Public Health England

Protecting and improving the nation's health

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

Technical briefing 13

27 May 2021

This briefing provides an update on previous briefings up to 22 May 2021

Contents

Summary

There are 5 variants of concern and 9 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-02 (C.36.3). 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 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. VOC-21APR-02 is likely to be the predominant variant in England although there is regional heterogeneity.

Iterated vaccine effectiveness analysis combined with additional neutralisation data from multiple samples tested at multiple laboratories continues to support the assessment of reduced vaccine effectiveness after the first dose.

The median time to onset of symptoms in household contacts, where the index case is B.1.617.2, is 4 days, which is the same as for B.1.1.7 (using routine contact tracing data). Longitudinal sampling studies have commenced.

Data on hospital admissions with vaccination status is now included and will form part of ongoing surveillance and vaccine effectiveness monitoring.

K417N, a receptor binding domain mutation associated with antigenic change and present in B.1.351 (VOC-20DEC-02), has been noted in a small number of cases of B.1.617.2, in addition to the standard mutations for this lineage.

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 on 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). Figure 1 shows the proportion of cases sequenced over time. Summary epidemiology on each variant is shown in Table 2, case numbers are also updated online. Tables 3a and 3b show hospitalisation and death data. Figure 2 shows cumulative cases of variants over time, indexed by the day of the fifth case.

Table 1. Variant lineage and designation as of 25 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	VUI
P.3	VUI-21MAR-02	Philippines	VUI
B.1.617.1	VUI-21APR-01	India	VUI
B.1.617.3	VUI-21APR-03	India	VUI
AV.1	VUI-21MAY-01	UK	VUI
C.36.3	VUI-21MAY-02	Thailand ex Egypt	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
B.1.621			Monitoring
B.1 with 214insQAS			Monitoring
AT.1			Monitoring

Sequencing coverage

Figure 1. Coverage of sequencing: percentage of SARS-CoV-2 cases sequenced over time as of 24 May 2021
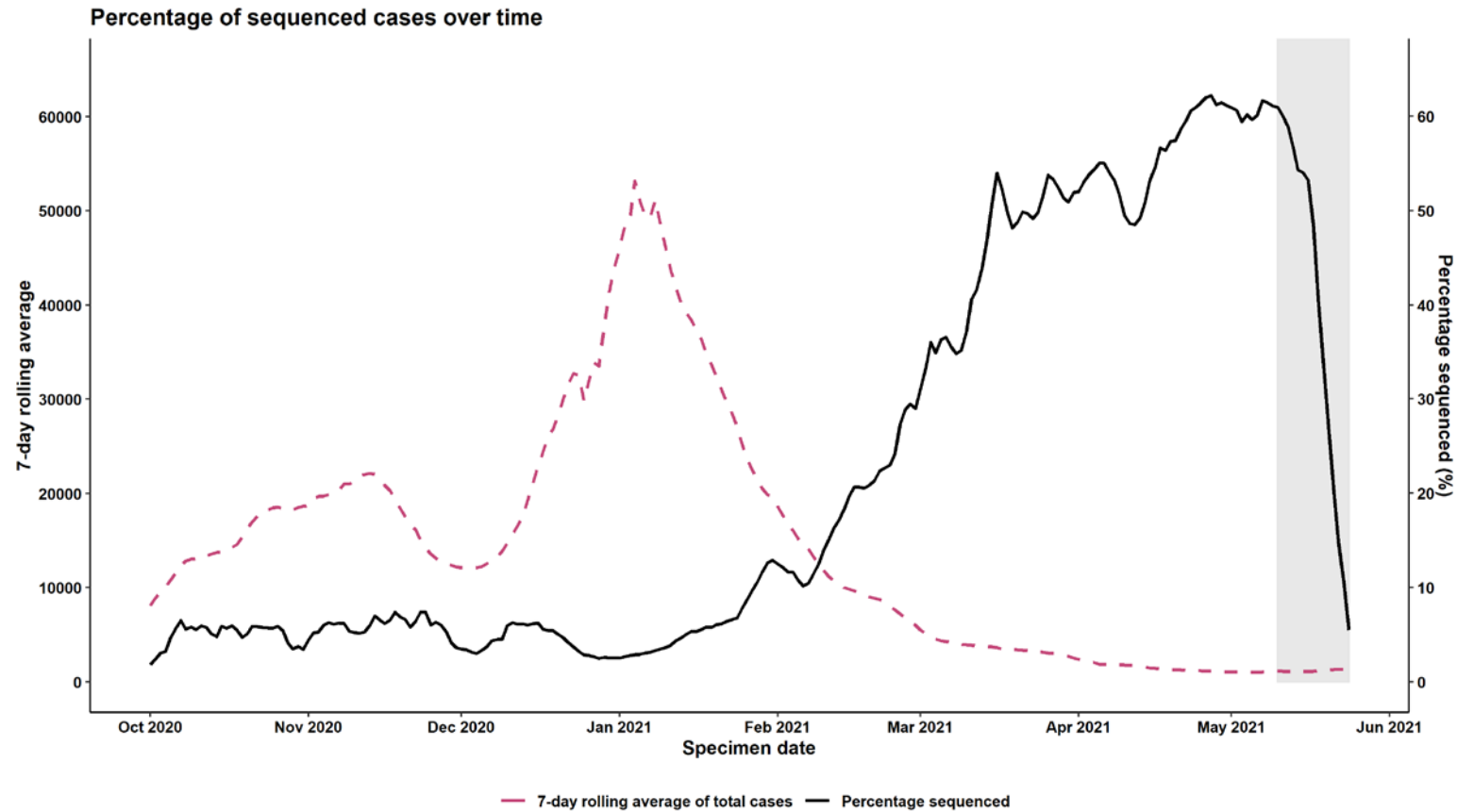
(Find accessible data used in this graph in underlying data)

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 25 May 2021

Variant	Case number	Case proportion	Deaths	Case fatality
VOC-20DEC-01	210,662	96.374%	4,152	2.0% (1.9 to 2.0%)
VOC-20DEC-02	831	0.38%	13	1.6% (0.8 to 2.7%)
VOC-21APR-02*	5,599	2.561%	12	0.2% (0.1 to 0.4%)
VOC-21FEB-02	43	0.02%	1	2.3% (0.1 to 12.3%)
VOC-21JAN-02	145	0.066%	0	0.0% (0.0 to 2.5%)
VUI-21APR-01	406	0.186%	0	0.0% (0.0 to 0.9%)
VUI-21APR-03	14	0.006%	0	0.0% (0.0 to 23.2%)
VUI-21FEB-01	79	0.036%	2	2.5% (0.3 to 8.8%)
VUI-21FEB-03	430	0.197%	12	2.8% (1.5 to 4.8%)
VUI-21FEB-04	228	0.104%	1	0.4% (0.0 to 2.4%)

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VUI-21JAN-01	54	0.025%		1	1.9% (0.0 to 9.9%)
VUI-21MAR-01	2	0.001%		0	0.0% (0.0 to 84.2%)
VUI-21MAR-02	6	0.003%		0	0.0% (0.0 to 45.9%)
VUI-21MAY-01	90	0.041%		0	0.0% (0.0 to 4.0%)

Excludes variant cases not linked to a known COVID-19 case or with provisional sequencing/genotyping results.
[a]Case number England genomic cases 25 May 2021.
[b]Deaths as of 25 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.
* VOC-21APR-02 includes a high proportion of recent cases who have not completed 28 days of follow up.

Table 3a. Attendance to emergency care and deaths among all COVID-19 sequenced cases in England, 1 February 2021 to 25 May 2021

Variant	Cases since 01 Feb 2021¥	Cases with specimen date in past 28 days		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	136,048	9,554	7.0	5,391	4.0	2,079	1.5	1,703	1.3
VOC-20DEC-02	628	74	11.8	26	4.1	9	1.	8	1.3
VOC-21JAN-02	145	36	24.8	7	4.8	1	0.7	0	NA
VOC-21FEB-02	17	0	NA	0	NA	0	NA	1	5.9
VOC-21APR-02	5,599	4,665	83.3	201	3.6	43	0.8	12	0.2
VUI-21JAN-01	24	0	NA	1	4.2	1	1.2	0	NA
VUI-21FEB-01	8	0	NA	0	NA	0	NA	0	NA
VUI-21FEB-03	376	39	10.4	10	2.7	3	0.8	7	1.9
VUI-21FEB-04	221	43	19.5	3	1.4	0	NA	1	0.5
VUI-21MAR-02	6	0	NA	0	NA	0	NA	0	NA
VUI-21APR-01	406	77	19.0	7	1.7	2	0.5	0	NA
VUI-21APR-03	14	2	14.3	0	NA	0	NA	0	NA
VUI-21MAY-01	90	76	84.4	0	NA	0	NA	0	NA

Table 3b. Attendance to emergency care and deaths by vaccination status among VOC-21APR-02 confirmed cases in England, 1 February 2021 to 25 May 2021

	Total	Cases with specimen date in past 28 days	Unlinked	Unvaccinated	<21 days post dose 1	≥21 days post dose 1	Received 2 doses
VOC-21APR-02 cases since 01 Feb 2021¥	5,599	4,665	962	3,367	157	936	177
Cases with an A&E visit§	201	NA	6	138	7	45	5
Cases where presentation to A&E resulted in overnight inpatient admission§	43	NA	2	29	1	10	1
Deaths^	12	NA	0	8	0	2	2

Data sources: A&E attendance and admissions from Emergency Care Dataset (ECDS), deaths from PHE daily death data series (deaths within 28 days)
¥ Cases without specimen dates and unlinked sequences (sequenced samples that could not be matched to individuals) are excluded from this table.
* Cases are assessed for any A&E attendance within 28 days of their positive specimen date. Cases still undergoing within 28-day period may have an emergency care 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 help remove cases whose primary cause of admission is not COVID-19 picked up via routine testing in healthcare settings. This underestimate the true number of cases who have attended emergency care due to COVID-19 but avoids overestimation due to asymptomatic people attending emergency care for unrelated conditions; validation of the dataset is being undertaken.
^ 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 25 May 2021
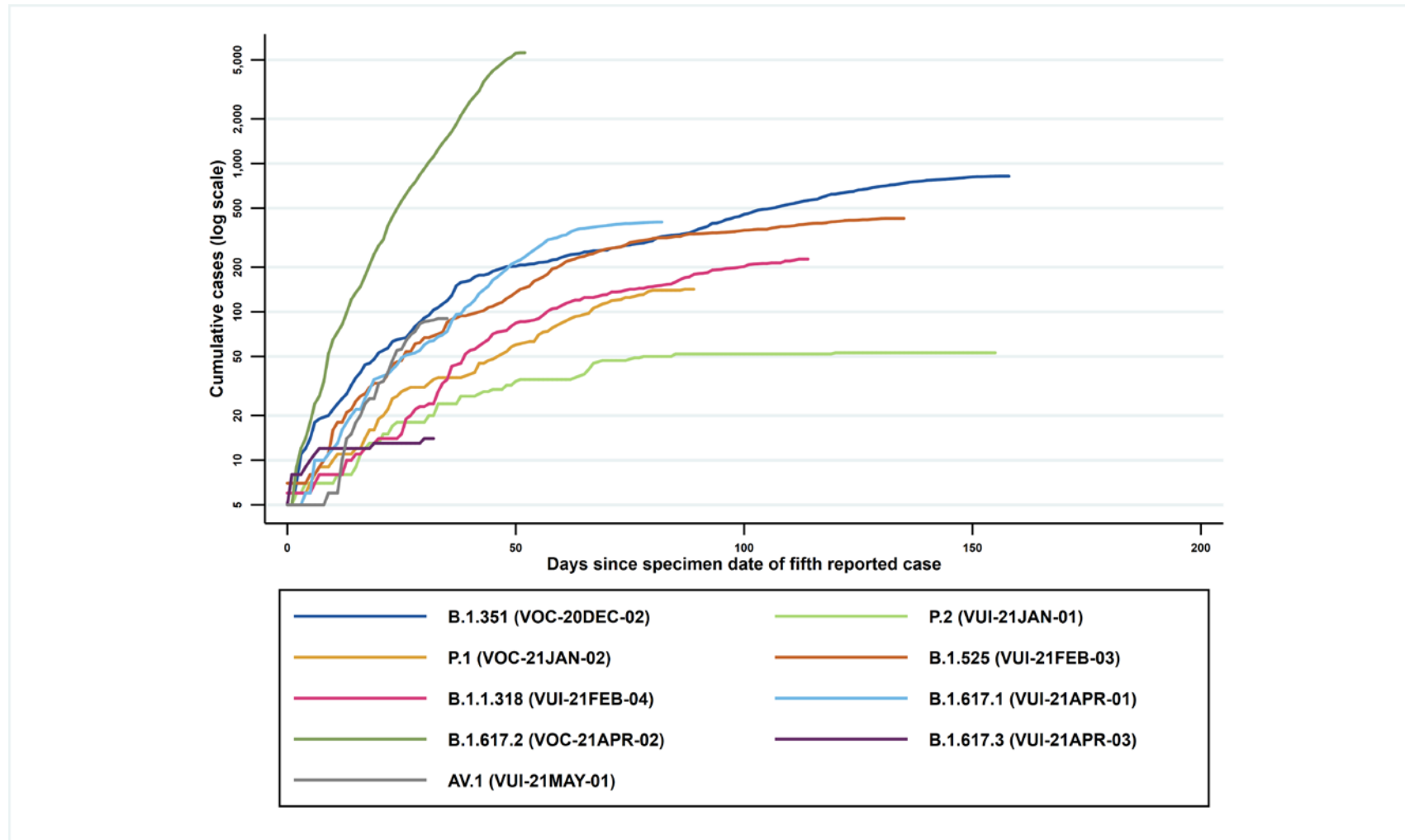

(Find accessible data used in this graph in underlying data).
Figure 2 demonstrates the rapid identification of VOC-21APR-02 (B.1.617.2) cases over a short period of time.

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 are available.

