Public Health England

Protecting and improving the nation's health

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

Technical briefing 11

13 May 2021

This briefing provides an update on previous briefings up to 7 May 2021

Contents

Summary

There are 5 variants of concern and 7 variants under investigation (Table 1).

This report has been published to continue to share detailed surveillance of VOC-21APR-02 (B.1.617.2). A separate report is published covering our routine data on all other VOCs and VUIs. These additional specialist technical briefings represent early data and analysis on an emerging variant and findings have a high level of uncertainty.

Whilst case numbers in general remain very low, the proportion of cases which are VOC-21APR-02 (B.1.617.2) has increased, as monitored through both genomic and S gene target data. This is most pronounced in London and the North West.

The proportion of S gene target positives continues to increase rapidly, but the proportion of VOC-21APR-02 (B.1.617.2) genomes amongst all sequenced cases has a slower increase in the most recent data. Genomic data from the most recent period shown is still being produced and this picture may be related to sequencing lag or alternatively to biases in the S gene data related to geographic coverage.

In a small number of areas there are both rising incidence rates and a high proportion of VOC-21APR-02 (B.1.617.2).

Surveillance of travellers from India shows a predominance of VOC-21APR-02 (B.1.617.2) amongst imported cases.

Secondary attack rates for VOC-21APR-02 (B.1.617.2) are similar to those for VOC-20DEC-01 (B.1.1.7) in non-travellers and slightly higher for travellers. Small numbers of non-travel VOC-21APR-02 (B.1.617.2) cases mean these results should be interpreted with caution and will be refined with further cases.

Routine reinfection surveillance shows a small number of potential reinfection cases with VOC-21APR-02 (B.1.617.2). This would be expected with any prevalent variant; comparative analyses have been initiated.

The updated VOC-21APR-02 (B.1.617.2) risk assessment will be published separately on 14 May 2021.

Published information on variants

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. Data on variants not detailed here is published in the variant data update. Variant risk assessments are available in prior technical briefings. A repository containing the up-to-date genomic definitions for all variants of concern (VOC) and variants under investigation (VUI) as curated by Public Health England was created 5 March 2021. The repository can be accessed on GitHub.

Part 1: Overview surveillance data

Variants under surveillance

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

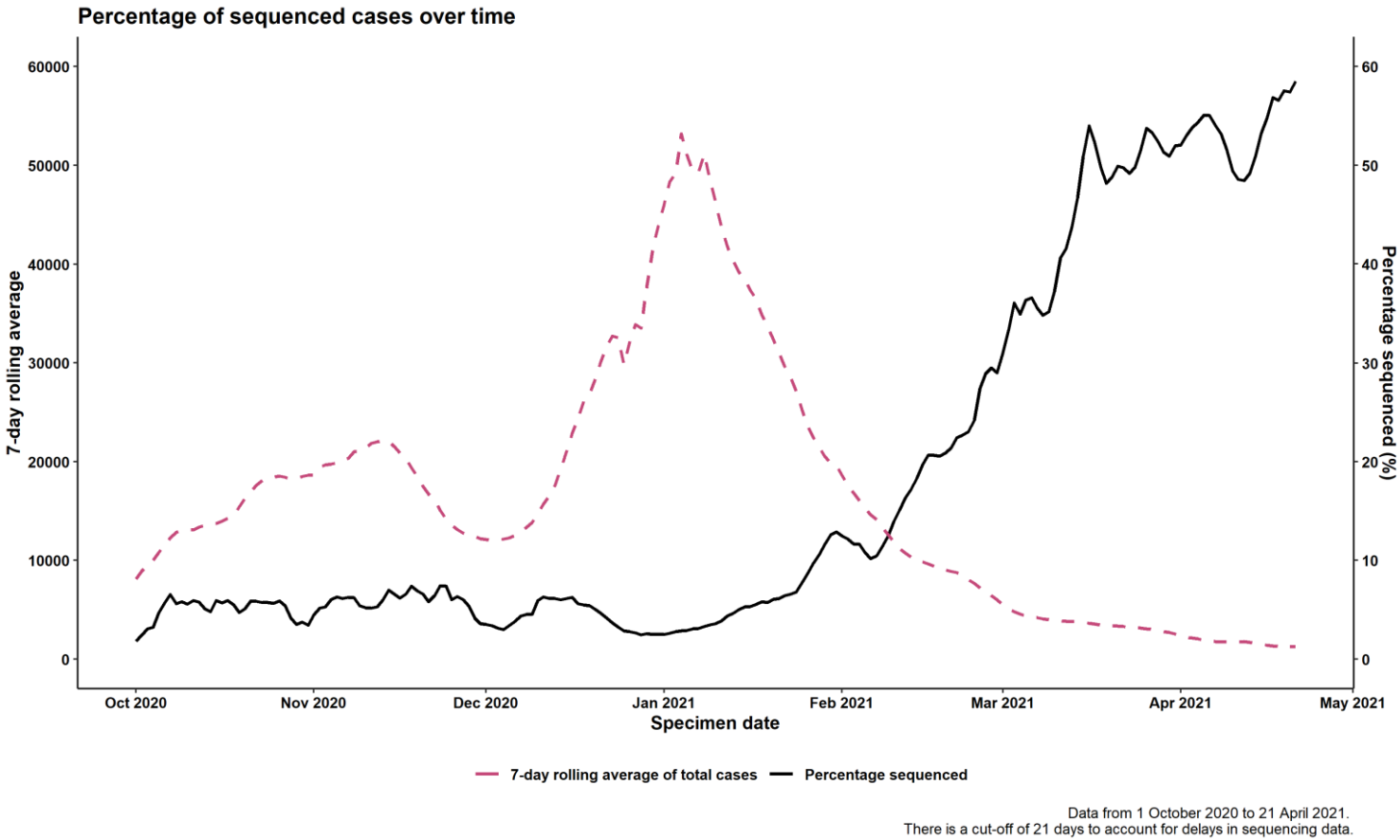
Table 1. Variant lineage and designation as of 12 May 2021 (provisionally extinct variants removed)

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
B.1.617.2	VOC-21APR-02	India	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
B.1.1.318	VUI-21FEB-04	UK England	VUI
P.3	VUI-21MAR-02	Philippines	VUI
B.1.617.1 with E484Q	VUI-21APR-01	India	VUI
B.1.617.3	VUI-21APR-03	India	VUI
B.1.429			Monitoring
B.1.1.7 with S494P			Monitoring
A.27			Monitoring
B.1.526			Monitoring
B.1.1.7 with Q677H			Monitoring
B.1.620			Monitoring
B1.214.2			Monitoring
B.1.1.1 with L452Q and F490S			Monitoring
R.1			Monitoring
B.1.1.28 with N501T and E484Q			Monitoring
C.36			Monitoring
B.1.621			Monitoring
B.1 with 214insQAS			Monitoring
AV.1			Monitoring

Sequencing coverage

Figure 1 shows the proportion of cases which are sequenced in England.

Figure 1. Coverage of sequencing: percentage of SARS-CoV-2 cases sequenced over time as of 12 May 2021
(Find accessible data used in this graph in underlying data)



VOC and VUI case numbers, proportion, deaths and case fatality rate

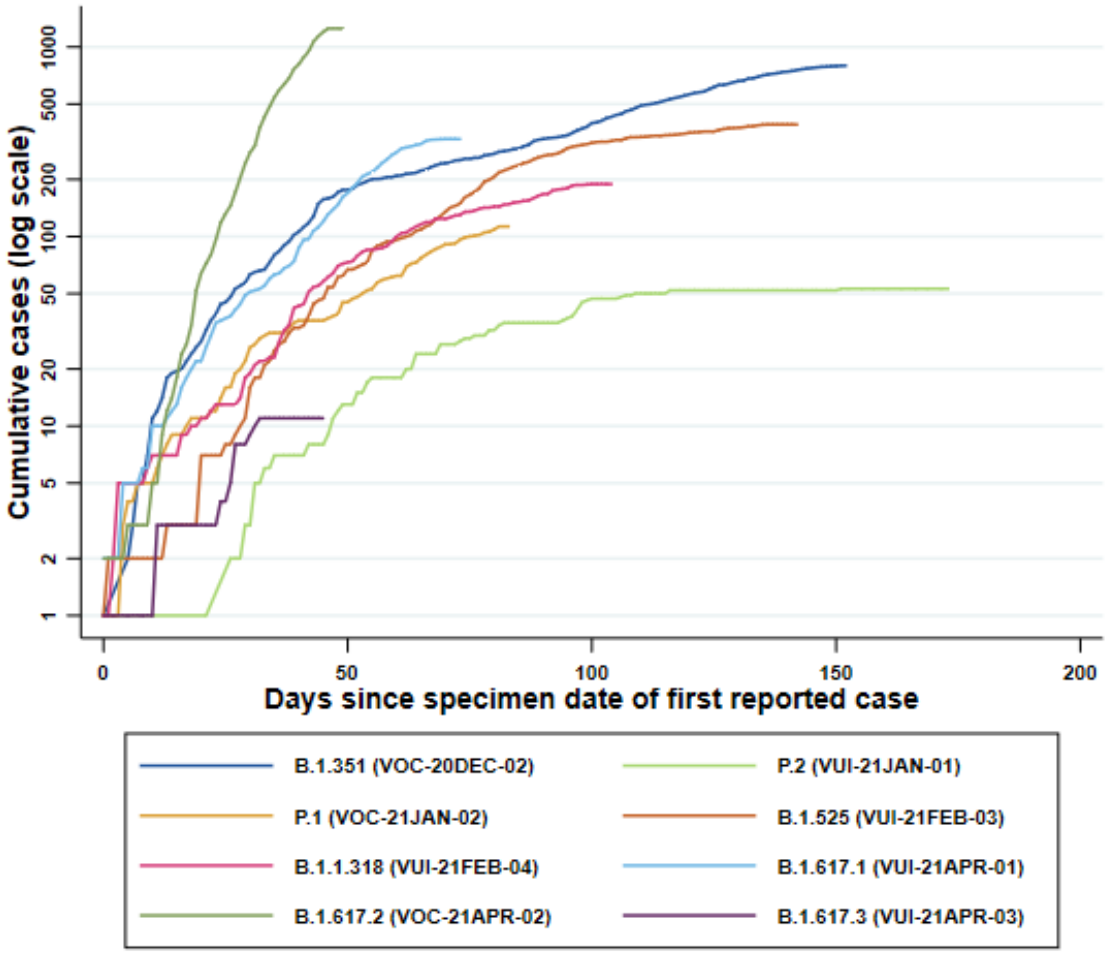
The number of cases of variants of concern and variant under investigation are shown in Table 2. including the proportion of variant cases compared to all sequenced cases, deaths and case fatality rate. Figure 2 shows the cumulative number of cases per variant indexed by days since first report.

Table 2. Case number, proportion, death and case fatality rate of variants of concern and variant under investigation from 1 October 2020 to 12 May 2021

Variant	Case Number[a]	Case Proportion	Deaths[b]	Case Fatality[c]
VOC-20DEC-01	202,229	98.425%	4,103	2.0% (2.0 - 2.1%)
VOC-20DEC-02	772	0.376%	12	1.6% (0.8 - 2.7%)
VOC-21FEB-02	43	0.021%	1	2.3% (0.1 - 12.3%)
VOC-21JAN-02	102	0.05%	0	0.0% (0.0 - 3.6%)
VUI-21APR-01	330	0.161%	0	0.0% (0.0 - 1.1%)
VOC-21APR-02	1,255	0.611%	4	0.3% (0.1 - 0.8%)
VUI-21APR-03	11	0.005%	0	0.0% (0.0 - 28.5%)
VUI-21FEB-01	79	0.038%	2	2.5% (0.3 - 8.8%)
VUI-21FEB-03	393	0.191%	12	3.1% (1.6 - 5.3%)
VUI-21FEB-04	190	0.092%	1	0.5% (0.0 - 2.9%)
VUI-21JAN-01	54	0.026%	1	1.9% (0.0 - 9.9%)
VUI-21MAR-02	6	0.003%	0	0.0% (0.0 - 45.9%)

Excludes variant cases not linked to a known COVID-19 case or with provisional sequencing/genotyping results.
[a]Case number England genomic cases 12 May 2021.
[b]Deaths As of 12 May 2021 (within 28 days) with confirmed or probable VOC or total cases.
[c]95% Confidence Intervals calculated with Clopper–Pearson exact method, using R package PropCIs.

