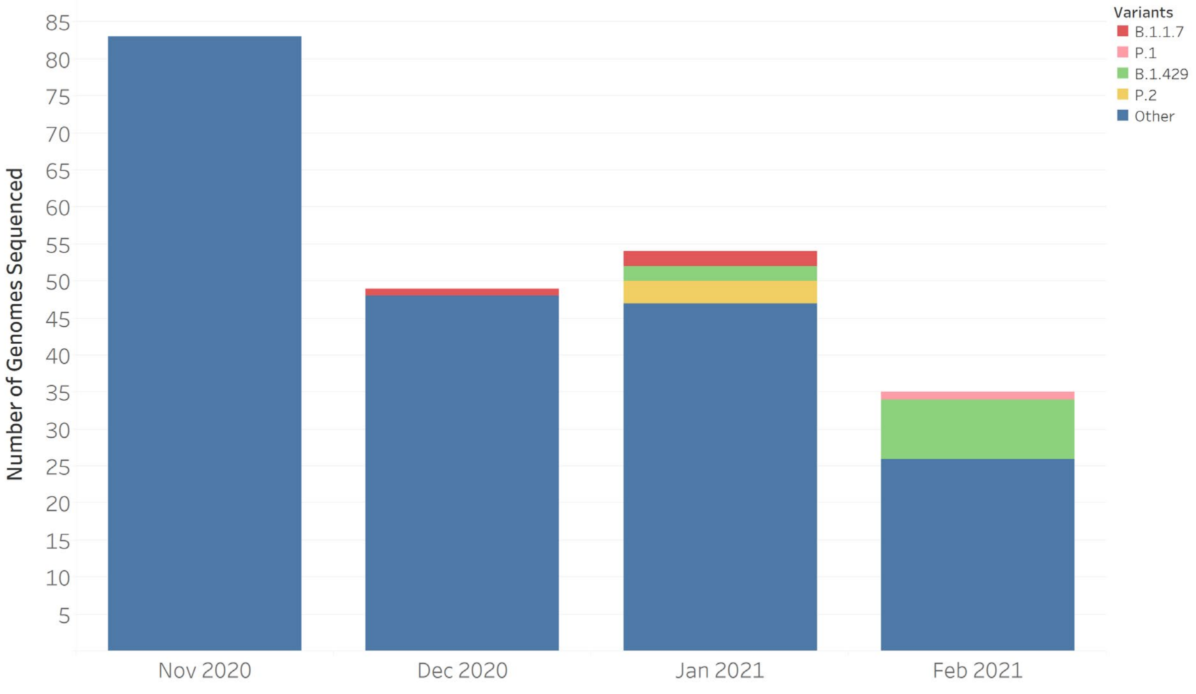
Variants of Concern Identified in Alaska

Lineage	Found	First Identified in Alaska
B.1.1.7	3	20 December 2020
B.1.351	0	Not detected
P.1	1	8 February 2021

Variants of Interest Identified in Alaska

Lineage	Found	First Identified in Alaska
B.1.429	10	8 January 2021
P.2	3	27 January 2021

Recent Variants Identified in Alaska



Variants of Concern, Individual Lineage Reports

B.1.1.7

B.1.1.7 was first identified in the United Kingdom, also known as: Variant of Concern 202012/01, VOC-202012/01, 20B/501Y.V1, 20I/501Y.V1. This variant contains the N501Y mutation and a short deletion in the Spike (S) protein. This variant is concerning because it has shown to be significantly more transmissible than the original SARS-CoV-2 lineages. B.1.1.7 is widely circulating in the US.

Epidemiology of B.1.1.7 VOC in Alaska: Phylogenetics analysis suggests B.1.1.7 may have been introduced twice into Alaska, one case in December 2020 and a separate case (sequenced twice) identified in January 2021. Both cases are in Anchorage/Mat-Su region.

Location	B.1.1.7 found	First Identified
Worldwide	86,721	20 September 2020
USA	1,071	17 December 2020
Alaska	3	20 December 2020

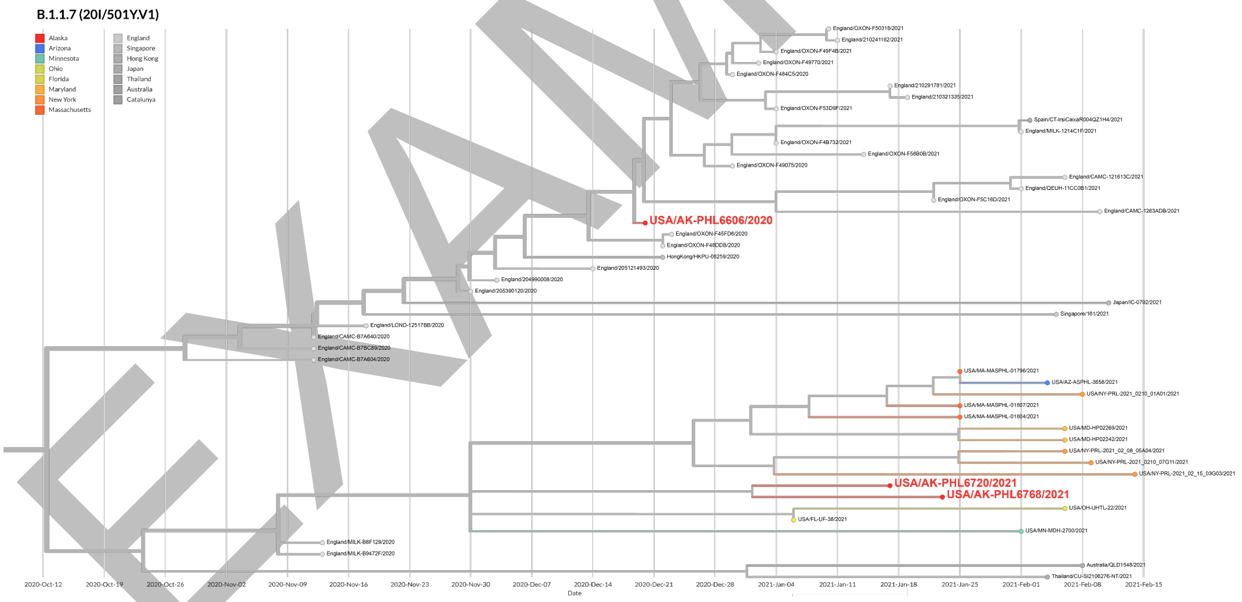


Figure: Phylogenetics analysis of B.1.1.7 cases identified in Alaska. Context of the B.1.1.7 cases sequenced in Alaska. The context of other genomes only represents a small sample of the globally sequenced genomes.

