Public Health England

Protecting and improving the nation's health

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

Technical briefing 14

3 June 2021

This briefing provides an update on previous briefings up to 27 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 Delta (VOC-21APR-02, B.1.617.2). A separate report is published covering our routine data on all other variants of concern and variants under investigation. These additional specialist technical briefings represent early data and analysis on an emerging variant and findings have a high level of uncertainty.

Principal changes and findings this week are:

- new WHO nomenclature is incorporated – a table incorporating WHO and UK designations and Pango lineages is provided; thereafter variants are referred to using their WHO designation where this exists, and the UK designation where it does not
- in the week commencing 17 May 2021, the most recent week where sequencing data are complete, 61% of sequenced cases are Delta
- growth rates using genomic and S gene target data continue to show a substantially increased growth rate for Delta compared to Alpha
- secondary attack rates have been iterated and remain higher for Delta than Alpha in both traveller and non-traveller cases and amongst both household and non-household contacts
- early data from both England and Scotland suggest an increased risk of hospitalisation with Delta compared to Alpha; confirmatory analyses are required
- new data on outbreaks managed by health protection teams and exposure settings identified through contact tracing are included
- the vaccine effectiveness analysis is being further updated and reviewed at present and no new estimates are provided this week

The risk assessment for Delta is published separately and has been updated this week.

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 3 and 4 show hospitalisation and death data. Figure 2 shows cumulative cases of variants over time, indexed by the day of the fifth case.

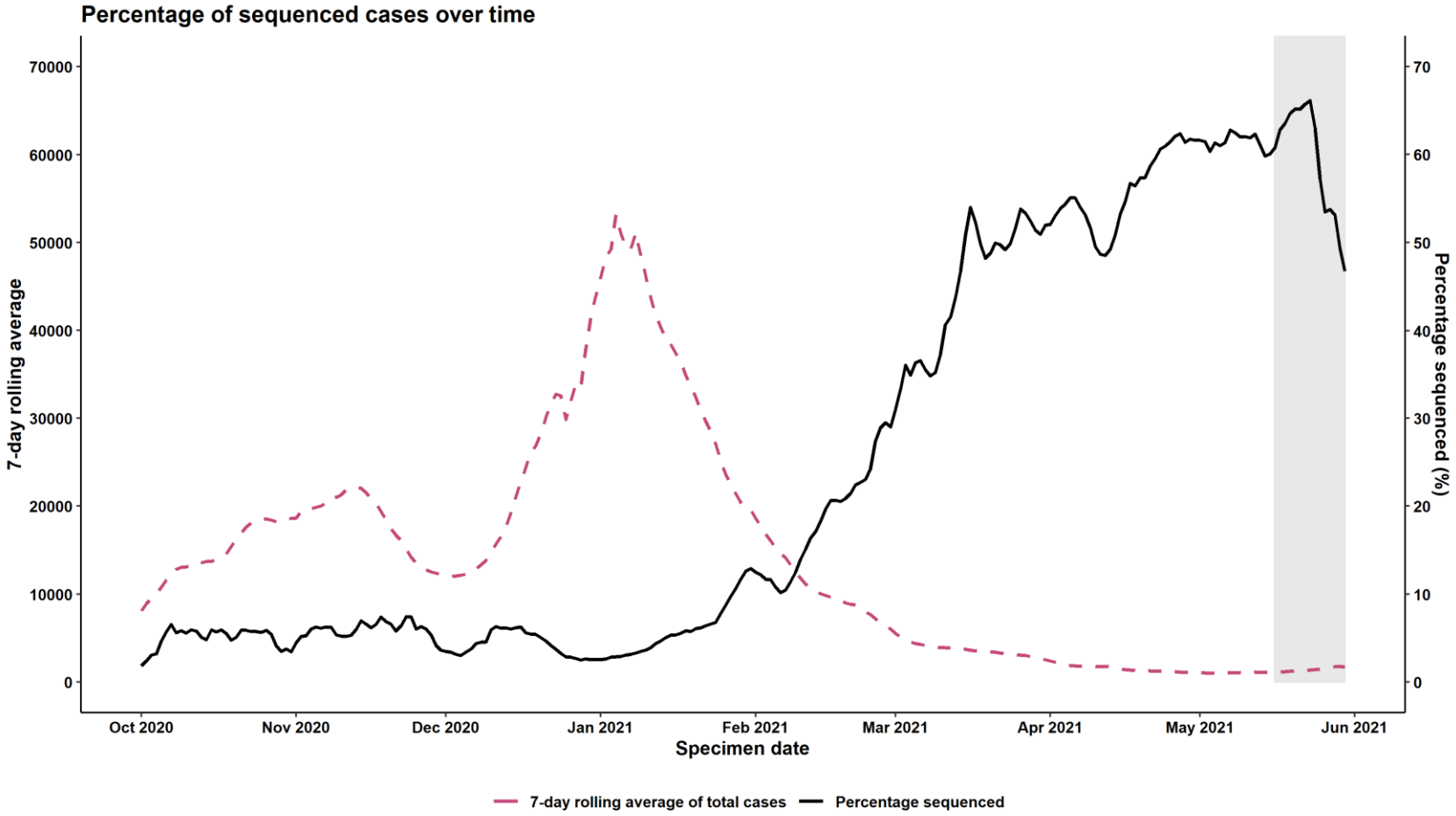
Table 1. Variant lineage and designation as of 2 June 2021 (provisionally extinct variants removed)

WHO nomenclature as of 31 May 2021	Pangolin Lineage	Designation	First detected in sequence from	Status
Alpha	B.1.1.7	VOC-20DEC-01	UK	VOC
Beta	B.1.351	VOC-20DEC-02	South Africa	VOC
Gamma	P.1	VOC-21JAN-02	Japan ex Brazil	VOC
	B1.1.7 with E484K	VOC-21FEB-02	UK	VOC
Delta	B.1.617.2	VOC-21APR-02	India	VOC
Zeta	P.2	VUI-21JAN-01	Brazil	VUI
	A.23.1 with E484K	VUI-21FEB-01	UK	VUI
Eta	B.1.525	VUI-21FEB-03	UK	VUI
	B.1.1.318	VUI-21FEB-04	UK	VUI
Theta	P.3	VUI-21MAR-02	Philippines	VUI
Kappa	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
Epsilon	B.1.427/B.1.429			Monitoring
	B.1.1.7 with S494P			Monitoring
	A.27			Monitoring
Iota	B.1.526			Monitoring
	B.1.1.7 with Q677H			Monitoring

WHO nomenclature as of 31 May 2021	Pangolin Lineage	Designation	First detected in sequence from	Status
	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 31 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 and 4 show the number of cases known to be infected with variants of concern/variants under investigation 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 31 May 2021

Variant	Case number	Case proportion	Deaths	Case fatality rate
Alpha (VOC-20DEC-01)	213,432	94.7%	4,171	2.0% (1.9 - 2.0%)
Beta (VOC-20DEC-02)	846	0.4%	13	1.5% (0.8 - 2.6%)
Gamma (VOC-21JAN-02)	151	0.07%	0	0.0% (0.0 - 2.4%)
VOC-21FEB-02	43	0.02%	1	2.3% (0.1 - 12.3%)
Delta (VOC-21APR-02)*	9,426	4.2%	17	0.2% (0.1 - 0.3%)
Zeta (VUI-21JAN-01)	54	0.02%	1	1.9% (0.0 - 9.9%)
VUI-21FEB-01	79	0.04%	2	2.5% (0.3 - 8.8%)
Eta (VUI-21FEB-03)	436	0.2%	12	2.8% (1.4 - 4.8%)
VUI-21FEB-04	243	0.1%	1	0.4% (0.0 - 2.3%)
VUI-21MAR-01	2	0.001%	0	0.0% (0.0 - 84.2%)
Theta (VUI-21MAR-02)	6	0.003%	0	0.0% (0.0 - 45.9%)
Kappa (VUI-21APR-01)	413	0.2%	0	0.0% (0.0 - 0.9%)
VUI-21APR-03	14	0.006%	0	0.0% (0.0 - 23.2%)
VUI-21MAY-01	122	0.05%	1	0.8% (0.0 - 4.5%)
VUI-21MAY-02	117	0.05%	0	0.0% (0.0 - 3.1%)

*Delta (VOC-21APR-02) includes a high proportion of recent cases who have not completed 28 days of follow up and therefore CFR is likely to be an underestimate.

Table 3. Attendance to emergency care and deaths among all COVID-19 sequenced cases in England, 1 February 2021 to 31 May 2021

Variant	Cases since 1 Feb 2021¥	Cases with specimen date in past 28 days*		Cases with an A&E visit§ (excluding cases with the same specimen and attendance dates)‡		Cases with an A&E visit§ (including cases with the same specimen and attendance dates)		Cases where presentation to A&E resulted in overnight inpatient admission§ (excluding cases with the same specimen and admission dates)‡		Cases where presentation to A&E resulted in overnight inpatient admission§ (including cases with the same specimen and admission dates)		Deaths^	
		N	%	N	%	N	%	N	%	N	%	N	%
Alpha	138,774	8,822	6.4	5,466	3.9	7,699	5.6	2,081	1.5	3,498	2.5	1,720	1.2
Beta	644	58	9.0	26	4.0	34	5.3	9	1.4	17	2.6	8	1.2
Gamma	151	27	17.9	7	4.6	7	4.6	1	0.7	1	0.7	0	NA
VOC-21FEB-02	17	0	NA	0	NA	0	NA	0	NA	0	NA	0	NA
Delta	9,427	7,744	82.1	364	3.9	479	5.1	89	0.9	137	1.5	17	0.2
Zeta	24	0	NA	1	4.2	1	4.2	1	4.2	1	4.2	0	NA
VUI-21FEB-01	8	0	NA	0	NA	1	12.5	0	NA	0	NA	0	NA
Eta	382	29	7.6	10	2.6	14	3.7	3	0.8	6	1.6	7	1.8

Variant	Cases since 1 Feb 2021¥	Cases with specimen date in past 28 days*		Cases with an A&E visit§ (excluding cases with the same specimen and attendance dates)‡		Cases with an A&E visit§ (including cases with the same specimen and attendance dates)		Cases where presentation to A&E resulted in overnight inpatient admission§ (excluding cases with the same specimen and admission dates)‡		Cases where presentation to A&E resulted in overnight inpatient admission§ (including cases with the same specimen and admission dates)		Deaths^	
		N	%	N	%	N	%	N	%	N	%	N	%
VUI-21FEB-04	236	44	18.6	3	1.3	6	2.5	0	NA	2	0.9	1	0.4
Theta	6	0	NA	0	NA	0	NA	0	NA	0	NA	0	NA
Kappa	413	41	9.9	7	1.7	8	1.9	1	0.2	2	0.5	0	NA
VUI-21APR-03	14	2	14.3	0	NA	0	NA	0	NA	0	NA	0	NA
VUI-21MAY-01	122	96	78.7	1	0.8	1	0.8	0	NA	0	NA	1	0.8
VUI-21MAY-02	117	21	17.9	3	2.6	4	3.4	0	NA	1	0.9	0	NA

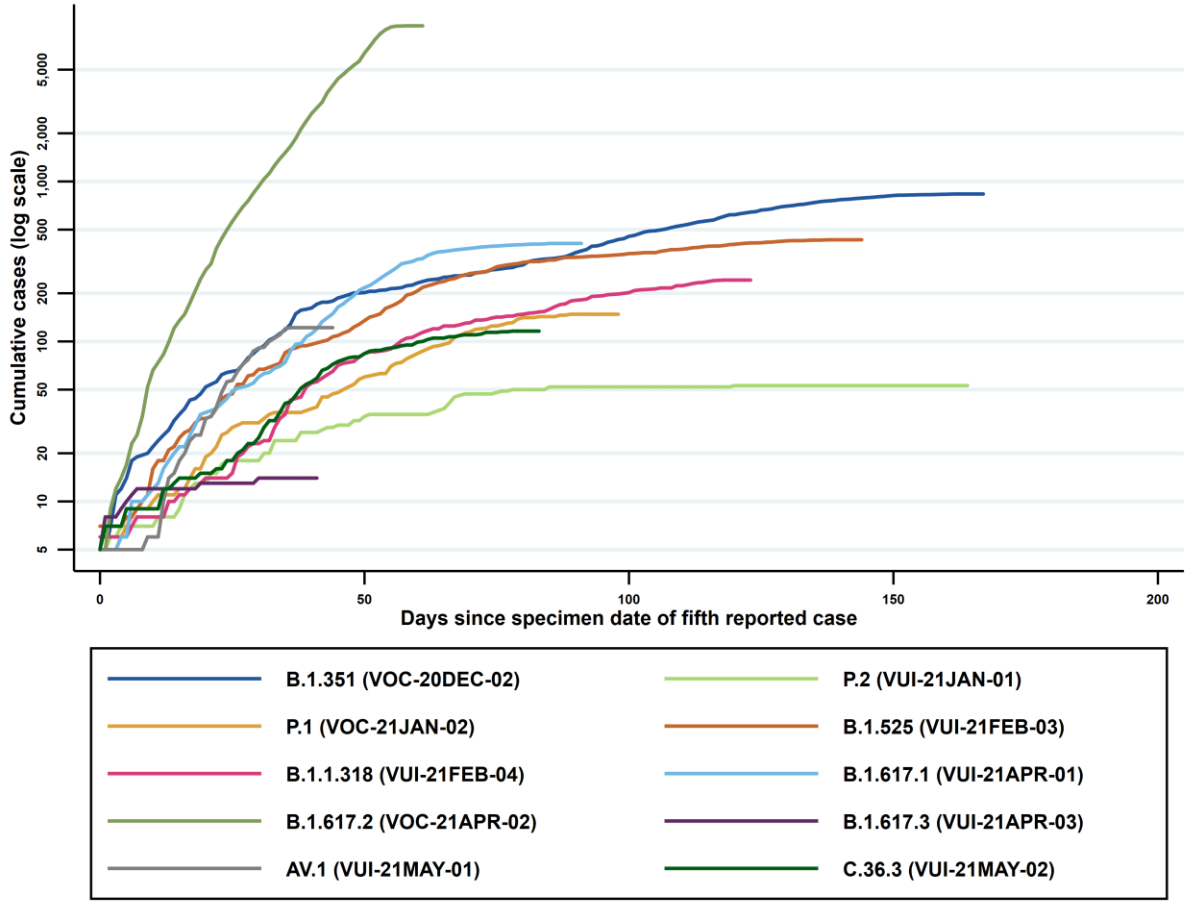
Table 4. Attendance to emergency care and deaths by vaccination status among Delta confirmed cases in England, 1 February 2021 to 31 May 2021

	Total	Cases with specimen date in past 28 days*	Unlinked	Unvaccinated	<21 days post dose 1	≥21 days post dose 1	Received 2 doses
Delta cases since 1 Feb 2021 ¥	9,427	7,744	2,321	5,172	303	1,364	267
Cases with an A&E visit§ (excluding cases with the same specimen and attendance dates)‡	364	NA	25	233	14	80	12
Cases with an A&E visit§ (including cases with the same specimen and attendance dates)	479	NA	32	309	22	98	18
Cases where presentation to A&E resulted in overnight inpatient admission§ (excluding cases with the same specimen and admission dates)‡	89	NA	8	59	1	18	3
Cases where presentation to A&E resulted in overnight inpatient admission§ (including	137	NA	11	90	5	24	7

cases with the same specimen and admission dates)							
Deaths^	17	NA	1	11	0	3	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 or admission within 28 days of positive specimen date
‡ Cases where specimen date is the same as date of A&E visit are excluded to help remove cases picked up via routine testing in healthcare settings whose primary cause of attendance is not COVID-19. This underestimates the number of individuals in hospital with COVID-19 but only includes those who tested positive prior to the day of their A&E visit. Some of the cases detected on the day of admission may have attended for another diagnosis.
^ Total deaths in any setting (regardless of hospitalisation status) within 28 days of positive specimen date.

