Public Health England

Protecting and improving the nation's health

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

Technical briefing 12

22 May 2021

This briefing provides an update on previous briefings up to 13 May 2021

Contents

Summary

There are 5 variants of concern and 8 variants under investigation (Table 1).

This report has been published to continue to share detailed surveillance of VOC-21APR-02 (B.1.617.2) and information on a new variant under investigation VUI-21MAY-01 (AV.1). 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 emerging variants, and findings have a high level of uncertainty.

This briefing contains a surveillance overview of variants, an update on investigations of VOC-21APR-02 (B.1.617.2) and details of a new variant under investigation (VUI-21MAY-01, AV.1).

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

A small number of areas have both high proportions of S gene target positive cases and elevated incidence rates.

Hospitalisation data is provided for the first time for all variants.

Secondary attack rates are higher for VOC-21APR-02 (B.1.617.2) than for VOC-20DEC-01 (B.1.1.7) in travellers and non-travellers.

There continue to be small numbers of reinfections, including with VOC-21APR-02 (B.1.617.2), detected through national surveillance, which is expected with any prevalent variant. Comparative analyses are underway. The SIREN national healthcare worker cohort shows no increase in reinfections or acute infections overall during the time period that VOC-21APR-02 (B.1.617.2) has been increasing in prevalence.

Analysis of vaccine effectiveness using the national immunisation and genomics datasets to compare VOC-20DEC-01 (B.1.1.7) and VOC-21APR-02 (B.1.617.2) suggest that while there is a reduction in vaccine effectiveness against VOC-21APR-02 (B.1.617.2) after one dose, any reduction in vaccine effectiveness after 2 doses of vaccine is likely to be small.

The risk assessment for VOC-21APR-02 (B.1.617.2) is published separately.

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: Surveillance overview

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.

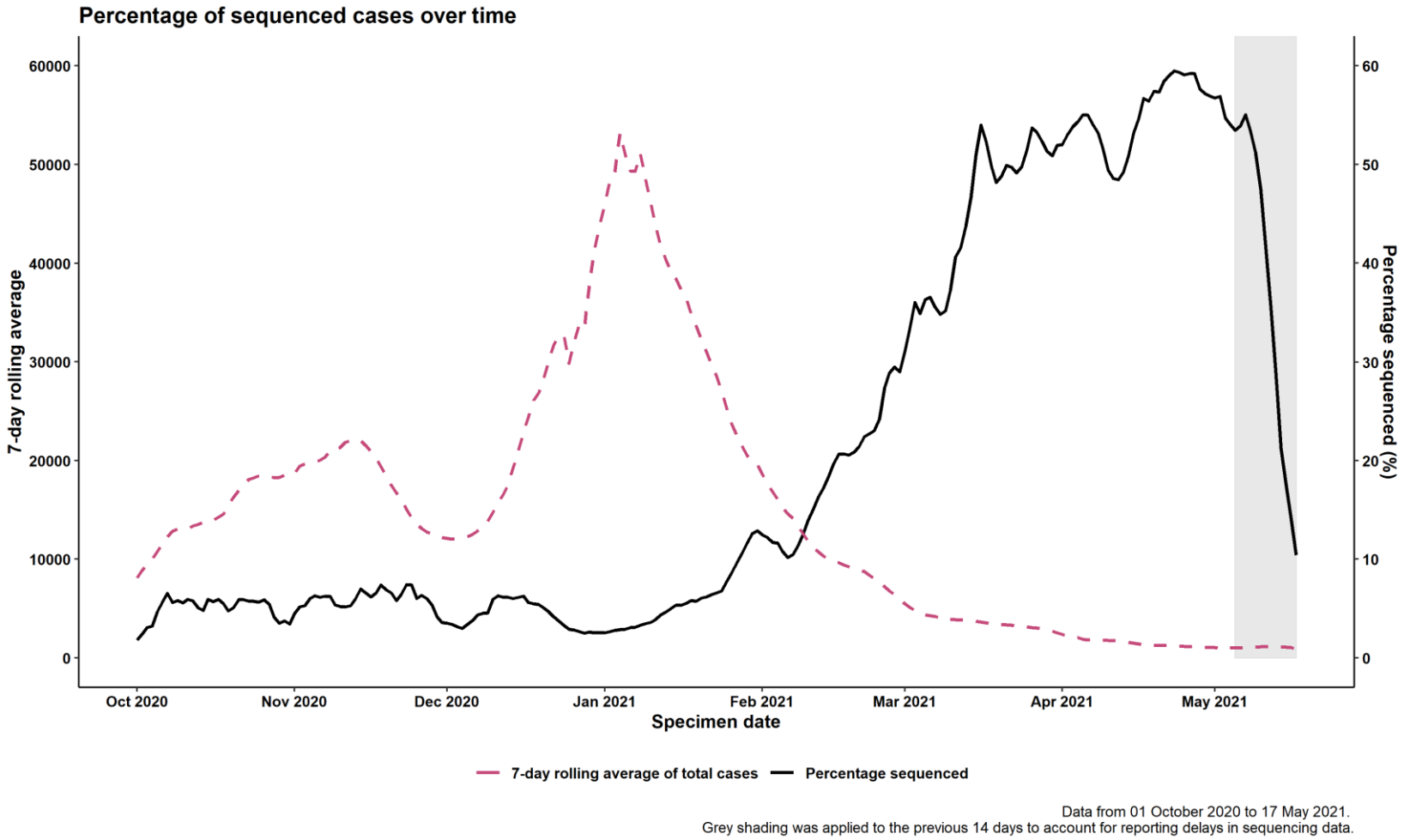
Table 1. Variant lineage and designation as of 18 May 2021 (provisionally extinct variants removed)

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
AV.1	VUI-21MAY-01	UK	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

Sequencing coverage

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

Figure 1. Coverage of sequencing: percentage of SARS-CoV-2 cases sequenced over time as of 18 May 2021
(Find accessible data used in this graph in underlying data)



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

Table 2 shows the number of cases and deaths associated with each variant of concern and variant under investigation, and the proportion of total sequenced cases accounted for by each variant. Table 3 shows the number of cases known to be infected with VOC/VUIs who visited an NHS Emergency Department, the number who were admitted, and the number who died in any setting (note data is shown from 1 February 2021 onwards to enable comparison). 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 18 May 2021

Variant	Case Number[a]	Case Proportion	Deaths[b]	Case Fatality[c]
VOC-20DEC-01	206,598	97.6%	4,127	2.0% (1.9 - 2.1%)
VOC-20DEC-02	800	0.4%	12	1.5% (0.8 - 2.6%)
VOC-21JAN-02	128	0.06%	0	0.0% (0.0 - 2.8%)
VOC-21FEB-02	43	0.02%	1	2.3% (0.1 - 12.3%)
VOC-21APR-02	2,854	1.3%	6	0.2% (0.1 - 0.5%)
VUI-21JAN-01	54	0.04%	1	1.9% (0.0 - 9.9%)
VUI-21FEB-01	79	0.05%	2	2.5% (0.3 - 8.8%)
VUI-21FEB-03	409	0.2%	12	2.9% (1.5 - 5.1%)
VUI-21FEB-04	205	0.1%	1	0.5% (0.0 - 2.7%)
VUI-21MAR-01	2	0.001%	0	0.0% (0.0 - 84.2%)
VUI-21MAR-02	6	0.003%	0	0.0% (0.0 - 45.9%)
VUI-21APR-01	373	0.2%	0	0.0% (0.0 - 1.0%)
VUI-21APR-03	12	0.006%	0	0.0% (0.0 - 26.5%)
VUI-21MAY-01	41	0.02%	0	0.0% (0.0 - 8.6%)

Excludes unlinked sequences (sequenced samples that could not be matched to individuals) and cases with only provisional sequencing/genotyping results.
[a]Case number England genomic cases 18 May 2021.
[b]Deaths as of 18 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.

Table 3. Attendance to emergency care and deaths among all COVID-19 sequenced cases (including provisional sequencing results) in England, 1 February 2021 to 18 May 2021

Variant	Cases since 01 Feb 2021¥	Cases still under follow-up*		Cases with an A&E visit§		Cases where presentation to A&E resulted in overnight inpatient admission§		Deaths^	
		Number	%	Number	%	Number	%	Number	%
VOC-20DEC-01	132,082	10,803	8.2	5,238	4.0	2,011	1.5	1,569	1.2
VOC-20DEC-02	665	107	16.1	31	4.7	11	1.7	12	1.8
VOC-21JAN-02	129	46	35.7	7	5.4	1	0.8	0	NA%
VOC-21FEB-02	34	1	2.9	1	2.9	0	NA%	1	2.9
VOC-21APR-02	2,889	2,455	85.0	104	3.6	31	1.1	6	0.2
VUI-21JAN-01	27	2	7.4	1	3.7	1	3.7	0	NA%
VUI-21FEB-01	8	0	NA%	0	NA%	0	NA%	0	NA%
VUI-21FEB-03	353	41	11.6	10	2.8	3	0.9	7	2.0
VUI-21FEB-04	197	46	23.4	3	1.5	0	NA%	1	0.5
VUI-21MAR-01	2	0	NA%	0	NA%	0	NA%	0	NA%
VUI-21MAR-02	6	1	16.7	0	NA%	0	NA%	0	NA%
VUI-21APR-01	373	127	34.0	4	1.1	1	0.3	0	NA%
VUI-21APR-03	12	4	33.3	0	NA%	0	NA%	0	NA%
VUI-21MAY-01	41	36	87.8	0	NA%	0	NA%	0	NA%
Non-variant	2,454	85	3.5	79	3.2	26	1.1	69	2.8

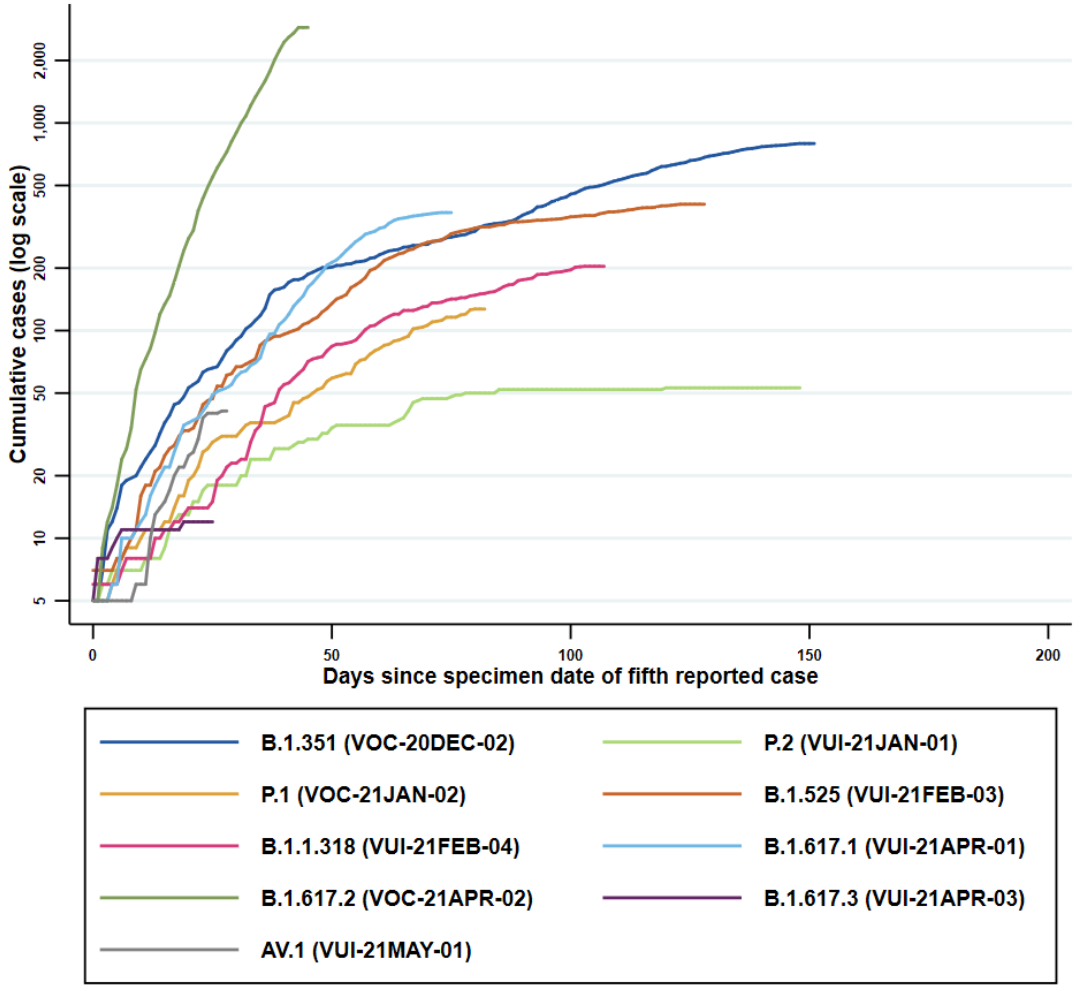
Data sources: A&E attendance and admissions from Emergency Care Dataset (ECDS), deaths from PHE daily death data series (deaths within 28 days)

¥ Excludes unlinked sequences (sequenced samples that could not be matched to individuals) and cases without specimen dates.

* This includes cases within 28 days of their specimen date. Cases are assessed for A&E attendance and hospitalisation within 28 days of their positive specimen date. Cases still within this 28 day period may have a hospital attendance reported at a later date.
§ At least one attendance within 28 days of positive specimen date; cases where specimen date is the same as or after the date of A&E visit are excluded to remove cases picked up via testing for the purpose of healthcare attendances. A&E visit and hospital attendance data are subject to reporting delay and therefore these data may be revised upwards.
^ Total deaths in any setting (regardless of hospitalisation status) within 28 days of positive specimen date.

Figure 2. Cumulative cases in England of variants indexed by days since the fifth reported, data as of 18 May 2021
(Find accessible data used in this graph in underlying data)

Figure 2 demonstrates the rapid identification of VOC-21APR-02 (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. Rapid genotyping assay results that have not been confirmed by sequencing have been removed from this dataset. The supplementary data for figures is available.

Figure 3. Variant prevalence for all England available case data from 1 February 2021 as of 18 May 2021 (excluding cases where the specimen date was unknown). The black line indicates proportion of cases sequenced in a 7-day rolling window. The area in grey shows weeks where the sequence data is still accumulating, therefore the proportions are less likely to accurately reflect prevalence. Rapid genotyping assay results that have not been confirmed by sequencing have been removed from this dataset. (Find accessible data used in this graph in underlying data).