Figure 2. Cumulative cases in England of variants indexed by days since first reported, data as of 12 May 2021
(Find accessible data used in this graph in underlying data). Figure 2 demonstrates the rapid identification of B.1.617.2 cases over a short period of time.



Variant prevalence

The prevalence of different variants amongst all sequenced cases is presented in Figure 3, split by region in Figure 4 and by travel status in Figure 5. The ‘Other’ category in Figure 3 and Figure 4 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. The total genomic dataset used for this assessment includes enhanced testing and sequencing from individuals who have travelled, and surge testing and sequencing in outbreak areas. Sequencing numbers and coverage fall in the last week shown due partly to sequencing lag time, and new sequences are still being produced relating to sample dates in that week. The supplementary data for figures is available.

Figure 3. Variant prevalence for all England available case data from 1 February 2021 as of 12 May 2021 (Excluding cases where the specimen date was unknown). (Find accessible data used in this graph in underlying data).

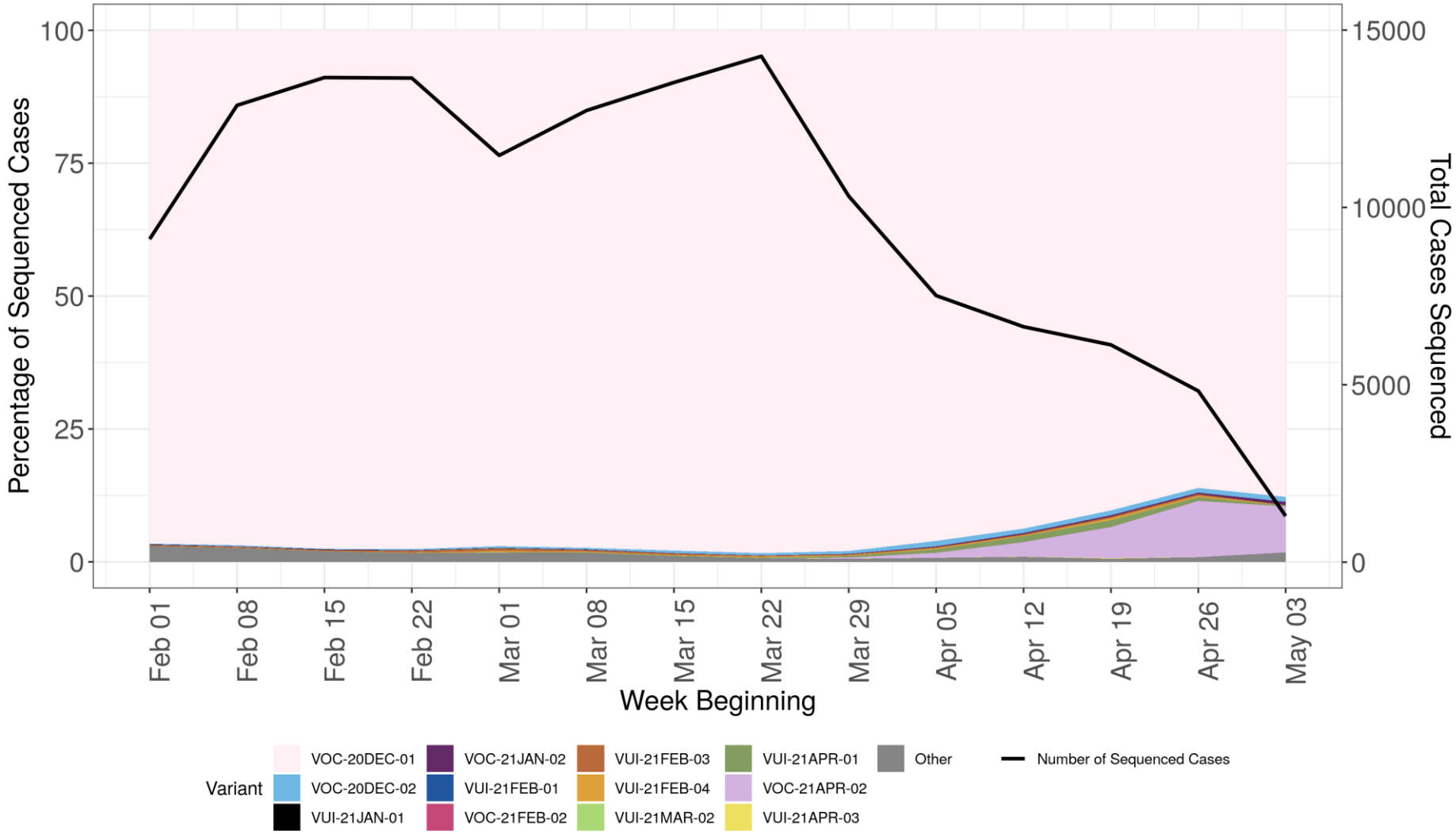


Figure 4. Variant prevalence for all England available case data from 1 February 2021 as of 12 May 2021 by region
(Excluding cases where the region or specimen date were unknown). Black line indicates total number of cases sequenced (Find accessible data used in this graph in underlying data). Data for most recent 2 weeks is incomplete.

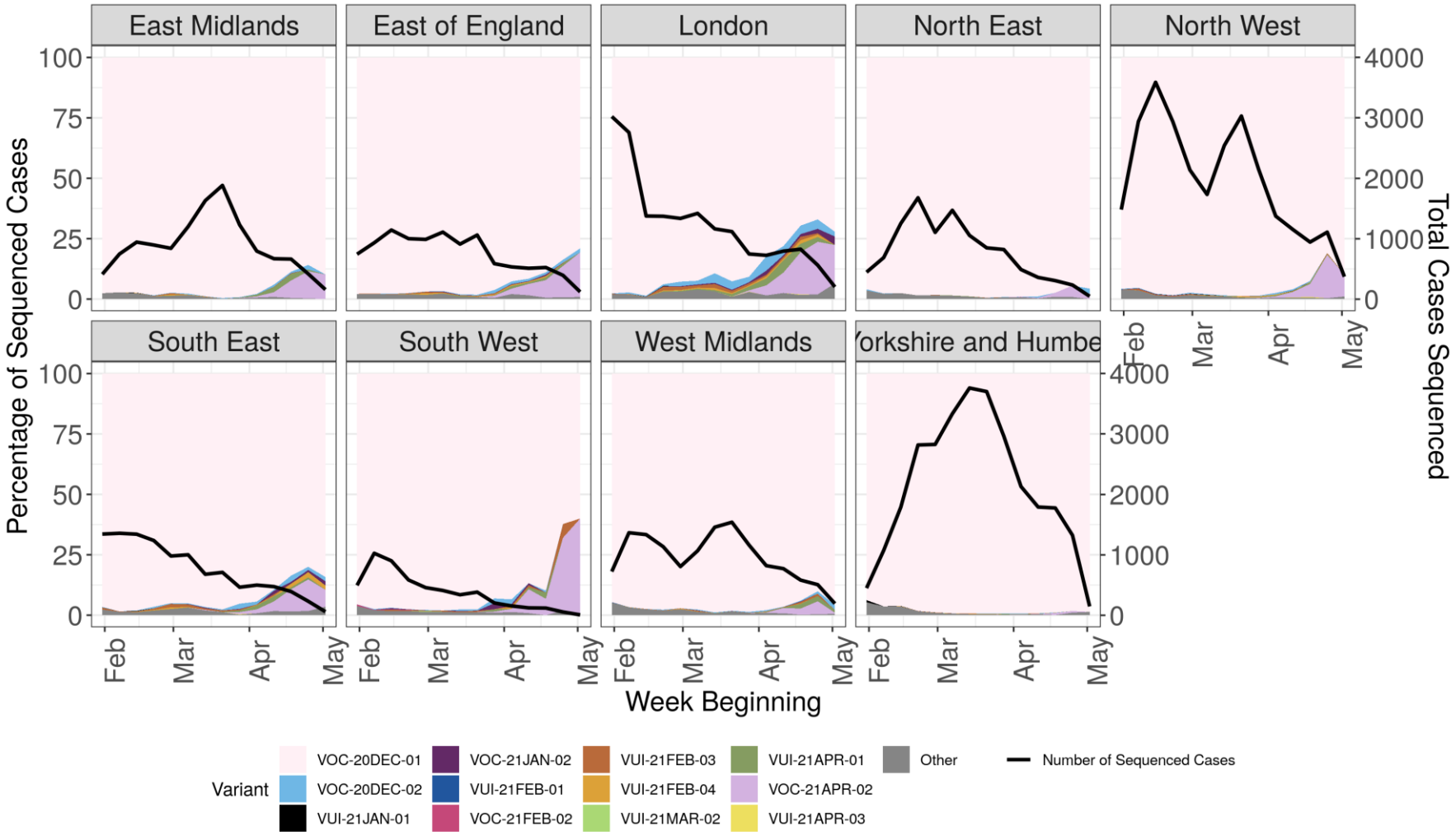
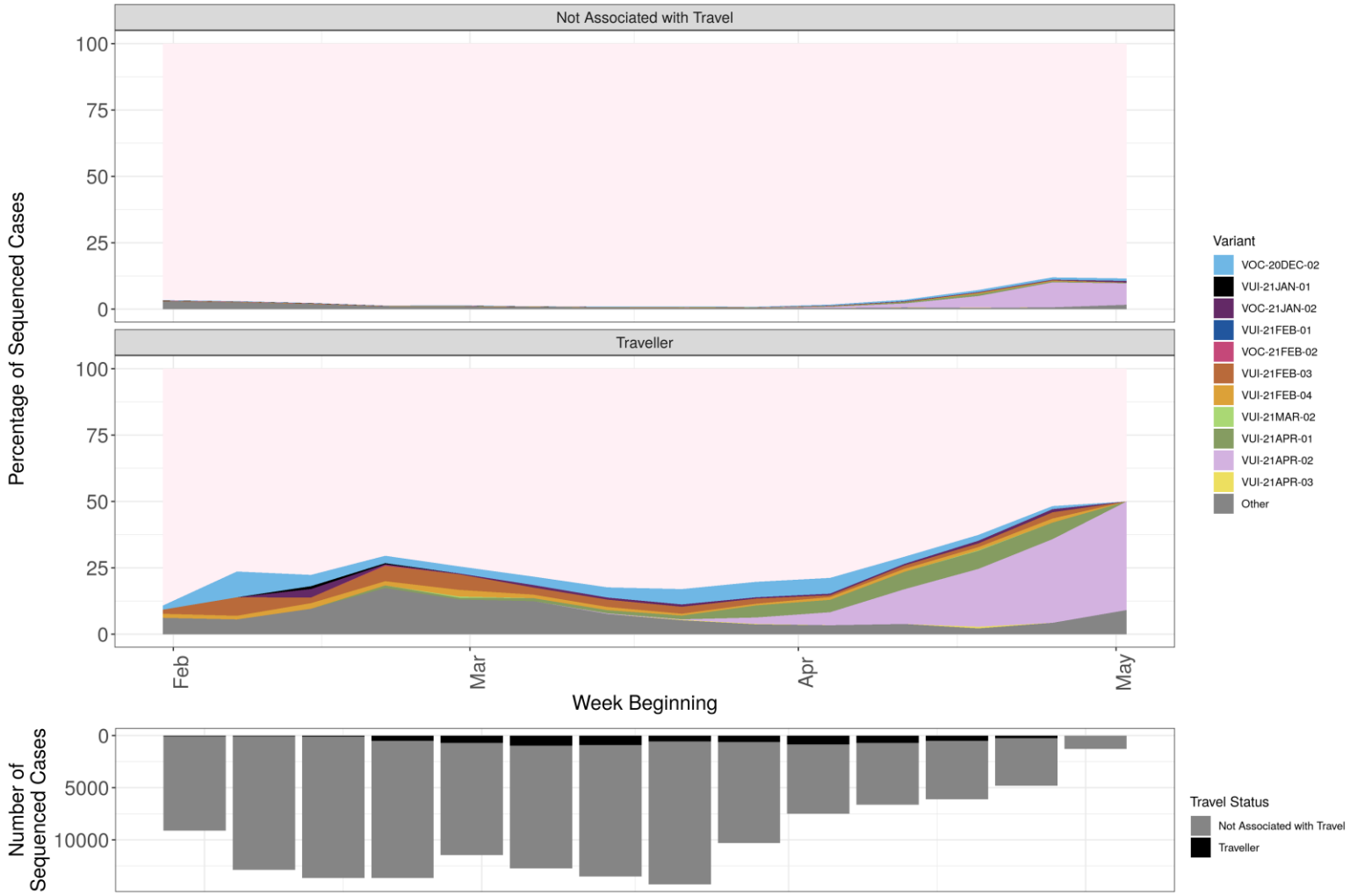


Figure 5. Prevalence of variants over time: all sequenced cases in England, split by travel status as of 12 May 2021
(Find accessible data used in this graph in underlying data). Travel status includes cases matched to Passenger Locator Form data and samples taken as part of the managed quarantine service or through private testing following travel. The total number of sequenced cases in each week is shown in the bars below, split by travel status.



