Public Health England

Protecting and improving the nation's health

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

Technical briefing 16

18 June 2021

This briefing provides an update on previous briefings up to 11 June 2021

Contents

Summary

There are 4 current variants of concern and 8 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:

- by combining genotyping and sequencing, more than 80% of cases in England now have a variant test undertaken
- the most recent data show that the Delta variant comprises 91% of sequenced cases
- deaths are now presented for those cases which have completed the 28-day follow-up period – the crude case fatality rate remains lower for Delta than other variants at present; however, mortality is a lagged indicator, which means that the number of cases who have completed 28 days of follow up is very low – therefore, it is too early to provide a formal assessment of the case fatality of Delta, stratified by age, compared to other variants
- secondary attack rates remain higher for Delta than Alpha – a small reduction in secondary attack rates is observed for Delta in recent weeks
- current evidence suggests vaccine effectiveness against hospitalisation is maintained for Delta
- the most common settings for reported exposures were education settings, for both Alpha and Delta variants – in the latest week presented, hospitality settings were a larger proportion of all common exposures reported by cases with both Alpha and Delta variants, and the proportion of common exposures related to travel also increased

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

As Delta is now the dominant variant in the UK, epidemiological data in the weekly surveillance report is also relevant and is available.

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.

WHO nomenclature as of 31 May 2021 is incorporated. A table incorporating WHO and UK designations and Pango lineages is provided (Table 1); thereafter variants are referred to using their WHO designation where this exists, and the UK designation where it does not.

Technical Briefing 16 includes variant diagnoses made both by whole-genome sequencing and by a genotyping PCR test, including the categorisation of confirmed and probable variant results and a rules-based decision algorithm (RBDA) to identify variant and mutation (VAM) profiles from genotype assay mutation profiles. Genotyping is used to identify variants Alpha, Beta, Delta and Gamma; targets were updated in mid-May 2021 to prioritise accurate identification of Delta over Alpha.

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 4, case numbers are also updated online. Tables 5 and 6 show hospitalisation and death data. Figure 2 shows cumulative cases of variants over time.

Table 1. Variant lineage and designation as of 14 June 2021 (provisionally extinct variants removed)

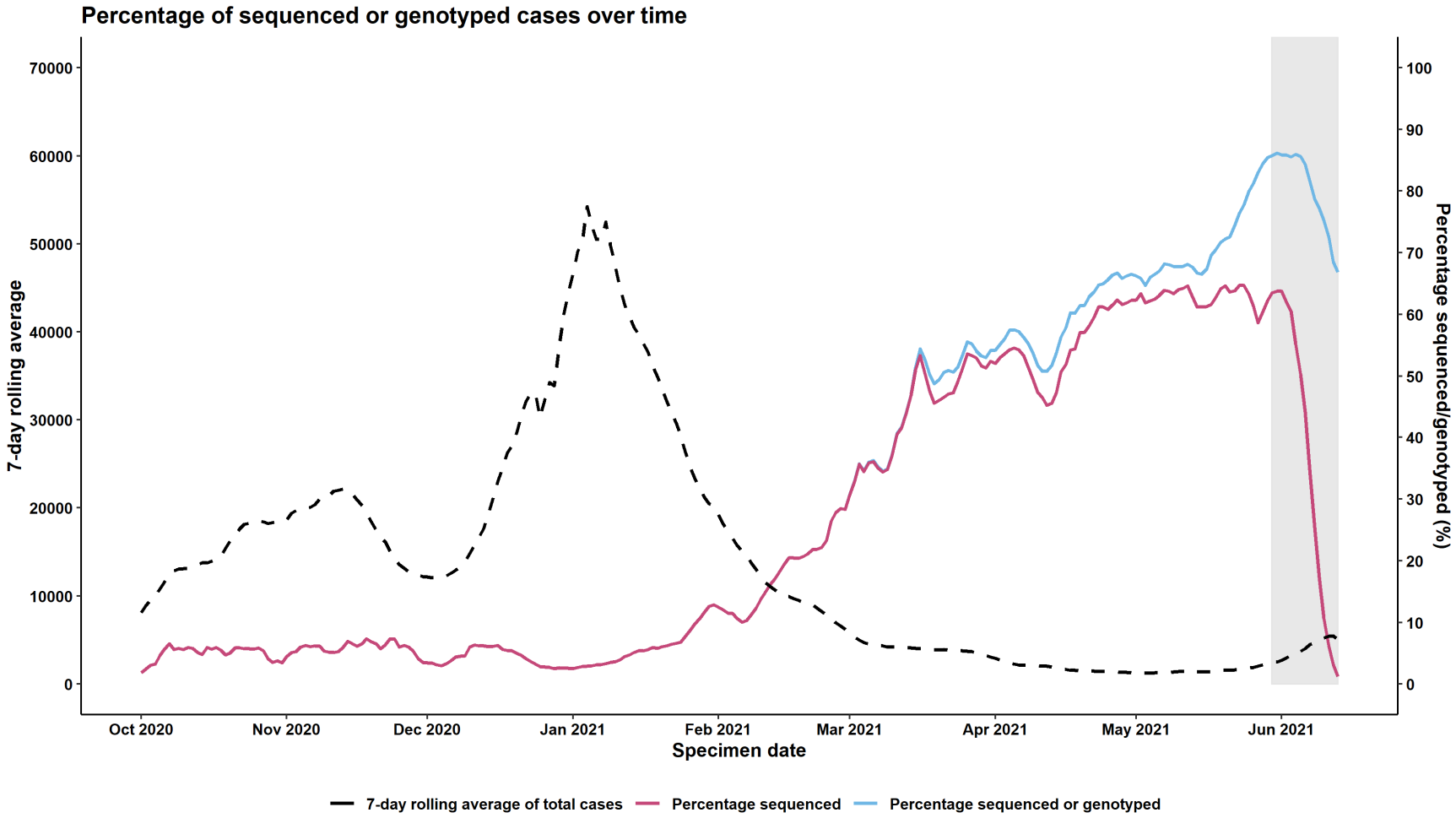
World Health Organization nomenclature as of 14 June 2021	Lineage	Designation	Status
Alpha	B.1.1.7	VOC-20DEC-01	VOC
Beta	B.1.351	VOC-20DEC-02	VOC
Gamma	P.1	VOC-21JAN-02	VOC
Delta	B.1.617.2, AY.1 and AY.2	VOC-21APR-02	VOC
Zeta	P.2	VUI-21JAN-01	VUI
Eta	B.1.525	VUI-21FEB-03	VUI
	B.1.1.318	VUI-21FEB-04	VUI
Theta	P.3	VUI-21MAR-02	VUI
Kappa	B.1.617.1	VUI-21APR-01	VUI
	B.1.617.3	VUI-21APR-03	VUI
	AV.1	VUI-21MAY-01	VUI
	C.36.3	VUI-21MAY-02	VUI
	B.1.1.7 with E484K	VOC-21FEB-02	*Monitoring
Epsilon	B.1.427/B.1.429		Monitoring

World Health Organization nomenclature as of 14 June 2021	Lineage	Designation	Status
	B.1.1.7 with S494P		Monitoring
	A.27		Monitoring
Iota	B.1.526		Monitoring
	B.1.1.7 with Q677H		Monitoring
	B.1.620		Monitoring
	B.1.214.2		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
	Lineage A with R346K, T478R and E484K		Monitoring
Lambda^	C.37		Monitoring

*VOC-21FEB-02 (B.1.1.7 with E484K). This specific clade of B.1.1.7 with E484K has not been detected in England since 1 March 2021. There is apparent transmission outside the UK based on international sequence data. It is no longer included in the data update but monitoring of international data continues.
^Designated as Variant of Interest by WHO, 14 June 2021.

Sequencing coverage

Figure 1. Coverage of sequencing: percentage of SARS-CoV-2 cases sequenced or genotyped over time as of 14 June 2021. (Find accessible data used in this graph in underlying data)



Data extract from 14 June 2021; data from 01 October 2020 to 13 June 2021.
Grey shading was applied to the previous 14 days to account for reporting delays in sequencing 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 the fifth reported case.

Table 2. Number of confirmed (sequencing) and probable (genotyping) cases by variant as of 14 June 2021

Variant	Confirmed (sequencing) case number	Probable (genotyping) case number*	Total case number	Case Proportion*	Deaths	Case Fatality	Cases with 28 day follow up	Deaths among those with 28 day follow up	Case Fatality among those with 28 day follow up
Alpha	218,332	5,689	224,021	77.9%	4,259	1.9% (1.8 to 2.0%)	217,228	4,252	2.0% (1.9 to 2.0%)
Beta	871	55	926	0.3%	13	1.4% (0.7 to 2.4%)	858	13	1.5% (0.8 to 2.6%)
Delta	31,132	29,523	60,655	21.1%	73	0.1% (0.1 to 0.2%)	5,762	17	0.3% (0.2 to 0.5%)
Eta	441	0	441	0.2%	12	2.7% (1.4 to 4.7%)	428	12	2.8% (1.5 to 4.8%)
Gamma	170	42	212	0.1%	0	0.0% (0.0 to 1.7%)	155	0	0.0% (0.0 to 2.4%)
Kappa	422	0	422	0.1%	1	0.2% (0.0 to 1.3%)	404	1	0.2% (0.0 to 1.4%)
Theta	7	0	7	0.0%	0	0.0% (0.0 to 41.0%)	5	0	0.0% (0.0 to 52.2%)

Variant	Confirmed (sequencing) case number	Probable (genotyping) case number*	Total case number	Case Proportion*	Deaths	Case Fatality	Cases with 28 day follow up	Deaths among those with 28 day follow up	Case Fatality among those with 28 day follow up
VOC-21FEB-02	45	0	45	0.0%	1	2.2% (0.1 to 11.8%)	44	1	2.3% (0.1 to 12.0%)
VUI-21APR-03	13	0	13	0.0%	0	0.0% (0.0 to 24.7%)	12	0	0.0% (0.0 to 26.5%)
VUI-21FEB-01	79	0	79	0.0%	2	2.5% (0.3 to 8.8%)	78	1	1.3% (0.0 to 6.9%)
VUI-21FEB-04	266	0	266	0.1%	1	0.4% (0.0 to 2.1%)	229	1	0.4% (0.0 to 2.4%)
VUI-21MAR-01	2	0	2	0.0%	0	0.0% (0.0 to 84.2%)	2	0	0.0% (0.0 to 84.2%)
VUI-21MAY-01	166	0	166	0.1%	1	0.6% (0.0 to 3.3%)	111	0	0.0% (0.0 to 3.3%)
VUI-21MAY-02	126	0	126	0.0%	0	0.0% (0.0 to 2.9%)	111	0	0.0% (0.0 to 3.3%)
Zeta	54	0	54	0.0%	1	1.9% (0.0 to 9.9%)	53	1	1.9% (0.0 to 10.1%)

*Genotyping is used to identify variants Alpha, Beta, Delta and Gamma; targets were updated in mid-May 2021 to prioritise accurate identification of Delta over Alpha

Table 3. Attendance to emergency care and deaths among all COVID-19 cases (sequencing and genotyping) in England, 1 February 2021 to 14 June 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	148,513	5,584	3.8	7,929	5.3	10,228	6.9	2,929	1.9	4,447	3.0	1,614	1.1
Beta	721	56	7.8	37	5.1	47	6.5	12	1.7	23	3.2	8	1.1
Gamma	212	51	24.1	8	3.8	8	3.8	1	0.5	1	0.5	0	NA
Delta	60,624	53,177	87.7	1,555	2.6	2,176	3.6	488	0.8	806	1.3	73	0.1
Zeta	24	0	NA	1	4.2	1	4.2	1	4.2	1	4.2	0	NA
Eta	387	9	2.3	15	3.9	20	5.2	6	1.6	9	2.3	6	1.6
VUI-21FEB-04	259	30	11.6	7	2.7	11	4.2	1	0.4	3	1.2	1	0.4
Theta	7	1	14.3	1	14.3	1	14.3	0	NA	0	NA	0	NA
Kappa	422	11	2.6	14	3.3	15	3.6	3	0.7	4	1.0	1	0.2

