Public Health England

Protecting and improving the nation's health

SARS-CoV-2 variants of concern and variants under investigation in England

Technical briefing 9

22 April 2021

This briefing provides an update on previous briefings up to 1 April 2021

Contents

Summary

There are 4 variants of concern and 7 variants under investigation (Table 1).

VOC-20DEC-01 (B.1.1.7) remains predominant in the UK. Other variants of concern and variants under investigation remain a very low proportion of the available sequence data.

VUI-21APR-01 (B.1.617.1) cases have been imported to England with increasing frequency. Phylogeny and surveillance data are presented.

The enhanced investigations for all variants under investigation and variants of concern have been updated, including secondary attack rates, spatial risk mapping, and growth rate estimates. Numbers of all variants under investigation remain low and estimates have low certainty. Travel data are now included.

A new clinical risk assessment for VOC-20DEC-01 (B.1.1.7) is provided in the Appendix.

Variant information

The collection page gives content on variants, including prior technical briefings. Definitions for variants of concern, variants under investigation and signals in monitoring are detailed in technical briefing 8.

Variant status and numbers

Table 1 shows the current variants of concern and variants under investigation (including new simplified naming convention). Summary epidemiology on each variant is shown in Table 2 (case numbers are also updated online Case numbers on variants of concern (VOC) and variants under investigation (VUI)).

Table 1. Variant lineage, designation and status as of 21 April 2021

Lineage	Designation	First detected in sequence from	Status
B.1.1.7	VOC-20DEC-01	UK	VOC
B.1.351	VOC-20DEC-02	South Africa	VOC
P.1	VOC-21JAN-02	Japan ex Brazil	VOC
B1.1.7 with E484K	VOC-21FEB-02	UK	VOC
P.2	VUI-21JAN-01	Brazil	VUI
A.23.1 with E484K	VUI-21FEB-01	UK	VUI
B.1.525	VUI-21FEB-03	UK	VUI

Lineage	Designation	First detected in sequence from	Status
B.1.1.318	VUI-21FEB-04	UK England	VUI
B.1.324.1 with E484K	VUI-21MAR-01	UK	VUI
P.3	VUI-21MAR-02	Philippines	VUI
B.1.617.1 with E484Q	VUI-21APR-01	India	VUI
B.1.429		California USA	Monitoring
B.1.1.7 with S494P		UK	Monitoring
A.27		France (Mayotte)	Monitoring
B.1.526		New York USA	Monitoring
B.1.1.7 with Q677H		UK	Monitoring
B.1 with profile: P26S, V126A, S477N, E484K, P681H, T1027I, D1118H, nsp6d, Sd68, Sd143		Imported cases to UK	Monitoring
B1.214.2		Belgium	Monitoring
B.1.1.1 with L452Q and F490S		Imported cases to UK	Monitoring
R.1		Multiple locations	Monitoring
B.1.1.28 with N501T and E484Q		Belo Horizonte (Brazil Lineage)	Monitoring
R346K, T478R and E484K		Variant associated with travellers	Monitoring
B.1.617.2		India	Monitoring
B.1.617.3		India	Monitoring

Variant prevalence

Variant prevalence for all available case data is presented in Figure 1 and Figure 2. The predominant variant remains VOC-20DEC-01; other variants of concern and under investigation represent a low proportion of available sequences. The ‘Other’ category in Figure 1 includes genomes where the quality is insufficient to determine variant status and genomes that do not meet the current definition for any designated variant under investigation or variant of concern; this category has been removed from Figure 2. These figures represent all available genomic data including enhanced testing and sequencing from individuals who have travelled, and surge testing and sequencing in outbreak areas. The supplementary data for figures is available.

Figure 1. Variant prevalence for all England available case data from 1 February 2021 to 21 April 2021
(Find accessible data used in this graph in underlying data)

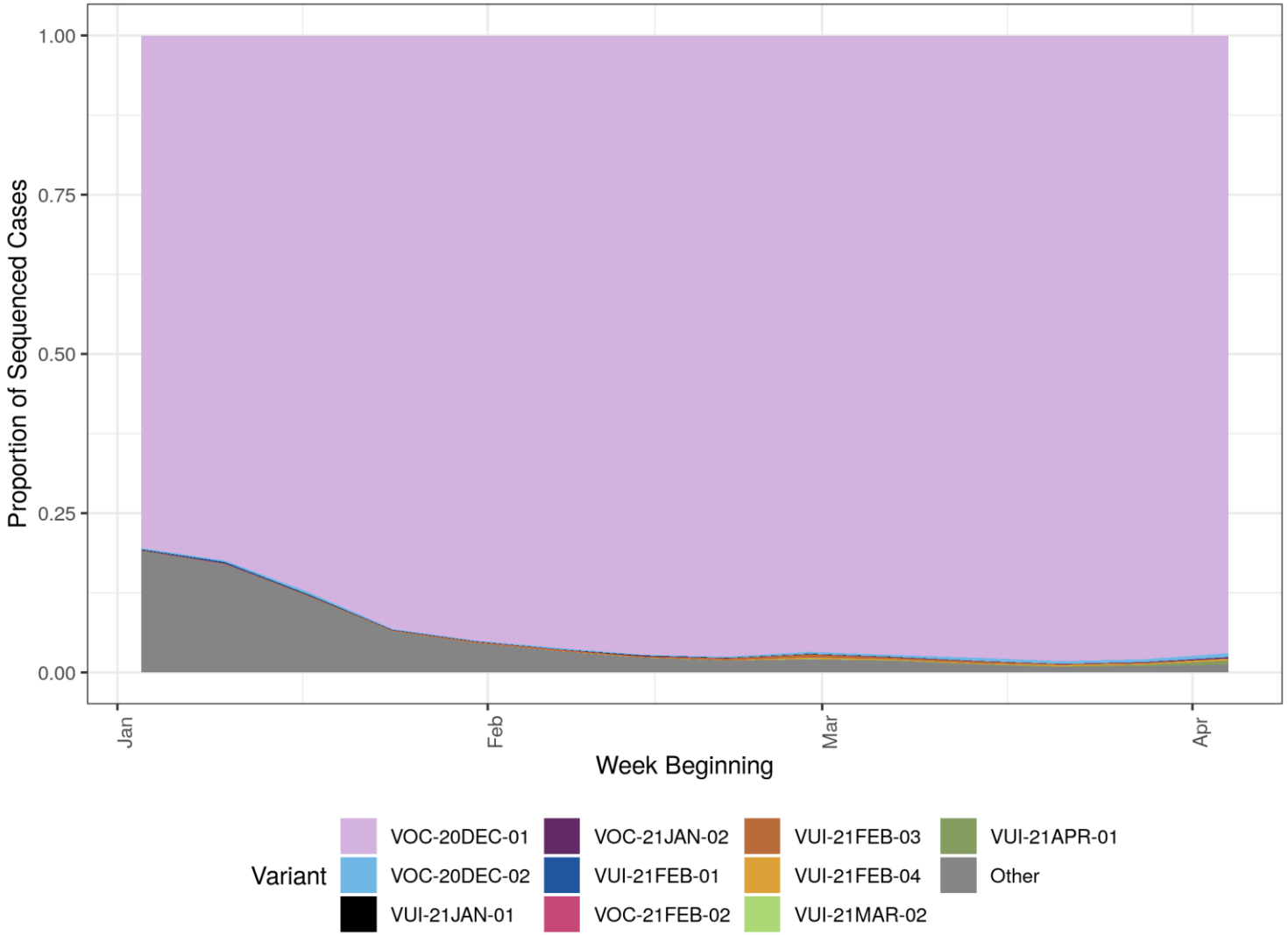
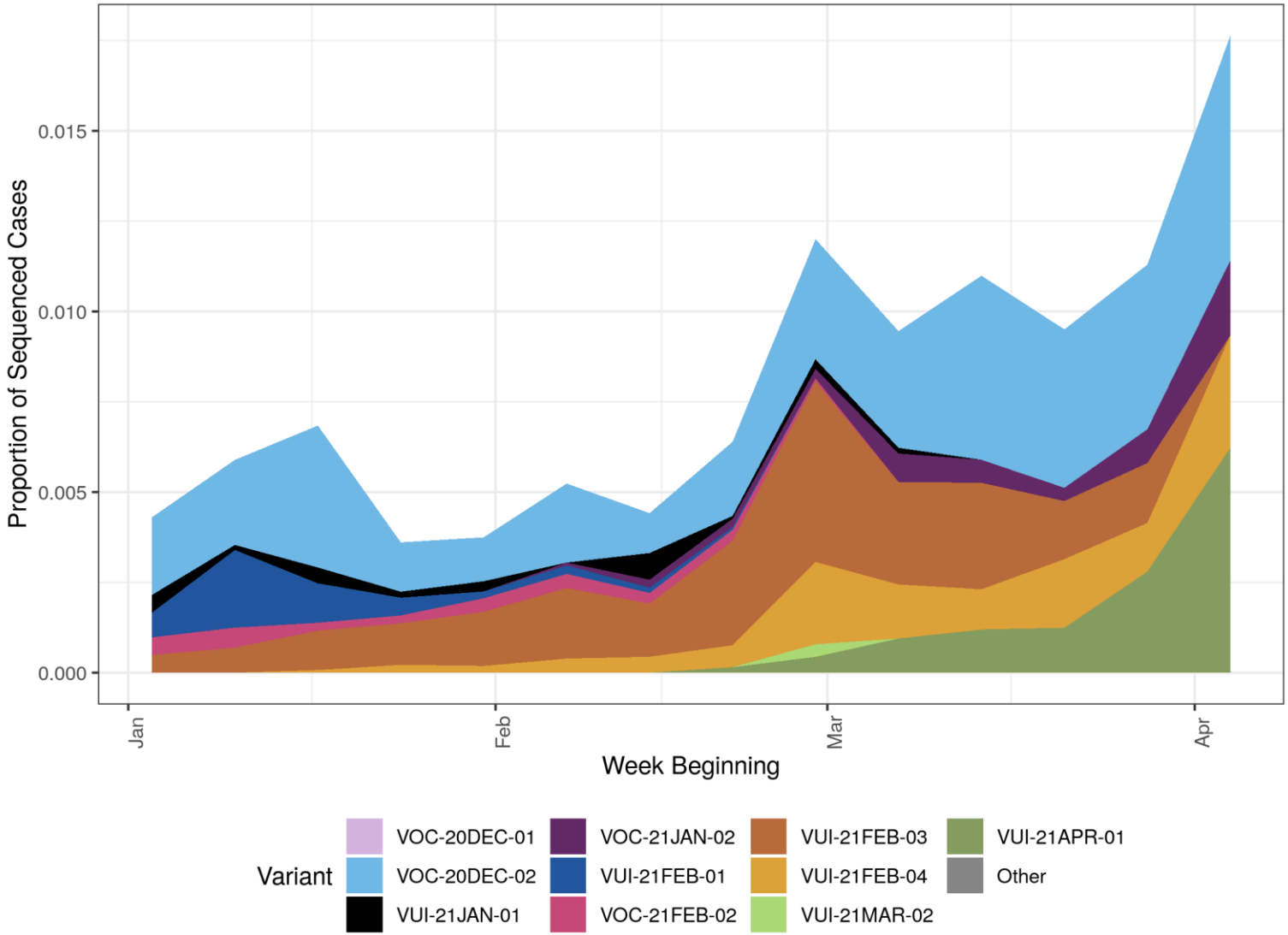


Figure 2. Variant prevalence for all England available case data from 1 February 2021 to 21 April 2021 excluding VOC-20DEC-01 and "Other" (Find accessible data used in this graph in underlying data)



New Variant Under Investigation: VUI-21APR-01 (B.1.617.1)

A variant first detected in sequences from India was designated under investigation on 1 April 2021 as VUI-21APR-01 (B.1.617.1).

Genomic profile

The complete mutation profile of VUI-21APR-01 (B.1.617.1) is shown in Table 2 and genomic case definition in Table 3.

Table 2. Variant defining mutations

Gene	Amino Acid	Actual Nucleotide	Note
orf1ab	-	C3457T	nsp3
	T1567I	C4965T	nsp3:T749I
	T3646A	A11201G	nsp6:T77A
	M5753I	G17523T	nsp13:M429I
	K6711R	A20396G	nsp15:K259R
S Gene	-	T21895C	
	E154K	G22022A	
	L452R	T22917G	
	E484Q	G23012C	
	P681R	C23604G	
ORF3a	S26L	C25469T	
ORF7a	V82A	T27638C	
N Gene	R203M	G28881T	

Table 3. Genomic case definition

CONFIRMED	All variant defining changes called as alternate base
PROBABLE	AT LEAST 5 variant defining changes called as alternate base and all other positions either N or mixed base
LOW_C	Fewer than 5 variant defining changes called as alternate base and all other positions either N or mixed base

Phylogeny

Genomic phylogeny of VUI-21APR-01 (B.1.617.1) and signals in monitoring B.1.617.2 and B.1.617.3 are shown in Figure 3a.

Based on available data from international and UK datasets, the lineage B.1.617 contains 3 clades with different mutation profiles which are:

- B.1.617.1 – includes a large number of sequences and has a spike profile including L452R and E484Q
- B.1.617.2 – has a different profile without E484Q and appears to have recent expansion
- B.1.617.3 – has L452R and E484Q but is distinct from B.1.617.1 and currently remains small

B.1.617.1 is designated VUI-21APR-01 on the basis of the mutation profile and apparent successful transmission and spread. B.1.617.2 with a lesser mutation profile, and B.1.617.3, not clearly spreading rapidly, are under surveillance and not designated as variants under investigation.

Numbers within this briefing are for the designated VUI-21APR-01 (B.1.617.1).

Figure 3b shows the number of sequences of Lineage B.1.1.7 and B.1.617 over time in sequences from individuals that have travelled from India as of 21 April 2021. There is an increase in detected B.1.617 sequences.

Figure 3a. Genomic phylogeny of VUI-21APR-01 (B.1.617.1) and signals in monitoring B.1.617.2 and B.1.617.3 as of 21 April 2021 (Supplementary data is not available for this figure). Sequences from India are shown in yellow, from the UK in blue and from other countries in grey.

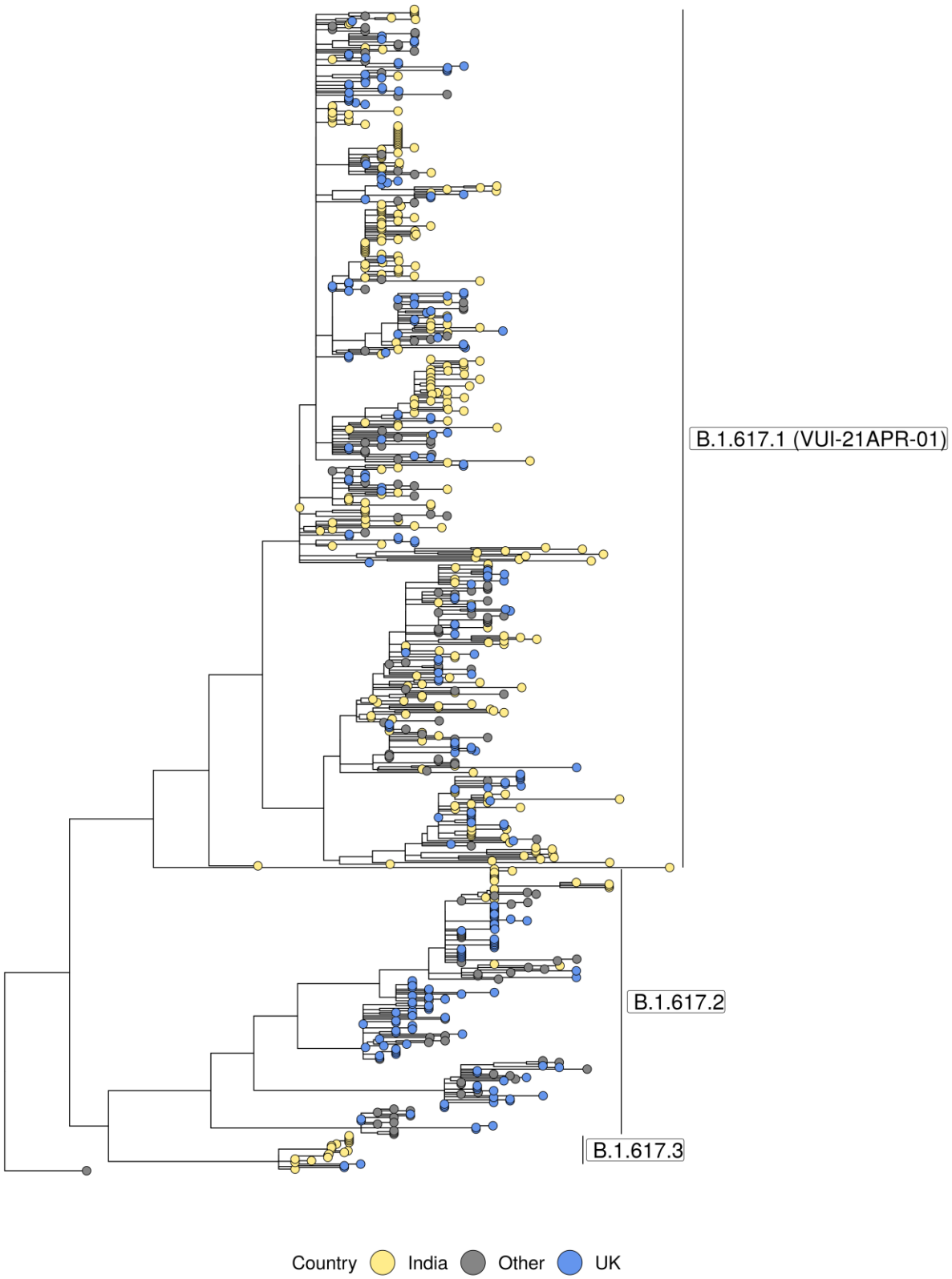
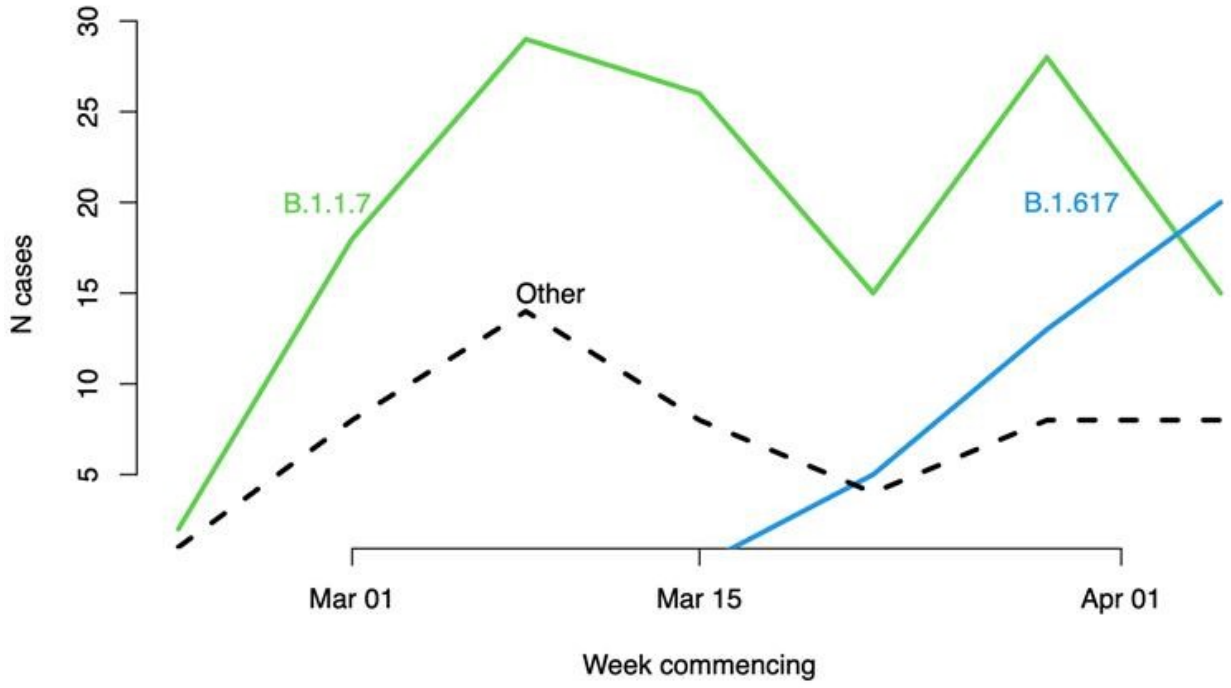


Figure 3b. Number of sequences of Lineage B.1.1.7, and B.1.617 over time in sequences from individuals that have travelled as of 21 April 2021 (Find accessible data used in this graph in underlying data). B.1.1.7 is shown in green, B.1.617 in blue and Other as dashed line.