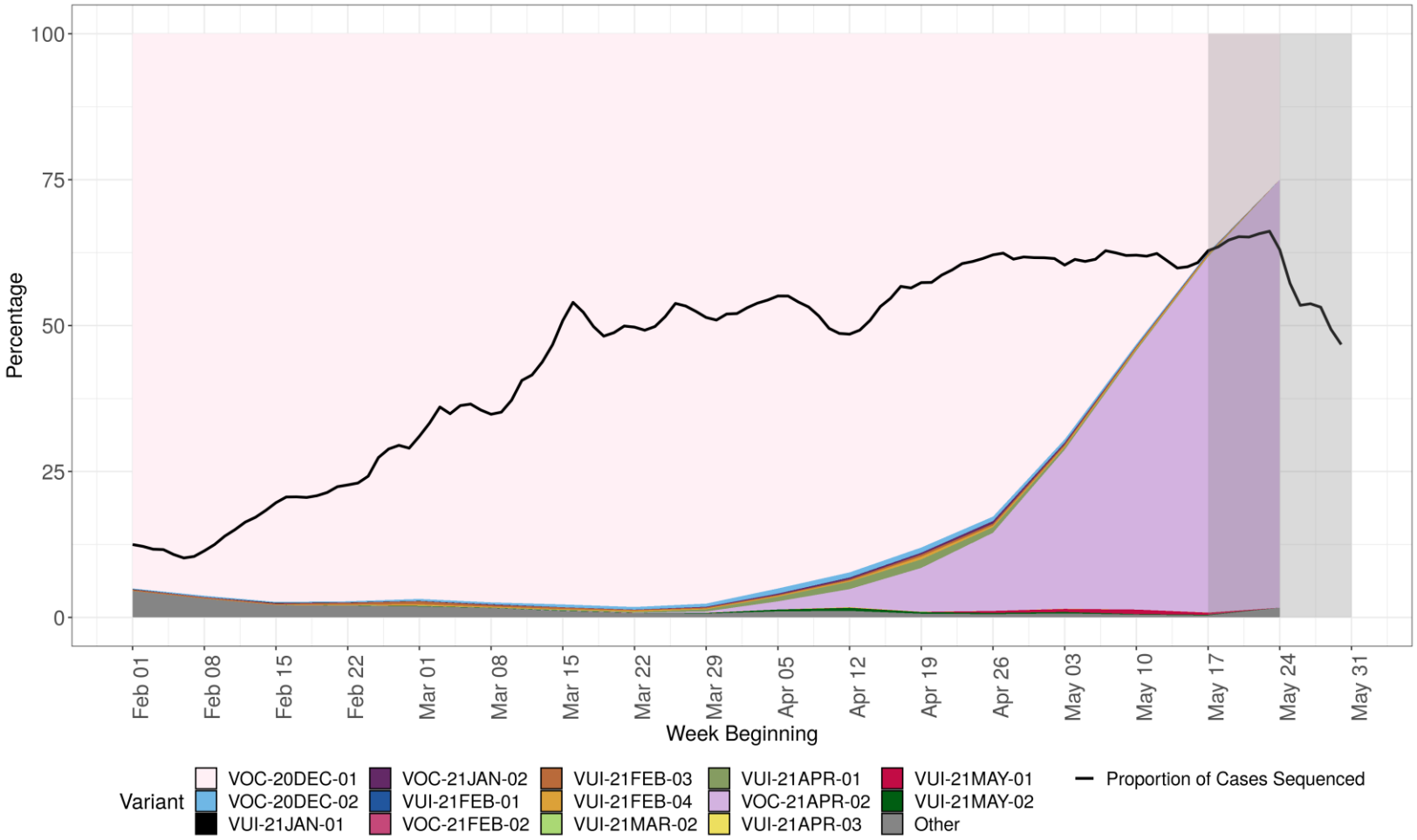
Figure 2. Cumulative cases in England of variants indexed by days since the fifth reported, data as of 31 May 2021
(Find accessible data used in this graph in underlying data).
Figure 2 demonstrates the rapid identification of Delta cases over a short period of time.



Variant prevalence

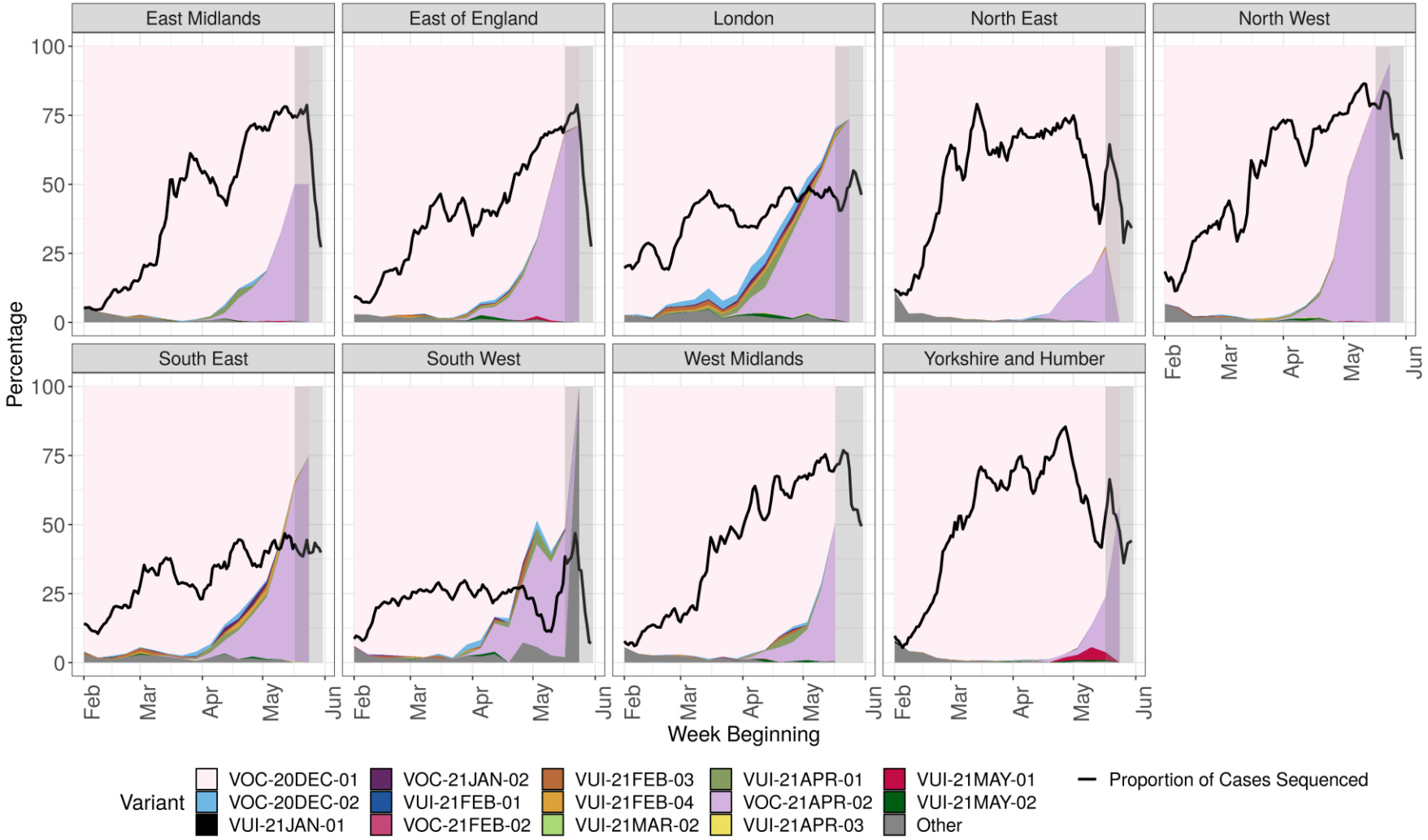
The prevalence of different variants amongst all sequenced cases is presented in Figure 3, split by region in Figure 4 and by travel status in Figure 5. The ‘Other’ category in Figure 3 and Figure 4 includes genomes where the quality is insufficient to determine variant status and genomes that do not 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 31 May 2021 (excluding 52 cases where the specimen date was unknown)



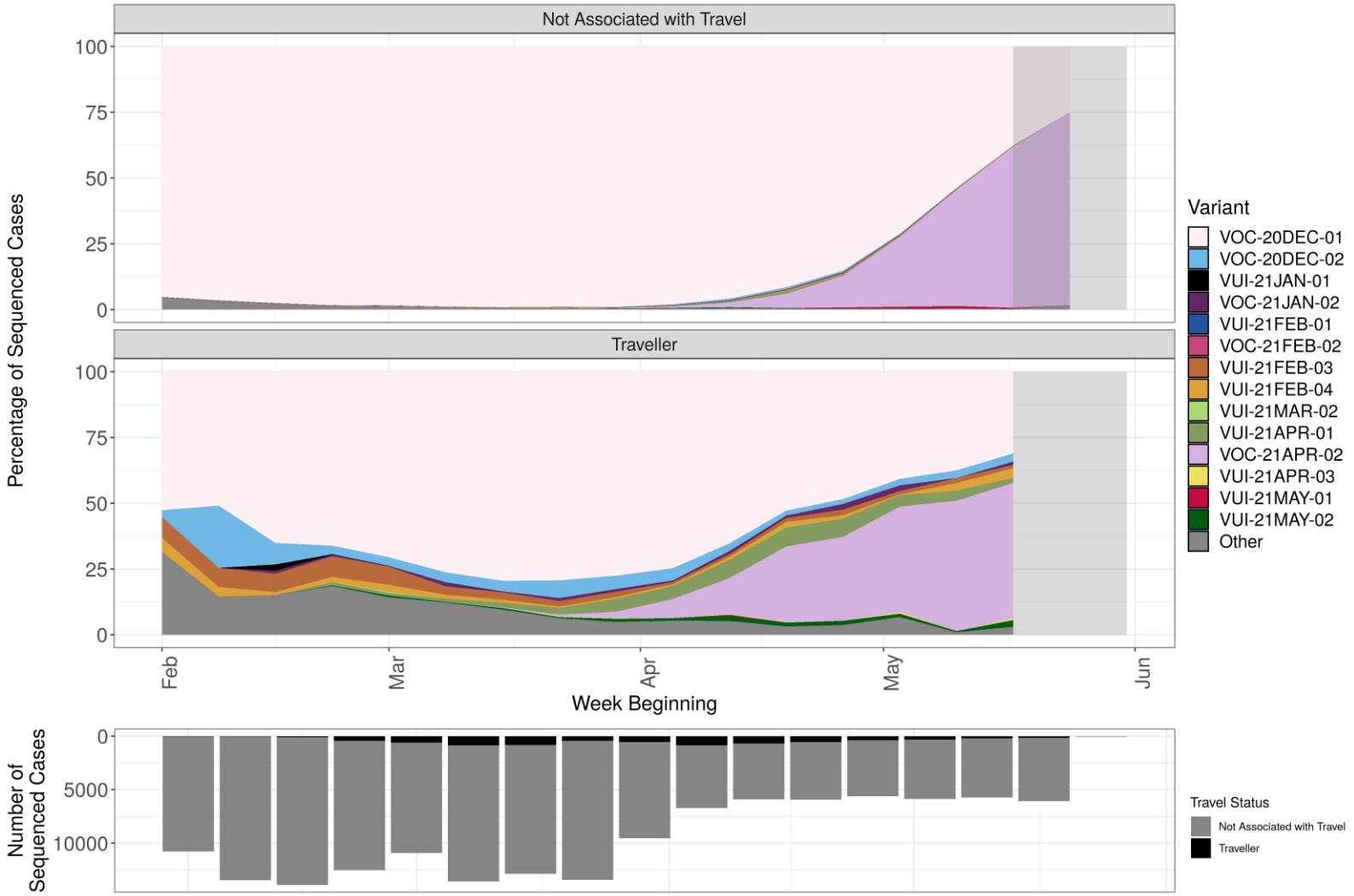
The most recent data show 73% of sequenced cases are Delta. At the latest data point where there is complete data (outside the grey region), 61% of sequenced cases are Delta. The black line indicates proportion of cases sequenced in a 7-day rolling window. The area in grey shows weeks where sequence data are 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 (13,431 have been excluded). (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 31 May 2021 by region (excluding 637 cases where the region or specimen date were unknown)



The black line indicates the proportion of cases sequenced in a 7-day sliding window. The area in grey shows weeks where sequence data are 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 (13,431 excluded). Data for most recent 2 weeks is incomplete. (Find accessible data used in this graph in underlying data).

Figure 5. Prevalence of variants over time: all sequenced cases in England, split by travel status as of 31 May 2021 (excluding 238 cases where the specimen date or travel status is unknown)
Travel-linked variant data available until 23 May only.



Travel status is assigned based an interval of ≤ 14 days between arrival date and positive specimen date. Travellers are derived through matching to Passenger Locator Forms, contact-tracing, international arrivals and local HPT survey data. Where no match to these datasets was found then the individuals are categorised as not-travel associated. Travel status was assigned on the basis of the individual's own history of travel, not contact with a traveller. The area in grey shows weeks where sequence data are 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 (13,431 excluded). 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 underlying data).

Variant growth rates

Logistic growth rates (1/week from 1 January 2021 as of 1 June 2021) relative to Alpha are calculated for each variant under investigation or variant of concern with more than 20 samples and shown in Table 5. 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.

In order to adjust for geographic variation in reproduction numbers and sample coverage, for each VOC/VUI variant under investigation or variant of concern a geographically matched subsample of Alpha cases is retained for analysis. Alpha cases are subsampled from each UTLA in proportion to the numbers of each VUI or VOC sampled in that UTLA. Any Alpha samples collected outside the period of time that the variant under investigation or variant of concern are observed are excluded as are Alpha samples collected in UTLAs where the variant under investigation or variant of concern 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 Alpha. Growth rate reflects both the biological properties of the virus and the context (that is population and place) in which it is transmitting.

Compared to Alpha, Delta displays an increased logistic growth rate indicating that the proportion of samples that are Delta is increasing.