Figure 3. Variant prevalence for all England available case data from 1 February 2021 as of 25 May 2021 (excluding cases where the specimen date was unknown)
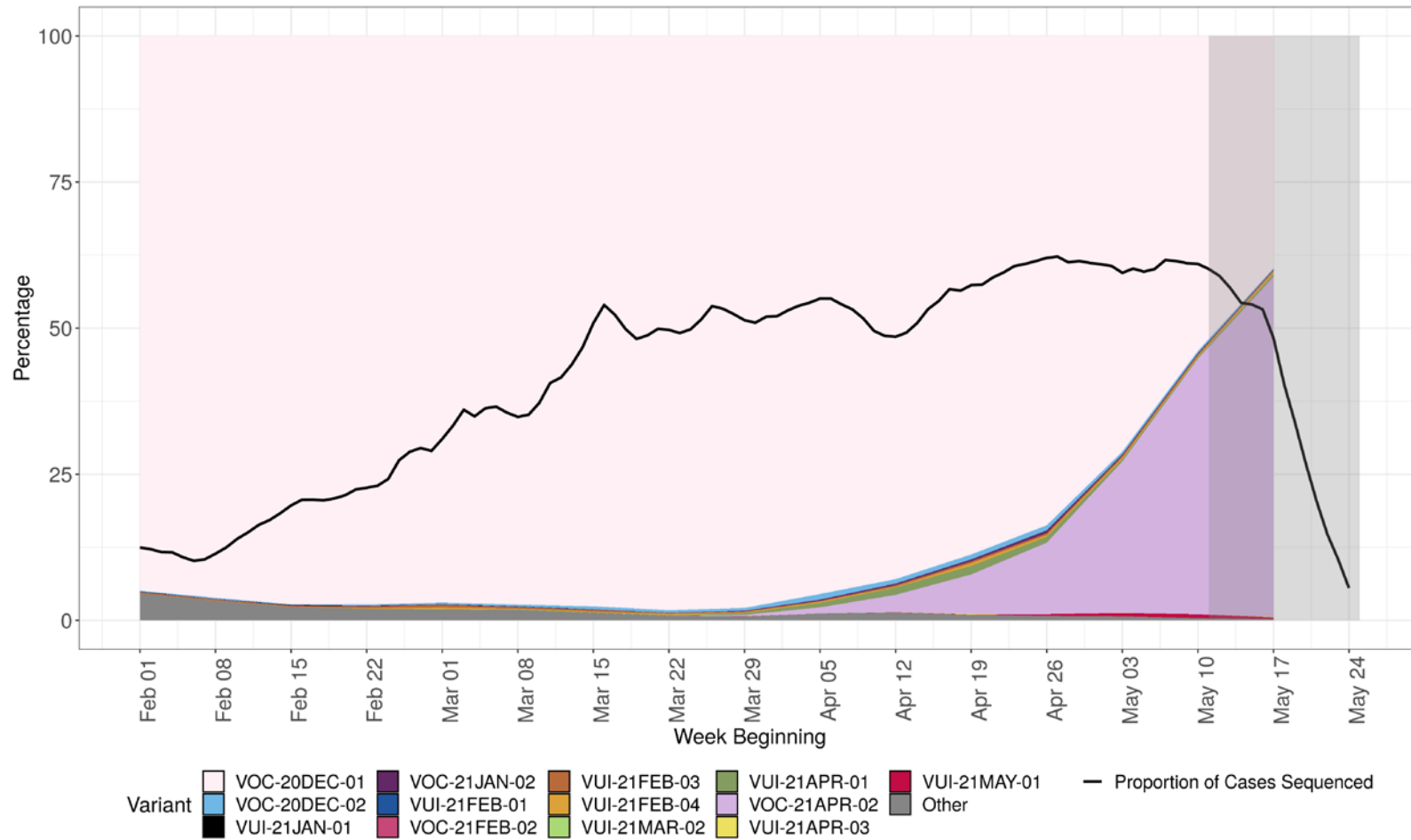
The most recent data shows 58% of sequenced cases are VOC-21APR-02. At the latest data point where there is complete data (outside the grey region), 43% of sequenced cases are VOC-21APR-02. The black line indicates proportion of cases sequenced in a 7-day rolling window. The area in grey shows weeks 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

Figure 4. Variant prevalence for all England available case data from 1 February 2021 as of 25 May 2021 by region (excluding cases where the region or specimen date were unknown)
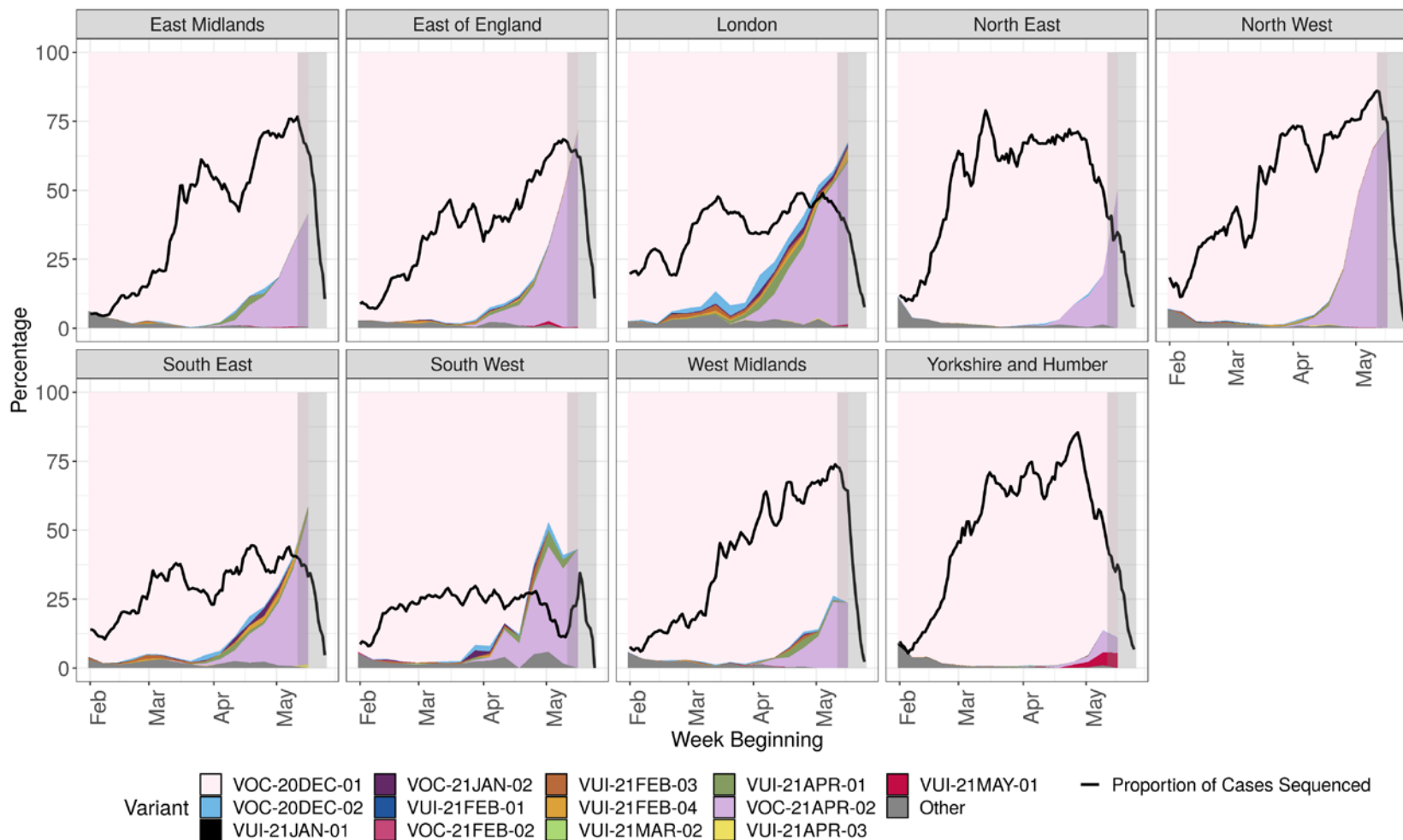
In figure 4, the black line indicates proportion of cases sequenced in a 7-day sliding window. The area in grey shows weeks where the sequence data is still accumulating, therefore the proportions are less likely to accurately reflect prevalence. Rapid genotyping assay results that have not been confirmed by sequencing have been removed from this dataset. Data for most recent 2 weeks is incomplete. (Find accessible data used in this graph in

Figure 5. Prevalence of variants over time: all sequenced cases in England, split by travel status as of 25 May 2021 (excluding cases where the specimen date is unknown)
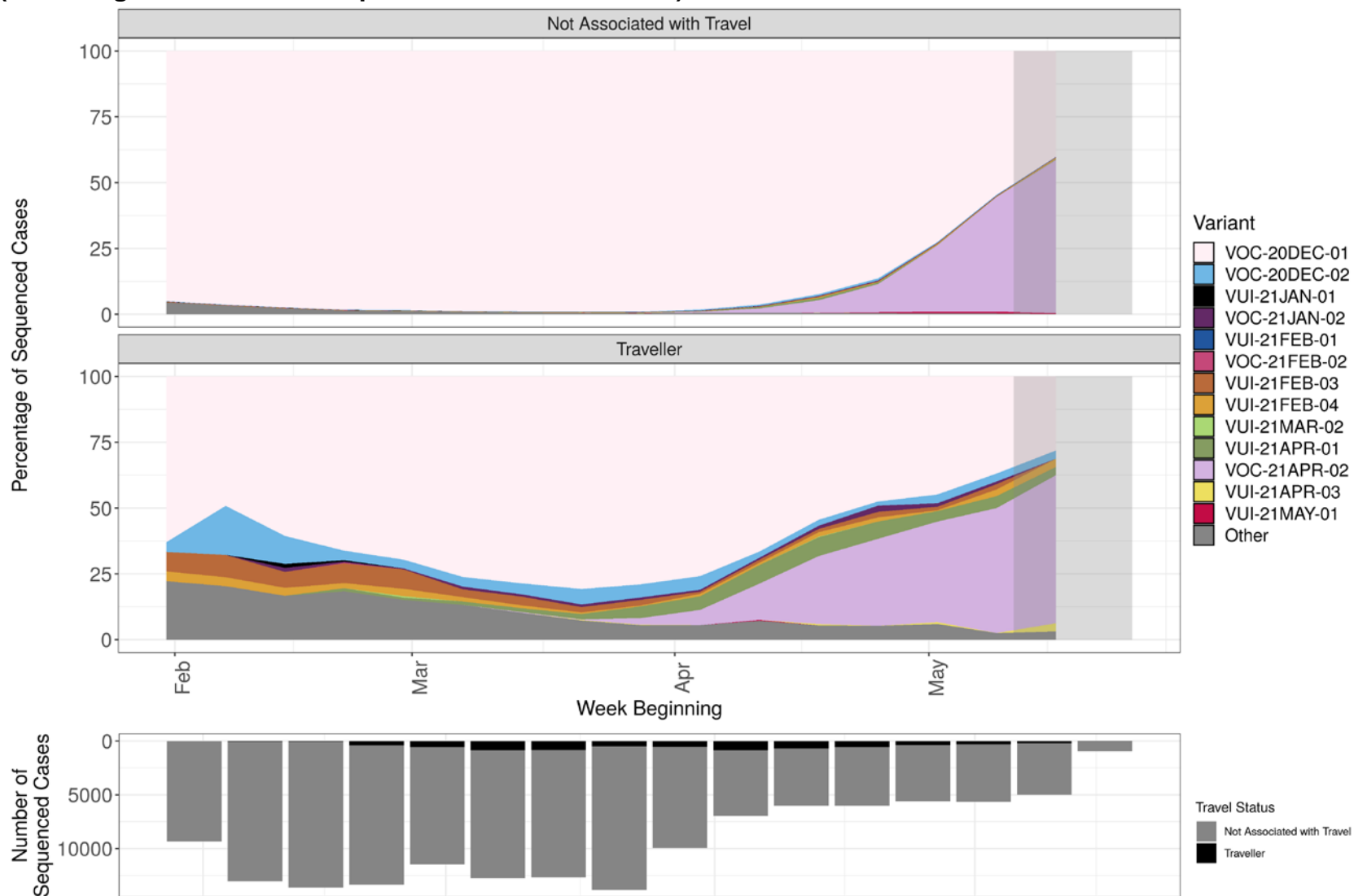
Travel status is assigned based an interval of <= 14 days between arrival date and positive specimen date. It is derived through matching to Passenger Locator Forms, contact-tracing, international arrivals and local HPT survey data. The area in grey shows weeks where the sequence data is still accumulating, 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. The total number of sequenced cases in each week is shown in the bars below, split by travel status. (Find accessible data used in this graph in

Variant growth rates

Logistic growth rates (1/week from 1 January 2021 as of 25 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: 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 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). Growth rate is context dependent and cannot be interpreted as a change in biological transmissibility.

Compared to VOC-20DEC-01 (B.1.1.7), VOC-21APR-02 (B.1.617.2) displays an increased logistic growth rate indicating that the proportion of samples that are VOC-21APR-02 is increasing.

Table 4. Growth rate of variants of concern and variants under investigation 1 January 2021 as of 25 May 2021

Variant	Growth rate (1/week)
VOC-20DEC-02	0.16 (p=9.366e-36, n=337)
VUI-21JAN-01	-0.098 (p=0.15, n=21)
VOC-21JAN-02	0.32 (p=1.191e-15, n=74)
VUI-21FEB-01	-0.31 (p=0.0004, n=55)
VUI-21FEB-03	0.11 (p=2.54e-11, n=192)
VUI-21FEB-04	0.19 (p=1.682e-15, n=126)
VUI-21APR-01	0.32 (p=4.27e-18, n=149)
VOC-21APR-02	0.94 (p=0, n=4,699)
VUI-21APR-03	0.98 (p=0.12, n=5)

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.

Use of rapid genotyping assays

Rapid genotyping assays are being rolled out across the testing laboratory network and have been amended to incorporate VOC-21APR-02 detection. At present the genotyping assay detects P681R, N501Y, K417N, K471T and deletion 69-70 ('S gene target failure'). Genotyping results are confirmed by sequencing. Data presented in the technical briefing currently uses either genomic or S gene target data. Genotyping assay results will be incorporated in the coming weeks.

Secondary attack rates

This section includes secondary attack rates for traveller and non-traveller cases, and separate household contact rates. It also includes a new analysis of time to onset of symptoms in household contacts.

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 4 May 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 4 May 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): 13.5% compared to 8.1%. 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. 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 4 May 2021. Secondary attack rates for contacts of non-travel cases with VOC-21FEB-02 and VUI-21MAY-01 were lower than for contacts of non-travel cases with VOC-20DEC-01 over this time. All other secondary attack rates for contacts of non-travel cases with the remaining variants of concern or under investigation are not significantly different from 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, due to the difference in contact definition.

Table 7 shows the secondary attack rates amongst household and non-household contacts of non-travel cases with VOC-21APR-02 (B.1.617.2) 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 4 May 2021 as in Table 5. Secondary attack rates are higher amongst household contacts than non-household contacts of non-travel cases with both variants and higher for contacts of non-travel cases with VOC-21APR-02 (B.1.617.2) than VOC-20DEC-01 (B.1.1.7); this is consistent with Table 5.

Fig 6 (and Table 8) shows the time interval between index and secondary case onset for household contacts, and between exposure date and secondary case onset for non-household contacts. The median interval for household exposures is 4 days for both VOC-20DEC-01 and VOC-21APR-02. For non-household exposures, the median interval from exposure date to secondary case onset is also 4 days for VOC-20DEC-01, but 5 days for VOC-21APR-02.

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 4 May 2021, variant data as at 18 May 2021, contact tracing data as at 25 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 cases 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	1,738 (71.2% with contacts)	26,437 (81.8% with contacts)	6.2%	1.7% (1.5% to 1.8%) [452/26,934]	8.1% (7.9% to 8.3%) [5,587/68,713]
VUI-21APR-01	158 (78.5% with contacts)	119 (79.0% with contacts)	57.0%	2.2% (1.7% to 2.9%) [56/2,509]	11.0% (7.9% to 15.0%) [33/301]
VOC-21APR-02	404 (70.8% with contacts)	1,446 (83.4% with contacts)	21.8%	2.9% (2.5% to 3.4%) [174/5,908]	13.5% (12.5% to 14.6%) [537/3,977]
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 4 May 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 4 May 2021, variant data as at 18 May 2021, contact tracing data as at 25 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 cases 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	3,906 (77.8% with contacts)	165,560 (74.4% with contacts)	2.3%	1.7% (1.6% to 1.8%) [1,170/69,210]	9.9% (9.8% to 10.0%) [34,166/344,947]
VOC-20DEC-02	291 (72.9% with contacts)	334 (66.5% with contacts)	46.6%	2.5% (2.1% to 3.1%) [106/4,162]	9.0% (7.1% to 11.4%) [63/698]
VUI-21JAN-01	3 (66.7% with contacts)	32 (75.0% with contacts)	8.6%	Unavailable [0/137]	8.1% (3.5% to 17.5%) [5/62]
VOC-21JAN-02	55 (60.0% with contacts)	60 (66.7% with contacts)	47.8%	0.9% (0.4% to 2.2%) [5/536]	11.0% (6.9% to 17.1%) [16/146]
VUI-21FEB-01	0 (0 with contacts)	63 (60.3% with contacts)	0.0%	Unavailable [0/0]	8.6% (4.4% to 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% to 3.3%) [0/111]
VUI-21FEB-03	190 (71.1% with contacts)	177 (73.4% with contacts)	51.8%	1.3% (1.0% to 1.7%) [55/4,184]	9.0% (6.3% to 12.5%) [30/335]
VUI-21FEB-04	79 (68.4% with contacts)	114 (75.4% with contacts)	40.9%	0.6% (0.3% - 1.0%) [13/2,193]	9.4% (6.3% - 13.8%) [22/235]

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 cases 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)	26 (84.6% with contacts)	7.1%	Unavailable [0/0]	3.3% (1.1% to 9.2%) [3/92]