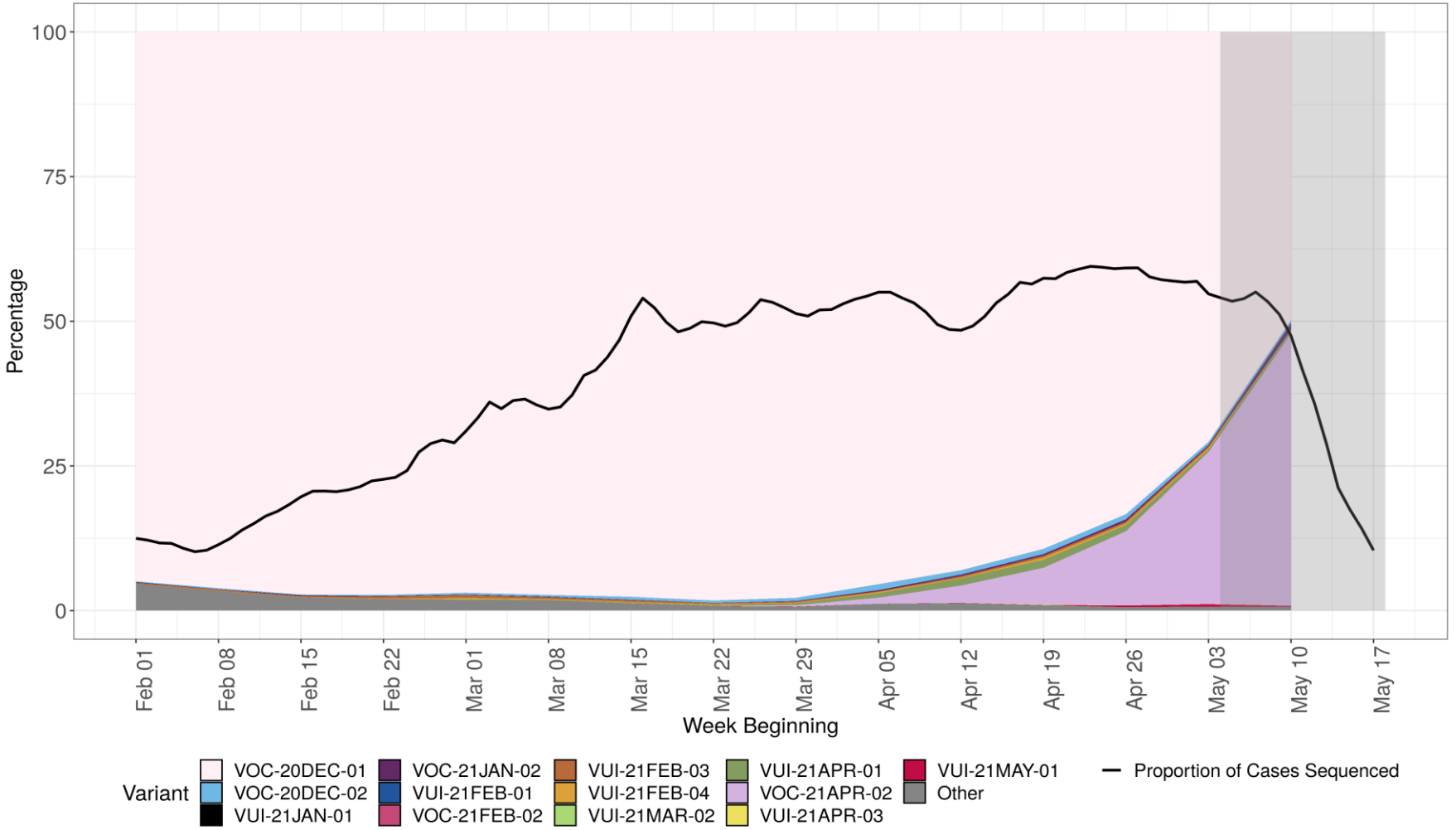


Figure 4. Variant prevalence for all England available case data from 1 February 2021 as of 18 May 2021 by region (excluding cases where the region or specimen date were unknown). Black line indicates proportion of cases sequenced in a 7-day sliding window. The area in grey shows weeks where the sequence data is incomplete, so the proportions are less likely to accurately reflect prevalence. (Find accessible data used in this graph in underlying data). Data for most recent 2 weeks is incomplete.

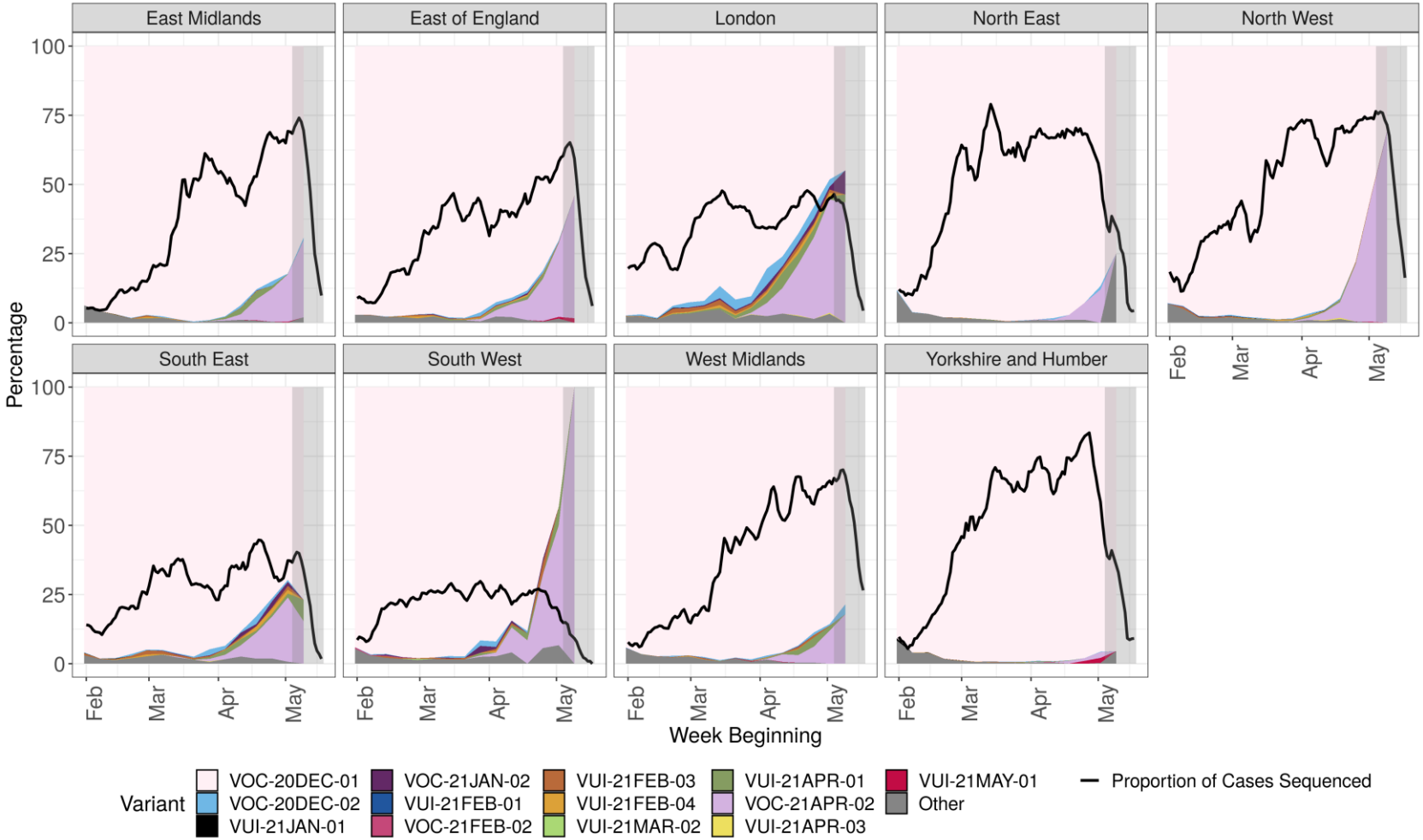
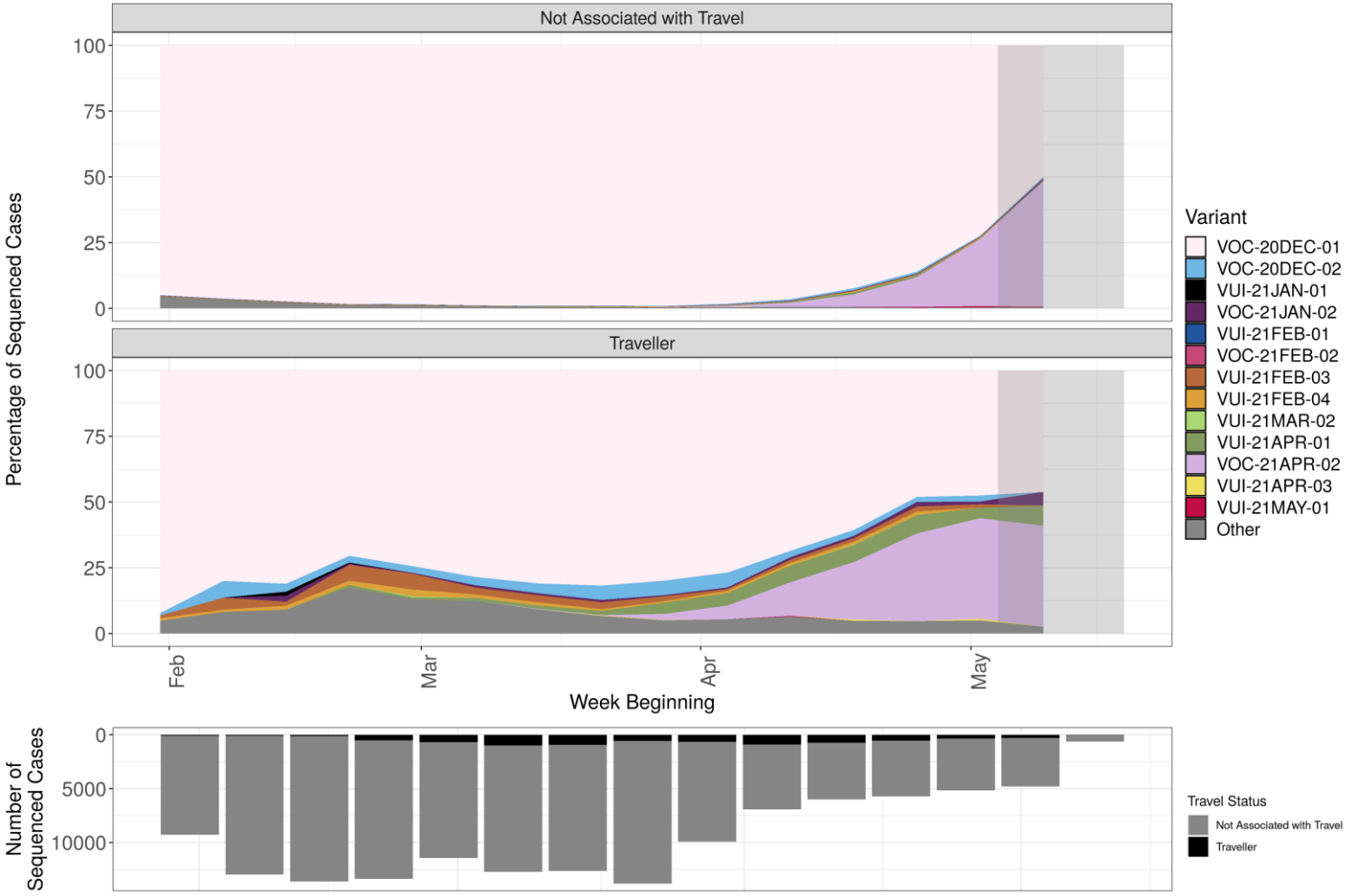


Figure 5. Prevalence of variants over time: all sequenced cases in England, split by travel status as of 18 May 2021
(Find accessible data used in this graph in underlying data). Travel status includes cases matched to Passenger Locator Form data and samples taken as part of the managed quarantine service or through private testing following travel. Greyed out area shows weeks where the sequence data is incomplete, so the proportions are less likely to accurately reflect prevalence. The total number of sequenced cases in each week is shown in the bars below, split by travel status**.**



Variant growth rates

Logistic growth rates (1/week from 1 January 2021 as of 18 May 2021) relative to VOC-20DEC-01 (B.1.1.7) are calculated for each VUI or VOC with more than 20 samples and shown in Table 4. Sample inclusion criteria are:

- a non-traveller as determined by matching each case against passenger locator forms and managed quarantine service test codes
- collected from Pillar 2 testing
- 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 VOC-20DEC-01 (B.1.1.7) is collected for measuring relative growth rates by weighting each VOC-20DEC-01 (B.1.1.7) sample by the proportion of the VUI or VOC which are sampled in each UTLA. Any VOC-20DEC-01 (B.1.1.7) samples collected outside the period of time that the VUI or VOC are observed are excluded as are VOC-20DEC-01 (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 VOC-20DEC-01 (B.1.1.7).

Compared to VOC-20DEC-01 (B.1.1.7), the growth rate for VOC-21APR-02 (B.1.617.2) displays an increased growth rate. The growth rate of VOC-21APR-02 (B.1.617.2) has decreased since 12 May 2021 (110% to 99%). Growth rate is context dependent and cannot be interpreted as a change in biological transmissibility.

Table 4. Growth rate of variants of concern and variants under investigation 1 January 2021 as of 18 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 VOC-20DEC-01 (B.1.1.7) growth rates.

Variant	Growth rate (1/week)
VOC-20DEC-02	0.17 (p=2.548e-32,n=292)
VOC-21JAN-02	0.52 (p=5.881e-14,n=50)
VUI-21JAN-01	-0.15 (p=0.016,n=22)
VUI-21FEB-03	0.071 (p=0.0002,n=160)
VUI-21FEB-01	-0.31 (p=0.0008,n=55)
VUI-21FEB-04	0.23 (p=1.4e-14,n=103)
VOC-21APR-02	0.99 (p=2.518e-304,n=1,802)
VUI-21APR-01	0.51 (p=2.062e-23,n=122)

Secondary attack rates

Secondary attack rates 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.

Table 5 shows the secondary attack rates for VOC-21APR-02 (B.1.617.2) compared to the other B.1.617 variants and VOC-20DEC-01 (B.1.1.7). The time period of study for secondary attack rates has been restricted to the period 29 March 2021 to 28 April 2021, to capture recent social restrictions and vaccination levels. A reduction in secondary attack rate for non-travel cases with VOC-20DEC-01 is observed in this shorter period when compared to Table 6 covering 05 January 2021 to 28 April 2021.

Secondary attack rates for contacts of cases with VOC-21APR-02 (B.1.617.2) and no travel history are higher than those for contacts of non-travel cases with VOC-20DEC-01 (B.1.1.7). 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 (B.1.617.2) were higher than those for travel cases with VOC-20DEC-01 (B.1.1.7).

Table 6 shows the secondary attack rates for variants (excluding B.1.617 variants) for the period 5 January 2021 to 28 April 2021. Secondary attack rates for contacts of non-travel cases with these 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 over this time. 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, due to the difference in contact definition.

Table 5. Secondary attack rates for VUI-21APR-01 (B.1.617.1), VOC-21APR-02 (B.1.617.2) and VUI-21APR-03 (B.1.617.3), presented with VOC-20DEC-01 (B.1.1.7), time restricted for comparison
(29 March 2021 to 28 April 2021, variant data as at 18 May 2021, contact tracing data as at 19 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	1,650 (71.3% with contacts)	23,697 (81.6% with contacts)	6.5%	1.7% (1.6% - 1.9%) [434/25,019]	8.1% (7.9% - 8.3%) [4,950/61,187]
VUI-21APR-01	140 (82.9% with contacts)	107 (81.3% with contacts)	56.7%	2.2% (1.7% - 2.9%) [55/2,490]	11.3% (8.1% - 15.6%) [31/275]
VOC-21APR-02	331 (70.4% with contacts)	698 (81.8% with contacts)	32.2%	3.3% (2.8% - 3.9%) [135/4,058]	12.5% (11.1% - 14.0%) [245/1,959]
VUI-21APR-03	4 (25.0% with contacts)	5 (100.0% with contacts)	44.4%	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, their contacts were traced by the international contact tracing team 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 29 March 2021 to 28 April 2021 in order to allow time for contacts to become cases, hence case counts are lower than other sources. Provisional results are excluded.