Table 5. Growth rate of variants of concern and variants under investigation 1 January 2021 as of 1 June 2021

Variant	Growth rate (1/week)
Beta	0.16 (p=7.3e-36,n=340)
Zeta	-0.079 (p=0.2015,n=22)
Gamma	0.35 (p=1.7e-17,n=76)
VUI-21FEB-01	-0.26 (p=0.003,n=55)
Eta	0.096 (p=6.525e-10,n=191)
VUI-21FEB-04	0.2 (p=7.242e-19,n=134)
Kappa	0.29 (p=1.3e-17,n=149)
Delta	0.92 (p=0,n=7,374)
VUI-21MAY-01	0.91 (p=4.3e-23,n=105)

Sample sizes (n) correspond to the number of variant under investigation or variant of concern used in the analysis. P values correspond to the null hypothesis that there is no difference in variant under investigation or variant of growth rates and Alpha growth rates.

Secondary attack rates

This section includes secondary attack rates for traveller and non-traveller cases, and separate household contact rates. It also includes an updated 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 6 shows the secondary attack rates for Delta compared to the other B.1.617 variants and Alpha. The time period of study for secondary attack rates has been restricted to the period 29 March 2021 to 11 May 2021, to capture recent social restrictions and vaccination levels. A reduction in secondary attack rate for non-travel cases with Alpha is observed in this shorter period when compared to Table 7 covering 05 January 2021 to 11 May 2021.

Secondary attack rates for contacts of cases with Delta and no travel history are higher than those for contacts of non-travel cases with Alpha: 12.4% compared to 8.2%. The estimate of secondary attack rate for contacts of cases with Delta represents a decrease compared to that published in Technical Briefing 13 for the period to 29 March to 4 May 2021, which was 13.5% (95% CI 12.5% to 14.6%). 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 Delta were higher than those for travel cases with Alpha.

Table 7 shows the secondary attack rates for variants (excluding variants of the B.1.617 lineage, that is Delta, Kappa, VUI-21APR-03) for the period 5 January 2021 to 11 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 Alpha 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 Alpha. 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 8 shows the secondary attack rates amongst household and non-household contacts of non-travel cases with Delta and Alpha. The time period of study for secondary attack rates has been restricted to the period 29 March 2021 to 11 May 2021 as in Table 6. 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 Delta than Alpha; this is consistent with Table 6.

Figure 6 (and Table 9) 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 Alpha and Delta. For non-household exposures, the median interval from exposure date to secondary case onset is also 4 days for Alpha, but 5 days for Delta.

Table 6. Secondary attack rates for Kappa, Delta and VUI-21APR-03 (B.1.617.3), presented with Alpha, time restricted for comparison (29 March 2021 to 11 May 2021, variant data as at 25 May 2021, contact tracing data as at 1 June 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]
Alpha	1,919 (70.3% with contacts)	29,459 (82.0% with contacts)	6.1%	1.6% (1.4% - 1.7%) [494/31,472]	8.2% (8.0% - 8.4%) [6,295/76,948]
Kappa	177 (77.4% with contacts)	123 (78.9% with contacts)	59.0%	2.0% (1.6% - 2.6%) [60/2,928]	11.0% (8.0% - 15.0%) [34/308]
Delta	545 (71.9% with contacts)	2883 (83.1% with contacts)	15.9%	2.6% (2.3% - 3.0%) [235/8,952]	12.4% (11.7% - 13.2%) [993/7,987]

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 11 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 all variants (excluding B.1.617 variants)
(5 January 2021 to 11 May 2021, variant data as at 25 May 2021, contact tracing data as at 1 June 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]
Alpha	4,087 (77.1% with contacts)	168,623 (74.5% with contacts)	2.4%	1.6% (1.6% - 1.7%) [1,212/73,748]	9.9% (9.8% - 10.0%) [34,878/35,3212]
Beta	301 (72.4% with contacts)	351 (66.7% with contacts)	46.2%	2.3% (1.9% - 2.7%) [106/4673]	8.7% (6.8% - 10.9%) [64/739]
Zeta	3 (66.7% with contacts)	32 (75.0% with contacts)	8.6%	Unavailable [0/137]	8.1% (3.5% - 17.5%) [5/62]
Gamma	65 (63.1% with contacts)	68 (70.6% with contacts)	48.9%	1.3% (0.7% - 2.4%) [9/716]	11.0% (7.1% - 16.7%) [18/164]
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]
Eta	193 (69.9% with contacts)	186 (73.1% with contacts)	50.9%	1.3% (1.0% - 1.7%) [55/4184]	9.3% (6.7% - 12.8%) [33/353]

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-21FEB-04	85 (68.2% with contacts)	120 (75.8% with contacts)	41.5%	0.6% (0.4% - 1.0%) [15/2502]	9.3% (6.3% - 13.5%) [23/248]
VUI-21MAR-01	1 (100.0% with contacts)	0 (0 with contacts)	100.0%	Unavailable [0/7]	Unavailable [0/0]
Theta	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)	56 (85.7% with contacts)	3.4%	Unavailable [0/0]	3.8% (1.9% - 7.3%) [8/212]

Note legend from Table 6. No variant data was available for VUI-21MAY-02 at time of production.

Table 8. Secondary attack rates for household contacts of non-travel cases of Alpha and Delta
(29 March 2021 to 11 May 2021, variant data as at 25 May 2021, contact tracing data as at 1 June 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]
Alpha	29,459 (79.8% with household, 17.8% with non-household contacts)	9.0% (8.7% - 9.2%) [5,657/63,145]	4.6% (4.3% - 5.0%) [638/13,803]
Delta	2,883 (81.1% with household, 16.3% with non-household contacts)	13.6% (12.8% - 14.5%) [910/6,668]	6.3% (5.1% - 7.7%) [83/1,319]

Note legend from Table 6. Data provided is for period 29 March 2021 to 11 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 Alpha and Delta (29 March 2021 to 11 May 2021, variant data as at 25 May, contact tracing data as at 1 June)
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).

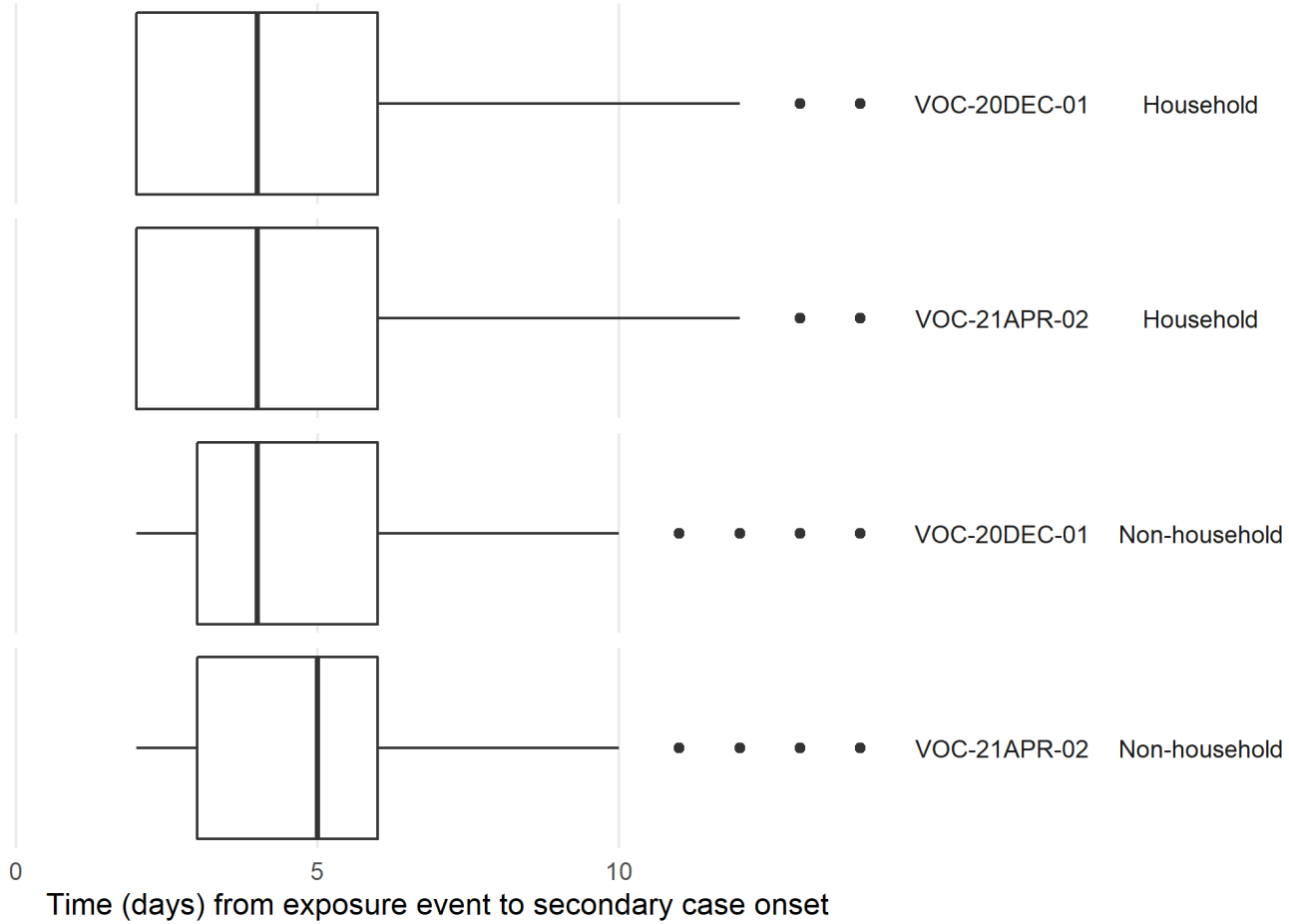


Table 9. Time interval to onset in secondary case, household and non-household contacts of cases of Alpha and Delta (29 March 2021 to 11 May 2021, variant data as at 25 May 2021, contact tracing data as at 1 June 2021)

Variant	Exposure type	Secondary cases	Median interval (days)
Alpha	Household	5,850	4
Alpha	Non-household	939	4
Delta	Household	1,016	4
Delta	Non-household	212	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.

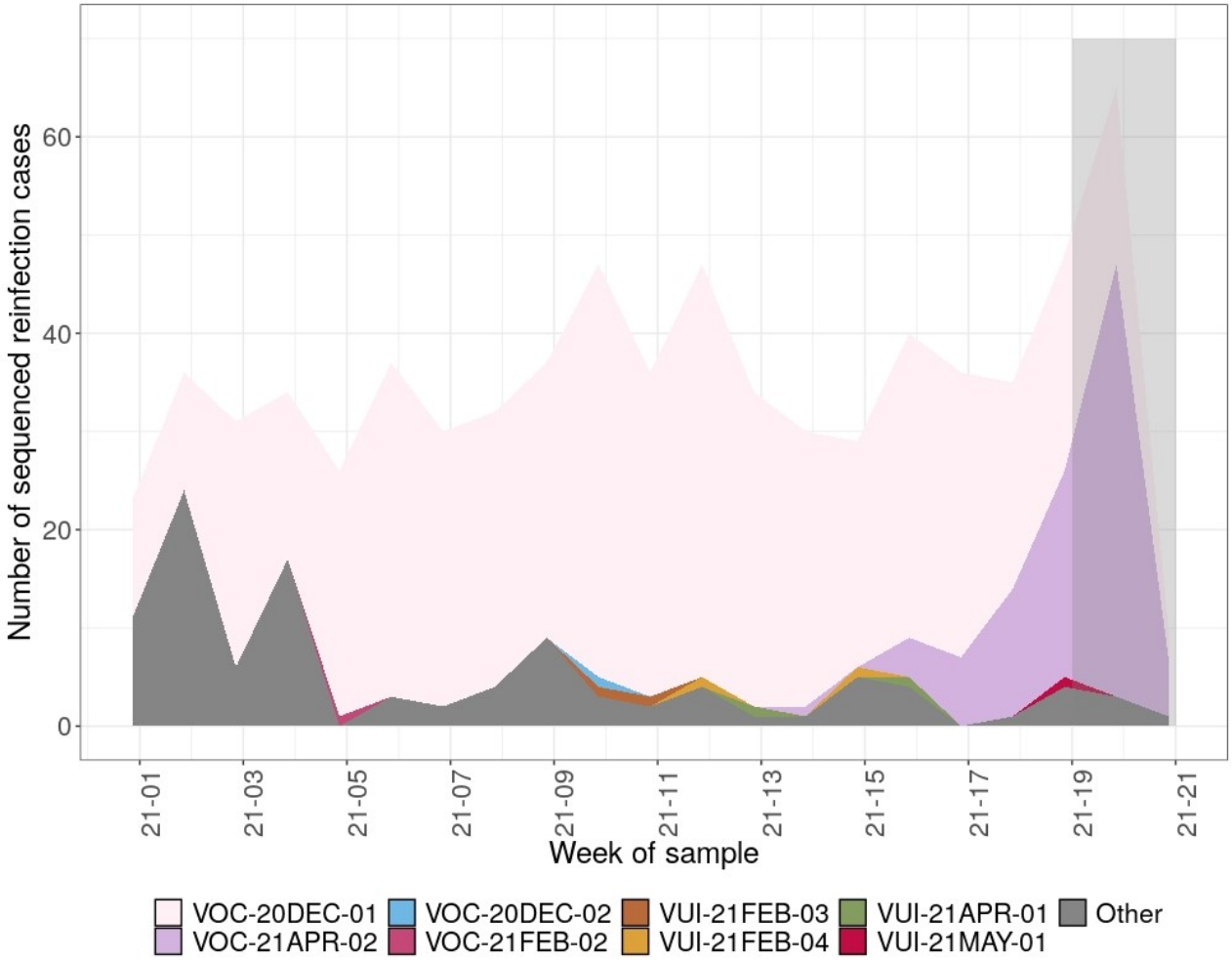
Surveillance of reinfections

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 10 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. 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 10. Number of sequenced reinfection cases and the variant assigned
(Data as of 31 May 2021)

Variant	Total
Alpha	556
Beta	1
Zeta	0
VOC-21FEB-02	1
Eta	2
VUI-21FEB-04	2
Kappa	2
Delta	96
VUI-21APR-03	0
VUI-21MAY-01	1
VUI-21MAY-02	0
Total sequenced	874

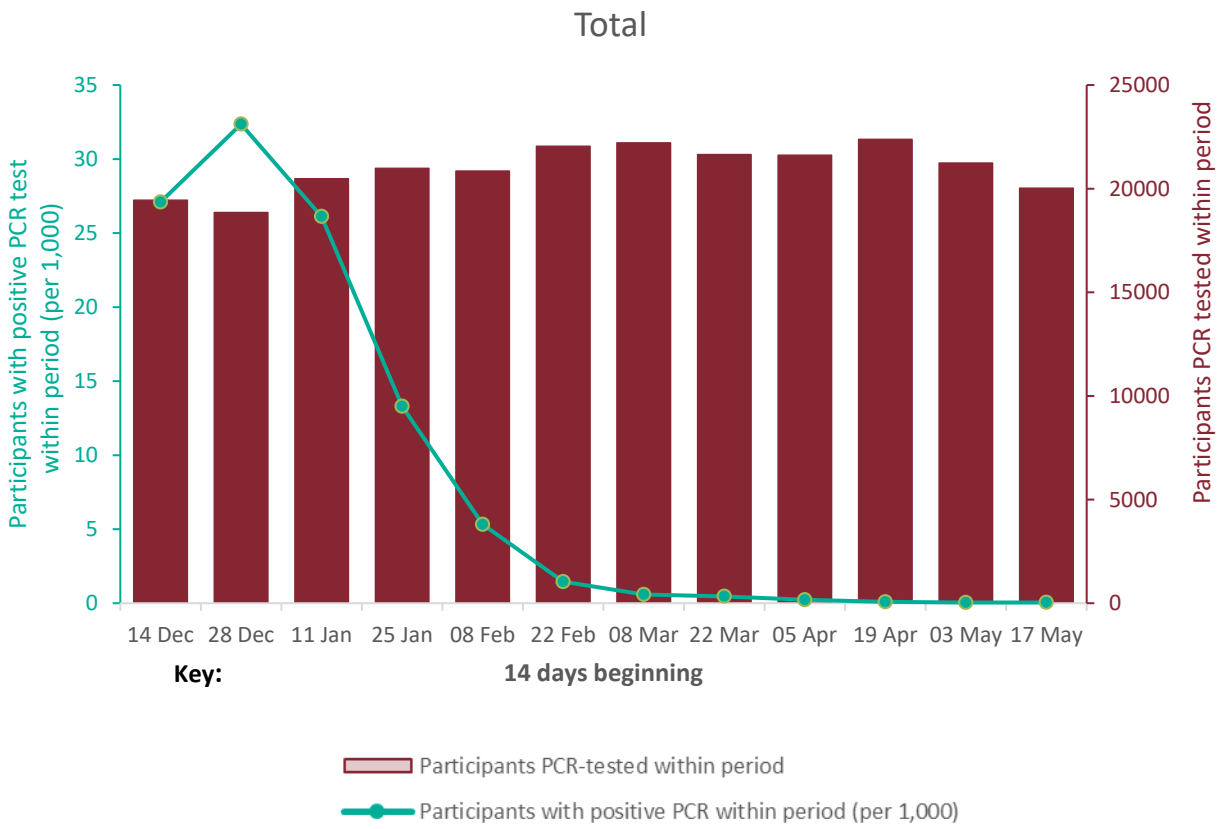
Figure 7. The number of reinfections cases from all sample sources, with the total number of reinfections cases with sequences, and the number of variant sequences over time as of 31 May 2021
(Find accessible data used in this graph in underlying data).



