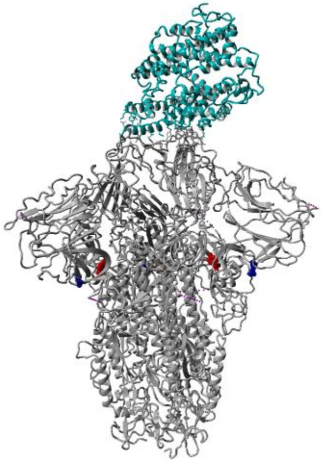
GISAID – CEPI
COVID-19 update

March 2021

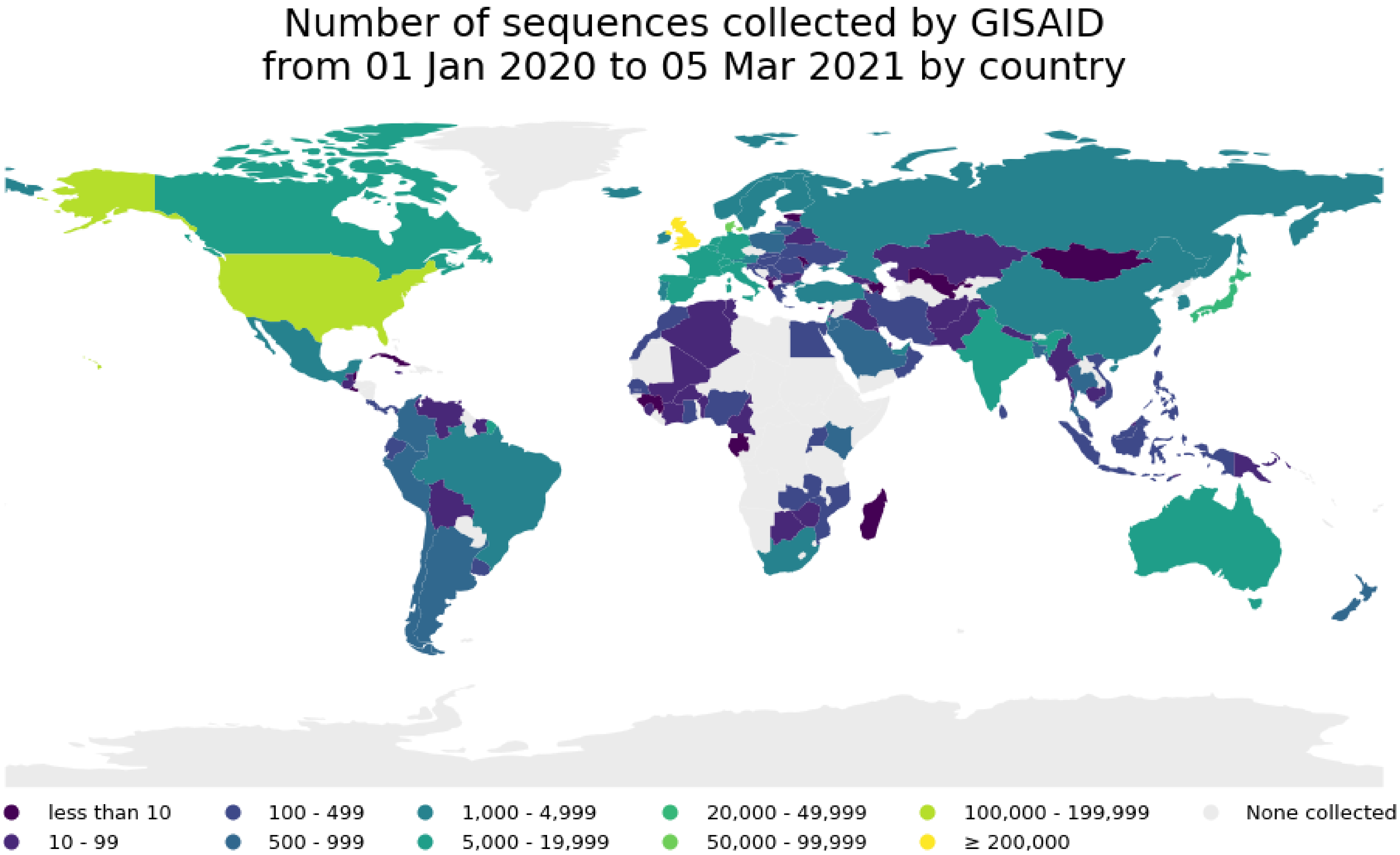


By: GISAID BII core team and GISAID TechDev team

GISAID Key Figures

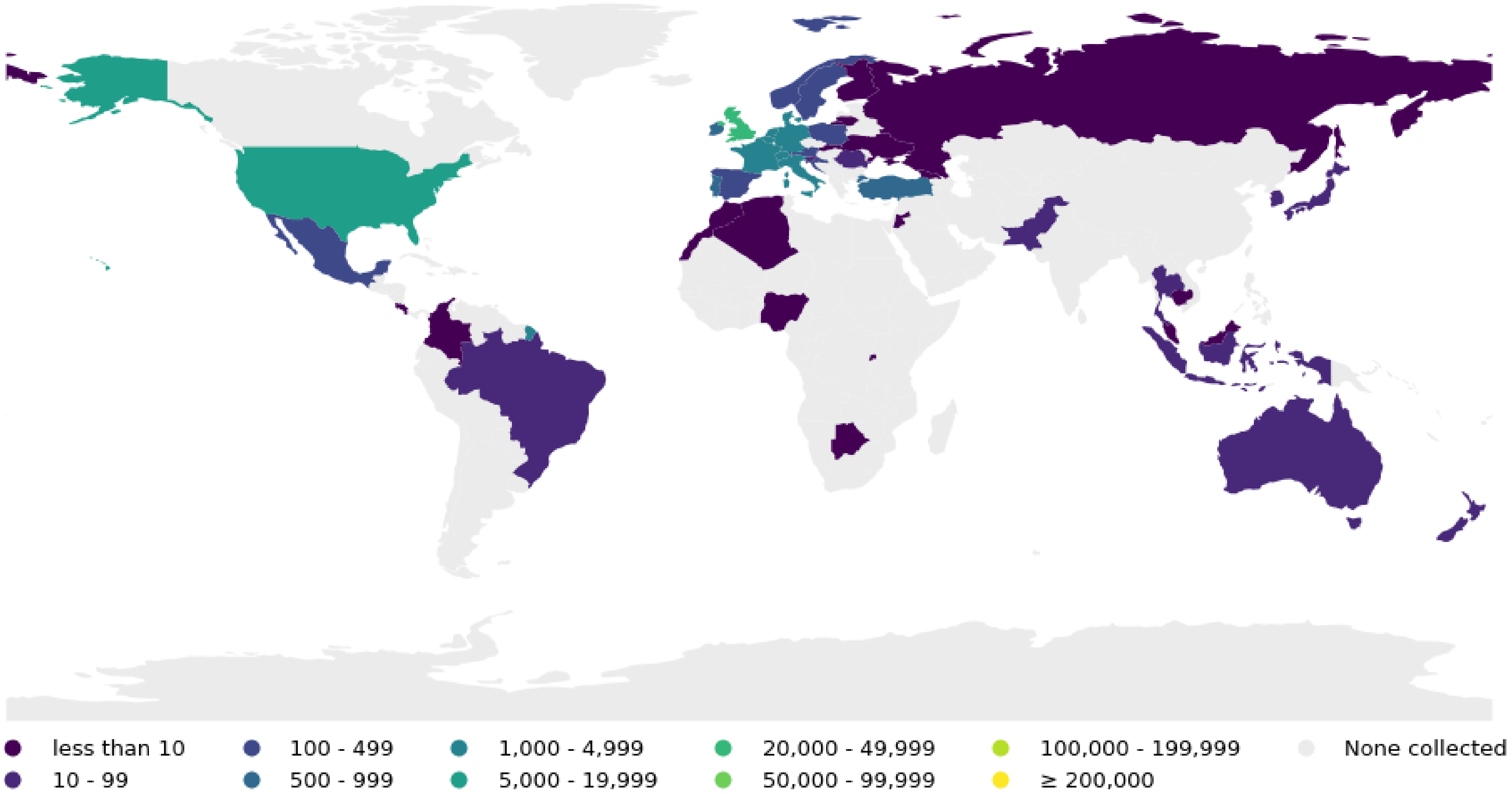
659,063	full genomes collected from 01 Jan 2020 to 04 Mar 2021
56,488	new genomes collected in the past 30 days
157	countries contributing to GISAID
51	variants of concern actively tracked

We gratefully acknowledge the Authors from Originating and Submitting laboratories of sequence data on which the analysis is based.