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-21APR-03	13	0	N/A	0	NA	0	NA	0	NA	0	NA	0	NA
VUI-21MAY-01	166	45	27.2	1	0.6	2	1.2	0	NA	1	0.6	1	0.6
VUI-21MAY-02	126	11	8.7	6	4.8	7	5.6	2	1.6	2	1.6	0	NA

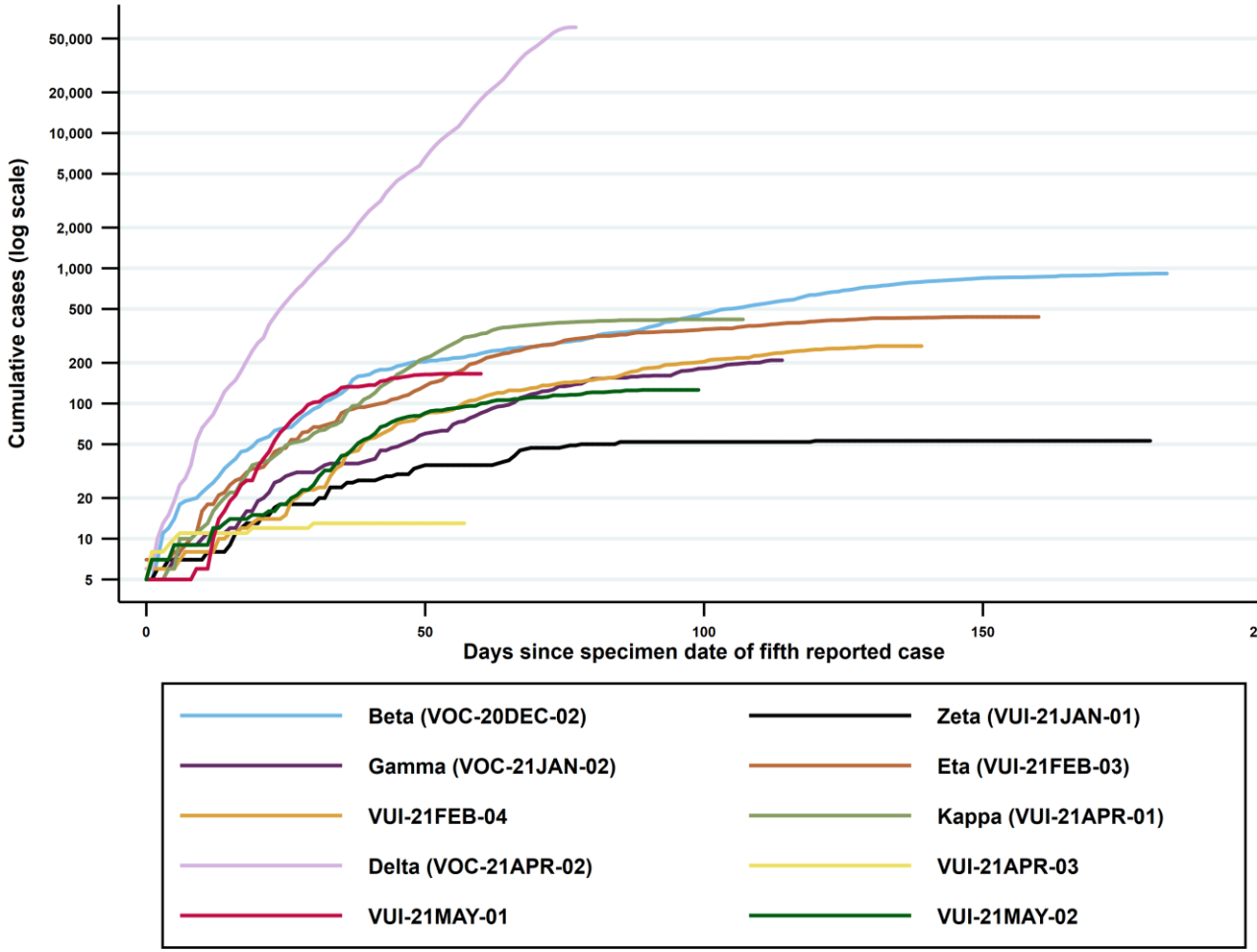
Table 4. Attendance to emergency care and deaths by vaccination status among Delta confirmed cases (sequencing and genotyping) in England, 1 February 2021 to 14 June 2021.

	Total	Cases with specimen date in past 28 days*	Unlinked	Unvaccinated	<21 days post dose 1	≥21 days post dose 1	≥14 days post dose 2
Delta cases since 1 Feb 2021 ¥	60,624	53,177	7,461	35,521	4,094	9,461	4,087
Cases with an A&E visit§ (excluding cases with the same specimen and attendance dates)‡	1,555	NA	14	1,038	116	285	102
Cases with an A&E visit§ (including cases with the same specimen and attendance dates)	2,176	NA	24	1,446	155	378	173
Cases where presentation to A&E resulted in overnight inpatient admission§ (excluding cases with the same specimen and admission dates)‡	488	NA	7	324	30	87	40
Cases where presentation to A&E resulted in overnight inpatient admission§ (including cases with the same specimen and admission dates)	806	NA	10	527	50	135	84
Deaths^	73	NA	2	34	1	10	26

Data sources: Emergency care 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 Emergency Care 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 1 attendance or admission within 28 days of positive specimen date
‡ Cases where specimen date is the same as date of Emergency Care 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 Emergency Care visit. Some of the cases detected on the day of admission may have attended for a diagnosis unrelated to COVID-19.
^ 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 14 June 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 changes in the use of genotyping over time should be considered when interpreting the prevalence incorporating genotypes. The ‘Other’ category in Figure 3 to 5 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 dataset used for this assessment includes enhanced testing and sequencing from individuals who have travelled, and surge testing and sequencing in outbreak areas. Sequencing numbers and coverage fall in the last week shown due partly to sequencing lag time, and new sequences are still being produced relating to sample dates in that week. The supplementary data for figures are available.

Figure 3. Variant prevalence for all England available sequenced cases from 1 February 2021 as of 14 June 2021 (excluding 48 cases where the specimen date was unknown). (Find accessible data used in this graph in underlying data).

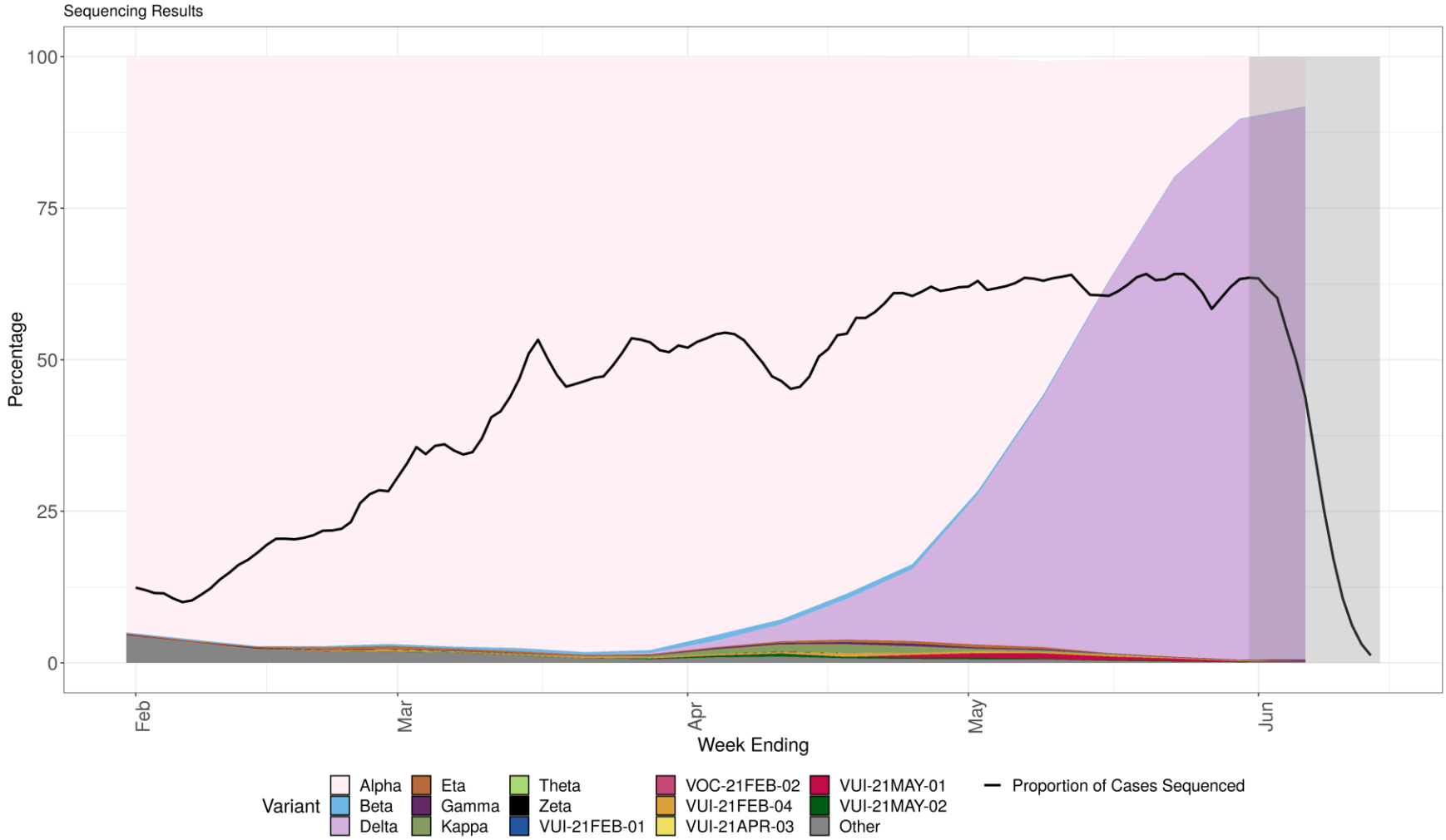


Figure 4. Variant prevalence from 1 February 2021 as of 14 June 2021 by region for all sequenced cases in England (excluding 744 cases where the region or specimen date were unknown). (Find accessible data used in this graph in underlying data).