Biological profile

VUI-21APR-01 (B.1.617.1) contains a number of spike mutations associated with antigenic escape or found in other variants of concern.

Mutations at position 484 are well described as having a large impact on virus antigenicity and are associated with the VOC-20DEC-02 (B.1.351) and VOC-21JAN-02 (P.1) variants, however VUI-21APR-01 contains E484Q rather than the better described E484K. The majority of antigenic escape studies (monoclonal antibody and/or polyclonal sera) that find changes at position 484 implicate E484K, and to a lesser extent E484G/D/A/Y, while E484Q is not seen. The studies where E484Q is routinely implicated, albeit at lower levels than E484K, are deep mutagenesis scanning studies which generally give a much larger variety of results, Unlike E484K, E484Q is not known to be associated with any change in receptor binding avidity.

B.1.617 also contains the mutation L452R which is associated with antigenic escape from both monoclonal antibodies and convalescent antisera, and found in several other variants including signals in monitoring B.1.429 and A.27. L452R is also associated with enhanced receptor binding affinity.

Additionally B.1.617 contains the furin cleavage site mutation P681R, similar to P681H. 681R/H are found in multiple variant lineages, such as VOC-20DEC-01 (B.1.1.7),

VUI-21FEB-04 (B.1.1.318) and VUI-21FEB-01 (A.23.1). Both P681H and P681R have been shown to optimise spike cleavage by furin; it has been hypothesised that this optimisation may enhance virus transmissibility.

VUI-21APR-01 contains several N-terminal domain mutations. G142D is associated with escape from some N-terminal domain targeting monoclonal antibodies but is unclear if this has a large impact on convalescent or vaccine-driven immunity.

Outside the spike gene, VUI-21APR-01 contains a number of mutations across its genome, however none of these mutations are currently associated with any phenotypic change.

Surveillance in England

As of 22 April 2021, 119 genomically confirmed cases of VUI-21APR-01 (B.1.617.1) have been identified in all regions of England; concentrated in the London, North West and East of England regions (Table 4). Number of cases by specimen date are shown in Figure 4, geospatial distribution in Figure 5 and Figure 11, age-sex distribution in Figure 6 and travel association in Figure 7. The supplementary data for figures is available here. Note contact tracing is included in Table 8.

Case detection indicates an increase in imported cases from March 2021. As of 22 April 2021 most cases of VUI-21APR-01 (B.1.617.1) in England occur as single cases with a few localised clusters detected. Only 3 cases in England have been identified without a known travel link, 94 have a link to travel, and 22 cases remain under investigation. No cases are known to have died in England with VUI-21APR-01 (B.1.617.1) as of 22 April 2021.

Cases of signals in monitoring (B.1.617.2 and B.1.617.3) have been noted in sequences from the UK (Figure 3). In addition to 119 VUI-21APR-01 (B.1.617.1) cases, there are 94 sequences from B.1.617.2 and 3 sequences B.1.617.3 detected.

The Amber border measures that remain until 23 April 2021 should limit both VUI-21APR-01 (B.1.617.1) and signals in monitoring (B.1.617.2 and B.1.617.3). Amber border measures require individuals to isolate on arrival to the UK for 10 days at their home address and perform PCR testing on day 2 and day 8. If either testing is positive, then individuals are required to isolate for 10 days from the date of the positive test. From Friday 23 April 2021, all arrivals from India will be required to isolate in managed quarantine facilities with day 2 and day 8 PCR tests. Any individual with a positive PCR test will be required to stay for 10 days from the date of the positive test in the managed quarantine facility.

Re-sampling of all PCR positive entrants from India is underway to provide materials for virological culture work and analysis (for both VUI-21APR-01 (B.1.617.1) and signals in monitoring (B.1.617.2 and B.1.617.3).

International surveillance

As of the 19 April 2021, international cases have been reported in 15 countries (including the UK).

GISAID includes data on sequences available internationally. As of 21 April 2021 284 sequences from; India (188), Singapore (35), USA (21), Australia (8), Bahrain (7), Germany (7), New Zealand (4), South Korea (4), Belgium (3), Ireland (3), Guadeloupe (2), Canada (1), and Sint Maarten (1) have been identified on GISAID.

Table 4. Number of confirmed and probable VUI-21APR-01 (B.1.617.1) cases, by region of residence as of 22 April 2021

Region	Case Number	Case Proportion	Cases that have travelled	Proportion of travellers among cases
East Midlands	8	6.7%	8	100%
East of England	13	10.9%	10	76.9%
London	55	46.2%	37	67.3%
North East	4	3.4%	2	50%
North West	17	14.3%	7	41.2%
South East	10	8.4%	7	70%
South West	2	1.7%	2	100%
West Midlands	3	2.5%	3	100%
Yorkshire and Humber	7	5.9%	4	57.1%

Figure 4. Confirmed and probable VUI-21APR-01 (B.1.617.1) cases by specimen date as of 22 April 2021. Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data)

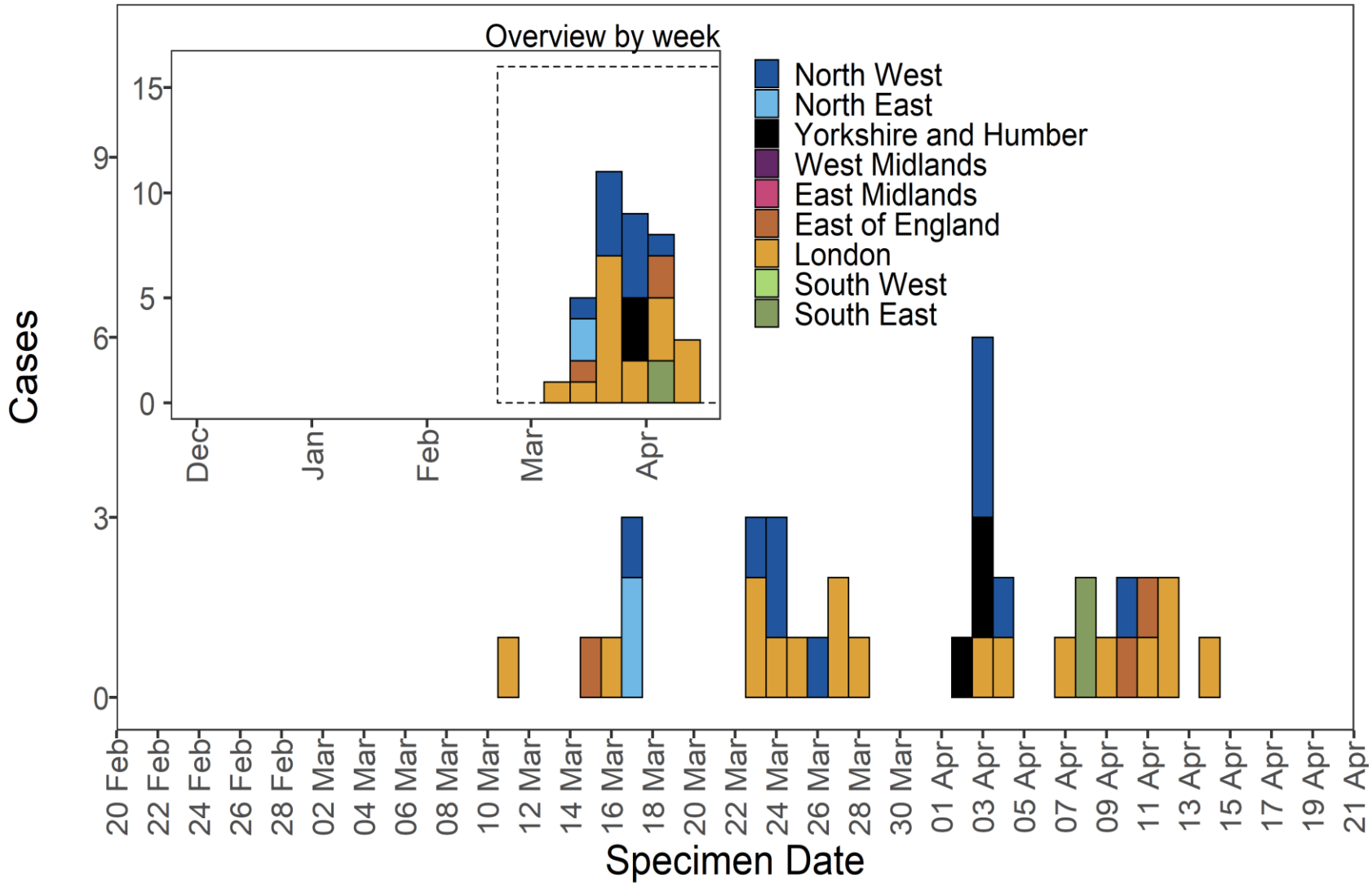


Figure 5. Geospatial distribution of confirmed and probable VUI-21APR-01 (B.1.617.1) cases by specimen date as of 22 April 2021. Larger plot includes last 60 days only. (Supplementary data is not available for this figure)

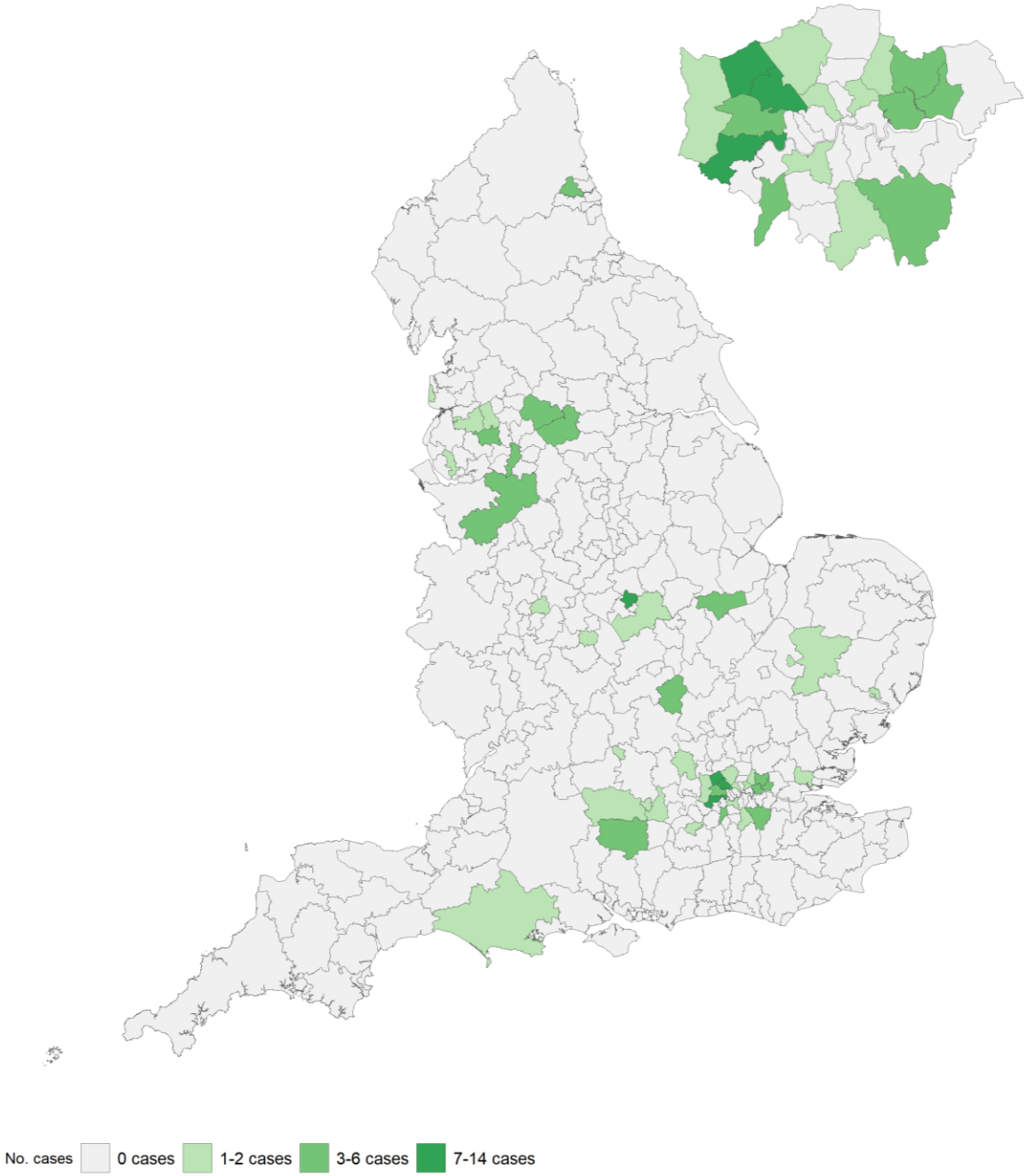
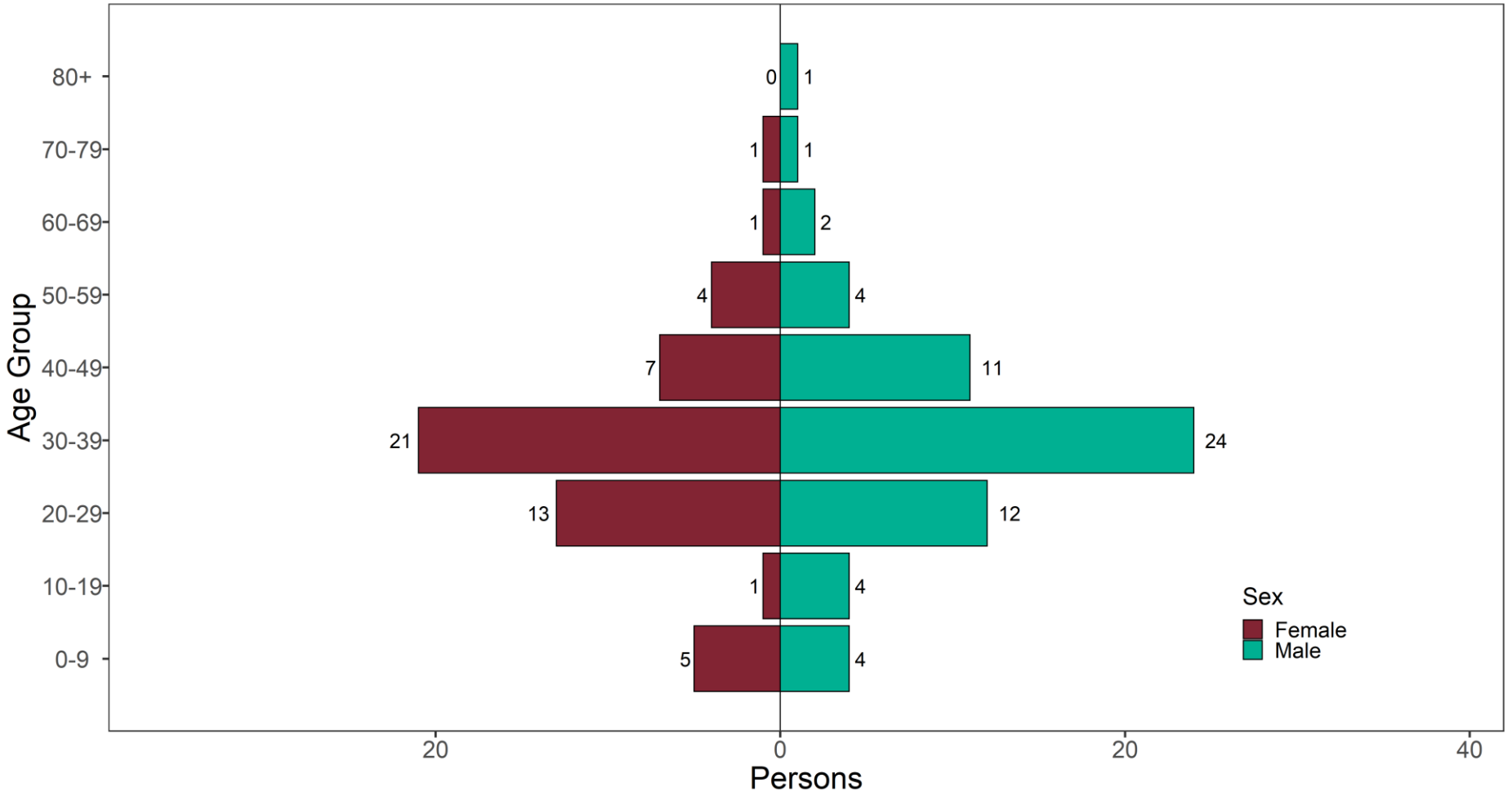
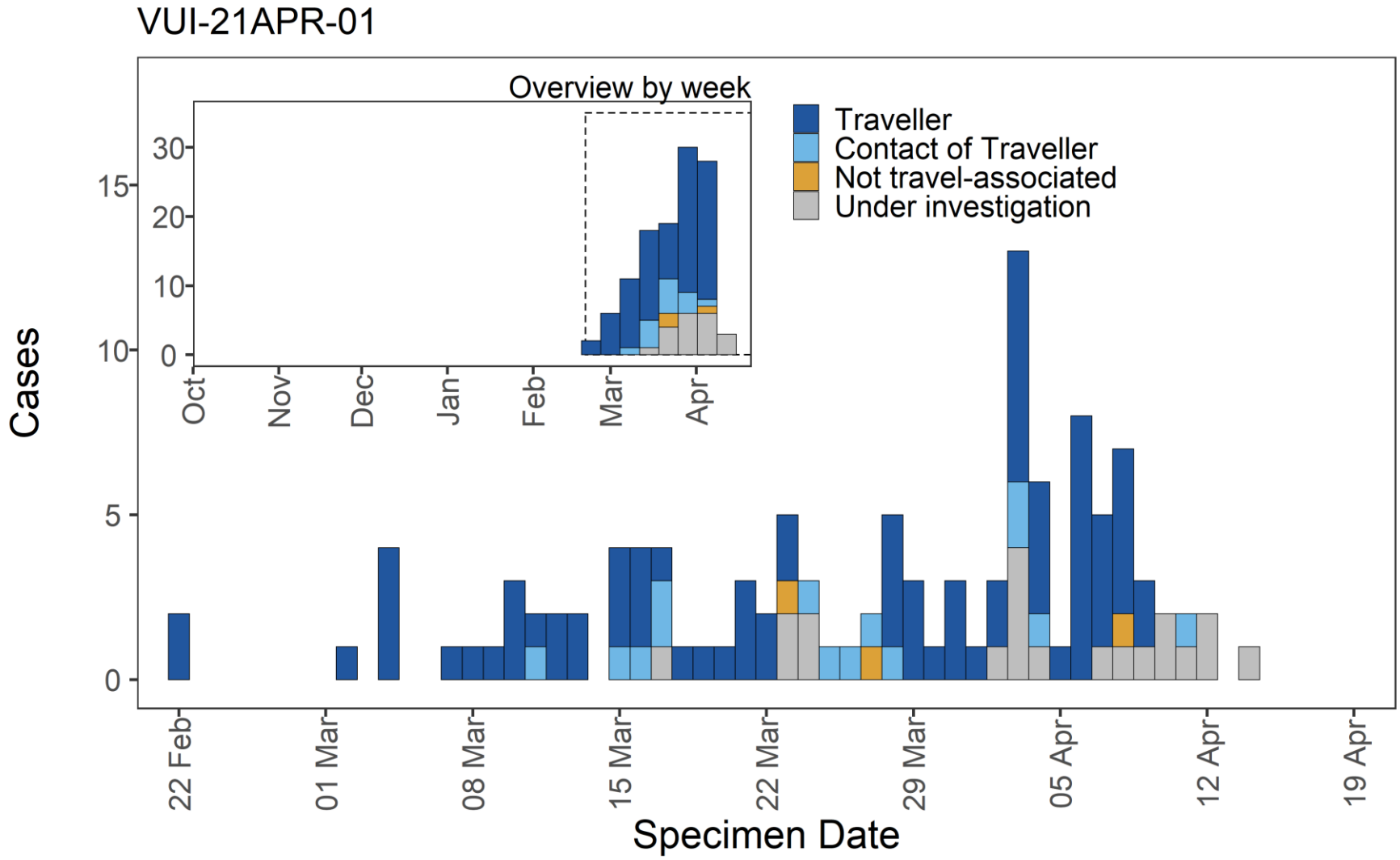


Figure 6. Age-sex distribution of confirmed and probable VUI-21APR-01 (B.1.617.1) cases by specimen date as of 22 April 2021. Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data)



1 cases excluded with missing sex or age data.