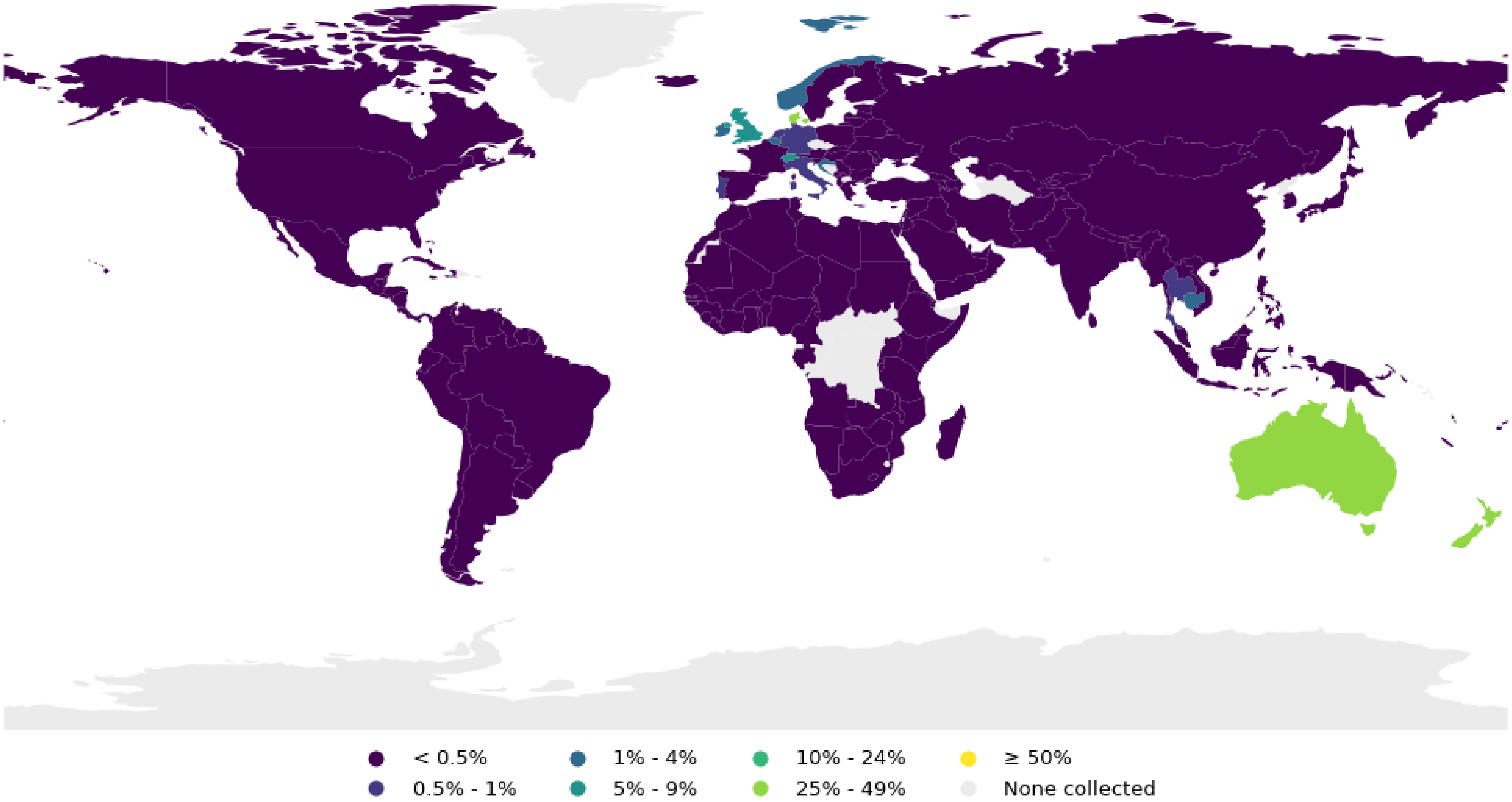


Number of sequences collected by GISAID
from 01 Jan 2020 to 05 Mar 2021 by country

Number of sequences collected by GISAID in last 30 days
from 02 Feb 2021 to 05 Mar 2021 by country

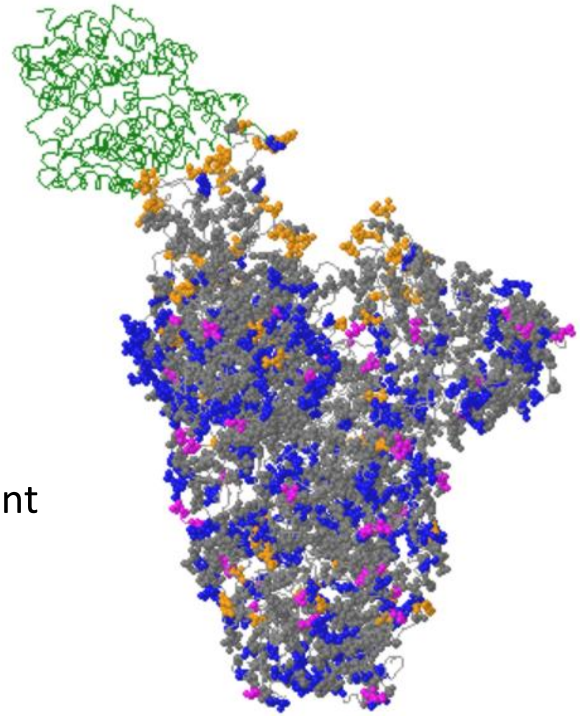


Proportion of sequenced cases submitted to GISAID in last 30 days
from 02 Feb 2021 to 05 Mar 2021 by country



Variant of concern

VUI 202012/01 GR501Y.V1 (B.1.1.7)



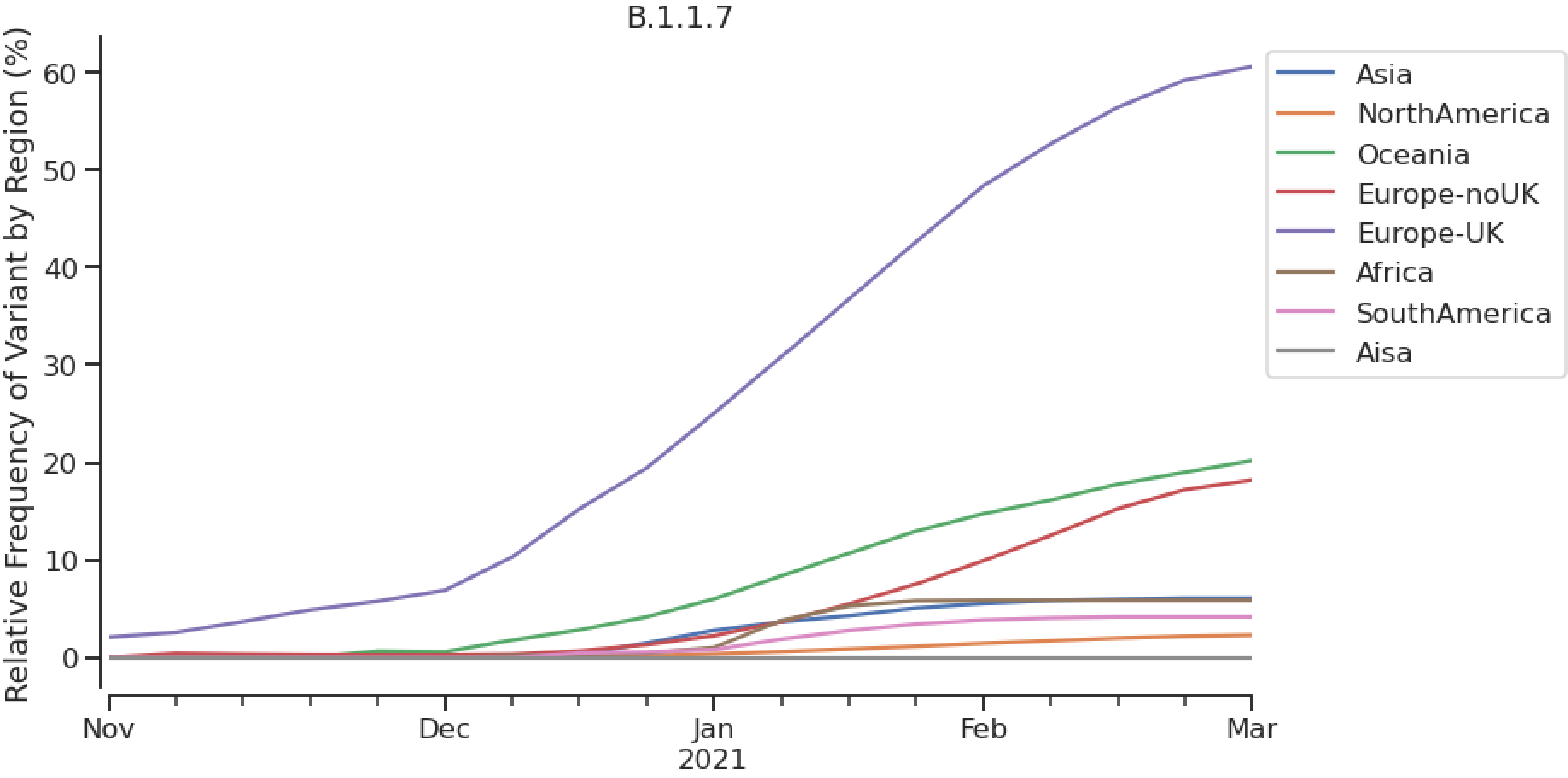
125,529	genomes in total
37,108	genomes collected in last 30 days
87	countries reporting this variant