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 4 May 2021 in order to allow time for contacts to become cases, hence case counts are lower than other sources. Provisional results are excluded.
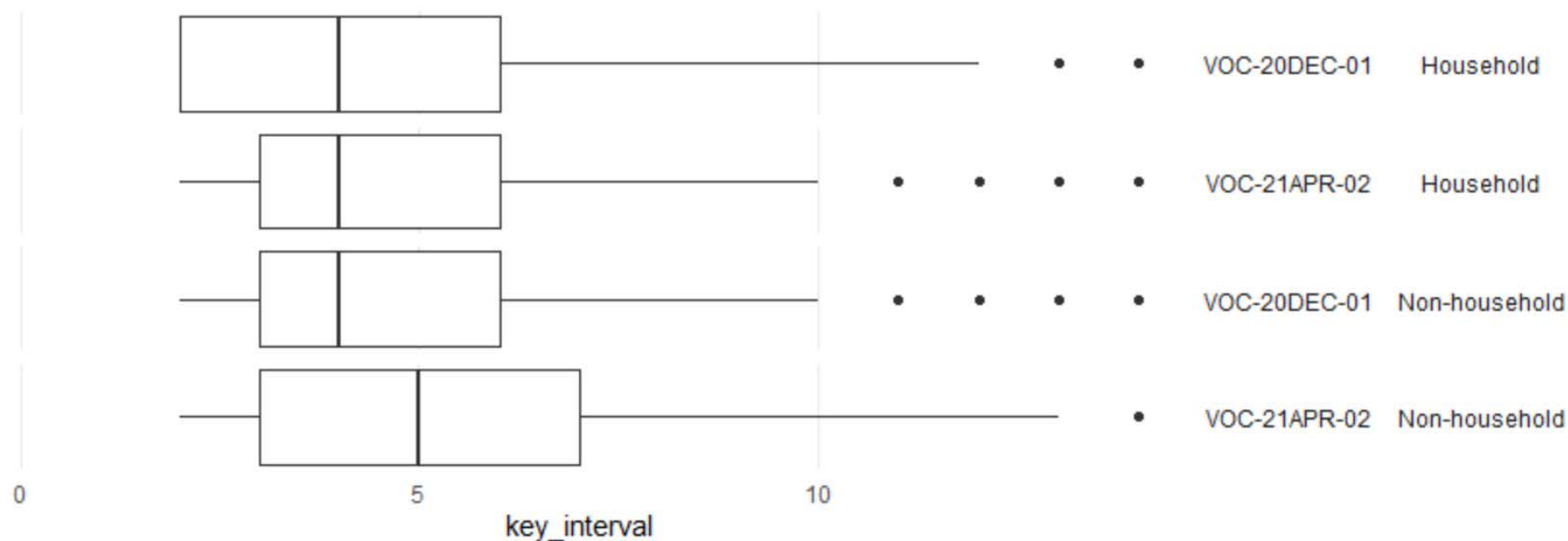
Table 7. Secondary attack rates for household contacts of non-travel cases of VOC-20DEC-01 (B.1.1.7) and VOC-21APR-02 (B.1.617.2) (29 March 2021 to 4 May 2021, variant data as at 18 May 2021, contact tracing data as at 25 May 2021)

Variant	Cases in those that have not travelled or unknown (with household contacts, with non-household contacts)	Secondary Attack Rate among household contacts of cases that have not travelled or unknown (95% CI) [secondary cases/contacts]	Secondary Attack Rate among non-household contacts of cases that have not travelled or unknown (95% CI) [secondary cases/contacts]
VOC-20DEC-01	2,6437 (79.7% with household, 17.9% with non-household contacts)	8.9% (8.7% to 9.1%) [5,019/56,374]	4.6% (4.2% to 5.0%) [568/12,339]
VOC-21APR-02	1,446 (81.3% with household, 16.2% with non-household contacts)	15.0% (13.8% to 16.2%) [490/3,274]	6.7% (5.1% to 8.8%) [47/703]

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

Fig. 6 Time interval to onset of symptoms in secondary case, household and non-household contacts of cases of VOC-20DEC-01 (B.1.1.7) and VOC-21APR-02 (B.1.617.2) (29 March 2021 to 5 May 2021, variant data as at 25 May, contact tracing data as at 26 May)

NHS Test and Trace data. Distribution of time in days from contact exposure to secondary case onset of symptoms. Periods restricted to between 2 to 14 days. Household exposure dates are taken as date of onset or test in primary case. (Find accessible data used in this graph in underlying data).

Table 8. Time interval to onset in secondary case, household and non-household contacts of cases of VOC-20DEC-01 (B.1.1.7) and VOC-21APR-02 (B.1.617.2) (29 March 2021 to 5 May 2021, variant data as at 25 May, contact tracing data as at 26 May)

Variant	Exposure type	Secondary cases	Median interval (days)
VOC-20DEC-01	Household	5,376	4
VOC-21APR-02	Household	618	4
VOC-20DEC-01	Non-household	888	4
VOC-21APR-02	Non-household	160	5

NHS Test and Trace data. Distribution of time in days from contact exposure to secondary case onset of symptoms. Periods restricted to between 2 to 14 days. Household exposure dates are taken as date of onset or test in primary case.

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 9 shows the total number of sequences available from second episodes of infection in possible reinfection cases, categorized by variant. Figure 7 shows the number of different variants identified through sequencing that are possible reinfection cases. In recent weeks there have been a number of reinfections 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 those weeks.

Table 9. Number of sequenced reinfection cases and the variant assigned. (Data as of 25 May 2021).

Variant	Total
VOC-20DEC-01	540
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	54
VUI-21APR-03	0
VUI-21MAY-01	1
Total sequenced	812

Figure 7. 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 25 May 2021
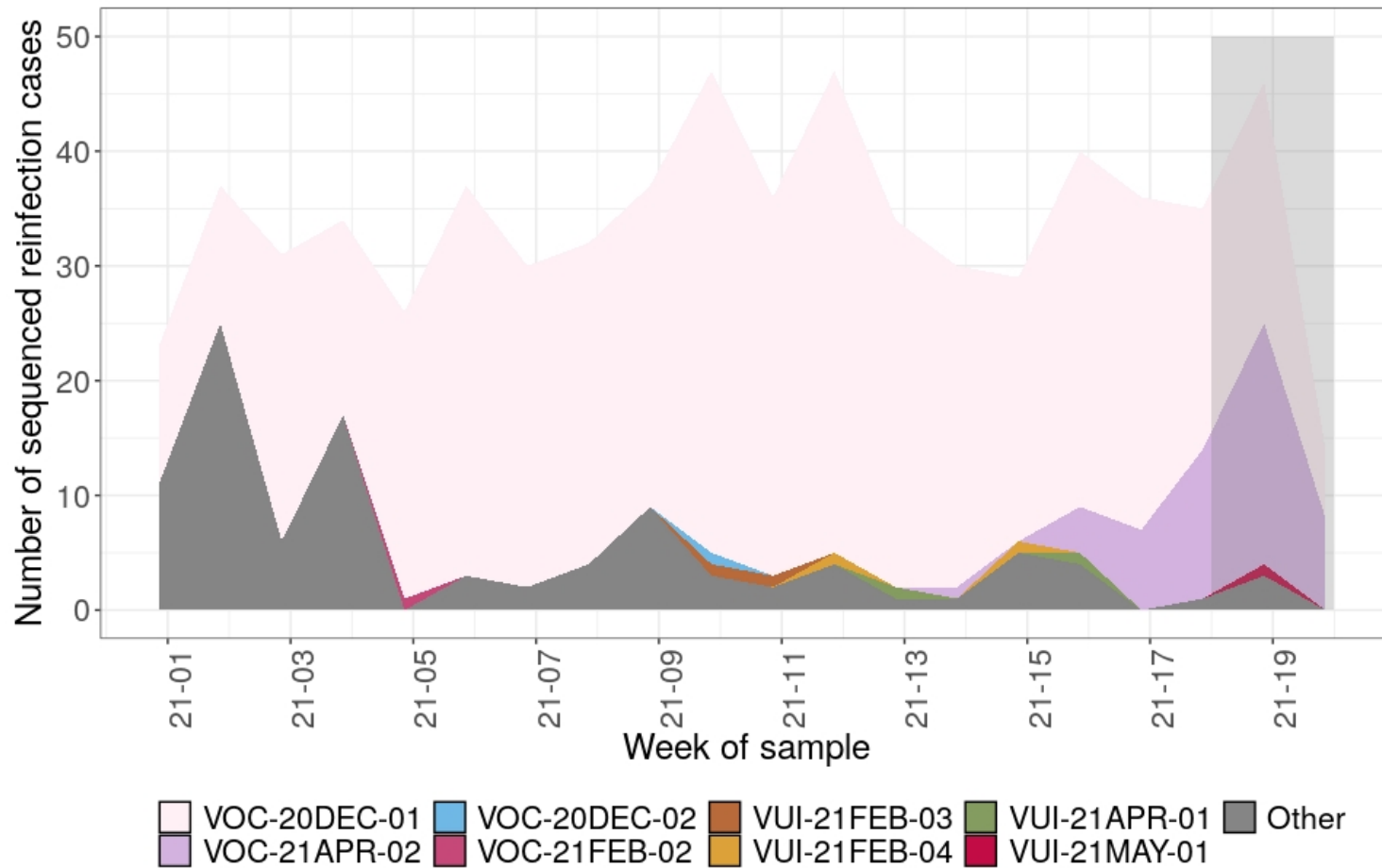

(Find accessible data used in this graph in underlying data).

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 8) and reinfections remain at very low numbers in individuals previously either PCR positive or seropositive (Figure 9).

Figure 8. PCR positivity within the SIREN study for all regions, England (fortnightly testing interval). Data up to 23 May 2021
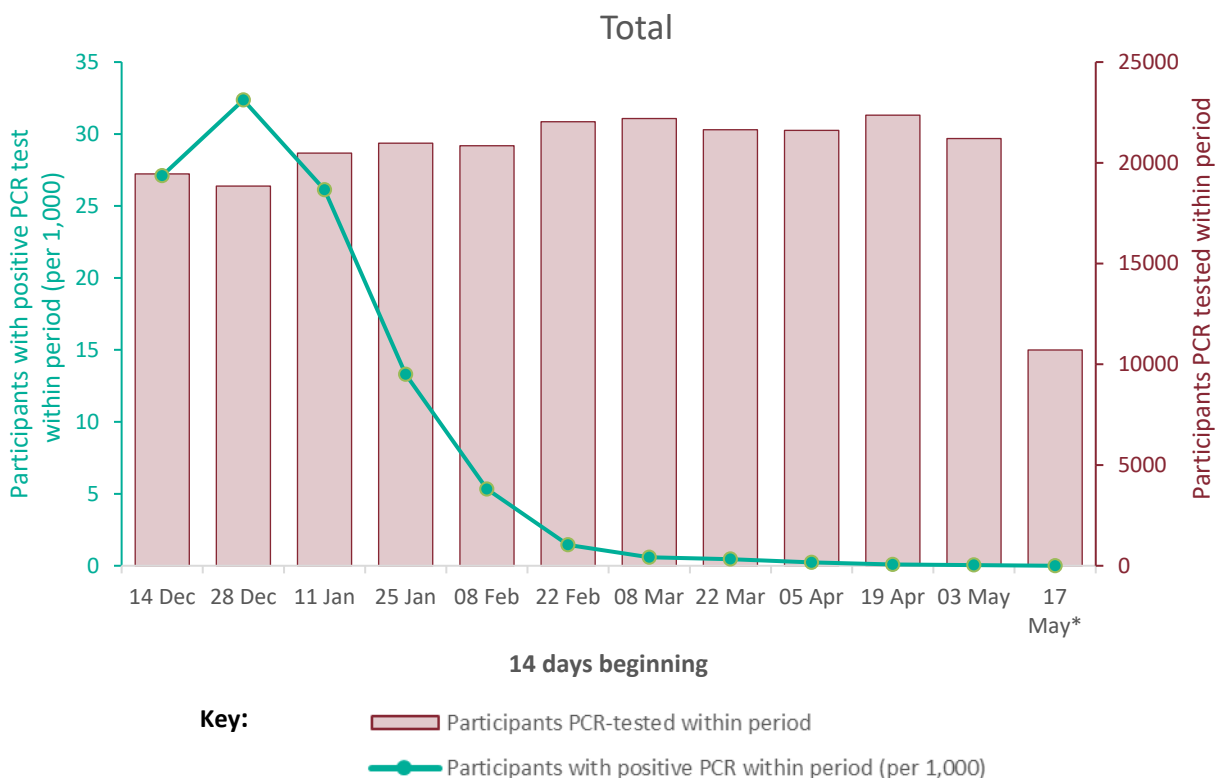
Contains only participants with at least one PCR test within given period; participants are counted as positive if at least one PCR test within given period is positive; only samples collected during the SIREN study (that is baseline and follow-up); figures have not been restricted by antibody status nor vaccination status, therefore will include participants presumed no longer susceptible to a new infection; includes only participants from England trusts.

* This is the number who enrolled and have not subsequently withdrawn and requested their data to be deleted (Find accessible data used in this graph in underlying data).

Figure 9. Monthly frequency of potential reinfections within SIREN. Data up to 25 May 2021
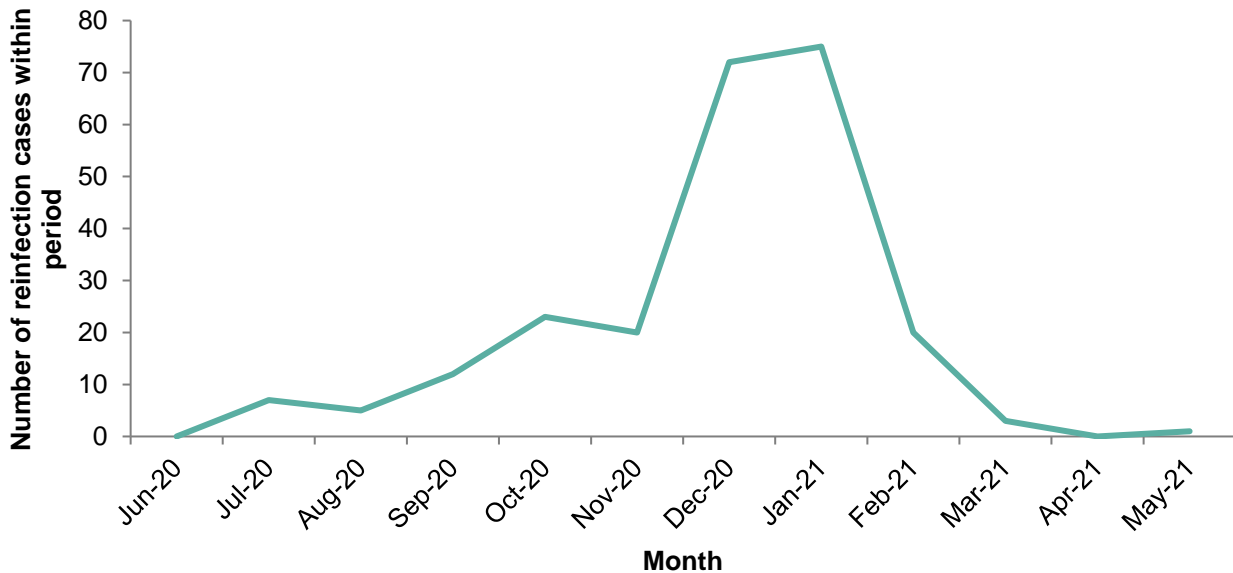
238 total potential reinfections (green line) within SIREN identified in England up to 25 May 2021. 9813* (31%) of SIREN cohort with prior infection at enrolment.

*This number has increased during follow-up as participants move from the negative to positive cohort after a primary infection.