P.1

P.1 was first identified in Brazil, also known as: Variant of Concern B.1.1.28.1, 20J/501Y.V3. This variant contains three key mutations in the S gene: E484K, N501Y, and K417T. Preliminary studies suggest the P.1, like B.1.351, may escape some vaccine-induced antibody responses although not the Pfizer and Moderna mRNA vaccines currently deployed in Alaska.

Epidemiology of P.1 in Alaska: P.1 was identified in early February 2021 in the Anchorage/Mat-Su region.

Location	P.1 found	First Identified
Worldwide	183	4 December 2020
USA	4	9 January 2021
Alaska	1	8 February 2021

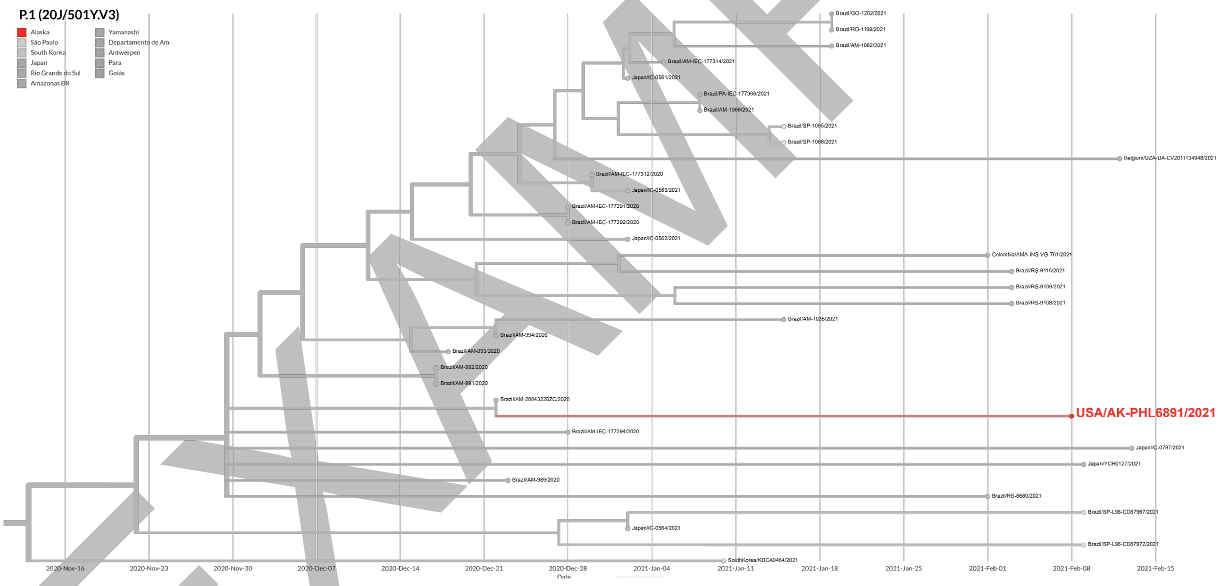


Figure: Phylogenetic analysis and context of the P.1 case sampled in Alaska. The context of other genomes only represents a small sample of the globally sequenced genomes.

B.1.351 - Not detected in Alaska

B.1.351 has not been detected in Alaska. This variant (also known as: 20H/501Y.V2) was first identified in South Africa and has begun circulating in other parts of the US. The B.1.351 has both N501Y and E484K mutations in the Spike protein. Preliminary studies suggest the B.1.351, like the P.1, may escape some vaccine-induced antibody responses, although not the Pfizer and Moderna mRNA vaccines currently deployed in Alaska.

Location	B.1.351 found	First Identified
Worldwide	1,821	8 October 2020
USA	14	8 January 20201
Alaska	0	Not detected

Variants of Interest, Individual Lineage Reports

B.1.429

B.1.429 was first identified in California and is also known as: CA VUI1. Little is known about this variant beyond that its prevalence grew in California. This variant is characterized by the L452R mutation in the S gene. This variant is genetically very similar to B.1.351 but lacks several key mutations.

Epidemiology of B.1.429 variant in Alaska: The B.1.429 variant has been introduced into Alaska with at least 6 groups of cases detected across the state by January-February, 2021.

Location	B.1.429 found	First Identified
Worldwide	4030	23 June 2020
USA	3941	13 July 2020
Alaska	10	8 January 2021

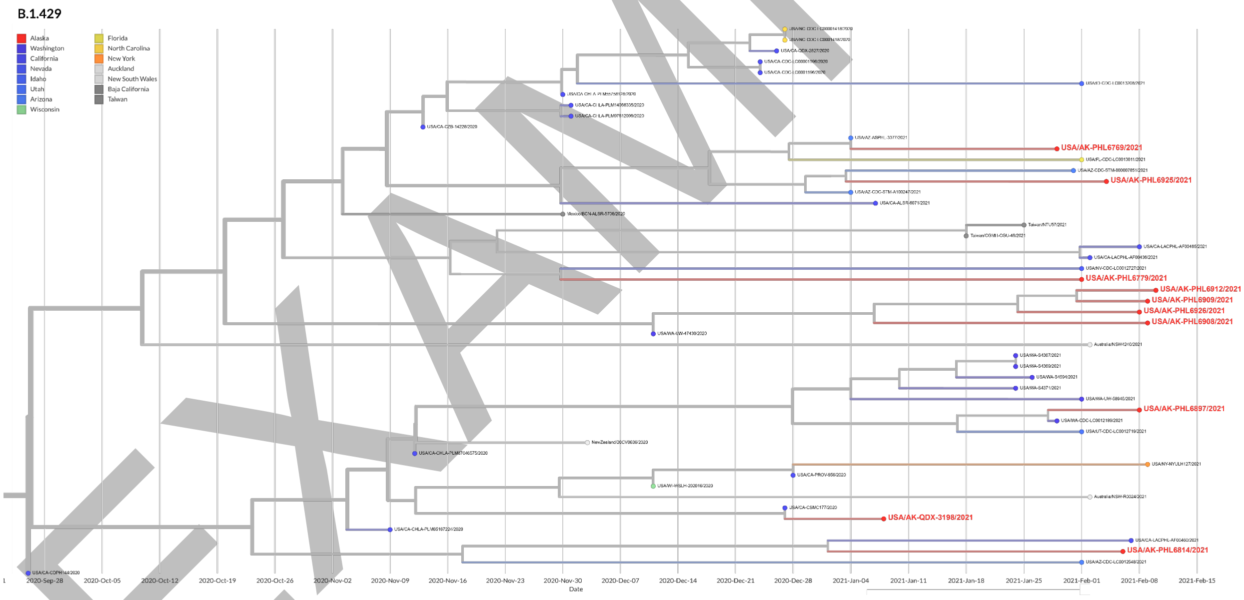
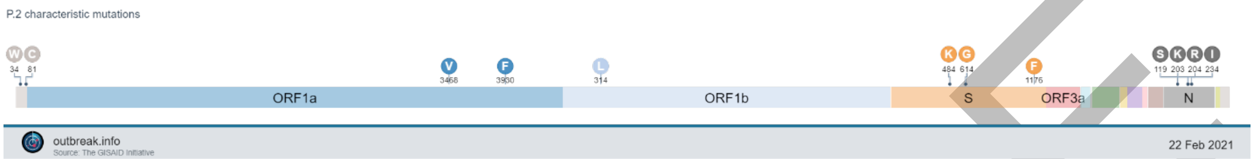