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, 35,717* 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 Delta 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).

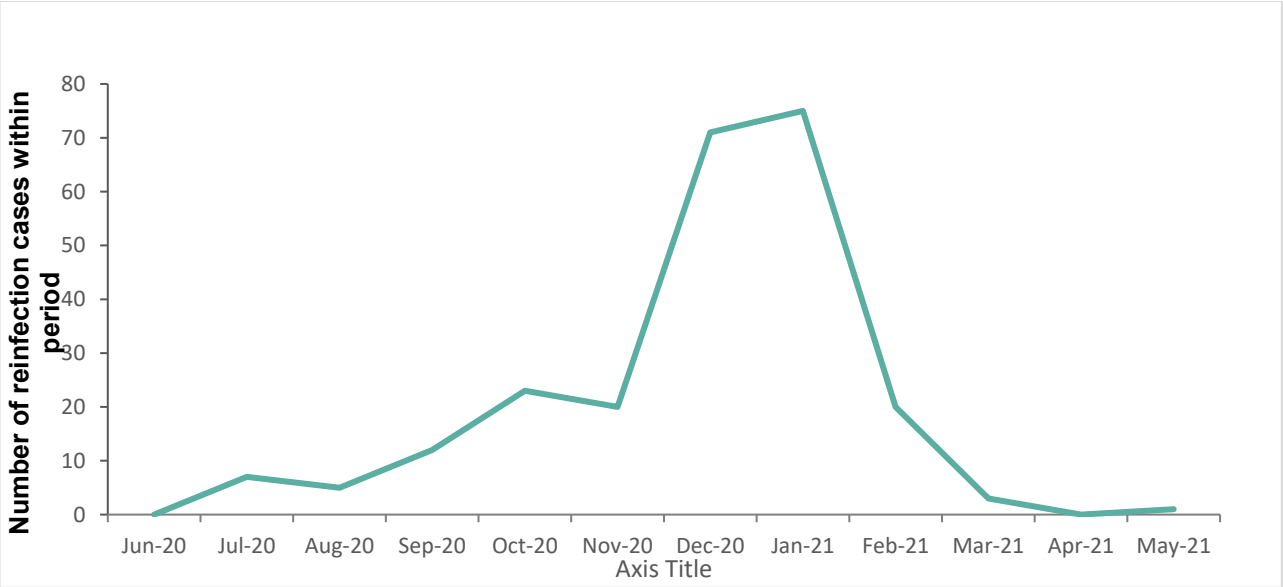
Figure 8. PCR positivity within the SIREN study for all regions, England (fortnightly testing interval) Data up to 30 May 2021



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 1 June 2021



Nine thousand, eight hundred and thirteen (31%) of the SIREN cohort had evidence of prior infection (previous PCR positive or antibody positive) at enrolment; 237 potential reinfections (green line) were identified in England up to 1 June 2021.

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

Variants linked to suspected SARS-CoV-2 outbreaks

Data on all new acute respiratory infection (ARI) incidents reported to Health Protection Teams (HPTs) and entered on the Case and Incident Management System (CIMS) in the previous reporting week are published in the weekly influenza/COVID-19 surveillance report.

Here we present information on a subset of these incidents – those suspected SARS-CoV-2 clusters and outbreaks that have at least one confirmed non-Alpha variant of concern or variant under investigation case identified and linked to them. Incidents are assigned a variant type through an automated data linkage process which brings together incident data, case data and genomics data. These are experimental data as the methodology is new and will continue to undergo further validation and enhancements. Alpha-related incidents are not included here because these outbreaks have not been recorded in an equivalent way since it became the dominant strain and an accurate comparison cannot be made.

It is important to note that there is a time lag from the suspected outbreak being reported to PHE to sequencing being undertaken and variant cases identified so data are provisional and likely to change in subsequent weeks.

Note that:

- an incident is an administrative record regarding a setting rather than an epidemiological classification and consequently complex, multi-variant incidents exist in a given setting
- household outbreaks and clusters that have been misclassified as outbreaks linked to settings are excluded
- suspected Alpha outbreaks and clusters are excluded
- supplementary data on Table 11, 12 and 13 are available in underlying data.
- the incidents captured on the CIMS represent a subset of all ongoing clusters and outbreaks in England – a variety of arrangements are in place with local authorities and other stakeholders supporting HPTs, however, data may not routinely be documented on the CIMS

Table 11. Incidents managed by Health Protection Teams involving SARS-CoV-2 variants by iso-week, by outbreak setting
(4 January 2021 up to 1 June 2021)

Setting/Year-Week	21-01	21-02	21-03	21-04	21-05	21-06	21-07	21-08	21-09	21-10	21-11	21-12	21-13	21-14	21-15	21-16	21-17	21-18	21-19	21-20	21-21	Total
Custodial Institution	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	2
Food Outlet/Restaurant	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	4	3	9
Healthcare	0	2	1	1	1	0	0	1	1	0	1	0	0	0	0	2	1	2	1	2	1	17
Care Home	2	0	1	1	2	2	0	1	0	0	0	0	0	1	0	1	1	0	0	1	5	18
Workplace	1	1	0	2	2	1	1	1	0	0	2	0	0	2	0	2	4	4	10	25	23	81
Educational Setting	0	0	0	0	0	0	1	1	0	0	2	1	1	2	1	2	8	19	23	42	69	172
Other	0	1	1	5	4	5	2	4	2	2	4	0	6	14	5	13	30	51	30	47	37	263
Total	3	4	3	10	9	8	4	8	3	2	9	1	7	19	6	20	44	77	65	122	138	562

Table 12. Incidents managed by Health Protection Teams involving SARS-CoV-2 variants by iso-week by variant
(4 January 2021 up to 1 June 2021)

Variant/Week	21-01	21-02	21-03	21-04	21-05	21-06	21-07	21-08	21-09	21-10	21-11	21-12	21-13	21-14	21-15	21-16	21-17	21-18	21-19	21-20	21-21	Total
Beta	0	0	0	3	3	2	2	1	2	1	2	0	2	9	3	3	5	3	3	0	2	46
VOC-20DEC-01+E484K	0	0	0	0	0	0	0	0	0	0	0	0	1	2	0	1	1	0	0	0	0	5
Zeta	0	1	2	1	0	1	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	8
Gamma	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	2	4	4	0	0	1	13
VUI-21FEB-01	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
Eta	0	0	0	0	4	1	1	1	0	0	4	0	3	1	1	3	1	0	1	0	1	22
VUI-21FEB-04	0	0	0	0	0	0	0	0	1	0	0	0	0	1	1	1	0	0	1	0	0	5
VOC-21FEB-02	1	1	1	1	2	3	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0	12
VUI-21APR-01	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	3	5	9	2	0	2	23
Delta	0	0	0	1	0	0	0	0	0	0	0	0	0	2	0	6	21	58	54	115	123	380
VUI-21APR-03	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	2
VUI-21MAY-01	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	2	1	4
Undetermined+E484K	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	3

Multiple variants identified	1	2	0	3	0	1	0	0	0	0	1	1	1	1	0	1	7	3	4	4	7	37
Total	3	4	3	10	9	8	4	8	3	2	9	1	7	19	6	20	44	77	65	122	138	562

Table 13. Incidents managed by Health Protection Teams involving SARS-CoV-2 variants by setting by variant
(4 January 2021 up to 1 June 2021)

Variant	Care Home	Custodial Institution	Educational Setting	Food outlet/restaurant	Healthcare	Other	Workplace	Total
Beta	1	1	3	1	4	31	5	46
VOC-20DEC-01+E484K	0	0	2	0	0	3	0	5
Zeta	0	0	0	0	1	6	1	8
Gamma	0	0	3	0	0	9	1	13
VUI-21FEB-01	0	0	0	0	0	0	2	2
Eta	3	0	4	0	3	11	1	22
VUI-21FEB-04	0	0	2	0	0	2	1	5
VOC-21FEB-02	3	0	1	0	0	5	3	12
VUI-21APR-01	0	0	5	0	0	18	0	23
Delta	10	1	140	7	5	155	62	380
VUI-21APR-03	0	0	0	0	0	2	0	2
VUI-21MAY-01	0	0	1	0	0	2	1	4
Undetermined+E484K	0	0	1	0	0	2	0	3

Multiple variants identified	1	0	10	1	4	17	4	37
Total	18	2	172	9	17	263	81	562

Suspected clusters and outbreaks linked to primary and secondary schools (including Special Educational Needs (SEN) settings) undergo further validation. Individual incident and case notes are reviewed by an epidemiologist on a weekly basis and an assessment made about whether the criteria for a confirmed SARS-CoV-2 cluster or outbreak are met. In the most recent 4 week period there have been 97 confirmed SARS-CoV-2 outbreaks linked to primary and secondary schools that have had at least one variant case linked to them. This represents around 1 in 250 schools.

Figure 10. Number of confirmed SARS-CoV-2 outbreaks or clusters in primary and secondary schools (including special educational needs settings) by variant type identified and epidemiological week, from 26 April to 30 May 2021
These data are provisional, excluding confirmed Alpha variant outbreaks.

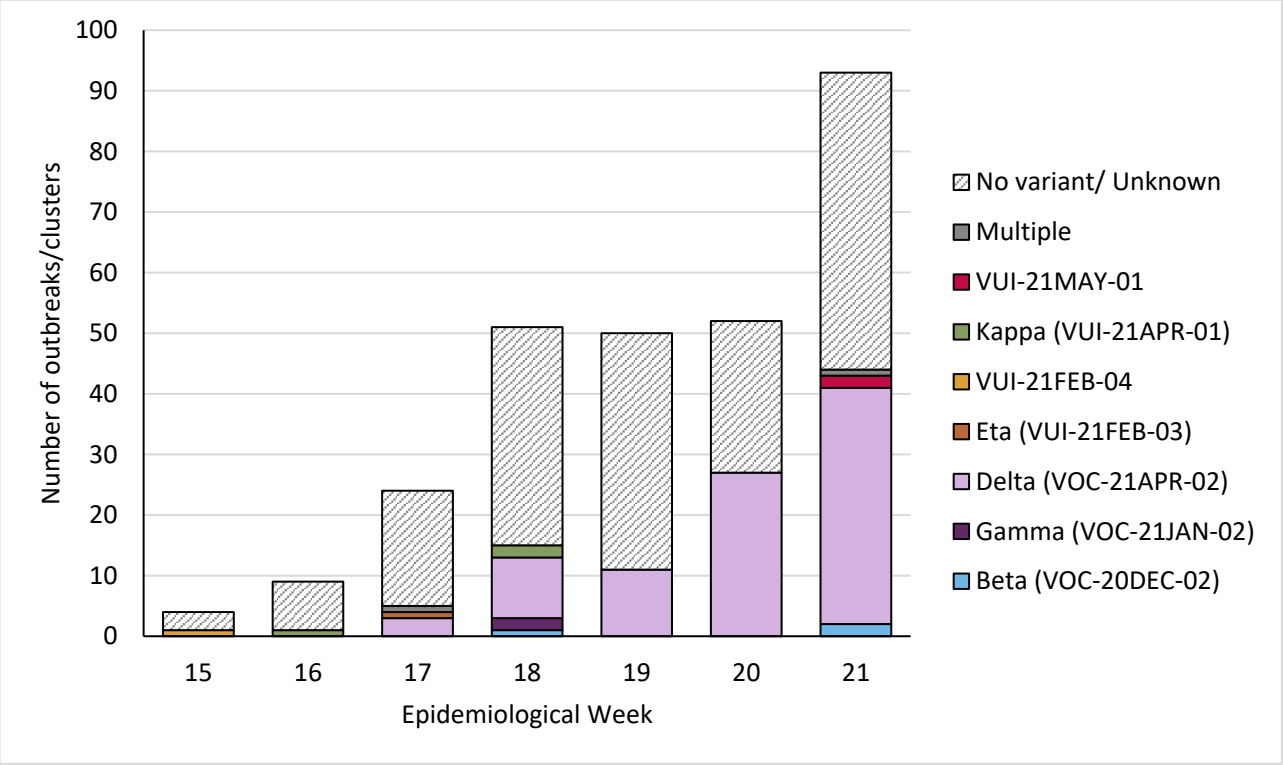


Table 14. Number of confirmed SARS-CoV-2 outbreaks or clusters in primary and secondary schools (including special educational needs settings) by variant type identified and epidemiological week, from 26 April to 30 May 2021
These data are provisional, excluding Alpha variant.