(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 10. Number of confirmed and probable VOC-21APR-02 (B.1.617.2) cases, by region of residence as of 25 May 2021

Region	Case Number	Case Proportion	Cases that have travelled	Proportion of travellers among cases*
East Midlands	535	9.6%	56	10.5%
East of England	713	12.7%	83	11.6%
London	991	17.7%	204	20.6%
North East	81	1.4%	10	12.3%
North West	2,486	44.4%	39	1.6%
South East	315	5.6%	87	27.6%
South West	98	1.8%	44	44.9%
West Midlands	258	4.6%	51	19.8%
Yorkshire and Humber	108	1.9%	22	20.4%
Unknown region	14	0.3%		NA
England	5,599	-	596	10.6%

*Denominator is all cases, including those with unknown or pending travel status

Figure 10. Confirmed and probable VOC-21APR-02 (B.1.617.2) cases by specimen date as of 25 May 2021
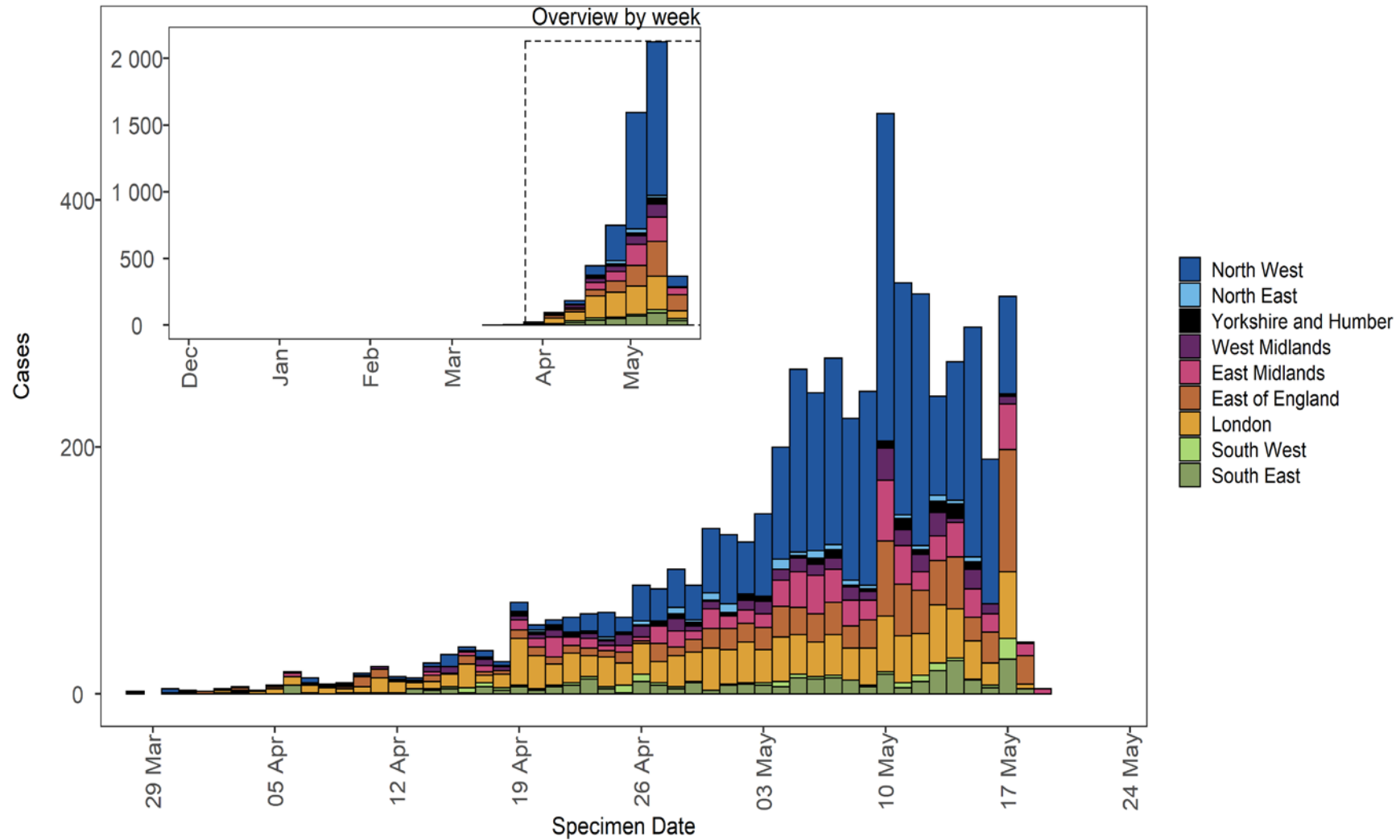
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data).

Figure 11. Travel data for confirmed and probable VOC-21APR-02 (B.1.617.2) cases by specimen date as of 25 May 2021
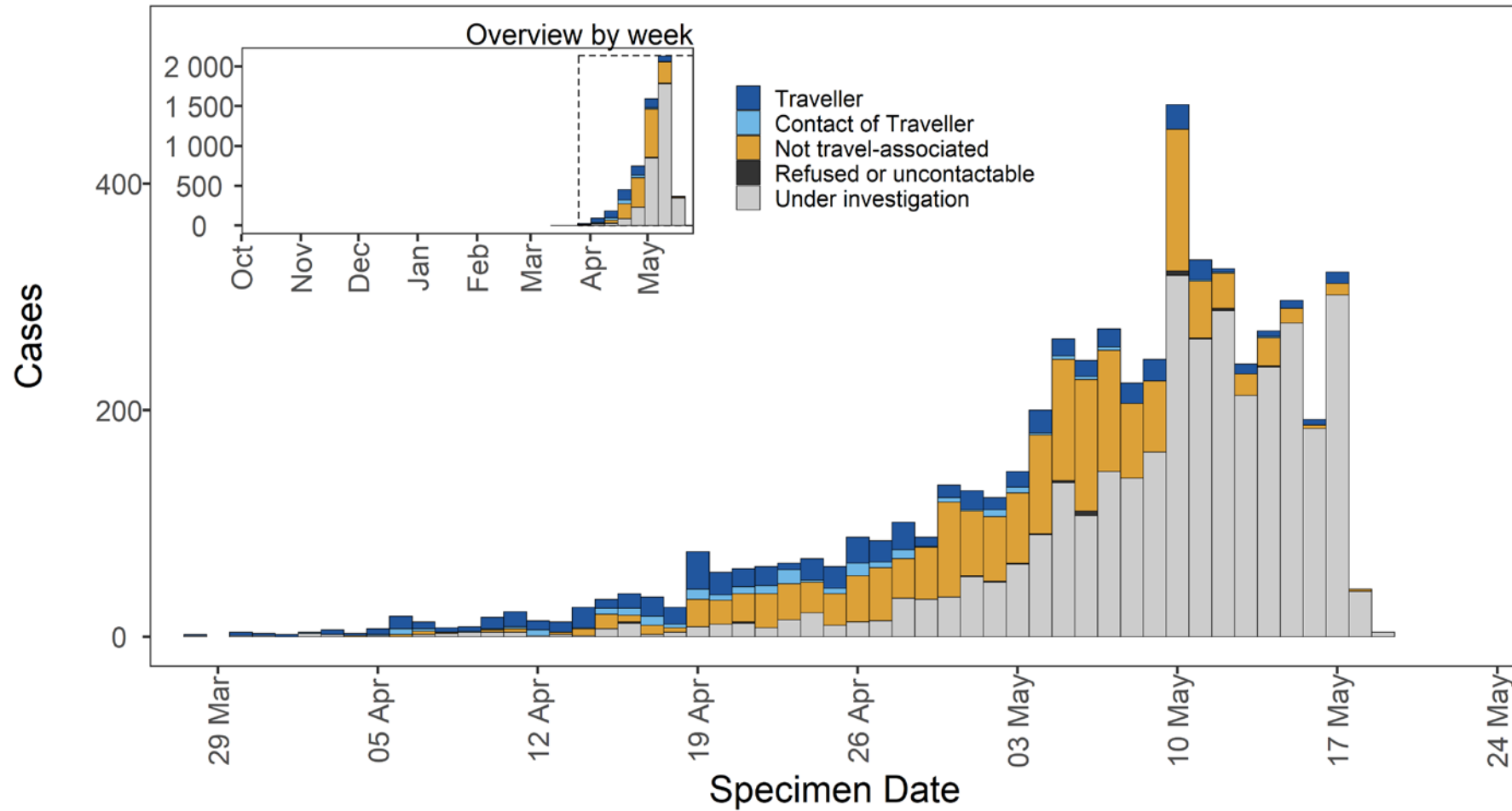
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data).

Table 11 Additional spike mutations of interest detected in VOC-21APR-02 genomes in the UK

Amino acid change	Nucleotide change	Total number of sequences (UK)	Number of sequences 26 February to 25 March	Number of sequences 26 March to 25 April	Number of sequences 26 April to 25 May
Total		7,388	4	813	6,570
P681R	23604G	7,372	4	810	6,557
L452R	22917G	7,262	4	809	6,448
G142D	21987A	4,466	3	583	3,880
K417N	22813T	29	0	1	28
G446V	22899T	9	0	4	5
Q677H	23593T	9	0	6	3
S255F	22326T	6	0	2	4
V503I	23069A	6	0	0	6
L244S	22293C	5	0	0	5
E484A	23013C	4	0	0	4
S494L	23043T	3	0	0	3
A701V	23664T	2	0	1	1
D80A	21801C	1	0	0	1
P251L	22314T	1	0	0	1
D405Y	22775T	1	0	0	1
L455F	22927T	1	0	1	0
S477I	22992T	1	0	0	1
P479S	22997T	1	0	0	1
V483F	23009T	1	0	0	1
E484Q	23012C	1	0	0	1
R682W	23606T	1	0	0	1
R683Q	23610A	1	0	0	1
R683L	23610T	1	0	0	1

This data uses the numbers of genomes in the national genomic dataset rather than case numbers. Further investigations of K417N genomes are being undertaken.

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 12 highlights areas of significantly increased risk identified for VOC-21APR-02 (B.1.617.2) and the differences between data presented in technical briefing 12 and 13. London is no longer demonstrating an increased intensity ratio.

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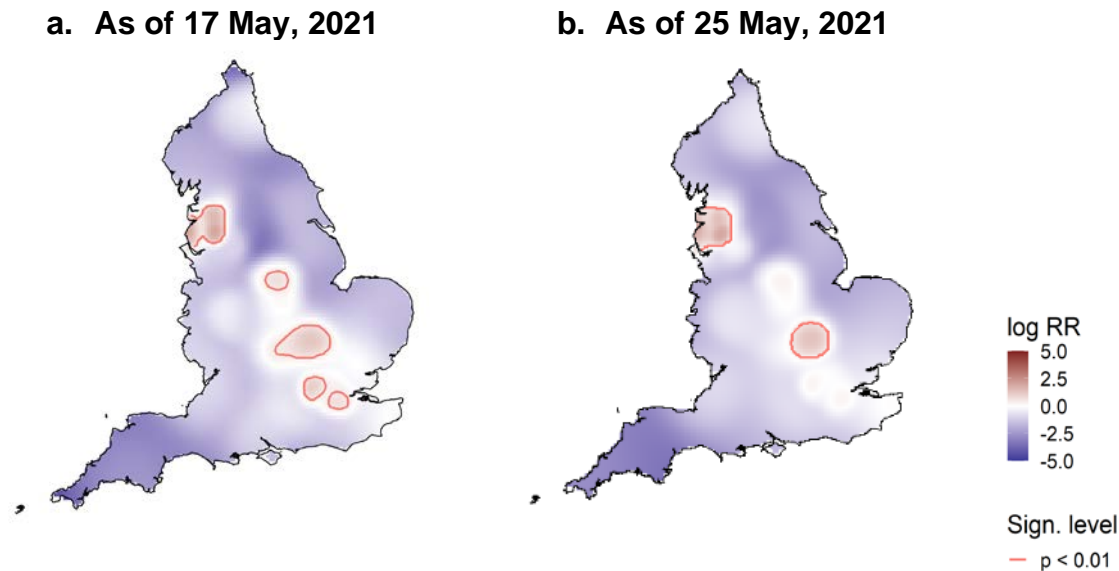
This figure excludes cases in managed quarantine facilities. Supplementary data is not available for this figure.

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 (Figure 13, negative binomial GLM $p = 0.0498$).

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, 104 VOC-21APR-02 (B.1.617.2) clusters were retained with a mean origin date of 26 April 2021 and a mean size of 20.3. A further 469 VOC-20DEC-01 (B.1.1.7) clusters were retained with a mean origin date of February 21, 2021 and a median size of 22.1.

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 principal findings in this iteration of the analysis are that the regional composition (NHS region) of clusters was not a significant predictor of cluster size ($p>0.13$), a larger number of traveller cases detected at the origin of each cluster was associated with larger cluster sizes ($p=0.0007$), and after adjusting for the number of travellers at the origin of each cluster, VOC-21APR-02 clusters were not significantly larger than VOC-20DEC-01 clusters ($p=0.19$).

Figure 13. Clustering of VOC-20DEC-01 (B.1.1.7) and VOC-21APR-02 (B.1.617.2) by region as of 25 May 2021
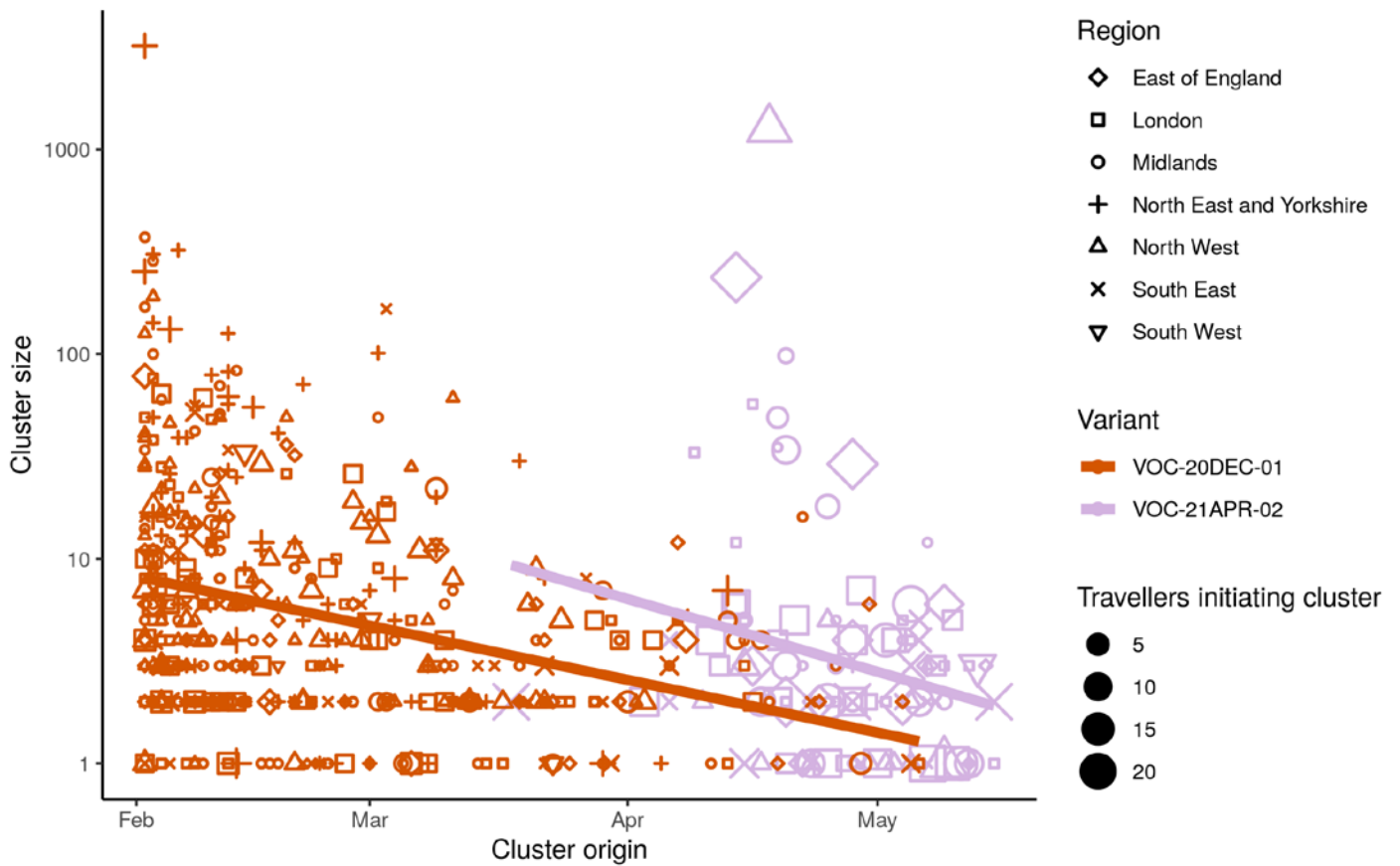
The size of phylogenetic clusters initiated by cases linked to travel from India is shown versus the time of origin of each cluster (time of first sample). Lines show a linear regression for lineages VOC-20DEC-01 (B.1.1.7) and VOC-21APR-02 (B.1.617.2). (Find accessible data used in this graph in underlying data).