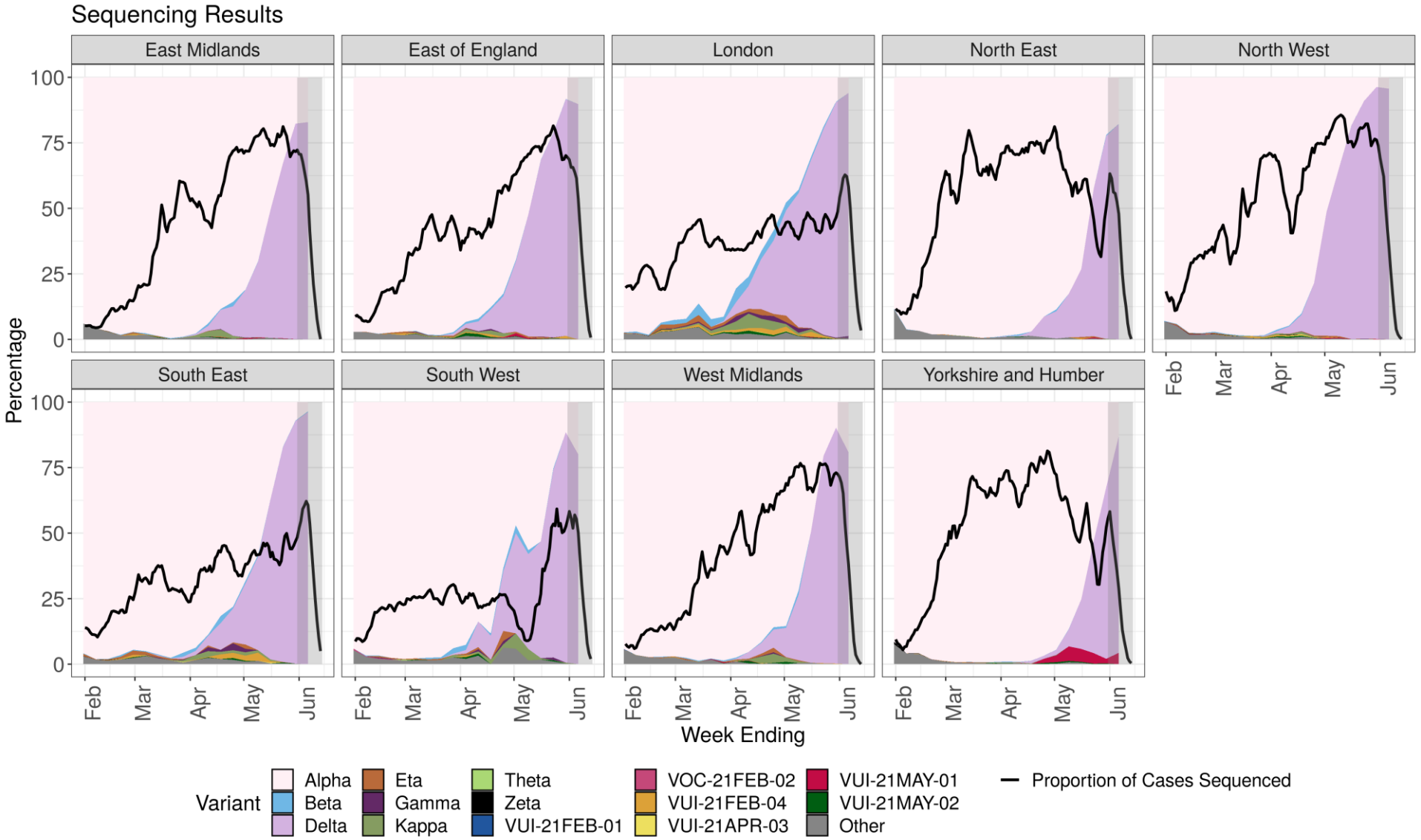
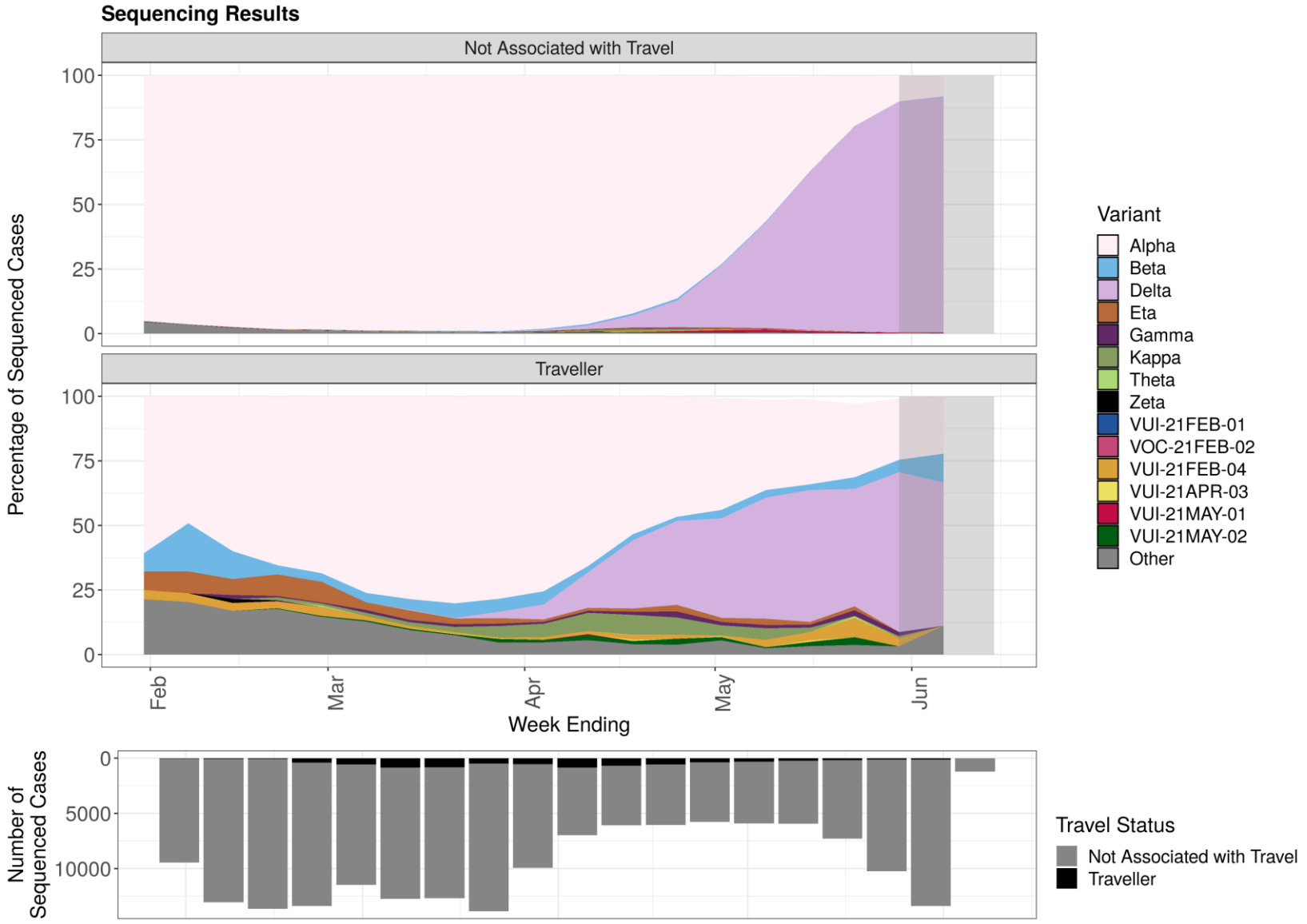


Figure 5. Prevalence of variants over time: all sequenced cases in England, split by travel status as of 14 June 2021 (excluding 428 cases where the specimen date or travel status is unknown). Travel-linked variant data available until 7 June 2021 only. (Find accessible data used in this graph in underlying data).



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. The total number of sequencing cases in each week is shown in the bars below, split by travel status. (Find accessible data used in this graph in underlying data).

Secondary attack rates

This section includes secondary attack rates for traveller and non-traveller cases, and separate household contact rates, including new analysis of rates for household and non-household contacts of non-traveller cases over time for Delta and Alpha variants.

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. Variant cases are identified using confirmed (sequencing) results as at 7 June 2021 supplemented with probable (genotyping) results as at 8 June 2021, and exclude LQ-HRG results.

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 8 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 25 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 8 covering 5 January 2021 to 25 May 2021.

Secondary attack rates for contacts of cases with Delta and no travel history are higher than those for contacts of cases with Alpha and no travel history: 11.4% (95% CI 11.1% to 11.7%) compared to 8.0% (95% CI 7.8% 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 Delta were higher than those for travel cases with Alpha.

Table 9 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 25 May 2021. Secondary attack rates for contacts of non-travel cases with 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 10 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 25 May 2021 as in Table 8. 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 8.

Figure 6 shows the secondary attack rates amongst household and non-household contacts of non-travel cases with Delta and Alpha over time for the period 29 March 2021 to 23 May 2021, with 95% confidence intervals. The estimate of secondary attack rate for household contacts of cases with Delta has fallen over the last 4 weeks of reporting, from 16.8% (95% CI 15.1% to 18.7%) for exposure events in week commencing 26 April 2021 to 11.8% (95% 11.3% to 12.3%) for exposure events in week commencing 17 May 2021. Over the period presented, secondary attack rates for both household and non-household contacts of cases with Delta remain higher than for Alpha (or other cases). A peak in secondary attack rates from cases with Delta was seen in both household and non-household contacts exposed during the week commencing 26 April 2021, while secondary attack rates from cases with Alpha were stable compared to earlier and later weeks.

Table 5. 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 25 May 2021, variant data as at 7 June 2021, contact tracing data as at 15 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	2,070 (70.0% with contacts)	38,284 (82.5% with contacts)	5.1%	1.5% (1.3% to 1.6%) [516/35,092]	8.0% (7.8% to 8.1%) [8,102/101,787]
Kappa	186 (76.3% with contacts)	136 (79.4% with contacts)	57.8%	2.0% (1.6% to 2.5%) [62/3,107]	10.7% (7.8% to 14.5%) [36/336]
Delta	724 (69.8% with contacts)	15,394 (84.3% with contacts)	4.5%	2.3% (2.0% to 2.5%) [268/11,910]	11.4% (11.1% to 11.7%) [5,118/44,745]
VUI-21APR-03	6 (16.7% with contacts)	5 (100.0% with contacts)	54.5%	Unavailable [0/201]	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 until 25 May 2021 in order to allow time for contacts to become cases, hence case counts are lower than other sources. Probable (genotyping) results are included, low quality genomic results are not.

Table 6. Secondary attack rates for all variants (excluding B.1.617 variants)
(5 January 2021 to 25 May 2021, variant data as at 7 June 2021, contact tracing data as at 15 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	4,264 (76.8% with contacts)	179,563 (75.0% with contacts)	2.3%	1.6% (1.5% - 1.7%) [1,243/78,032]	9.7% (9.6% - 9.8%) [37,109/383,194]
Beta	315 (72.1% with contacts)	392 (67.3% with contacts)	44.6%	2.1% (1.8% - 2.5%) [109/5,171]	8.8% (7.1% - 10.9%) [77/874]
Zeta	4 (75.0% with contacts)	29 (79.3% with contacts)	12.1%	Unavailable [0/160]	8.2% (3.6% - 17.8%) [5/61]
Gamma	67 (67.2% with contacts)	89 (74.2% with contacts)	42.9%	1.1% (0.6% - 2.1%) [9/806]	10.6% (7.2% - 15.4%) [23/217]
Eta	192 (70.3% with contacts)	196 (73.0% with contacts)	49.5%	1.2% (0.9% - 1.5%) [47/4,076]	8.5% (6.1% - 11.7%) [32/377]
VUI-21FEB-04	98 (68.4% with contacts)	140 (78.6% with contacts)	41.2%	0.5% (0.3% - 0.8%) [16/3,054]	8.5% (6.0% - 12.0%) [28/329]
Theta	5 (40.0% with contacts)	1 (100.0% with contacts)	83.3%	Unavailable [0/5]	Unavailable [0/3]

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-21MAY-01	2 (0.0% with contacts)	136 (84.6% with contacts)	1.4%	Unavailable [0/0]	5.8% (4.0% - 8.4%) [25/432]
VUI-21MAY-02	61 (73.8% with contacts)	47 (80.9% with contacts)	56.5%	0.9% (0.5% - 1.6%) [11/1,248]	7.5% (3.8% - 14.1%) [8/107]

Note legend from Table 5. Data provided is for period until 25 May 2021 in order to allow time for contacts to become cases, hence case counts are lower than other sources. Probable (reflex PCR) results are included, low quality genomic results are not.