Variant / Week	21-15	21-16	21-17	21-18	21-19	21-20	21-21	Total
Beta				1			2	3
Gamma				2				2
Delta			3	10	11	27	39	90
Eta			1					1
VUI-21FEB-04	1							1
Kappa		1		2				3
VUI-21MAY-01							2	2
Multiple			1				1	2
No variant/ Unknown	3	8	19	36	39	25	49	179
Total	4	9	24	51	50	52	93	283

Common exposures derived from contact tracing data

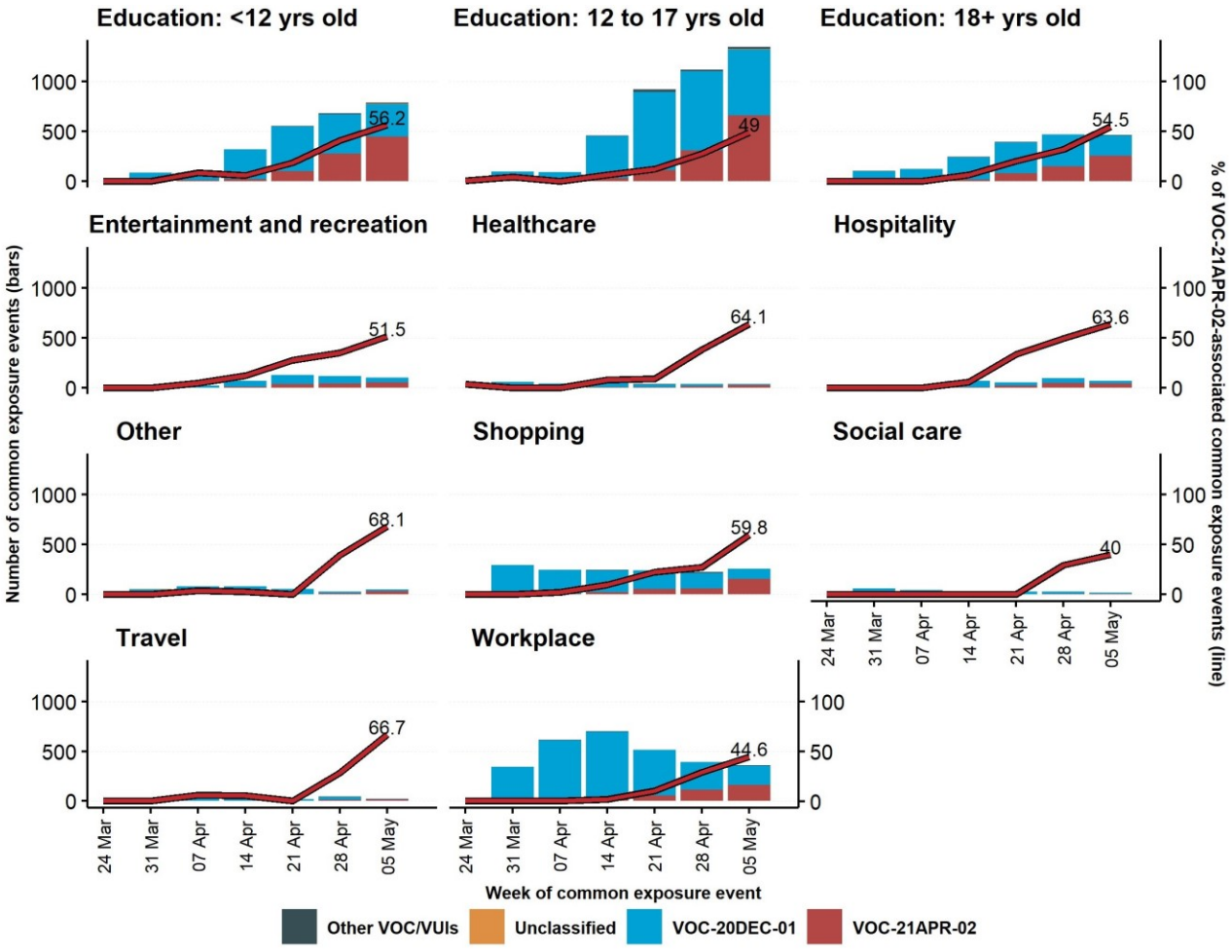
Figure 11 shows the number of common exposure events reported per week, by setting. This figure only includes common exposures reported by cases who have been sequenced, to enable a comparison of trends by variant. Common exposures are derived from contact tracing data, and are defined as specific venues visited outside the home by at least 2 cases during their pre-symptomatic period (2 to 7 days before symptom onset), on the same day or up to 7 days apart. A single common exposure event represents a visit by a case on a particular day to the common exposure setting.

Common exposure events can represent possible transmission events between known cases but also from unknown cases. However, they can also simply represent commonly visited locations and so are interpreted with caution. In particular, settings visited regularly (for example daily school or workplace attendance), can be enhanced in the data as each of the separate visits are counted. Fewer common exposures occur when settings are closed or limited due to restrictions.

Recent weeks of data suggest that the number of common exposure events reported by sequenced cases in educational settings increased between 24 March and 11 May 2021; more recent complete data is not yet available. The number of common exposure events in work and shopping settings stayed relatively consistent or decreased, whereas other settings have low total numbers of events reported. Note that these data are before the easing of restriction on 17 May 2021, and the beginning of the study period coincides with the Easter holiday when schools were closed. The number and proportion of common exposure events linked specifically to Delta cases (red bar and line respectively in Figure 11) has also increased over time. In the most recent week of presented data (starting 5 May 2021), the proportion ranged from 45% to 67% across all presented settings. The increase over the time period reflects the overall increase in to Delta prevalence.

Figure 11. Weekly number of common exposure events among sequenced cases, by setting and variant of cases (bars), and proportion of weekly common exposure events among sequenced cases associated with Delta (red line)

Common exposure events reported from 30 March 2021 to 11 May 2021. Variant data as of 1 June 2021, contact tracing data as of 2 June 2021. Percent for most recent week of data labelled, only settings with at least 100 common exposure events since 30 March included.



Part 2: Delta (B.1.617.2) surveillance

The lineage B.1.617.2 was escalated to a variant of concern in the UK on 6 May 2021 (VOC-21APR-02). This variant was named Delta by WHO on 31 May 2021.

Severity

Complementary analyses undertaken in England and Scotland found an increased risk of hospitalisation in cases who were S gene target positive (Scotland) or had sequence-confirmed Delta variant infection (England). Confirmatory analyses are required to confirm the magnitude of the change in risk and to explore the link to vaccination in more detail.

England

Based on a record linkage of sequence-confirmed Delta and Alpha cases in England tested between 29 March 2021 and 20 May 2021, an analysis of 38,805 sequenced cases was performed to assess the risk of hospitalisation and emergency care attendance. Using stratified Cox proportional hazard regression, there was a significantly increased risk of hospitalisation within 14 days of specimen date (HR 2.61, 95% CI 1.56-4.36, $p<0.001$), and emergency care attendance or hospitalisation within 14 days (HR 1.67, 1.25-2.23, $p<0.001$), for Delta cases compared to Alpha cases after adjustment for confounders (age, sex, ethnicity, area of residence, index of multiple deprivation, week of diagnosis and vaccination status).

Scotland

In the Public Health Scotland/EAVE II study, Cox proportional hazard regression was used to estimate risk factors for the time from test to hospitalisation among individuals who tested positive. Hospitalisation with COVID-19 was defined as any admission within 14 days of a positive test or where there was a positive test within 2 days of admission. The model was adjusted for age and days from 1 April 2021 as spline terms together with number of co morbid conditions, gender and vaccination status. Vaccination status was determined at the data of the PCR test. Only individual who tested positive from 1 April 2021 onwards (until 30 May 2021) were included in this analysis. There was an increased hazard ratio of hospitalisation for those who were S-gene positive compared with those with S gene target failure (2.39, 95% 1.72 to 3.31).

International surveillance

GISAID includes data on sequences available internationally. As of 1 June 2021, sequences from the following countries (excluding UK) have been identified in GISAID of Delta: In total 4,972 sequences from: Argentina, 1, Aruba, 3, Australia, 116, Austria, 4, Bahrain, 14, Bangladesh, 25, Belgium, 118, Brazil, 1, Canada, 125, China, 2, Czech Republic, 9, Democratic Republic of the Congo, 6, Denmark, 80, France, 70, Georgia, 4, Germany, 351, Ghana, 1, Greece, 1, Hong Kong, 3, India, 1709, Indonesia, 27, Iran, 9, Ireland, 99, Israel, 37, Italy, 62, Japan, 153, Jordan, 1, Luxembourg, 2, Malaysia, 4, Mexico, 22, Morocco, 1, Nepal, 12, Netherlands, 44, New Zealand, 11, Norway, 30, Pakistan, 1, Poland, 26, Portugal, 72, Qatar, 6, Romania, 5, Russia, 1, Reunion, 1, Saint Martin, 1, Singapore, 232, Slovenia, 1, South Africa, 16, South Korea, 1, Spain, 69, Sweden, 12, Switzerland, 45, Thailand, 8, Turkey, 1, USA, 1314, Uganda, 3

Surveillance through genomic data

Table 15. Number of confirmed and probable Delta cases, by region of residence as of 31 May 2021

[1]Calculated as a proportion of all cases, including those with unknown or pending travel status

Region	Case Number	Case Proportion	Cases that have travelled	Proportion of travellers among cases[1]
East Midlands	826	8.8%	66	8%
East of England	1,137	12.1%	81	7.1%
London	1,526	16.2%	247	16.2%
North East	149	1.6%	10	6.7%
North West	4,273	45.3%	39	0.9%
South East	530	5.6%	103	19.4%
South West	154	1.6%	48	31.2%
West Midlands	499	5.3%	67	13.4%
Yorkshire and Humber	278	2.9%	26	9.4%
Unknown region	54	0.6%	18	33.3%
Total	9,426	-	705	7.5%

Figure 12. Confirmed and probable Delta cases by specimen date as of 31 May 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data).

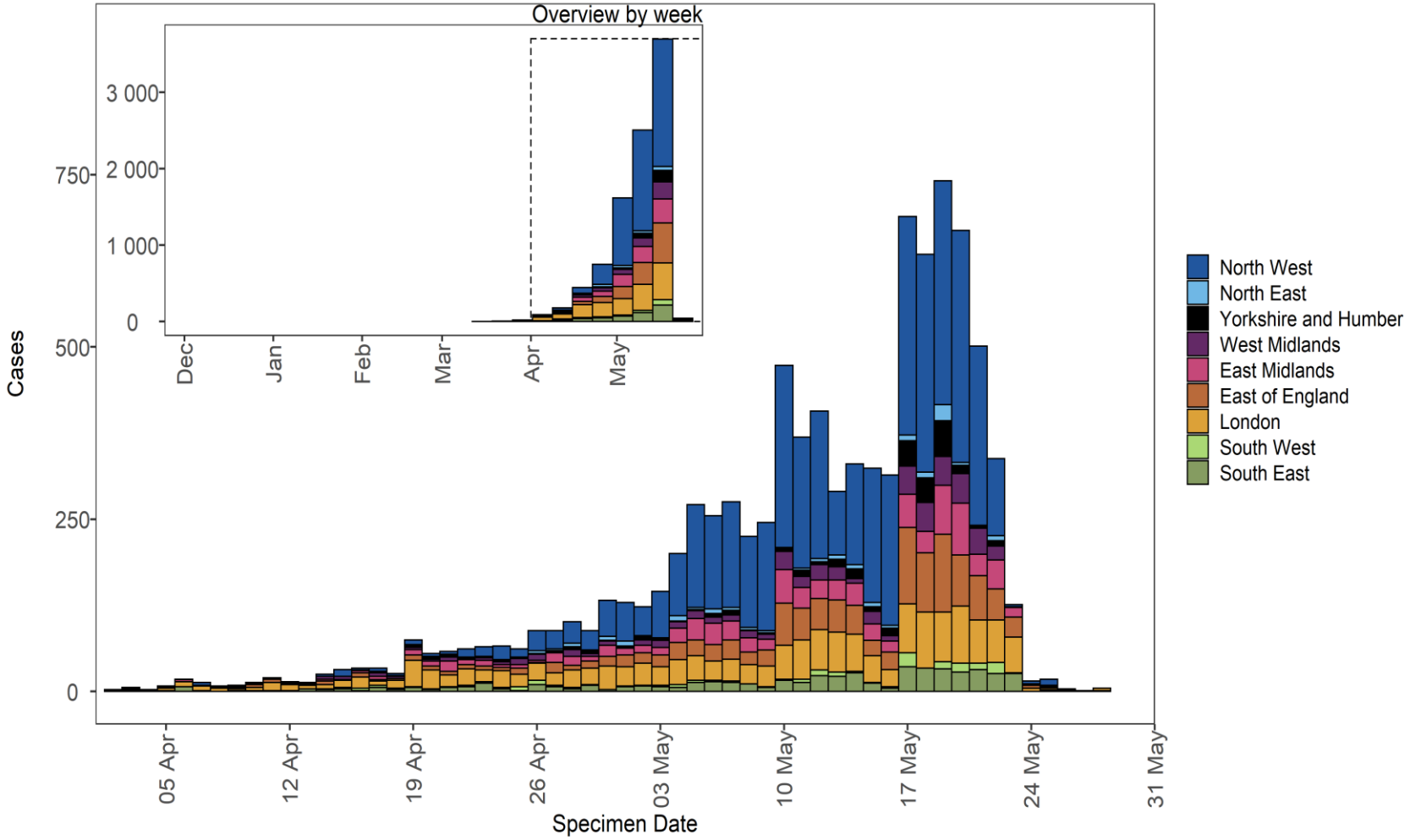


Figure 13. Travel data for confirmed and probable Delta cases by specimen date as of 31 May 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.