Growth rates

Logistic growth rates (1/week from 1 January 2021 as of 12 May 2021) relative to lineage B.1.1.7 are calculated for each VUI or VOC with more than 20 samples and shown in Table 3. Sample inclusion criteria are: 1) A non-traveller as determined by matching each case against passenger locator forms and managed quarantine service test codes 2) Collected from Pillar 2 testing. 3) If multiple sequences are collected from the same patient which show the same variant, the first sample is retained. Additionally, samples with missing or unknown date of sample collection or upper tier local authority (UTLA) of residence are excluded.

A sample of B.1.1.7 is collected for measuring relative growth rates by weighting each B.1.1.7 sample by the proportion of the VUI or VOC which are sampled in each UTLA. Any B.1.1.7 samples collected outside the period of time that the VUI or VOC are observed are excluded as are B.1.1.7 samples collected in UTLAs where the VUI or VOC have not yet been detected. The growth rate is estimated by logistic regression of the variant on time of sample collection. A growth rate of 0 would indicate parity with B.1.1.7.

Compared to lineage B.1.1.7, the growth rate for B.1.617.2 displays an increased growth rate. Growth rate is context dependent and cannot be interpreted as a change in biological transmissibility.

Table 3. Growth rate of variants of concern and variants under investigation 1 January 2021 as of 12 May 2021. Sample sizes (n) correspond to the number of VUI or VOC used in the analysis. P values correspond to the null hypothesis that there is no difference in VUI/VOC growth rates and B.1.1.7 growth rates.

Variant	Growth rate
VOC-20DEC-02	0.19 (p=4.336e-34,n=283)
VUI-21JAN-01	-0.16 (p=0.01946,n=22)
VOC-21JAN-02	0.62 (p=1.569e-11,n=40)
VUI-21FEB-01	-0.25 (p=0.004,n=55)
VUI-21FEB-03	0.041 (p=0.045,n=150)
VUI-21FEB-04	0.19 (p=1.854e-09,n=90)
VUI-21APR-01	0.61 (p=5.089e-22,n=111)
VOC-21APR-02	1.1 (p=6.591e-142,n=835)

Surveillance of reinfections

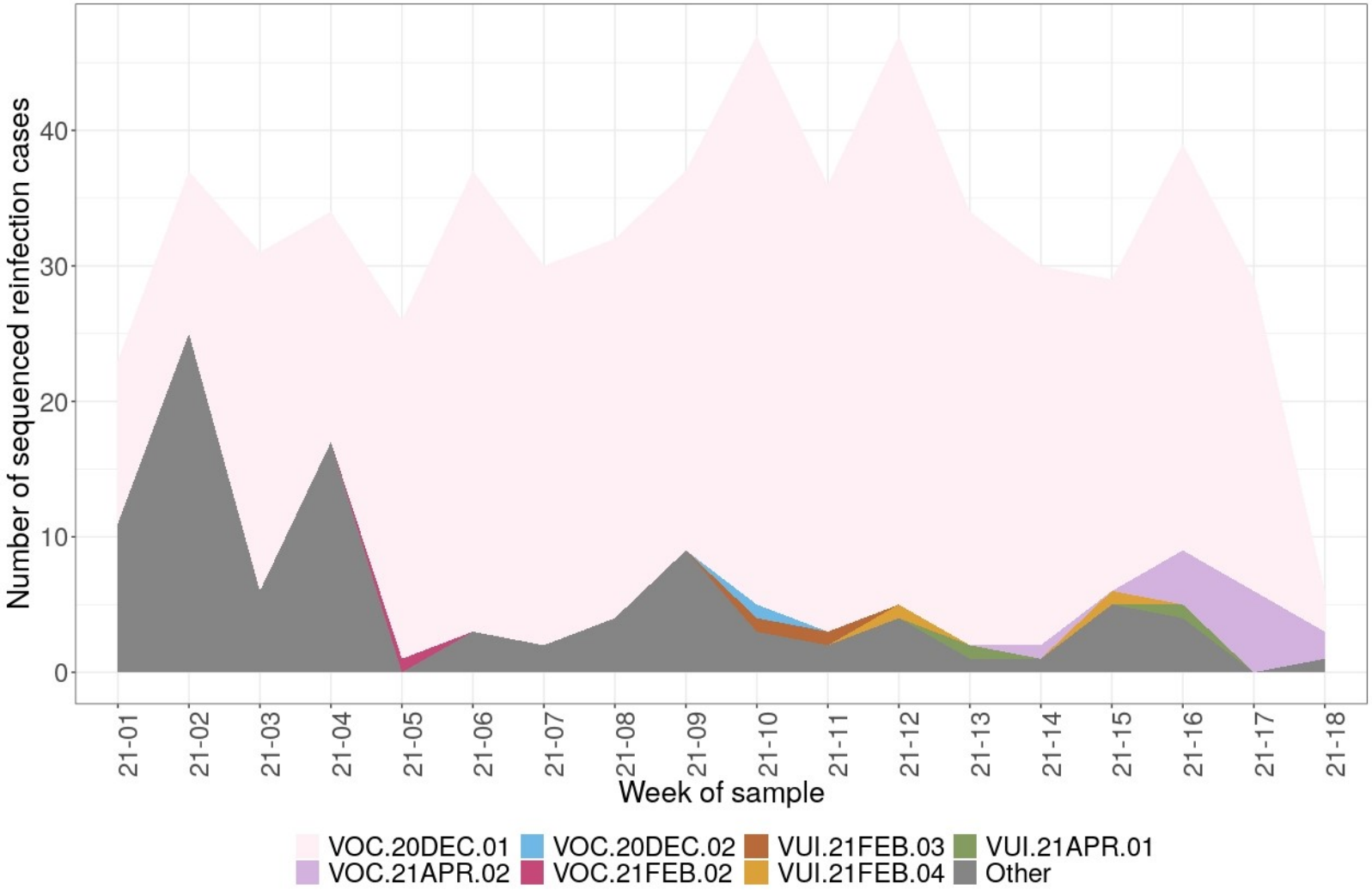
Individuals who have 2 positive tests (PCR and/or LFD) at least 90 days apart are classed as possible reinfection cases. A small proportion of reinfections have been sequenced through standard national surveillance sequencing. Table 4 shows the total number of sequences available from second episodes of infection in possible reinfection cases, categorized by variant. Figure 6 shows the number of different variants identified through sequencing that are possible reinfection cases. In recent weeks there have been small numbers of reinfection with VOC-21APR-02. This is expected with any prevalent variant; comparative analyses are underway.

Table 4. Number of sequenced reinfection cases and the variant assigned. (Data as of 12 May 2021)

Variant	Total
VOC-20DEC-01	487
VOC-20DEC-02	1
VUI-21JAN-01	0
VOC-21FEB-02	1
VUI-21FEB-03	2
VUI-21FEB-04	2
VUI-21APR-01	2
VOC-21APR-02	13
VUI-21APR-03	0
Total sequenced	714

The total potential reinfection figure includes all tests (for example lateral flow devices as well as PCR tests).

Figure 6. The number of reinfections cases from all sample sources, with the total number of reinfections cases with sequences, and the number of variant sequences over time (Find accessible data used in this graph in underlying data)



Part 2: VOC-21APR-02 surveillance

Surveillance through genomic data

Table 5. Number of confirmed and probable VOC-21APR-02 (B.1.617.2) cases, by region of residence as of 12 May 2021

Region	Case Number	Case Proportion	Cases that have travelled	Proportion of travellers among cases
East Midlands	129	10.3%	31	24%
East of England	152	12.1%	46	30.3%
London	400	31.9%	106	26.5%
North East	19	1.5%	3	15.8%
North West	319	25.4%	24	7.5%
South East	98	7.8%	46	46.9%
South West	39	3.1%	26	66.7%
West Midlands	62	4.9%	28	45.2%
Yorkshire and Humber	31	2.5%	16	51.6%
Unknown region	6	0.5%		NA%

Figure 7. Confirmed and probable VOC-21APR-02 (B.1.617.2) cases by specimen date as of 12 May 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data)