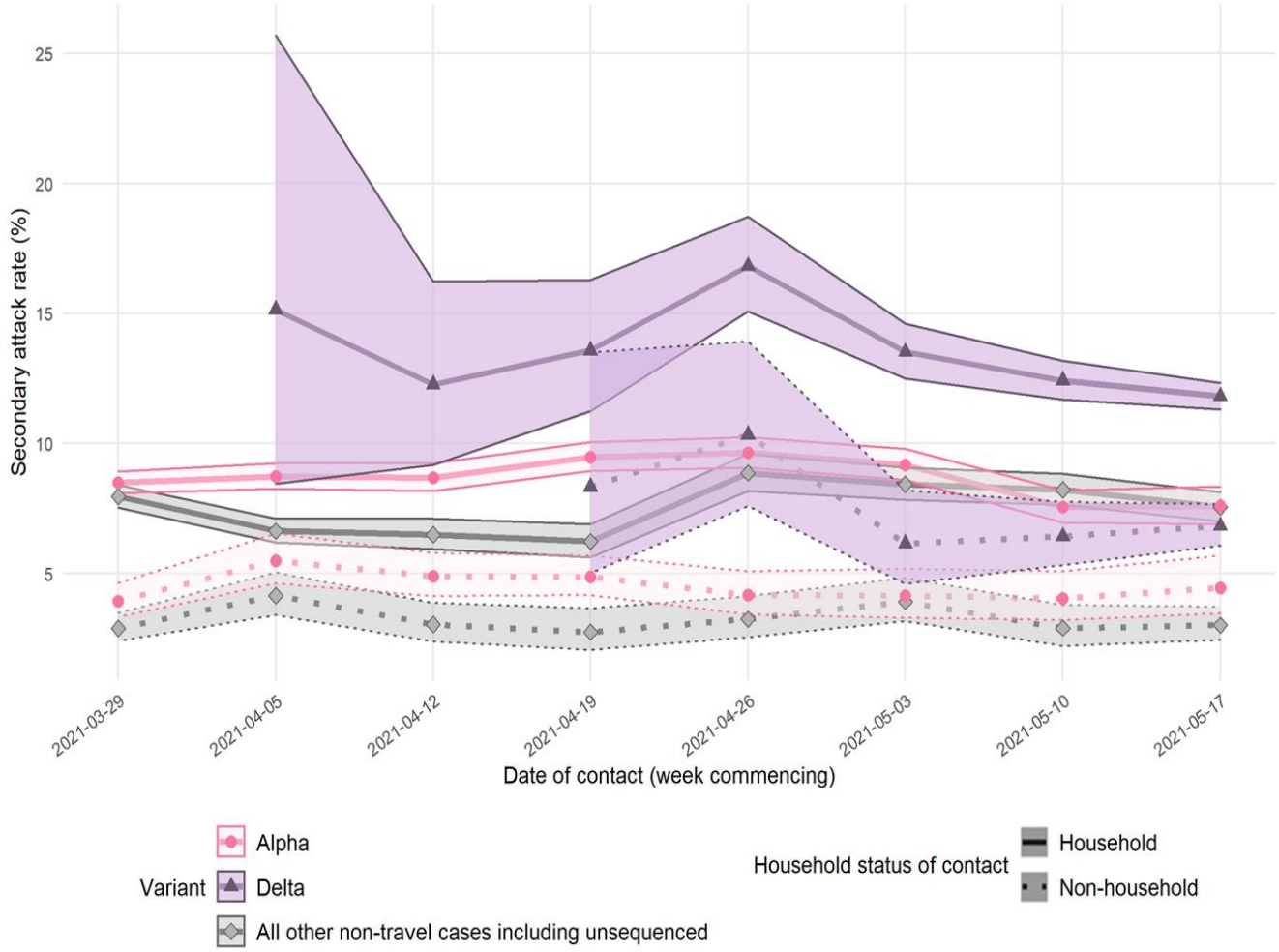
Table 7. Secondary attack rates for household contacts of non-travel cases of Alpha and Delta
(29 March 2021 to 25 May 2021, variant data as at 7 June 2021, contact tracing data as at 15 June 2021)

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	38,284 (80.4% with household, 18.3% with non-household contacts)	8.7% (8.5% - 8.9%) [7,264/83,150]	4.5% (4.2% - 4.8%) [838/18,637]
Delta	15,394 (82.3% with household, 18.0% with non-household contacts)	12.4% (12.1% - 12.7%) [4,566/36,804]	7.0% (6.4% - 7.5%) [552/7,941]

Note legend from Table 5. Data provided is for period until 25 May 2021 in order to allow time for contacts to become cases, hence case counts are lower than other sources. Probable (reflex PCR) results are included, low quality genomic results are not.

Figure 6. Secondary attack rates amongst household and non-household contacts of non-travel cases of Alpha, Delta and all others including unsequenced cases, with 95% confidence intervals

(29 March 2021 to 23 May 2021, variant data as at 7 June 2021, contact tracing data as at 15 June 2021). (Find accessible data used in this graph in underlying data).



Note legend from Table 5. Secondary attack rates are suppressed when count of contacts is less than 50 or count of exposing cases is less than 20. Data provided is for period until 23 May 2021 in order to allow time for contacts to become cases and complete weeks to be shown. Probable (reflex PCR) results are included, low quality genomic results are not.

Surveillance of reinfections

The COVID-19 reinfection surveillance programme aims to look at how long immunity lasts, protection against clinical disease (disease with symptoms) and protection against more severe disease. It is also important to understand whether those who become reinfected can pass the virus on to other people.

Figure 7 shows the weekly rate of possible COVID-19 reinfections with cumulation of first infections becoming eligible for reinfection and total first positives.

Individuals who have 2 positive detections (with PCR and/or lateral flow devices 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 8 shows the total number of sequences available from first and second episodes of infection in possible reinfection cases, categorized by variant. Figure 8 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 8. Number of sequenced reinfection cases and the variant assigned
(Data as of 14 June 2021). These numbers include cases where a sequence is available for both a first and second reinfection.

Variant	Total
Alpha	646
Beta	1
Zeta	0
VOC-21FEB-02	1
Eta	2
VUI-21FEB-04	2
Kappa	2
Delta	311
VUI-21APR-03	0
VUI-21MAY-01	2
VUI-21MAY-02	0
Total sequenced	1,260

Figure 7. The weekly rate of possible COVID-19 reinfections with cumulation of first infections becoming eligible for reinfection and total first positives (England, week 2021 to 2022) (Find accessible data used in this graph in underlying data).

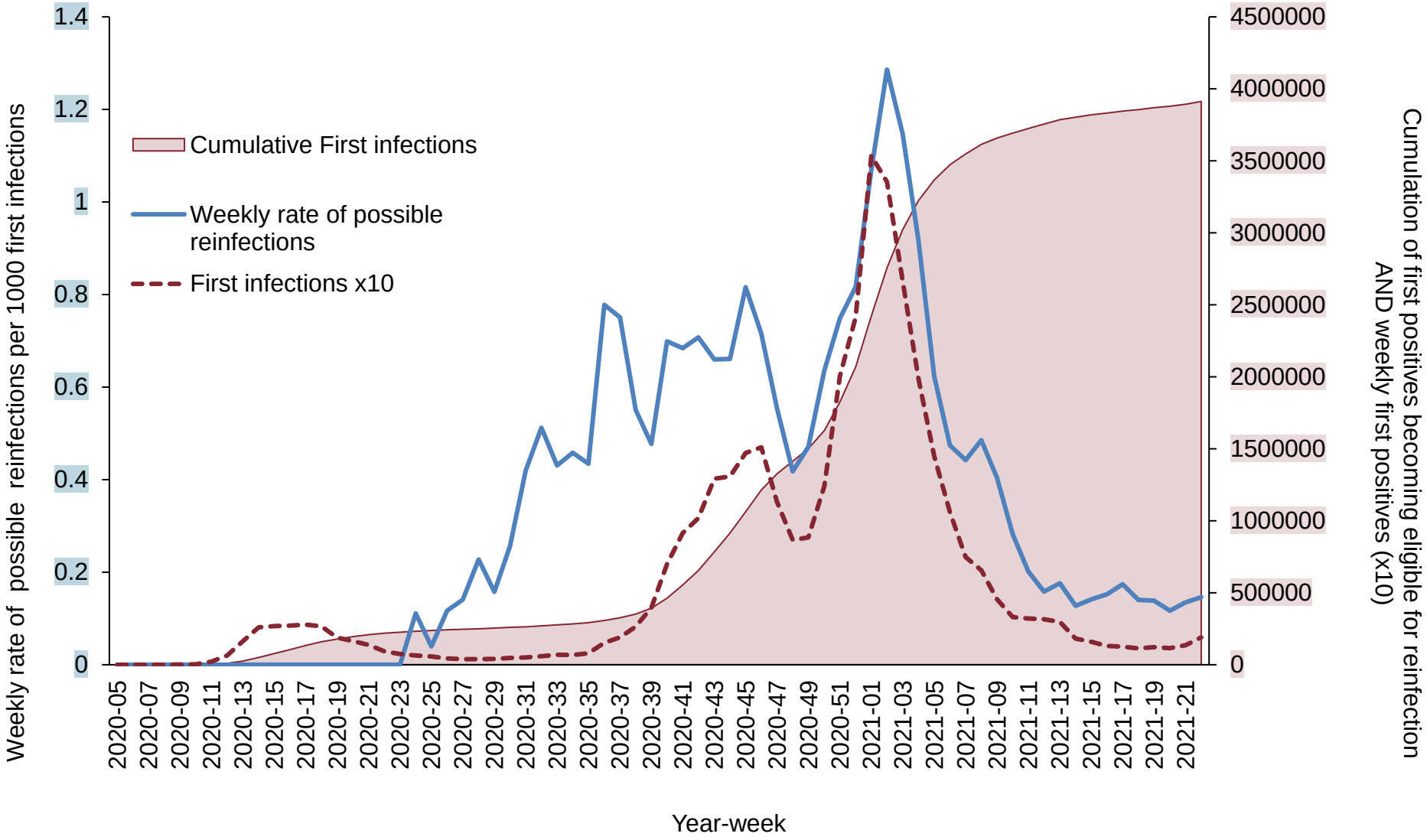
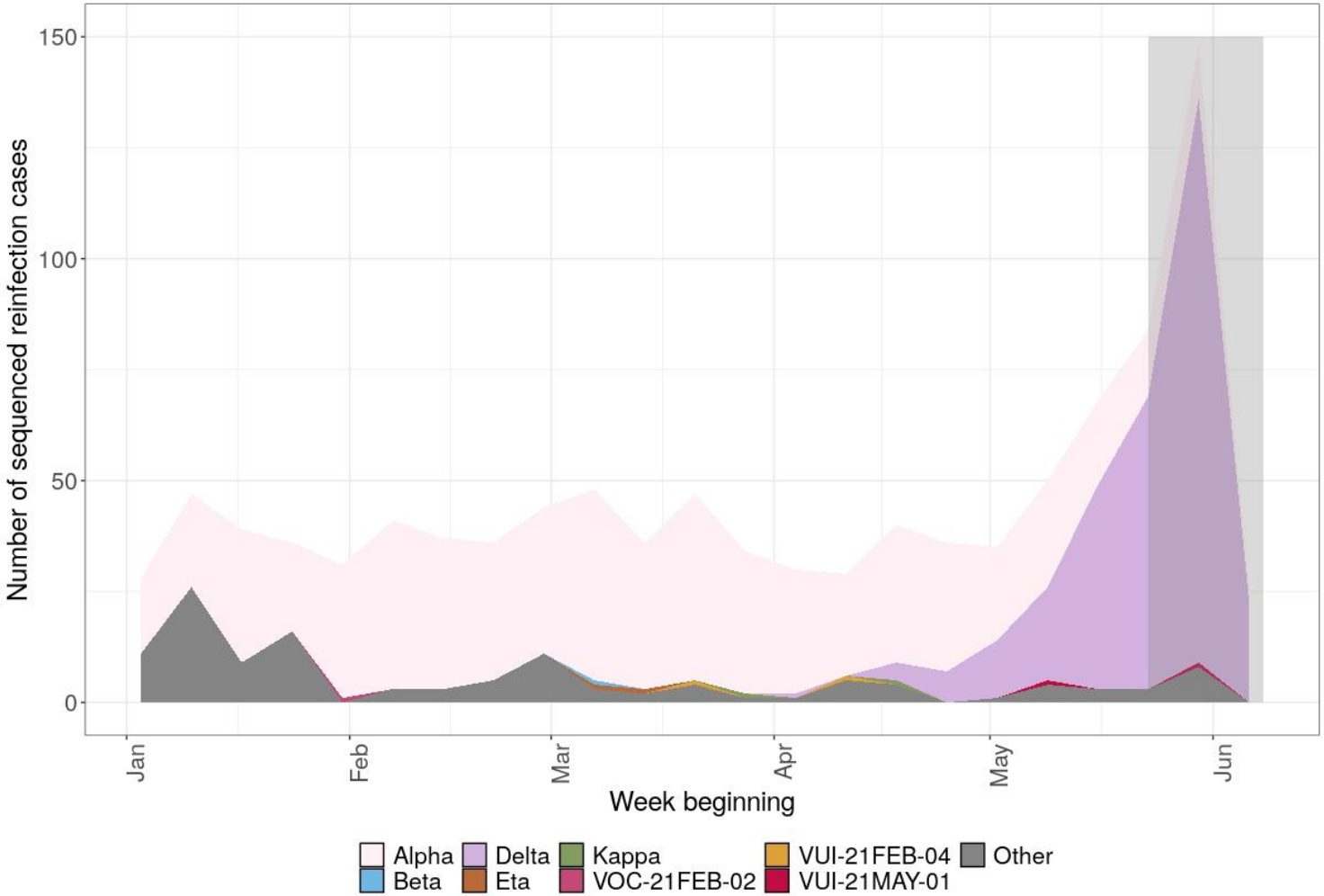