Table 6. Secondary attack rates for all variants (excluding B.1.617 variants)
(5 January 2021 to 28 April 2021, variant data as at 18 May 2021, contact tracing data as at 19 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	3,818 (78.0% with contacts)	162,820 (74.2% with contacts)	2.3%	1.7% (1.6% - 1.8%) [1,152/67,295]	9.9% (9.8% - 10.0%) [33,529/337,421]
VOC-20DEC-02	288 (73.3% with contacts)	318 (65.4% with contacts)	47.5%	2.5% (2.1% - 3.1%) [106/4,158]	9.1% (7.2% - 11.6%) [60/656]
VUI-21JAN-01	3 (66.7% with contacts)	32 (75.0% with contacts)	8.6%	Unavailable [0/137]	8.1% (3.5% - 17.5%) [5/62]
VOC-21JAN-02	53 (58.5% with contacts)	53 (64.2% with contacts)	50.0%	1.2% (0.5% - 2.7%) [5/428]	12.1% (7.3% - 19.2%) [14/116]
VUI-21FEB-01	0 (0 with contacts)	63 (60.3% with contacts)	0.0%	Unavailable [0/0]	8.6% (4.4% - 16.1%) [8/93]
VOC-21FEB-02	1 (100.0% with contacts)	33 (81.8% with contacts)	2.9%	Unavailable [0/96]	0.0% (0.0% - 3.3%) [0/111]
VUI-21FEB-03	186 (71.0% with contacts)	168 (72.0% with contacts)	52.5%	1.2% (0.9% - 1.5%) [45/3,892]	9.3% (6.5% - 13.0%) [29/313]
VUI-21FEB-04	77 (67.5% with contacts)	104 (74.0% with contacts)	42.5%	0.6% (0.4% - 1.0%) [13/2,141]	9.8% (6.5% - 14.5%) [21/215]

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]
VUI-21MAR-01	1 (100.0% with contacts)	0 (0 with contacts)	100.0%	Unavailable [0/7]	Unavailable [0/0]
VUI-21MAR-02	4 (25.0% with contacts)	1 (100.0% with contacts)	80.0%	Unavailable [0/4]	Unavailable [0/3]
VUI-21MAY-01	2 (0.0% with contacts)	12 (91.7% with contacts)	14.3%	Unavailable [0/0]	Unavailable [1/52]

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, their contacts were traced by the international contact tracing team 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 28 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 reinfections

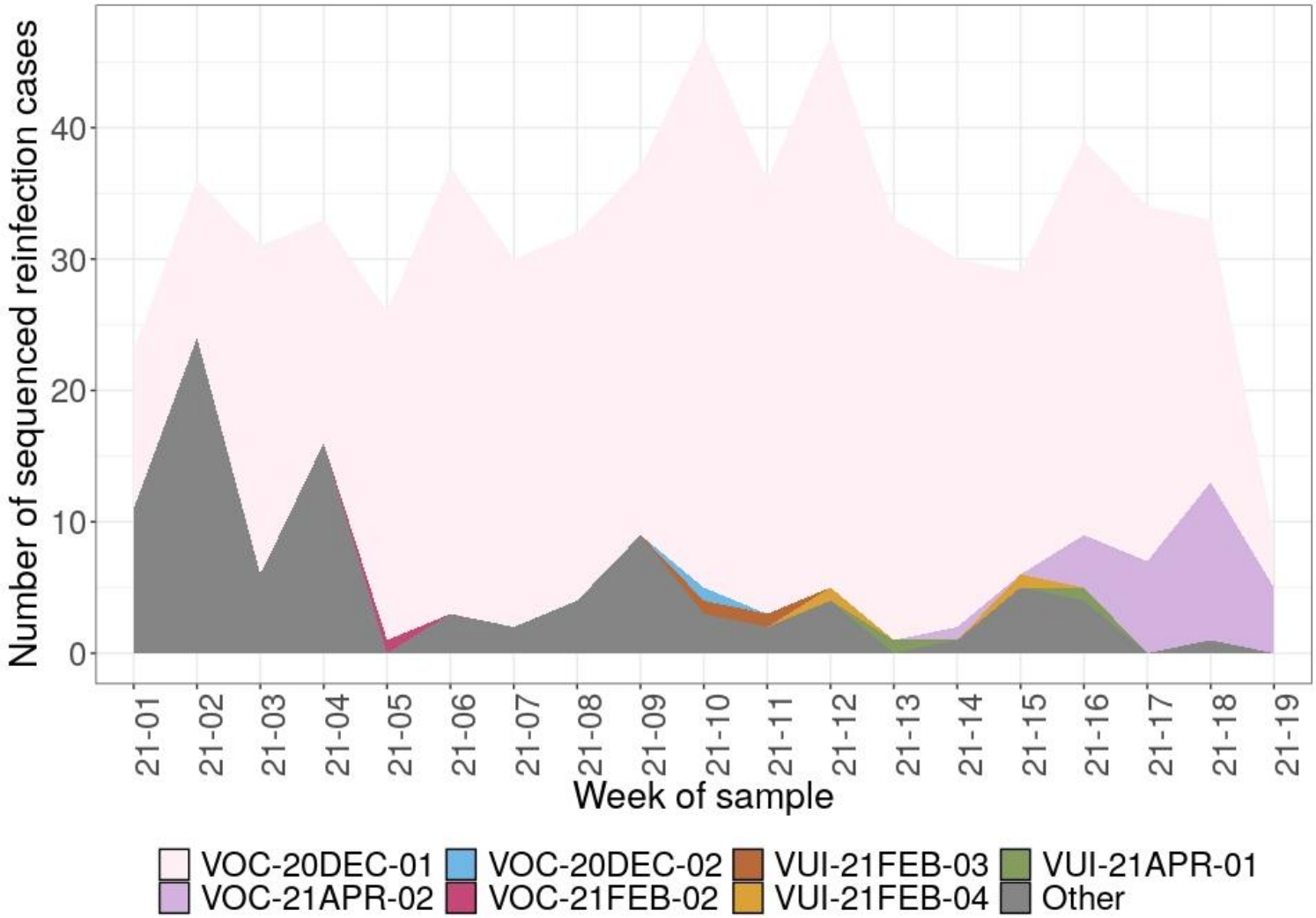
Individuals who have 2 positive tests (PCR and/or LFD) at least 90 days apart are classed as possible reinfection cases. A small proportion of reinfections have been sequenced through standard national surveillance sequencing. Table 7 shows the total number of sequences available from second episodes 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 (B.1.617.2). This is expected with any prevalent variant; comparative analyses are underway. Sequencing numbers fall in the last 2 weeks shown due partly to sequencing lag time, and new sequences are still being produced relating to sample dates in that week.

Table 7. Number of sequenced reinfection cases and the variant assigned
(Data as of 18 May 2021)

Variant	Total
VOC-20DEC-01	513
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	29
VUI-21APR-03	0
Total sequenced	753

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 as of 18 May 2021
(Find accessible data used in this graph in underlying data)



SARS-CoV-2 Immunity and Reinfection Evaluation (The SIREN study) cohort monitoring

The SIREN study is a cohort of National Health Service healthcare workers, including 135 sites and 44,549 participants across the UK, (35,720 in England), who are tested every 2 weeks for COVID-19 by PCR, and who have monthly serological testing. This cohort had a high seropositivity on recruitment (30% before the second wave) and is now vaccinated (95%). The incidence of new infections and potential reinfections in SIREN is monitored and would be expected to rise if a new variant became highly prevalent and was able to escape either natural or vaccine-derived immunity. During the period of time that VOC-21APR-02 (B.1.617.2) became prevalent, there has been no increase in PCR-positive participants in the SIREN cohort overall (Figure 7) and reinfections remain at very low numbers in individuals previously either PCR positive or seropositive (Figure 8).

Figure 7. PCR positivity within the SIREN study for all regions, England and fortnightly testing interval as of 18 May 2021

The black line indicates participants with positive PCR within period (per 1,000). The blue bar indicates participants PCR tested within period. Note: Contains only participants with at least one PCR test within given period; participants are counted as positive if at least one PCR test within given period is positive; only samples collected during the SIREN study (that is baseline and follow-up); figures have not been restricted by antibody status nor vaccination status, therefore will include participants presumed no longer susceptible to a new infection; includes only participants from England trusts. *Incomplete fortnight. (Find accessible data used in this graph in underlying data).

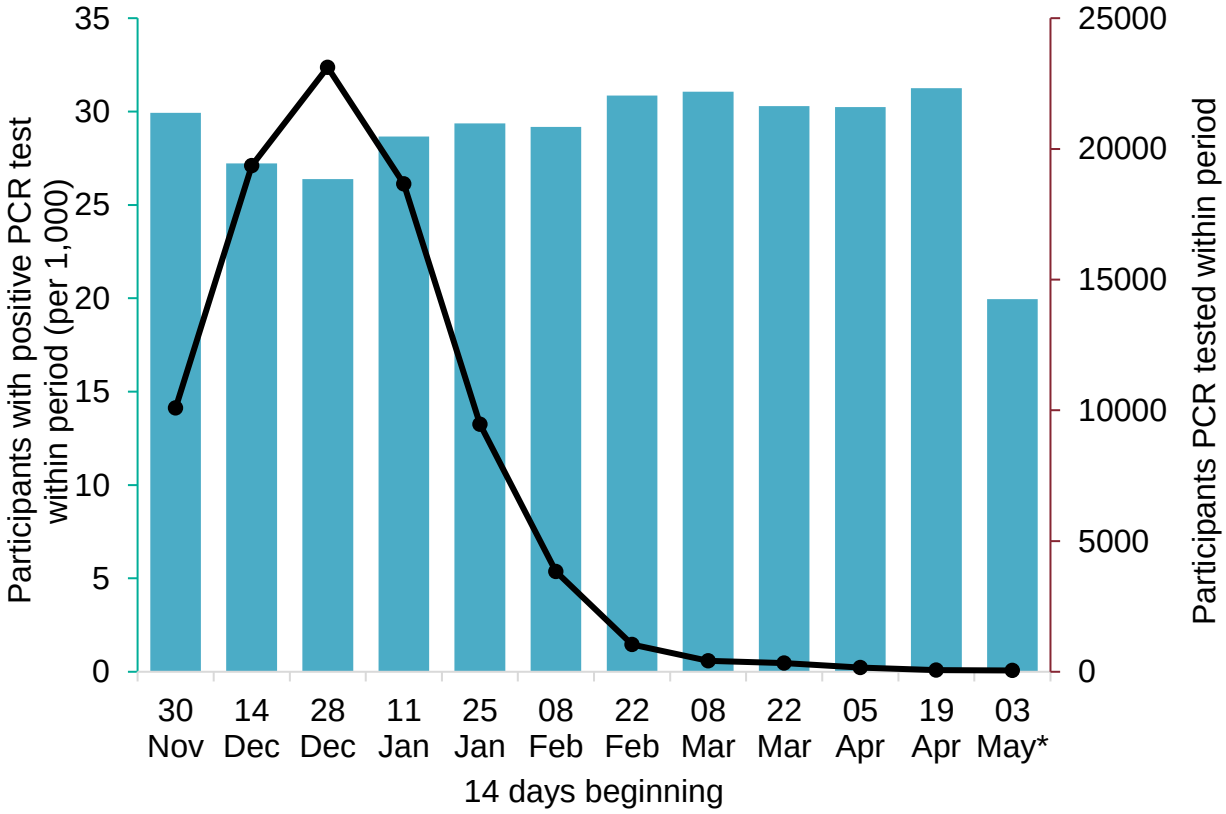
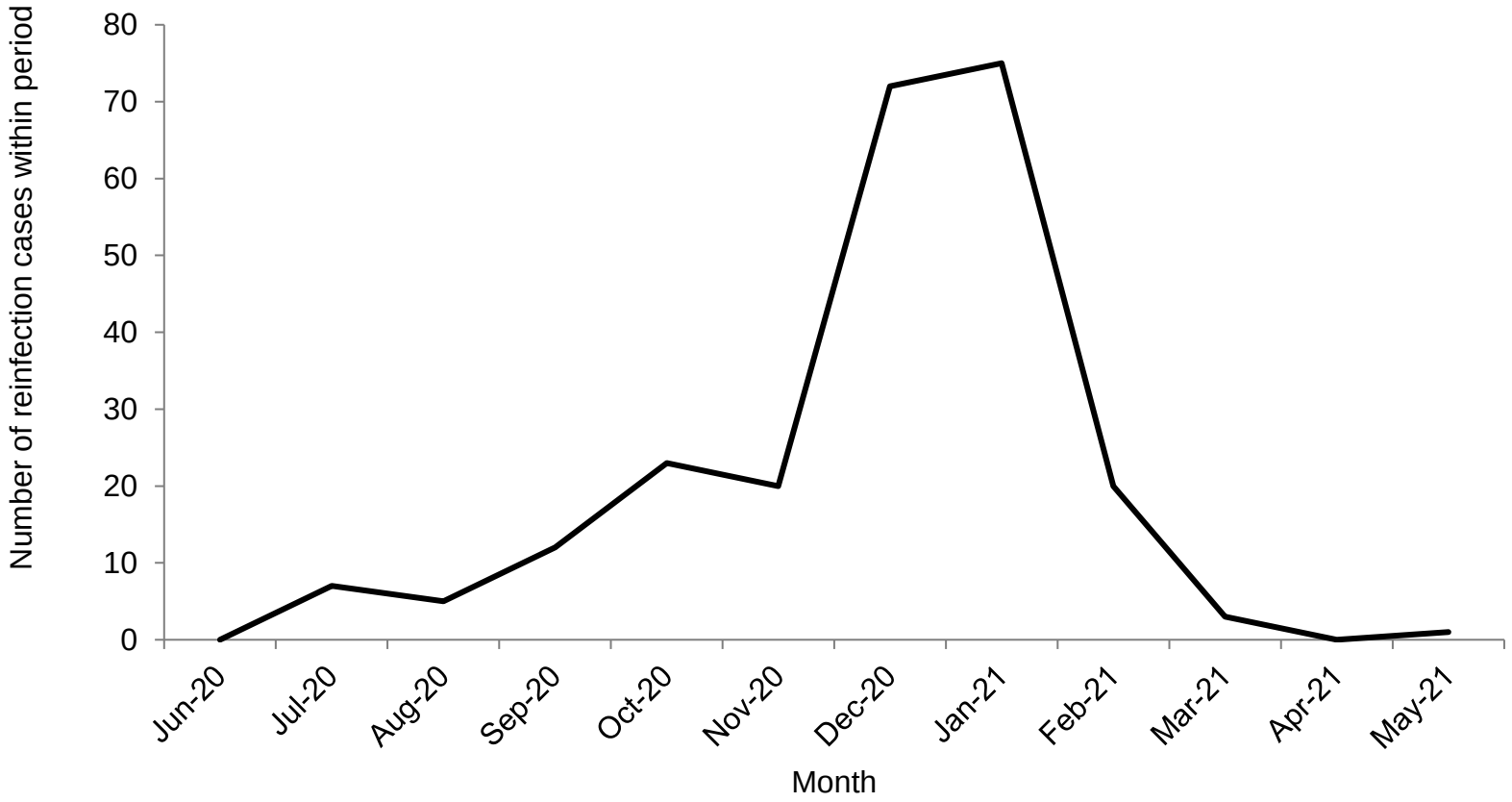


Figure 8. Monthly frequency of potential reinfections within SIREN June 2020 to May 2021
(Find accessible data used in this graph in underlying data)



Part 2: VOC-21APR-02 (B.1.617.2) surveillance

VUI-21APR-02 (B.1.617.2) was escalated to a variant of concern on 6 May 2021 (VOC-21APR-02).