Surveillance of cases in travellers from India

Figure 14. Lineages of cases with recent travel history from India
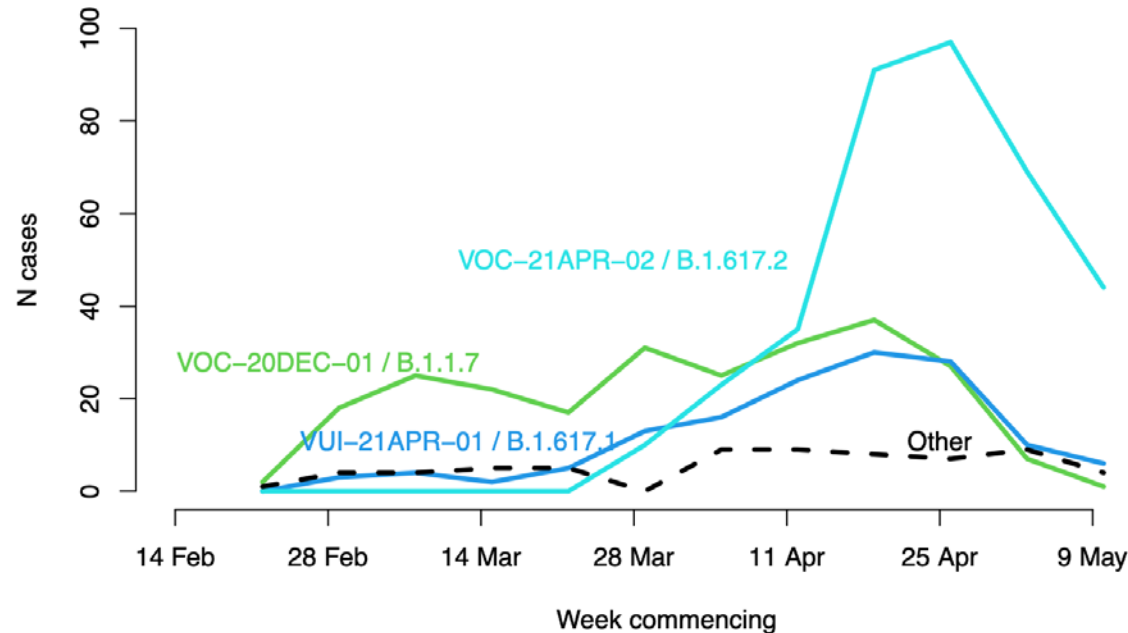
Each line shows the count of cases by test date of that lineage with known travel history from India within 14 days of testing positive: VOC-20DEC-01 (B.1.1.7) in green, VUI-21APR-01 (B.1.617.1) in blue, VOC-21-APR-02 (B.1.617.2) in cyan, other lineages as dashed line (22 February 2021 to 16 May 2021, final week incomplete). (Find accessible data used in this graph in underlying data).

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Surveillance through S gene detection

The S gene target in a 3-target assay (S, N and ORF1ab) used in some Lighthouse Laboratories fails in VOC-20DEC-01 (B.1.1.7) the previously dominant variant. However, this S gene 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. It is also detected in VOC-20DEC02 (B.1.351) and other variants. 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 January 2021 (data as of 25 May 2021), as well as the distribution of identified variants among these specimens. Unclassified variants refer to those not currently considered a VOC or VUI; these dominated the sequenced S gene positive specimens at the beginning of 2021 and have decreased to less than 1% in the most recent week of data (11 May to 17 May 2021, Figure 16). Comparatively, the proportion of confirmed VOC-21APR-02 specimens among S gene positives continues to increase, to 97.3% in the week starting 11 May 2021 (note incomplete week due to reporting delays). This is largely consistent across regions, however lower in Yorkshire and Humber where variant VUI-21MAY-01, which is also S gene positive, is present. Additionally, this proxy is limited by variable TaqPath laboratory coverage across England (Figure 17), and biases in sequencing, for instance targeting of contacts of variant cases in outbreak settings.
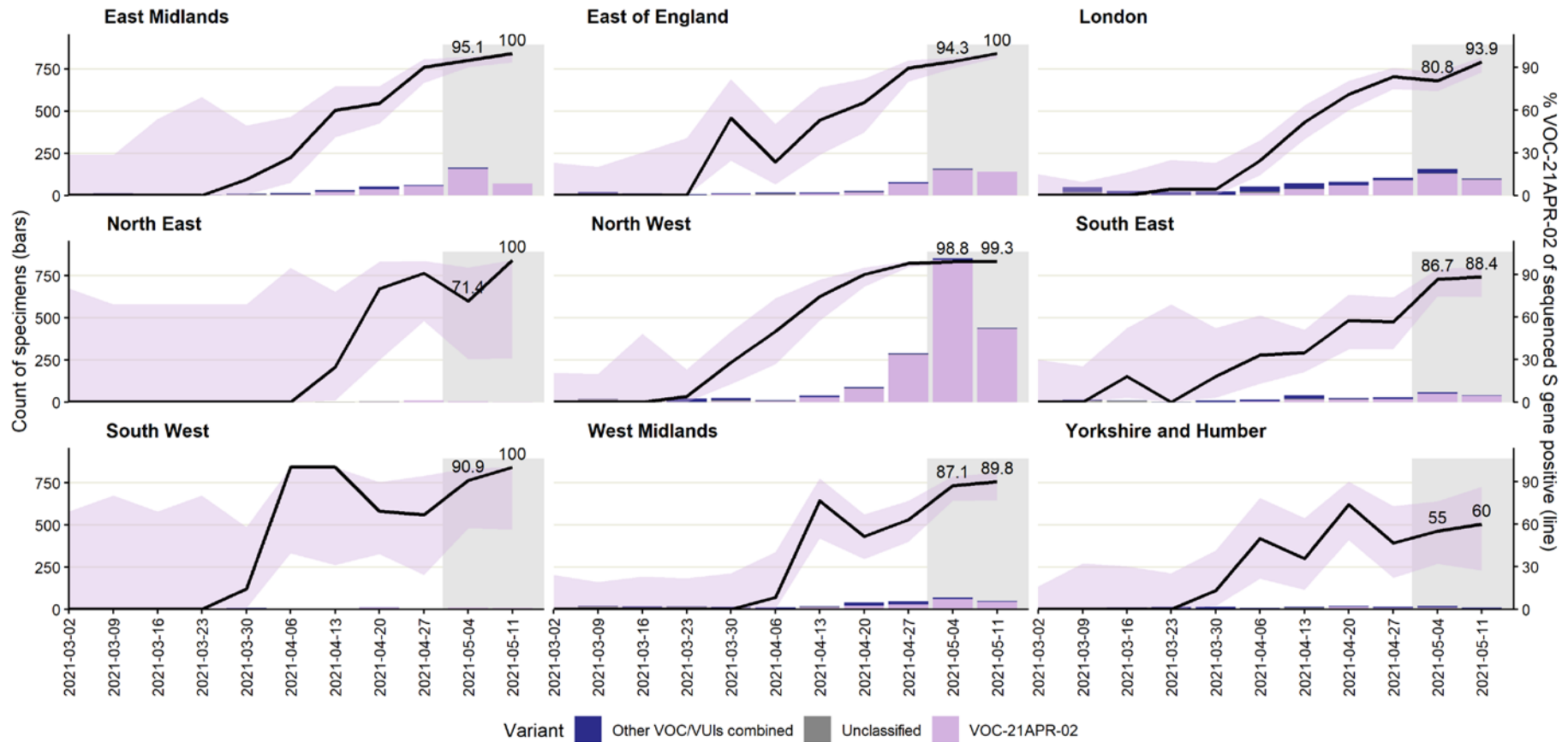
The number and proportion of S gene positive samples in England (Figure 18) has also steadily increased since mid-April, with more than 4,000 in the week starting 18 May; 73.5% of all cases tested on the TaqPath assay and reported to PHE that week. Almost all regions now have majority S gene positive cases in the most recent week (Figure 19), although with highest numbers concentrated in a small number of local authorities (Figures 17 and 20). Several of these areas, in particular Bolton, Blackburn with Darwen, and Bedford, also have high total case rates (Figure 20), although are also located in areas where a higher proportion of specimens are tested in laboratories which use the TaqPath PCR assay (Figure 17).

Figure 15. Weekly distribution of variants among sequenced S gene positive SARS-CoV-2 specimens
Specimen dates between 1 January 2021 and 15 May 2021, data as of 25 May 2021. Gray shading applied to 14 most recent days of data as these are affected by reporting delay. (Find accessible data used in this graph in underlying data).
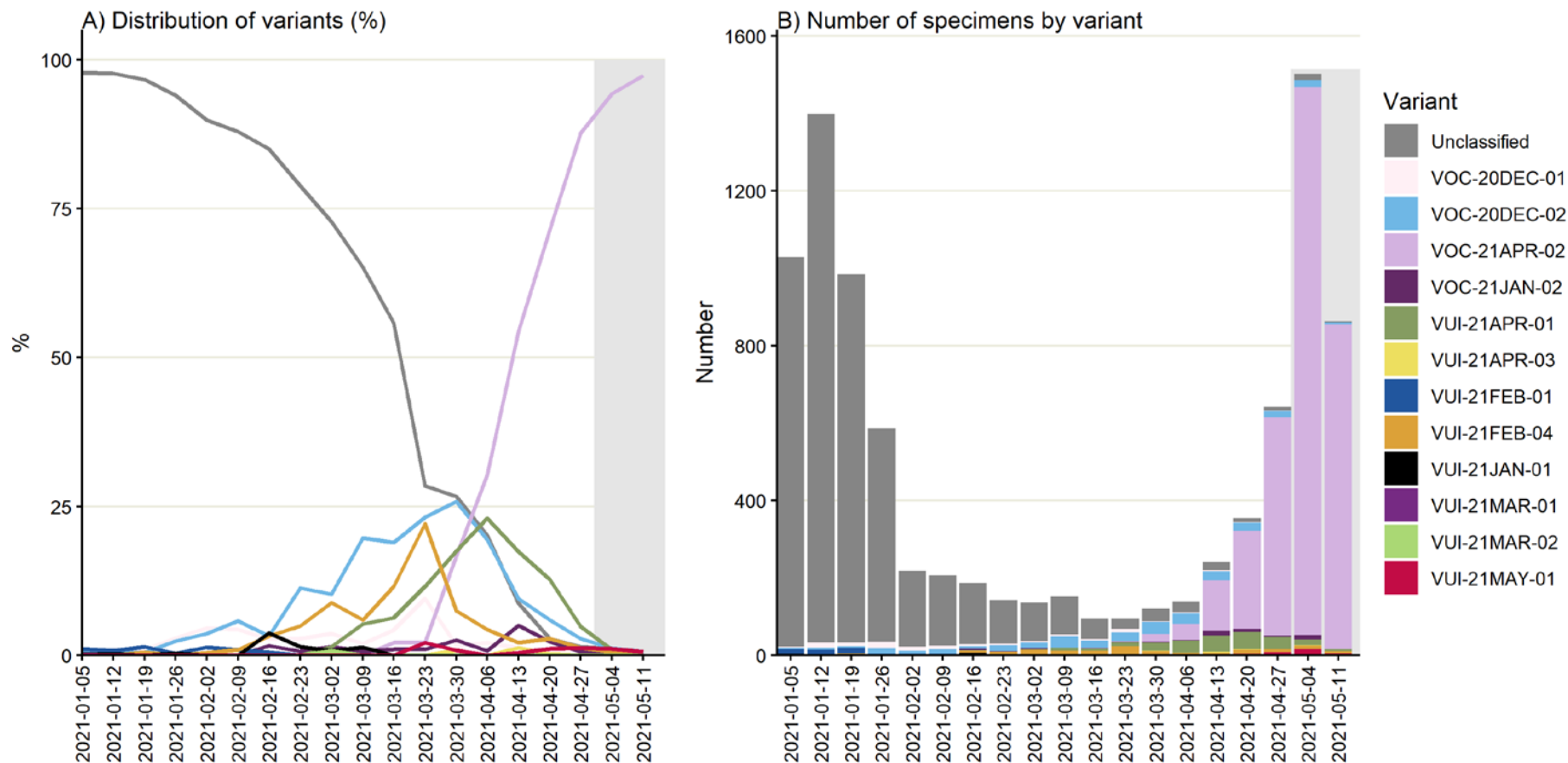
Source: SGSS and COG-UK sequencing data, restricted to sequenced positive S-gene positive tests from Alderley Park, Glasgow, and Milton Keynes Lighthouse Laboratories.
S gene +ve defined as positive SARS-CoV-2 test with CT values <=30 for S, N, and ORF1ab.

Figure 16. Weekly distribution of variants among sequenced S gene positive SARS-CoV-2 specimens, by region of residence

In figure 16 the black line represents weekly proportion of specimens that are VOC-21APR-02 with most recent 2 weeks labelled and 95% confidence intervals in lilac. Proportions for other variants not shown but are grouped for counts (bars). Specimen dates between 1 January 2021 and 15 May 2021, data as of 25 May 2021. Gray shading applied to 14 most recent days of data as these are affected by reporting delay. (Find accessible data used in this graph in underlying data).