First sampled in United Kingdom on 20 September 2020

Key Mutations on Spike Protein
N501Y, A570D, P681H, T716I, S982A, D1118H

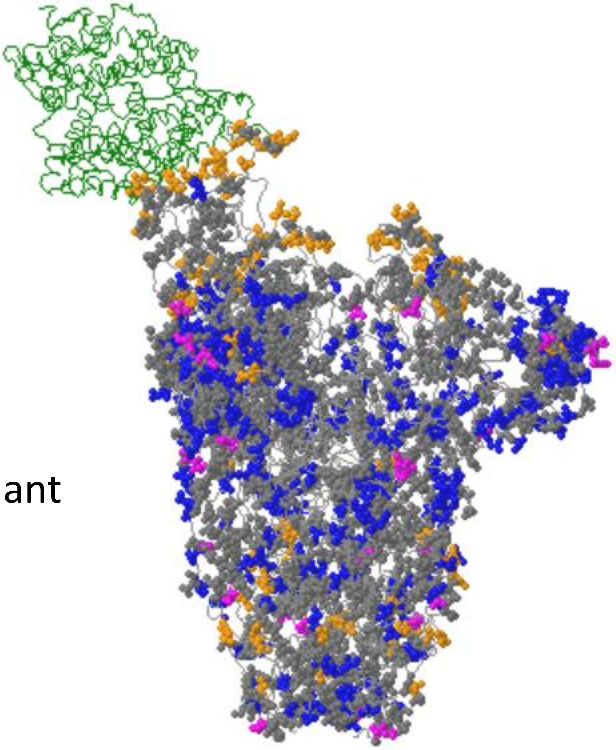
Variant of concern

VUI 202012/01 GRY (B.1.1.7)



Variant of concern

GH/501Y.V2 (B.1.351)



2,631 genomes in total

389 genomes collected in last 30 days

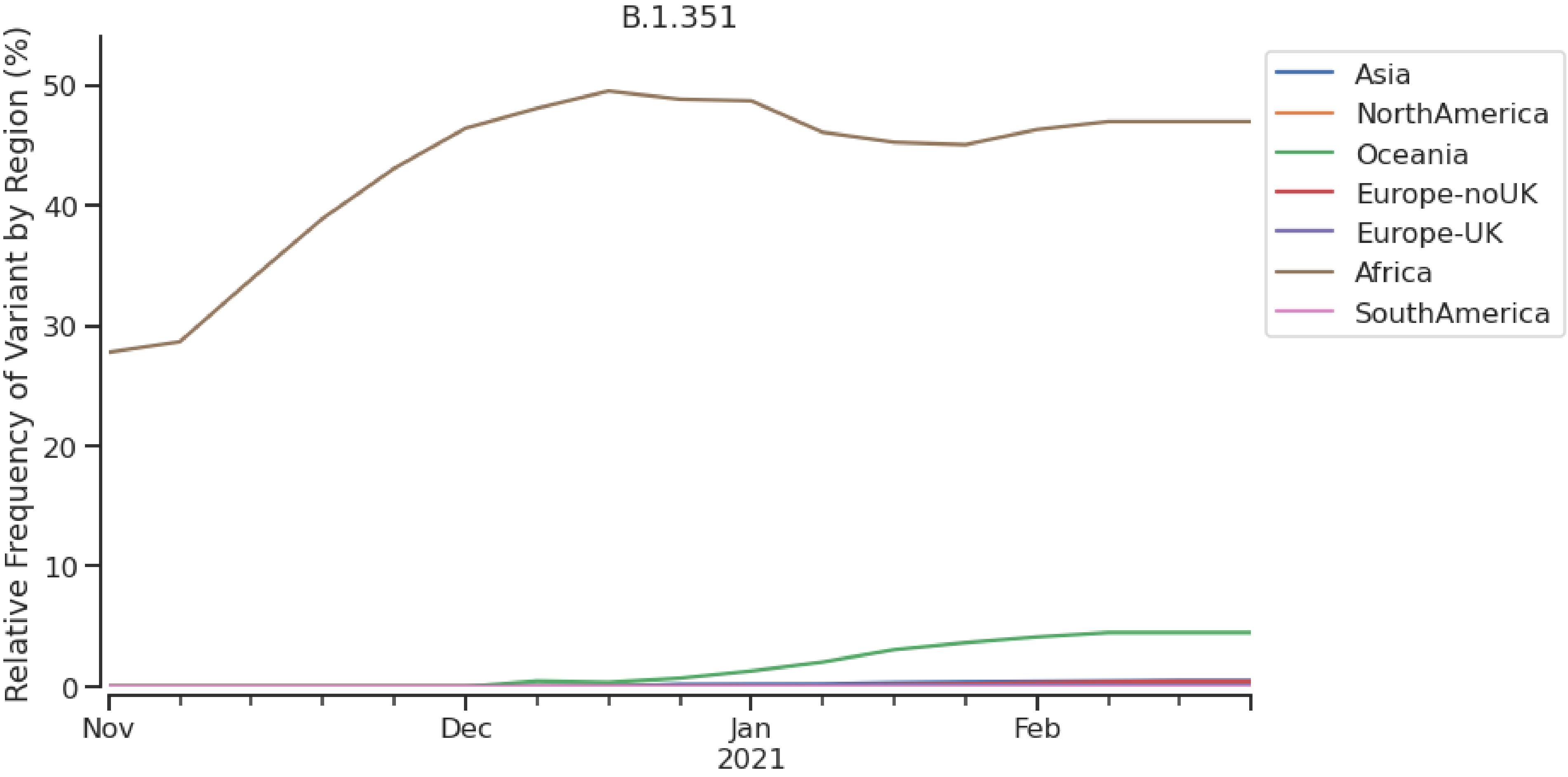
42 countries reporting this variant

First sampled in South Africa on 8 October 2020

Key Mutations on Spike Protein
D80A, D215G, K417N, A701V, N501Y, E484K

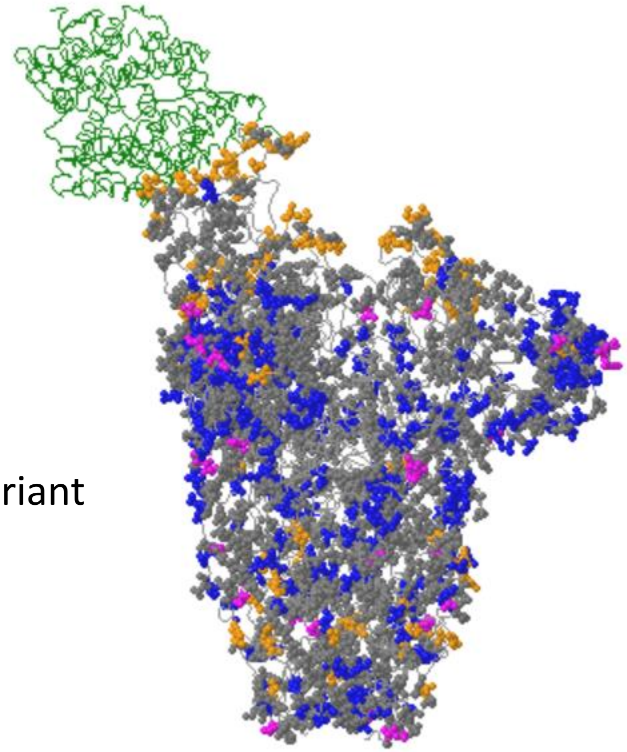
Variant of concern

GH/501Y.V2 (B.1.351)



Variant of concern

GR/484K.V2 (P1)