Figure: Phylogenetics analysis of B.1.429 cases sampled in Alaska. Context of the B.1.429 cases sampled in Alaska. The context of other genomes only represents a small sample of the globally sequenced genomes.

P.2

P.2 was first identified in Brazil and is also known as: B.1.1.28.2. Little is known about this variant beyond that its prevalence grew in Brazil. This variant contains the E484K mutation in the Spike protein but lacks many key mutations in other variants of concern.

Epidemiology of P.2 variant in Alaska: The P.2 variant was identified in January 2021, in the Southwest Alaska region. The immediate origin of this lineage is unknown.



Location	P.2 found	First Identified
Worldwide	484	15 April 2020
USA	119	10 November 2020
Alaska	3	27 January 2021

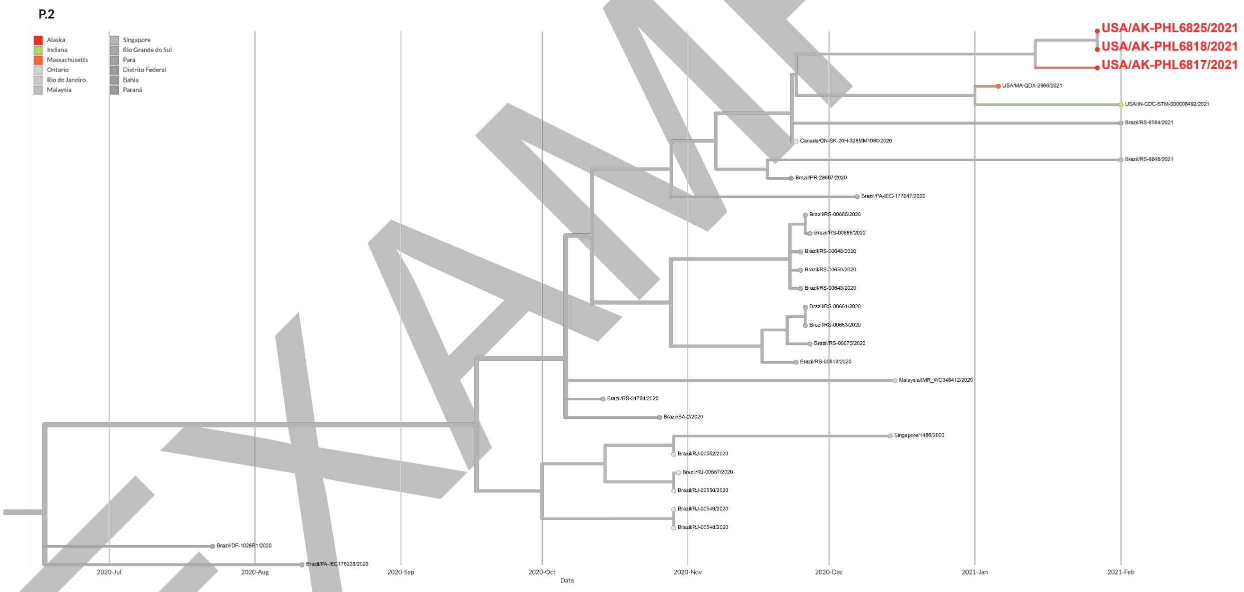
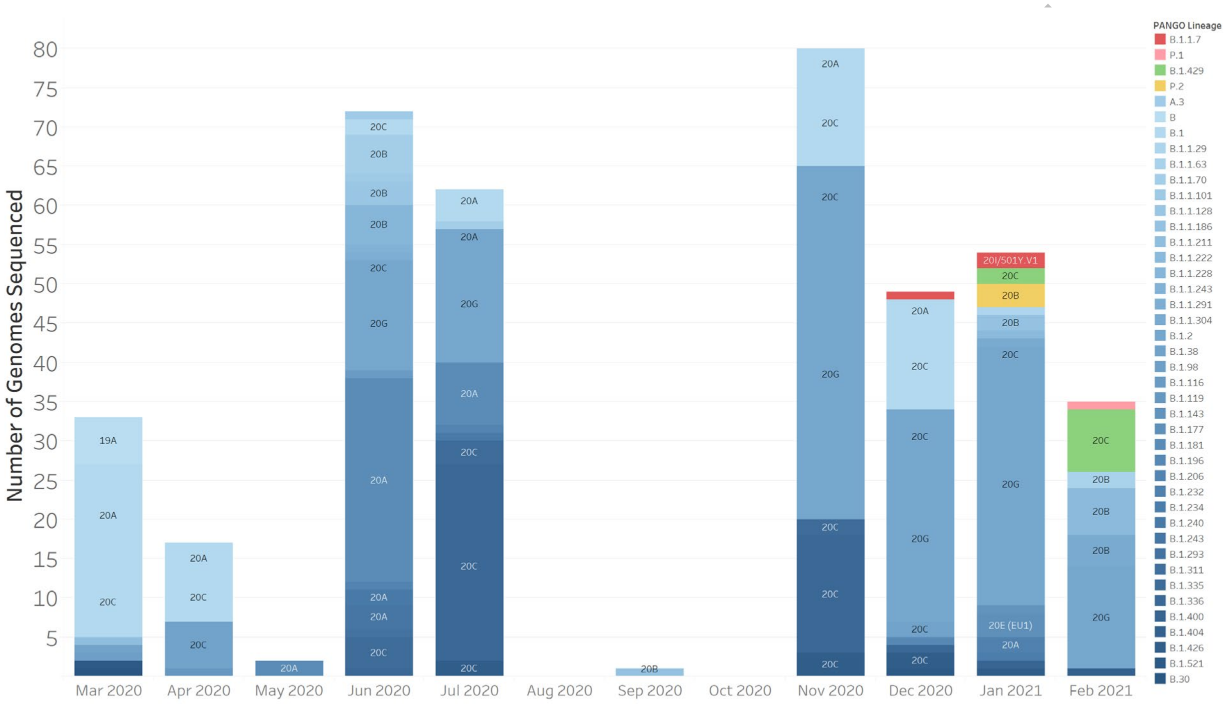


Figure: Phylogenetic context of the P.2 cases sampled in Alaska. The context of other genomes only represents a small sample of the globally sequenced genomes.