Figure 10 shows the weekly rates of possible reinfections per 1000 first infections based on a cumulative denominator derived from total individuals with a first SARS-CoV-2 positive test result at a point 13 weeks (91 days) before the second positive test result together (solid line); the cumulative total of first infections in the solid area (right Y-axis); total first infections (dashed maroon line, right Y-axis) by week of onset (these numbers are amplified x10 so the line can be clearly seen). Reinfections are identified on the basis of 2 sequential positive detection results (with PCR or Lateral flow device) at least 90 days apart.

Figure 8. 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 14 June 2021
(Find accessible data used in this graph in underlying data). These numbers include cases where a sequence is available for both a first and second reinfection.



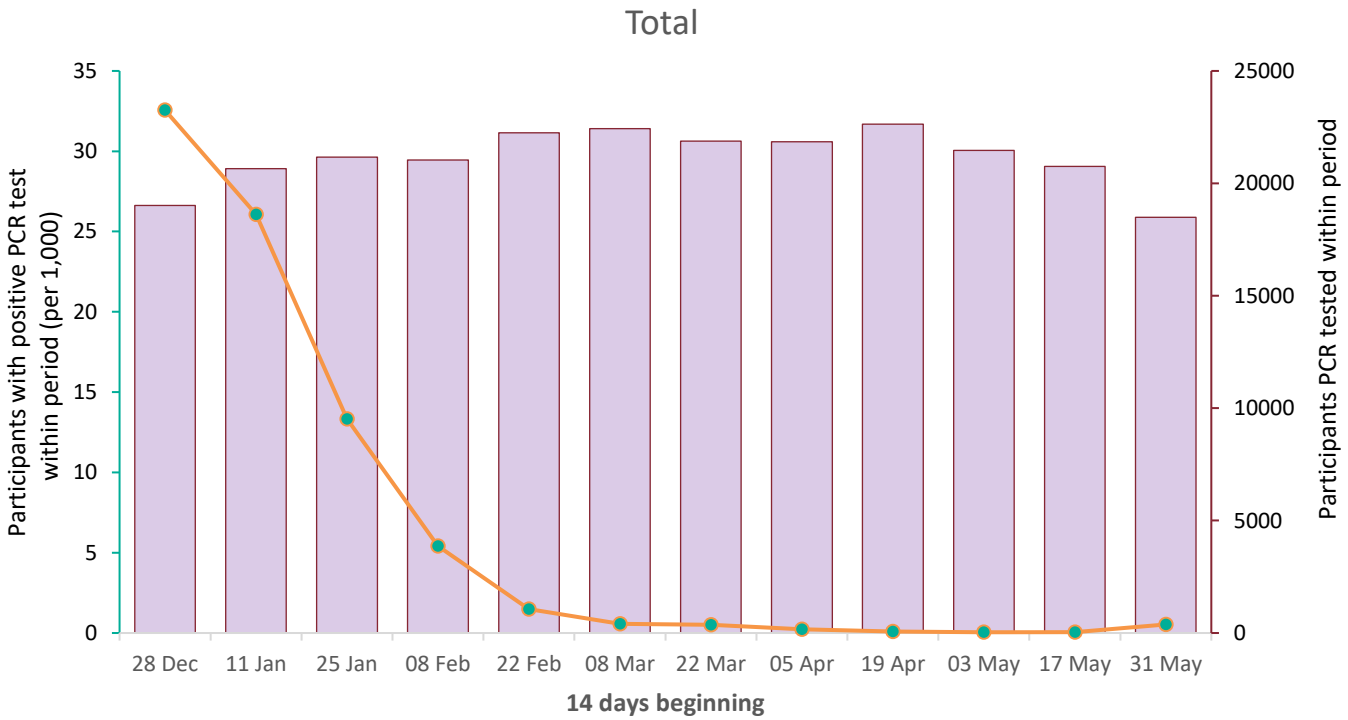
SARS-CoV-2 Immunity and Reinfection Evaluation (the SIREN study) cohort monitoring

The SIREN study is a cohort of National Health Service healthcare workers, including 135 sites and 44,546 participants across the UK, 35,710* in England, who remain under active follow-up with PCR testing every 2 weeks for COVID-19 by PCR. This cohort had a high seropositivity on recruitment (30% before the second wave) and is now highly 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 predominantly 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 9) and reinfections remain at very low numbers in individuals previously either PCR positive or seropositive (Figure 9). Of the 20 participants with a new PCR positive since April 2021 in the SIREN cohort overall, 13 (65%) occurred 14 days or more following their second vaccine dose. Figure 12 shows the monthly frequency of potential reinfection events within SIREN.

*Number excludes participants who have withdrawn from the study and requested their data to be removed and participants recruited in hospitals in the devolved administrations.

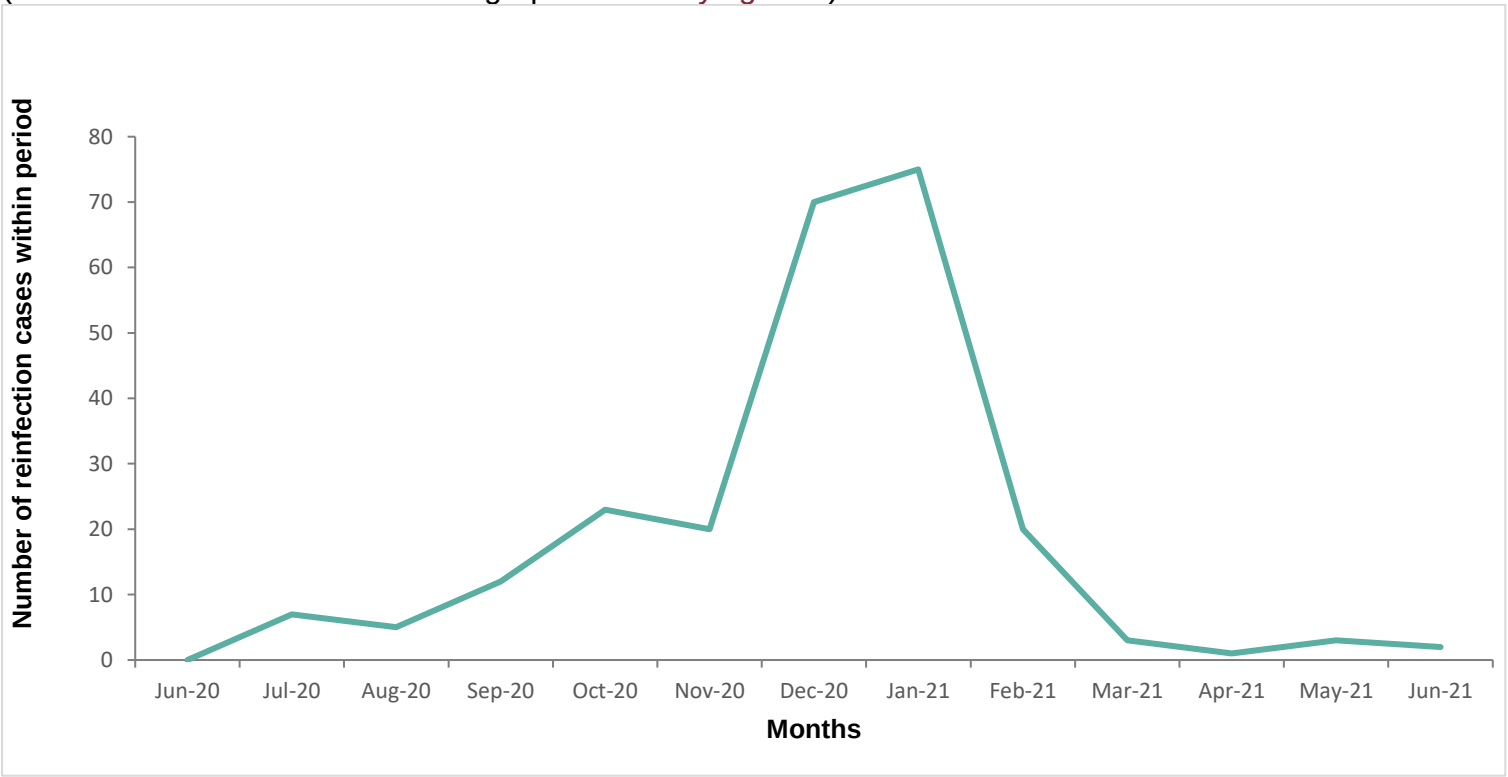
Figure 9. PCR positivity within the SIREN study for all regions, England (fortnightly testing interval)
Data up to 13 June 2021

Purple bars indicate participants PCR-tested within period (right axis), Orange line indicates participants with positive PCR within period (per 1,000) (left axis). (Find accessible data used in this graph in underlying data).



*Contains only participants with at least 1 PCR test within given period; participants are counted as positive if at least 1 PCR test within given period is positive. Figures have not been restricted by antibody status nor vaccination status; includes only participants from England trusts.

Figure 10. Monthly frequency of potential reinfection events within SIREN. Data up to 6 June 2021
(Find accessible data used in this graph in underlying data).



Nine thousand, eight hundred and thirteen (31%) of the SIREN cohort had evidence of prior infection (previous PCR positive or antibody positive) at enrolment. This number has increased during follow-up as participants move from the negative to positive cohort after a primary infection. From 18 June 2020 to 6 June 2021, there were 241 potential reinfections (blue line) identified in England. This is provisional data as potential reinfection cases flagged are undergoing further investigation, and some may subsequently be excluded. This number has decreased by one event in December (excluded) and increased by one event in April (reported retrospectively by site) since the last report. There were 6 potential reinfections since April 2021, all of which occurred at least 14 days after participants received their second vaccine dose.

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 during the period that this was the dominant strain and an accurate comparison cannot be made.

Due to the dominance of Delta variant, all outbreaks reported from week 20 onwards can be attributed to Delta unless the outcome of sequencing confirms otherwise. Reporting on the number of outbreaks that have a confirmed linked Delta variant case will therefore lead to an under-estimation of the total burden of outbreaks associated with Delta. In order to track the Delta variant it is best to refer to the total number of outbreaks by setting which are reported in the weekly influenza/COVID-19 surveillance report. In keeping with our approach to reporting on Alpha variant outbreaks, Delta-related outbreaks will not be included in subsequent Variants of Concern Technical Briefings, however information on emerging variants will be included where relevant.

In this technical briefing the data are presented as a chart (Figure 11) rather than 3 tables, as were presented in technical briefings 14 and 15. Auxiliary data of this chart is available in underlying data.