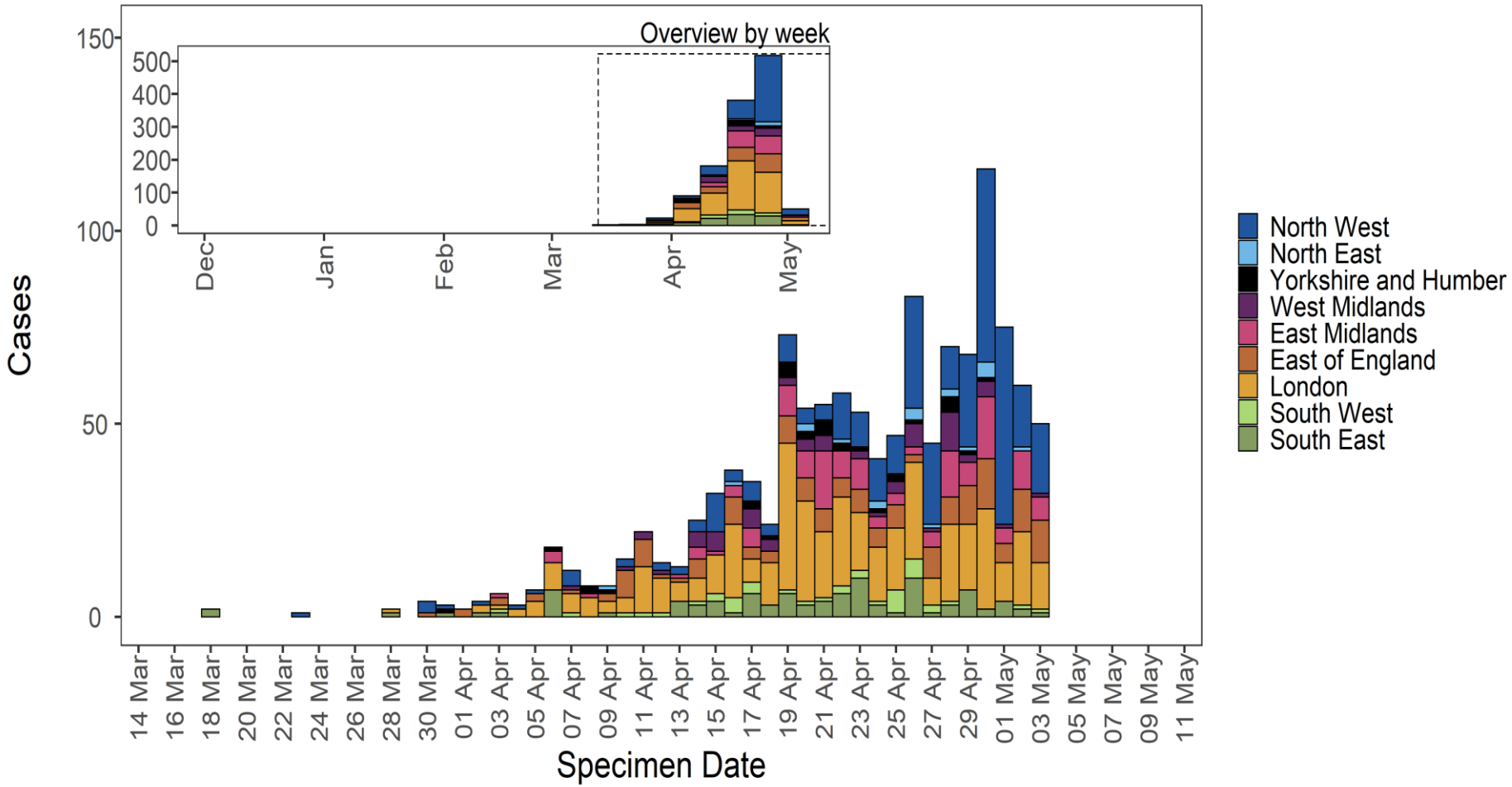
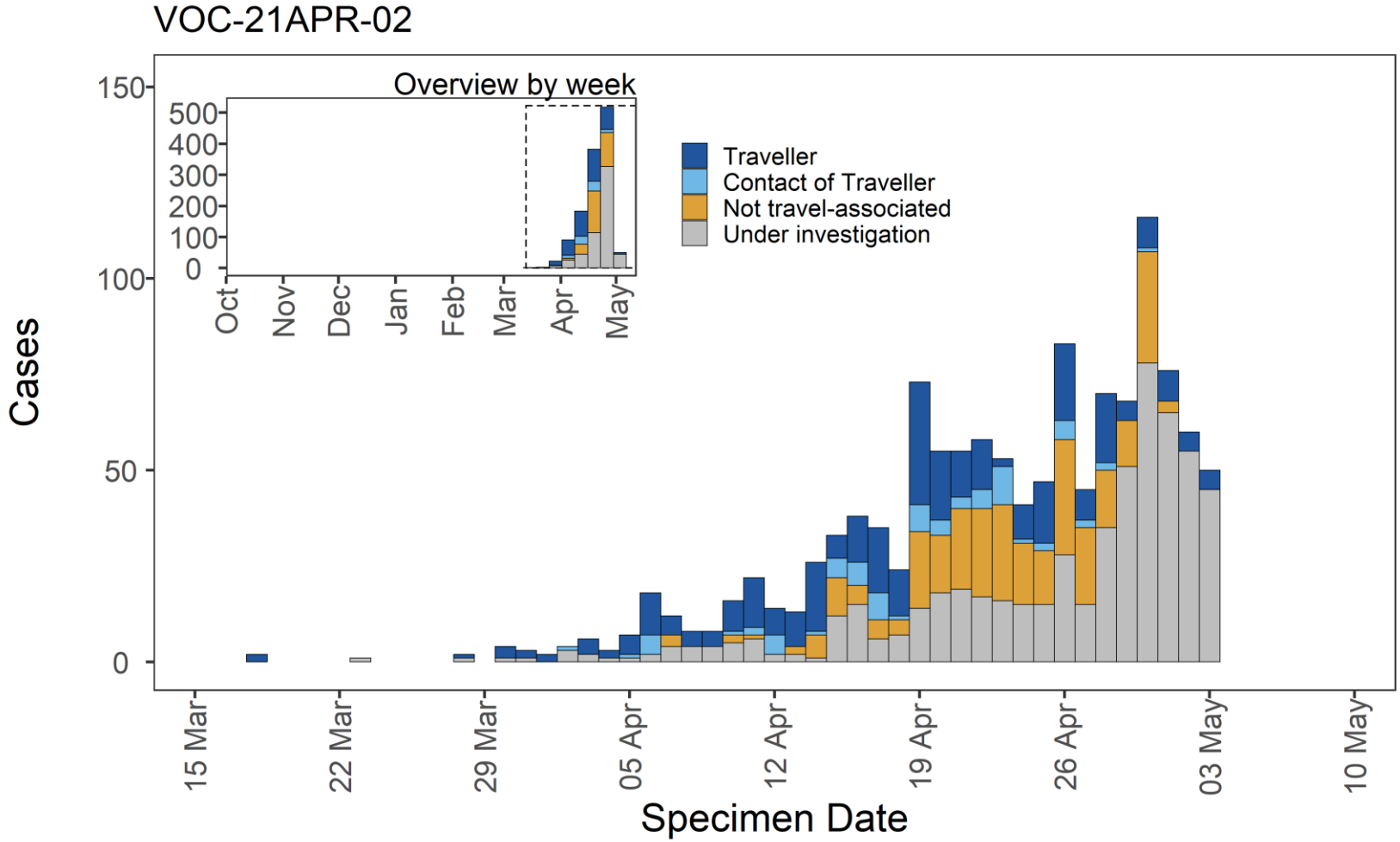


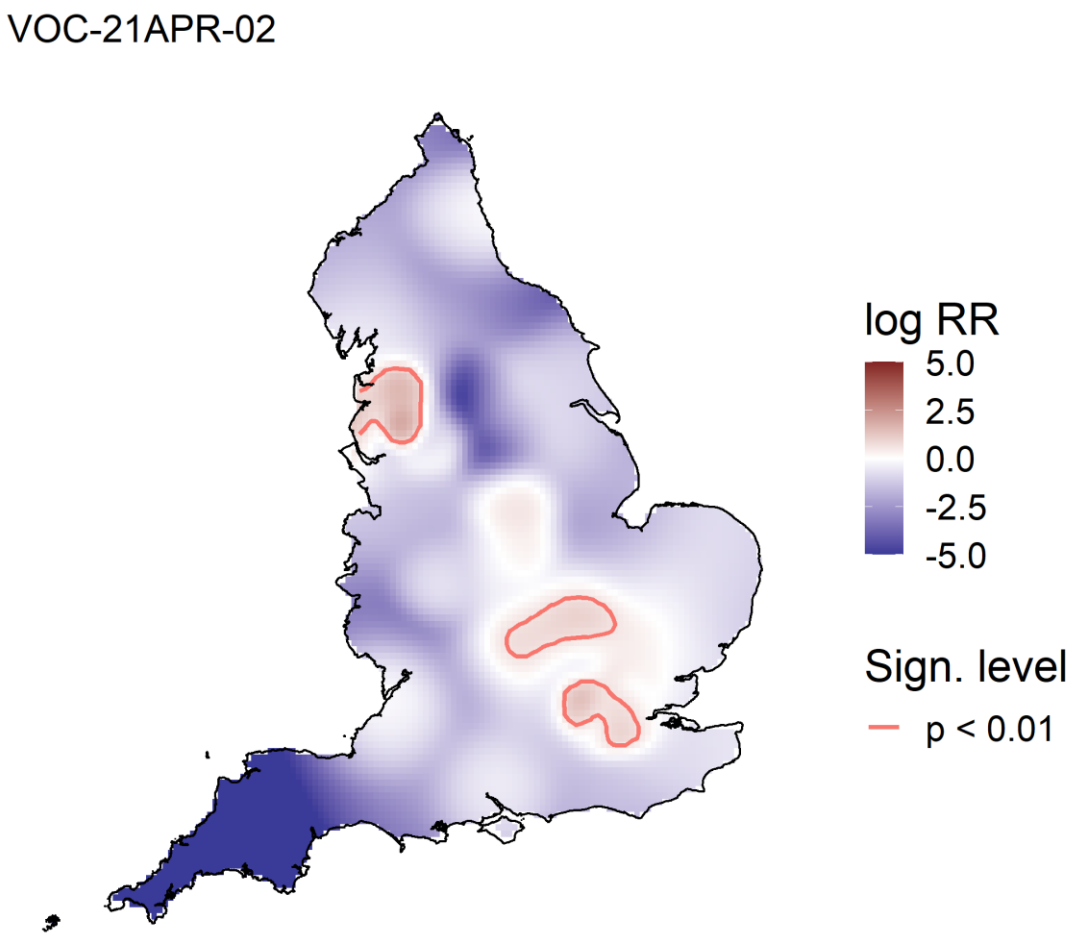
Figure 8. Travel data for confirmed and probable VOC-21APR-02 (B.1.617.2) cases by specimen date as of 12 May 2021
Larger plot includes last 60 days only.
(Find accessible data used in this graph in underlying data)
N/A indicates information is pending or not available.



Spatial variation in risk for variants

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 9 highlights areas of significantly increased risk identified for VOC-21APR-02.

Figure 9. Spatial variation in risk for VOC-21APR-02 (B.1.617.2) data from 1 October 2020, as of 12 May 2021, excluding cases that are known to have travelled
Supplementary data is not available for this figure). This figure excludes cases in managed quarantine facilities. Supplementary data is not available for this figure.



Secondary attack rates

Secondary attack rates for VOC-21APR-02 (B.1.617.2) compared to the other B.1.617.2 lineages and VOC-20DEC-01 (B.1.1.7) are shown in Table 6. 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 VUI-21APR-01, VOC-21APR-02 or VUI-21APR-03 were not significantly different from that for contacts of non-travel cases with VOC-20DEC-01. 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. Secondary attack rates for contacts of travel cases with VOC-21APR-02 were higher than those for travel cases with VOC-20DEC-01.

Table 6. Secondary attack rates for the 3 B.1.617.2 sublineages, presented with B.1.1.7 for comparison
(5 January 2021 to 21 April 2021, data as at 12 May 2021)

Variant	Cases in those that have travelled (% with contacts)	Cases in those that have not travelled or unknown (% with contacts)	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	3663 (78.5% with contacts)	158692 (74.0% with contacts)	2.3%	1.7% (1.6% - 1.8%) [1128/65383]	10.0% (9.9% - 10.1%) [32591/326364]
VUI-21APR-01	171 (80.7% with contacts)	81 (77.8% with contacts)	67.9%	2.0% (1.6% - 2.5%) [70/3469]	12.0% (8.1% - 17.3%) [23/192]
VOC-21APR-02	250 (72.4% with contacts)	287 (80.5% with contacts)	46.6%	3.3% (2.8% - 3.9%) [128/3884]	11.5% (9.6% - 13.9%) [98/850]
VUI-21APR-03	5 (20.0% with contacts)	5 (100.0% with contacts)	50.0%	Unavailable [1/3]	Unavailable [1/12]

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 or 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 21 April 2021 in order to allow time for contacts to become cases, hence case counts are lower than other sources. Provisional results are excluded.

Surveillance of cases in travellers from India

Figure 10. Lineages of cases with recent travel history from India
Each line shows the count of cases of that lineage with known travel history from India: B.1.1.7 in green, B.1.617.1 in blue, B.1.617.2 in cyan, other lineages as dashed line (22 February 2021 to 2 May 2021).(Find accessible data used in this graph in underlying data).