Figure 7. Travel data for confirmed and probable VUI-21APR-01 (B.1.617.1) cases by specimen date as of 22 April 2021. Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data). N/A indicates information is pending or not available.



Mutations at position Q498 of SARS-COV-2 spike

Mutations at position Q498 of SARS-CoV-2 spike have been predicted, in combination with N501Y, to greatly enhance human ACE2 binding (Zahradník et al., 2020[1]). It is hypothesised that greatly enhanced ACE2 binding could potentially lead to escape from neutralising antibodies in an 'avidity effect' like that described in influenza, or lead to a virus that was more transmissible or pathogenic. In the study Q498R was the specific substitution described, however it is likely Q498K may have a similar effect based on the similarity between R and K as both are positively charged.

Recently, more changes at position 498 have been identified in GISAID. This may be due to enhanced sequencing but remains under surveillance. As of the 20 April 2021 there were 21,767 sequences on GISAID that did not have the reference codon at position 498. The majority of sequences contained either a missing base, an unresolved base or a nucleotide change that did not change the amino acid. There were a total of 26 sequences with an alternate amino acid coded at position 498 of which 12 were sequences derived from viral infection of humans. These 12 sequences were assessed by Pangolin lineage and for mutations at positions 498, 484 and 501 (Table 5).

Table 5. Q498R and other changes at position 498 identified in GISAID

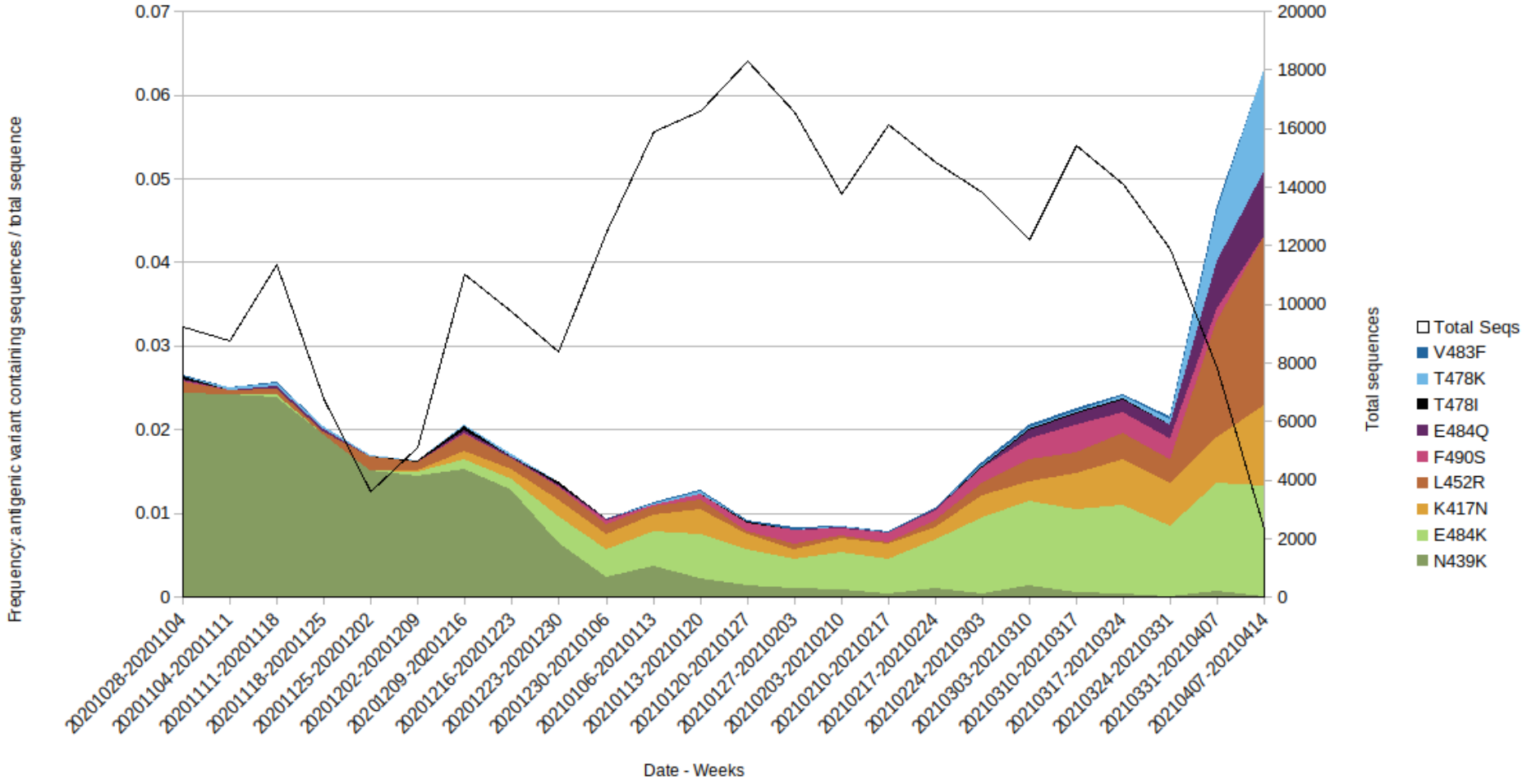
Lineage	Country	Date	Reference sequence NC045512 Amino Acid	Detected 498 mutation Amino Acid	501 Variant	484 Variant
B.1.1.144	Switzerland	2020-09-09	Q (glutamine)	Z (glutamine or glutamic acid)		
B.1.1.222	USA	2021-02-26	Q (glutamine)	H (histidine)		
B.1.1.7	Ireland	2021-02-02	Q (glutamine)	K (lysine)	Y (tyrosine)	
B.1.1.7	USA	2021-03-12	Q (glutamine)	K (lysine)	Y (tyrosine)	
B.1.1.7	USA	2021-02-24	Q (glutamine)	H (histidine)	Y (tyrosine)	
B.1.240	USA	2021-03-16	Q (glutamine)	R (arginine)		
B.1.240	USA	2021-03-04	Q (glutamine)	R (arginine)		
B.1.240		2021-03-10	Q (glutamine)	R (arginine)		
B.1.429	USA	2021-02-09	Q (glutamine)	H (histidine)		
B.1.429	USA	2021-03-25	Q (glutamine)	R (arginine)		
B.1.608	USA	2021-03-09	Q (glutamine)	L (leucine)	Y (tyrosine)	
None	Iran	2020-02-24	Q (glutamine)	P (proline)		

[1] SARS-CoV-2 RBD in vitro evolution follows contagious mutation spread, yet generates an able infection inhibitor

Antigenic change mutation monitoring

Mutations potentially associated with antigenic change are monitored as part of horizon scanning. Figure 8 shows the proportion of these mutations over time in the all England genomic dataset, illustrating the decline of N439K and an increase in E484K. Only those mutations which were present at a count of > 50 within the 6 month time frame are shown. The supplementary data for figures is available.

Figure 8. Proportion of mutations conferring antigenic change over time from 28 October 2020 to 21 April 2021
(Find accessible data used in this graph in underlying data). Note sequencing data from the past 10 days is incomplete



Case numbers, proportion, deaths and case fatality rate

The number of cases of variants of concern and variant under investigation are shown in Table 6. including the proportion of variant cases compared to all sequenced cases, deaths and case fatality rate.

Table 6. Case number, proportion, death and case fatality rate of variants of concern and variant under investigation from 1 October 2020 to 22 April 2021

Variant	Case Number[a]	Case Proportion[b]	Deaths[c]	Case Fatality (95%CI)[d]
VOC-20DEC-01	185,216	99.243%	3,846	2.1% (2.0 - 2.1%)
VOC-20DEC-02	592	0.317%	10	1.7% (0.8 - 3.1%)
VOC-21JAN-02	51	0.027%	0	0.0% (0.0 - 7.0%)
VOC-21FEB-02	43	0.023%	1	2.3% (0.1 - 12.3%)
VUI-21JAN-01	53	0.028%	1	1.9% (0.0 - 10.1%)
VUI-21FEB-01	79	0.042%	1	1.3% (0.0 - 6.9%)
VUI-21FEB-03	334	0.179%	12	3.6% (1.9 - 6.2%)
VUI-21FEB-04	135	0.072%	0	0.0% (0.0 - 2.7%)
VUI-21APR-01	119	0.064%	0	0.0% (0.0 - 3.1%)

Excludes variant cases not linked to a known COVID-19 case.
[a]Case number England genomic cases 22 April 2021.
[b]Proportion of sequences UK/England as of 22 April 2021.
[c]Deaths As of 22 April 2021 (within 28 days) with confirmed or probable VOC or total cases.
[d]95% Confidence Intervals calculated with Clopper–Pearson exact method, using R package PropCIs.

Enhanced investigations

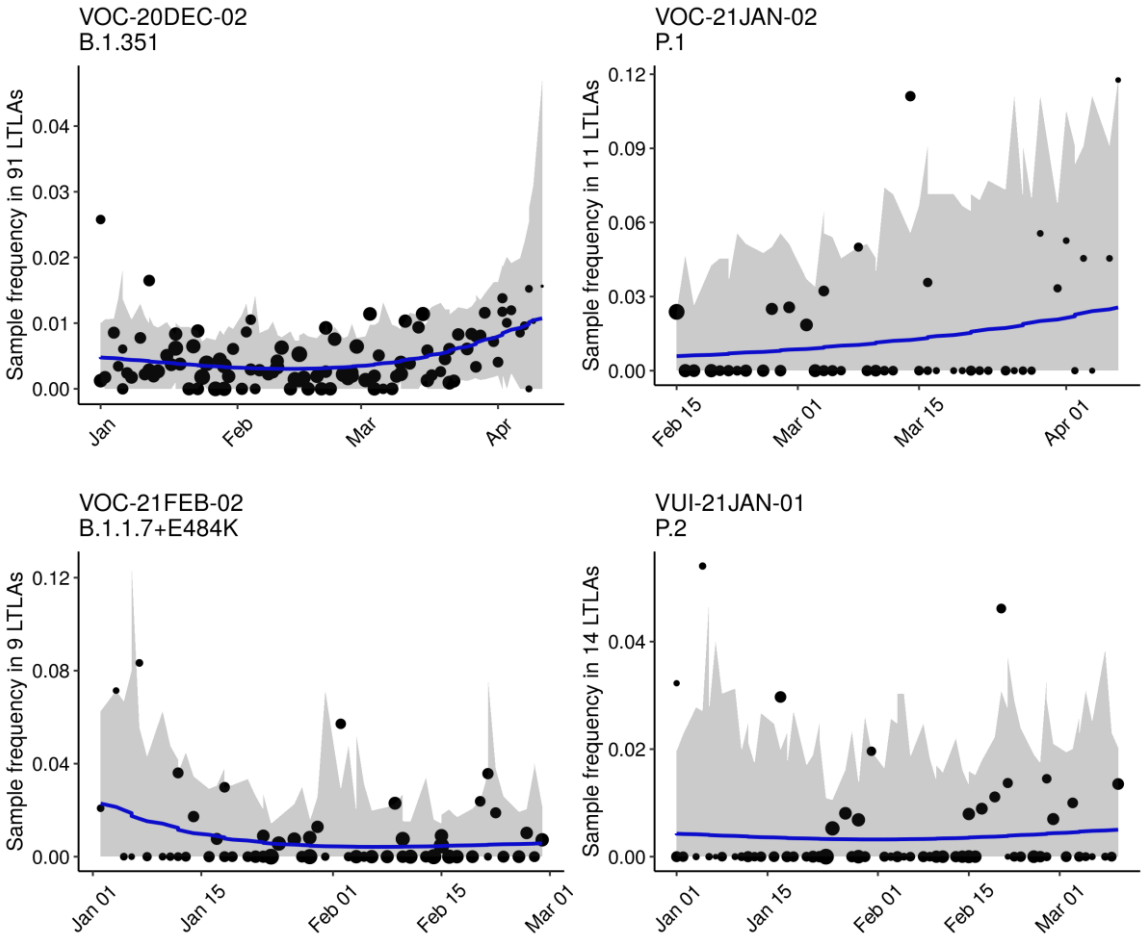
Growth rates

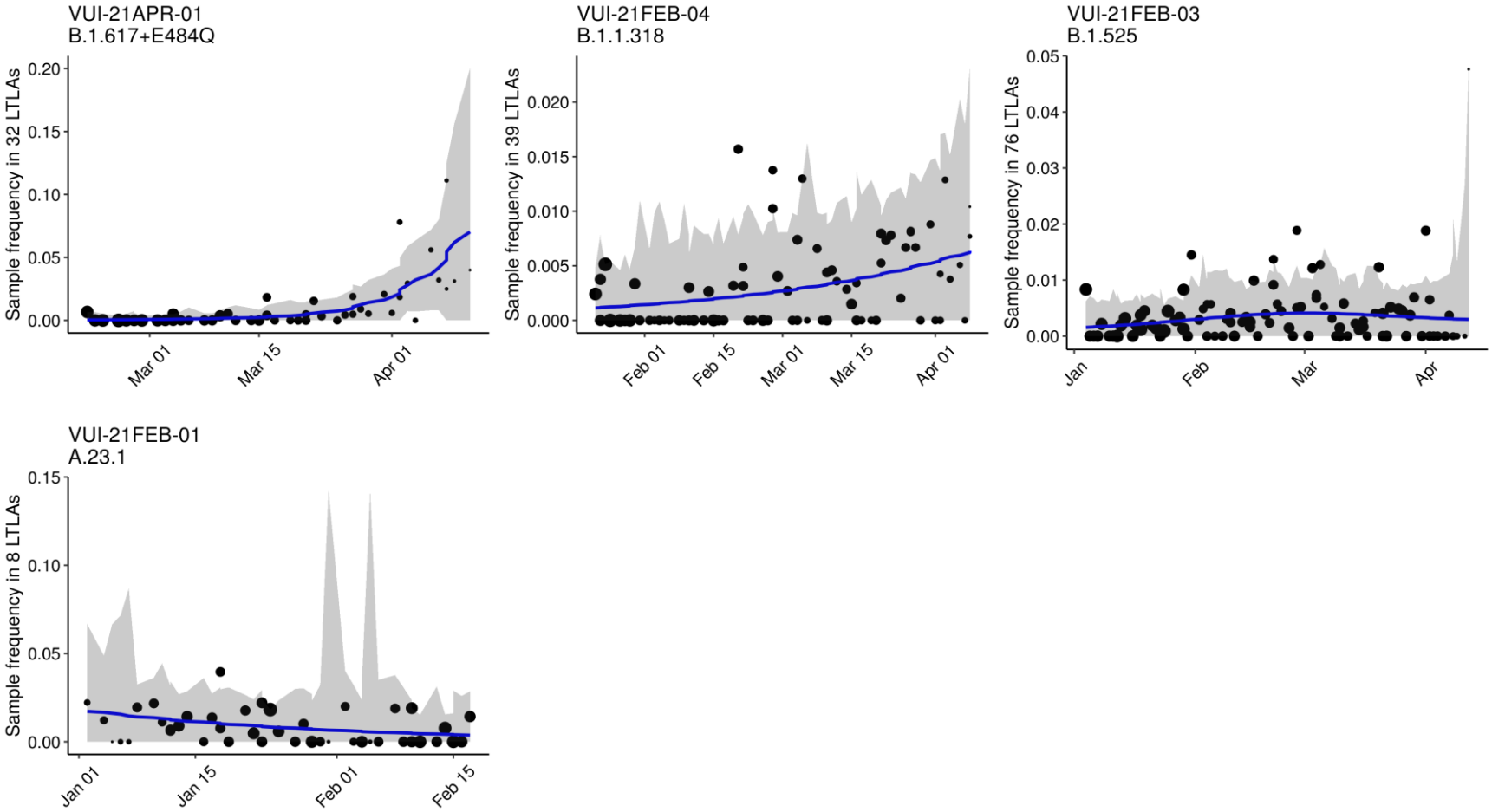
The growth rate estimates from a logistic growth model for variants of concern and variants under investigation (with sufficient numbers of cases) are shown in Table 8 and Figure 9 . Growth rates for each VUI or VOC are computed relative to a B.1.1.7 baseline and based on 2 sample sets. Set 1: Sequences randomly selected from Pillar 2 testing. Set 2: As Set 1 which further excludes surge testing and recently-returned travellers. Table 7 and Figure 9 shows Set 1 data, that the variants with significant positive growth rates compared to other circulating lineages in the same area are VUI-21APR-01 (B.1.617.1) and VUI-21FEB-04 (B.1.1.318). This version is updated to use PHE variant definitions. The supplementary data for figures is available.