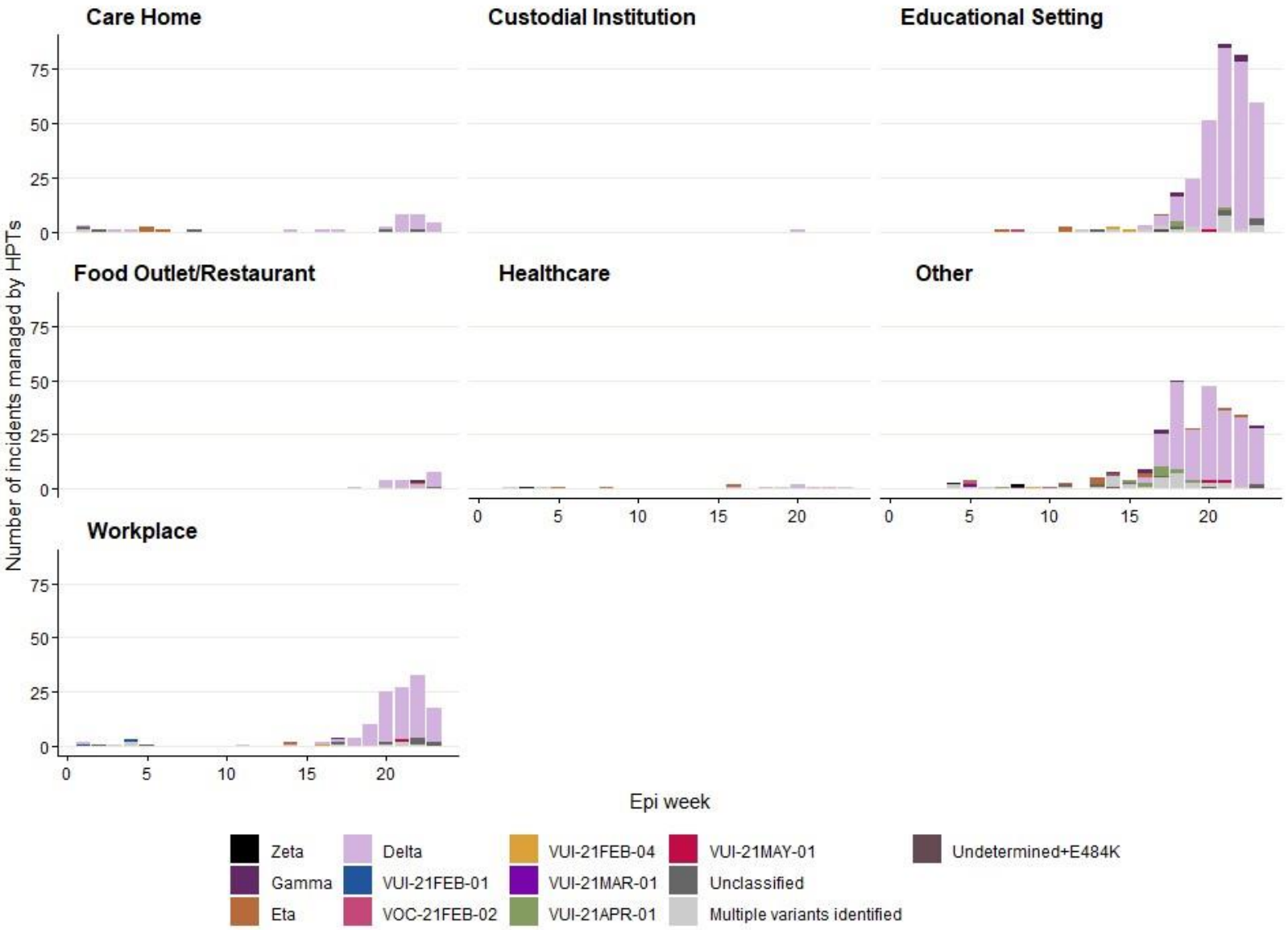
It is important to note that there is a time lag from the suspected outbreak being reported to PHE to genotyping and sequencing being undertaken and variant cases identified so data are provisional and likely to change in subsequent technical briefings.

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
- 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

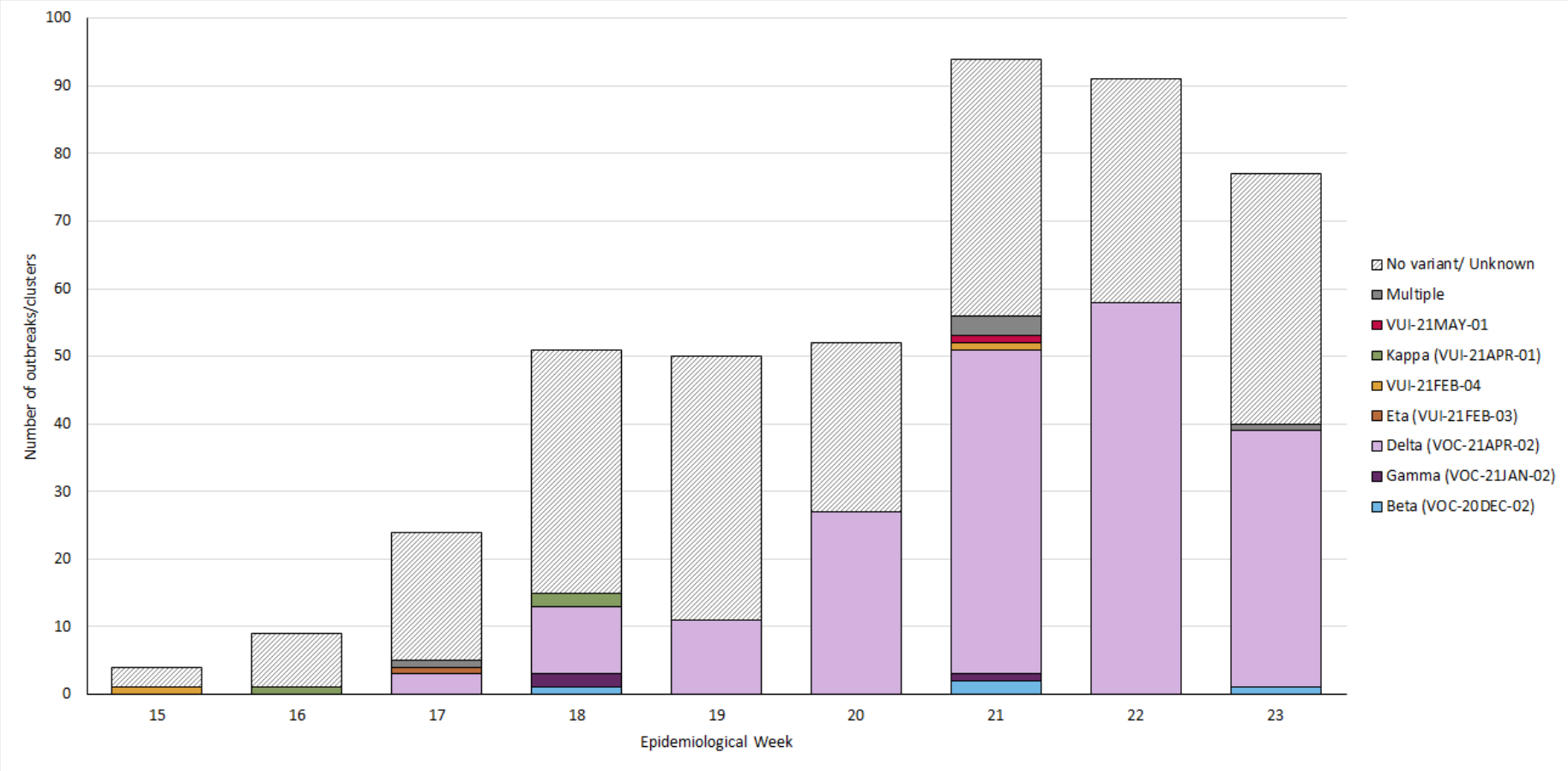
Figure 11. Incidents managed by Health Protection Teams involving SARS-CoV-2 variants by iso-week, by outbreak setting (4 January 2021 up to 13 June 2021) (Find accessible and auxiliary data used in this graph in underlying data).



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 181 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 0.8% of all schools.

For the reasons outlined, the weekly surveillance report provides the optimal data to track the total burden of Delta outbreaks linked to schools and other settings. These data will not be included in subsequent Variants of Concern Technical Briefings, however information on emerging variants linked to educational settings will be included where relevant.

Figure 12. 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 13 June 2021



These data are provisional, excluding confirmed Alpha variant outbreaks. Data used in Figure 12 is detailed in Table 9**.**

Table 9. 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 13 June 2021

These data are provisional, excluding Alpha variant.

Variant / Week	21-15	21-16	21-17	21-18	21-19	21-20	21-21	21-22	21-23	Total
Beta				1			2		1	**4**
Gamma				2			1			**3**
Delta)			3	10	11	27	48	58	38	**195**
Eta			1							**1**
VUI-21FEB-04	1						1			**2**
Kappa		1		2						**3**
VUI-21MAY-01							1			**1**
Multiple			1				3		1	**5**
No variant/ Unknown	3	8	19	36	39	25	38	33	37	**238**
Total	**4**	**9**	**24**	**51**	**50**	**52**	**94**	**91**	**77**	**452**

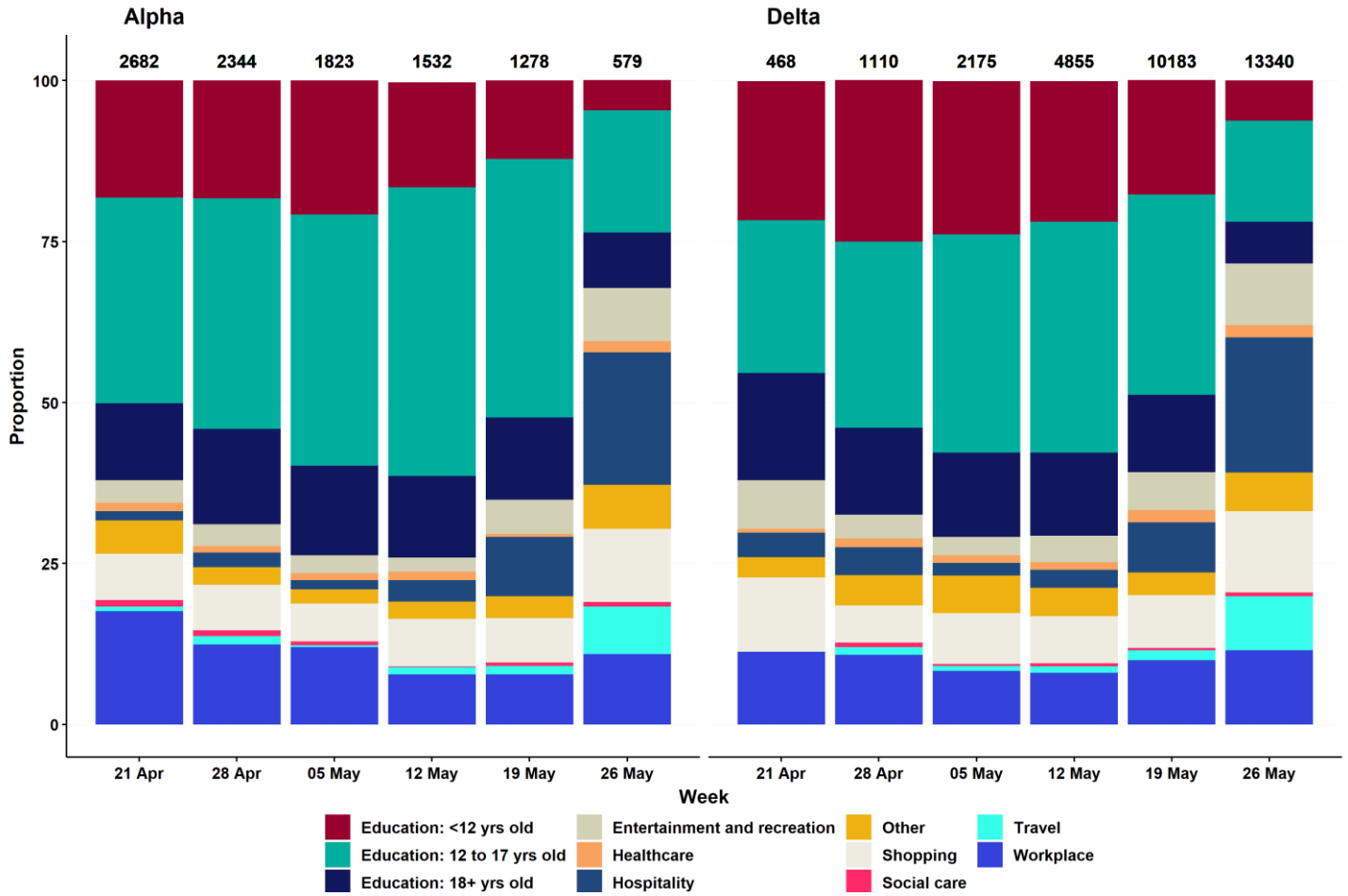
Common exposures derived from contact tracing data

Figure 13 shows the number of common exposure events reported per week, by setting, from week commencing 21 April to week of 26 May 2021. This figure only includes common exposures reported during contact tracing by cases who have been sequenced and confirmed as Alpha or Delta 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 may represent transmission events between known cases but also from unknown cases. However, they can also simply represent commonly visited locations and so should be interpreted with caution. 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, so should be interpreted in the context of national policy as well as other events such as school holiday periods.