1,437 genomes in total

24 genomes collected in last 30 days

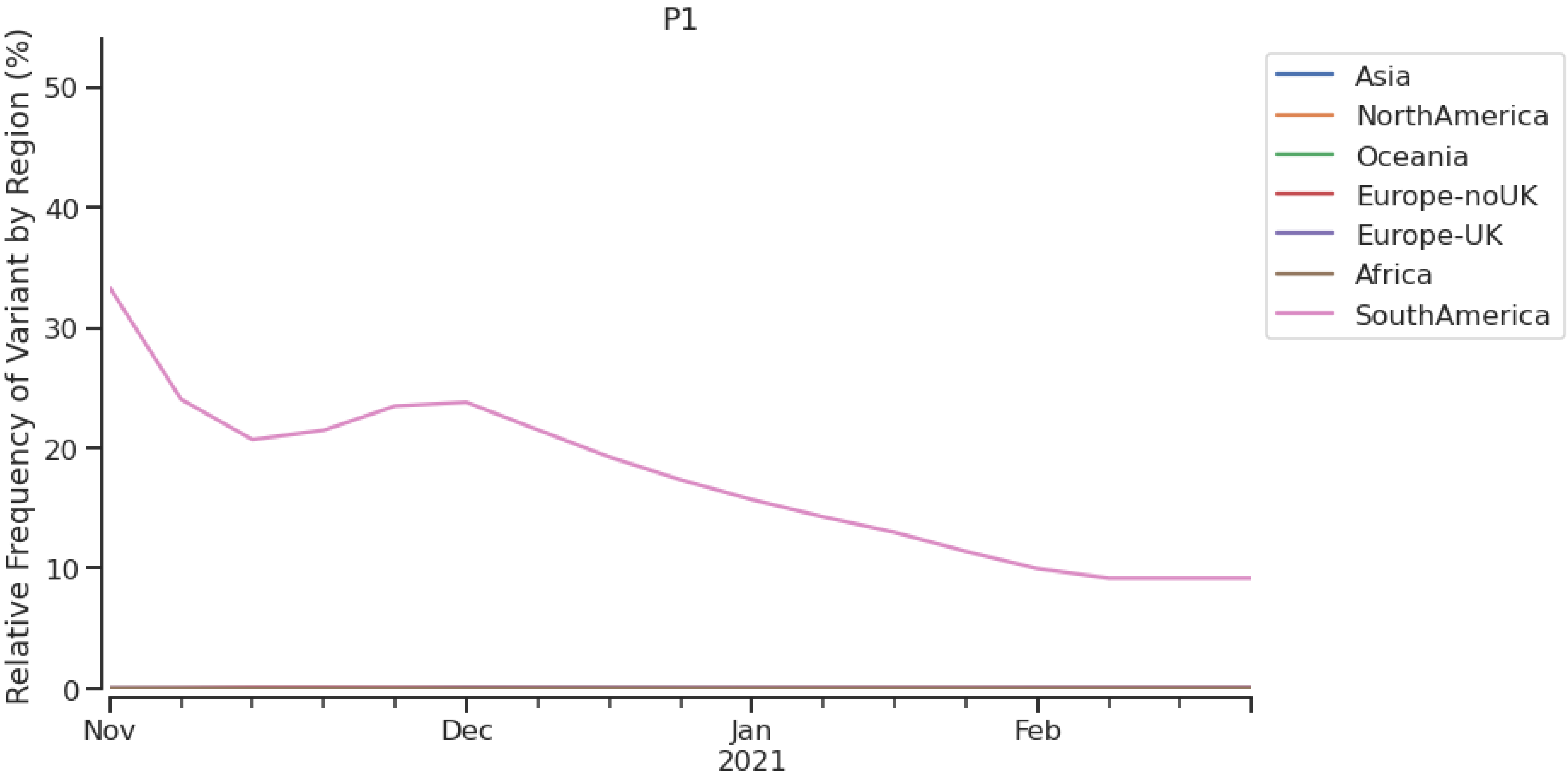
39 countries reporting this variant

First sampled in Brazil on 9 Oct 2020

Key Mutations on Spike Protein
L18F, T20N, P26S, D138Y, R190S, K417T, E484K, N501Y, H655Y, T1027I

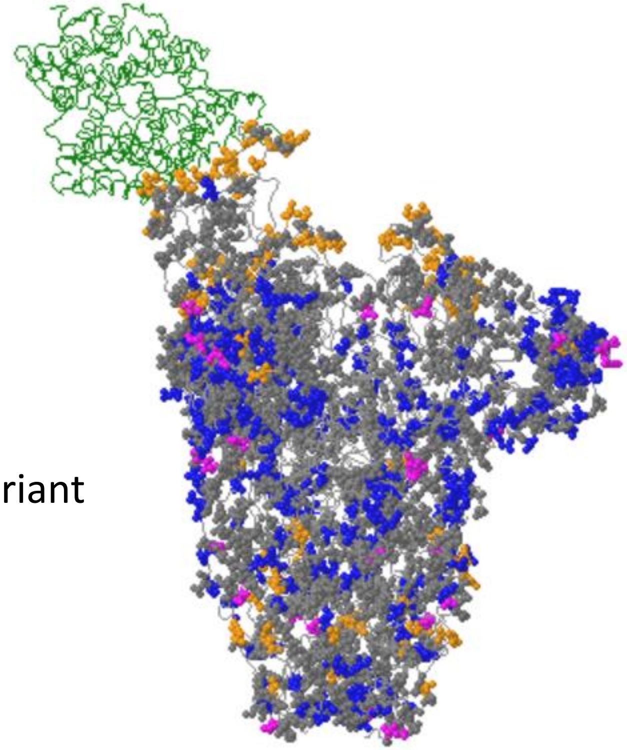
Variant of concern

GR/484K.V2 (P1)



Variant of concern

GH/452R.V1 (B.1.429+B.1.427)