Figure 17. Number of cases with detectable S gene target and TaqPath lab test coverage by local authority of residence
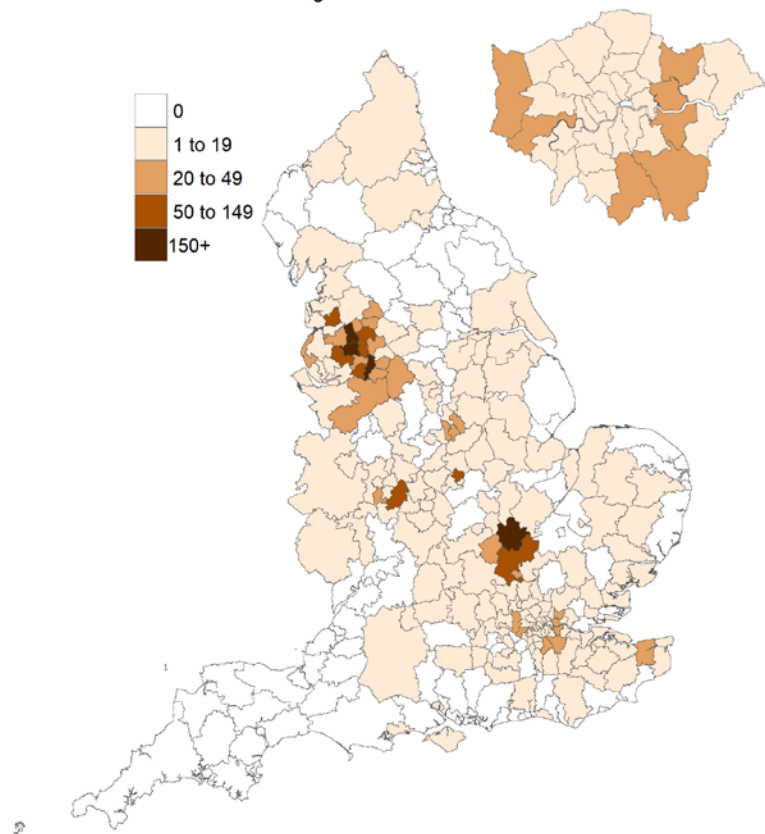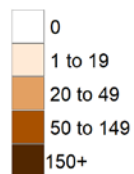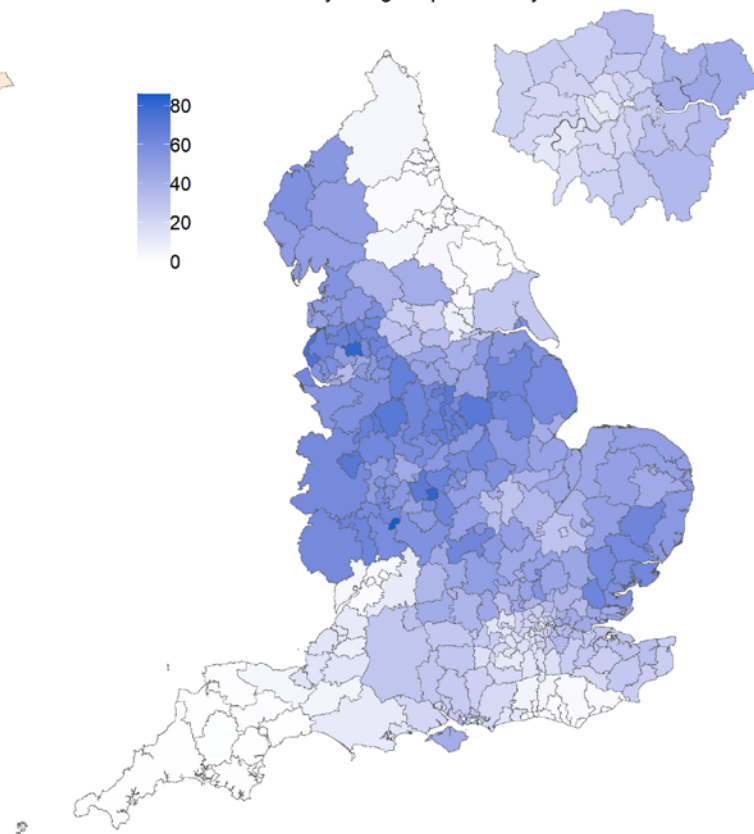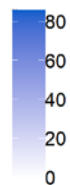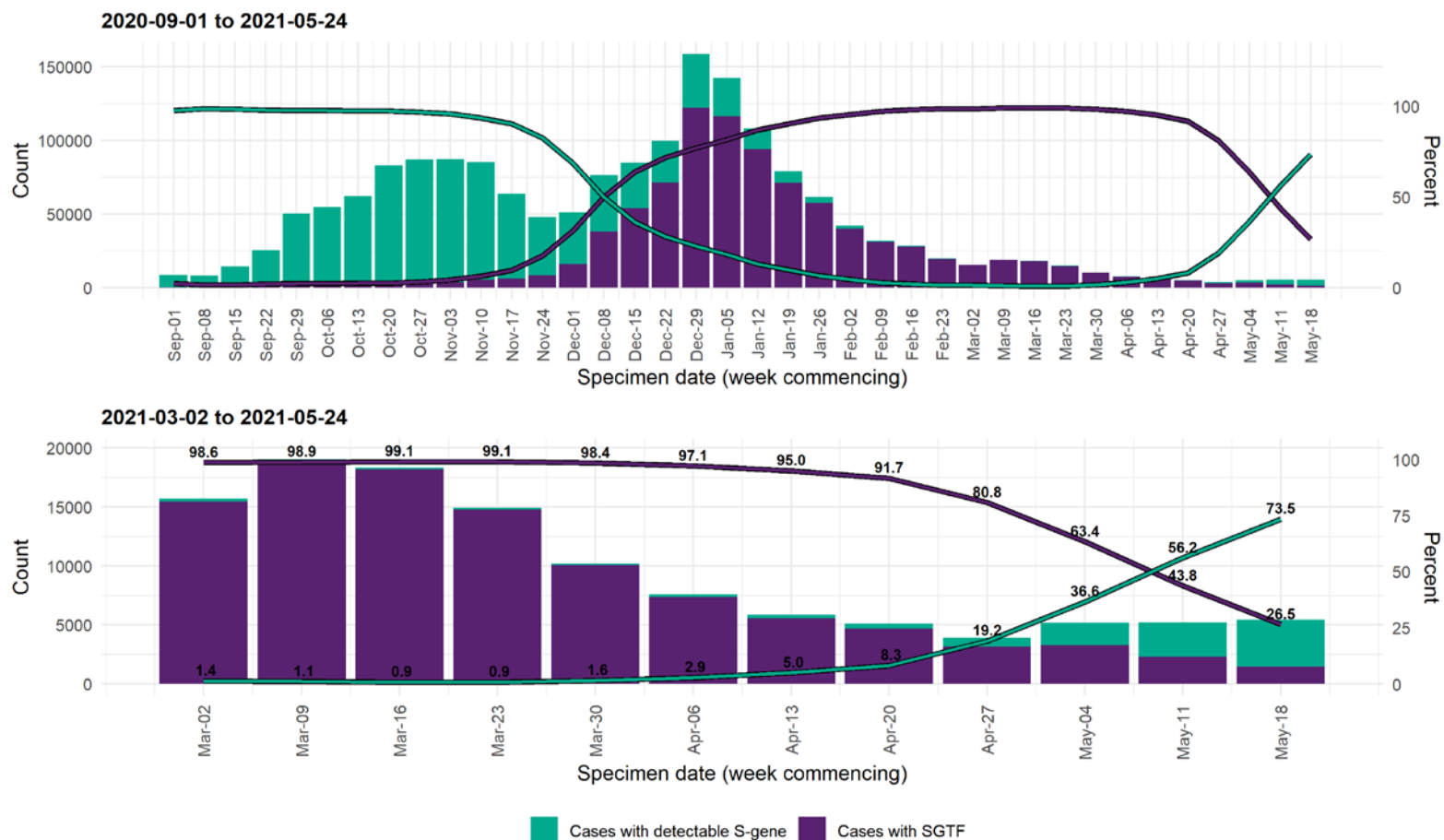

A detectable S gene (<=30 CT values for S, N, and ORF1ab genes) may currently indicate a VOC case; this continues to be monitored.
Only tests carried out with the TaqPath PCR assay and with confirmed SGTF or S gene results included, from Alderley Park, Milton Keynes and Glasgow Lighthouse Labs.
Local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

Specimen dates for figure 17; 15 May 2021 to 21 May 2021, data as of 25 May 2021; most recent 3 days excluded to reporting delay (Find accessible data used in this graph in underlying data).

Figure 18. 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 24 May 2021, data as of 25 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.

Figure 19. 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
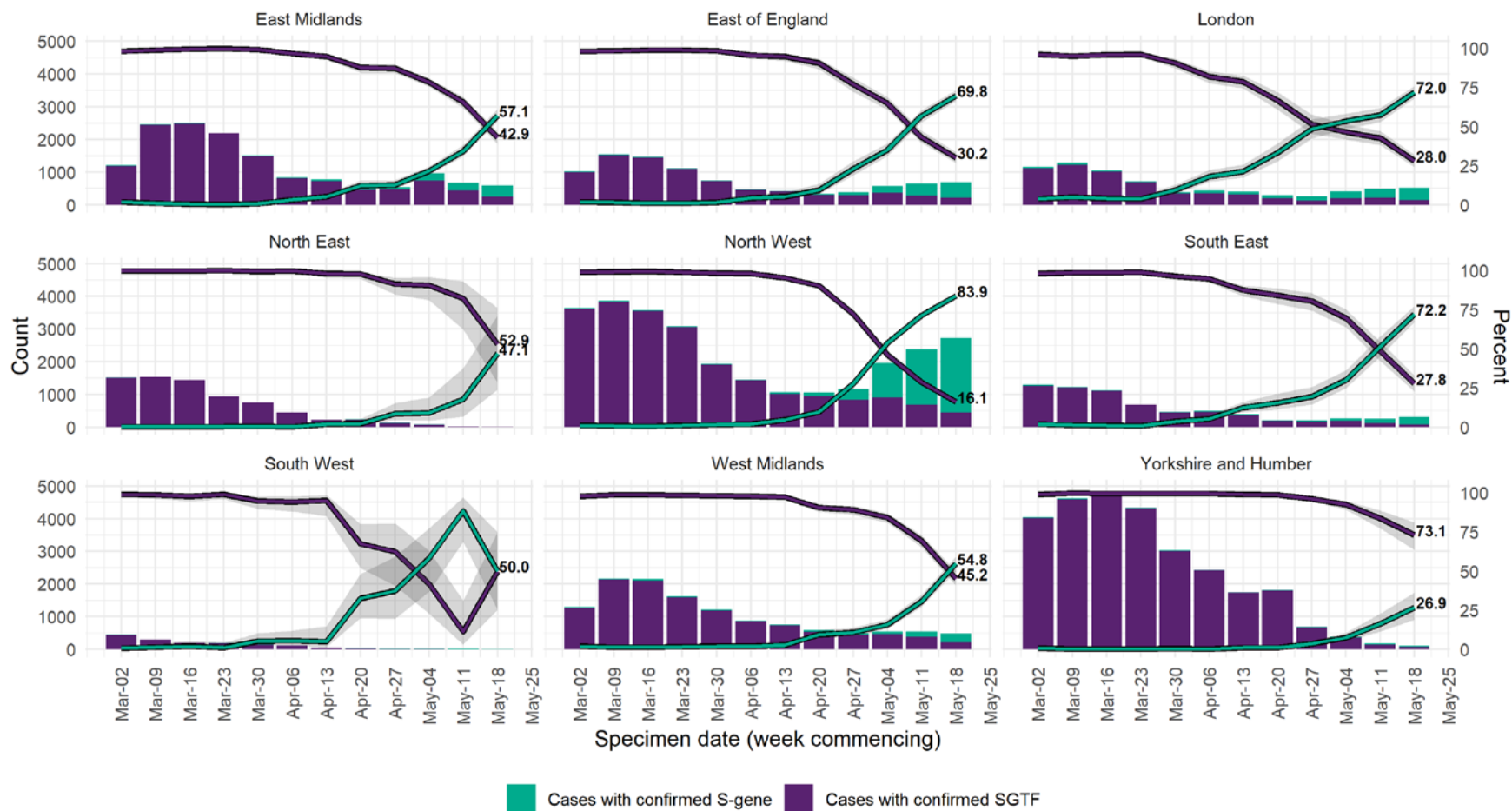
Only tests carried out with the TaqPath PCR assay and with confirmed SGTF or S gene positive results included, from Alderley Park, Milton Keynes and Glasgow Lighthouse Laboratories.
Case with SGTF: Positive SARS-CoV-2 test with non-detectable S gene and <=30 CT values for N and ORF1ab genes.
Case with 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 199 persons, excluded from figure.

In figure 19; specimen dates between 2 March 2021 and 24 May 2021, data as of 25 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).

Figure 20. 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
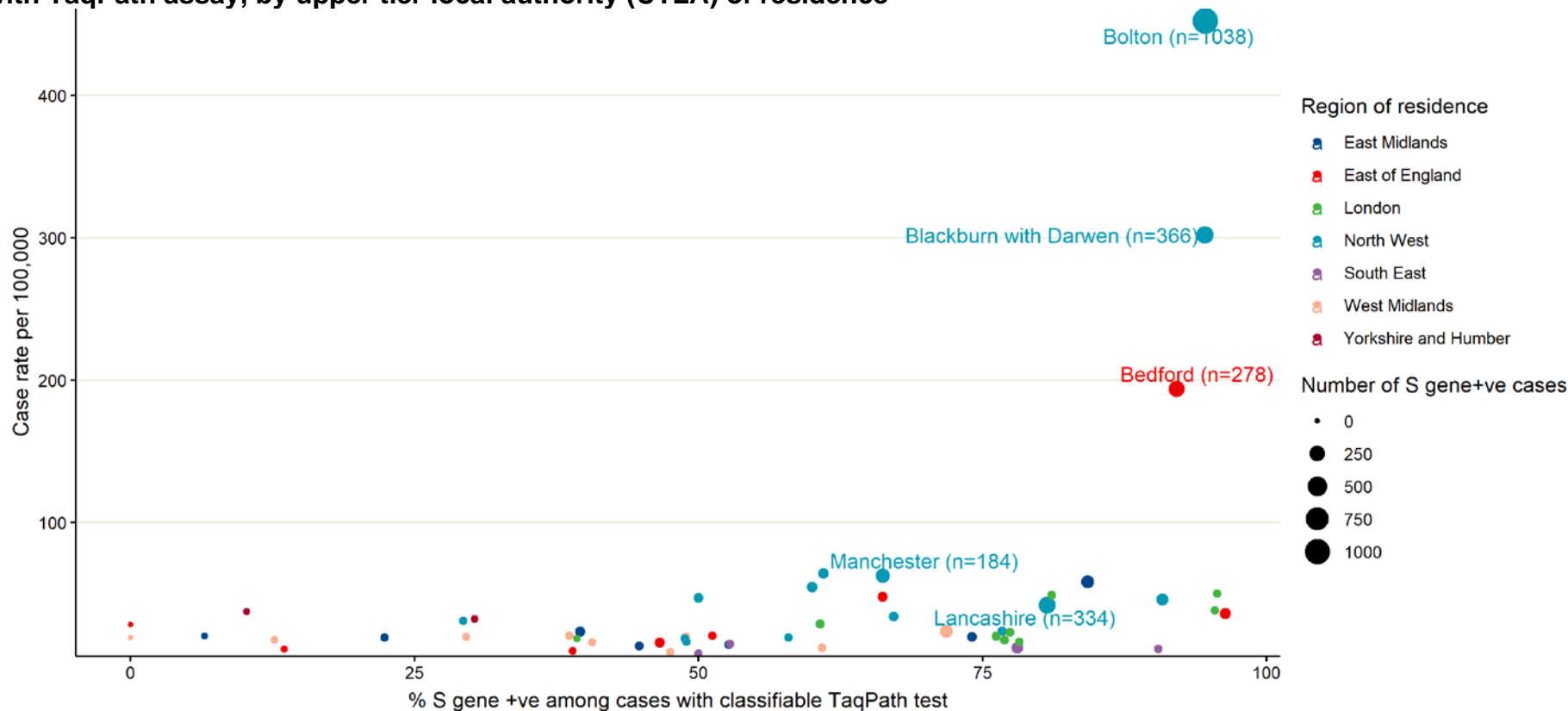
Total case rates include PCR and LFD positive.
Proportion S gene positive calculated out of cases with classifiable S gene detection results and tested with TaqPath PCR assay in Alderley Park, Milton Keynes or Glasgow Lighthouse Laboratory.
Case with detectable S-gene: Positive SARS-CoV-2 test with <=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.

Specimen dates between 15 May 2021 and 21 May 2021, data as of 25 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).

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Growth rate of S gene positive and negative cases

Figures 21 and 22 show growth rate and doubling time of S gene positive and negative (S gene target failure), for region and ethnicity, produced by fitting a generalized additive model with a quasi-Poisson.

The left vertical axis in both figures describe 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

Figure 21. Growth rate and doubling time of S gene positive and negative cases by region as of 20 May 2021
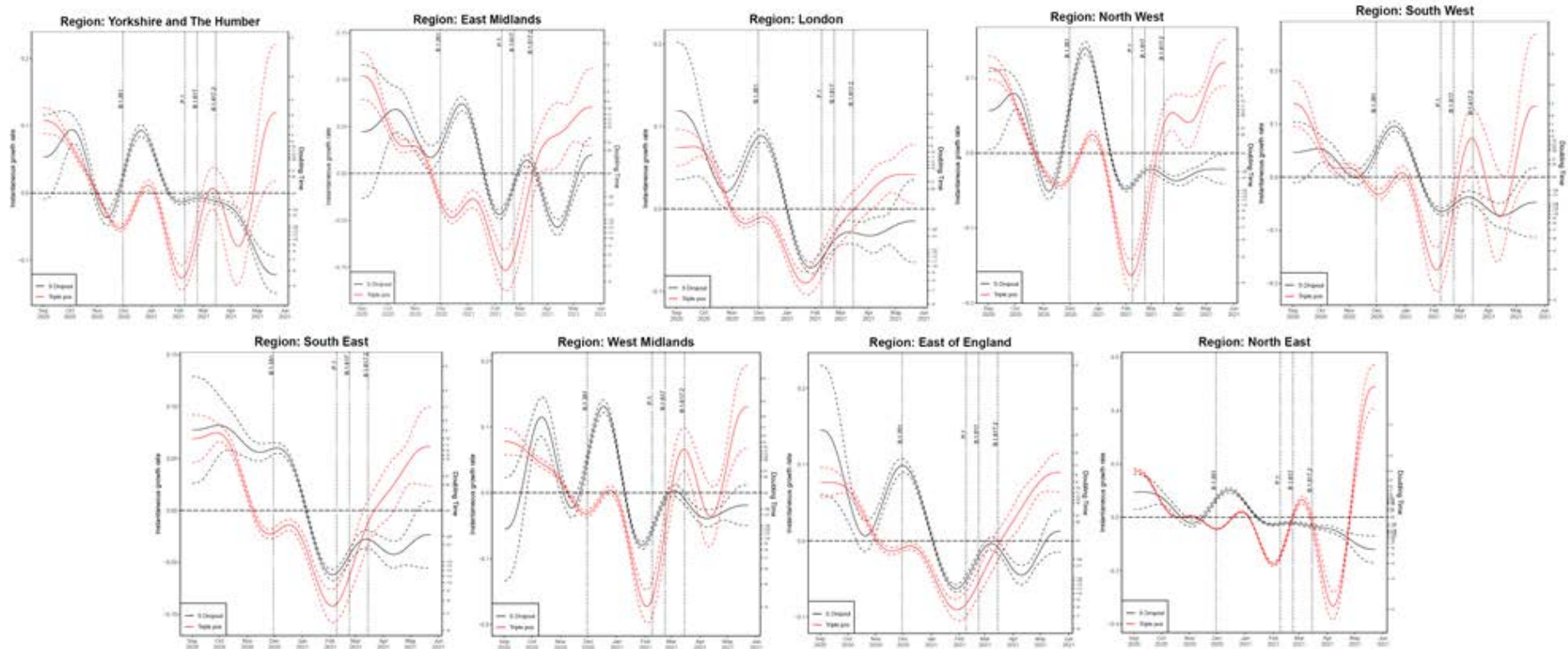
The growth rate for cases with all 3 PCR targets positive has been increasing over the course of April and May in all regions. The East Midlands and the East of England are the only regions seeing growth in cases with the S-dropout. Confidence intervals are wide for most regions, and data on PCR targets is low in some regions (East of England, South West, North East, Yorkshire and Humber). (Find accessible data used in this graph in underlying data).