Surveillance through genomic data

Table 8. Number of confirmed and probable VOC-21APR-02 (B.1.617.2) cases, by region of residence as of 18 May 2021

Region	Case Number	Case Proportion	Cases that have travelled	Proportion of travellers among cases
East Midlands	300	10.5%	49	16.3%
East of England	315	11.0%	61	19.4%
London	650	22.8%	148	22.8%
North East	43	1.5%	9	20.9%
North West	1,122	39.3%	28	2.5%
South East	175	6.1%	65	37.1%
South West	56	2.0%	35	62.5%
West Midlands	136	4.8%	39	28.7%
Yorkshire and Humber	49	1.7%	19	38.8%
Unknown region	8	0.3%	1	12.5%

Figure 9. Confirmed and probable VOC-21APR-02 (B.1.617.2) cases by specimen date as of 18 May 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data)

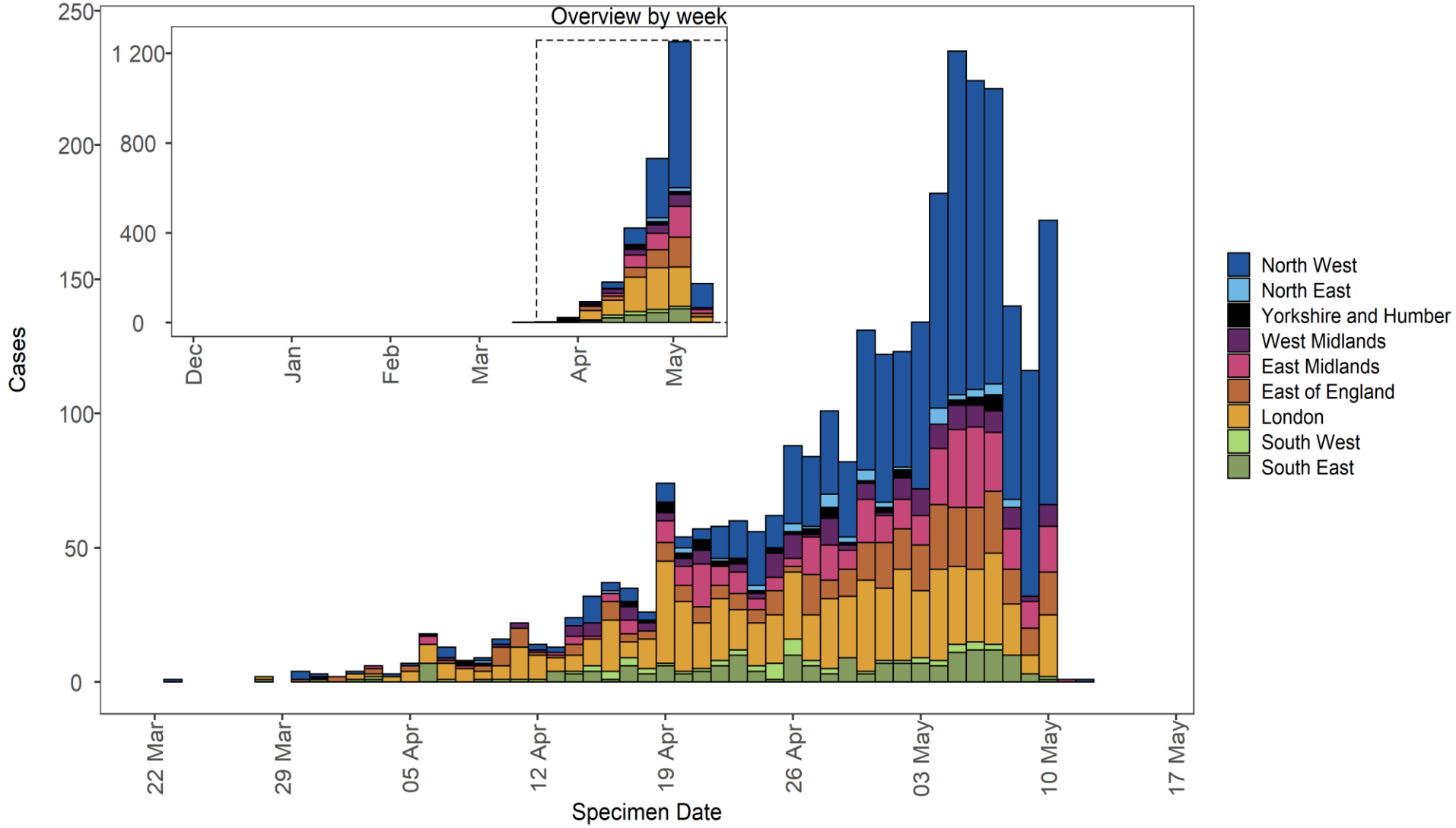
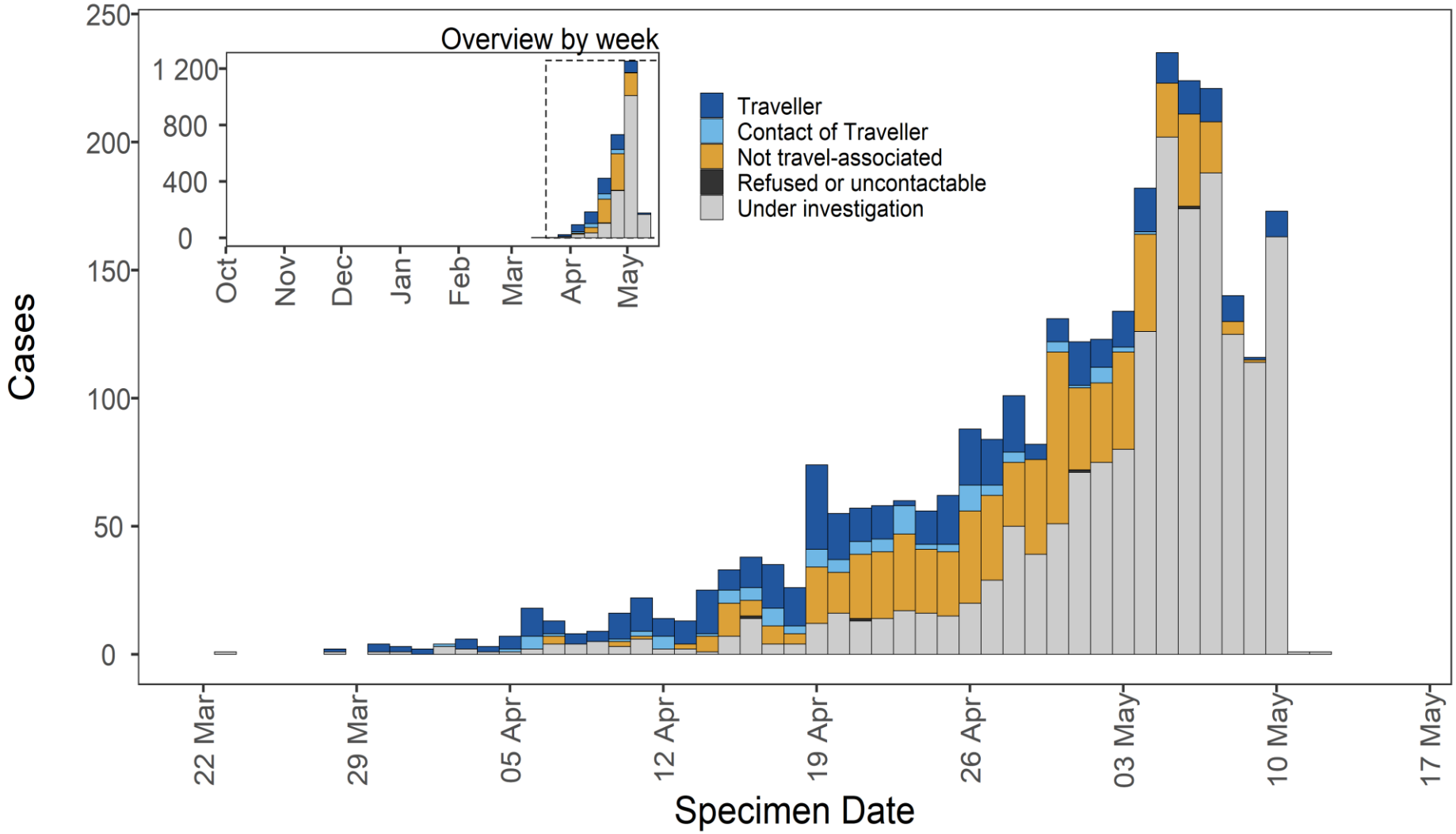


Figure 10. Travel data for confirmed and probable VOC-21APR-02 (B.1.617.2) cases by specimen date as of 18 May 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data). N/A indicates information is pending or not available.

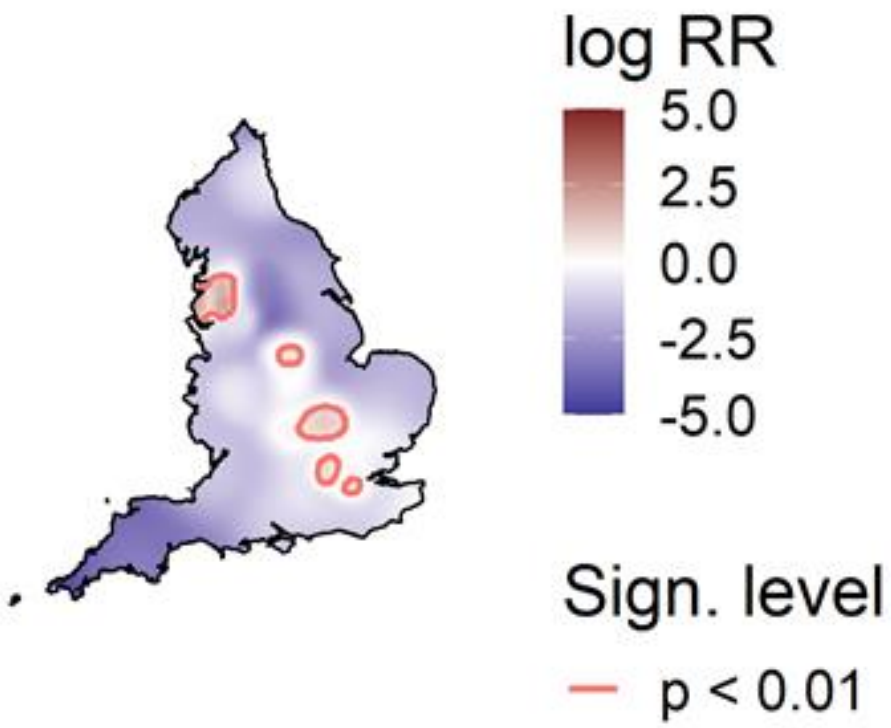


Spatial variation in risk

The spatial risk surface is estimated by comparing the smoothed intensity of cases (variants of concern) and controls (PCR positive, 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 11 highlights areas of significantly increased risk identified for VOC-21APR-02 (B.1.617.2).

Figure 11. Spatial variation in risk for VOC-21APR-02 (B.1.617.2) data from 1 October 2020, as of 18 May 2021, excluding cases that are known to have travelled

This figure excludes cases in managed quarantine facilities. Supplementary data is not available for this figure.

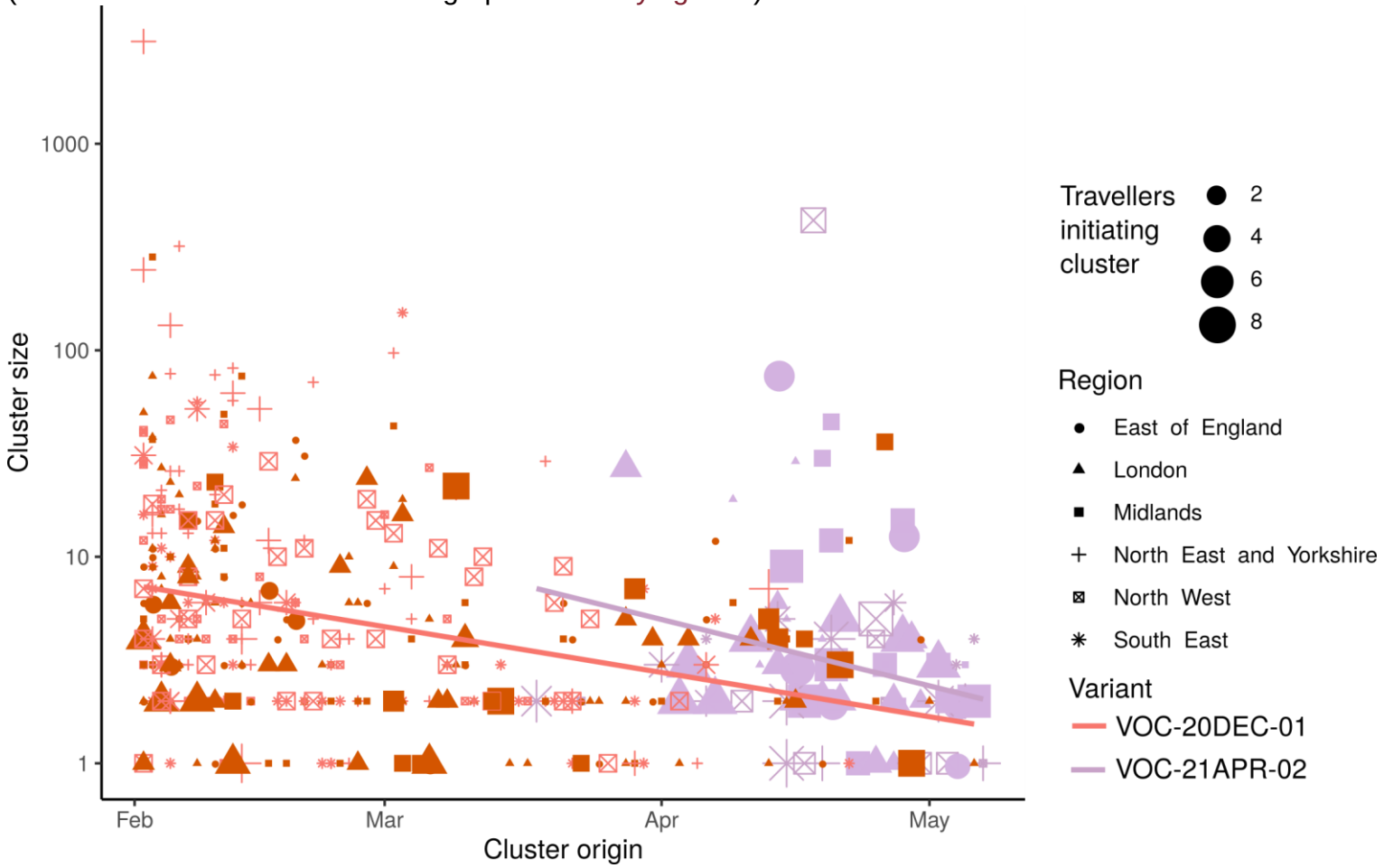


Cluster analysis

SARS-CoV-2 clusters initiated by cases linked to recent India travel tend to be larger if the traveller carries VOC-21APR-02 (B.1.617.2) in comparison to VOC-20DEC-01 (B.1.1.7) after adjusting for time of the first case in each cluster, however this difference is not significant (Figure 12), (negative binomial GLM p = 0.1267). Older clusters tend to be larger than recently introduced clusters, and VOC-21APR-02 (B.1.617.2) India-linked clusters were introduced later on average than VOC-20DEC-01 (B.1.1.7) India-linked clusters. The regional composition (NHS region) of clusters was not a significant predictor of cluster size (ordinary least squares p>0.19) except for the North East (p=0.02) which had larger cluster sizes. The number of traveller cases detected at the origin of each cluster was not significant (OLS p=0.868). Clusters were derived by a maximum parsimony reconstruction of the geographic location in a maximum likelihood SARS-CoV-2 phylogeny provided by the UK COVID-19 Genomics Consortium. When comparing cluster sizes, only sequences sampled in England Pillar 2 and excluding travellers were included. Persons under the age of 20 were excluded. After identifying clusters linked to India travel, 84 VOC-21APR-02 (B.1.617.2) clusters were retained with a mean origin date of 21 April 2021 and a median size of 10.5. A further 381 VOC-20DEC-01 (B.1.1.7) clusters were retained with a mean origin date of February 23, 2021 and a median size of 20.36.