The most common settings for common exposures were education, for Alpha and Delta variants, apart from the most recent week beginning 26 May (which includes the bank holiday weekend and start of school half term week). In the latest week presented (from 26 May 2021), hospitality settings were a larger proportion (around 20%) of all common exposures reported by cases with both Alpha and Delta variants, and the proportion of common exposures related to travel also increased substantially.

Figure 13. Weekly number and proportion of common exposure events among sequenced cases, by setting and variant of cases (for alpha and delta only)



Common exposure events reported from week commencing 21 April 2021 to week commencing 26 May 2021. Variant data as of 14 June 2021, contact tracing data as of 16 June 2021. Number of common exposures per week of data labelled. (Find accessible data used in this graph in underlying data).

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). Further analyses are required to reduce the uncertainty related to the change in risk and to explore the link to vaccination in more detail.

England

No new data in this report.

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. Individuals who tested positive from 1 April 2021 onwards (until 14 June 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 (1.8, 95% 1.4 to 2.3).

Monitoring of vaccine effectiveness

Analysis of routine testing data up to the 11 June 2021, linked to sequencing and S-gene target status has been used to estimate vaccine effectiveness against symptomatic disease using a test negative case control design. Methods and detailed results are available in Effectiveness of COVID-19 vaccines against the Delta variant. After a single dose there was an 18% absolute reduction in vaccine effectiveness against symptomatic disease with Delta compared to Alpha, but only a modest reduction in vaccine effectiveness after 2 doses (Table 10).

Table 10. Vaccine effectiveness against symptomatic disease for Alpha and Delta variants

Vaccination status	Vaccine Effectiveness (%)	
	Alpha	Delta
Dose 1	49 (46 to 52)	31 (25 to 36)
Dose 2	88 (85 to 90)	80 (77 to 82)

Vaccine effectiveness against hospitalisation was estimated by evaluating hospitalisation rates via emergency care among symptomatic confirmed cases using survival analysis (Stowe et al., 2021 pre-print). This analyses used available data from linkage of symptomatic cases, 12 April to the 4 June 2021. Hazard ratios for hospitalisation are combined with odds ratios against symptomatic disease from the test negative case control analysis described above to estimate vaccine effectiveness against hospitalisation. Methods and detailed results are available in Stowe et al., 2021. Similar vaccine effectiveness against hospitalisation was seen with the Alpha and Delta variants (Table 11).

Table 11. Vaccine effectiveness against hospitalisation for Alpha and Delta variants

Vaccination status	Vaccine Effectiveness (%)	
	Alpha	Delta
Dose 1	78 (65 to 86)	75 (57 to 85)
Dose 2	92 (78 to 97)	94 (85 to 98)

International surveillance

GISAID includes data on sequences available internationally. As of 14 June 2021, sequences from 61 countries (excluding UK) have been identified in GISAID of Delta. In total 9,810 sequences from: Anguilla (1), Argentina (1), Aruba (3), Australia (164), Austria (7), Bahrain (15), Bangladesh (47), Belgium (217), Brazil (3), Bulgaria (1), Canada (354), China (2), Czech Republic (13), Democratic Republic of the Congo (6), Denmark (94), Finland (2), France (117), Georgia (4), Germany (692), Ghana (1), Greece (4), Hong Kong (3), India (3,813), Indonesia (40), Iran (9), Ireland (141), Israel (37), Italy (143), Japan (178), Jordan (1), Luxembourg (52), Malawi (5), Malaysia (11), Malta (1), Mexico (27), Morocco (1), Nepal (45), Netherlands (88), New Zealand (13), Norway (68), Pakistan (5), Poland (63), Portugal (91), Qatar (26), Reunion (2), Romania (5), Russia (166), Saint Martin (1), Singapore (242), Slovenia (4), South Africa (17), South Korea (20), Spain (183), Sri Lanka (1), Sweden (36), Switzerland (86), Thailand (88), Turkey (1), USA (2,278), Uganda (3), Vietnam (68)

Surveillance through genomic data

Table 12. Number of confirmed (sequencing) and probable (genotyping) cases, by region of residence as of 14 June 2021

Region	Confirmed (sequencing) case number	Probable (genotyping) case number	Total case number	Proportion of all cases[1]
East Midlands	2,121	969	3,090	5.1%
East of England	2,694	831	3,525	5.8%
London	5,027	4,299	9,326	15.4%
North East	720	1,894	2,614	4.3%
North West	13,098	12,104	25,202	41.5%
South East	2,982	2,500	5,482	9.0%
South West	828	455	1,283	2.1%
West Midlands	2,085	2,202	4,287	7.1%
Yorkshire and Humber	1,424	4,164	5,588	9.2%
Unknown region	153	105	258	0.4%
Total	31,132	29,523	60,655	-

[1] Genotyping is used to identify variants Alpha, Beta, Delta and Gamma; targets were updated in mid-May 2021 to prioritise accurate identification of Delta over Alpha

Figure 14. Confirmed (sequencing) and probable (genotyping) Delta cases by specimen date and detection method as of 14 June 2021 (Find accessible data used in this graph in underlying data)

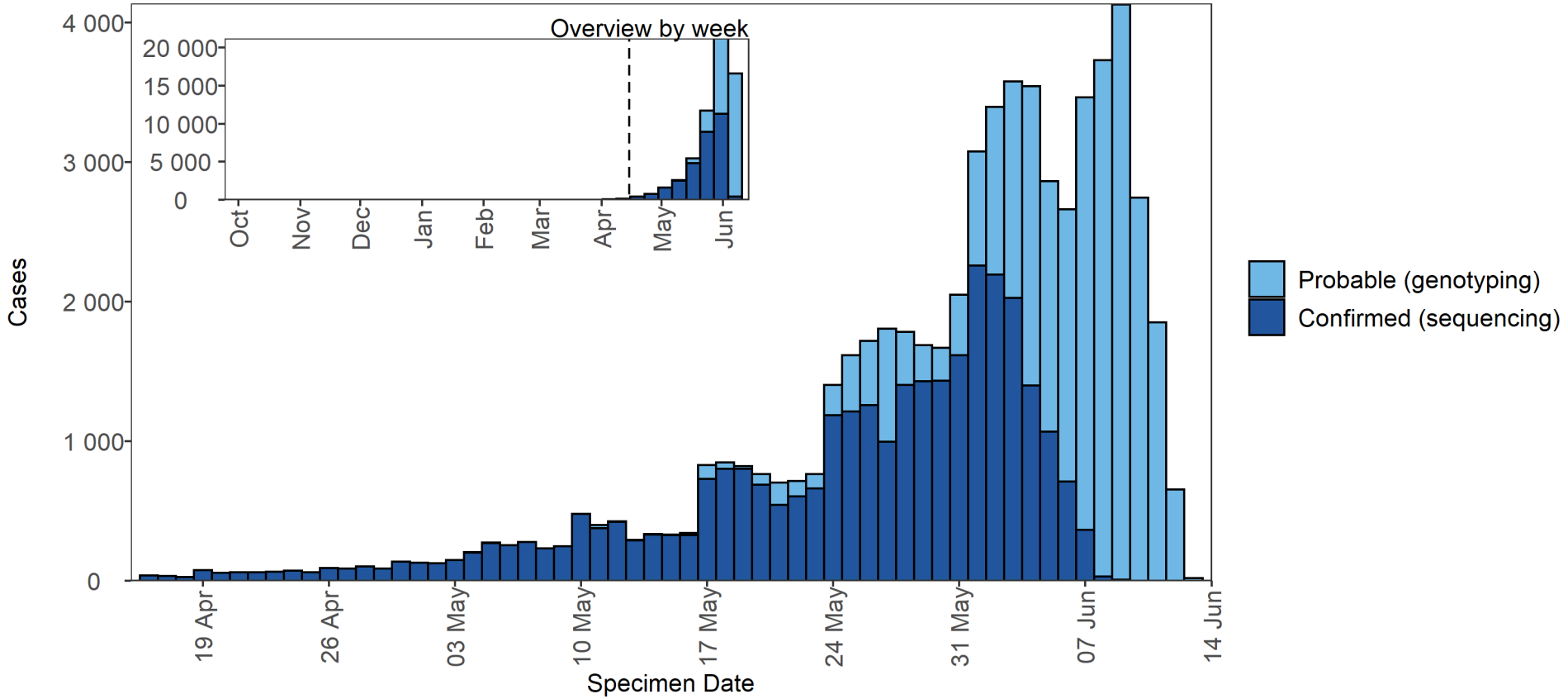


Figure 15. Confirmed (sequencing) and probable (genotyping) Delta cases by specimen date and region of residence as of 14 June 2021 (Find accessible data used in this graph in underlying data)