Lineages in Alaska

Lineages Over Time

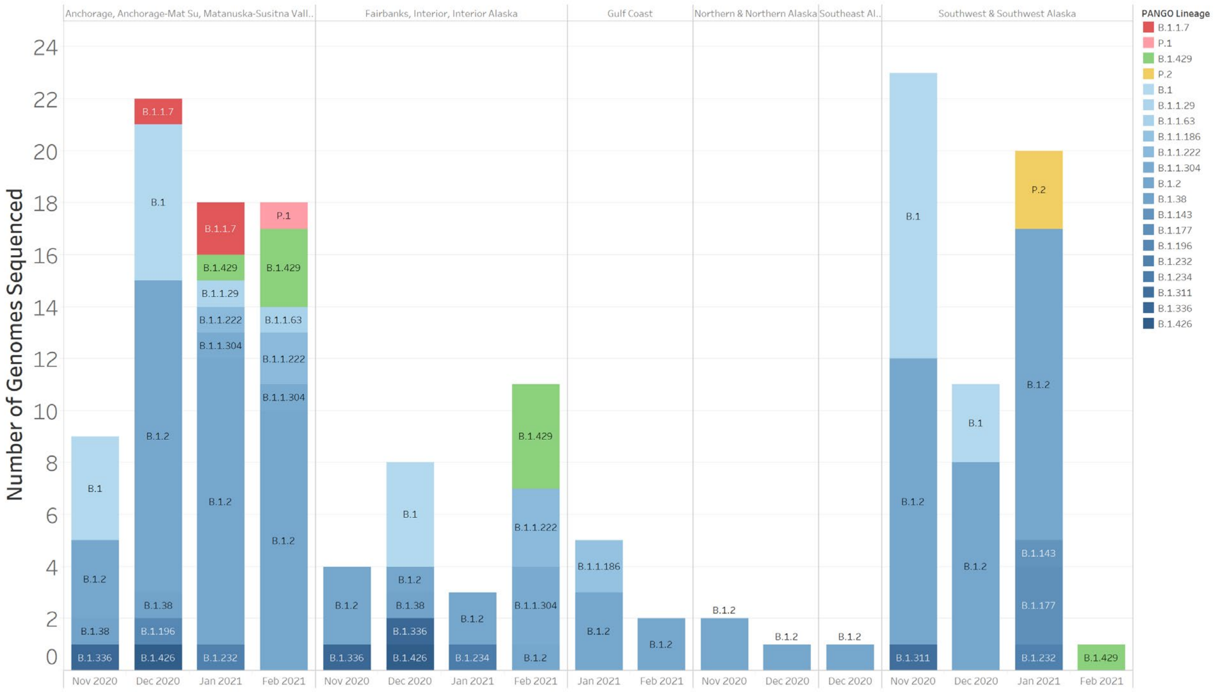
The graphs below indicate the number of genomes sequenced from Alaska cases per month (starting in March 2020). Colors indicate PANGO lineages and Nextstrain clades (groups of lineages) label the sections.



*Note that SARS-CoV-2 genome sequencing is not a random sample of all cases. As a result, the indicated prevalence only reflects an estimate based on the genomes sequenced. The report does not estimate the prevalence of the population. As sequencing effort increases and the number of genome sequences increases, the estimate will better reflect the population.

Lineages by Alaska Location

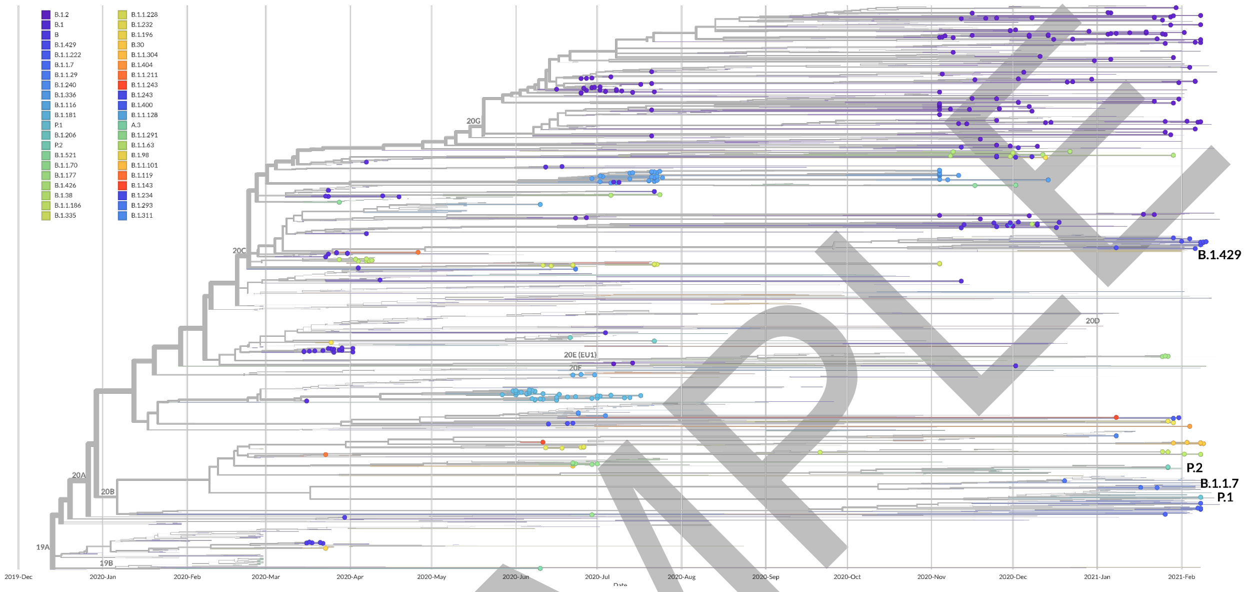
The graphs below indicate the number of genomes sequenced from Alaska cases per month (starting in November 2020). Colors and labels indicate PANGO lineages label the sections.