Figure 12. Clustering of VOC-20DEC-01 (B.1.1.7) and VOC-21APR-02 (B.1.617.2) by region as of 18 May 2021

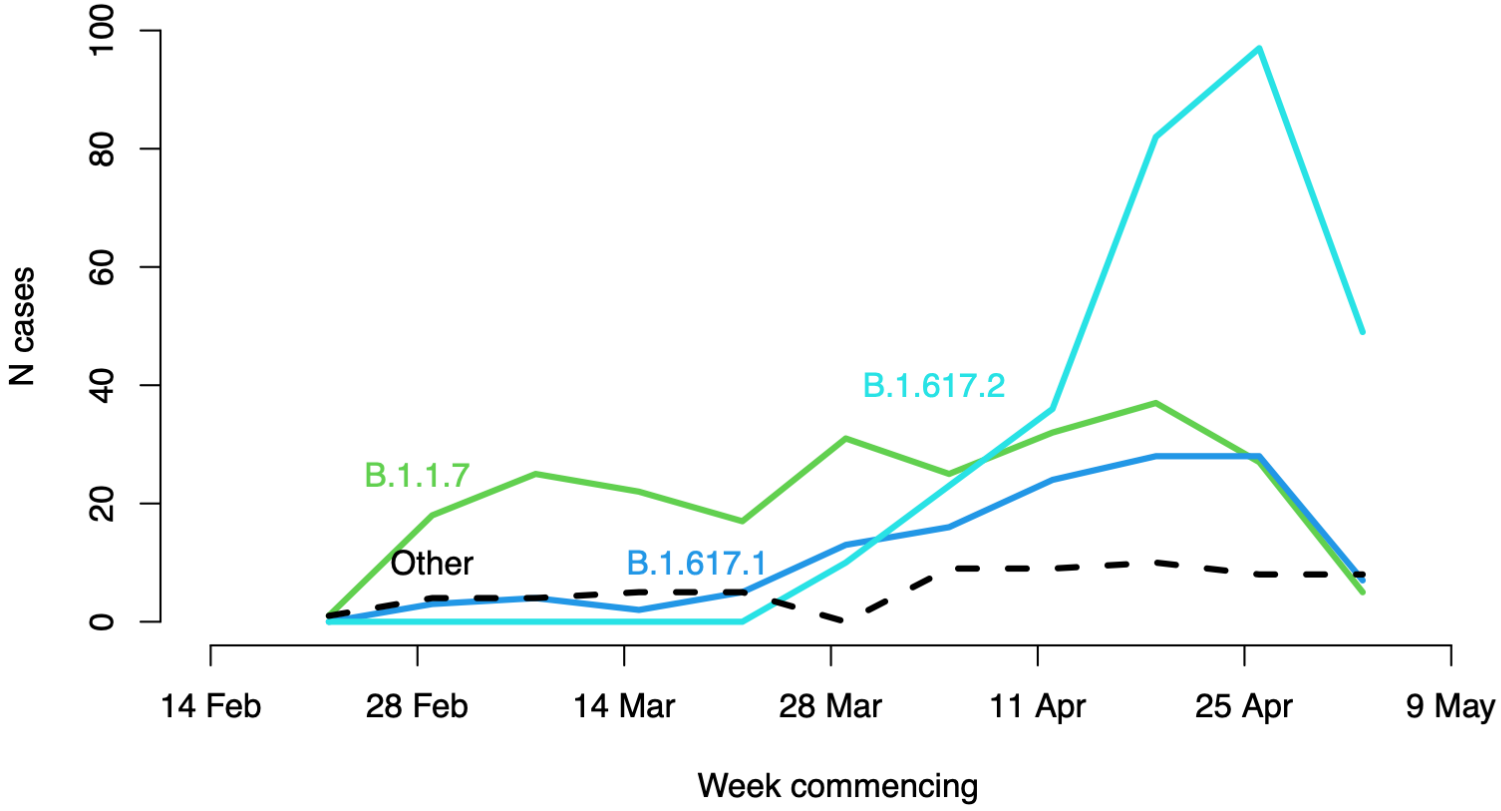
The size of phylogenetic clusters initiated by cases linked to travel from India is shown versus the time of origin of each cluster (time of first sample). Lines show a linear regression for lineages VOC-20DEC-01 (B.1.1.7) and VOC-21APR-02 (B.1.617.2). (Find accessible data used in this graph in underlying data).



Surveillance of cases in travellers from India

Figure 13. Lineages of cases with recent travel history from India

Each line shows the count of cases by test date of that lineage with known travel history from India within 14 days of testing positive: VOC-20DEC-01 (B.1.1.7) in green, VUI-21APR-01 (B.1.617.1) in blue, VOC-21-APR-02 (B.1.617.2) in cyan, other lineages as dashed line (22 February 2021 to 9 May 2021, final week incomplete). (Find accessible data used in this graph in underlying data).



Surveillance through S gene detection

The S gene target in a specific 3-target assay used in some Lighthouse Laboratories fails in VOC-20DEC-01 (B.1.1.7) that was previously predominant, but is detected in VUI-21APR-01 (B.1.617.1), VOC-21APR-02 (B.1.617.2) and VUI-21APR-03 (B.1.617.3) 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.

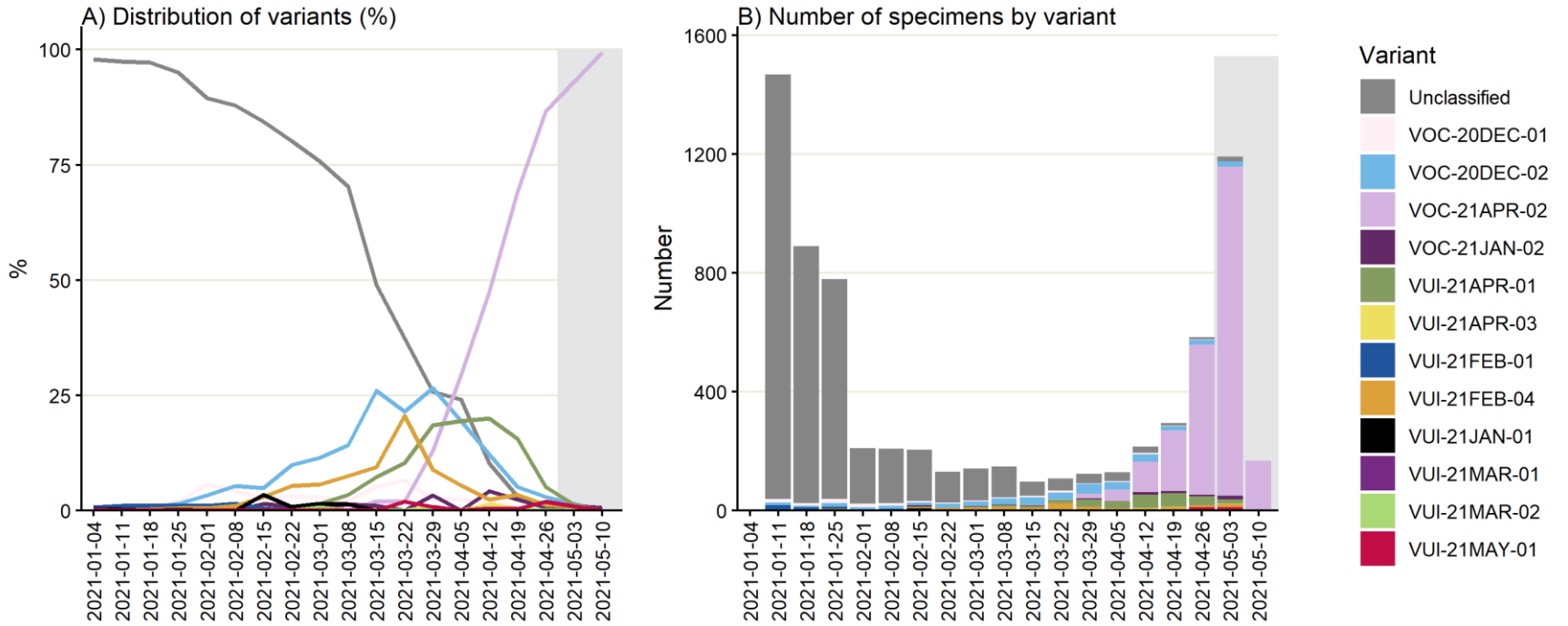
Figure 15 shows the number of sequenced S gene positive isolates over time since 1 January 2021 (data as of 18 May 2021), as well as the distribution of identified variants among these specimens. Unclassified variants refer to those not considered a VOC or VUI; these dominated the sequenced S gene positive specimens at the beginning of 2021, and decreased in proportion towards mid-May 2021 (Figure 14).

Among 1,192 sequenced S gene positive specimens from the week starting 3 May 2021, 98.6% (1,176) were variants under investigation or of concern, and 93% (1,109) were VOC-21APR-02 (B.1.617.2). This suggests S gene positive cases are currently indicative of additional VOC-21APR-02 (B.1.617.2) cases not detected through sequencing or before sequencing results are available. However, this proxy is limited by variable TaqPath laboratory coverage across England (Figure 15). 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 14) as well as the number and proportion of S gene positive samples nationally (Figure 16) has increased in recent weeks, particularly in North West England and London (Figure 17). 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, and Bedford (Figures 15 and 18). Some of these are located in areas where a higher proportion of specimens are tested in laboratories which use the TaqPath PCR assay (Figure 15).

Figure 14. Weekly distribution of variants among sequenced S gene positive SARS-CoV-2 specimens.

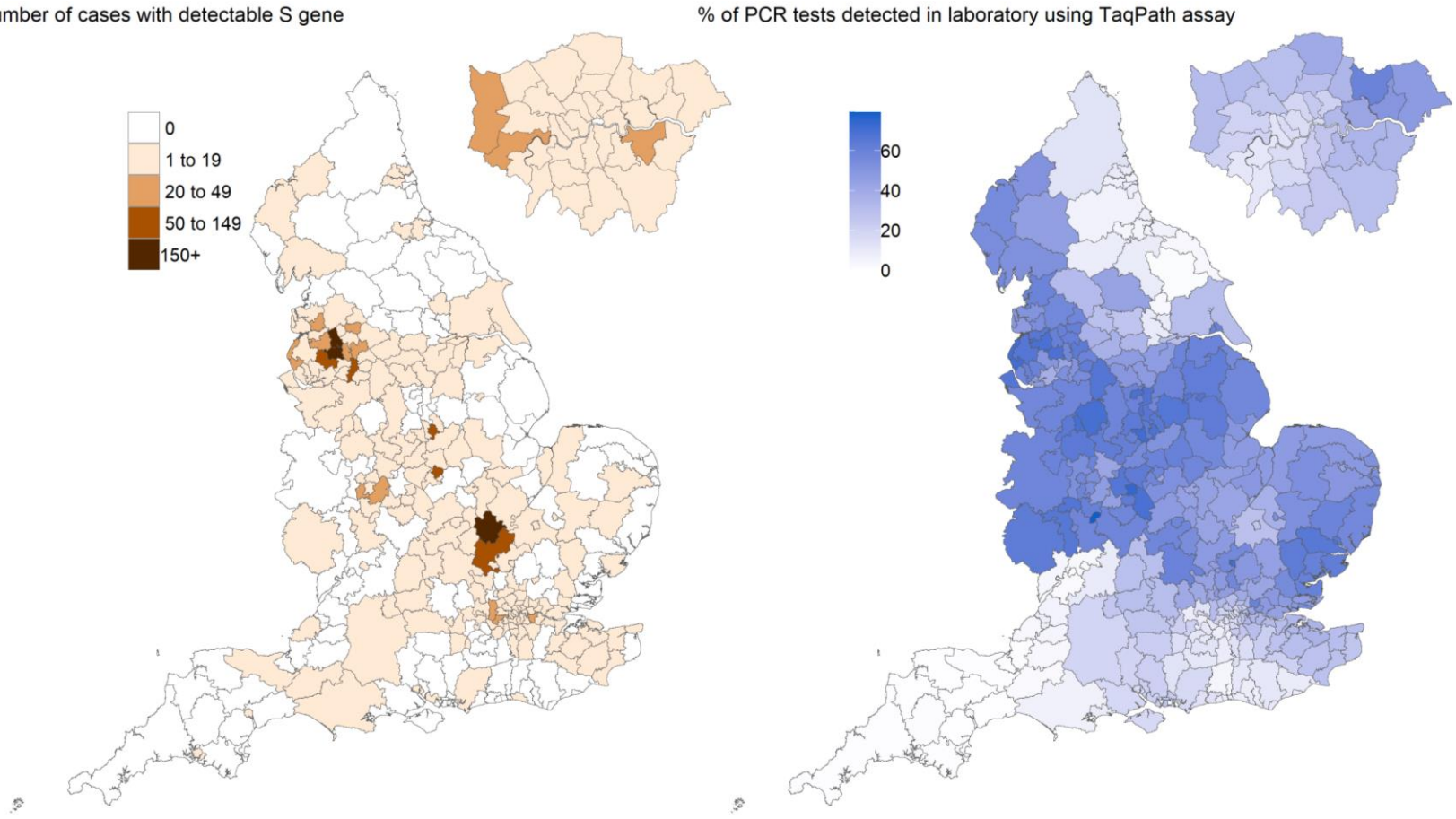
Specimen dates between 1 January 2021 and 12 May 2021, data as of 18 May 2021. Gray shading applied to weeks with 14 most recent days of data as these are affected by reporting delay. (Find accessible data used in this graph in underlying data).



Source: SGSS and COG-UK sequencing data, restricted to sequenced positive S-gene positive tests from Alderley Park, Glasgow, and Milton Keynes Lighthouse Laboratories.
S gene +ve defined as positive SARS-CoV-2 test with CT values <=30 for S, N, and ORF1ab.