8,839 genomes in total

1,938 genomes collected in last 30 days

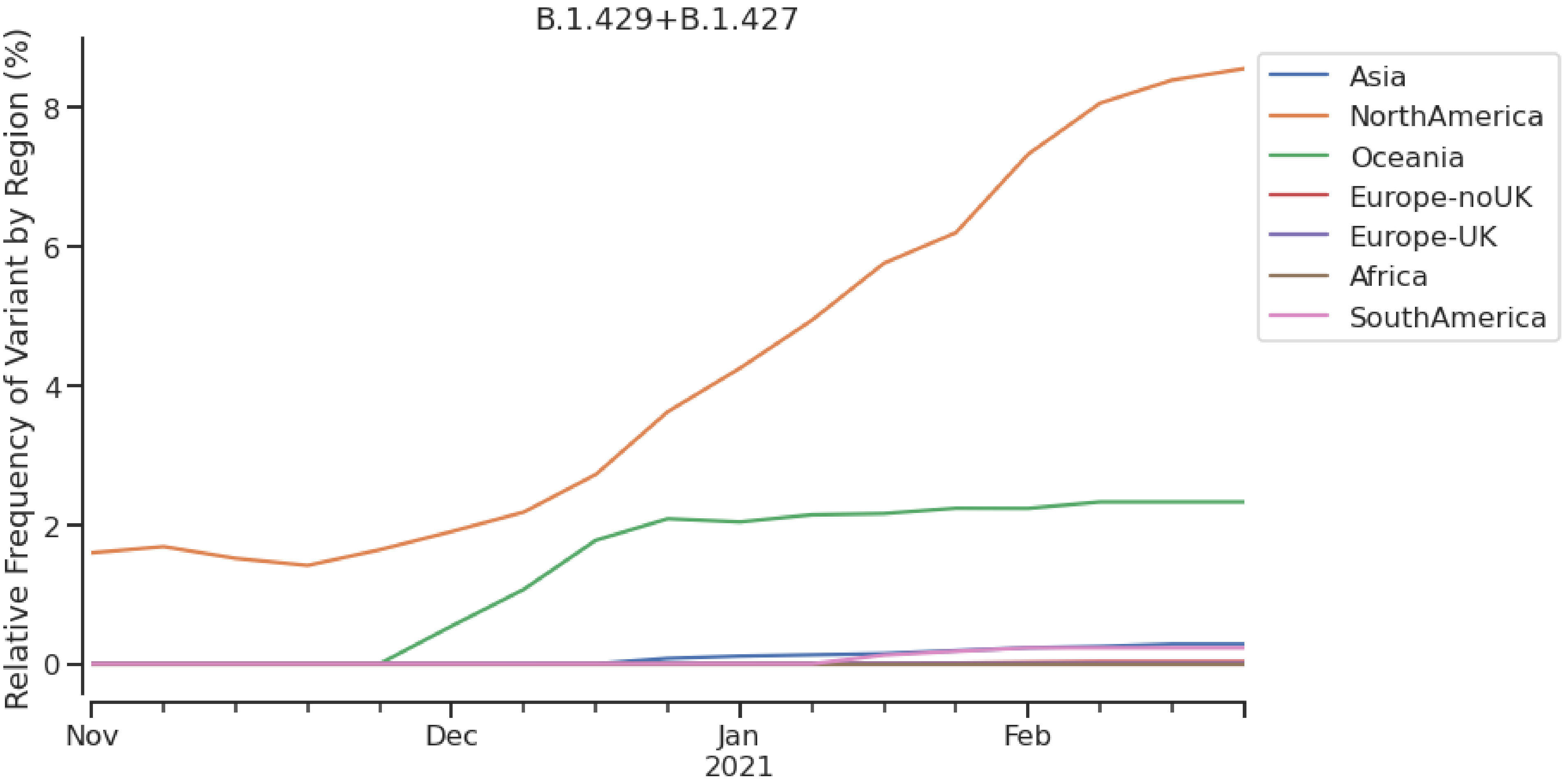
25 countries reporting this variant

First reported in USA on 12 September 2020

Key Mutations on Spike Protein
S13I, W152C, L452R, D614G

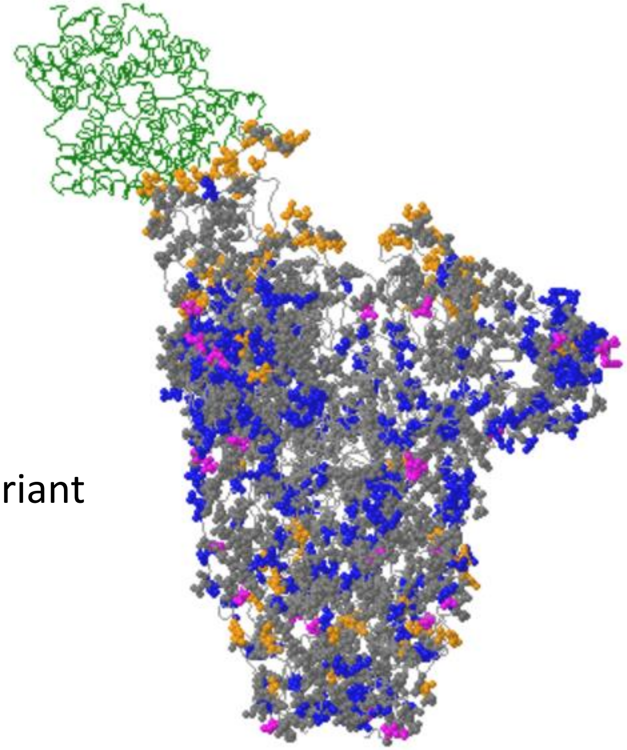
Variant of concern

GH/452R.V1 (B.1.429+B.1.427)



Variant of concern

G/484K.V3 (B.1.525)



351 genomes in total

128 genomes collected in last 30 days

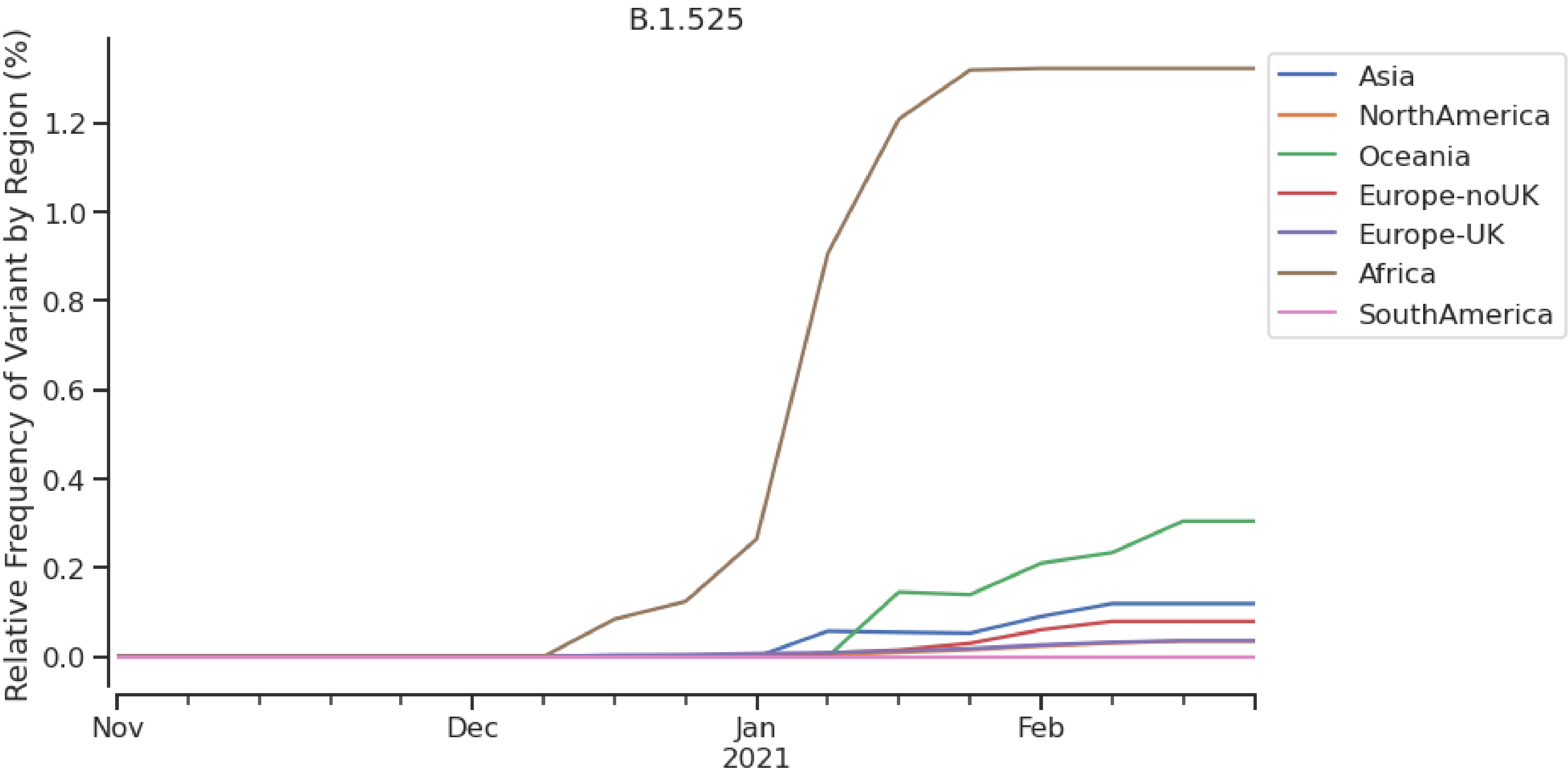
24 countries reporting this variant

First reported in United Kingdom on 15 December 2020

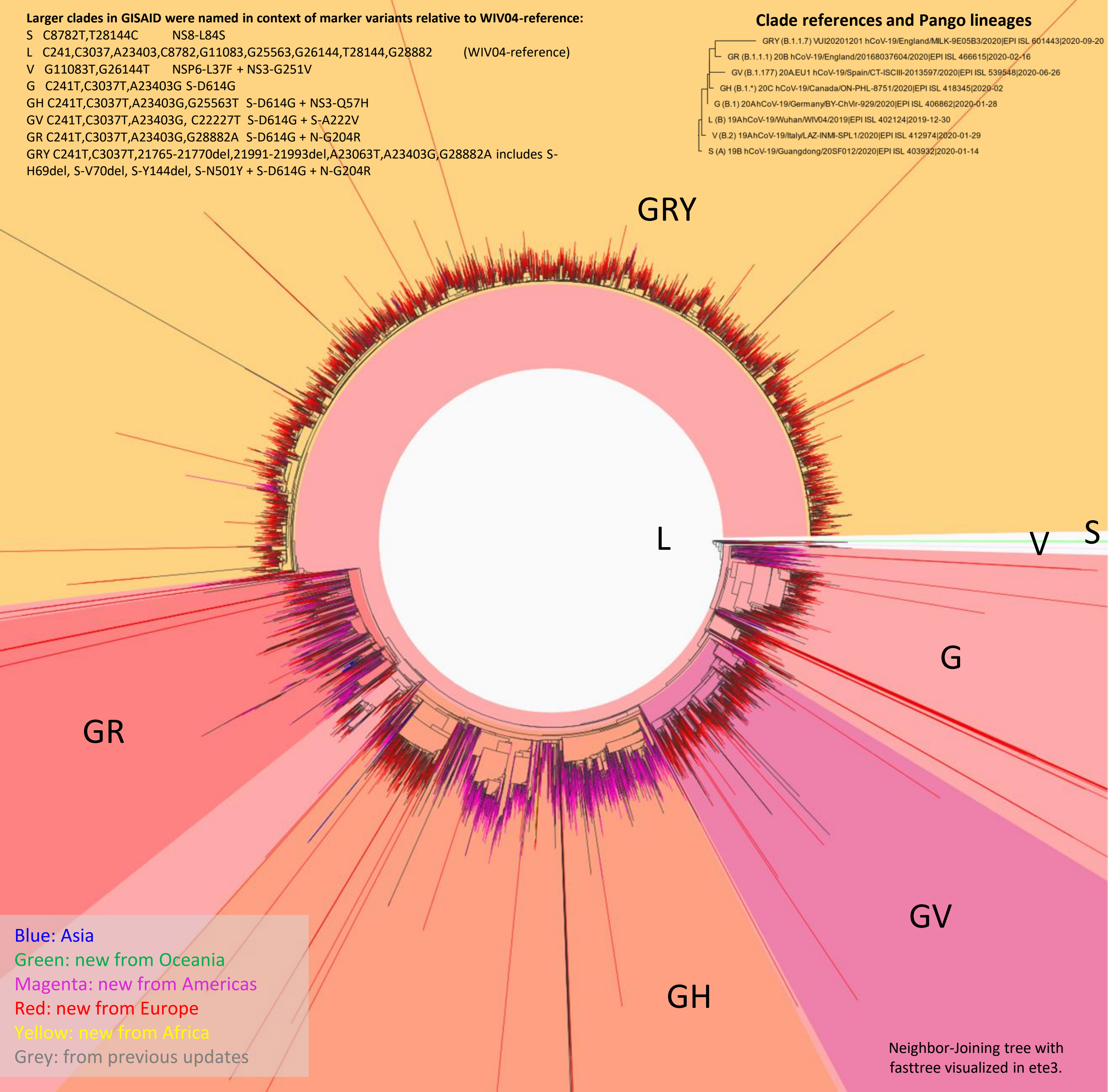
Key Mutations on Spike Protein
Q52R, E484K, Q677H, F888L