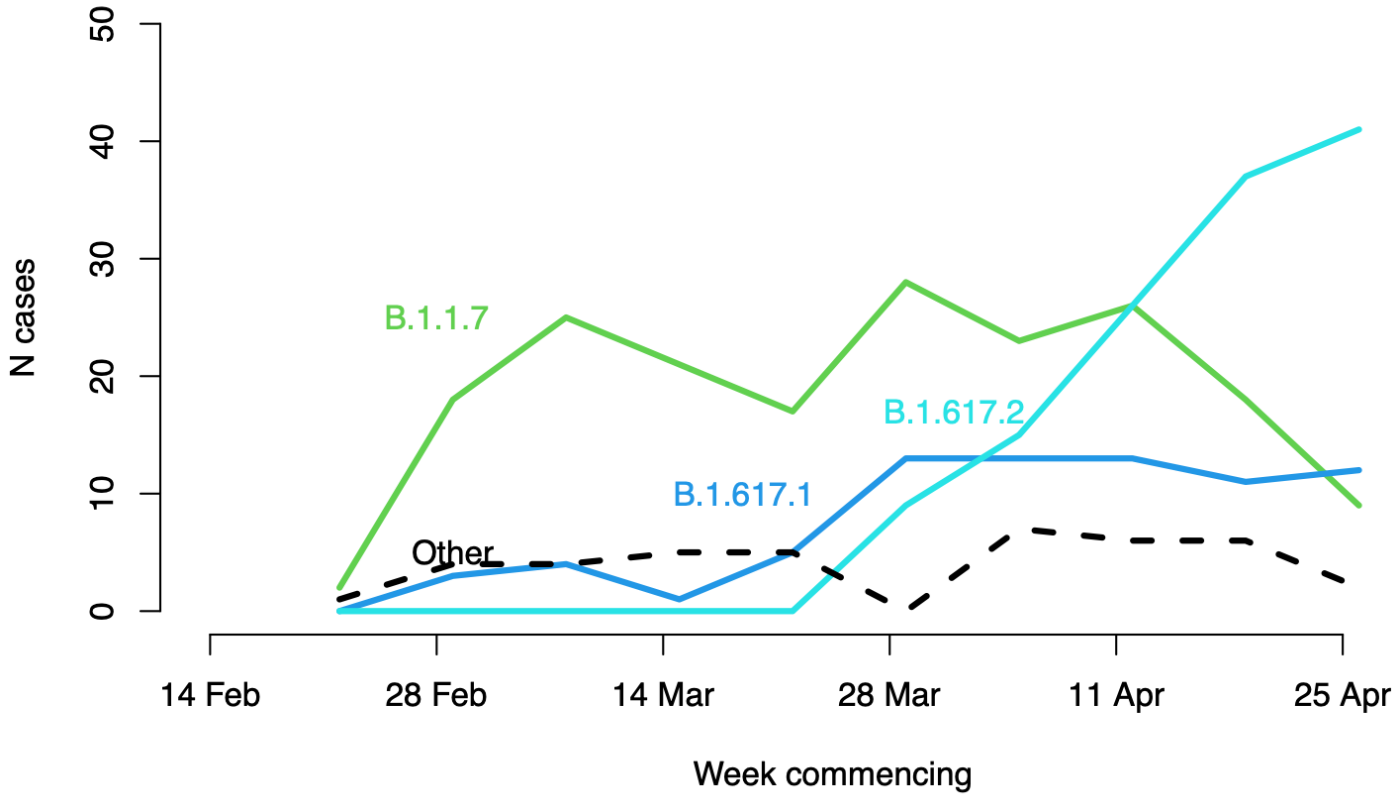
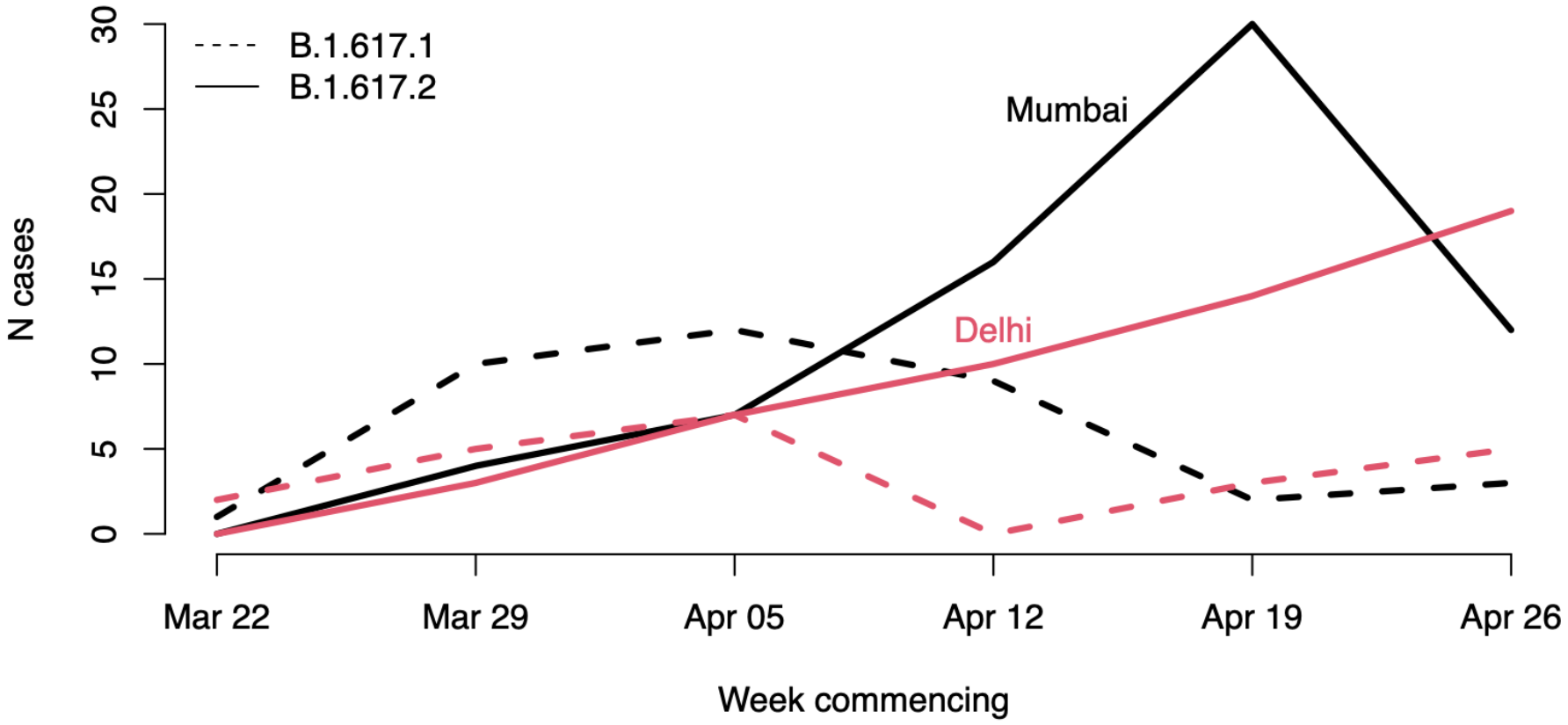


Figure 11. Lineages of cases from selected cities of departure within India. Each line shows the count of cases of that lineage with a listed port of departure from a particular city: Mumbai in black, Delhi in red. For each city, the dashed line is B.1.617.1, the solid line B.1.617.2. (22 February 2021 to 2 May 2021).



Surveillance through S gene detection

The S gene target in a specific 3-target assay used in some Lighthouse Laboratories fails in B.1.1.7, previously predominant, but is detected in VUI-21APR-01, VOC-21APR-02 and VUI-21APR-03 variants as well as VOC-20DEC02 (B.1.351) and some others. Specimens with a detectable S gene (also referred to as S gene positive) are defined as those with cycle threshold (CT) values of ≤30 in all 3 gene targets: S, N, and ORF1ab.

Figure 12 shows the number of sequenced S gene positive isolates over time since 1 January 2021 (data as of 12 May 2021), as well as the distribution of identified variants among these specimens. Unclassified variants refer to those not considered a VOC or VUI; these dominated the sequenced S gene positive specimens at the beginning of 2021, and decreased in proportion towards the end of April 2021 (Figure 12). Among 789 sequenced S gene positive samples in the second half of April 2021, 96% (n = 754) were variants under investigation or of concern, and 72.2% were VOC-21APR-02 (n=570). Among 397 specimens taken in May so far, 93% are VOC-21APR-02 (n=368). This suggests trends in S gene positive cases may currently capture additional VOC-21APR-02 cases not detected through sequencing, however this proxy is limited by variable TaqPath laboratory coverage across England (Figure 13). Additionally biases in sequencing, for instance targeting of contacts of variant cases in outbreak settings, may result in overrepresentation of variants among the S gene positive sequences.

The number of sequenced S gene positive samples (Figure 12) as well as the number and proportion of S gene positive samples nationally (Figure 14) has increased in recent weeks, particularly in North West England and London (Figure 15). Many of the recent S gene positive cases have been detected in a small number of local authorities which have high total case rates, including Bolton, Blackburn with Darwen, Bedford, and Sefton (Figures 13 and 16). Some of these are located in areas where a higher proportion of specimens are tested in laboratories which use the TaqPath PCR assay (Figure 13).

Figure 12. Distribution of variants among sequenced S gene positive SARS-CoV-2 specimens, by half-months as of 12 May 2021. Specimen dates between 1 January 2021 and 7 May 2021, data as of 12 May 2021 (latest period incomplete. Find accessible data used in this graph in underlying data).

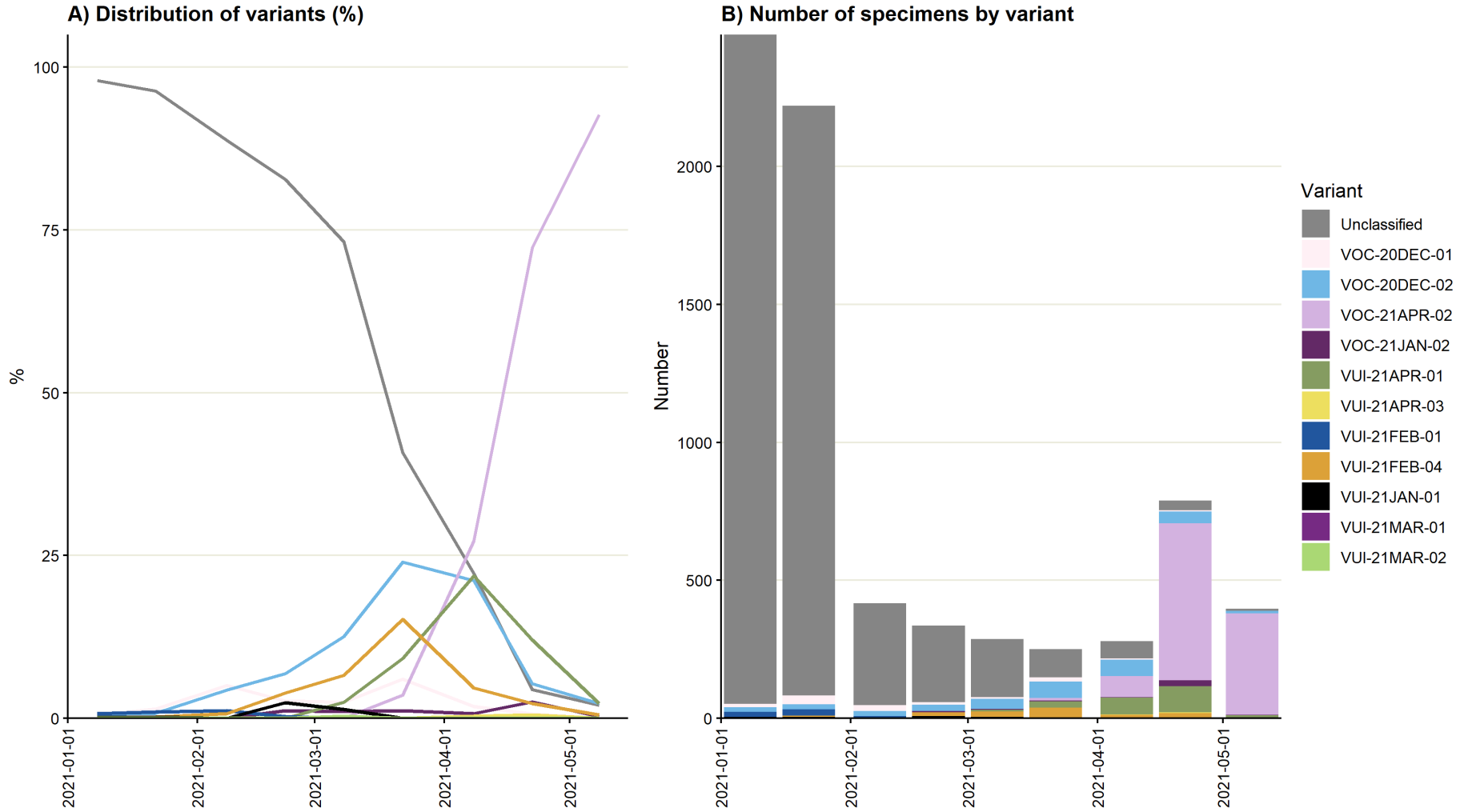


Figure 13. Proportion and number of cases with detectable S gene and TaqPath lab test coverage by local authority of residence. Interpret percentages with caution due to small numbers. Specimen dates 2 May 2021 to 8 May 2021, data as of 12 May 2021; most recent 3 days excluded to reporting delay (Find accessible data used in this graph in underlying data).