Table 7. Growth rate of variants of concern and variants under investigation 1 January 2021 as of 20 April 2021

Variant	Lineage	Growth rate (1/week) Set 1	Growth rate (1/week) Set 2
VOC-20DEC-02	B.1.351	0.076 (n=250,p=9.139e-06)	0.056 (n=141, p=0.014)
VOC-21JAN-02	P.1	0.27 (n=19, p=0.035)	0.17 (n=9,p=0.34)
VOC-21FEB-02	B.1.1.7 with E484K	-0.16 (n=33,p=0.06)	-0.23 (n=28, p=0.032)
VUI-21JAN-01	P.2	0.034 (n=22,p=0.70)	0.044 (n=22,p=0.62)
VUI-21FEB-01	A.23.1 with E484K	-0.19 (n=43,p=0.077)	-0.25 (n=46, p=0.022)
VUI-21FEB-03	B.1.525	0.051 (n=142,p=0.039)	0.0063 (n=77, p=0.84)
VUI-21FEB-04	B.1.1.318	0.16 (n=79,p=0.0001)	0.23 (n=54, p=4.65e-05)
VUI-21APR-01	B.1.617.1	0.81 (n=68, p=1.217e-12)	0.51 (n=21, p=0.006)

Figure 9. Growth estimates of variants of concern and under investigation as of 21 April 2021 (set 1 data)
(Find accessible data used in this graph in underlying data)




VUI-21APR-01
B.1.617+E484Q
Sample frequency in 32 LTLAs
0.20
0.15
0.10
0.05
0.00
Mar 01
Mar 15
Apr 01
VUI-21FEB-04
B.1.1.318
Sample frequency in 39 LTLAs
0.020
0.015
0.010
0.005
0.000
Feb 01
Feb 15
Mar 01
Mar 15
Apr 01
VUI-21FEB-03
B.1.525
Sample frequency in 76 LTLAs
0.05
0.04
0.03
0.02
0.01
0.00
Jan
Feb
Mar
Apr
VUI-21FEB-01
A.23.1
Sample frequency in 8 LTLAs
0.15
0.10
0.05
0.00
Jan 01
Jan 15
Feb 01
Feb 15

Secondary attack rates

Secondary attack rates are shown in Table 8. These are based on positive tests amongst contacts named to NHS Test and Trace by an original case identified with a confirmed or probable variant of concern or variant under investigation.

Secondary attack rates are shown for cases with and without travel history. In non-travel settings, only close contacts (household members, face to face contact, people within 1 metre of the case for 1 minute or longer, or people within 2 metres for 15 minutes) named by the original case are included. In travel settings the contacts reported are not restricted to only close contacts named by the case (for example, they may include contacts on a plane linked by additional contact tracing efforts), leading to likely deflation of secondary attack rates amongst travellers compared to non-travellers. In addition, people recently returning from overseas are subject to stricter quarantine measures and may moderate their behaviour towards contacts. Travel history indicates, but does not confirm, where infection of the original case occurred.

Secondary attack rates for contacts of non-travel cases with variants of concern or under investigation except VOC-21FEB-02 are not significantly different from that for contacts of non-travel cases with VOC-20DEC-01. No transmission events were identified to contacts of cases with VOC-21FEB-02. Estimates of secondary attack rates for contacts of those that have travelled with variants of concern or variants under investigation were all considerably lower than those that have not travelled.

Table 8. Case numbers and travel status including proportion and secondary attack rate for 5 January 2021 to 28 March 2021, data as of 20 April 2021

Variant	Lineage	Cases in those that have travelled	Cases in those that have not travelled or unknown	Case proportion that have travelled	Secondary Attack Rate among contacts of those that have travelled (95% CI) [secondary cases/contacts]	Secondary Attack Rate among contacts of cases that have not travelled or unknown (95% CI) [secondary cases/contacts]
VOC-20DEC-01	B.1.1.7	2220 (81.6% with contacts)	136936 (73.4% with contacts)	1.6%	1.7% (1.6% - 1.9%) [702/40371]	10.3% (10.2% - 10.5%) [28345/273897]
VOC-20DEC-02	B.1.351	197 (71.6% with contacts)	180 (61.7% with contacts)	52.3%	2.5% (2.0% - 3.1%) [76/3075]	8.9% (6.2% - 12.6%) [27/305]
VOC-21JAN-02	P.1	25 (80.0% with contacts)	7 (71.4% with contacts)	78.1%	1.2% (0.4% - 3.6%) [3/242]	Unavailable [1/9]
VOC-21FEB-02	B.1.1.7 with E484K	1 (100.0% with contacts)	33 (81.8% with contacts)	2.9%	Unavailable [0/96]	0.0% (0.0% - 3.3%) [0/111]
VUI-21JAN-01	P.2	3 (66.7% with contacts)	31 (77.4% with contacts)	8.8%	Unavailable [0/137]	10.8% (5.3% - 20.6%) [7/65]
VUI-21FEB-01	A.23.1 with E484K	0 (0% with contacts)	63 (60.3% with contacts)	0.0%	Unavailable [0/0]	8.6% (4.4% - 16.1%) [8/93]
VUI-21FEB-03	B.1.525	138 (71.0% with contacts)	139 (71.9% with contacts)	49.8%	1.3% (0.9% - 1.8%) [36/2805]	9.2% (6.2% - 13.5%) [23/249]
VUI-21FEB-04	B.1.1.318	32 (75.0% with contacts)	71 (73.2% with contacts)	31.1%	0.9% (0.5% - 1.6%) [11/1,214]	7.8% (4.4% - 13.4%) [11/141]

Variant	Lineage	Cases in those that have travelled	Cases in those that have not travelled or unknown	Case proportion that have travelled	Secondary Attack Rate among contacts of those that have travelled (95% CI) [secondary cases/contacts]	Secondary Attack Rate among contacts of cases that have not travelled or unknown (95% CI) [secondary cases/contacts]
VUI-21MAR-01	B.1.324.1 with E484K	1 (100.0% with contacts)	0 (0% with contacts)	100.0%	Unavailable [0/7]	Unavailable [0/0]
VUI-21MAR-02	P.3	4 (50.0% with contacts)	1 (100.0% with contacts)	80.0%	Unavailable [0/10]	Unavailable [0/3]
VUI-21APR-01	B.1.617.1	42 (83.3% with contacts)	14 (71.4% with contacts)	75.0%	1.4% (0.9% - 2.2%) [17/1,210]	Unavailable [1/29]

Secondary attack rates are marked as ‘Unavailable’ when count of contacts is less than 50 or count of exposing cases is less than 20. Travel-linked cases for secondary attack rates are identified positively in NHS Test and Trace data using multiple PHE sources. A case is considered as being travel-linked if:

- EpiCell or Health Protection Teams have found evidence of international travel
- their NHS Test and Trace record mentions an event associated with international travel
- their NHS Test and Trace record was created after notification via IHR NFP
- they have been marked for priority contact tracing in NHS Test and Trace for reasons of travel

Some travel-linked cases may be missed by these methods and would be marked as non-travel-linked or unknown. Secondary attack rates from NHS Test and Trace should generally be considered lower bounds due to the nature of contact tracing and testing. Data provided is for period 5 January 2021 to 28 March 2021 in order to allow time for contacts to become cases, hence case counts are lower than other sources.

Spatial variation in risk for variants

Spatial variation in risk

The spatial risk surface is estimated by comparing the smoothed intensity of cases (variants of concern) and controls (PCR +ve, non-variants of concern) across a defined geographical area to produce an intensity (or risk) ratio. If the ratio is ~1, this suggests that the risk of infection is unrelated to spatial location. Evidence of spatial variation in risk occurs where the intensities differ. Ratio values >1 indicate an increased risk and values <1 indicate lower risk. Figure 10 highlights areas of significantly increased risks for variants of concern, areas of significantly increased risk were identified for all variants of concern other than VOC-21JAN-02 (P.1). Supplementary data is not available for this figure. Figure 11 highlights areas of significantly increased risks for variants under investigation, areas of significantly increased risk were identified for multiple variants under investigation. Supplementary data is not available for this figure.

Figure 10. Spatial variation in risk for VOC data from 1 October 2020, as of 22 April 2021, excluding cases that have travelled. Supplementary data is not available for this figure) (Note data for VUI-21APR-01 is detailed in Figure 5 above).

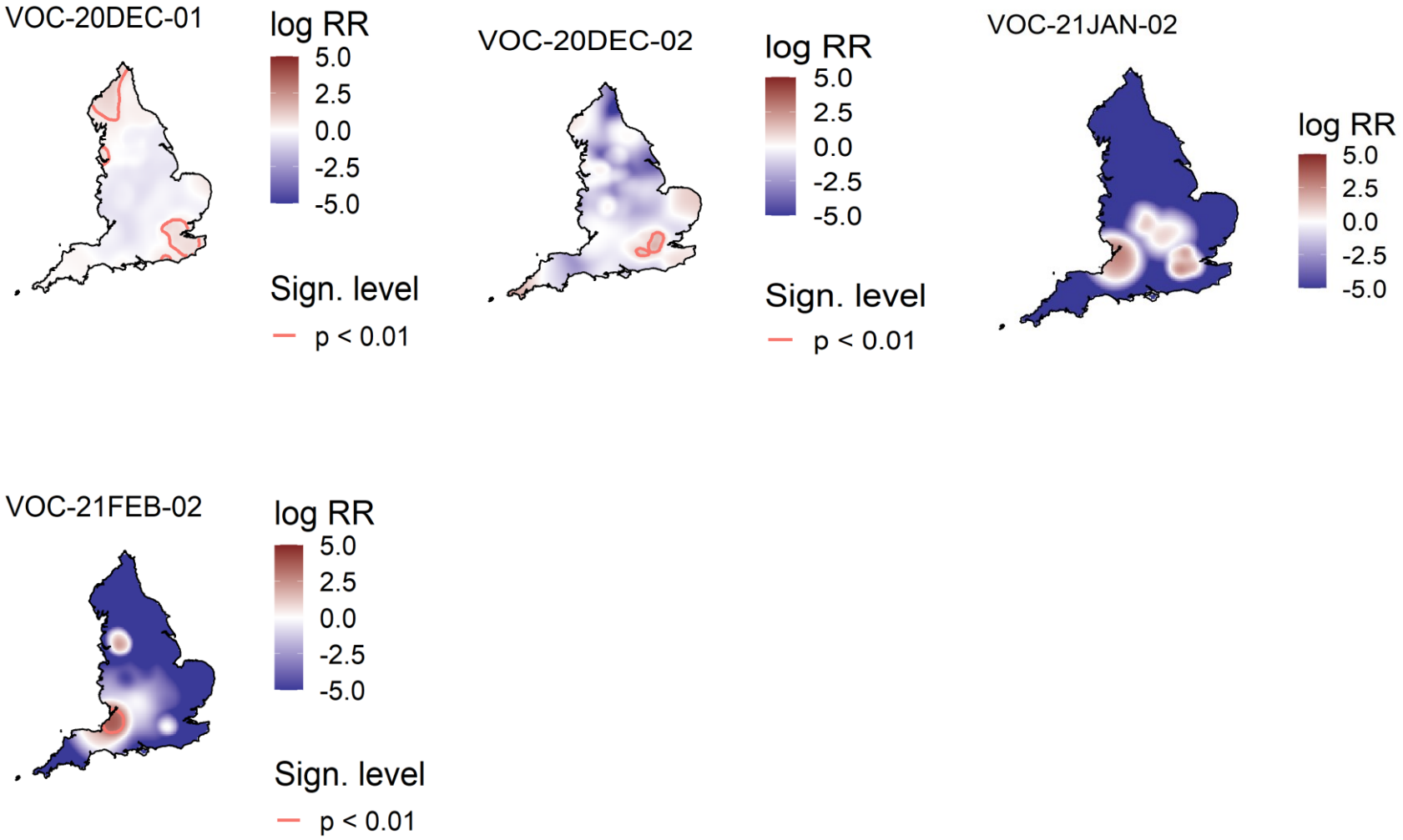
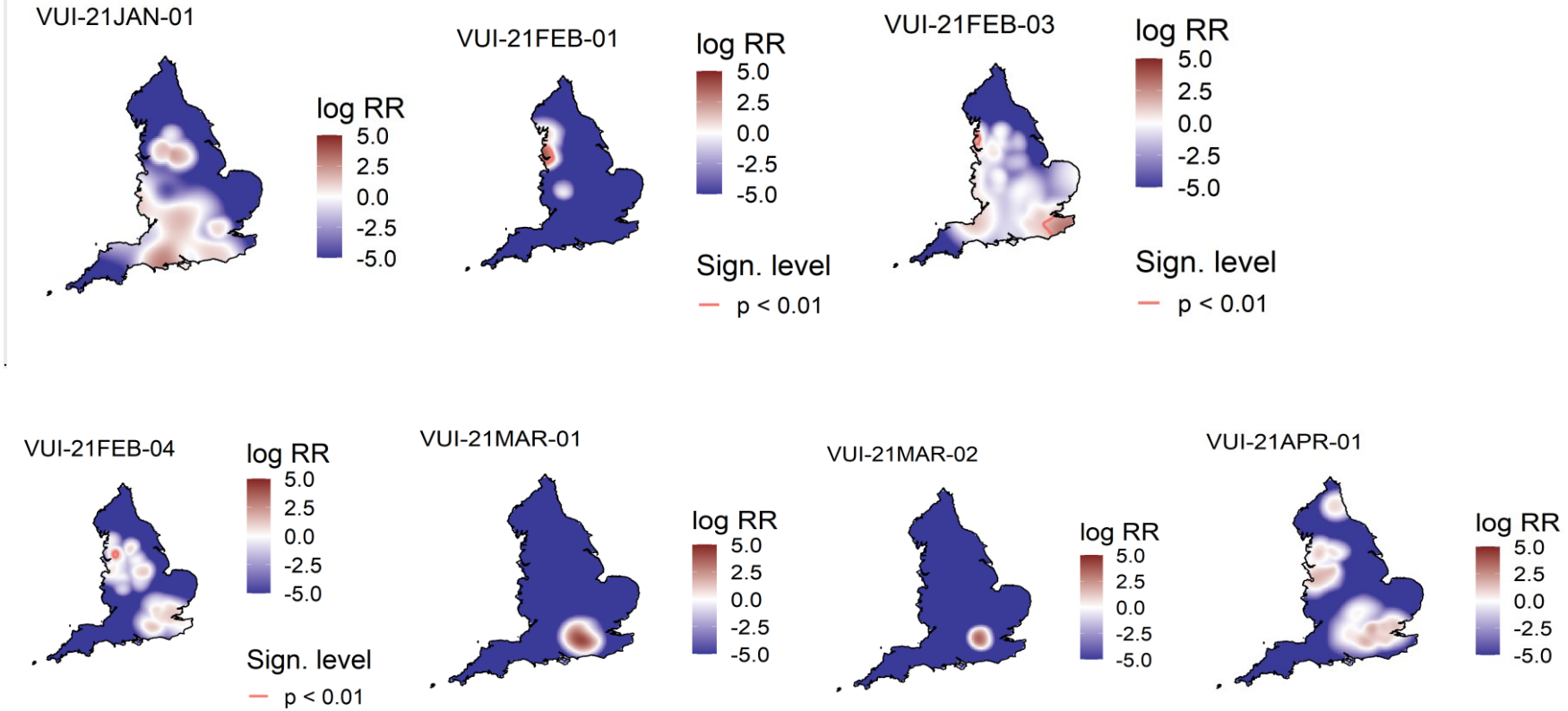


Figure 11. Spatial variation in risk for VUI data from 1 October 2020, as of 22 April 2021, excluding cases that have travelled (Supplementary data is not available for this figure)



Appendices

Appendix 1. Variant assessment tools

Repository of human and machine readable genomic case definitions

A repository containing the up-to-date genomic definitions for all VOC and VUI as curated by Public Health England was created 5 March 2021. The repository can be accessed on GitHub. They are provided in order to facilitate standardised VOC and VUI calling across sequencing sites and bioinformatics pipelines and are the same definitions used internally at Public Health England. Definition files are provided in YAML format so are compatible with a range of computational platforms. The repository will be regularly updated. The genomic and biological profiles of VOC and VUI are also detailed on first description in prior technical briefings.

Variant risk assessment framework

Variant risk assessment includes the following confidence grading categorisations and utilises the framework in Table 9.

1. Low: Little or poor-quality evidence, uncertainty or conflicting views amongst experts, no experience with previous similar incidents.
2. Moderate: Adequate quality evidence, including consistent results published only in grey literature, reliable source(s), assumptions made on analogy and agreement between experts or opinion of at least 2 trusted experts.
3. High: Good quality evidence, multiple reliable sources, verified, expert opinion concurs, experience of previous similar incidents.

Table 9. Variant risk assessment framework

Indicator	Risk assessment framework			
Zoonotic emergence and transmission to humans	Animal reservoir identified but no evidence of transmission from animals to humans	Sporadic transmission from animals to humans	Frequent transmission from animals to humans	
Transmissibility between humans	No demonstrated person to person transmission	Limited human case clusters	Established human to human transmission, which appears similar to wild type virus	Transmissibility appears greater than the wild type virus
Infection severity	Evidence of less severe clinical picture or lower infection fatality than from wild type SARS-CoV-2 infections	Similar clinical picture and infection fatality to wild type SARS-CoV-2 infections OR experimental animal data suggesting potential for increased disease severity humans	More severe clinical picture or higher infection fatality than from wild type SARS-CoV-2 infections (limited to specific risk groups)	More severe clinical picture or higher infection fatality than from wild type SARS-CoV-2 infections
Susceptibility and immunity – natural infection	Evidence of no antigenic difference from other circulating wild type virus	Structural data suggesting antigenic difference from other circulating wild type virus	Experimental evidence of functional evasion of naturally acquired immunity	Evidence of frequent infection in humans with known prior infection with earlier virus variant.

Indicator	Risk assessment framework			
Vaccines	Evidence of no structural or antigenic difference in vaccine targets	Structural data suggesting difference in vaccine target epitopes	Experimental evidence of functional evasion of vaccine derived immunity	Evidence of frequent vaccine failure or decreased effectiveness in humans
Drugs and therapeutics	Evidence of no structural or antigenic difference in therapeutic targets	Structural data suggesting difference in therapeutic target epitopes	Experimental evidence of reduced drug susceptibility	Evidence of frequent drug or therapeutic failure or decreased effectiveness in humans

Appendix 2. Data on individual variants

VOC-20DEC-01 (B.1.1.7)

This variant was designated VUI 202012/01 (B.1.1.7) on detection and on review re-designated as VOC-20DEC-01 (202012/01, B.1.1.7) on 18 December 2020. The clinical risk assessment for VOC-20DEC-01 (B.1.1.7) is shown in Table 10.

Table 10. Risk assessment for VOC-20DEC-01 (B.1.1.7)

Indicator	RAG*	Confidence	Assessment and rationale
Zoonotic emergence		NA	There is no evidence that VOC-20DEC-01 (B.1.1.7) emerged from a zoonotic source. Reports of infection with VOC-20DEC-01 (B.1.1.7) in companion animals are noted.
Transmissibility between human		HIGH	**Transmissibility appears greater than the wild type (first wave) virus.** The lineage rapidly became dominant in the UK and spread internationally. Epidemiological and genomic modelling in multiple studies and countries, and secondary attack rate studies using contact tracing data in the UK, support increased transmissibility.
Infection severity		MODERATE	**More severe clinical picture or higher infection fatality than from wild type (first wave) SARS-CoV-2 infections.** Multiple studies have now been undertaken. Although there are varying results from individual cohorts, the larger cohorts indicate an association with more severe disease (represented by either hospitalisation or death), compared to infection with non B.1.1.7 viruses.
Naturally acquired immunity		MODERATE	**Evidence of no increase in reinfection rate.** Although there is laboratory evidence supporting some antigenic distance between VOC-20DEC-01 (B.1.1.7) and older virus, with small reductions in the neutralising activity of convalescent plasma in some studies, there was no increase in reinfections in a large cohort study during the time that VOC-20DEC-01 (B.1.1.7) became prevalent in the UK. Antigenic distance may be affected by the acquisition of further mutations in this lineage.