Note: Some genomes are not included because of missing geographic locations within Alaska.

Phylogenetic Tree of Lineages

Using virus genome sequencing data, each genome can be placed into a broader context of SARS-CoV-2 lineages. Here, we are showing 389 Alaska samples placed into a phylogenetic or evolutionary context of 1958 global samples (Mar 2020 and Feb 2021). The horizontal axis shows the date of collection. Lineage of interest are marked on the phylogenetic tree. Branches are colored by PANGO lineage.

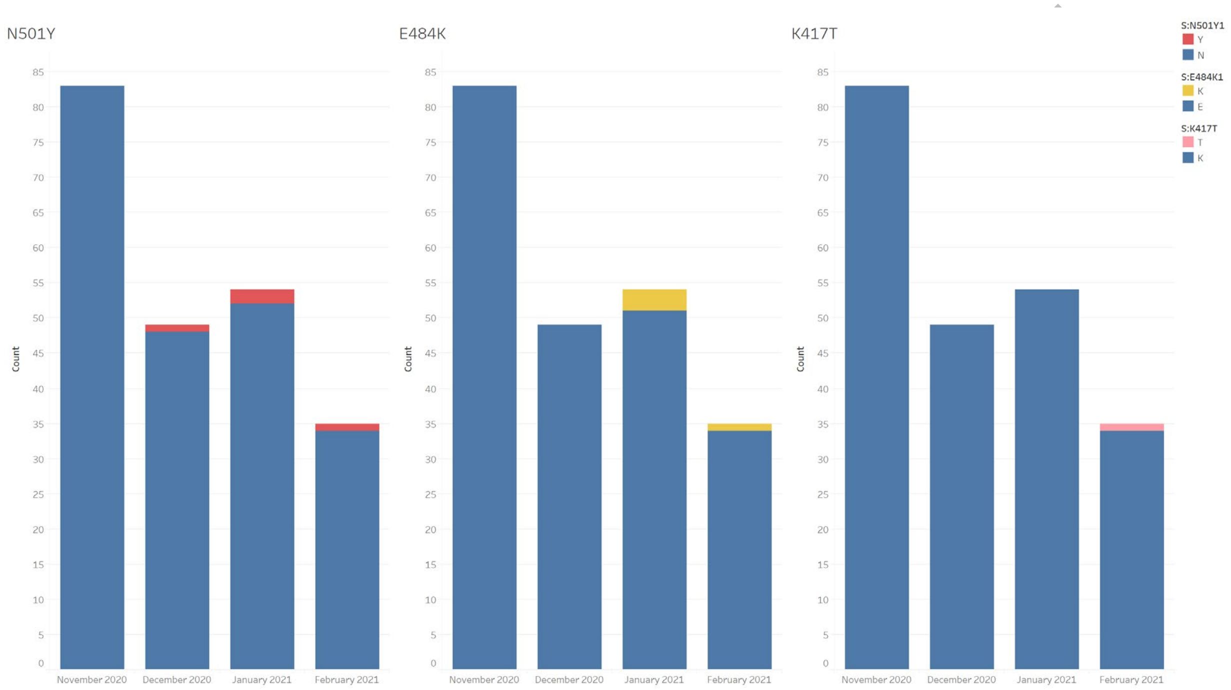


Methodology: We include as many of the Alaska genomes for phylogenetic analysis as possible. This includes all genomes that have at least 25000 nucleotides (greater than ~80% of the complete SARS-CoV-2 genome). So, while we might have enough genomic information to identify mutations and possibly identify lineage, we do exclude some sequenced genomes. We evenly sample 800 genomes across time from other states, prioritizing samples that are that are genetically like Alaska sequences. We also evenly sample 800 genomes across time from the rest of the world excluding the USA. This scheme includes as much local diversity for Alaska as possible and contextual samples from the rest of the USA and the world.

Mutations Reports

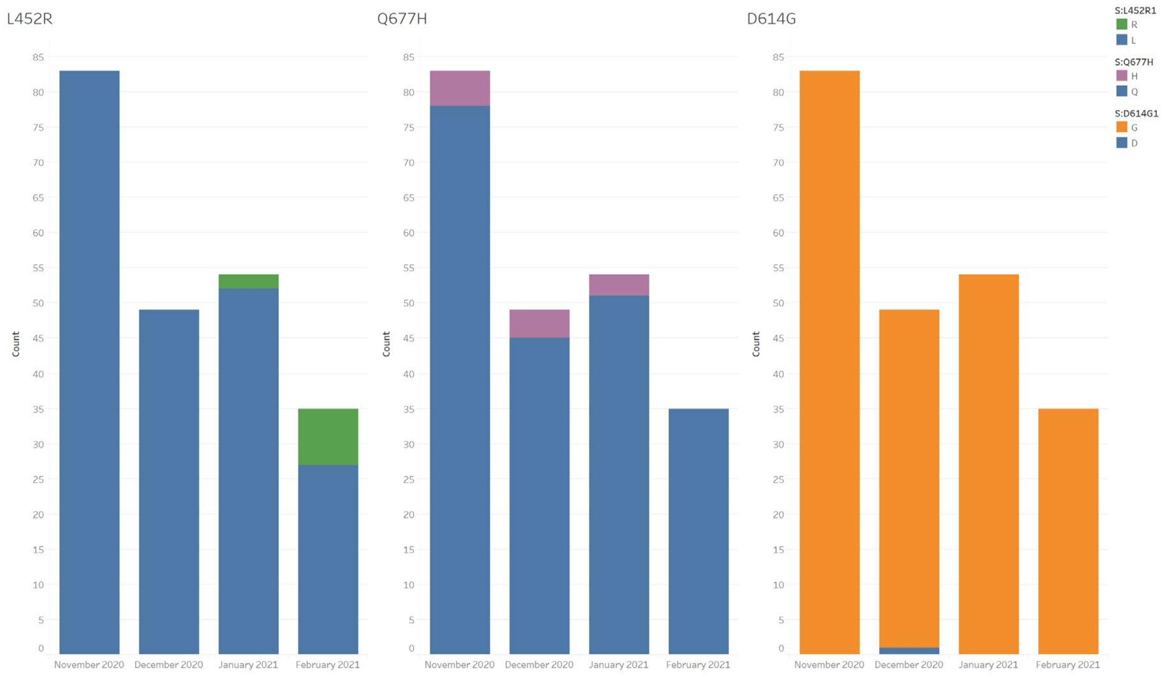
Mutations of Concern

Below are graphs with the count of genomes containing mutations of concern per month (starting in November 2020). Three mutations in the S gene (N501Y, E484K, K417T) are present in the Alaska sequenced genomes. In each graph, the blue color represents the ancestral state for each amino acid.