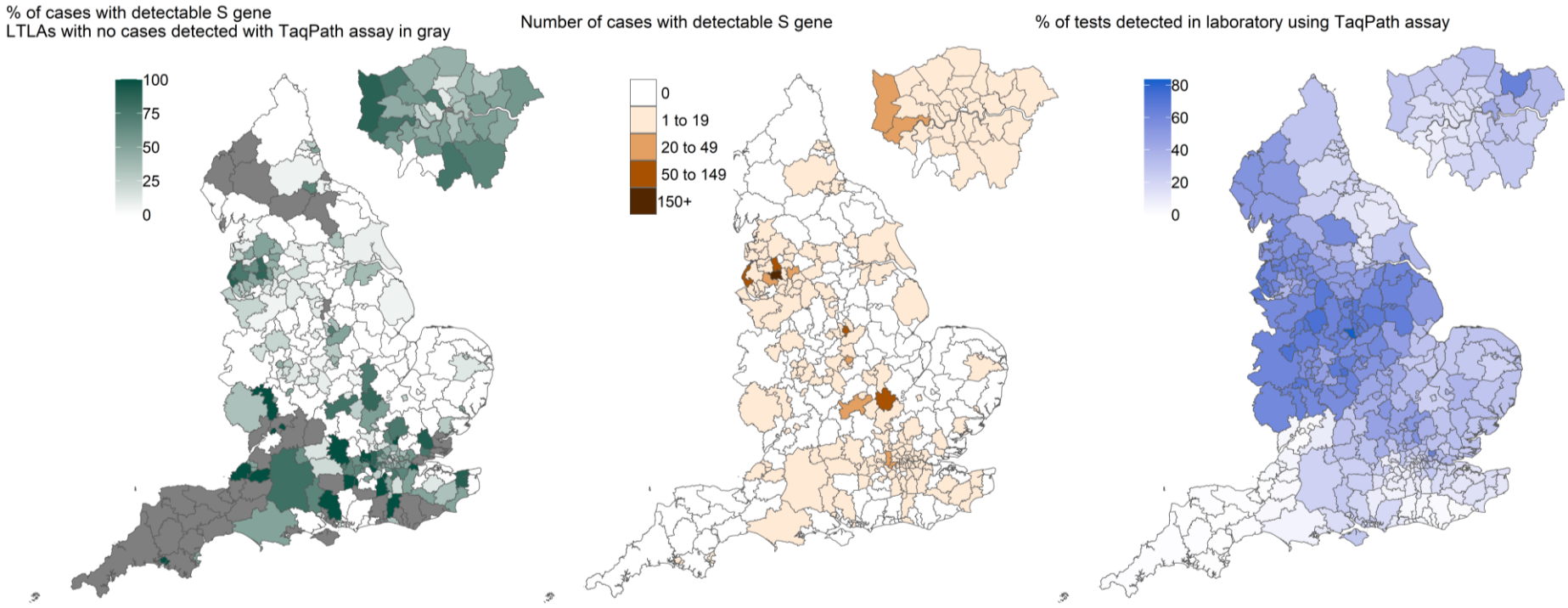
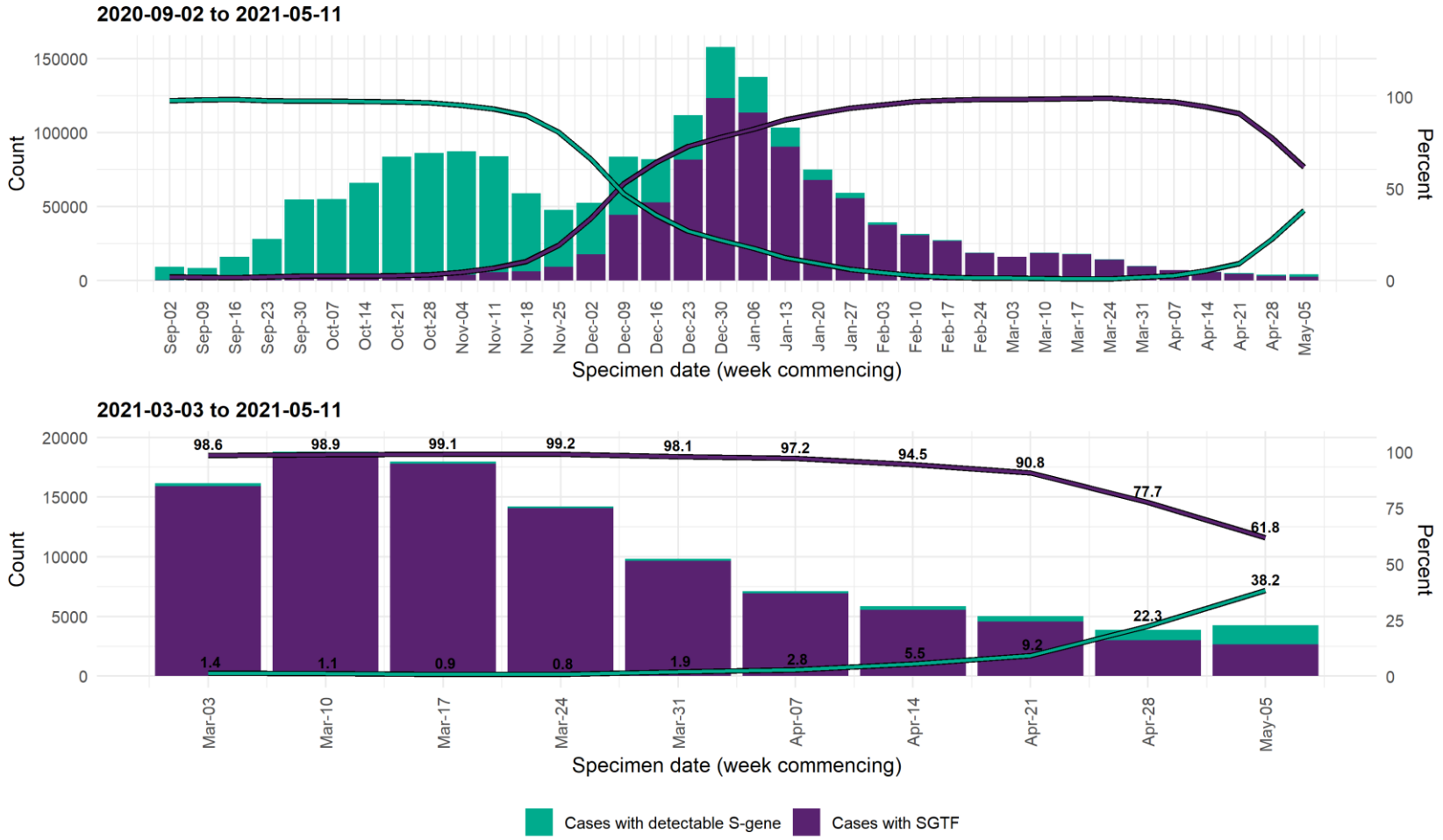


Figure 14. Weekly number and proportion of England Pillar 2 COVID-19 cases with SGTF and detectable S gene among those tested with the TaqPath assay. Specimen dates between 2 September 2020 to 11 May 2021, data as of 12 May 2021 (Find accessible data used in this graph in underlying data).



Only tests carried out with the TaqPath PCR assay and with confirmed SGTF or S gene positive results included, from Alderley Park, Milton Keynes and Glasgow Lighthouse Laboratories.
Case with SGTF: Positive SARS-CoV-2 test with non-detectable S gene and <=30 CT values for N and ORF1ab genes.
Case with detectable S gene: Positive SARS-CoV-2 test with <=30 CT values for S, N, and ORF1ab genes.
Data source: SGSS. Cases deduplicated to one positive test per person per week, prioritising SGTF tests.

Figure 15. Weekly number and proportion of England Pillar 2 COVID-19 cases with detectable S gene or SGTF among those tested with the TaqPath assay, by region of residence. Specimen dates between 3 March 2021 and 11 May 2021, data as of 12 May 2021; 95% confidence intervals indicated by grey shading and percentage for most recent week labelled (Find accessible data used in this graph in underlying data).

Only tests carried out with the TaqPath PCR assay and with confirmed SGTF or S gene positive results included, from Alderley Park, Milton Keynes and Glasgow Lighthouse Laboratories.
Case with SGTF: Positive SARS-CoV-2 test with non-detectable S gene and <=30 CT values for N and ORF1ab genes.
Case with detectable S gene: Positive SARS-CoV-2 test with <=30 CT values for S, N, and ORF1ab genes.
Data source: SGSS. Cases deduplicated to one positive test per person per week, prioritising SGTF tests.
Region missing for 168 persons, excluded from figure.

Figure 16. 7-day COVID-19 case rates per 100,000 population vs proportion S gene positive cases among those tested with TaqPath assay, by upper tier local authority (UTLA) of residence. Specimen dates between 2 May 2021 and 8 May 2021, data as of 12 May 2021 (3 most recent days excluded due to reporting delay). Five UTLAs with highest number of S gene positive cases labelled. Find accessible data used in this graph in underlying data).

Total case rates include PCR and LFD positive.
Proportion S gene positive calculated out of cases with classifiable S gene detection results and tested with TaqPath PCR assay in Alderley Park, Milton Keynes or Glasgow Lighthouse Laboratory.
Case with detectable S-gene: Positive SARS-CoV-2 test with <=30 CT values for S, N, and ORF1ab genes.
Local trends in these data may be affected by decisions to direct the processing of samples via a TaqPath laboratory.
Data source: SGSS. Deduplicated to one test per person within time period, prioritising SGTF.

Part 3: Other B.1.617 sublineages

VUI-21APR-01 (B.1.617.1)

Table 7. Number of confirmed and probable VUI-21APR-01 (B.1.617.1) cases, by region of residence as of 12 May 2021. Travel status in this table and all subsequent travel data in this document is based on information provided through the Contact Tracing Advisory Service (CTAS) and passenger locator forms where available. Travel status for cases under investigation is confirmed after follow up and is updated regularly.

Region	Case Number	Case Proportion	Cases that have travelled	Proportion of travellers among cases
East Midlands	44	13.3%	23	52.3%
East of England	27	8.2%	17	63%
London	145	43.9%	81	55.9%
North East	4	1.2%	2	50%
North West	29	8.8%	20	69%
South East	30	9.1%	19	63.3%
South West	6	1.8%	4	66.7%
West Midlands	30	9.1%	10	33.3%
Yorkshire and Humber	15	4.5%	11	73.3%

Figure 17. Spatial variation in risk for VUI-21APR-01 (B.1.617.1) data from 1 October 2020, as of 12 May 2021, excluding cases that are known to have travelled. Supplementary data is not available for this figure). This figure excludes cases in managed quarantine facilities. Supplementary data is not available for this figure.