Indicator	RAG*	Confidence	Assessment and rationale
Vaccine derived immunity		HIGH	**Evidence that vaccine performance is preserved**. Although there is laboratory evidence supporting some antigenic distance between VOC-20DEC-01 (B.1.1.7) and older virus, including small reductions in the neutralising activity of vaccinee sera, vaccine efficacy has been shown to be similar against VOC-20DEC-01 (B.1.1.7) compared to non B.1.1.7 lineages, in more than one study and with more than one vaccine. Antigenic distance may be affected by the acquisition of further mutations in this lineage.
Drugs and Therapeutics			The drugs and therapeutics risk assessment is under revision.
Overall assessment of level and nature of risk, and level of confidence			VOC-20DEC-01 (B.1.1.7) remains the predominant virus in the UK. There is strong supporting UK and international evidence for increased transmissibility, and accumulating evidence on increased severity, but limited understanding of the biological mechanisms underlying these characteristics. There is a growing body of evidence suggesting the limited changes in susceptibility to polyclonal sera observed in vitro do not translate to substantial changes in either reinfection or vaccine efficacy. Continued worldwide transmission of VOC-20DEC-01 (B.1.1.7) is allowing it to acquire further mutations but at present none predominate sufficiently to change the risk assessment.

Genomic profile

Lineage defining mutations are shown in technical briefing 6. In addition, VOC-20DEC-01 has acquired other mutations in some cases (Table 11).

Table 11. VOC-20DEC-01 (B.1.1.7) Spike mutations acquired in addition to the variant defining mutations 21 January 2021 to 20 April 2021

Percentages are the proportion of all sequences of VOC-20DEC-01 (B.1.1.7) per time period with the mutation.

VOC-20DEC-01 (B.1.1.7) Spike variants				
Amino acid change	Total number of instances in VOC-20DEC-01 (B.1.1.7) (UK data) to 20 April 2021	21 January 2021 to 20 February 2021	21 February 2021 to 20 March 2021	21 March 2021 to 20 April 2021
L18F	5,789 (2.43%)	1,383 (1.96%)	931 (1.67%)	506 (1.62%)
Q677H	1,915 (0.8%)	467 (0.66%)	760 (1.37%)	351 (1.13%)
P384L	388 (0.16%)	74 (0.11%)	164 (0.29%)	105 (0.34%)
A701V	456 (0.19%)	35 (0.05%)	122 (0.22%)	71 (0.23%)
F490S	320 (0.13%)	78 (0.11%)	130 (0.23%)	60 (0.19%)
S255F	154 (0.06%)	35 (0.05%)	32 (0.06%)	47 (0.15%)
P9L	125 (0.05%)	25 (0.04%)	43 (0.08%)	40 (0.13%)
K458N	66 (0.03%)	0 (0%)	24 (0.04%)	34 (0.11%)
S494P	895 (0.38%)	313 (0.44%)	98 (0.18%)	30 (0.1%)
P384S	339 (0.14%)	26 (0.04%)	21 (0.04%)	29 (0.09%)
A684T	40 (0.02%)	4 (0.01%)	3 (0.01%)	27 (0.09%)
E484K	124 (0.05%)	36 (0.05%)	24 (0.04%)	26 (0.08%)
S12P	55 (0.02%)	5 (0.01%)	18 (0.03%)	25 (0.08%)
L455F	105 (0.04%)	32 (0.05%)	35 (0.06%)	21 (0.07%)
G476S	69 (0.03%)	6 (0.01%)	40 (0.07%)	16 (0.05%)
Q677R	39 (0.02%)	6 (0.01%)	11 (0.02%)	16 (0.05%)
K147E	23 (0.01%)	0 (0%)	2 (0%)	15 (0.05%)
A684S	35 (0.01%)	1 (0%)	13 (0.02%)	11 (0.04%)
P9S	99 (0.04%)	35 (0.05%)	29 (0.05%)	11 (0.04%)
K150R	36 (0.02%)	10 (0.01%)	14 (0.03%)	11 (0.04%)
Q493R	41 (0.02%)	4 (0.01%)	19 (0.03%)	11 (0.04%)
A684V	94 (0.04%)	28 (0.04%)	31 (0.06%)	10 (0.03%)
H146Y	122 (0.05%)	34 (0.05%)	37 (0.07%)	10 (0.03%)
Q493K	30 (0.01%)	4 (0.01%)	12 (0.02%)	10 (0.03%)
D253G	40 (0.02%)	11 (0.02%)	8 (0.01%)	10 (0.03%)

Epidemiological profile

Lineage B.1.1.7 is dispersed across the UK. Confirmed cases are those identified by whole genome sequencing. As of 22 April 2021, there were 185,216 confirmed and probable cases of VOC 202012/01 (B.1.1.7) in England. The use of S gene target failure (SGTF) in the Taqpath assay as a good proxy for cases of this variant of concern has been described in prior technical briefings. In samples tested with this assay in the Lighthouse Laboratories, samples with SGTF have predominated since mid-December 2020, reaching 99% of cases in the week starting 3 March 2021. Proportions in all regions were >97% in March 2021 (prior technical briefings). An online B.1.1.7 tracking tool is available at Covid-19 Genomic Surveillance.

Figure 12 and Figure 13 show the weekly number and proportion of England Pillar 2 (community testing) COVID-19 cases with SGTF among those tested with the TaqPath assay, and with S gene detection results, showing cases with SGTF account for more than 98% of cases from community testing nationally. The supplementary data for figures is available.

International epidemiology

As of the 19 April 2021, there are 137 countries or territories (including the UK) reporting cases of VOC-20DEC-01 globally. Of countries or territories outside of the UK, 35 report, or there is evidence of, community transmission. However, for many countries the information available on the extent of transmission within the country is not clear.

Figure 12. Weekly number and proportion of England Pillar 2 COVID-19 cases with SGTF among those tested with the TaqPath assay and with S gene detection results (1 September 2020 to 21 April 2021)
(Find accessible data used in this graph in underlying data)

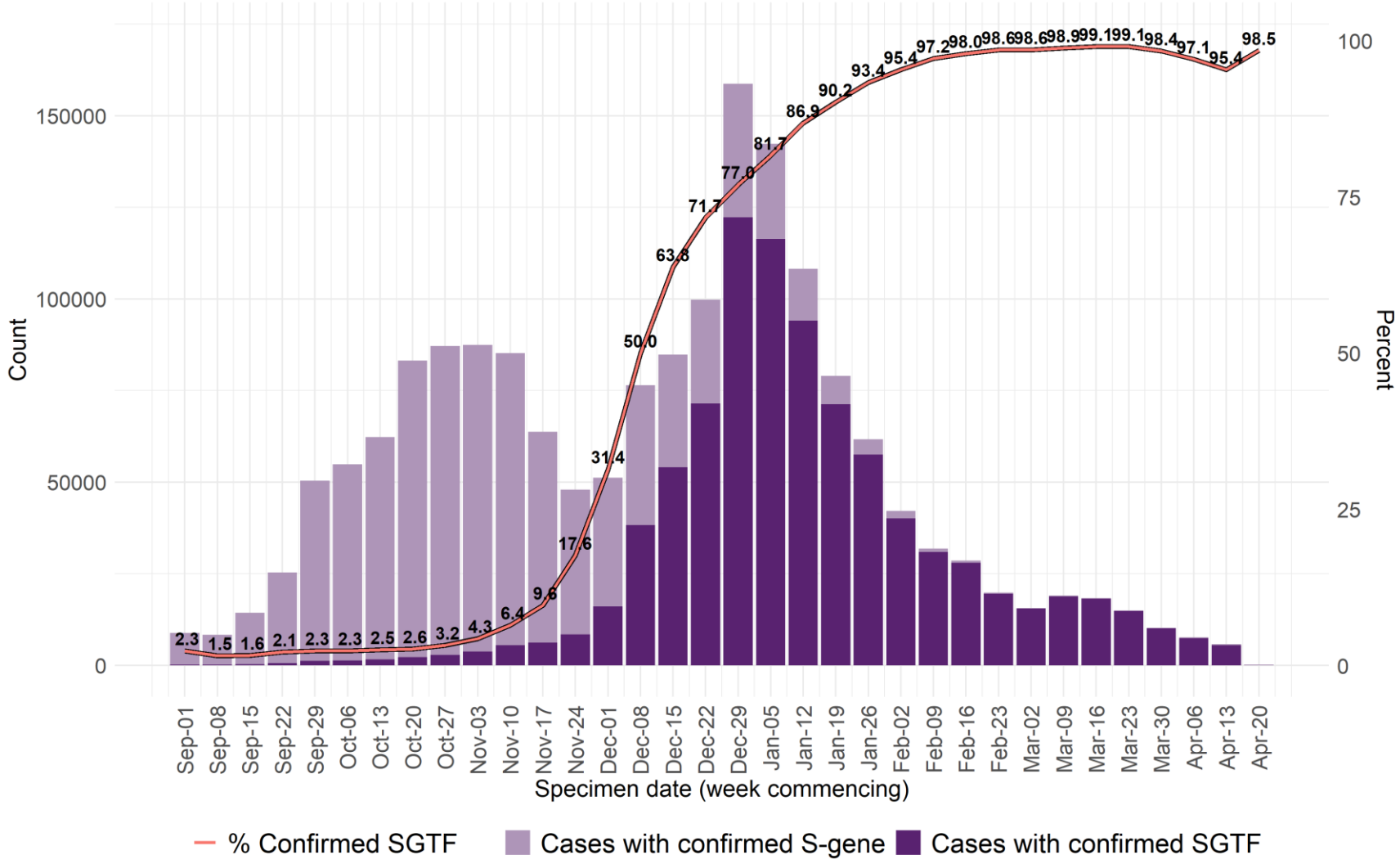
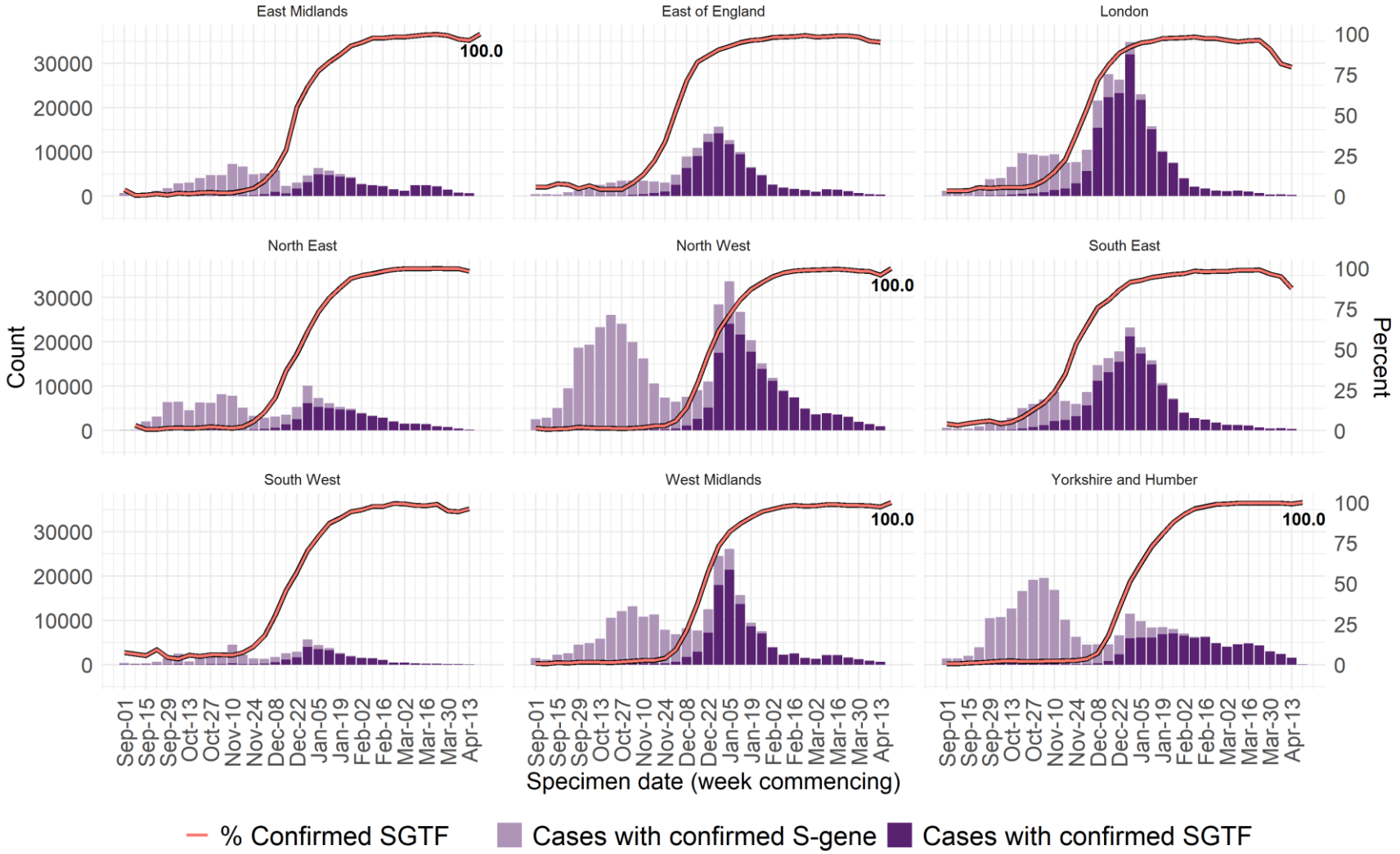


Figure 13. Weekly number and proportion of England Pillar 2 COVID-19 cases with SGTF among those tested with the TaqPath assay and with S gene detection results, by region of residence (1 September 2020 to 21 April 2021)
(Find accessible data used in this graph in underlying data)



VOC-21FEB-02 (B.1.1.7 cluster with E484K)

Through routine scanning of variation in VOC-20DEC-01 (B.1.1.7) a small number of B.1.1.7 sequences had acquired the spike protein mutation E484K. Information suggested more than one independent acquisition event. One cluster was predominant with evidence of community transmission and was designated variant under investigation on detection and on review re-designated as variant of concern VOC-21FEB-02 (VOC202102/02, B.1.1.7 cluster with E484K) on 5 February 2021. The genomic and biological profile is as previously described in Technical briefing documents on novel SARS-CoV-2 variants.

Epidemiological profile

As of 22 April 2021, 43 genomically confirmed cases of VOC-21FEB-02 (B.1.1.7 cluster with E484K) have been identified; concentrated in the South West and North West (Table 12). Cases by specimen date are shown in Figure 14 and shows cases have not been detected since 1 March 2021. The supplementary data for figures is available.

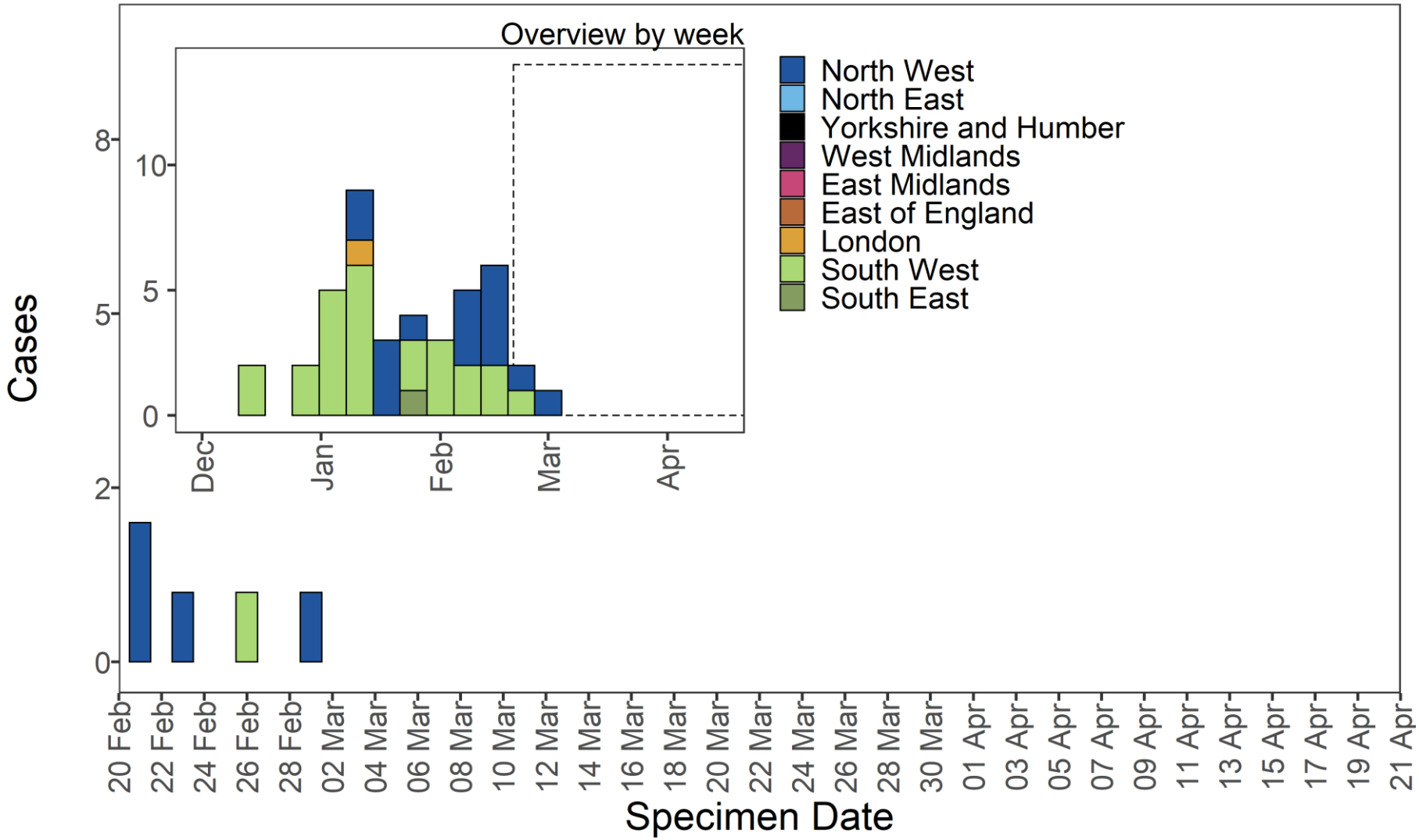
International epidemiology

As of the 19 April 2021, international cases have been reported in 8 countries (including the UK) as of 21 April 2021, 6 sequences from the Netherlands have been identified on GISAID.

Table 12. Number of confirmed and probable VOC-21FEB-02 (B.1.1.7 cluster with E484K) cases, by region of residence as of 22 April 2021

Region	Case Number	Case Proportion	Cases that have travelled	Proportion of travellers among cases
London	1	2.3%	0	0%
North West	15	34.9%	0	0%
South East	1	2.3%	0	0%
South West	26	60.5%	0	0%

Figure 14. Confirmed and probable VOC-21FEB-02 (B.1.1.7 cluster with E484K) cases by specimen date as of 22 April 2021
(Find accessible data used in this graph in underlying data)



VOC-20DEC-02 (B.1.351)

B.1.351 was initially detected in South Africa. This variant was designated variant under investigation on detection and on review re-designated as VOC-20DEC-02 (B.1.351) on 24 December 2020. The clinical risk assessment is detailed in Technical briefing 8.

Epidemiological profile

VOC-20DEC-02 (B.1.351) is dispersed across the UK in low numbers. Confirmed cases are those identified by whole genome sequencing. As of 22 April 2021, 592 confirmed cases of VOC-20DEC-02 (B.1.351) were identified. An international travel link was identified for 386 cases, and 154 had no travel link (47 cases awaiting further information). Confirmed and probable cases by specimen date are shown in Figure 15, and regional breakdown in Table 13. Figure 15 shows cases predominate in the London area. Travel data is shown in Figure 16. The supplementary data for figures is available.