Mutations of Interest

Below are graphs with counts of genomes containing mutations of interest. Three mutations in the S gene (L452R, Q677H, and D614G) are present in the Alaska sequenced genomes. Little is known about the L452R mutation beyond that its prevalence grew in California. The Q677 mutation has arisen multiple times and little is known about this mutant beyond that its prevalence is spreading in the United States. The D614G mutations became common globally very early in the pandemic and now the G (orange) version is present in nearly all genomes.



Mutation Report, S:N501Y

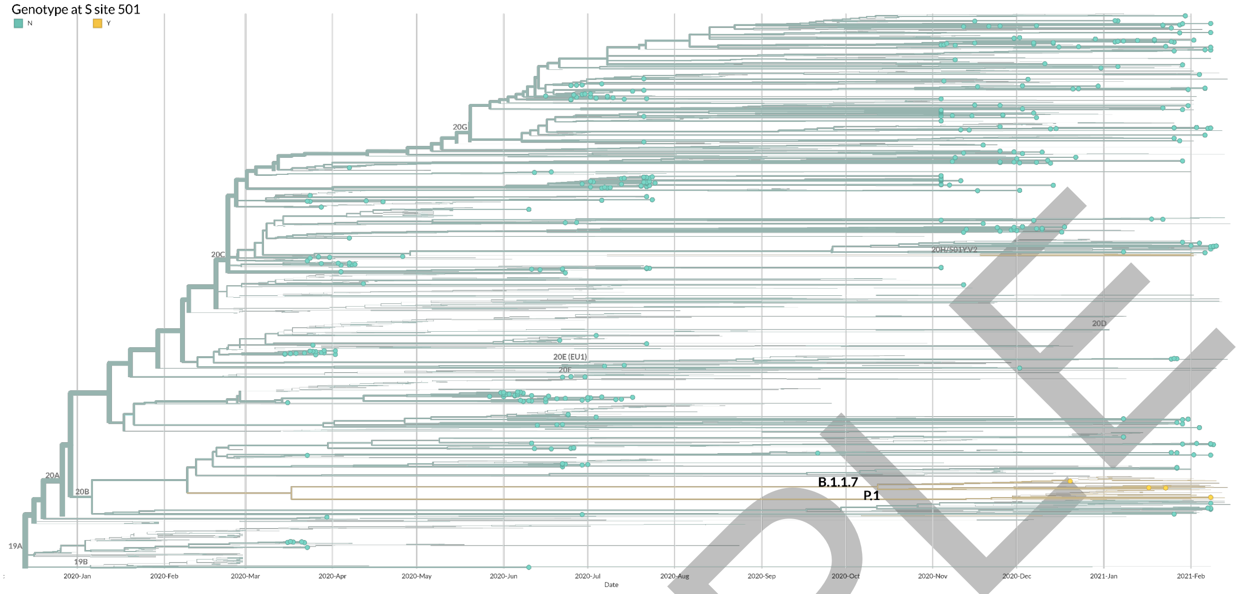


Figure: Alaska samples containing the N501Y mutation are colored yellow. This mutation is present in the Alaska cases in the B.1.1.7 and P.1 lineages. The N501Y mutation has appeared multiple times independently and appears in multiple lineages across the tree including the B.1.351 lineage (not shown).

Mutation Report, S:E484K

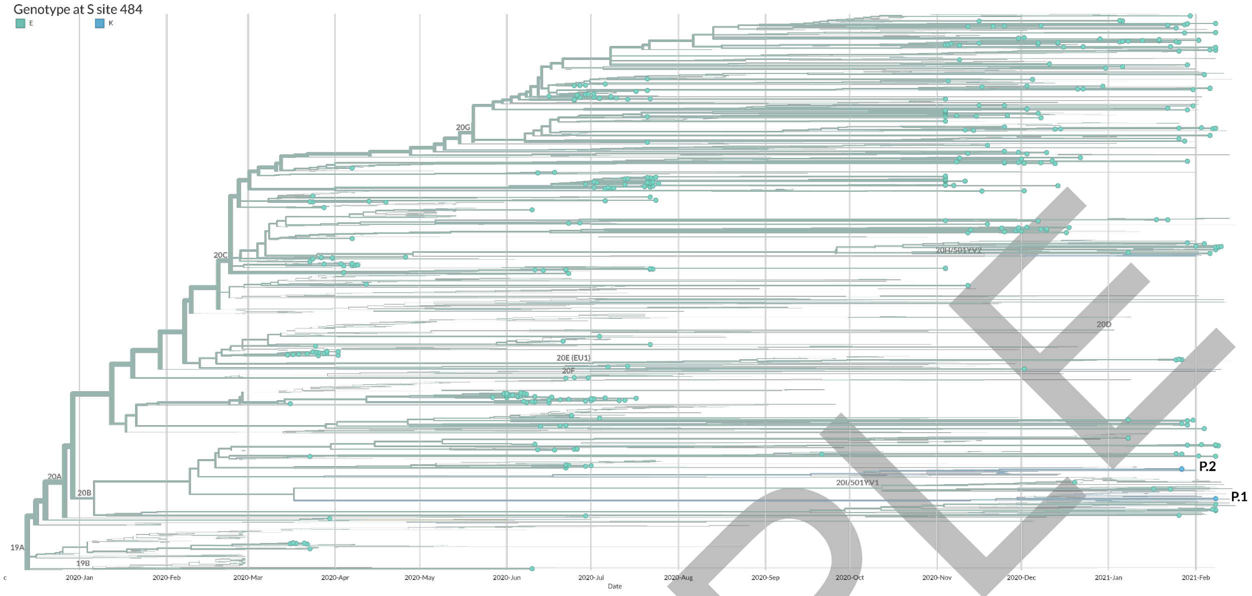


Figure: The E484K mutation has appeared multiple times independently. The specific mutation is found in two variants of concern P.1 (Brazil 20J/501Y.V3) and B.1.351 (not present in any Alaska genome) as well as variant of interest P.2. Recently, this mutation has also been found in a minority of B.1.1.7 (UK 20I/501Y.V1) genomes and is an indication of convergent evolution in this virus.