Variant of concern

G/484K.V3 (B.1.525)



Full genome tree derived from all outbreak sequences 2021-03-05



Larger clades in GISAID were named in context of marker variants relative to WIV04-reference:
S C8782T,T28144C NS8-L84S
L C241,C3037,A23403,C8782,G11083,G25563,G26144,T28144,G28882 (WIV04-reference)
V G11083T,G26144T NSP6-L37F + NS3-G251V
G C241T,C3037T,A23403G S-D614G
GH C241T,C3037T,A23403G,G25563T S-D614G + NS3-Q57H
GV C241T,C3037T,A23403G, C22227T S-D614G + S-A222V
GR C241T,C3037T,A23403G,G28882A S-D614G + N-G204R
GRY C241T,C3037T,21765-21770del,21991-21993del,A23063T,A23403G,G28882A includes S-H69del, S-V70del, S-Y144del, S-N501Y + S-D614G + N-G204R

Clade references and Pango lineages
GRY (B.1.1.7) VUI20201201 hCoV-19/England/MILK-9E05B3/2020|EPI ISL 601443|2020-09-20
GR (B.1.1.1) 20B hCoV-19/England/20168037604/2020|EPI ISL 466615|2020-02-16
GV (B.1.177) 20A.EU1 hCoV-19/Spain/CT-ISCIII-2013597/2020|EPI ISL 539548|2020-06-26
GH (B.1.*) 20C hCoV-19/Canada/ON-PHL-8751/2020|EPI ISL 418345|2020-02
G (B.1) 20AhCoV-19/Germany/BY-ChVir-929/2020|EPI ISL 406862|2020-01-28
L (B) 19AhCoV-19/Wuhan/WIV04/2019|EPI ISL 402124|2019-12-30
V (B.2) 19AhCoV-19/Italy/LAZ-INMI-SPL1/2020|EPI ISL 412974|2020-01-29
S (A) 19B hCoV-19/Guangdong/20SF012/2020|EPI ISL 403932|2020-01-14

Blue: Asia
Green: new from Oceania
Magenta: new from Americas
Red: new from Europe
Yellow: new from Africa
Grey: from previous updates

Neighbor-Joining tree with fasttree visualized in ete3.

Notable changes

617,323 full genomes (+23,012) (excluding low coverage, out of 658,134 entries)

Updated clades

RBDx: relevant changes near receptor and antibody binding sites

S clade 8,953 [RBDx 365] (+71 [+50])
L clade 5,033 [RBDx 13] (+13 [+3])
V clade 5,942 [RBDx 5] (+2 [+0])
G clade 82,301 [RBDx 16,663] (+2,083 [+1,114])
GR clade 135,140 [RBDx 17,957] (+2,353 [+760])
GRY clade 115,977 [RBDx 3,159] (+11,933 [+221])
GH clade 140,092 [RBDx 29,373] (+4,551 [+2,018])
GV clade 116,874 [RBDx 494] (+1,868 [+57])
Other clades 7,011 [RBDx 494] (+138 [+76])

We gratefully acknowledge the Authors from Originating and Submitting laboratories of sequence data on which the analysis is based.

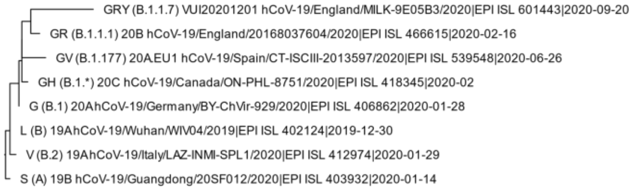
by BII/GIS, A*STAR Singapore

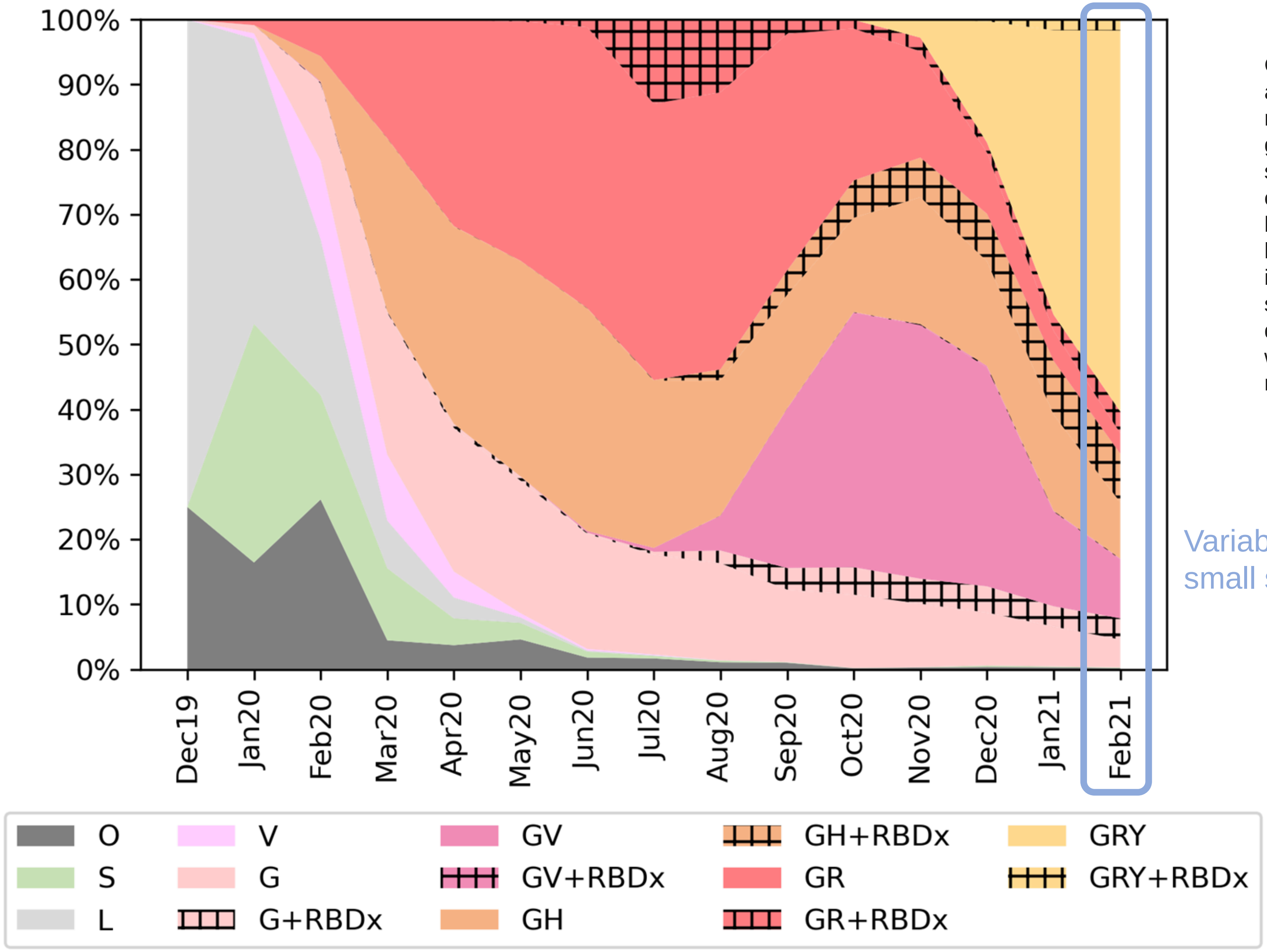
Timecourse of clade distribution in collected sequences 2021-03-05