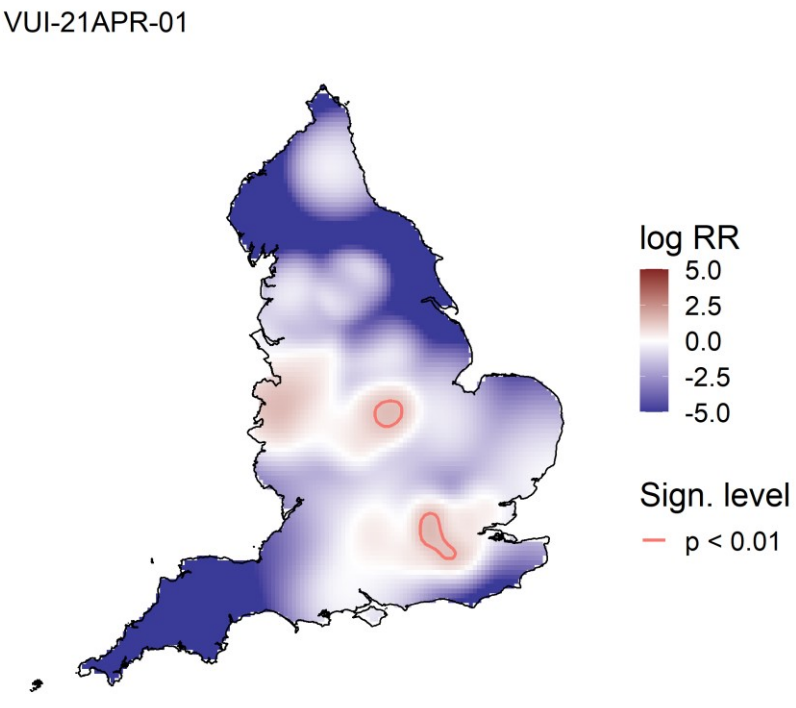


Figure 18. Confirmed and probable VUI-21APR-01 (B.1.617.1) cases by specimen date as of 12 May 2021. Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data).

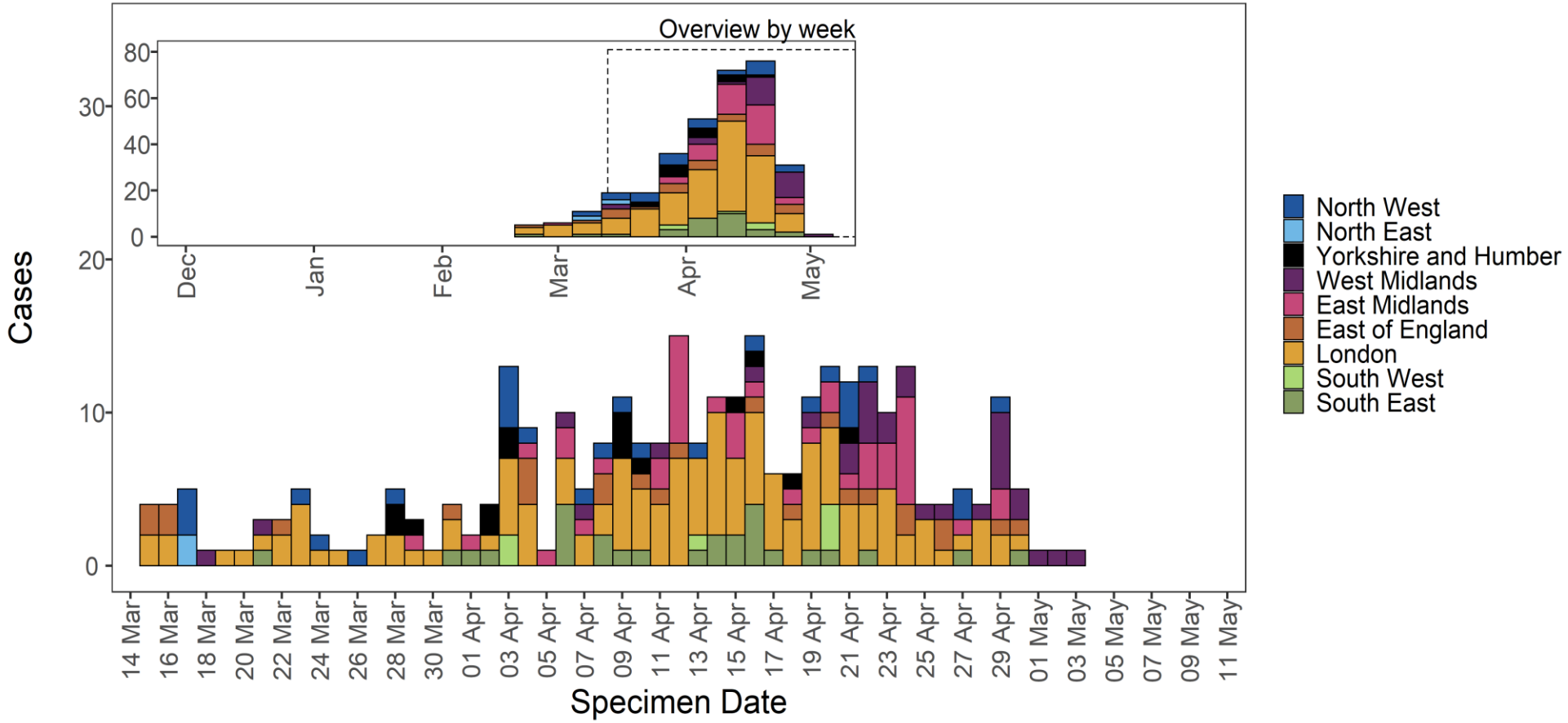
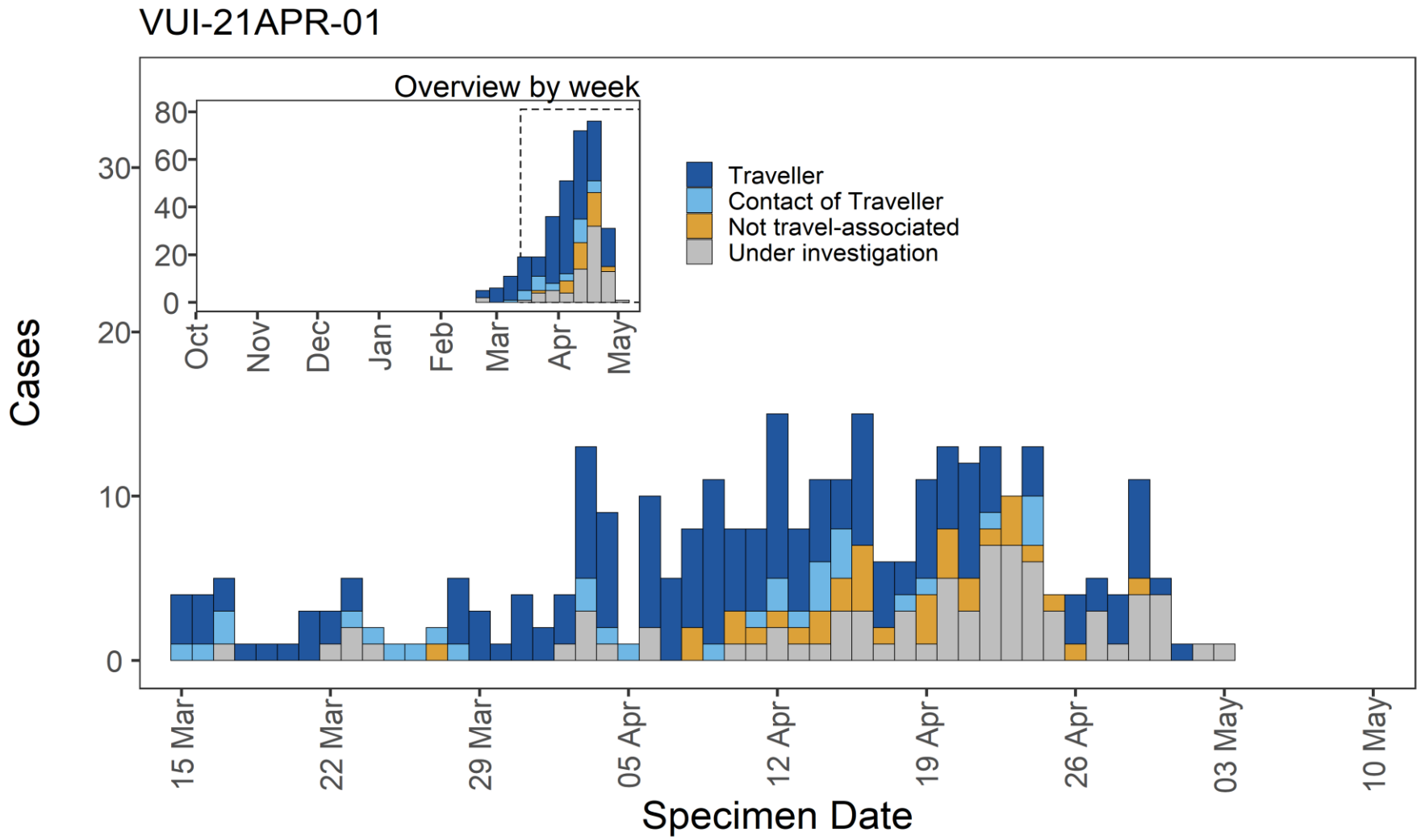


Figure 19. Travel data for confirmed and probable VUI-21APR-01 (B.1.617.1) cases by specimen date as of 12 May 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data). N/A indicates information is pending or not available.



VUI-21APR-03 (B.1.617.3)

Table 8. Number of confirmed and probable VUI-21APR-03 (B.1.617.3) cases, by region of residence as of 12 May 2021

Region	Case Number	Case Proportion	Cases that have travelled	Proportion of travellers among cases
London	4	36.4%	2	50%
North West	6	54.5%	2	33.3%
South East	1	9.1%	0	0%

Figure 20. Spatial variation in risk for VUI-21APR-03 (B.1.617.3) data from 1 October 2020, as of 12 May 2021, excluding cases that are known to have travelled Supplementary data is not available for this figure). This figure excludes cases in managed quarantine facilities. Supplementary data is not available for this figure.