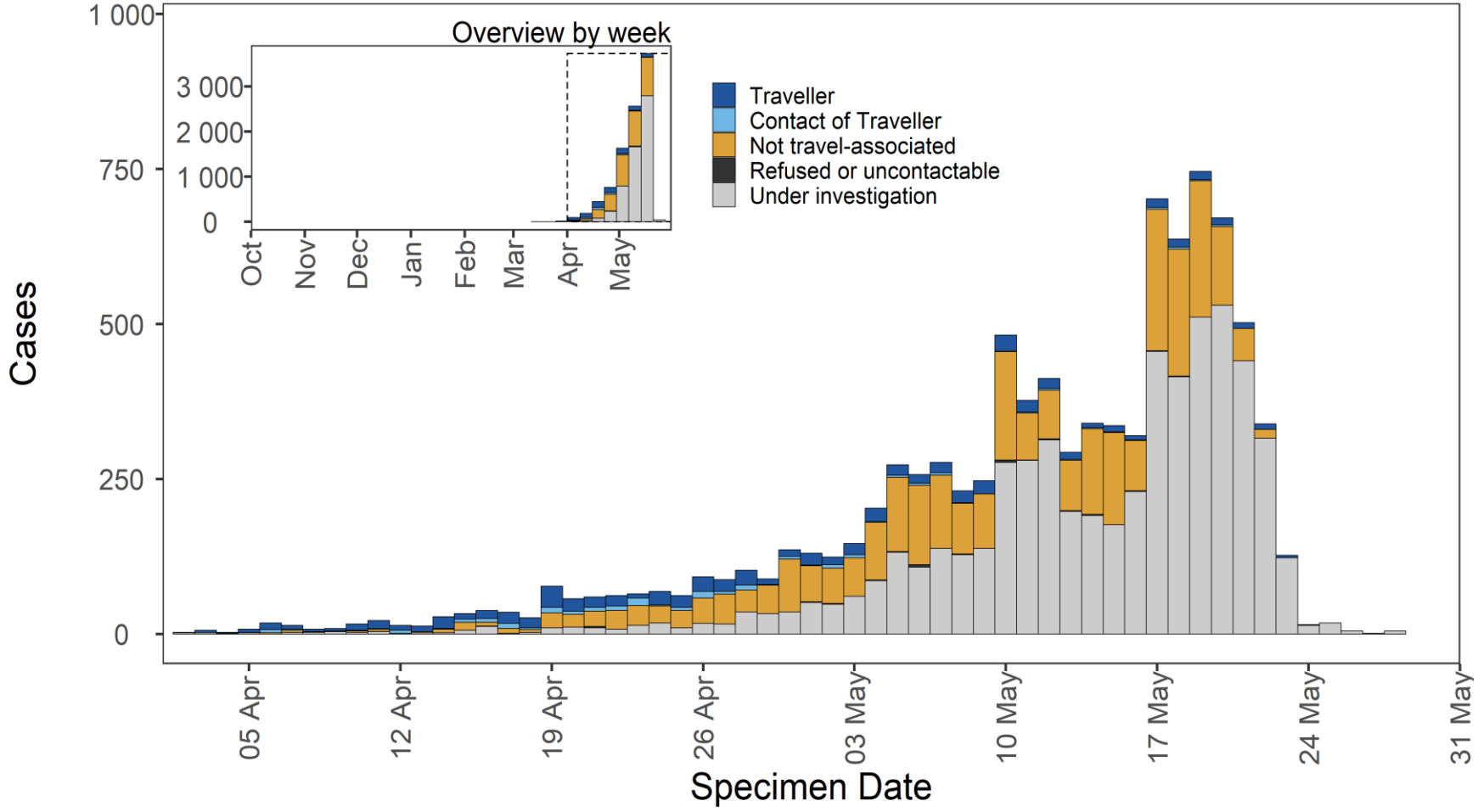


Table 16. Additional spike mutations of interest detected in Delta genomes in the UK, as of 1 June 2021

Amino acid change	Nucleotide change	Total number of sequences (UK)	Number of unlinked sequences	Number of sequences 2nd March to 1st April	Number of sequences 2nd April to 1st May	Number of sequences 2nd May to 1st June
P681R	C23604G	13,258	2,057	17	1,540	9,644
L452R	T22917G	13,073	2,023	18	1,530	9,502
G142D	G21987A	8,596	1,259	11	1,054	6,272
R158G	A22034G	43	14	0	0	29
K417N	G22813T	43	8	0	8	27
G446V	G22899T	11	4	0	0	7
Q677H	G23593T	9	0	1	8	0
V503I	G23069A	8	0	0	0	8
L244S	T22293C	8	2	0	0	6
S255F	C22326T	6	0	0	4	2
P251L	C22314T	5	4	0	0	1
E484A	A23013C	4	0	0	4	0
S494L	C23043T	3	0	0	0	3
L18F	C21614T	2	0	0	0	2
D405Y	G22775T	2	2	0	0	0
A701V	C23664T	2	1	0	1	0

This data uses the numbers of genomes in the national genomic dataset rather than case numbers. Unlinked sequences refers to genomes which have not been linked to a primary PCR result in the English database and include individuals from outside of England. Further investigations of K417N genomes are being undertaken.

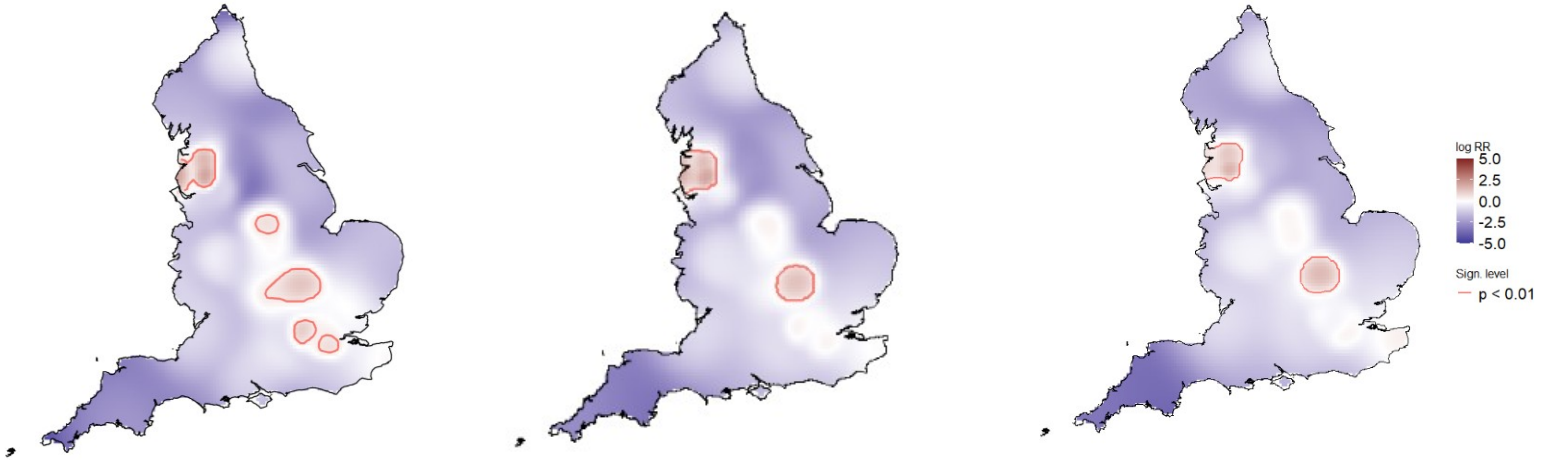
Spatial variation in risk

The spatial risk surface is estimated by comparing the smoothed intensity of cases (variants of concern) and controls (PCR-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 14 highlights areas of significantly increased risk identified for Delta and the differences between data presented in technical briefing 12 and 13. Areas where risk remains significantly are in Bedfordshire and the North West.

Figure 14. Spatial variation in risk for Delta data from 1 October 2020, excluding cases that are known to have travelled

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

a. As of 17 May 2021 **b. As of 25 May 2021** **c. As of 31 May 2021**



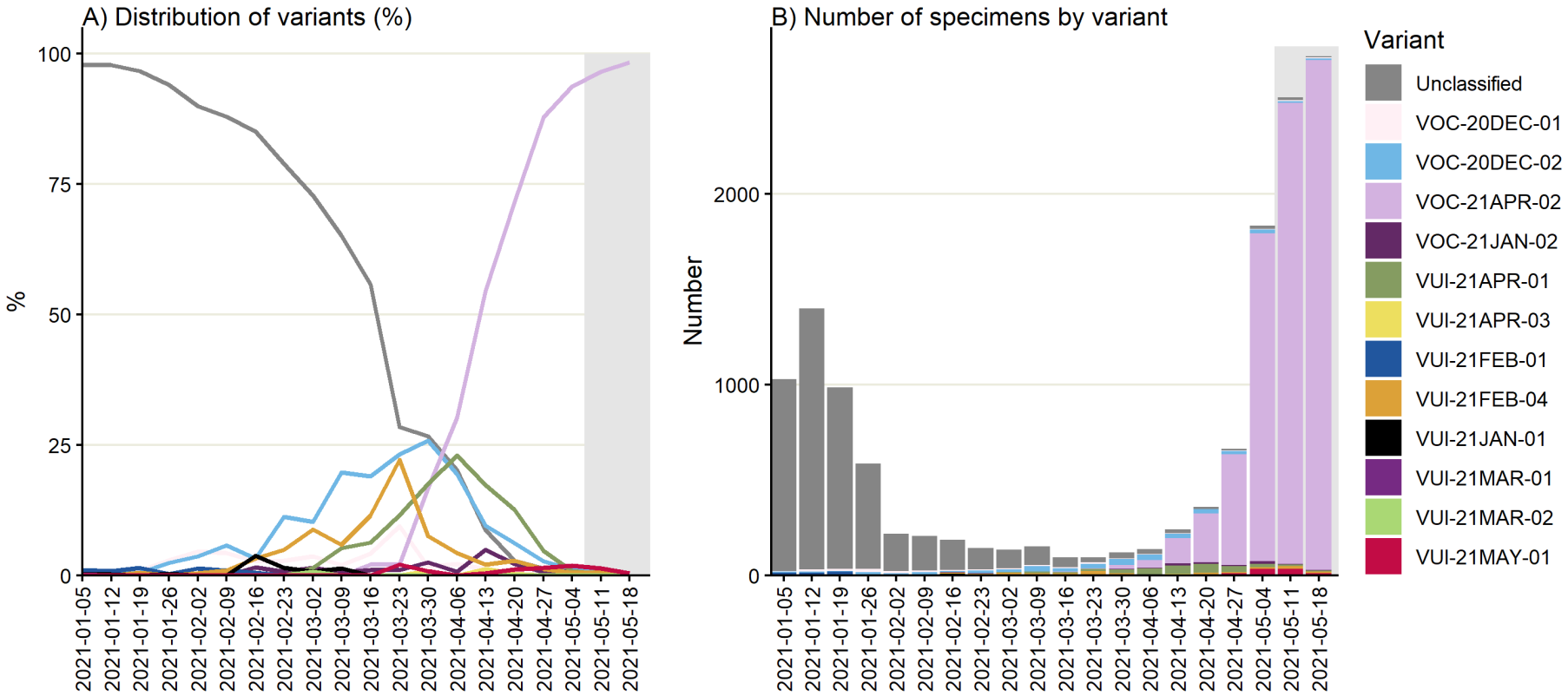
Surveillance through S gene detection

The S gene target in a 3-target assay (S, N and ORF1ab) used in some Lighthouse Laboratories is not detected in Alpha. However, this S gene is detected in Kappa, Delta and VUI-21APR-03 (B.1.617.3) variants. It is also detected in Beta 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 1 June 2021), as well as the distribution of identified variants among these specimens. Unclassified variants refer to those not currently considered a variant of concern or variant under investigation; these dominated the sequenced S gene positive specimens at the beginning of 2021 and have decreased to less than 1% since the end of April 2021. The proportion of confirmed Delta specimens among S gene positives continues to increase, and has been above 95% in the most recent 2 weeks of data (since 11 May2021). This is largely consistent across regions (Figure 16), although lower in the South West and Yorkshire and Humber where total numbers are lower. Additionally variant VUI-21MAY-01 is present in Yorkshire and Humber, which is also S gene positive. 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.

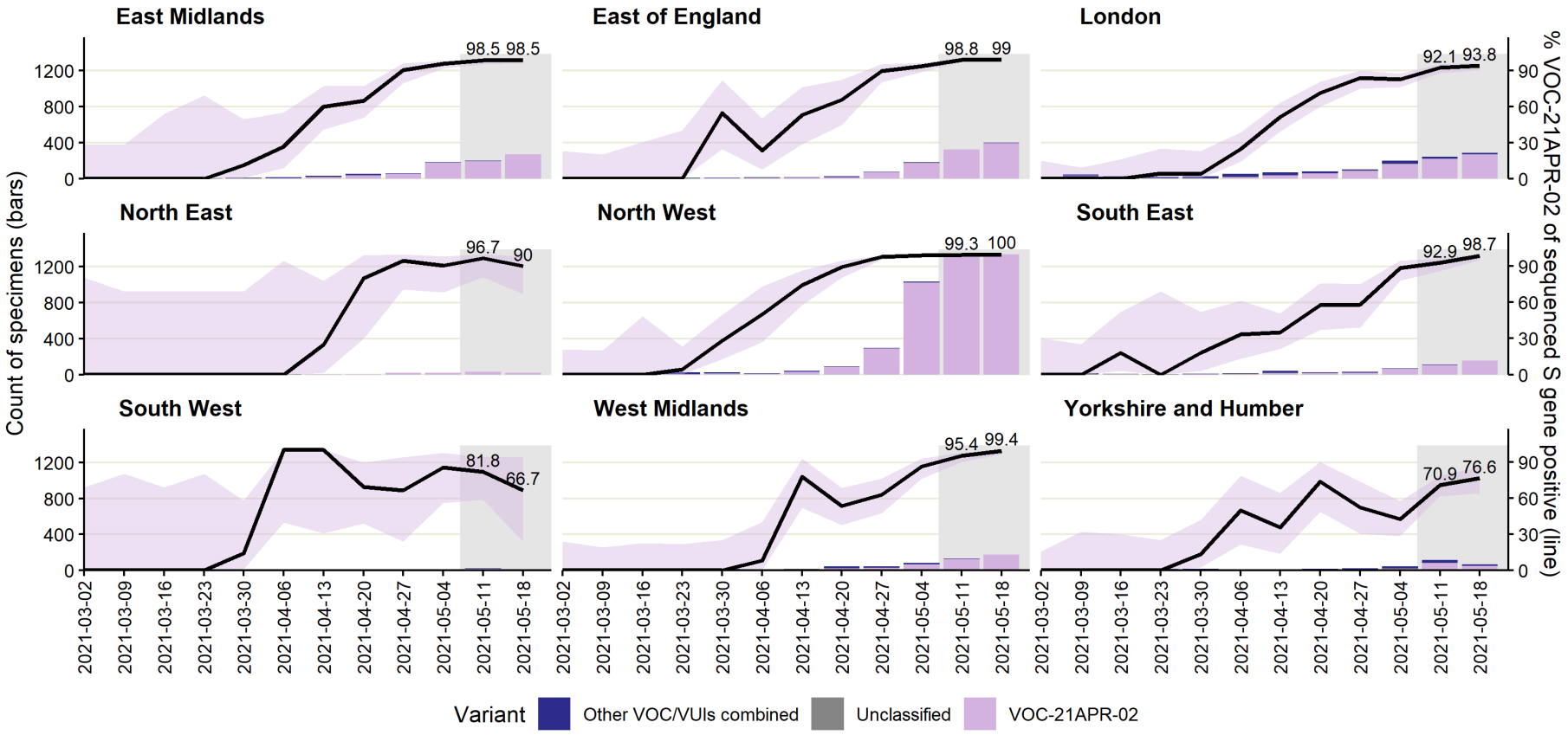
The number and proportion of S gene positive samples in England (Figure 18) has also steadily increased since mid-April, with 7600 cases reported in the week starting 25 May; 85.4% of all cases tested on the TaqPath assay and reported to PHE that week. The recent addition of Newcastle Lighthouse Laboratory to S gene surveillance is partially responsible for the absolute increase, particularly in comparison to Technical Briefing 13, with S gene data from this laboratory available since the end of April 2021. 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 and Blackburn with Darwen, 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 5 January 2021 and 23 May 2021, data as of 1 June 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).