Larger clades in GISAID were named in context of marker variants relative to WIV04-reference:

S C8782T,T28144C NS8-L84S
L C241,C3037,A23403,C8782,G11083,G25563,G26144,T28144,G28882 (WIV04-reference)
V G11083T,G26144T NSP6-L37F + NS3-G251V
G C241T,C3037T,A23403G S-D614G
GH C241T,C3037T,A23403G,G25563T S-D614G + NS3-Q57H
GV C241T,C3037T,A23403G, C22227T S-D614G + S-A222V
GR C241T,C3037T,A23403G,G28882A S-D614G + N-G204R
GRY C241T,C3037T,21765-21770del,21991-21993del,A23063T,A23403G,G28882A includes S-H69del, S-V70del, S-Y144del, S-N501Y + S-D614G + N-G204R

Clade references and Pango lineages





Variable, small sample size

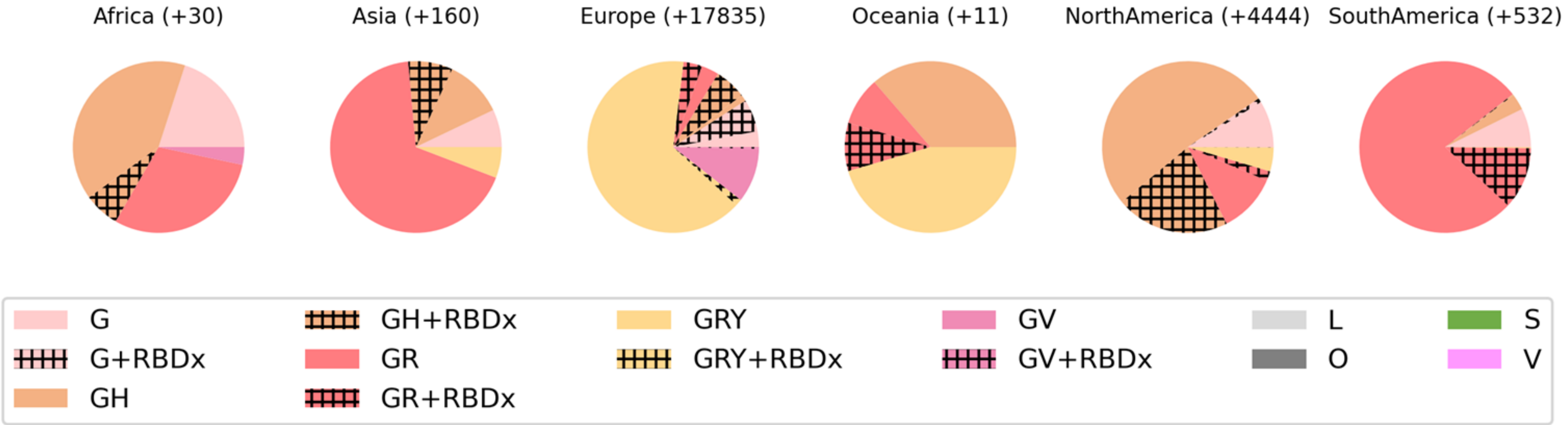
RBDx: *Relevant changes near receptor and antibody binding sites (relative to clade reference)*

Given the widespread appearance and large numbers of B.1.1.7 genomes globally surpassing numbers of other existing clades, we have elevated the B.1.1.7 lineage (GR/501Y.V1) to its own clade GRY for simple purposes, descending from clade GR with addition of spike markers including N501Y.

We gratefully acknowledge the Authors from Originating and Submitting laboratories of sequence data on which the analysis is based.

by BII/GIS, A*STAR Singapore

Regional clade distribution of new sequences 2021-03-05



S clade 8,953 [RBDx 365] (+71 [+50]): 32 [32] France, 8 USA/AZ, 8 Peru, 6 [6] USA/NY, 5 [5] Italy, 3 [1] England, 2 [2] Slovenia, 1 Switzerland, 1 [1] USA/CO, 1 Canada, 1 [1] Ireland, 1 Netherlands, 1 [1] Spain, 1 [1] USA/NM
L clade 5,033 [RBDx 13] (+13 [+3]): 7 [2] Belgium, 3 Netherlands, 1 France, 1 [1] England, 1 Peru
V clade 5,942 [RBDx 5] (+2 [+0]): 2 Canada
G clade 82,301 [RBDx 16,663] (+2,083 [+1,114]): 576 [562] Slovenia, 204 [11] Netherlands, 150 [51] Switzerland, 137 [101] Turkey, 93 [87] Italy, 87 [9] USA/AZ, 87 [83] Croatia, 73 [18] Belgium, 70 [11] USA/NY, 67 [46] France, 47 [25] Norway, 43 [34] England, 42 USA/TX, 42 [9] Spain, 38 [37] Austria, 37 Peru, 34 [4] USA/WA, 33 [1] Canada, 30 [1] USA/CA, 29 [1] USA/FL, 16 [3] USA/NM, 14 [1] USA/CO, 13 USA/MI, 12 USA/KS, 10 [1] Portugal, 10 Malaysia, 8 Hungary, 6 Morocco, 6 Poland, 5 [4] Romania, 5 [1] USA/AL, 5 USA/UT, 4 [1] USA/VA, 4 USA/WI, 4 [2] Wales, 4 Ukraine, 4 USA/PA, 4 [2] Ireland, 4 [4] NorthMacedonia, 4 USA/OR, 3 USA/MA, 3 Mexico, 2 [1] USA/OH, 2 [1] Scotland, 2 USA/NV, 2 USA/MN, 1 [1] NorthernIreland, 1 Singapore, 1 USA/WY, 1 USA/NJ, 1 USA/CT, 1 Brazil, 1 [1] USA/IL, 1 USA/ME
GR clade 135,140 [RBDx 17,957] (+2,353 [+760]): 375 [41] Peru, 263 [232] England, 169 [4] Norway, 162 [21] Switzerland, 157 [14] Canada, 108 [63] Portugal, 95 Japan, 91 [19] USA/NY, 88 [62] Turkey, 88 [18] Brazil, 66 [54] Belgium, 60 [4] Mexico, 46 [43] Scotland, 45 [4] USA/TX, 45 [26] France, 44 [18] Netherlands, 43 [29] Austria, 36 Ukraine, 34 [24] Italy, 32 [15] USA/WA, 31 [1] USA/AZ, 31 [1] USA/CA, 29 [15] USA/VA, 26 [12] Slovenia, 24 USA/NM, 14 [14] Wales, 14 Croatia, 12 Greece, 11 [4] Spain, 10 USA/FL, 7 Egypt, 7 [1] USA/NJ, 6 [1] USA/CO, 6 [5] Ireland, 6 USA/MI, 5 USA/LA, 5 USA/OH, 5 Indonesia, 4 [1] USA/MA, 4 USA/KS, 4 USA/PA, 4 [1] USA/AL, 3 Hungary, 3 Beijing, 3 [3] Romania, 3 [2] NorthMacedonia, 3 USA/IL, 2 USA/GA, 2 USA/NH, 2 [1] USA/WI, 2 [2] NorthernIreland, 2 USA/NV, 2 Morocco, 2 [1] USA/CT, 2 [2] French Guiana, 2 [1] Australia/NSW, 2 Malaysia, 1 USA/WY, 1 Germany, 1 USA/OR, 1 Poland, 1 [1] USA/TN, 1 USA/WV
GRY clade 115,977 [RBDx 3,159] (+11,933 [+221]): 7,642 [174] England, 1,090 [11] Scotland, 635 [21] Wales, 485 [2] NorthernIreland, 408 Italy, 336 [1] Portugal, 273 [4] Switzerland, 169 France, 152 [5] Norway, 139 Belgium, 102 [1] USA/NY, 76 Turkey, 66 Ireland, 65 Austria, 45 Poland, 43 Spain, 38 [1] Croatia, 27 USA/CO, 24 Romania, 20 Slovenia, 14 USA/PA, 11 USA/UT, 10 Netherlands, 7 USA/KS, 7 USA/CA, 7 Cambodia, 5 [1] USA/FL, 4 USA/VA, 4 Canada, 3 USA/MA, 3 NewZealand, 3 USA/NJ, 2 USA/GA, 2 USA/OH, 2 USA/PR, 2 Singapore, 2 USA/WA, 2 USA/TX, 2 USA/NM, 2 Australia/NSW, 2 USA/AL, 1 Estonia, 1 Brazil
GH clade 140,092 [RBDx 29,373] (+4,551 [+2,018]): 726 [396] USA/NY, 389 [307] USA/CA, 382 [8] Canada, 334 [300] Switzerland, 282 [23] USA/AZ, 212 [194] France, 199 [60] USA/WA, 197 [22] USA/TX, 172 [161] Turkey, 128 [22] USA/CO, 124 [4] USA/MI, 113 [113] Austria, 107 [9] USA/FL, 88 [12] USA/VA, 87 [80] Belgium, 80 [20] Norway, 78 [12] USA/NM, 75 [6] USA/WI, 72 [57] Portugal, 69 [38] Netherlands, 69 [2] USA/AL, 50 [1] USA/MA, 47 USA/KS, 43 [6] USA/OH, 42 [7] USA/WY, 37 [37] Italy, 31 [2] USA/OR, 26 [16] England, 24 [13] USA/NV, 24 [10] USA/PA, 23 [10] USA/NJ, 19 [2] USA/IL, 17 [6] Indonesia, 15 Peru, 14 [11] Slovenia, 12 [11] Croatia, 12 Greece, 10 [10] Spain, 9 USA/NH, 8 [1] USA/CT, 8 USA/LA, 8 [5] USA/KY, 7 [1] USA/ME, 7 USA/UT, 5 [3] Ireland, 5 Morocco, 5 [2] Tunisia, 5 [1] USA/WV, 4 Egypt, 4 Australia/NSW, 4 [2] Cambodia, 3 [2] USA/HI, 3 [3] Wales, 3 USA/IN, 3 Poland, 3 [1] USA/IA, 3 USA/MN, 3 [3] Malaysia, 2 Hungary, 2 [2] Scotland, 2 [1] NorthernIreland, 2 India, 2 Thailand, 2 [2] Singapore, 1 Estonia, 1 USA/VT, 1 USA/RI, 1 Mexico, 1 USA/NE, 1 USA/AK, 1 [1] French Guiana, 1 USA/NC, 1 USA/TN, 1 USA/AR
GV clade 116,874 [RBDx 494] (+1,868 [+57]): 248 Netherlands, 222 [2] Wales, 221 [1] Switzerland, 209 [30] Italy, 209 [1] Spain, 198 [1] England, 195 [1] Portugal, 121 Scotland, 67 [9] Norway, 51 Belgium, 45 France, 32 [1] NorthernIreland, 23 [11] Croatia, 9 Slovenia, 6 Ireland, 3 Turkey, 3 Austria, 2 Romania, 1 Morocco, 1 Poland, 1 USA/WA, 1 Ukraine
Other clades 7,011 [RBDx 494] (+138 [+76]): 49 [48] Turkey, 49 [18] Belgium, 16 [4] Spain, 7 [2] USA/OR, 4 [1] Indonesia, 3 Hungary, 2 Peru, 2 [2] Switzerland, 2 USA/MT, 1 France, 1 [1] Italy, 1 Mexico, 1 Lu'an