Mutation Report, S:L452R

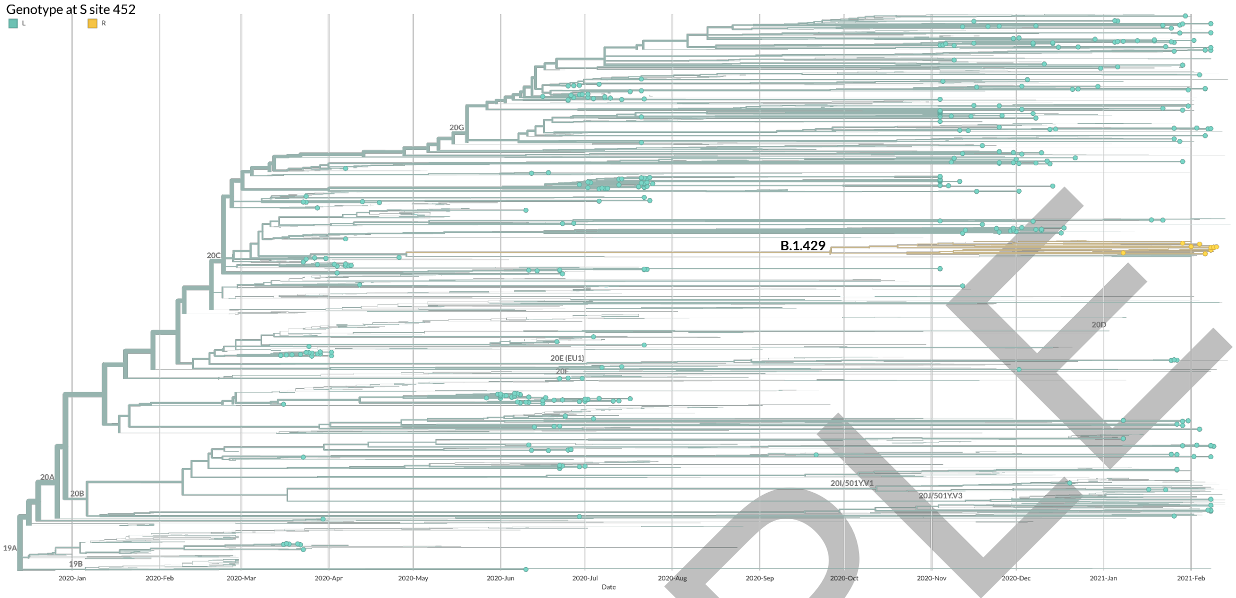


Figure: The L452R mutation was first detected in California and is present in the variant of interest B.1.429. This mutation is present in the Alaska cases in the B.1.429 lineage.

Mutation Report, S:Q677H

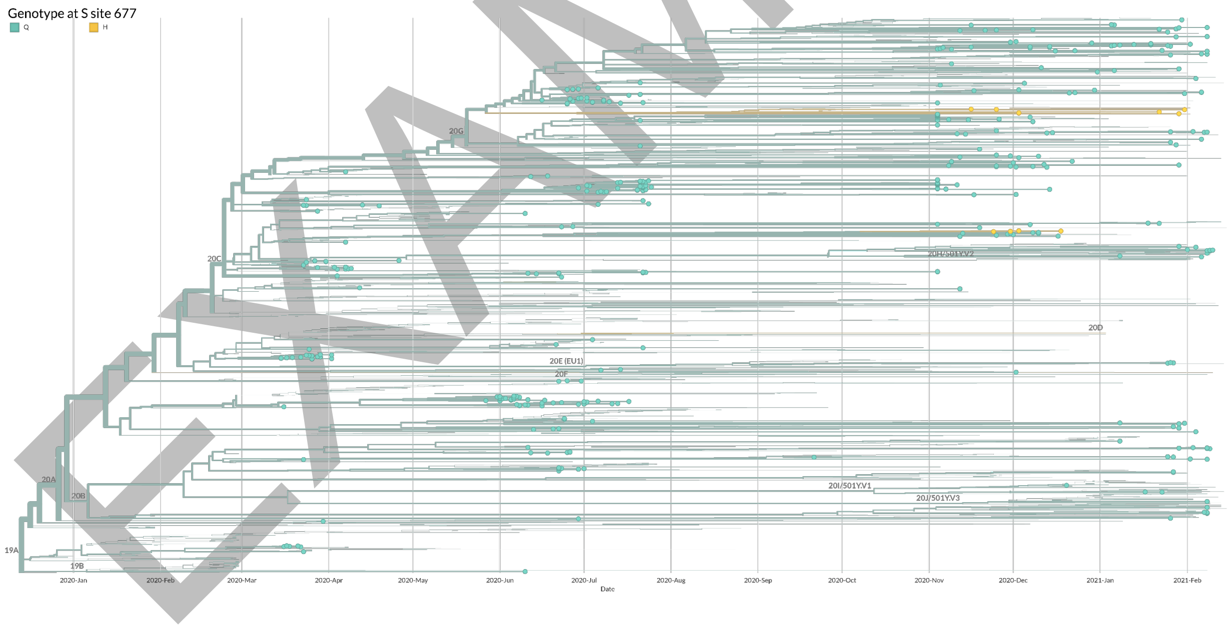


Figure: The Q677 mutation has arisen multiple times and little is known about this mutant beyond that its prevalence is spreading in the United States.