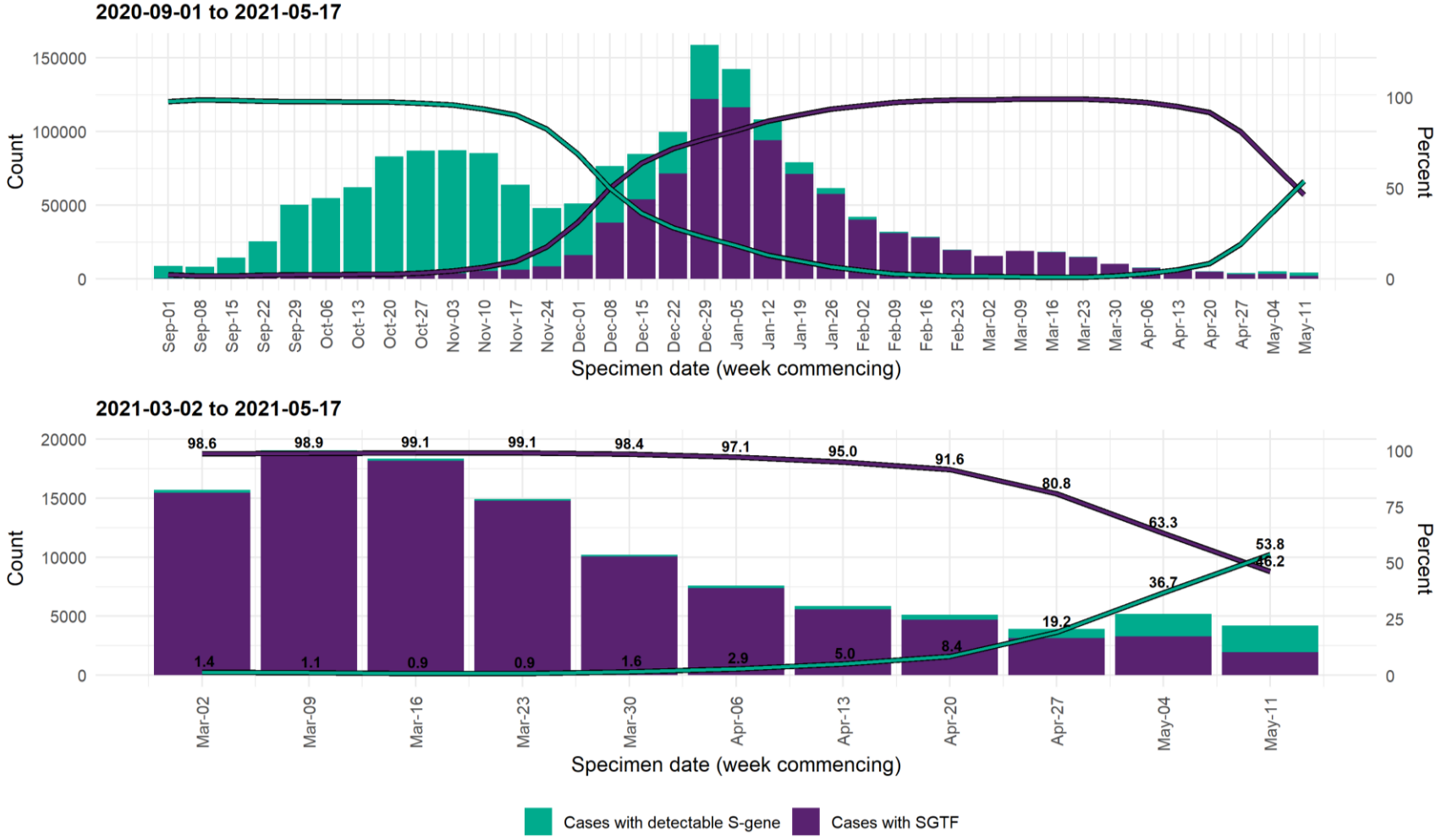
Figure 15. Number of cases with detectable S gene target and TaqPath lab test coverage by local authority of residence

Specimen dates 8 May 2021 to 14 May 2021; most recent 3 days excluded to reporting delay (Find accessible data used in this graph in underlying data).



A detectable S gene (<=30 CT values for S, N, and ORF1ab genes) may currently indicate a VOC case; this continues to be monitored.
Only tests carried out with the TaqPath PCR assay and with confirmed SGTF or S gene results included, from Alderley Park, Milton Keynes and Glasgow Lighthouse Labs.
Local trends in these data may be affected by decisions to direct the processing of samples via a TaqPath laboratory.

Figure 16. Weekly number and proportion of England Pillar 2 COVID-19 cases with SGTF and detectable S gene target among those tested with the TaqPath assay. Specimen dates between 1 September 2020 to 17 May 2021, data as of 18 May 2021 (Find accessible data used in this graph in underlying data).

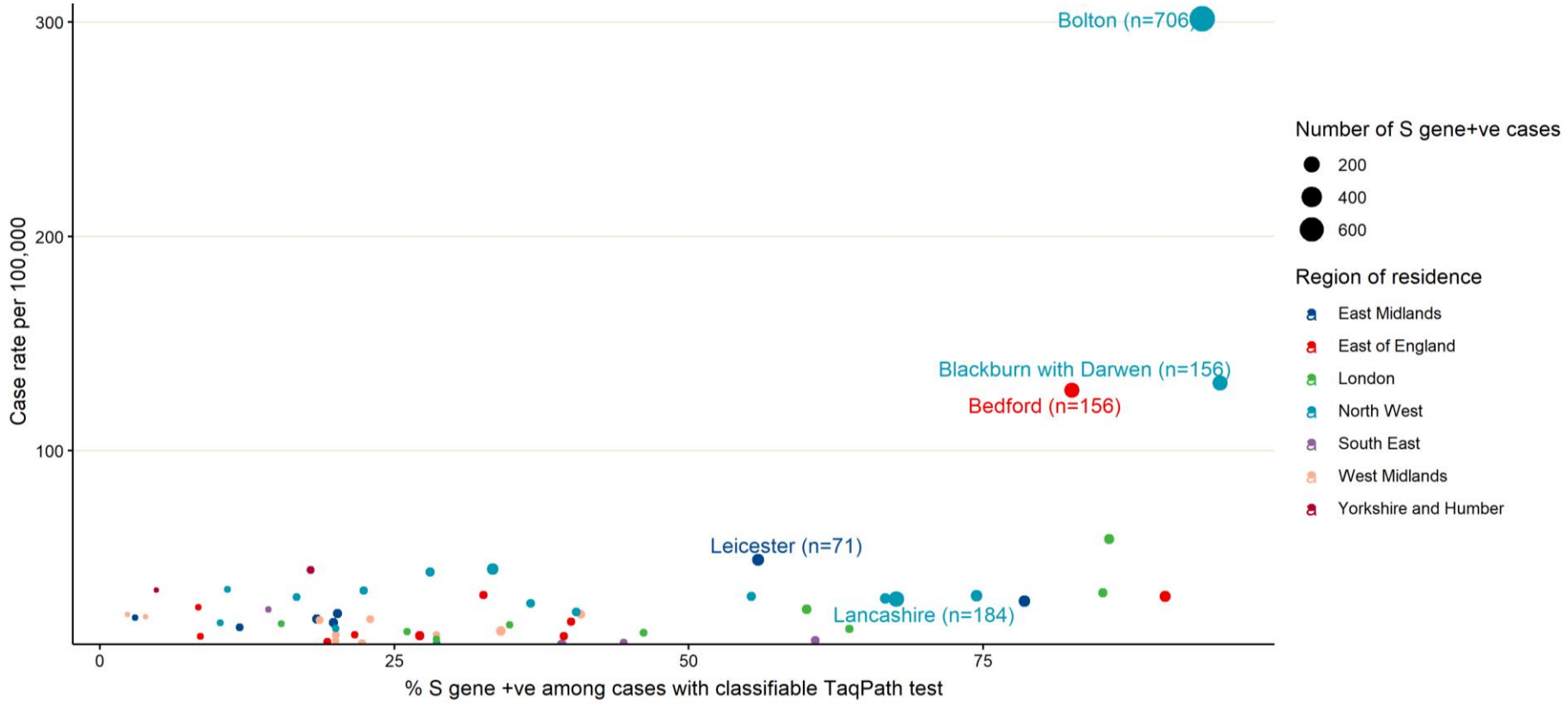


Only tests carried out with the TaqPath PCR assay and with confirmed SGTF or S gene positive results included, from Alderley Park, Milton Keynes and Glasgow Lighthouse Laboratories.
Case with SGTF: Positive SARS-CoV-2 test with non-detectable S gene and <=30 CT values for N and ORF1ab genes.
Case with 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 17. Weekly number and proportion of England Pillar 2 COVID-19 cases with detectable S gene target or SGTF among those tested with the TaqPath assay, by region of residence. Specimen dates between 2 March 2021 and 17 May 2021, data as of 18 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.
Region missing for 189 persons, excluded from figure.

Figure 18. 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 8 May 2021 and 14 May 2021, data as of 18 May 2021 (3 most recent days excluded due to reporting delay). Restricted to UTLAs with >20 cases tested on TaqPath assay. 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.

Growth rate of S gene positive and negative cases

Figure 19 shows growth rate and doubling time of S gene positive and negative (S gene target failure), produced by fitting a generalized additive model with a quasi-Poisson.

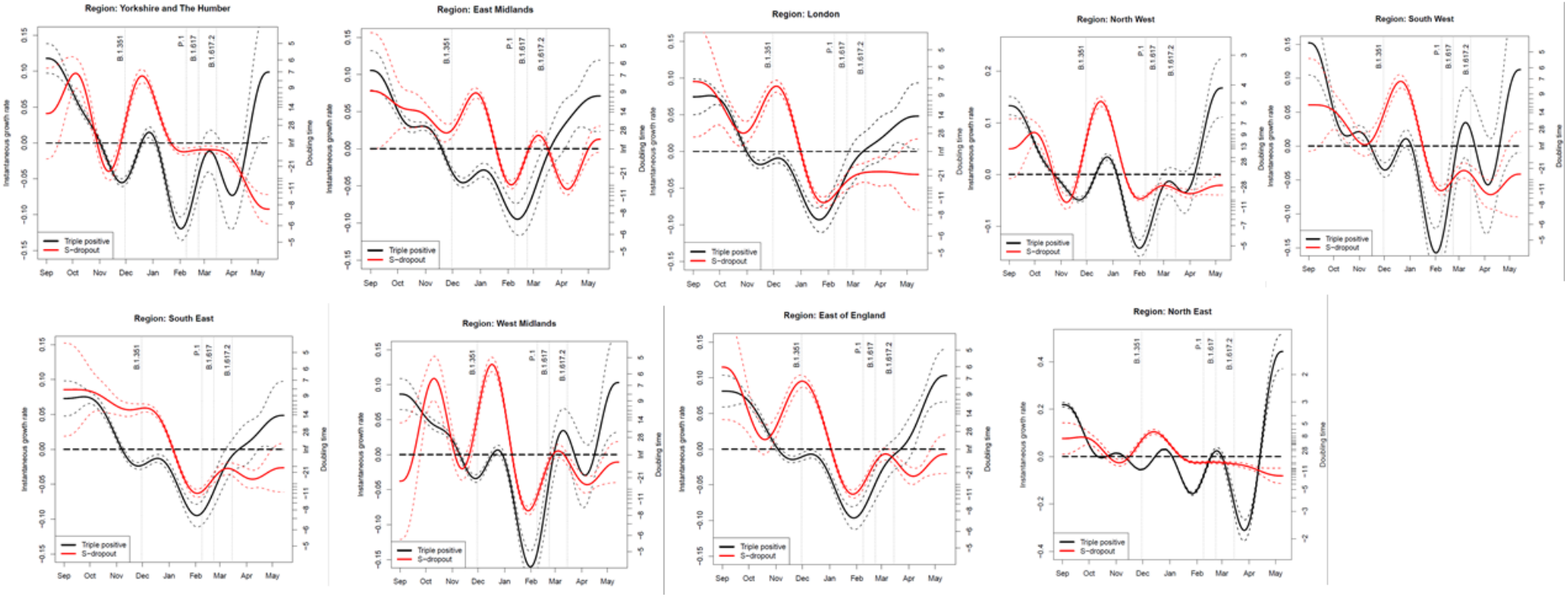
The growth rate for cases with all 3 PCR targets positive has been increasing over the course of April and May in all regions, most rapid in the North West. The East Midlands is the only region seeing growth in S-dropout.

London, the East Midlands and the South East have the lowest rates of growth in triple (S, ORF and N-gene) gene positives with a doubling time of around 2 weeks.

Confidence intervals are very wide for most regions, and data on PCR targets is low in some regions (East of England, South West, North East).

Figure 19. Growth rate and doubling time of S gene positive and negative cases by region as of 14 May 2021

The left vertical axis describes the daily rates of exponential growth; and the right vertical axis the corresponding daily doubling times, that is number of days required for cases to double at that particular growth rate. The dashed lines represent uncertainty (95% CI), which grows approaching the plot edges because the number of data points used for the estimation becomes smaller. Note that, if an epidemic trend changes from growth to decline, the growth rates change from positive to negative, while the doubling times become longer and longer, cross infinity when the trend is temporarily flat, and turn into halving times (that is number of days it takes for cases to halve), represented as negative doubling times. (Find accessible data used in this graph in underlying data).



Live virus and pseudovirus neutralization

Neutralisation studies of VOC-21APR-02 (B.1.617.2) have been conducted by 3 independent groups, PHE Colindale, Genotype to Phenotype Consortium laboratories (Imperial College London and Centre for Virus Research Glasgow) and Oxford University using both live virus and pseudovirus neutralisation assays and a range of different virus strains and sera, including convalescent and post vaccine sera. There are some reductions in neutralisation activity, both of first wave convalescent sera tested against live virus, and vaccinee sera tested against pseudovirus with VOC-21APR-02 (B.1.617.2) spike. The changes noted are generally greater than or comparable to the reduction seen for VOC-20DEC-01 (B.1.1.7) and less than that seen for VOC-20DEC-02 (B.1.351). The magnitude of the change differs between assays and further assessment is in process.

Effectiveness of COVID-19 vaccines against VOC-21APR-02 (B.1.617.2).

PHE has undertaken analysis of vaccine effectiveness against symptomatic disease with VOC21-APR-02 (B.1.617.2), using the national genomic and immunisation datasets. The full methodology and analysis will be published here. These findings suggest that while there is a reduction in vaccine effectiveness against VOC-21APR-02 (B.1.617.2) after one dose, any reduction in vaccine effectiveness after 2 doses of vaccine is likely to be small (Table 9). These data combine all vaccines, and a breakdown by vaccine is provided in the full analysis.