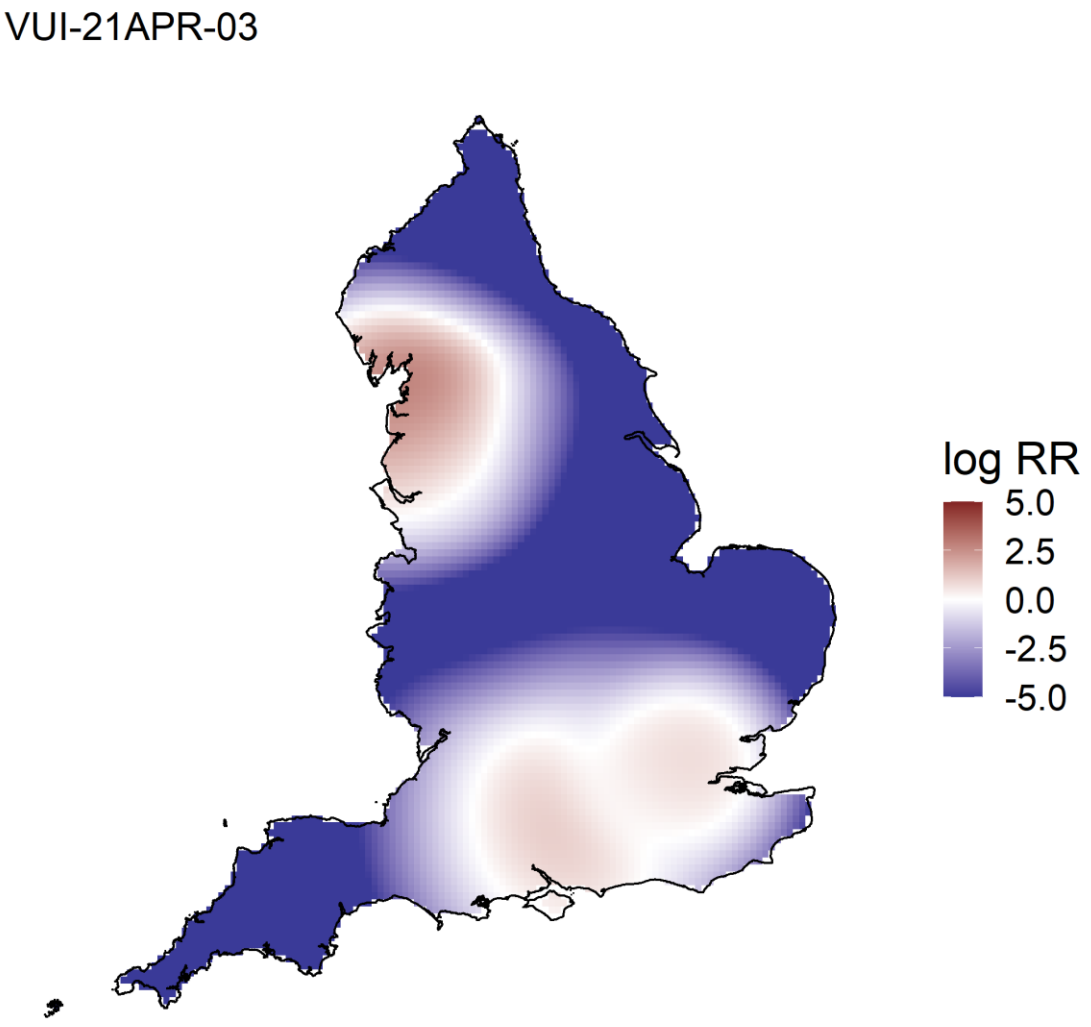


Figure 21. Confirmed and probable VUI-21APR-03 (B.1.617.3) cases by specimen date as of 12 May 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data).

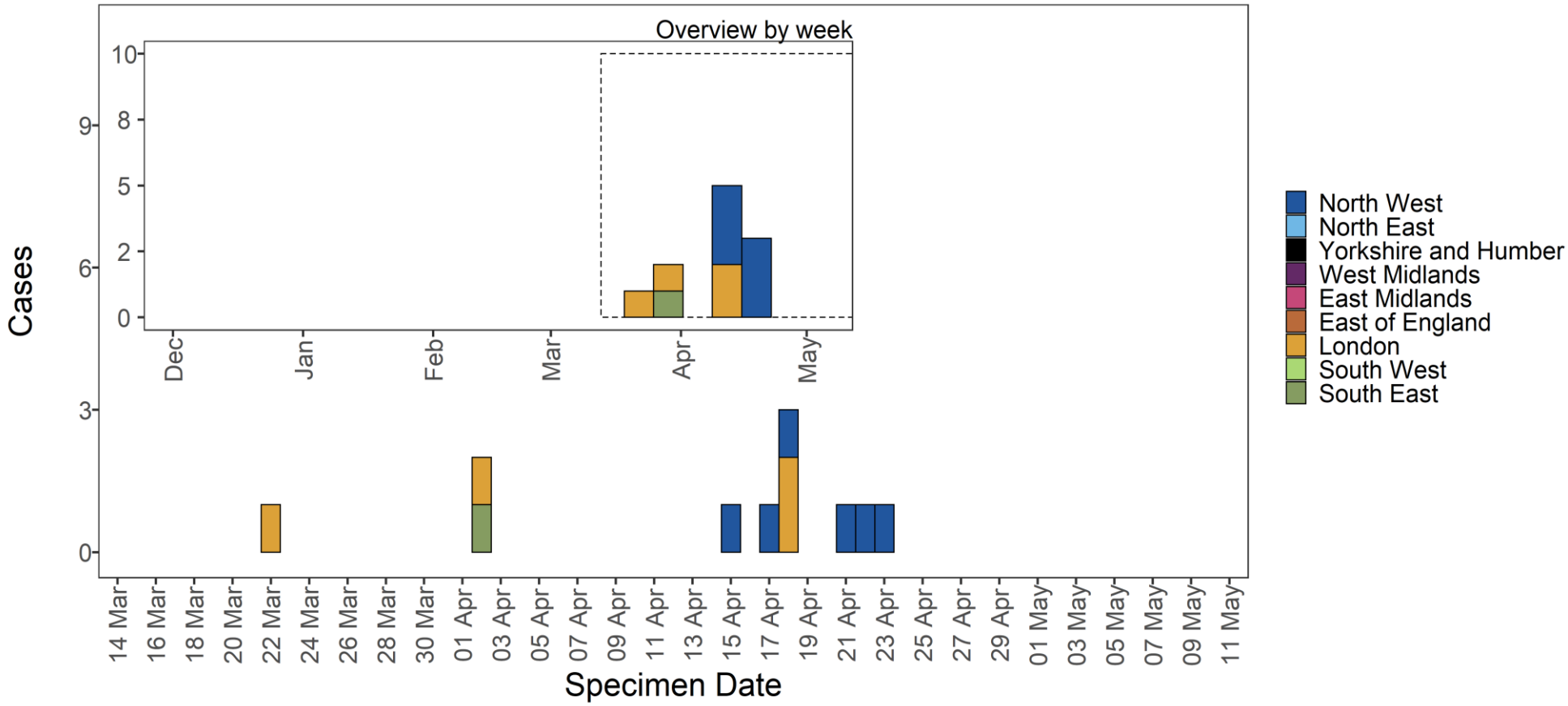
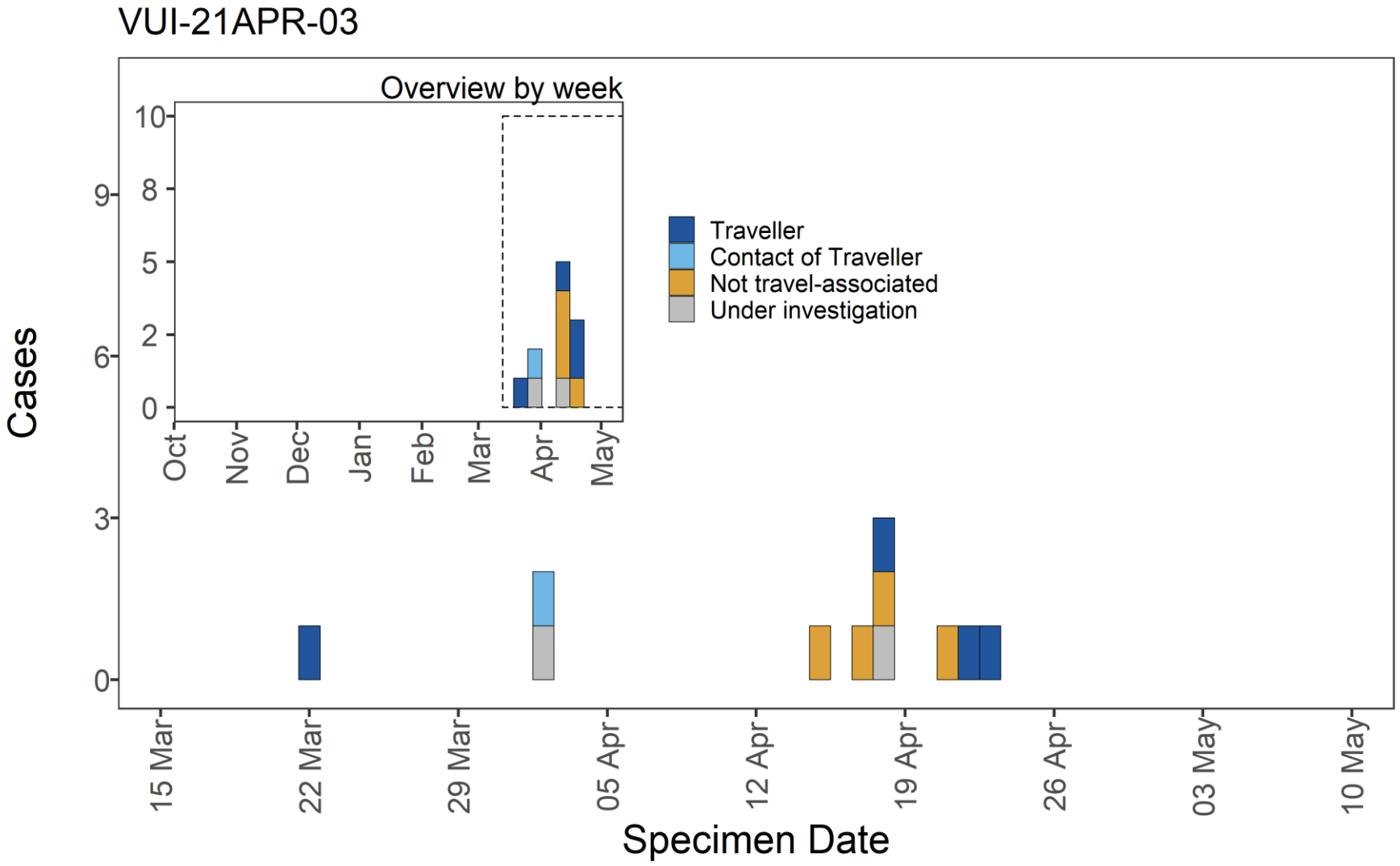


Figure 22. Travel data for confirmed and probable VUI-21APR-03 (B.1.617.3) cases by specimen date as of 12 May 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data). N/A indicates information is pending or not available.



International surveillance

In total, 59 countries have reported at least one case of the VUI-21APR-01, VOC-21APR-02 and VUI-21APR-03 variants via GISAID, or official or media sources, or via IHR/EWRS. GISAID includes data on sequences available internationally. As of 12 May 2021 sequences from the following countries (excluding UK) have been identified in GISAID:

- **VUI-21APR-01 (B.1.617.1)** Australia (21), Bahrain (8), Belgium (6), Canada (5), Czech Republic (3), Denmark (21), France (2), Germany (32), Greece (1), Guadeloupe (2), Hong Kong (9), India (1,069), Ireland (9), Italy (1), Japan (9), Jordan (3), Luxembourg (5), Malaysia (1), Mexico (1), Netherlands (6), New Zealand (4), Portugal (7), Saint Martin (2), Singapore (58), South Korea (5), Spain (1), Sweden (4), Switzerland (6), Thailand (1), USA (137), Uganda (1)
- **VOC-21APR-02 (B.1.617.2)** Aruba (3), Australia (64), Austria (1), Bahrain (14), Bangladesh (6), Belgium (15), Canada (1), China (2), Denmark (17), France (13), Germany (46), Greece (1), Hong Kong (3), India (452), Indonesia (4), Ireland (28), Italy (18), Japan (19), Luxembourg (2), Malaysia (1), Mexico (1), Netherlands (5), New Zealand (9), Norway (1), Poland (5), Romania (1), Singapore (100), Slovenia (1), South Korea (1), Spain (5), Sweden (3), Switzerland (13), USA (211), Uganda (3)
- **VUI-21APR-03 (B.1.617.3)** India (47), Russia (2), USA (1)

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).

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 Technical Group

Authors of this report

PHE Genomics Cell
PHE Outbreak Surveillance Team
PHE Epidemiology Cell
PHE Contact Tracing Cell Data Team

Variant Technical Group Membership

The PHE Variant Technical Group includes representation from the following organisations: PHE, DHSC, 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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