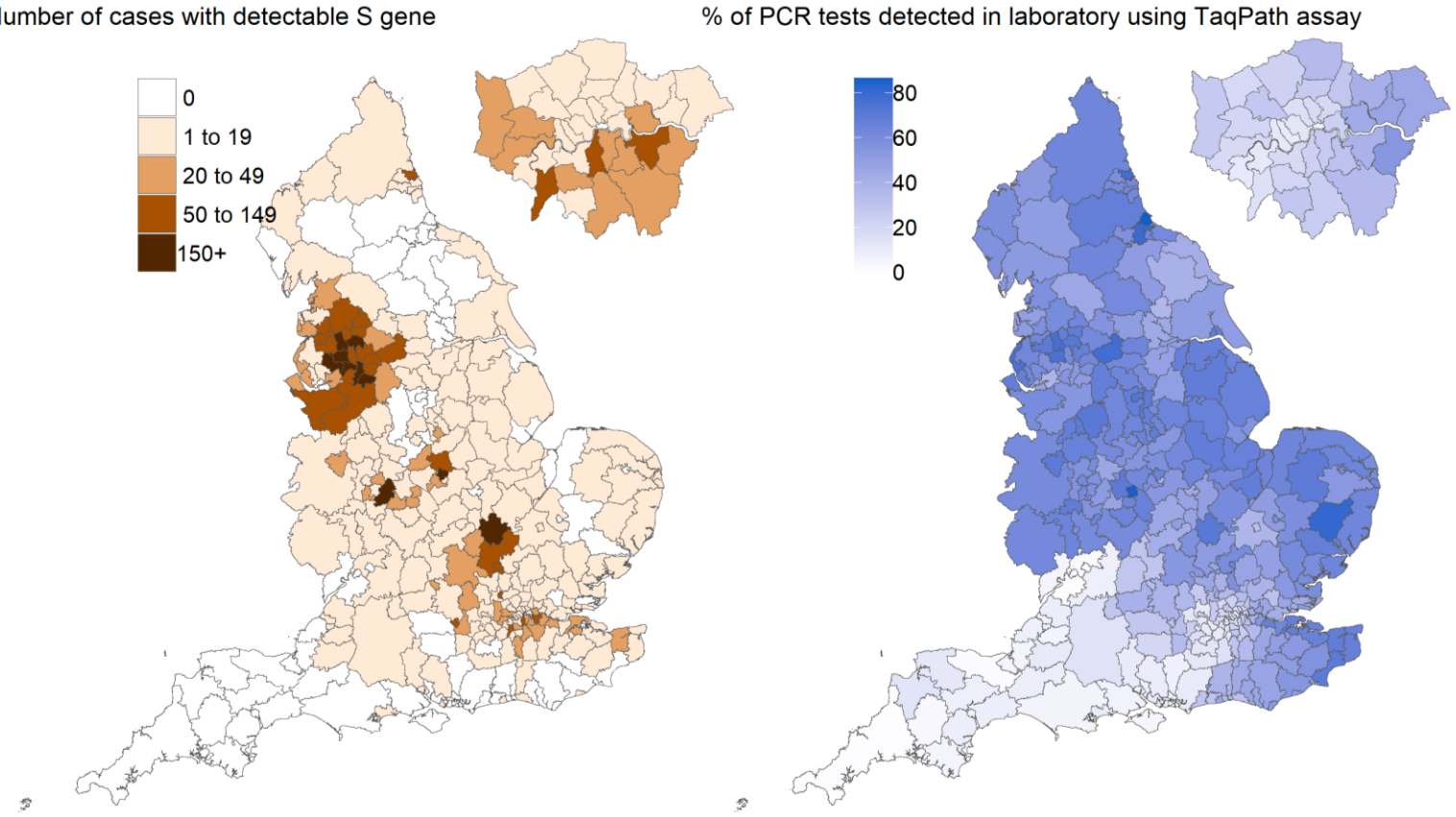
Source: SGSS and COG-UK sequencing data, restricted to sequenced positive S-gene positive tests from Newcastle, Alderley Park, Glasgow, and Milton Keynes Lighthouse Laboratories.
S gene +ve defined as positive SARS-CoV-2 test with CT values <=30 for S, N, and ORF1ab.

Figure 16. Weekly distribution of variants among sequenced S gene positive SARS-CoV-2 specimens, by region of residence. Black line represents weekly proportion of specimens that are Delta 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 2 March 2021 and 23 May 2021, data as of 1 June 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).



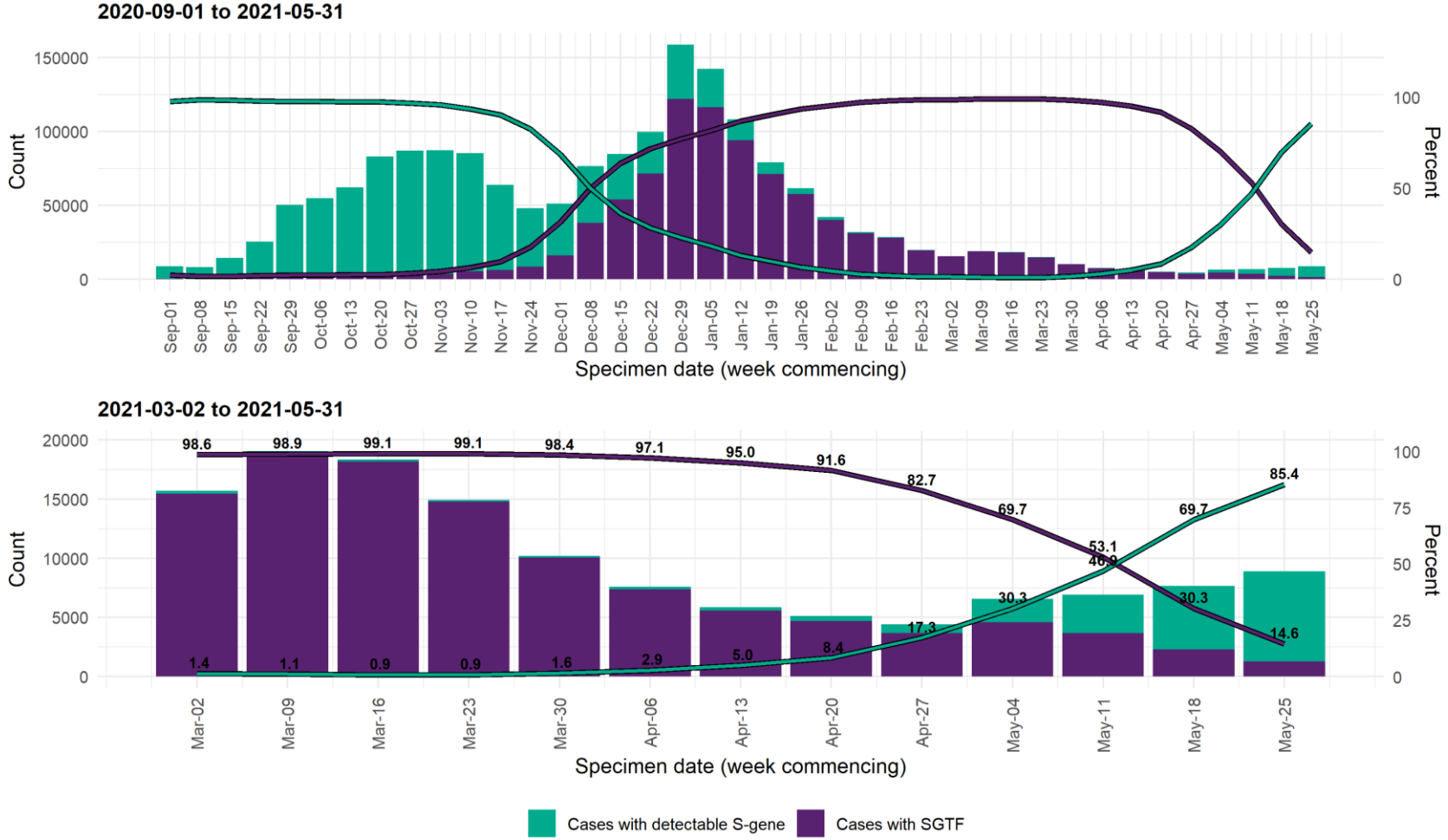
Source: SGSS and COG-UK sequencing data, restricted to sequenced positive S-gene positive tests from Newcastle, Alderley Park, Glasgow, and Milton Keynes Lighthouse Laboratories.
S gene +ve defined as positive SARS-CoV-2 test with CT values <=30 for S, N, and ORF1ab.
Patterns in sequenced S gene +ve cases may not reflect all S gene +ve cases, and S gene +ve cases are not detected uniformly across England.

Figure 17. Number of cases with detectable S gene target and TaqPath lab test coverage by local authority of residence
Specimen dates for figure 17; 22 May 2021 to 28 May 2021, data as of 1 June 2021; most recent 3 days excluded to reporting delay (Find accessible data used in this graph in underlying data).



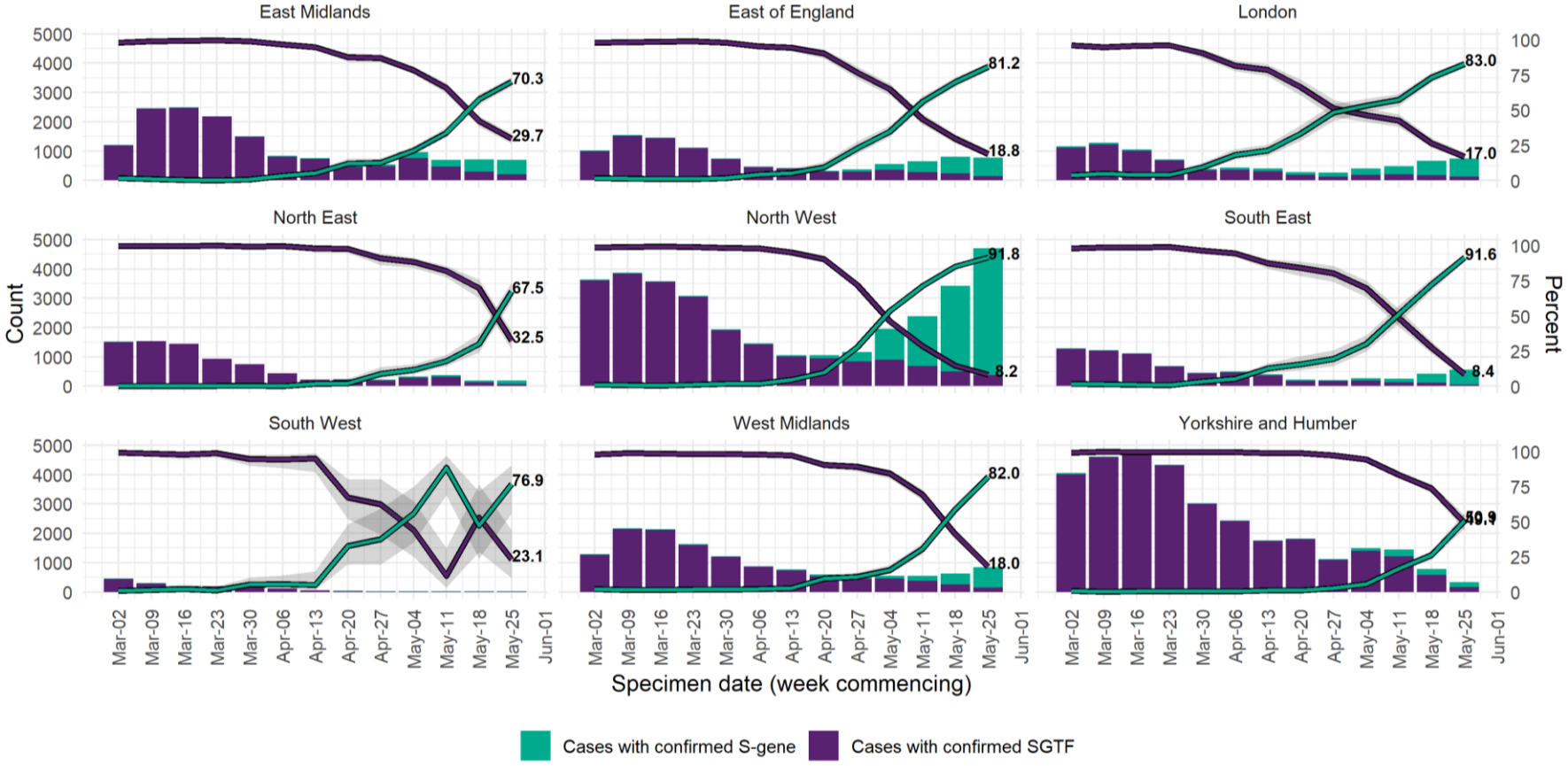
A detectable S gene (<=30 CT values for S, N, and ORF1ab genes) may currently indicate a VOC case; this continues to be monitored.
Only tests carried out with TaqPath PCR assay and with confirmed SGTF or S gene results included, from Newcastle, Alderley Park, Milton Keynes and Glasgow Lighthouse Labs.
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.

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 31 May 2021, data as of 1 June 2021 (Find accessible data used in this graph in underlying data).



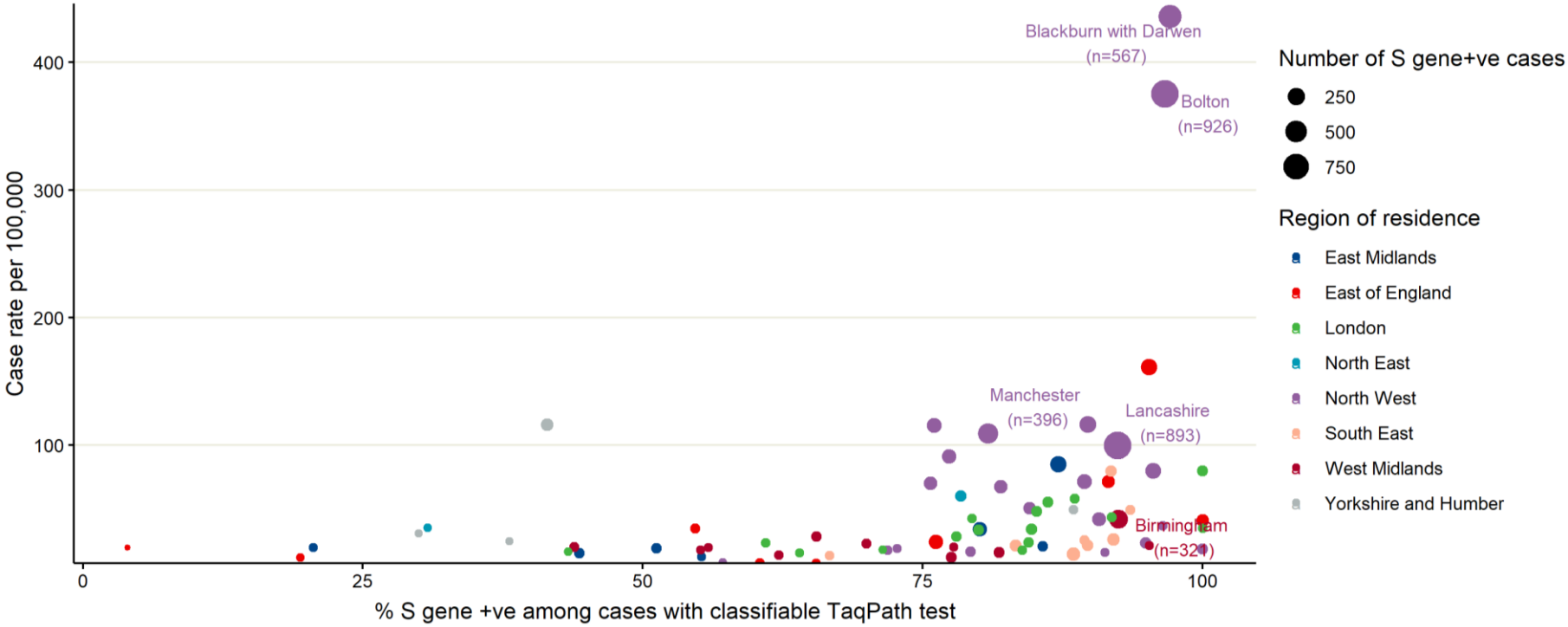
Only tests carried out with the TaqPath PCR assay and with confirmed SGTF or S gene positive results included, from Newcastle, Alderley Park, Milton Keynes and Glasgow Lighthouse Laboratories.
Case with SGTF: Positive SARS-CoV-2 test with non-detectable S gene and <=30 CT values for N and ORF1ab genes.
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. Specimen dates between 2 March 2021 and 31 May 2021, data as of 1 June 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 Newcastle, 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 221 persons, excluded from figure.