Table 9. Vaccination status and vaccine effectiveness for VOC-20DEC-01 (B.1.1.7), VOC21-APR-02 (B.1.617.2)

Vaccination status	Vaccine Effectiveness	
	VOC-20DEC-01 (B.1.1.7)	VOC21-APR-02 (B.1.617.2)
Dose 1	51.1% (47.3 to 54.7)	33.5% (20.6 to 44.3)
Dose 2	86.8% (83.1 to 89.6)	80.9% (70.7 to 87.6)

VUI-21APR-01 (B.1.617.1)

Table 10. 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	48	12.9%	24	50%
East of England	30	8.0%	19	63.3%
London	159	42.6%	87	54.7%
North East	4	1.1%	2	50%
North West	29	7.8%	20	69%
South East	37	9.9%	24	64.9%
South West	8	2.1%	6	75%
West Midlands	43	11.5%	17	39.5%
Yorkshire and Humber	15	4.0%	11	73.3%

Figure 20. Spatial variation in risk for VUI-21APR-01 (B.1.617.1) data from 1 October 2020, as of 18 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.

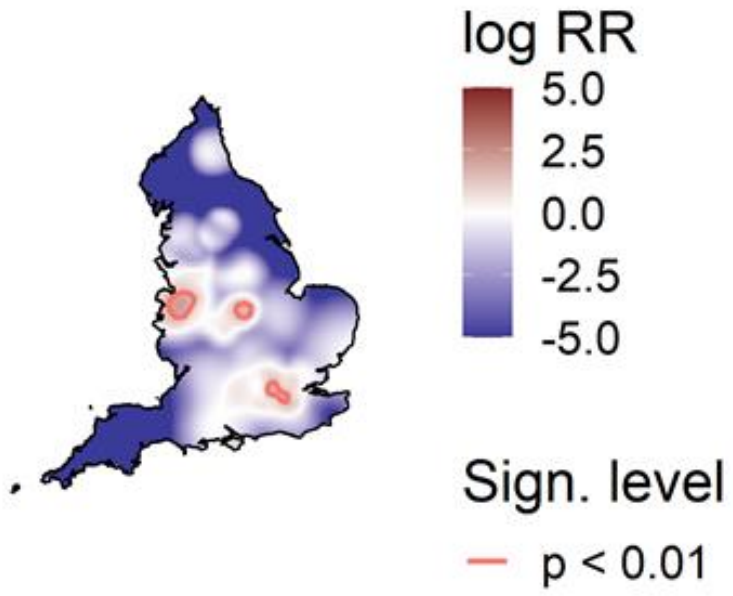


Figure 21. Confirmed and probable VUI-21APR-01 (B.1.617.1) cases by specimen date as of 18 May 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data).

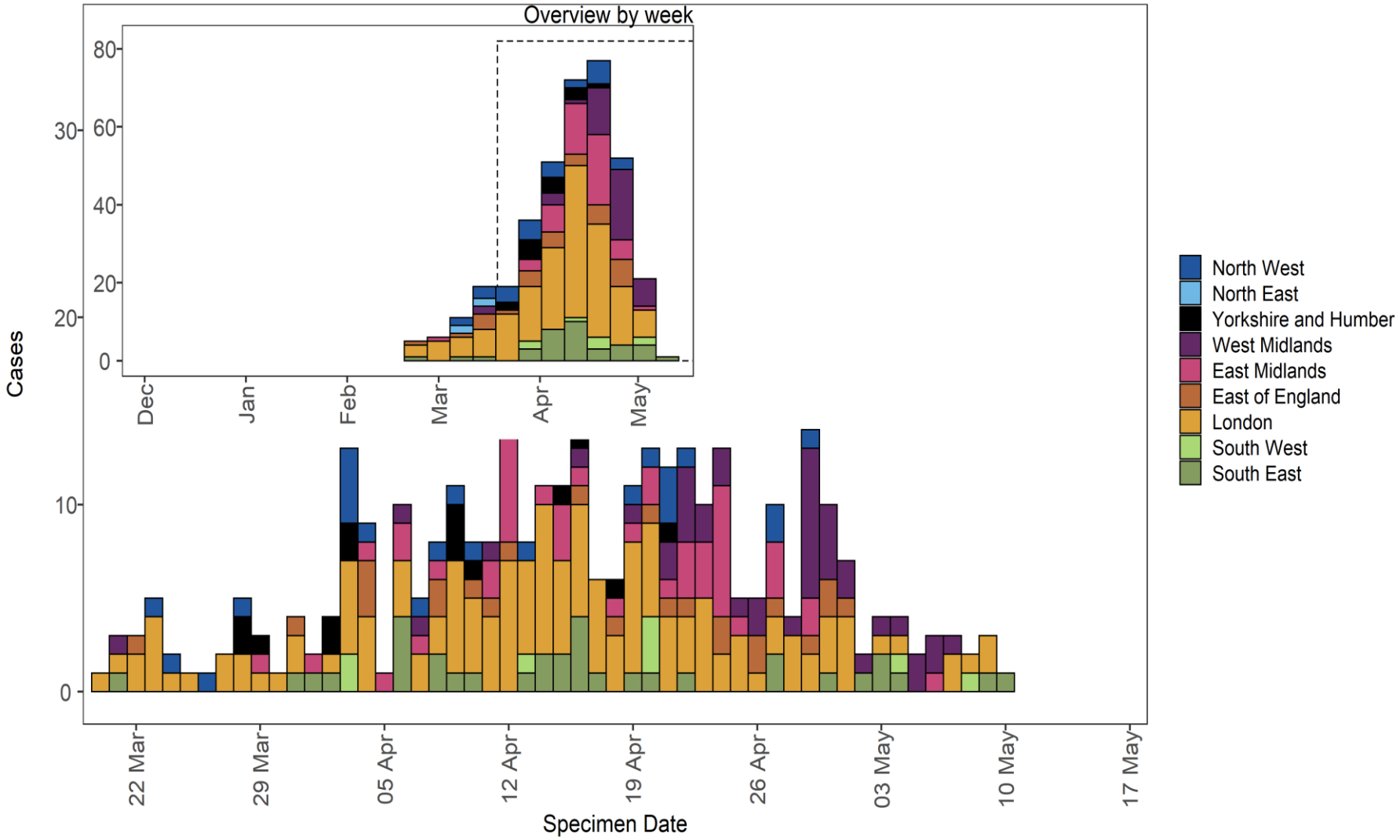
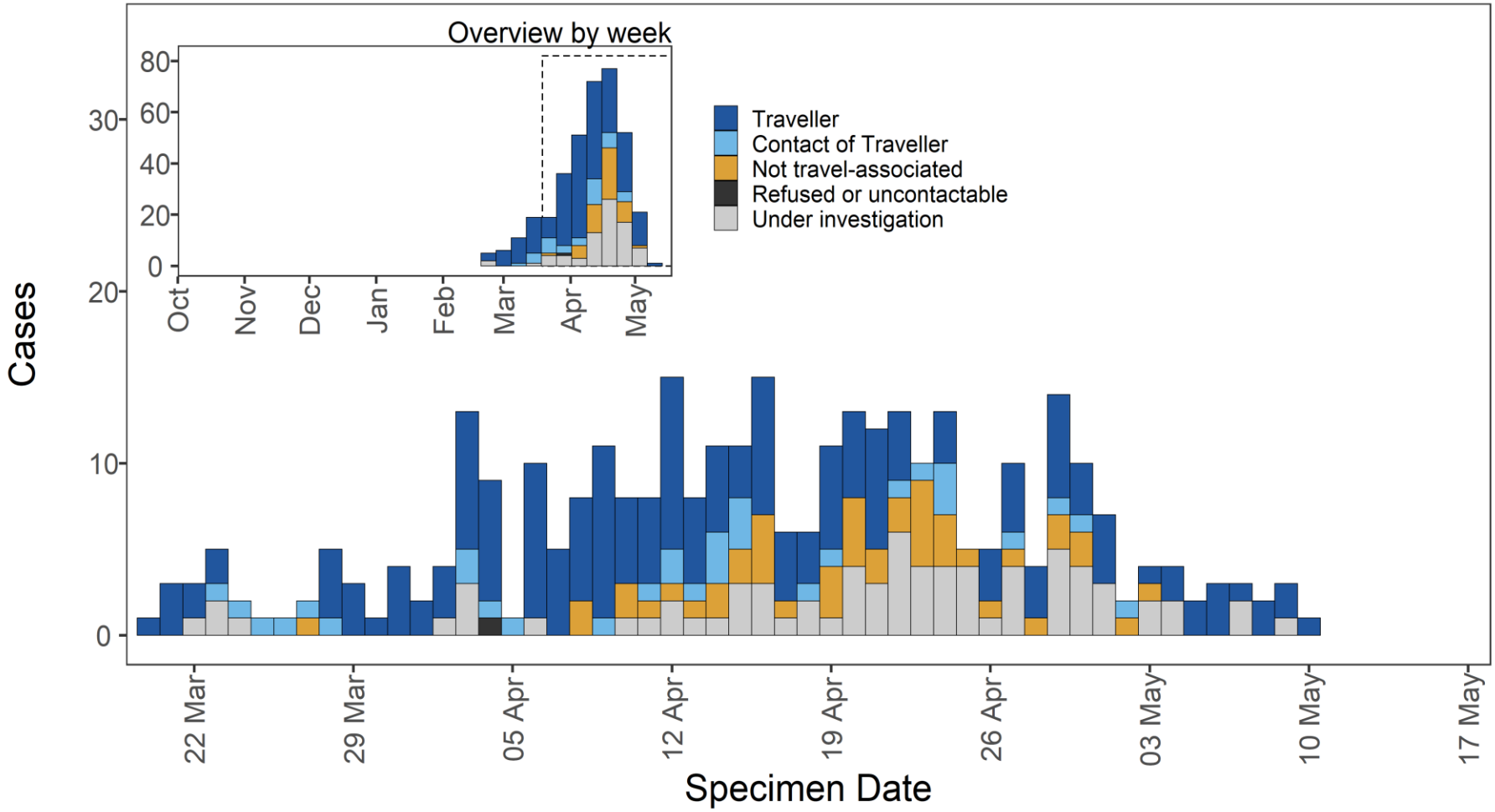


Figure 22. Travel data for confirmed and probable VUI-21APR-01 (B.1.617.1) cases by specimen date as of 18 May 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data). N/A indicates information is pending or not available.



VUI-21APR-03 (B.1.617.3)

Table 11. Number of confirmed and probable VUI-21APR-03 (B.1.617.3) cases, by region of residence as of 18 May 2021

Region	Case Number	Case Proportion	Cases that have travelled	Proportion of travellers among cases
London	5	41.7%	3	60%
North West	6	50.0%	2	33.3%
South East	1	8.3%	0	0%

Figure 23. Spatial variation in risk for VUI-21APR-03 (B.1.617.3) data from 1 October 2020, as of 18 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.

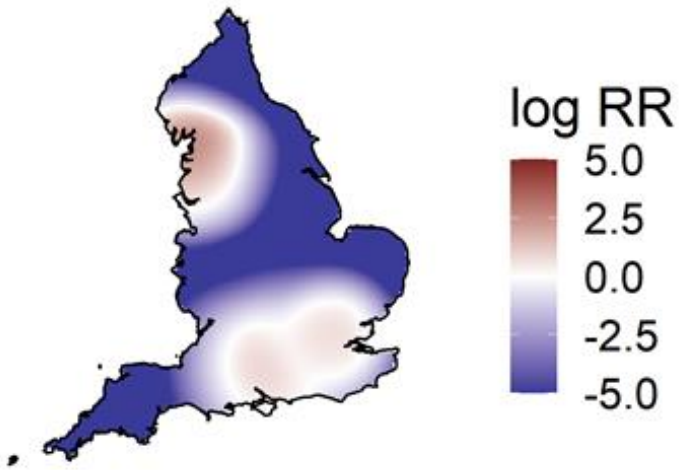


Figure 24. Confirmed and probable VUI-21APR-03 (B.1.617.3) cases by specimen date as of 18 May 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data).

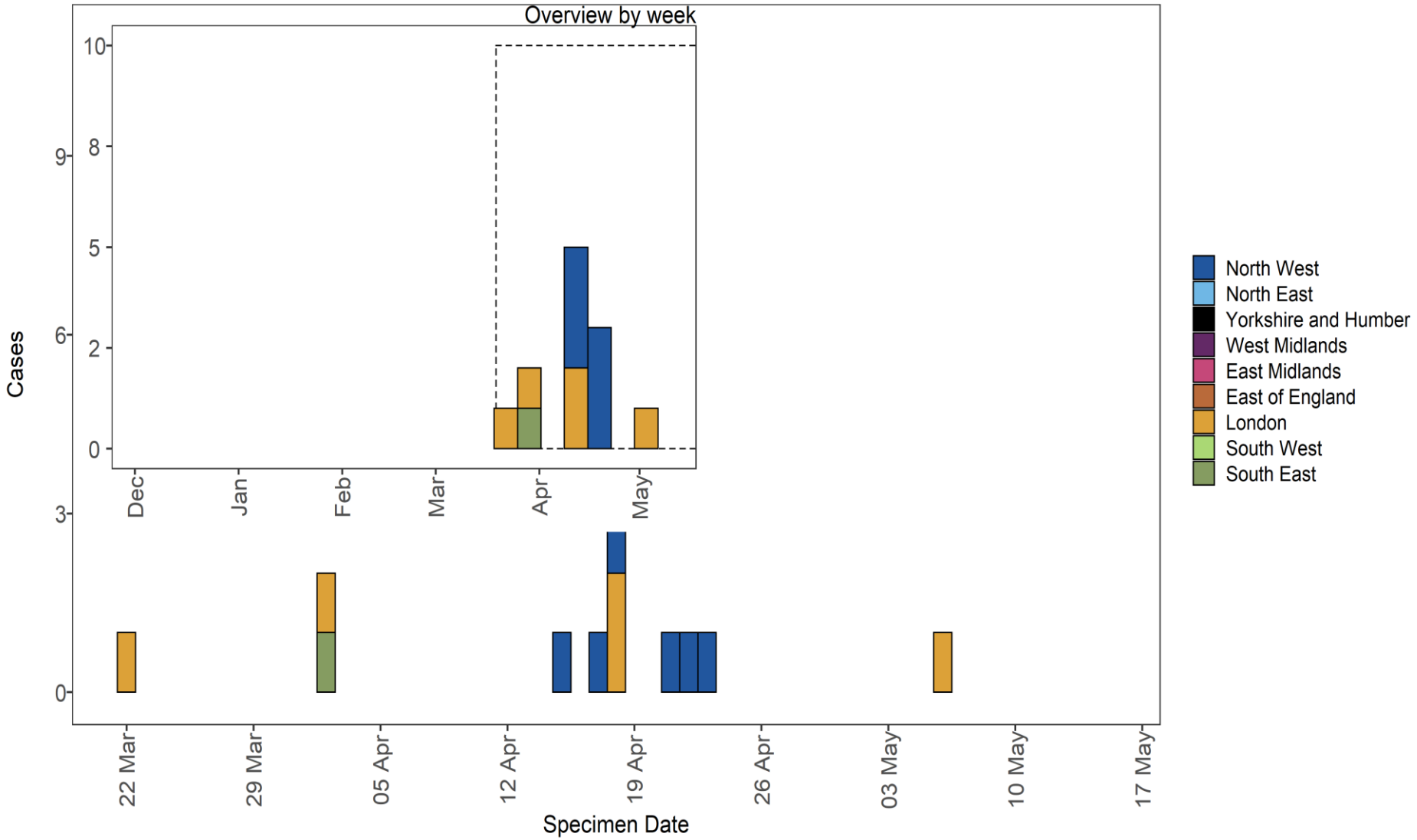
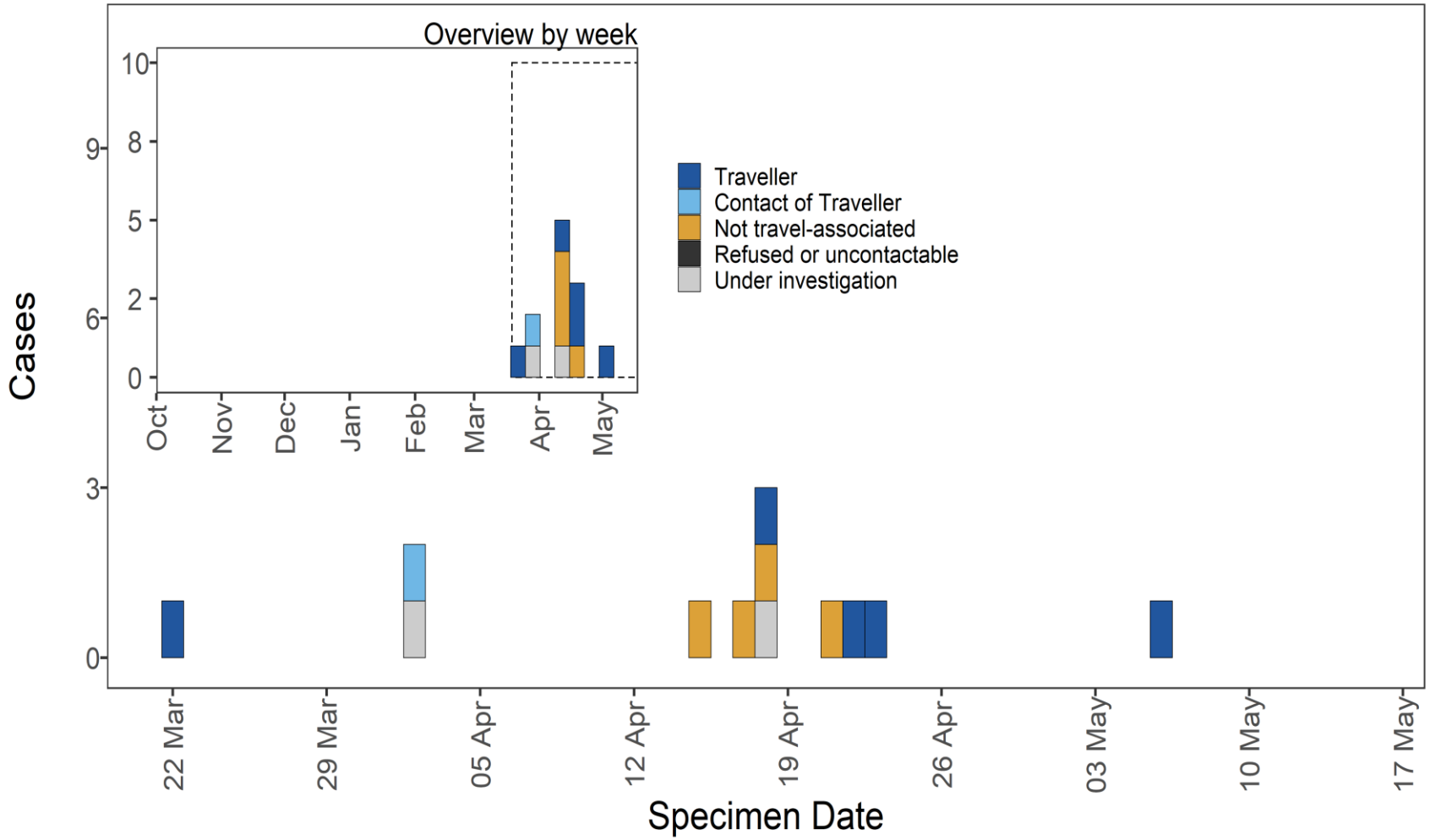