Figure 15. Confirmed and probable VOC-20DEC-02 (B.1.351) cases by specimen date as of 22 April 2021
(Find accessible data used in this graph in underlying data)

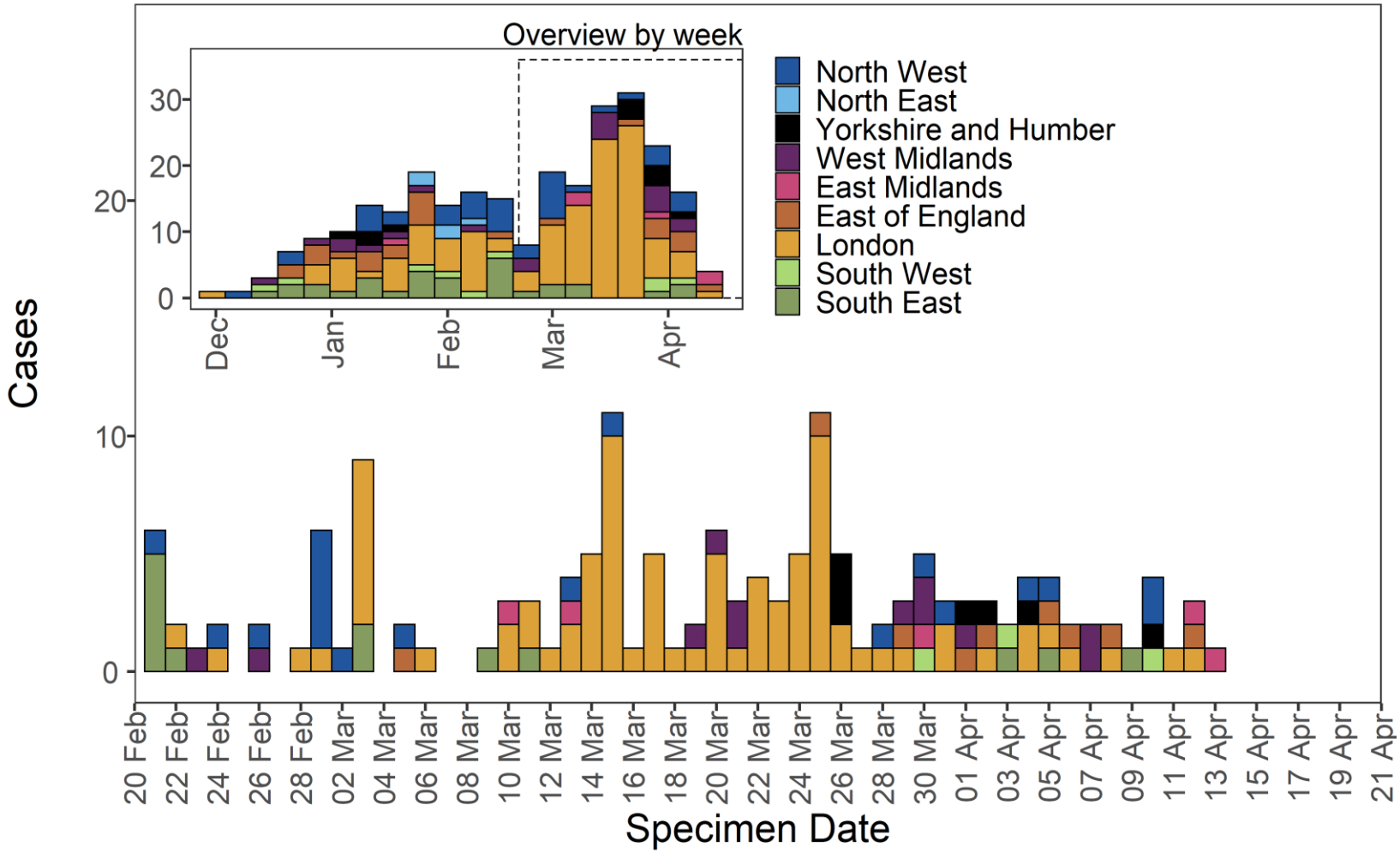


Figure 16. Travel data for confirmed and probable VOC-20DEC-02 (B.1.351) cases by specimen date as of 22 April 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data)

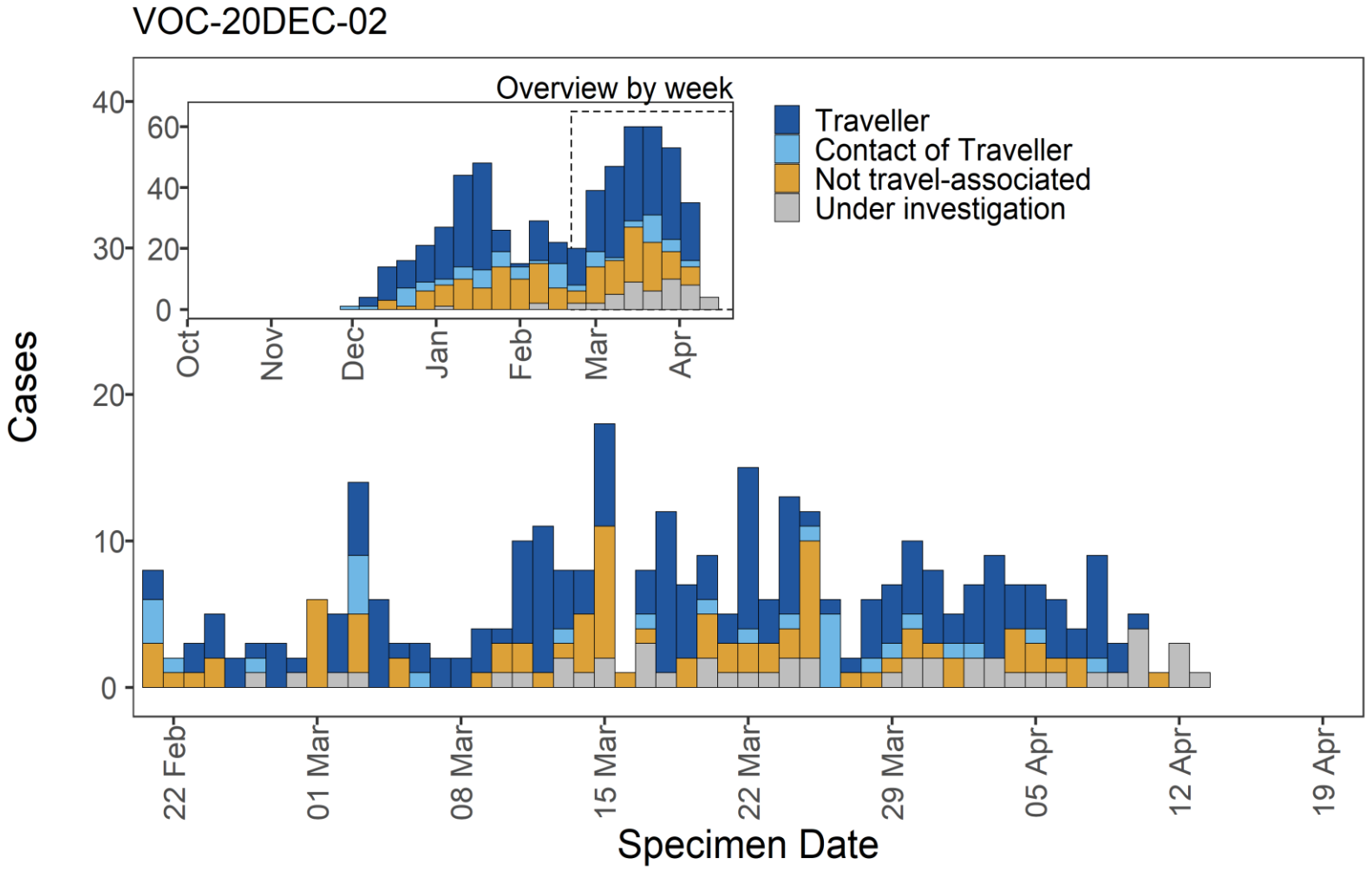


Table 13. Confirmed and probable cases of VOC-20DEC-02 by region as of 22 April 2021

Region	Case Number	Case Proportion	Cases that have travelled	Proportion of travellers among cases
East Midlands	27	4.6%	21	77.8%
East of England	61	10.3%	34	55.7%
London	259	43.8%	135	52.1%
North East	8	1.4%	3	37.5%
North West	67	11.3%	28	41.8%
South East	79	13.3%	47	59.5%
South West	23	3.9%	13	56.5%
West Midlands	43	7.3%	23	53.5%
Yorkshire and Humber	25	4.2%	14	56%

International epidemiology

As of 19 April 2021 there are 97 countries (including the UK) that have reported cases of this variant globally. GISAID includes data on sequences available internationally. As of the 21 April 2021 9,198 sequences of VOC-20DEC-02, excluding UK, are listed from 70 countries and territories.

VOC-21JAN-02 (P.1)

First identified in Japan amongst travellers from Brazil, the P.1 lineage is a descendant of B.1.1.28. This variant was designated variant under investigation on detection and on review re-designated as VOC-21JAN-02 (P.1) on 13 January 2021. The clinical risk assessment for P1 is detailed in technical briefing 7.

Epidemiological profile

As of 22 April 2021, 51 genomically confirmed and probable cases of VOC-21JAN-02 (P.1) have been identified in England. 36 cases have been linked to international travel, 1 case has no travel link, 14 under investigation. Regional breakdown of cases in shown in Table 14 and cases by specimen date are shown in Figure 17. Travel data is shown in Figure 18. The supplementary data for figures is available.

Table 14. Number of confirmed and probable cases VOC-21JAN-02 (P.1), by region of residence as of 22 April 2021

Region	Case Number	Case Proportion	Cases that have travelled	Proportion of travellers among cases
East of England	5	9.8%	4	80%
London	28	54.9%	16	57.1%
South East	4	7.8%	4	100%
South West	11	21.6%	1	9.1%
West Midlands	2	3.9%	1	50%
Yorkshire and Humber	1	2.0%	1	100%

Figure 17. Confirmed and probable VOC-21JAN-02 (P.1) cases by specimen date as of 22 April 2021
(Find accessible data used in this graph in underlying data)

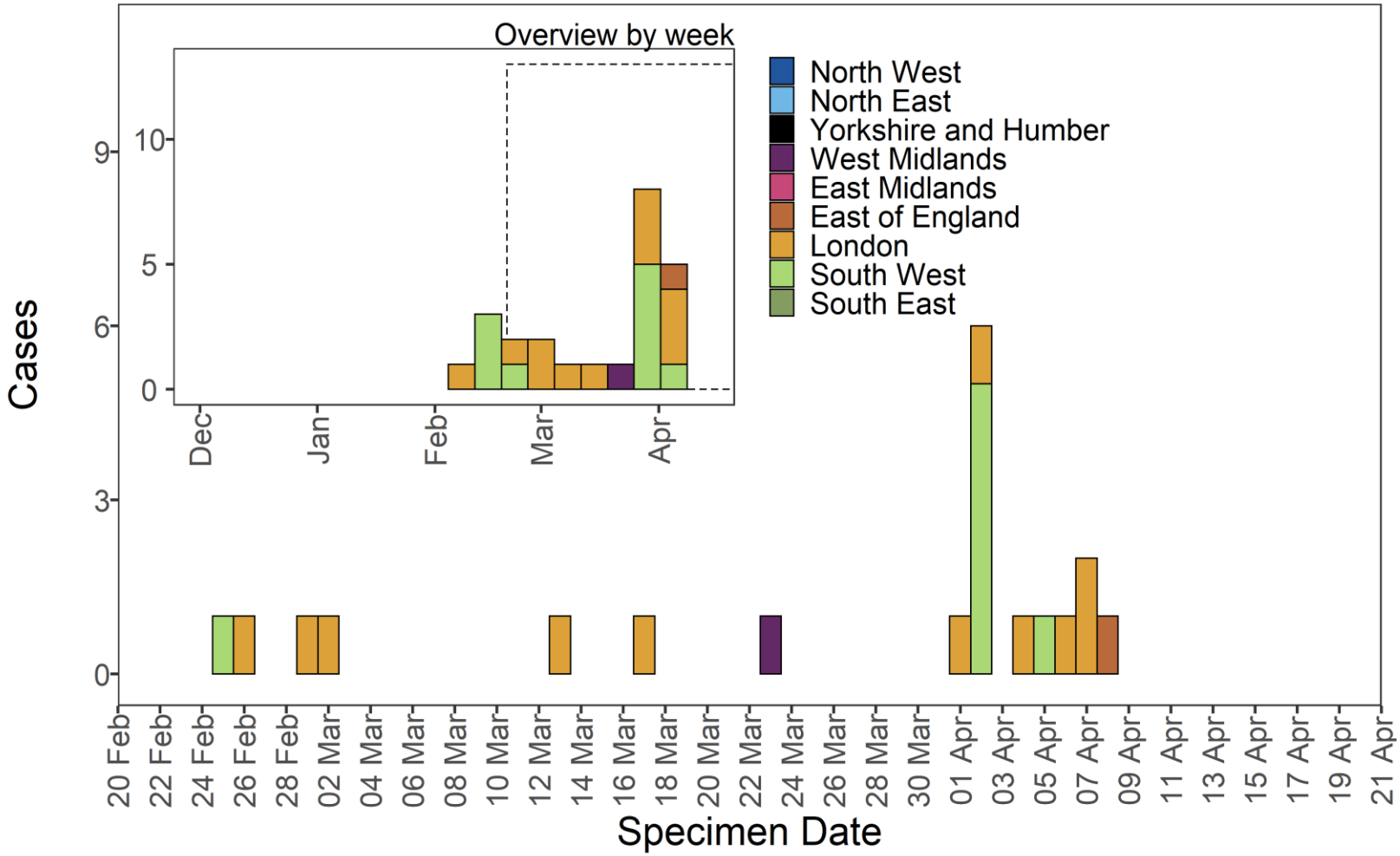
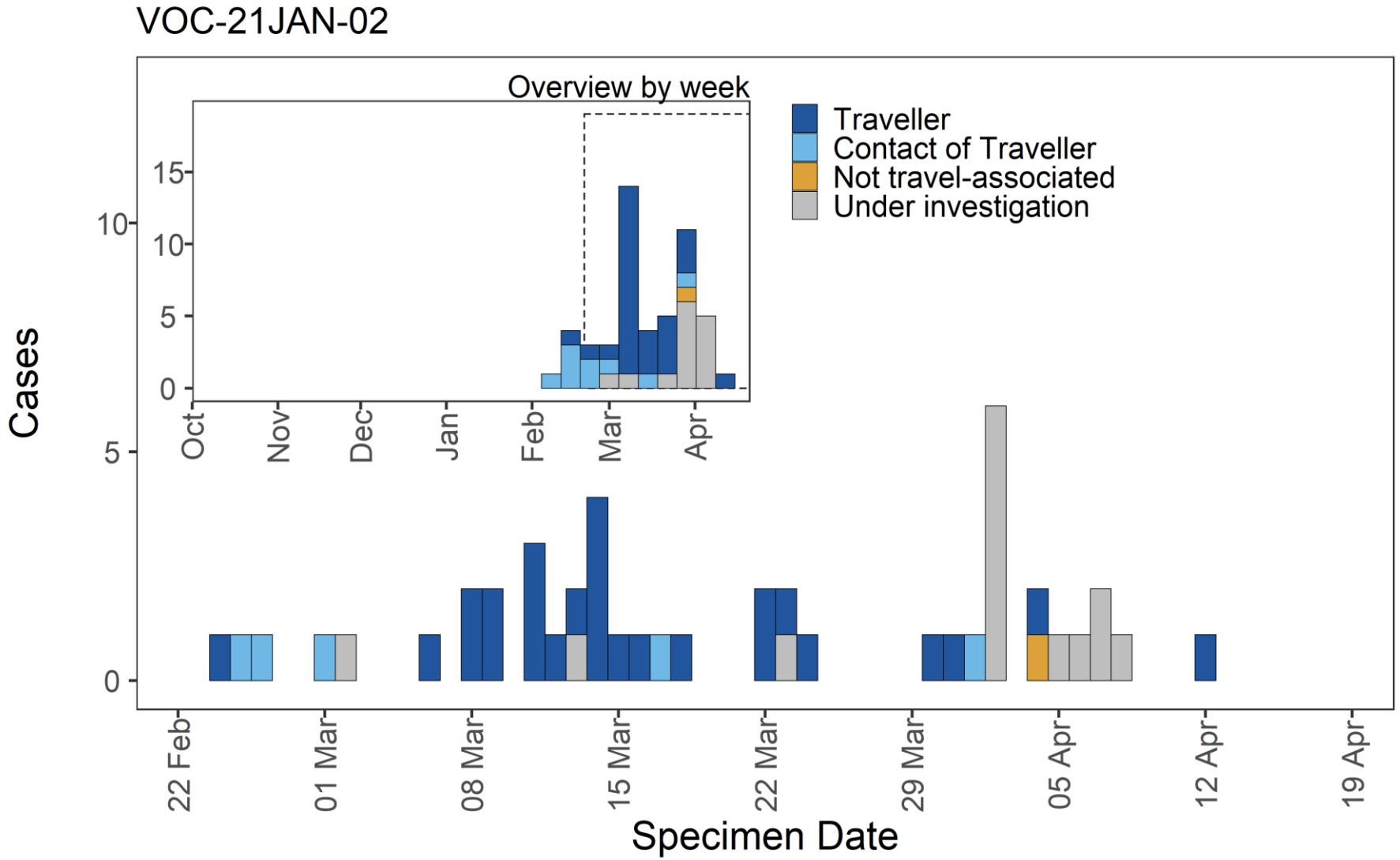


Figure 18. Travel data for confirmed and probable VOC-21JAN-02 (P.1) cases by specimen date as of 22 April 2021 Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data)



International epidemiology

As of 19 April 2021, cases of VOC-21JAN-02 (P.1) have been reported in 55 countries or territories (including the UK). Five countries have reported cases of a Brazilian variant but additional information is awaited to clarify if this is with VOC-21JAN-02 (P.1).

GISAID includes data on sequences available internationally. As of the 21 April 2021 3,618 sequences of VOC-21JAN-02 are listed from 39 countries excluding the UK.

VUI-21JAN-01 (P2)

First identified in Brazil, the P.2 lineage is a descendant of B.1.1.28. This variant was designated VUI-21JAN-01 (P.2) on 13 January 2021. It was first sequenced in the UK in November 2020.

Epidemiological profile

As of 22 April 2021, 53 cases of VUI-21JAN-01 (P.2) have been identified in England. 9 cases have been linked to international travel, and 41 cases had no travel link (3 cases awaiting further information). Regional breakdown of cases in shown in Table 15 and confirmed and probable cases by specimen date are shown in Figure 19. Figure 19 shows a limited number of cases in different regions. Travel data is shown in Figure 20. The supplementary data for figures is available.

Table 15. Number of confirmed and probable cases VUI-21JAN-01 (P.2), by region of residence as of 22 April 2021

Region	Case Number	Case Proportion	Cases that have travelled	Proportion of travellers among cases
East Midlands	1	1.9%	0	0%
East of England	2	3.8%	1	50%
London	14	26.4%	6	42.9%
North West	11	20.8%	0	0%
South East	6	11.3%	0	0%
South West	7	13.2%	0	0%
West Midlands	1	1.9%	0	0%
Yorkshire and Humber	11	20.8%	0	0%

International epidemiology

As of 19 April 2021, cases of VUI-21JAN-01 (P.2) have been reported in 39 countries or territories (including the UK).