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. Specimen dates between 22 May 2021 and 28 May 2021, data as of 1 June 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).



% S gene +ve calculated out of cases with S gene detection results and tested with TaqPath PCR assay in Newcastle, Alderley Park, Milton Keynes or Glasgow Lighthouse Labs.
Total case rates include PCR and LFD positive. 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.

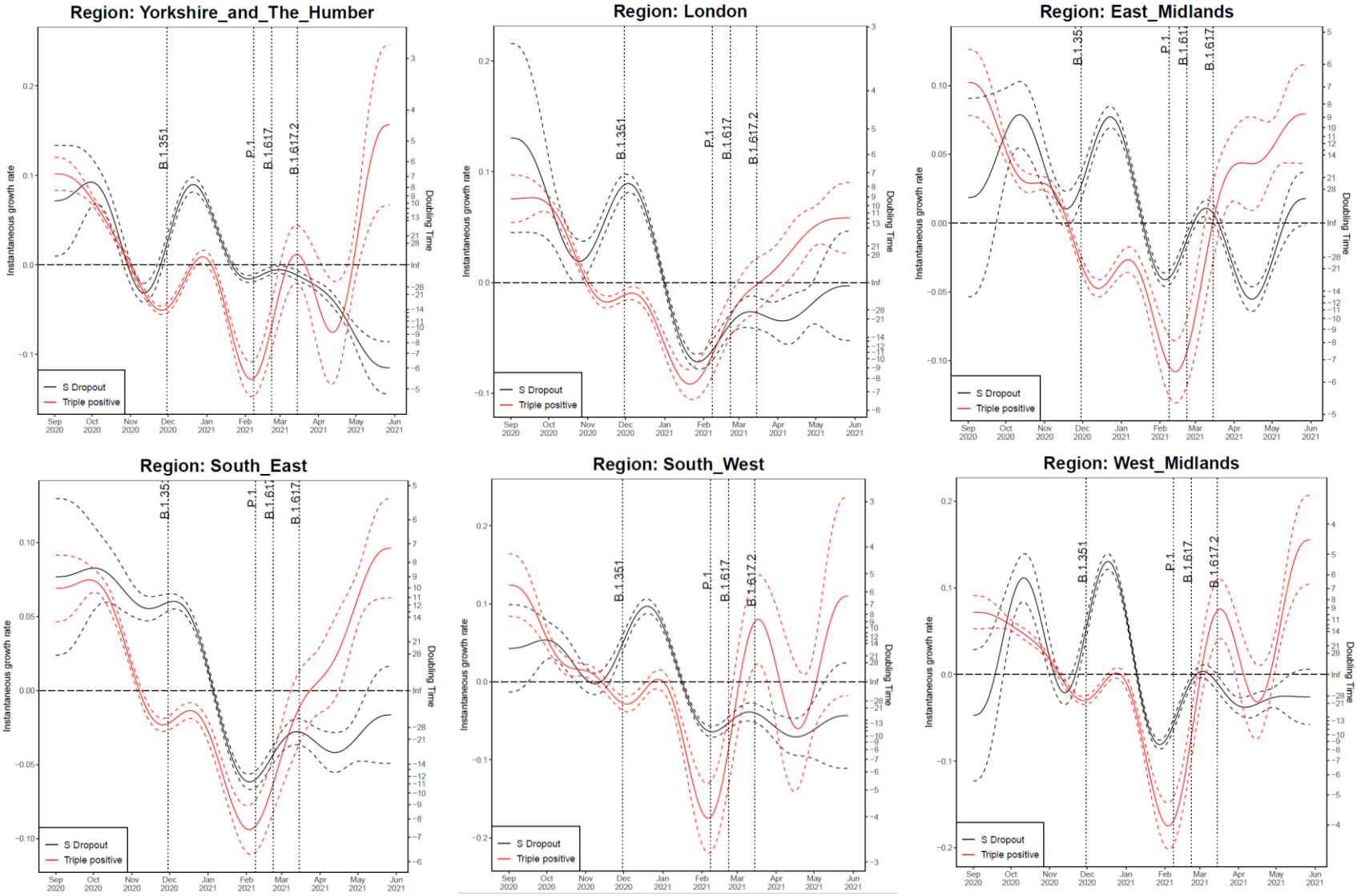
Growth rate of S gene positive and negative cases[1]

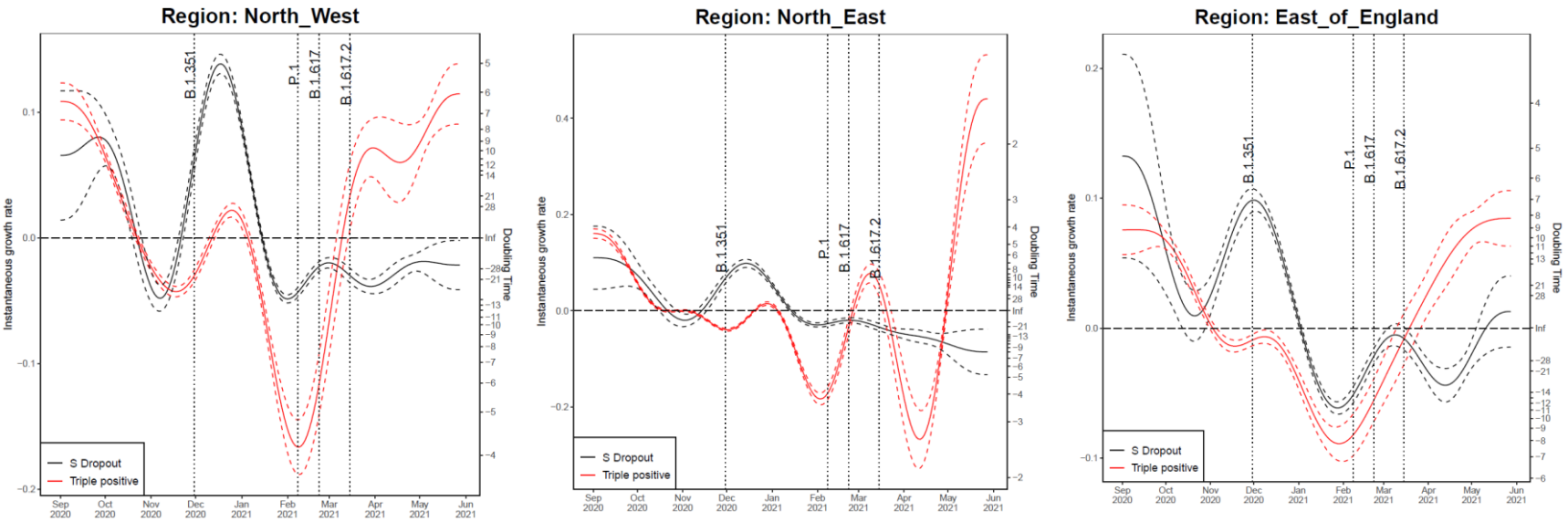
Figures 21 and 22 show growth rate and doubling time of S gene positive (all 3 PCR targets positive) and negative (S gene target failure), produced by fitting a generalized additive model with a quasi-Poisson.

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.

[1] This information is provided by the Joint Biosecurity Centre

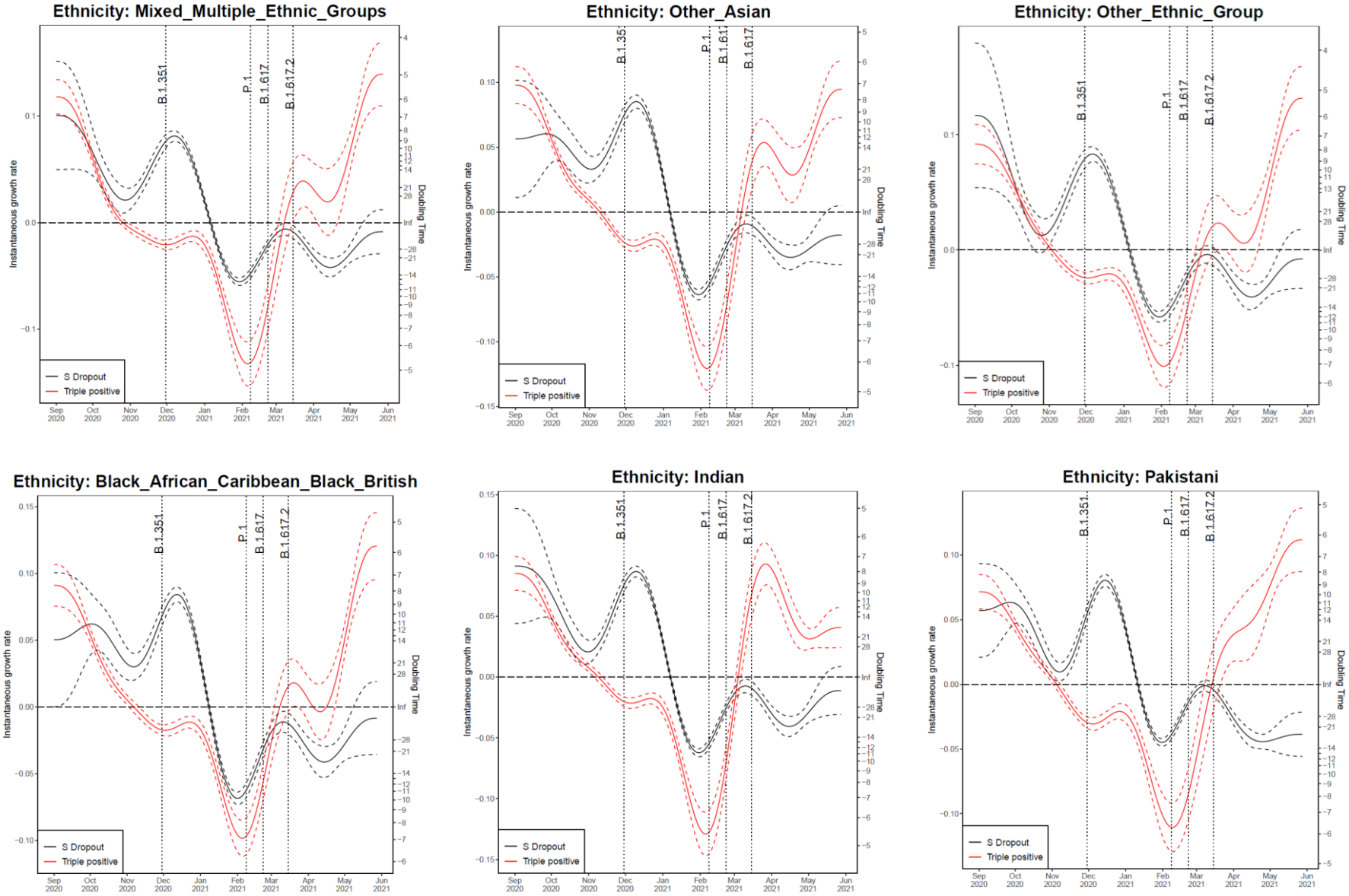
Figure 21. Growth rate and doubling time of S gene positive and negative cases by region as of 31 May 2021

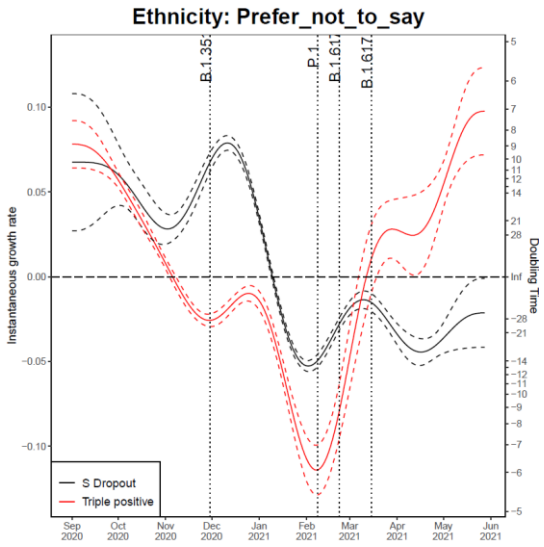


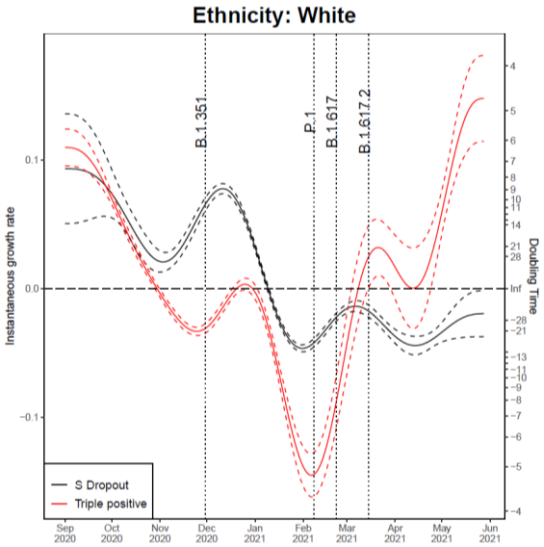


The growth rate for cases with all 3 PCR targets positive (S+) has been increasing over the course of April and May in all regions. There is very rapid growth in S+ (doubling times <7 days) in the North West and West Midlands, where PCR target data coverage is good. There is also rapid growth in the South East and East of England (doubling times around a week) and London (doubling times around 2 weeks). In Yorkshire and The Humber, the North East, South West, there is very rapid growth, but PCR target data coverage is lower overall in these regions, and confidence intervals are wide, particularly in the South West. There have also been changes in the proportion of PCR tests with PCR target data, particularly in the North East, which may artificially inflate growth. 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 31 May 2021







The growth rate for cases with all 3 PCR targets positive has been increasing over the course of April and May in most ethnicities, to around 5 to 7 days. The growth rates for the Indian ethnicity appear to have now plateaued at around 21 days.
(Find accessible data used in this graph in underlying data).

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.

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, Emergency Care Data Set (ECDS), and the PHE Case and Incident Management System (CIMS). 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

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Public Health Scotland and EAVE group
Contributions from the Variant Technical Group Members

Variant Technical Group members and contributors

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Acknowledgements

The authors are grateful to those teams and groups providing data for these analyses including: the Lighthouse Laboratories, NHS, COG-UK, the Wellcome Sanger Institute, Health Protection Data Science teams, the Joint Biosecurity Centre and the Genotype to Phenotype Consortium.

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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Published: June 2021
PHE gateway number: GOV-8530

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