Figure 25. Travel data for confirmed and probable VUI-21APR-03 (B.1.617.3) cases by specimen date as of 18 May 2021
Larger plot includes last 60 days only (Find accessible data used in this graph in underlying data). N/A indicates information is pending or not available.



International surveillance

GISAID includes data on sequences available internationally. As of 19 May 2021 sequences from the following countries (excluding UK) have been identified in GISAID:

- **VUI-21APR-01 (B.1.617.1)** In total 1,667 sequences from: Australia 21, Bahrain 8, Belgium 7, Canada 18, Curacao 1, Czech Republic 3, Denmark 25, France 4, Germany 68, Greece 1, Guadeloupe 2, Hong Kong 9, India 1153, Ireland 22, Italy 3, Japan 17, Jordan 4, Luxembourg 5, Malaysia 1, Mexico 3, Nepal 1, Netherlands 7, New Zealand 4, Portugal 8, Saint Martin 2, Singapore 58, South Korea 5, Spain 1, Sweden 4, Switzerland 9, Thailand 1, USA 191, Uganda 1.
- **VOC-21APR-02 (B.1.617.2)** In total 2,199 sequences from: Aruba 3, Australia 83, Austria 1, Bahrain 14, Bangladesh 7, Belgium 51, Canada 8, China 2, Democratic Republic of Congo 6, Denmark 39, France 25, Germany 177, Greece 1, Hong Kong 3, India 730, Indonesia 5, Ireland 59, Italy 45, Japan 127, Jordan 1, Luxembourg 2, Malaysia 3, Mexico 2, Morocco 1, Nepal 7, Netherlands 20, New Zealand 11, Norway 4, Poland 10, Portugal 1, Reunion 1, Romania 3, Russia 1, Singapore 100, Slovenia 1, South Africa 9, South Korea 1, Spain 33, Sweden 8, Switzerland 27, Thailand 1, USA 563, Uganda 3.
- **VUI-21APR-03 (B.1.617.3)** In total 57 sequences from: India 54, Russia 2, USA 1

Part 3: New variant under investigation VUI-21MAY-01 (AV.1)

A variant first detected in UK sequences was designated under investigation on 14 May 2021 as VUI-21MAY-01 (AV.1) on the basis of the mutation profile and apparent localised cluster in Yorkshire and Humber region.

Genomic profile

The complete mutation profile of VUI-21MAY-01 (AV.1) is shown in Table 12 and genomic case definition in Table 13.

Table 12. Variant defining mutations.

Gene	Mutations
ORF1ab	G519S, A591V, H1160Y, P1640L, N2405S, A3209V, 3675-3677del, S4826A, A6044V
S	D80G, T95I, G142D, 144del, N439K, E484K, D614G, P681H, I1130V, D1139H
M	A63T, H125Y
ORF3a	26158-26161del
N	I157V, R203K, G204R

Table 13. Genomic case definition

CONFIRMED	All variant defining changes called as alternate base
PROBABLE	AT LEAST 7 variant defining changes called as alternate base and all other positions either N or mixed base
LOW_QC	Fewer than 7 variant defining changes called as alternate base and all other positions either N or mixed base

Biological profile

VUI-21MAY-01 (AV.1) contains several mutations strongly linked to antigenic change including both N439K and E484K, as well as P681H, a mutation at a site hypothesised to affect transmissibility. It also contains deletions associated with other Variants of Concern.

Surveillance in England

As of 18 May 2021, 41 genomically confirmed cases of VUI-21MAY-01 (AV.1) have been identified in 4 regions of England; concentrated in the Yorkshire and Humber, East of England, West Midlands and East Midlands regions (Table 14). Number of cases by specimen date are shown in Figure 26, geospatial distribution in Figure 27. The supplementary data for figures is available here. Note contact tracing is included in Table 6.

As of 18 May 2021 several cases in England occur as part of a cluster in Yorkshire. 1 case is known to have overseas travel link, 0 cases have been confirmed as having no link to travel identified, and 40 cases remain under investigation. No cases are known to have died in England with VUI-21MAY-01 (AV.1) as of 18 May 2021.

All E484K-containing variants are subject to enhanced public health management.

International surveillance

GISAID includes data on sequences available internationally. As of 19 May 2021, one sequence of VUI-21MAY-01 (AV.1) from France has been identified on GISAID.

Table 14. Number of confirmed and probable VUI-21MAY-01 (AV.1) cases, by region of residence as of 18 May 2021

Region	Case Number	Case Proportion	Cases that have travelled	Proportion of travellers among cases
East Midlands	3	7.3%	0	0%
East of England	5	12.2%	0	0%
North West	3	7.3%	0	0%
West Midlands	4	9.8%	0	0%
Yorkshire and Humber	26	63.4%	1	3.8%

Figure 26. Confirmed and probable VUI-21MAY-01 (AV.1) cases by specimen date as of 18 May 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data).

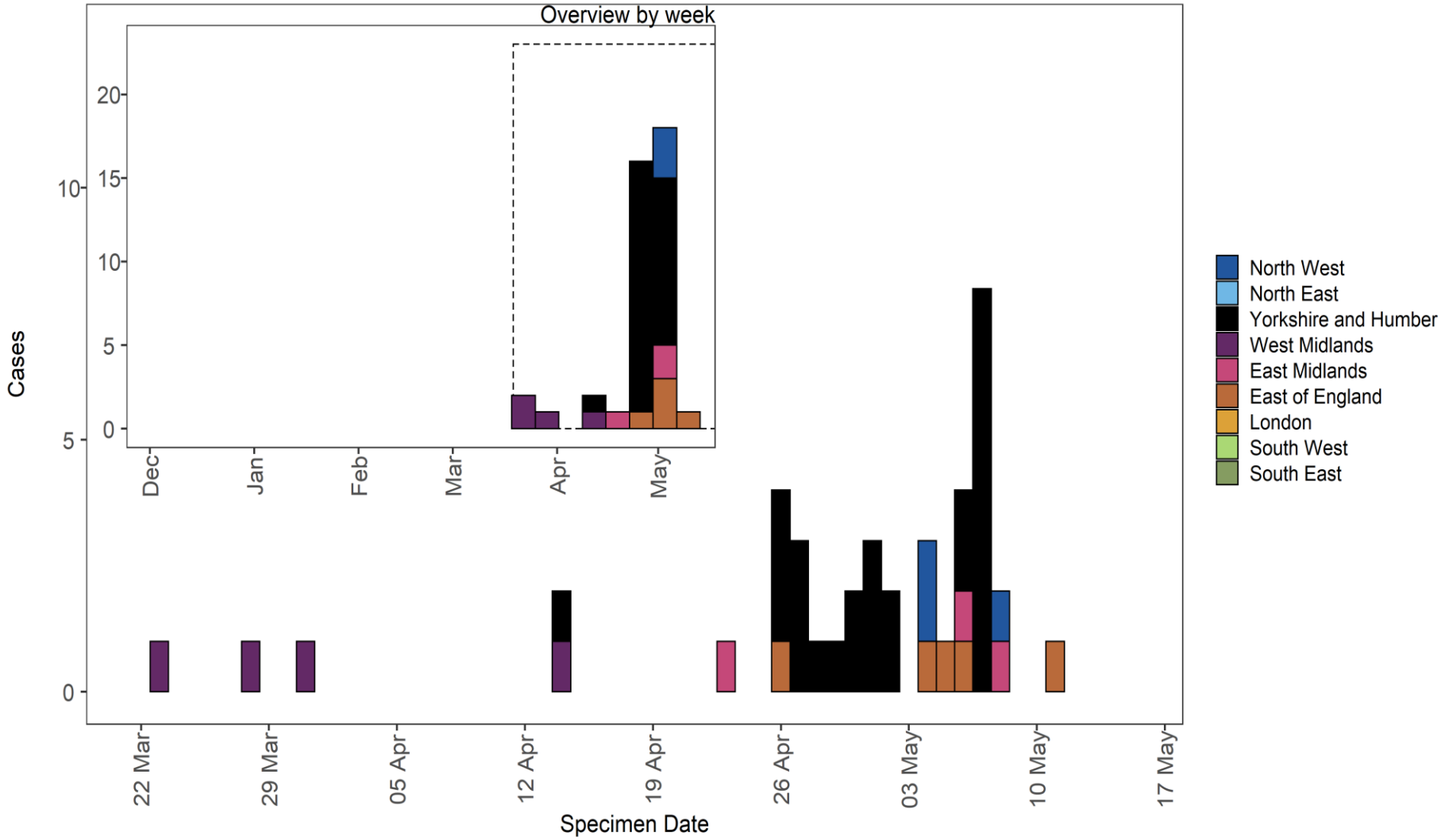
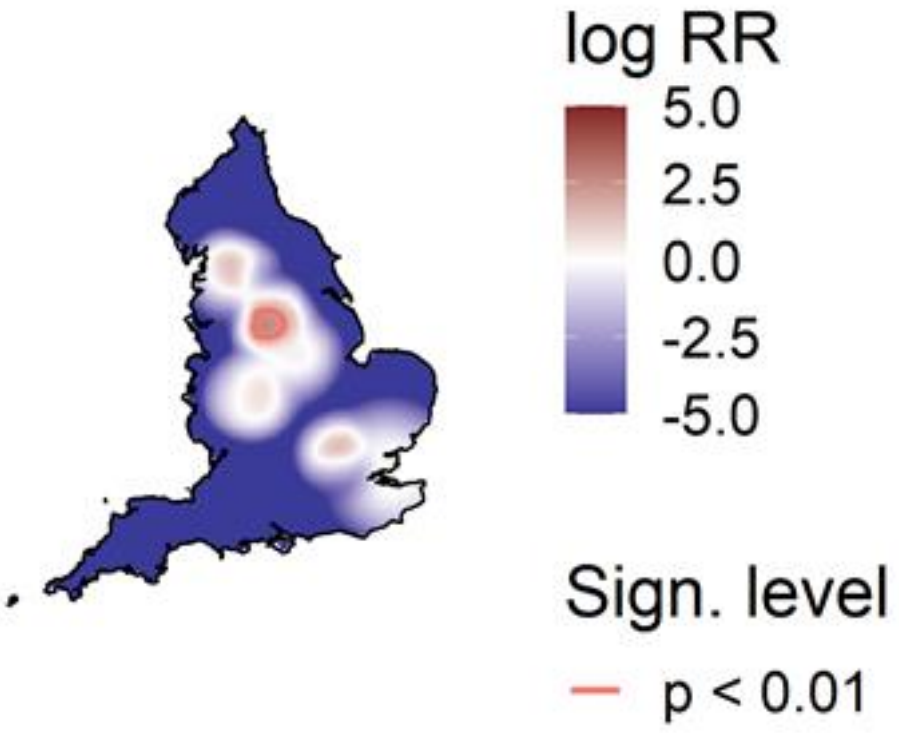


Figure 27. Spatial variation in risk for VUI-21MAY-01 (AV.1) data from 1 October 2020, as of 18 May 2021, excluding cases that are known to have travelled

Supplementary data is not available for this figure. This figure excludes cases in managed quarantine facilities.



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: Public Health England, Public Health Wales , Public Health Scotland, Public Health Agency Northern Ireland, the Department of Health and Social Care, 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, the Joint Biosecurity Centre.

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About Public Health England

Public Health England exists to protect and improve the nation's health and wellbeing, and reduce health inequalities. We do this through world-leading science, research, knowledge and intelligence, advocacy, partnerships and the delivery of specialist public health services. We are an executive agency of the Department of Health and Social Care, and a distinct delivery organisation with operational autonomy. We provide government, local government, the NHS, Parliament, industry and the public with evidence-based professional, scientific and delivery expertise and support.

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