Figure 22. Growth rate and doubling time of S gene positive and negative cases by ethnicity as of 20 May 2021
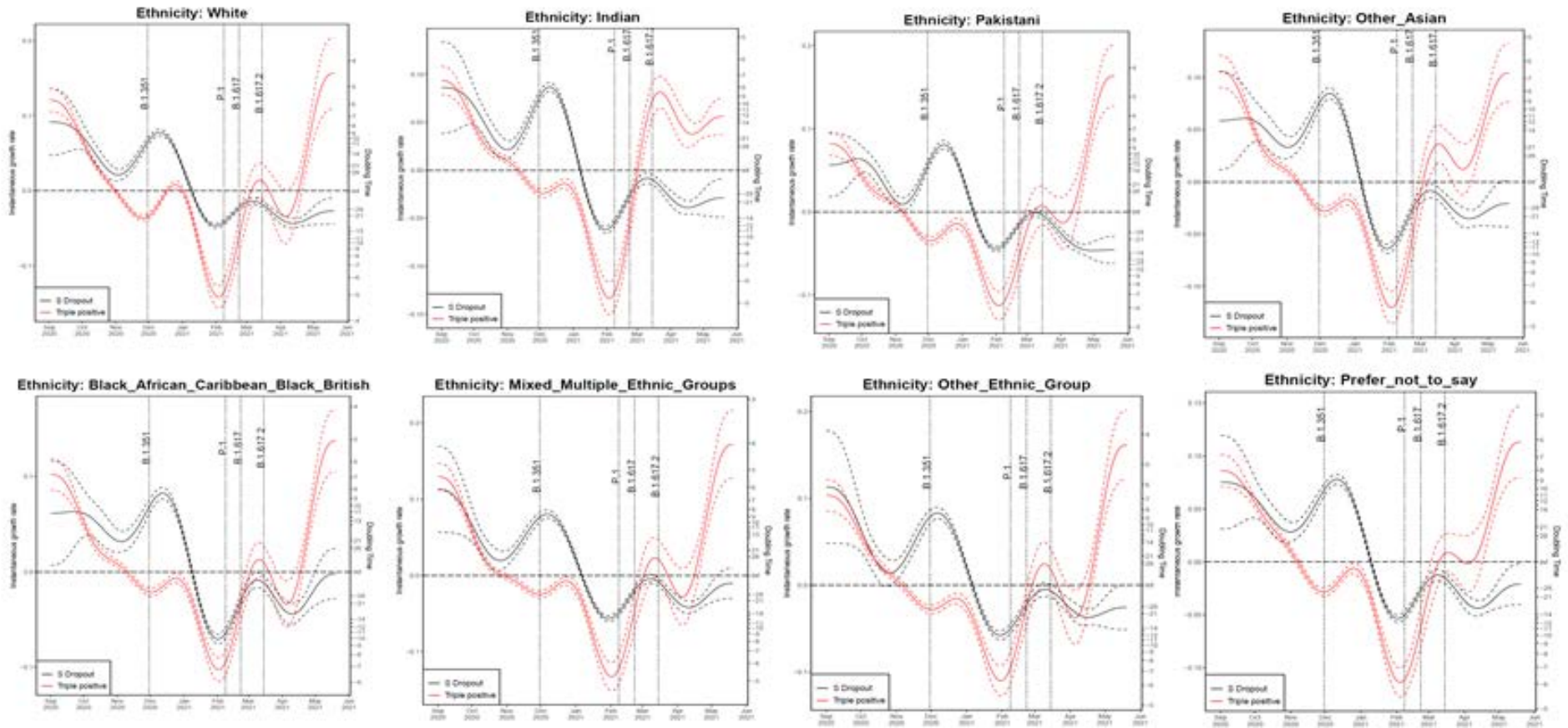
The growth rate for cases with all 3 PCR targets positive has been increasing over the course of April and May in all ethnicities. The growth rates for the Indian ethnicity appear to have levelled, whilst growth rate in other ethnicities continues to rise. (Find accessible data used in this graph in underlying data). Confidence intervals are wide, and data on PCR targets is low in some regions.

Live virus and pseudovirus neutralization

Neutralisation studies of VOC-21APR-02 (B.1.617.2) have been conducted by the Genotype to Phenotype Consortium laboratories (Imperial College London, Centre for Virus Research Glasgow, Pirbright Virology Institute, the Francis Crick Institute), PHE Colindale and Oxford University. There are reductions in neutralising activity seen across multiple sera and laboratories including:

- first wave convalescent sera tested against live virus
- vaccinee sera tested against pseudovirus with B.1.617.2. spike
- a panel of 220 vaccinee sera from the Legacy study (University College London Hospitals/Francis Crick Institute) tested against live virus

These changes are greater than the reduction seen for VOC-20DEC-01 (B.1.1.7). Whilst outputs from individual assays vary, the consensus view is that the magnitude of the change is likely to lie between that seen for B.1.1.7 and B.1.351. Further assessment is in process.

Monitoring of vaccine effectiveness

The vaccine effectiveness analyses undertaken previously were iterated including data up to the end of week 21. This provides estimates of vaccine effectiveness against symptomatic disease, methods are described in Effectiveness of COVID-19 vaccines against the B.1.617.2 variant. The analysis now includes 7673 symptomatic cases identified as B.1.1.7 and 2934 cases identified as B.1.617.2. Results remain similar to those seen last week, though with increased precision. After a single dose there was a 17% absolute reduction in vaccine effectiveness against symptomatic disease with B.1.617.2 compared to B.1.1.7, but only a modest reduction in vaccine effectiveness after 2 doses (Table 12).

Table 12.

Vaccination status	Vaccine Effectiveness	
	VOC-20DEC-01 (B.1.1.7)	**VOC21-APR-02 (B.1.617.2)**
Dose 1	50.2 (46.7 to 53.5)	33.2 (25.8 to 39.9)
Dose 2	88.4 (85.7 to 90.7)	80.8 (76.3 to 84.4)

Serial interval and viral load dynamics

The Assessment of Transmission and Contagiousness of COVID-19 in Contacts (ATACCC) study (NIHR Health Protection Research Unit in Respiratory Infections, PHE and Imperial College London) has been reopened to recruitment as of 24 May 2021 to assist with characterisation of B.1.617.2.

The study analyses secondary attack rates, serial intervals and viral load dynamics, by performing intensive, longitudinal PCR sampling of contacts of newly diagnosed COVID-19 cases in the community, accompanied by collection of symptom diaries and demographic data.
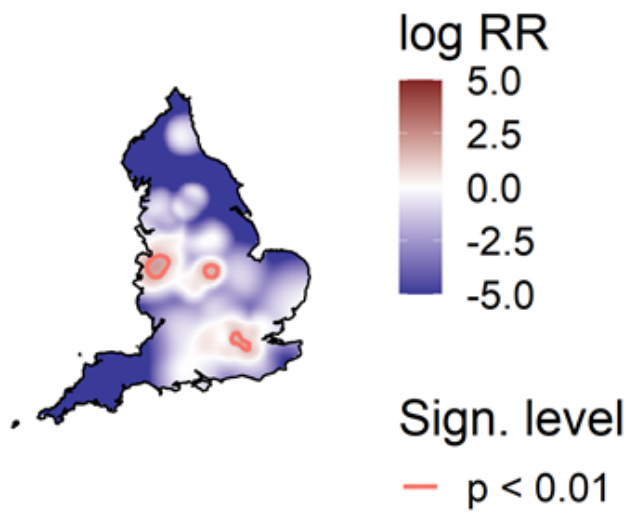
VUI-21APR-01 (B.1.617.1)

Table 13. Number of confirmed and probable VUI-21APR-01 (B.1.617.1) cases, by region of residence as of 25 May 2021

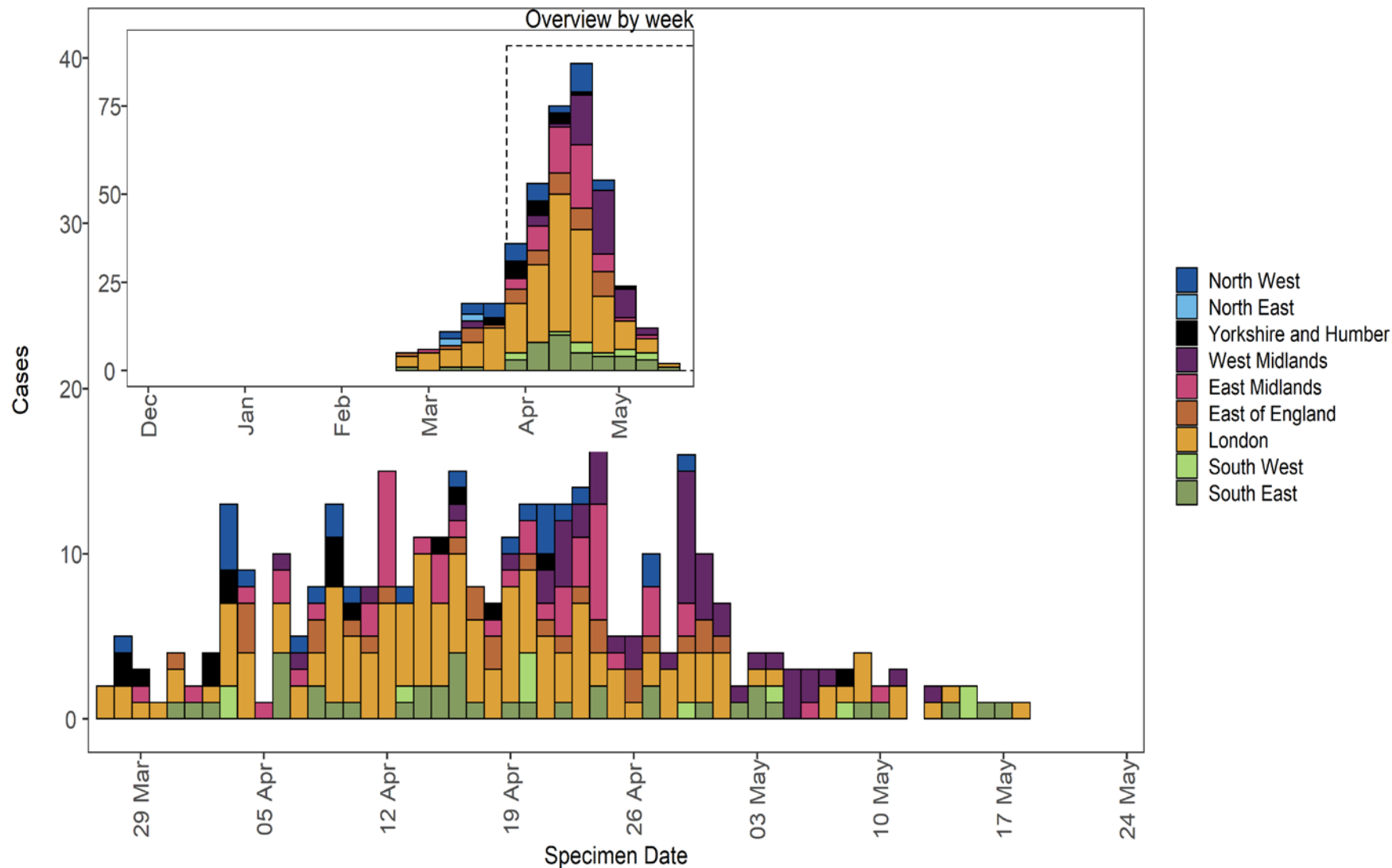| Region	Case Number	Case Proportion	Cases that have travelled	Proportion of travellers among cases*
East Midlands	49	12.1%	25	51.0%
East of England	34	8.4%	20	58.8%
London	170	41.9%	96	56.5%
North East	4	1.0%	2	50.0%
North West	32	7.9%	21	65.6%
South East	42	10.3%	25	59.5%
South West	11	2.7%	8	72.7%
West Midlands	48	11.8%	19	39.6%
Yorkshire and Humber	16	3.9%	12	75.0%
England	**406**	-	**228**	**56.2%**

*Denominator is all cases, including those with unknown or pending travel status. 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.