GISAID includes data on sequences available internationally, as of 21 April 2021 2,072 sequences (excluding UK) of VUI-21JAN-01 from 33 countries.

Figure 19. Confirmed and probable VUI-21JAN-01 (P.2) cases by specimen date, as of 22 April 2021
(Find accessible data used in this graph in underlying data)

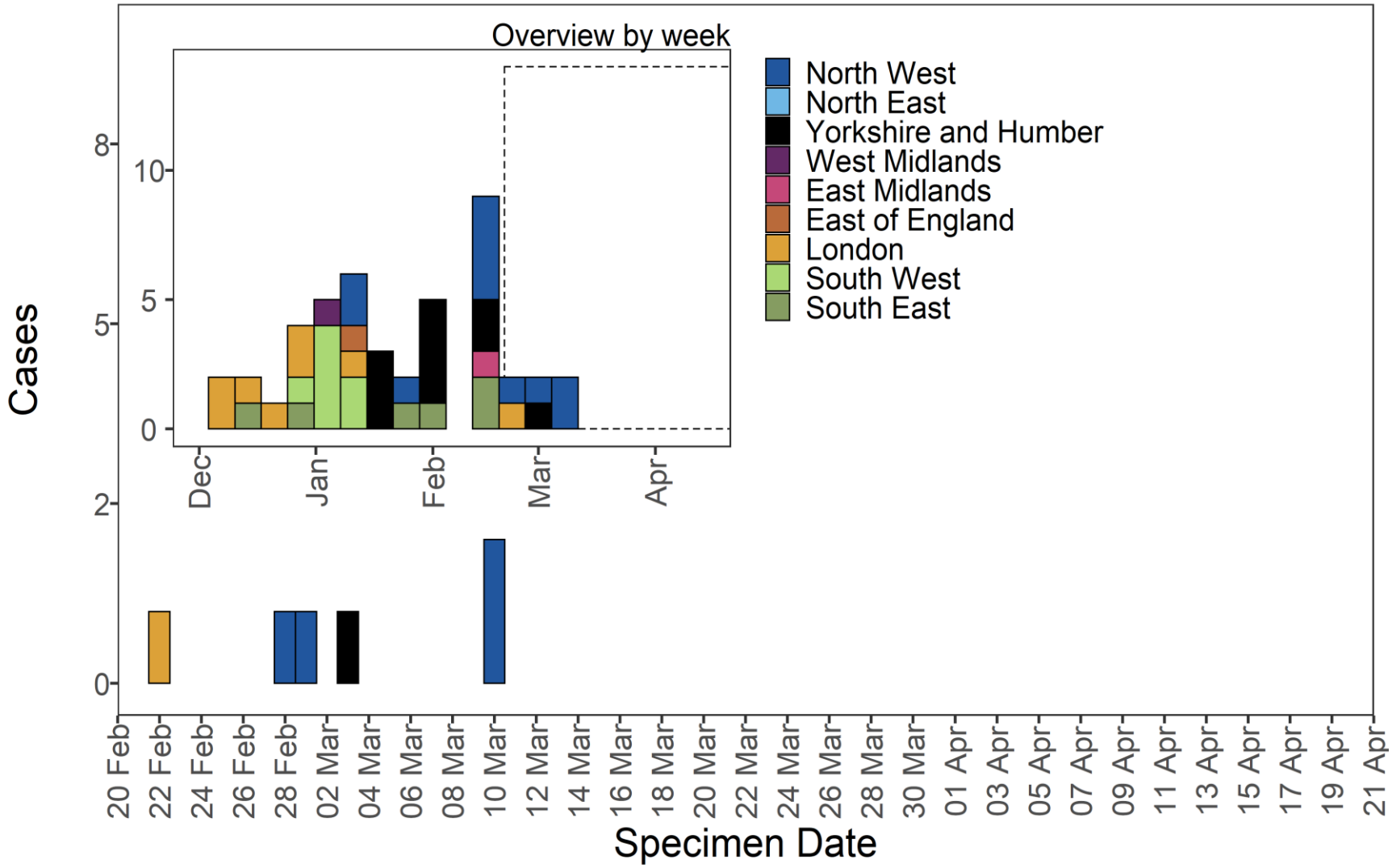
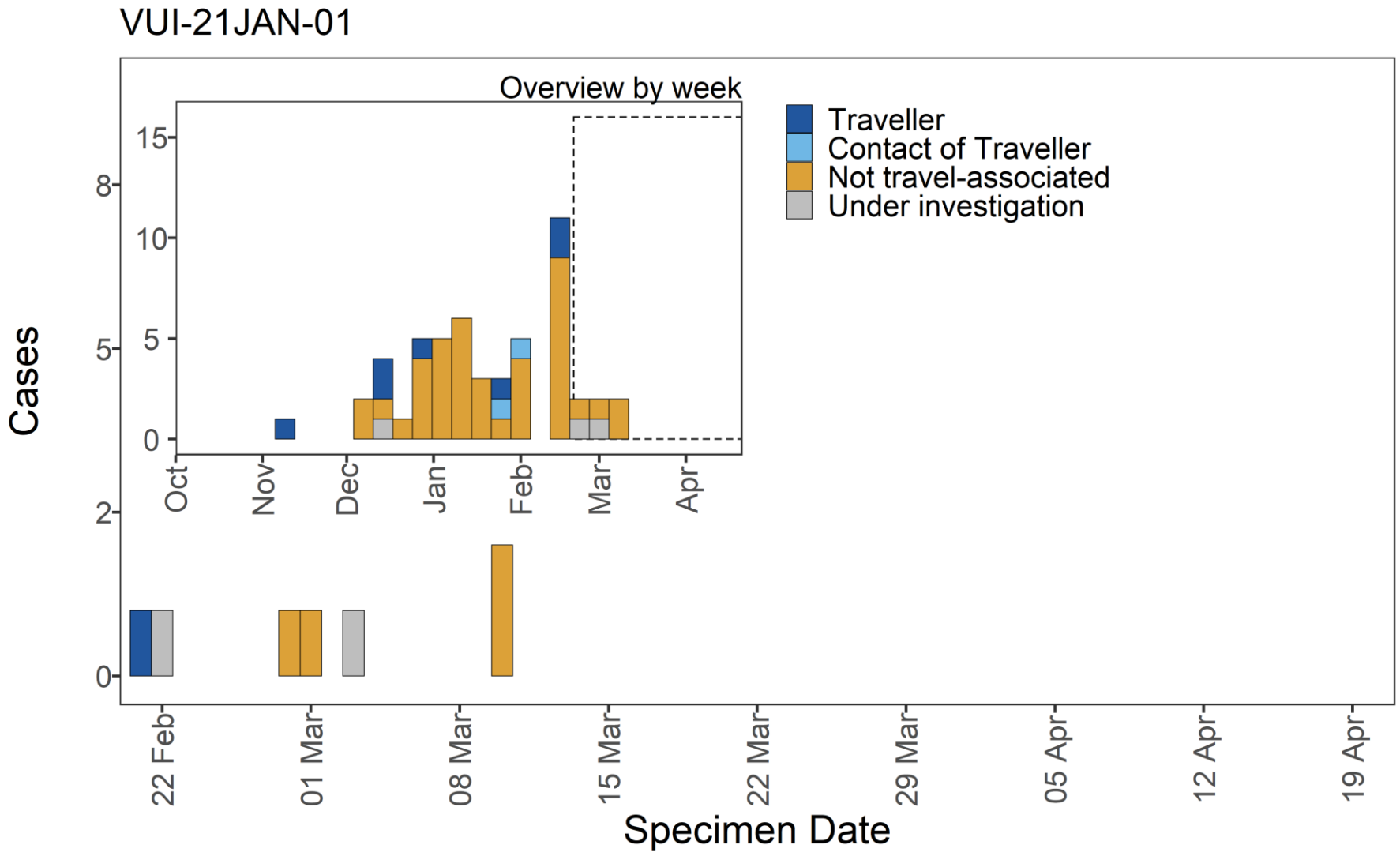


Figure 20. Travel data for confirmed and probable VUI-21JAN-01 (P.2) cases by specimen date as of 22 April 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data)



VUI-21FEB-01 (A.23.1 with E484K)

This variant was first identified in Liverpool, UK, derived from a lineage first identified in Uganda without E484K. The variant was designated VUI-21FEB-01 (A.23.1 with E484K) on 5 February 2021. It was first detected in the UK in December 2020.

Epidemiological profile

As of 22 April 2021, 79 genomically confirmed cases of VUI-21FEB-01 (A.23.1 with E484K) have been identified. The majority of these are residents of the North West of England (Table 16). Confirmed and probable cases by specimen date are shown in Figure 21. Figure 21 shows cases predominate in the North West. Travel data is shown in Figure 22. The supplementary data for figures is available.

International epidemiology

As of 19 April 2021, cases of VUI-21FEB-01 (A.23.1 with E484K) have been reported in the UK and the Netherlands only.

GISAID includes data on sequences available internationally. As of 21 April 2021 1 sequence is listed of VUI-21FEB-01 (A.23.1 with E484K) (excluding UK) from Netherlands.

Table 16. Number of confirmed and probable VUI-21FEB-01 (A.23.1 with E484K) cases, by region of residence as of 22 April 2021

Region	Case Number	Case Proportion	Cases that have travelled	Proportion of travellers among cases
North West	78	98.7%	0	0%
West Midlands	1	1.3%	0	0%

Figure 21. Confirmed and probable VUI-21FEB-01 (A.23.1 with E484K) cases by specimen date as of 22 April 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data)

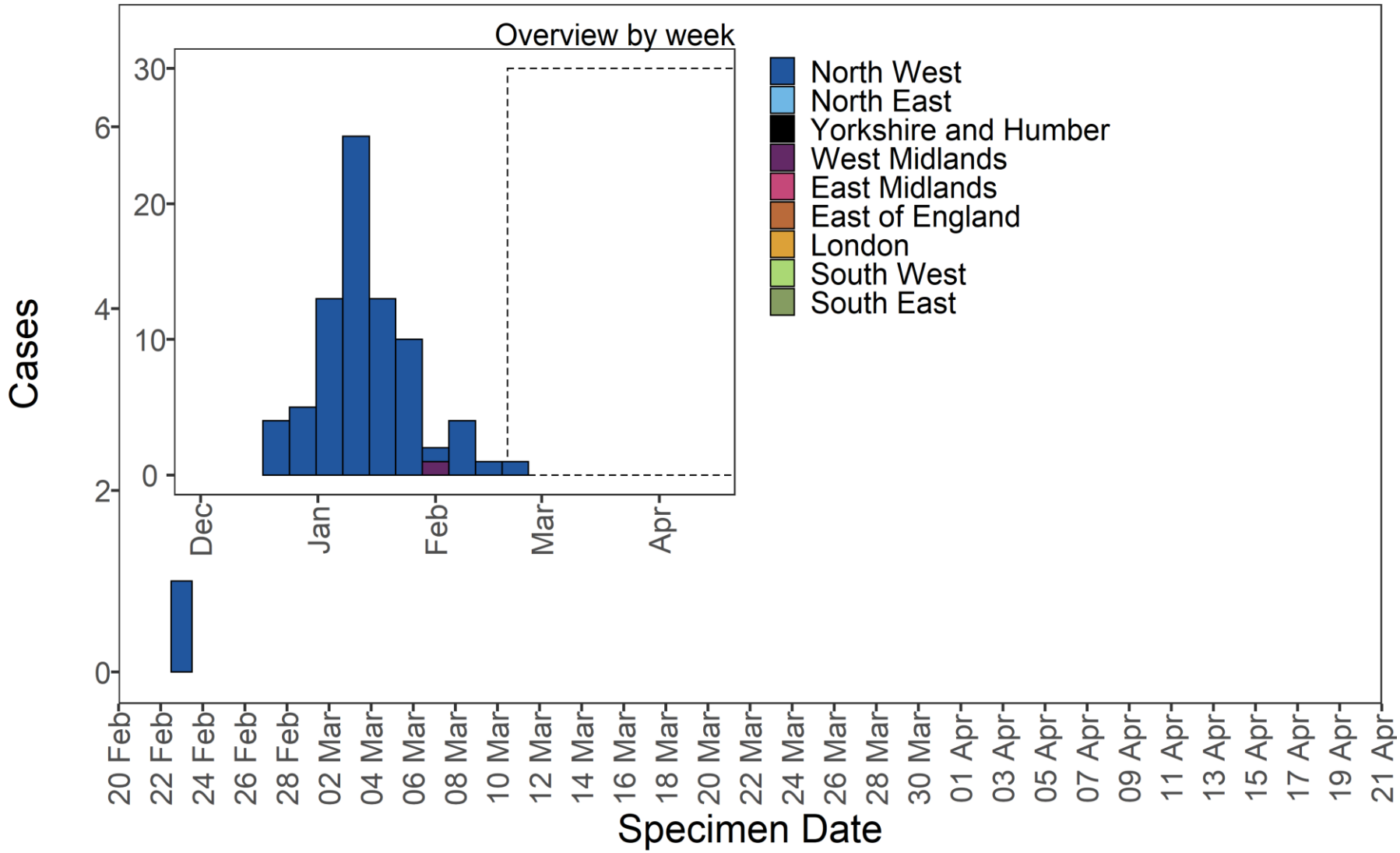
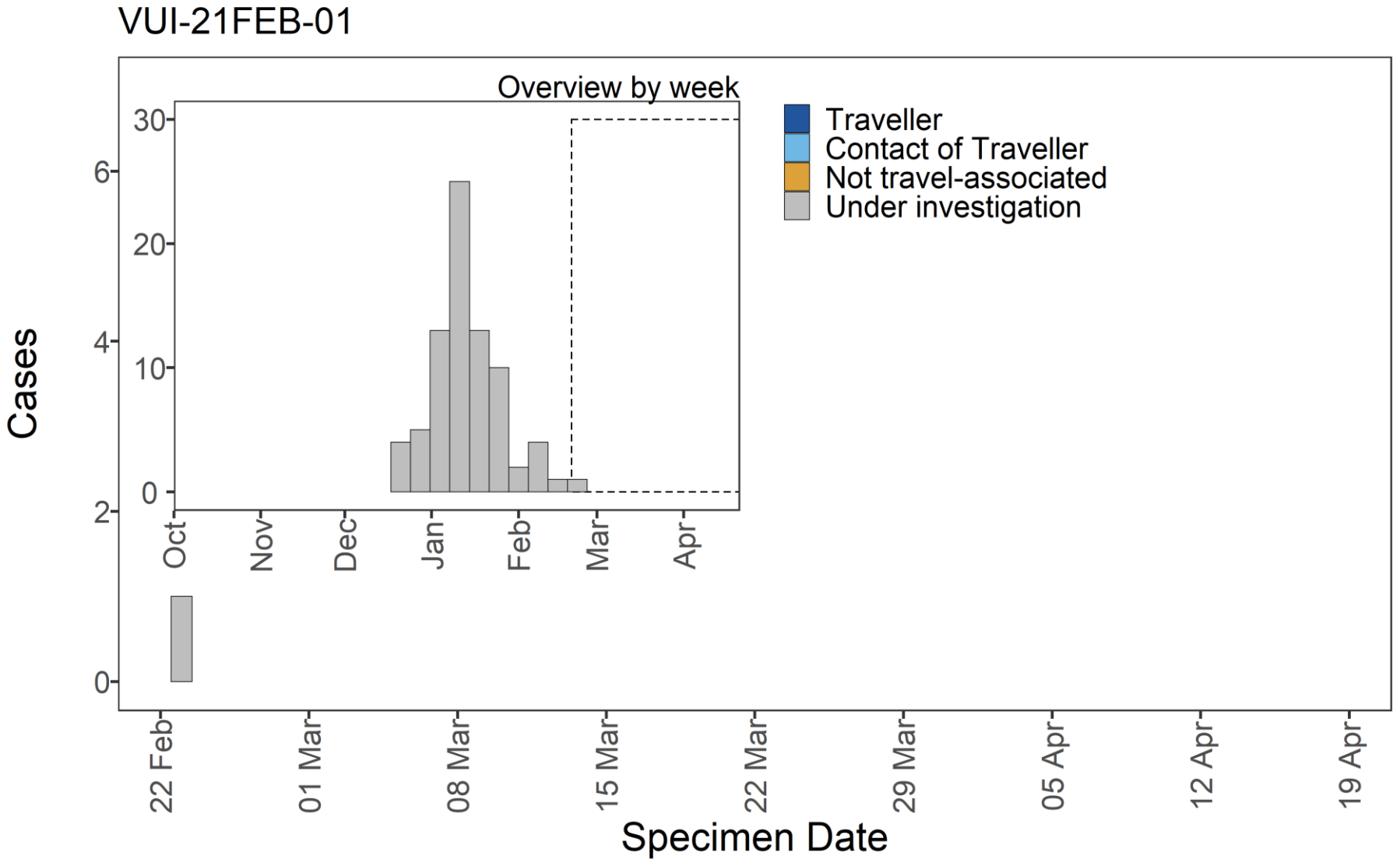


Figure 22. Travel data for confirmed and probable VUI-21FEB-01 (A.23.1 with E484K) cases by specimen date as of 22 April 2021. Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data)



VUI-21FEB-03 (B.1.525)

First identified as a geographically dispersed cluster in UK on the 2 February 2021. This variant was designated VUI-21FEB-03 (B.1.525) on 12 February 2021. The earliest sample date for VUI-21FEB-03 (B.1.525) in England was 15 December 2020. The biological profile is described in technical briefing 7.

Epidemiological profile

As of 22 April 2021, there were 334 cases of VUI-21FEB-03 (B.1.525) in England In this geographically dispersed genomic cluster with likely community transmission. Regional cases are shown in Table 17 and confirmed and probable cases by specimen date are shown in Figure 23. Figure 23 shows cases are in several regions, predominating in London and South East and North West. Travel data is shown in Figure 24. The supplementary data for figures is available.