Mutation Report, S:D614G

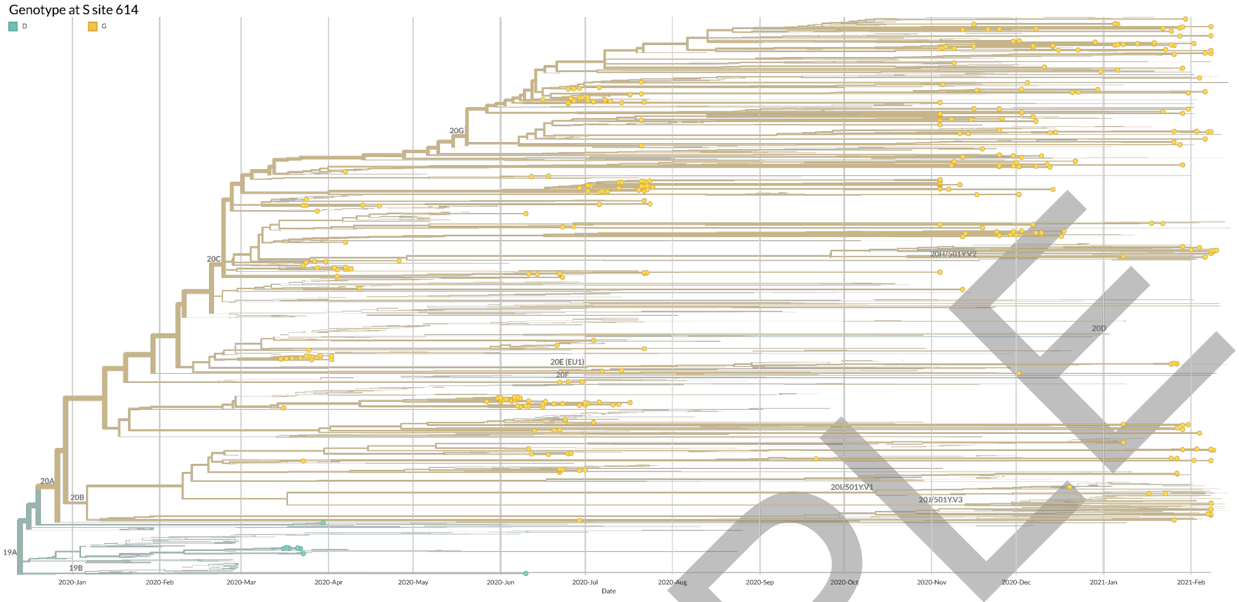


Figure: The D614G mutation arose early in the evolution of SARS-CoV-2 along the 20A clade. Nearly all Alaska genomes contain this mutation (yellow). Although not seen in Alaska, there have been independent emergences of 614G and 614N mutations during the resurgence of 19A and 19B lineages in recent months (https://nextstrain.org/groups/blab/narratives/ncov/19B/2020-02-16?n=3).


B.1.2
B.1
B
B.1.429
B.1.1.222
B.1.1.7
B.1.1.29
B.1.240
B.1.336
B.1.116
B.1.181
P.1
B.1.206
P.2
B.1.521
B.1.1.70
B.1.177
B.1.426
B.1.38
B.1.1.186
B.1.335
B.1.1.228
B.1.232
B.1.196
B.30
B.1.1.304
B.1.404
B.1.1.211
B.1.1.243
B.1.243
B.1.400
B.1.1.128
A.3
B.1.1.291
B.1.1.63
B.1.98
B.1.1.101
B.1.119
B.1.143
B.1.234
B.1.293
B.1.311
20G
20C
20D
20E (EU1)
20F
20A
20B
19A
19B
B.1.429
P.2
B.1.1.7
P.1
2019-Dec
2020-Jan
2020-Feb
2020-Mar
2020-Apr
2020-May
2020-Jun
2020-Jul
2020-Aug
2020-Sep
2020-Oct
2020-Nov
2020-Dec
2021-Jan
2021-Feb
Date

B.1.1.7 (20I/501Y.V1)

B.1.429

🟥 Alaska
🟦 Washington
🟦 California
🟦 Nevada
🟦 Idaho
🟦 Utah
🟦 Arizona
🟩 Wisconsin
🟨 Florida
🟨 North Carolina
🟧 New York
⬜ Auckland
⬜ New South Wales
⬛ Baja California
⬛ Taiwan
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USA/CA-QDX-2827/2020
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Mexico/BCN-ALSR-5708/2020
Taiwan/NTU57/2021
Taiwan/CGMH-CGU-48/2021
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2020-Oct-26
2020-Nov-02
2020-Nov-09
2020-Nov-16
2020-Nov-23
2020-Nov-30
2020-Dec-07
2020-Dec-14
2020-Dec-21
2020-Dec-28
2021-Jan-04
2021-Jan-11
2021-Jan-18
2021-Jan-25
2021-Feb-01
2021-Feb-08
2021-Feb-15
Date


P.1 (20J/501Y.V3)
🟥 Alaska
São Paulo
South Korea
Japan
Rio Grande do Sul
Amazonas BR
Yamanashi
Departamento de Am
Antwerpen
Para
Goiás
Brazil/GO-1202/2021
Brazil/RO-1199/2021
Brazil/AM-1062/2021
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Japan/IC-0561/2021
Brazil/PA-IEC-177366/2021
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SouthKorea/KDCA0464/2021
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2020-Nov-23
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2020-Dec-14
2020-Dec-21
2020-Dec-28
2021-Jan-04
2021-Jan-11
2021-Jan-18
2021-Jan-25
2021-Feb-01
2021-Feb-08
2021-Feb-15
Date

P.2


Alaska
Indiana
Massachusetts
Ontario
Rio de Janeiro
Malaysia
Singapore
Rio Grande do Sul
Para
Distrito Federal
Bahia
Paraná
USA/AK-PHL6825/2021
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Brazil/RJ-00548/2020
Brazil/DF-1028R1/2020
Brazil/PA-IEC176228/2020
2020-Jul
2020-Aug
2020-Sep
2020-Oct
2020-Nov
2020-Dec
2021-Jan
2021-Feb
Date


Genotype at S site 501
N
Y
20G
20C
20H/501Y.V2
20D
20E (EU1)
20F
20A
20B
19A
19B
B.1.1.7
P.1
2020-Jan
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2020-Nov
2020-Dec
2021-Jan
2021-Feb
Date


Genotype at S site 484
🟩 E
🟦 K
20G
20C
20H/501Y.V2
20D
20E (EU1)
20F
P.2
20I/501Y.V1
P.1
20A
20B
19A
19B
2020-Jan
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2020-Dec
2021-Jan
2021-Feb
Date


Genotype at S site 452
🟩 L
🟨 R
20G
20C
B.1.429
20D
20E (EU1)
20F
20A
20B
19A
19B
20I/501Y.V1
20J/501Y.V3
2020-Jan
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2020-Apr
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2020-Jul
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2020-Sep
2020-Oct
2020-Nov
2020-Dec
2021-Jan
2021-Feb
Date


Genotype at S site 677
Q
H
20G
20C
20H/501Y.V2
20D
20E (EU1)
20F
20A
20B
20I/501Y.V1
20J/501Y.V3
19A
19B
2020-Jan
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2021-Jan
2021-Feb
Date


Genotype at S site 614
🟩 D
🟨 G
20G
20C
20H/501Y.V2
20D
20E (EU1)
20F
20A
20B
20I/501Y.V1
20J/501Y.V3
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19B
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Additional Resources

CDC COVID-19 National Genomic Surveillance Dashboard - https://www.cdc.gov/coronavirus/2019-ncov/cases-updates/variant-surveillance/genomic-surveillance-dashboard.html

SARS-CoV-2 (hCoV-19) Mutation Situation Reports - https://outbreak.info/situation-reports

Nextstrain SARS-CoV-2 resources - https://nextstrain.org/sars-cov-2/

CoVariants - https://covariants.org/

PANGO Lineage Reports -https://cov-lineages.org/global_report.html