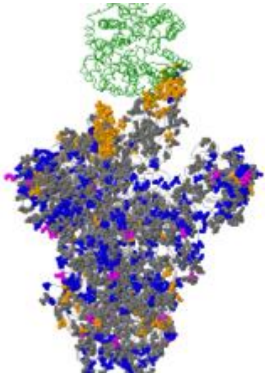
	Africa	*Asia*	*Europe*	*Oceania*	*North America*	*South America*
Total	7,335	37,879	399,478	17,198	148,830	6,603
New	30	160	17,835	11	4,444	532

by BII/GIS, A*STAR Singapore

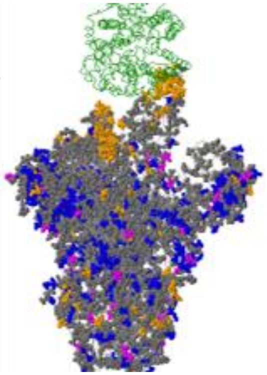
Receptor binding surveillance for complete genomes 2021-03-05

New occurrence of receptor binding changes 7744x N501Y in England, 1098x N501Y in Scotland, 653x N501Y in Wales, 486x N501Y in Northern Ireland, 441x N501Y in Italy, 408x N501Y in Turkey, 351x N501Y in Portugal, 283x N501Y in Switzerland, 256x N501Y in France, 228x N501Y in Belgium, 169x N501Y in Austria, 162x N501Y in Norway, 122x N501Y in USA/NY, 74x N501Y in Ireland, 53x N501Y in Spain, 45x N501Y in Poland, 39x N501Y in Croatia, 33x N501Y in Slovenia, 27x N501Y in USA/CO, 25x N501Y in Romania, 24x N501Y in Netherlands, 23x N501Y in Peru, 17x N501Y in USA/PA, 16x N501Y in Canada, 15x N501Y in USA/WA, 12x N501Y in Brazil, 11x N501Y in USA/UT, 519x N439K in Slovenia, 83x N439K in Croatia, 72x N439K in Italy, 49x N439K in Switzerland, 35x N439K in Austria, 23x N439K in Norway, 14x N439K in Belgium, 14x N439K in France, 284x S477N in Switzerland, 175x S477N in France, 103x S477N in USA/NY, 56x S477N in Portugal, 43x S477N in Belgium, 38x S477N in Netherlands, 34x S477N in Italy, 17x S477N in Peru, 11x S477N in Austria, 11x S477N in Spain, 215x E484K in USA/NY, 128x E484K in Austria, 44x E484K in Belgium, 42x E484K in England, 24x E484K in France, 22x E484K in Peru, 19x E484K in Italy, 18x E484K in Brazil, 17x E484K in USA/VA, 13x E484K in Norway, 249x K417N in Turkey, 103x K417N in Austria, 35x K417N in Belgium, 20x K417N in France, 15x K417N in Norway, 12x K417N in England, 78x S494P in USA/NY, 48x S494P in England, 55x T478K in Mexico, 20x T478K in USA/NY, 18x T478K in USA/TX, 23x K417T in Peru, 12x K417T in Italy, 11x K417T in Brazil, 21x F490S in Peru, 16x F490S in England, 13x N501T in USA/MA, 13x S477R in Scotland (only locations >10 occurrences are shown)

E484Q K417N T478I Y453F N439K V503I Q493H G446V F490S S477I S477N N501T R403K V445I N501Y L455F Q498H G504N E484K G446S G485A T478K S494P
in GH clade (B.1.*)



Q493R E484Q V445F K417N T478I F490Y A475S N439K G504S Q493H A475V G485V F456L G446V S477R F490S Q493K S477N Y489H N501T K417T G496S N501Y L455F G446S E484K Q493L T478K S494P G447D G476A
in GR & GRY clade
(B.1.1.1 & B.1.1.7)

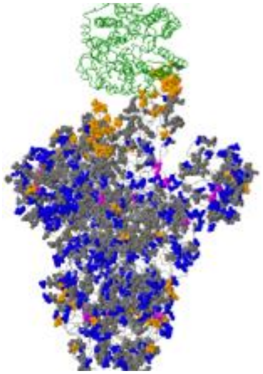


Changes in the spike glycoprotein for the 23012 new complete genomes.

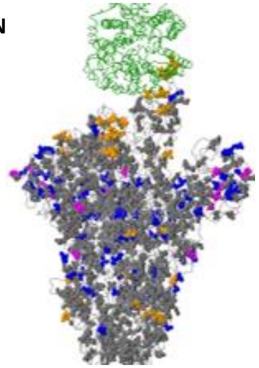
We gratefully acknowledge the Authors from Originating and Submitting laboratories of sequence data on which the analysis is based.

Green ... ACE2 human host receptor
Gray ... CoV spike glycoprotein trimer
Gray balls ... Spike glycoprotein variation occurring 100 times or less
Blue balls ... Spike glycoprotein variation occurring greater than 100 times
Red balls ... Spike glycoprotein variation near host receptor with effect history
Orange balls ... Spike glycoprotein variation near host receptor, or other functional annotation
Cyan ... Insertion/deletion
Magenta balls ... Spike glycoprotein variation altering potential N-glycosylation sites

V455F E484Q E484G K417N N439K V503I Q493H S494L A475V S477R F490S G446V F490L S477N K417T T478R V445I N501Y E484K T478K S494P
in G & GV clades
(B.1 & B.1.177)



E484K N439K G476S K417N C488G Y453F S477N F486S N501Y
in nonG clade
(A, B & B.2)



Full list online at gisaid.org/spike

Equivalent positions have been studied for V483A and V483I in MERS (DOI: 10.1128/JVI.01381-18) and G476S, L455I, F456L, F456V, S494P, A475V, N439K, K444R and V503F in SARS (DOI: 10.1074/jbc.M111.325803 DOI: 10.1086/651022 DOI:10.1186/1743-422X-2-73 DOI:10.1093/molbev/msq056) where they most often weakly reduced host receptor binding and altered antigenicity.

Numbering relative to start codon 21563 in hCoV-19/Wuhan/WIV04/2019

by BII/GIS, A*STAR Singapore