Figure 23. Spatial variation in risk for VUI-21APR-01 (B.1.617.1) data from 1 October 2020, as of 25 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-01 (B.1.617.1) cases by specimen date as of 25 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-01 (B.1.617.1) cases by specimen date as of 25 May 2021
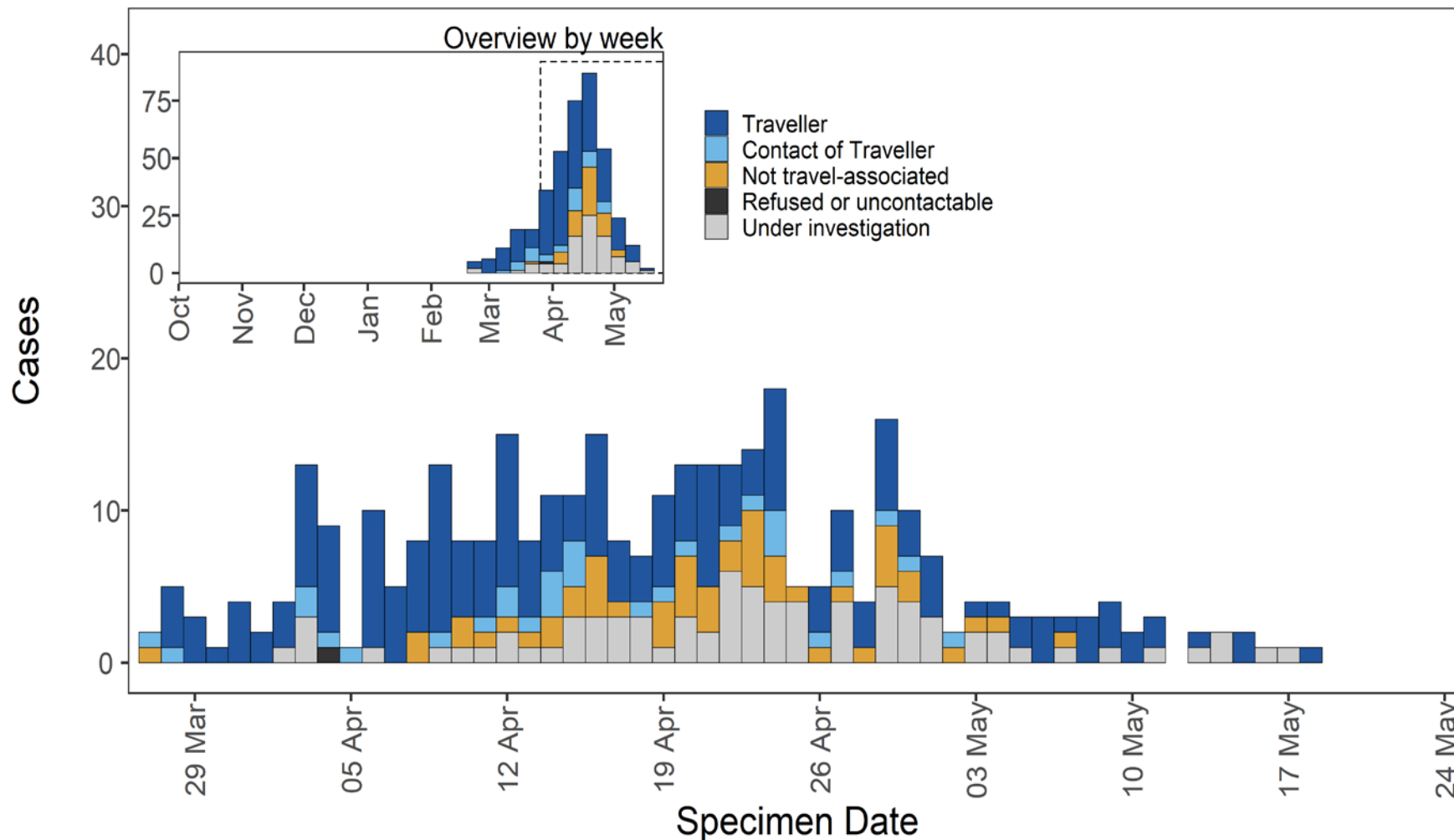
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data). N/A indicates information is pending or not available.
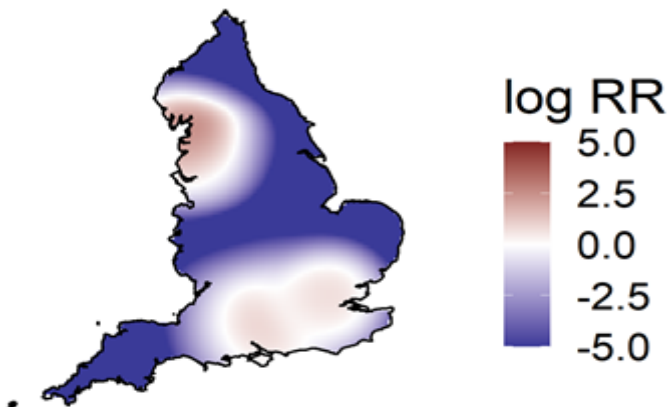
VUI-21APR-03 (B.1.617.3)

Table 14. Number of confirmed and probable VUI-21APR-03 (B.1.617.3) cases, by region of residence as of 25 May 2021

| Region	Case Number	Case Proportion	Cases that have travelled	Proportion of travellers among cases
East Midlands	0	0.0%	0	NA
East of England	0	0.0%	0	NA
London	5	35.7%	3	60.0%
North East	0	0.0%	0	NA
North West	7	50.0%	3	42.9%
South East	2	14.3%	1	50.0%
South West	0	0.0%	0	NA
West Midlands	0	0.0%	0	NA
Yorkshire and Humber	0	0.0%	0	NA
England	**14**	-	**7**	**50.0%**

*Denominator is all cases, including those with unknown or pending travel status

Figure 26. Spatial variation in risk for VUI-21APR-03 (B.1.617.3) data from 1 October 2020, as of 25 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 27. Confirmed and probable VUI-21APR-03 (B.1.617.3) cases by specimen date as of 25 May 2021
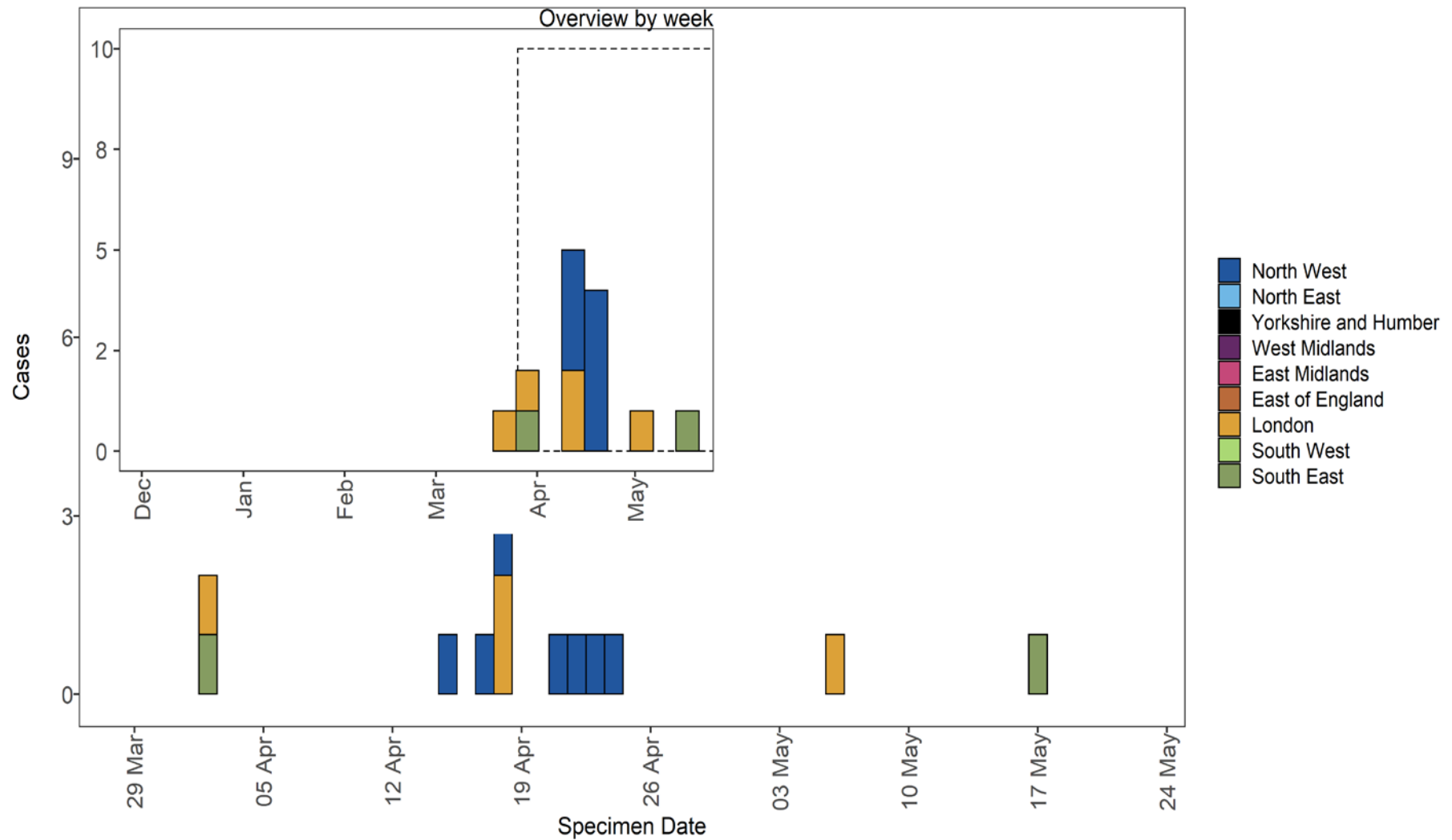
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data).

Figure 28. Travel data for confirmed and probable VUI-21APR-03 (B.1.617.3) cases by specimen date as of 25 May 2021
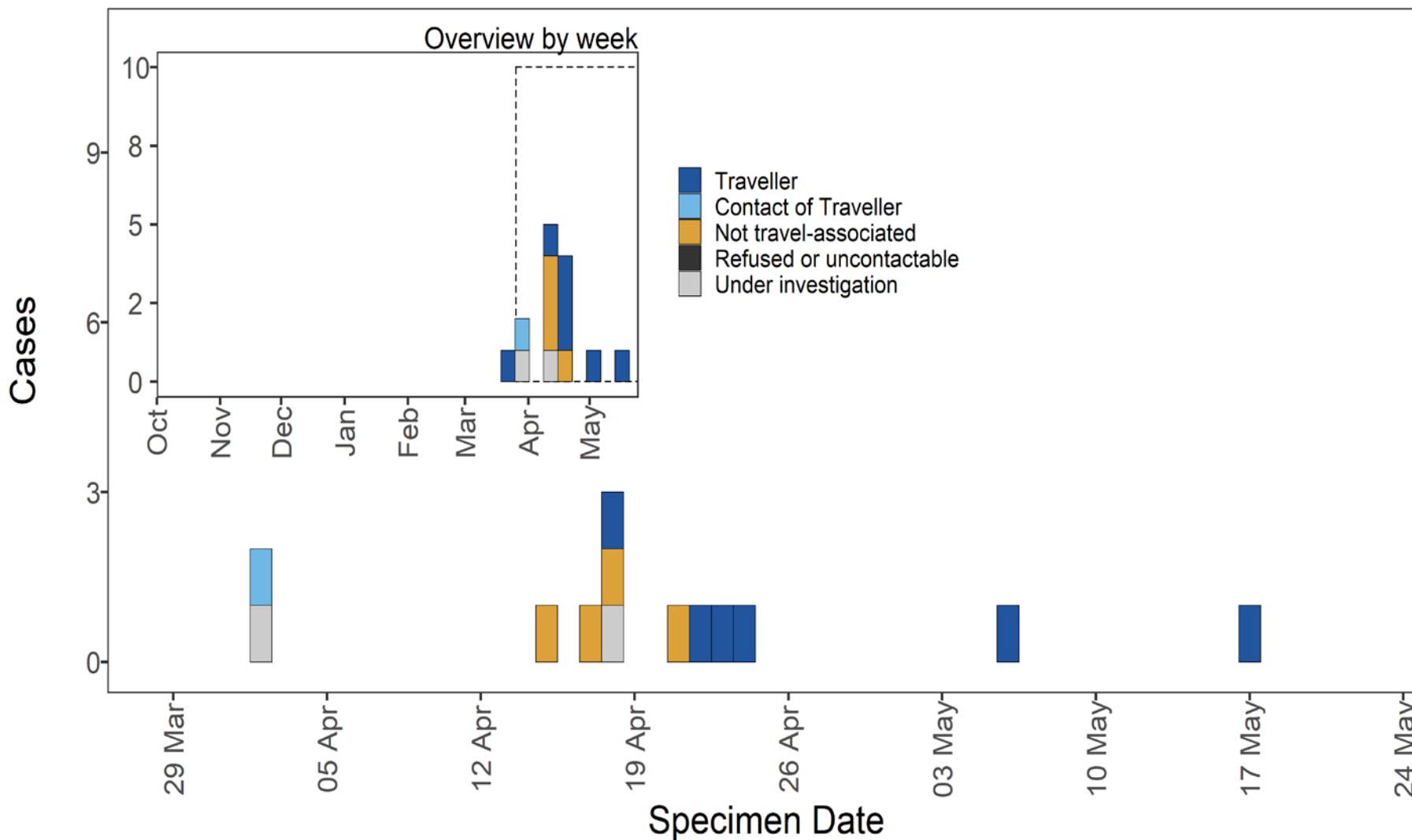
Larger plot includes last 60 days only (Find accessible data used in this graph in underlying data). N/A indicates information is pending or not available.

International surveillance

GISAID includes data on sequences available internationally. As of 26 May 2021, sequences from the following countries (excluding UK) have been identified in GISAID:

VUI-21APR-01 (B.1.617.1) In total 2,099 sequences from: Australia, 29, Austria, 1, Bahrain, 8, Belgium, 8, Canada, 38, Curacao, 1, Czech Republic, 3, Denmark, 27, Finland, 1, France, 7, Germany, 84, Greece, 1, Guadeloupe, 2, Hong Kong, 9, India, 1472, Ireland, 39, Italy, 5, Japan, 19, Jordan, 4, Luxembourg, 5, Malaysia, 1, Mexico, 3, Nepal, 2, Netherlands, 9, New Zealand, 4, Portugal, 9, Saint Martin, 2, Singapore, 58, South Korea, 5, Spain, 4, Sweden, 5, Switzerland, 9, Thailand, 1, USA, 223, Uganda, 1

VOC-21APR-02 (B.1.617.2) In total 3,744 sequences from: Argentina, 1, Aruba, 3, Australia, 106, Austria, 3, Bahrain, 14, Bangladesh, 11, Belgium, 79, Canada, 125, China, 2, Democratic Republic of the Congo, 6, Denmark, 62, France, 50, Germany, 264, Greece, 1, Hong Kong, 3, India, 1309, Indonesia, 27, Iran, 4, Ireland, 89, Israel, 37, Italy, 51, Japan, 138, Jordan, 1, Luxembourg, 2, Malaysia, 4, Mexico, 20, Morocco, 1, Nepal, 12, Netherlands, 31, New Zealand, 11, Norway, 5, Poland, 24, Portugal, 29, Reunion, 1, Romania, 4, Russia, 1, Singapore, 100, Slovenia, 1, South Africa, 16, South Korea, 1, Spain, 43, Sweden, 11, Switzerland, 33, Thailand, 1, Turkey, 1, USA, 1003, Uganda, 3

VUI-21APR-03 (B.1.617.3) In total 64 sequences from: India, 61, Russia, 2, USA, 1

Part 3: New variant under investigation VUI-21MAY-02 (C.36.3)

C.36.3 was designated a Variant Under Investigation on 24 May 2021 (VUI-21MAY-02) on the basis of the mutation profile and increased importation from a widening international area.

Genomic profile

The complete mutation profile of VUI-21MAY-02 (C.36.3) is shown in Table 15.

Table 15. C.36.3 Mutation profile

Gene	Mutations
orf1ab	E102K, A859V, T1246I, D1639N, P2287S, D2980N, D3222N, G3278S, S3687L, L3691S, T4090I, P4715L, D5429Y
S	S12F, del69-70, W152R, R346S, L452R, D614G, Q677H, A899S
M	I82T
N	R203K, G204R, G212V

Biological profile

VUI-21MAY-02 (C.36.3) contains several spike receptor binding domain (RBD) mutations linked to antigenic change including both L452R and R346S. Furthermore, it contains N-terminal domain (NTD) mutations potentially associated with antigenic change such as S12F and W152R. VUI-21MAY-02 also contains deletion 69-70 and Q677H, mutations also observed in other VOC/VUIs. Deletion 69-70 is associated with S gene target failure in the Taqpath assay which is used in surveillance analyses.

Surveillance in England

As of 25 May 2021, 109 genomically confirmed cases of VUI-21MAY-02 (C.36.3) have been identified in England. The regional distribution is shown in table 16.

Table 16: Cases of VUI-21MAY-02 (C.36.3) by region

Region	Number of cases of C.36.3
East Midlands	6
East of England	18
London	33
North East	1
North West	11
South East	8
South West	3
West Midlands	9
Yorkshire and Humber	20

International surveillance

GISAID includes data on sequences available internationally. As of 26 May 2021, sequences of VUI-21MAY-02 (C.36.3) from 34 countries has been identified on GISAID (Table 17)

Table 17. Country and number of sequences uploaded to GISAID as of 26th May 2021 for VUI-21MAY-02 (C.36.3)

Country	Number of Sequences
Germany	148
USA	144
Switzerland	62
Egypt	33
Belgium	26
France	18
Denmark	16
Italy	14
Sweden	11
Ireland	10
Norway	6
Austria	6
Canada	4
Indonesia	4
Spain	4
Israel	4
New Zealand	3
Latvia	2
Turkey	2
Lithuania	2
Slovenia	2
Belarus	1
Colombia	1
Greece	1
Poland	1
Lebanon	1
Singapore	1
India	1
Portugal	1
Philippines	1
Thailand	1
Chile	1
Australia	1
Netherlands	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 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, Genotype to Phenotype Consortium, SPI-M.

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Public Health England
Wellington House
133-155 Waterloo Road
London SE1 8UG
Tel: 020 7654 8000

Website: www.gov.uk/phe
Twitter: @PHE_uk
Facebook: www.facebook.com/PublicHealthEngland

Contact: All enquiries should be addressed to phe.enquiries@phe.gov.uk

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