Table 17. Number of confirmed and probable cases VUI-21FEB-03 (B.1.525) by region of residence as of 22 April 2021

Region	Case Number	Case Proportion	Cases that have travelled	Proportion of travellers among cases
East Midlands	9	2.7%	5	55.6%
East of England	24	7.2%	17	70.8%
London	113	33.8%	73	64.6%
North East	3	0.9%	3	100%
North West	62	18.6%	16	25.8%
South East	71	21.3%	24	33.8%
South West	14	4.2%	4	28.6%
West Midlands	20	6.0%	8	40%
Yorkshire and Humber	18	5.4%	8	44.4%

Figure 23. Confirmed and probable cases VUI-21FEB-03 (B.1.525) by specimen date as of 22 April 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data)

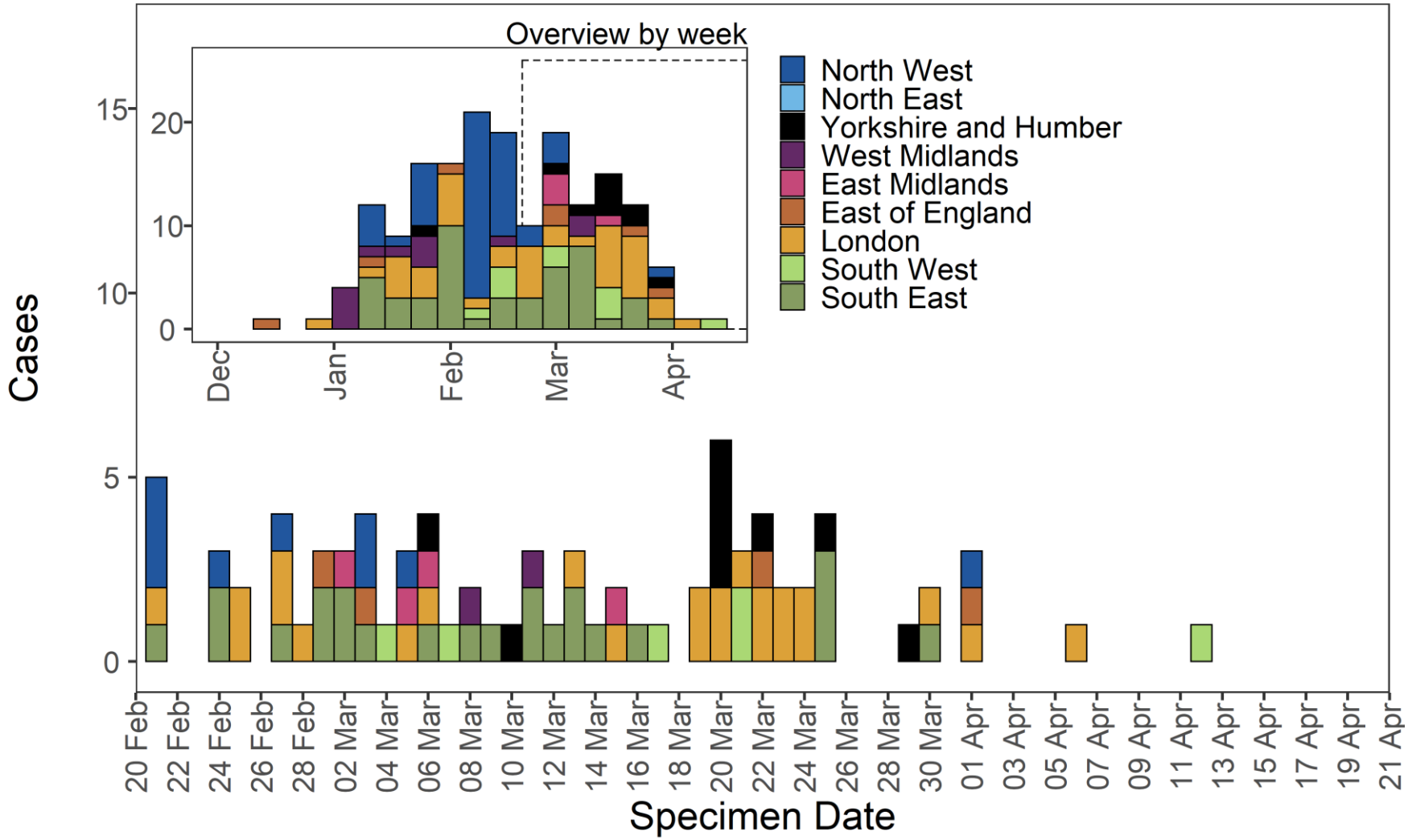
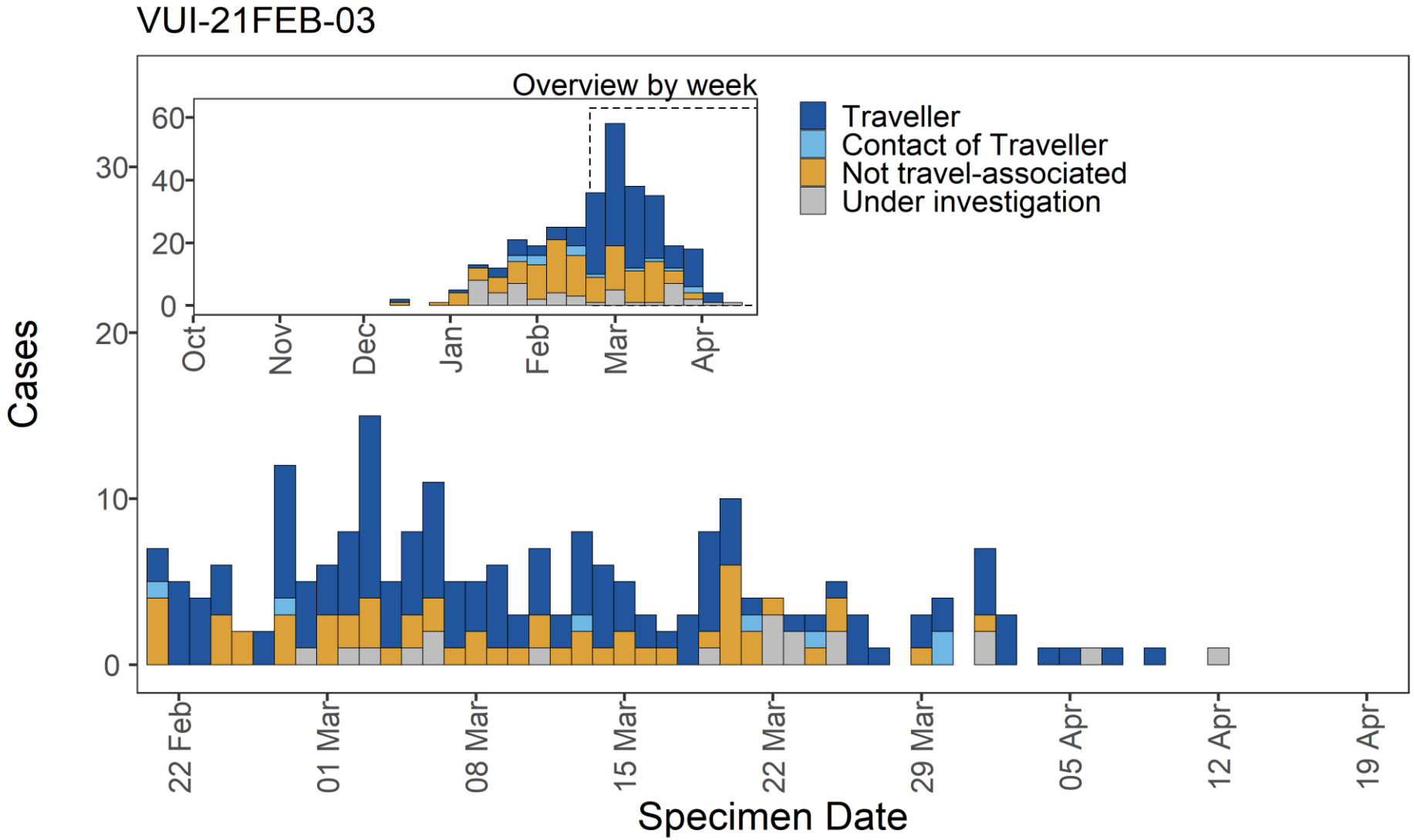


Figure 24. Travel data for confirmed and probable VUI-21FEB-03 (B.1.525) cases by specimen date as of 22 April 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data)



International epidemiology

As of 19 April 2021, cases of VUI-21FEB-03 (B.1.525) have been reported in 51 countries or territories (including the UK).

GISAID includes data on sequences available internationally. As of the 21 April 2021 1,331 sequences of VUI-21FEB-03 are listed, from 43 countries or territories excluding UK.

VUI-21FEB-04 (B.1.1.318)

The VUI-21FEB-04 is lineage B.1.1.318 and was identified in England in mid-February 2021 through routine horizon scanning for the development of new clusters of genomes containing E484K. This analysis identified an initial cluster of 6 cases containing E484K and other spike mutations, designated VUI-21FEB-04 (B.1.1.318) on 23 February 2021.

Epidemiological profile

As of 22 April 2021, there were 135 genomically confirmed cases of VUI-21FEB-04 (B.1.1.318). Cases have occurred in most regions of England, concentrated in London and the North West (Table 18). Regional cases are shown in Table 18 and confirmed and probable cases by specimen date are shown in Figure 25. Figure 25 shows sporadic cases in several regions. Travel data is shown in Figure 26. The supplementary data for figures is available. Of the 135 cases, 54 had a link to travel, 42 cases had no known link to travel, 39 are under investigation.

International epidemiology

As of 19 April 2021, cases of VUI-21FEB-04 (B.1.1.318) have been reported in 8 countries (including the UK).

GISAID (gisaid.org) includes data on sequences available internationally. As of the 21 April 2021, there are 24 international VUI-21FEB-04 sequences, excluding UK. (USA 10, Germany 6, Italy 4, Sweden 3, Bangladesh 1).

Table 18. Number of confirmed and probable VUI-21FEB-04 (B.1.1.318) cases, by region of residence as of 22 April 2021

Region	Case Number	Case Proportion	Cases that have travelled	Proportion of travellers among cases
East Midlands	9	6.7%	2	22.2%
East of England	16	11.9%	8	50%
London	41	30.4%	23	56.1%
North East	1	0.7%	1	100%
North West	35	25.9%	3	8.6%
South East	16	11.9%	9	56.2%
South West	1	0.7%	1	100%
West Midlands	5	3.7%	3	60%

Region	Case Number	Case Proportion	Cases that have travelled	Proportion of travellers among cases
Yorkshire and Humber	11	8.1%	1	9.1%

Figure 25. Confirmed and probable VUI-21FEB-04 (B.1.1.318) cases by specimen date as of 22 April 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data)

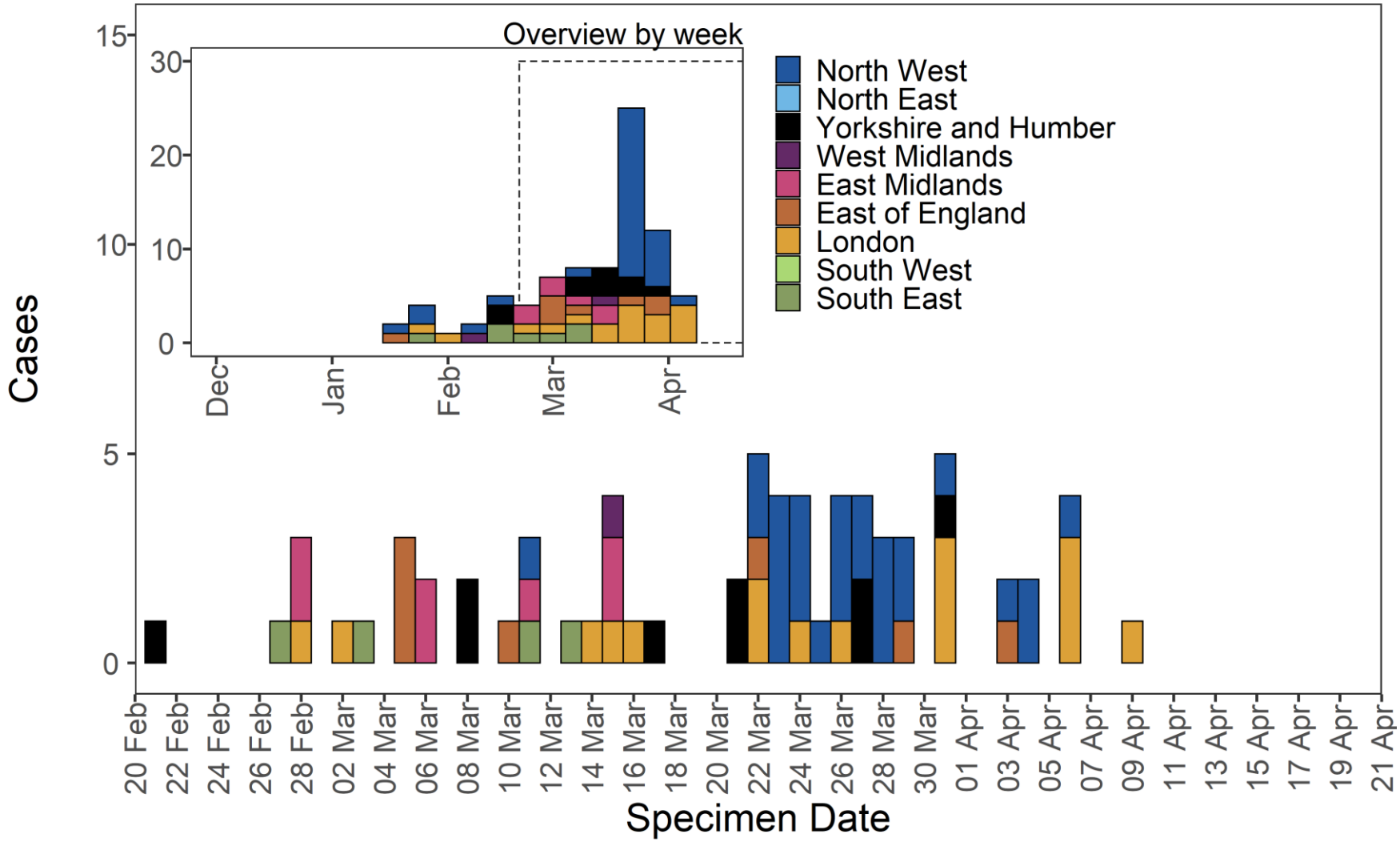
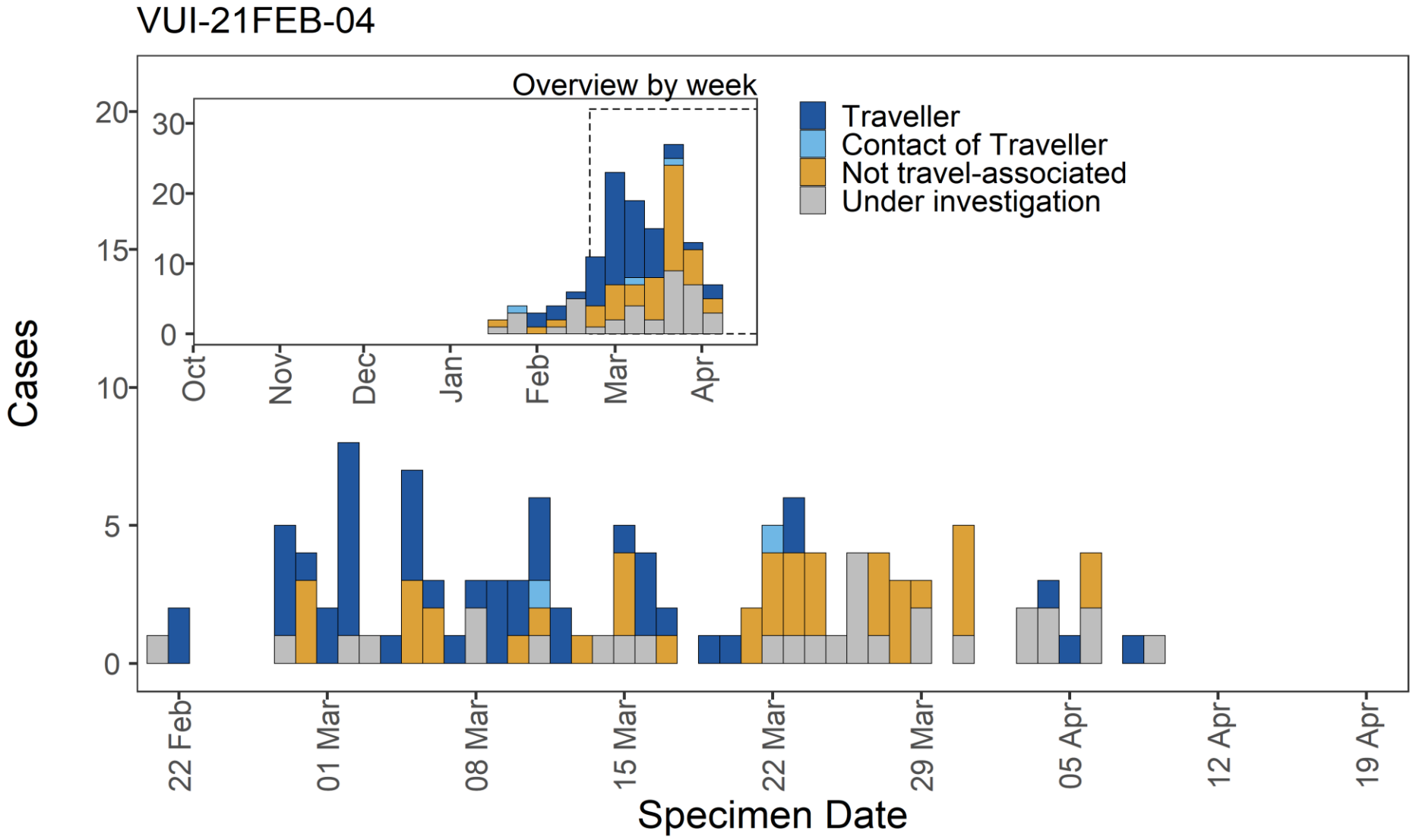


Figure 26. Travel data for confirmed and probable VUI-21FEB-04 (B.1.1.318) cases by specimen date as of 22 April 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data)



VUI-21MAR-01 (B.1.324.1 with E484K)

First identified via horizon scanning of genomes with spike mutations characteristic of VOCs (including both N501Y and E484K) on 3 March 2021, the variant VUI-21MAR-01 (B.1.324.1 with E484K) was designated VUI on detection as VUI-21MAR-01 (B.1.324.1 with E484K) on 4 March 2021.

Epidemiological profile

As of 22 April 2021, there are 2 confirmed cases in the UK in a group of returning travellers, with links to additional unsequenced cases.

International epidemiology

As of 19 April 2021 there are no cases reported internationally.

GISAID includes data on sequences available internationally. As of the 21 April 2021, 0 sequences are listed internationally of VUI-21MAR-01.

VUI-21MAR-02 (P.3)

The VUI-21MAR-02 (P.3) was identified on 9 March 2021 in a report of 33 genomes from the Philippines with 13 lineage defining mutations. This variant shares important mutations with Variants of Concern including E484K, N501Y and P681H. Based on genomic profile, PHE has designated VUI-21MAR-02 (P.3) on the 11 March 2021. This variant arises from B.1.1.28, the same parent lineage that gave rise to P.1 and P.2 in Brazil. Phylogenetic analysis of P.3 shows diversity indicating circulation prior to detection.

Epidemiological profile

As of 22 April 2021, there are 5 confirmed cases in the UK , of which 4 have recent travel history.

International epidemiology

As of 19 April 2021, cases of VUI-21MAR-02 (P.3) have been reported in 9 countries or territories (including the UK).

GISAID includes data on sequences available internationally. As of the 21 April 2021, 107 sequences are listed internationally of VUI-21MAR-02 excluding UK. (Australia 2, China 1, Germany 7, Japan 3, Netherlands 4, New Zealand 3, Norway 2, Philippines 81, Singapore 1, South Korea 1, USA 2).

Sources and acknowledgments

Data sources

Data used in this investigation is derived from the COG-UK dataset, the PHE Second Generation Surveillance System (SGSS), NHS Test and Trace, the Secondary Uses Service (SUS) dataset and Emergency Care Data Set (ECDS). Data on international cases are derived from reports in GISAID, the media and information received via the International Health Regulations National Focal Point (IHRNFP) and Early Warning and Response System (EWRS).

Variant Technical Group

Authors of this report

PHE Genomics Cell
PHE Outbreak Surveillance Team
PHE Epidemiology Cell
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Variant Technical Group membership

The PHE Variant Technical Group includes representation from:

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- DHSC
- BEIS
- Public Health Wales
- Public Health Scotland
- Public Health Agency Northern Ireland
- Imperial College London
- London School of Hygiene and Tropical Medicine
- University of Birmingham
- University of Cambridge
- University of Edinburgh
- University of Liverpool
- the Wellcome Sanger Institute

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About Public Health England

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