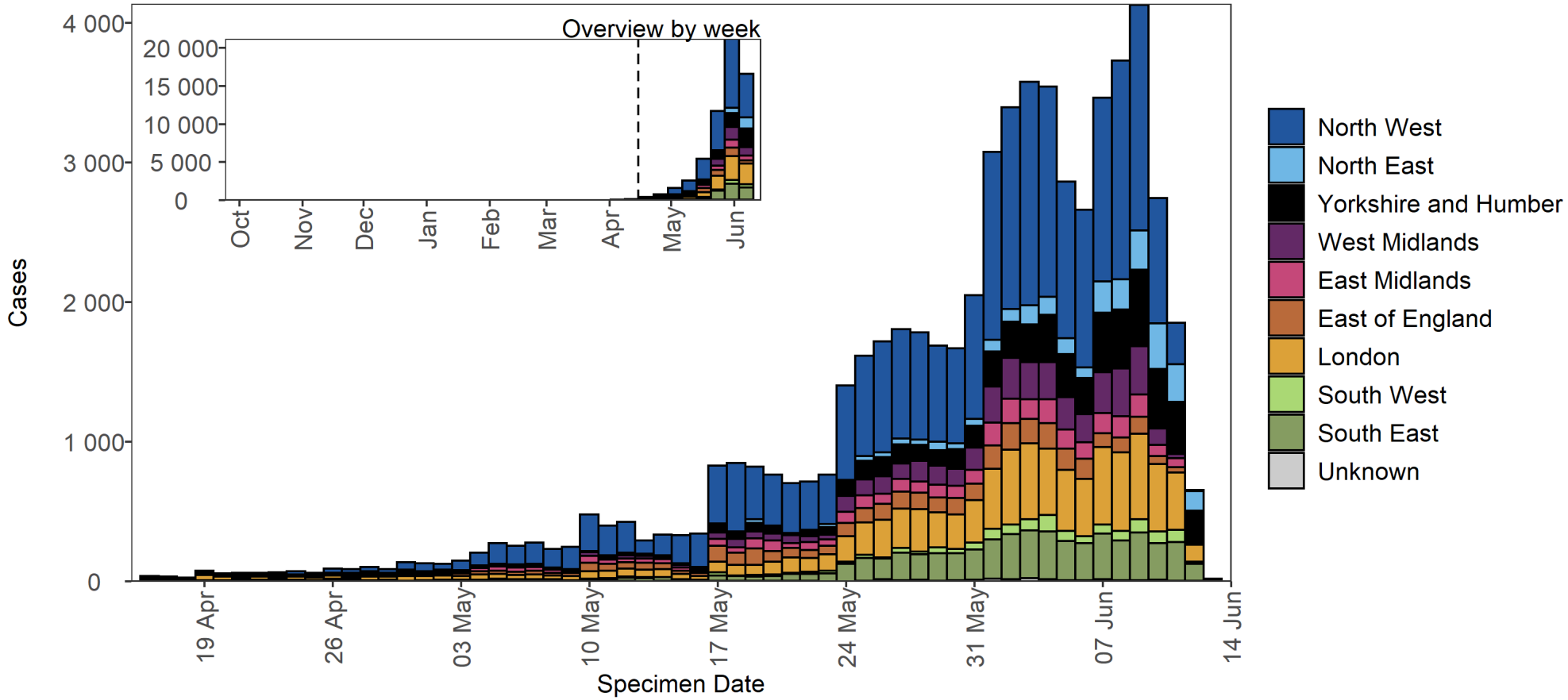
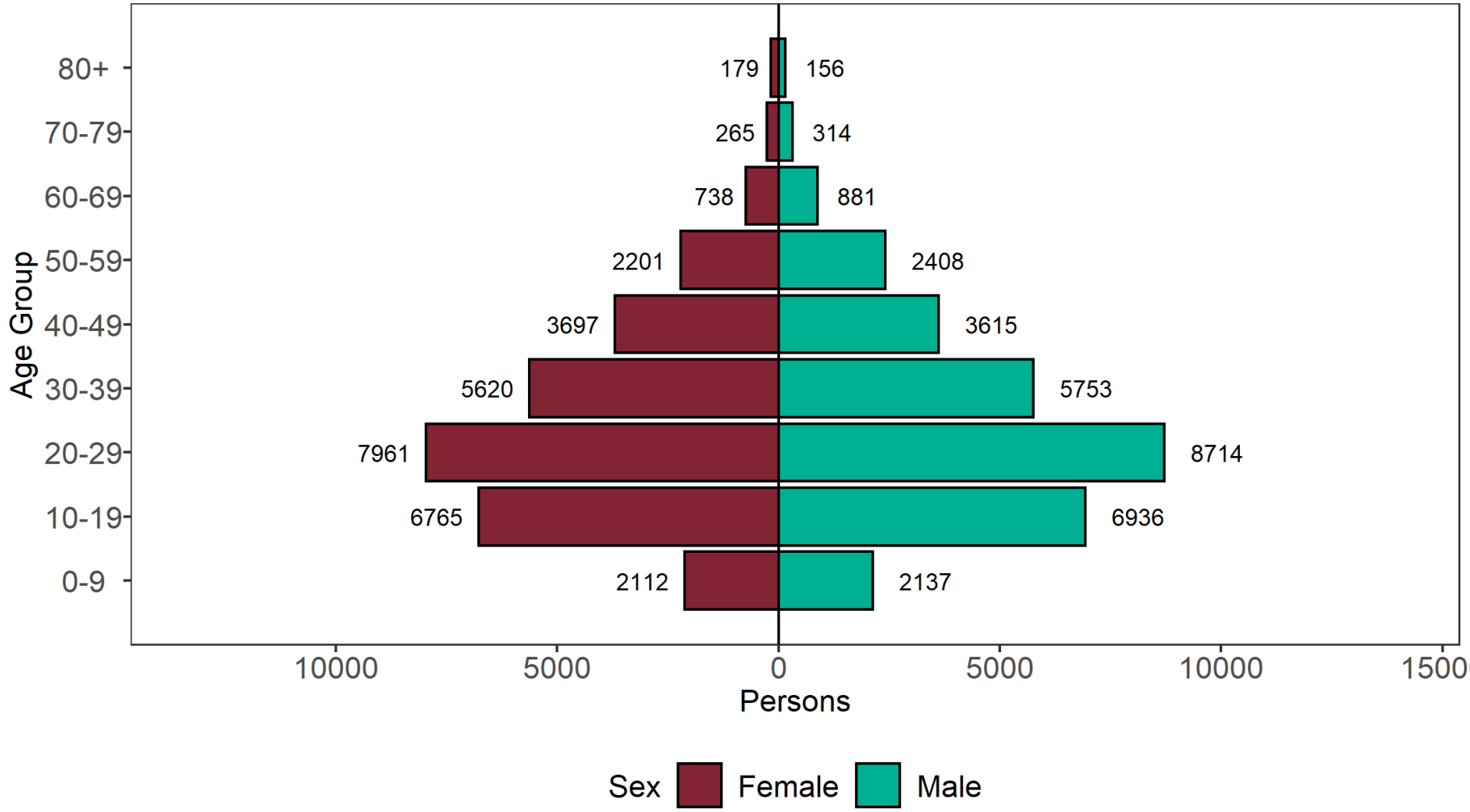


Figure 16. Age-sex pyramid of confirmed (sequencing) and probable (genotyping) Delta cases as of 14 June 2021
(Find accessible data used in this graph in underlying data)



175 cases excluded where sex or age not reported

Table 13. Additional spike mutations of interest detected in Delta genomes in the UK, as of 15 June 2021.

Amino acid change	Nucleotide change	Total number of sequences (UK)	Number of unlinked sequences	Number of sequences 16 March to 15 April 2021	Number of sequences 16 April to 15 May 2021	Number of sequences 16 May to 15 June 2021
P681R	C23604G	44844	7353	251	5618	31622
L452R	T22917G	43029	7159	251	5520	30099
G142D*	G21987A	27424	4456	180	3314	19474
P251L	C22314T	245	233	0	1	11
G446V	G22899T	120	59	0	5	56
R158G	A22034G	76	3	0	0	73
L452R	G22918A	50	2	0	12	36
K417N	G22813T	49	8	0	23	18
Q677H	G23593T	22	0	4	5	13
R683Q	G23610A	15	0	0	1	14
S255F	C22326T	14	0	0	6	8
V503I	G23069A	12	1	0	6	5
L244S	T22293C	8	2	0	5	1
T716I	C23709T	8	4	0	0	4
S477I	G22992T	7	1	0	1	5
S494L	C23043T	7	1	0	3	3
K444N	G22894T	7	5	0	0	2
P384S	C22712T	6	0	0	0	6
D215G	A22206G	5	0	0	0	5
E484A	A23013C	5	0	0	4	1
P681L	C23604T	5	0	0	0	5

L18F	C21614T	4	1	0	0	3
V483F	G23009T	4	1	0	1	2
P479S	C22997T	3	0	0	1	2
S494A	T23042G	3	0	0	0	3
D405Y	G22775T	3	2	0	0	1
R683L	G23610T	3	0	0	1	2
E484Q	G23012C	2	0	0	1	1
G142A	G21987C	2	0	0	0	2
R346G	A22598G	2	0	0	0	2
Q321L	A22524T	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. * Note that G142D is in a part of the genome with consistently reduced coverage in the Delta variant (due to the lineage-defining deletion from position 22029-22035, which affects one of the PCR primer sites in the ARTIC v3 protocol). While it is only reported as detected in ~60% of sequences, the remaining 40% of sequences are almost all “N” at that position (the code for “insufficient data”), rather than being confirmed ”G” (the reference allele). As the mutation occurred early in the history of the lineage the majority of sequences (>99%) in this lineage can be assumed to harbour the mutation.

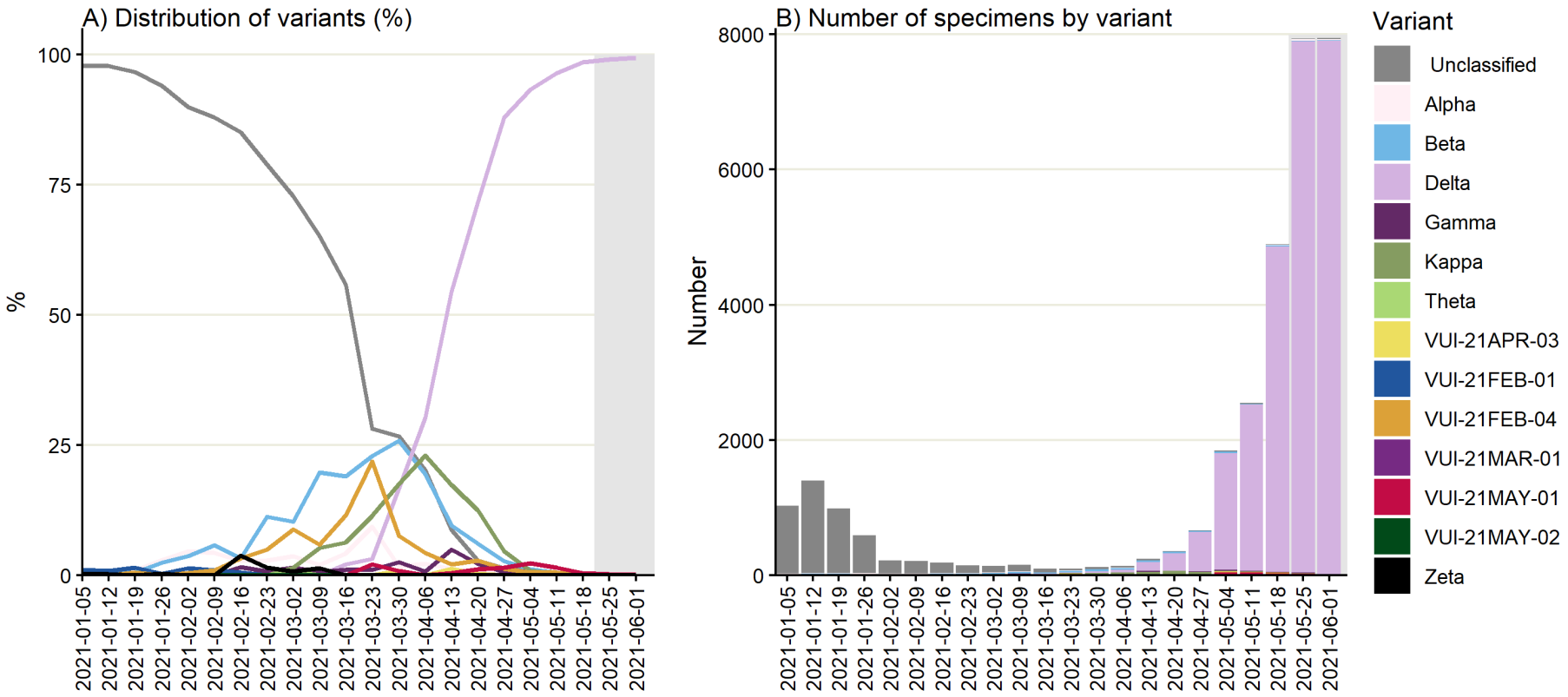
Surveillance through S gene detection

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 also detected in Beta, Kappa, Delta, VUI-21APR-03 (B.1.617.3) 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.

A detectable S gene in a positive SARS-CoV-2 sample has been established as a useful proxy for the Delta variant in England since mid-May 2021. The proportion of confirmed Delta specimens among S gene positives has been above 95% in the most recent 4 weeks of data (since 11 May 2021).

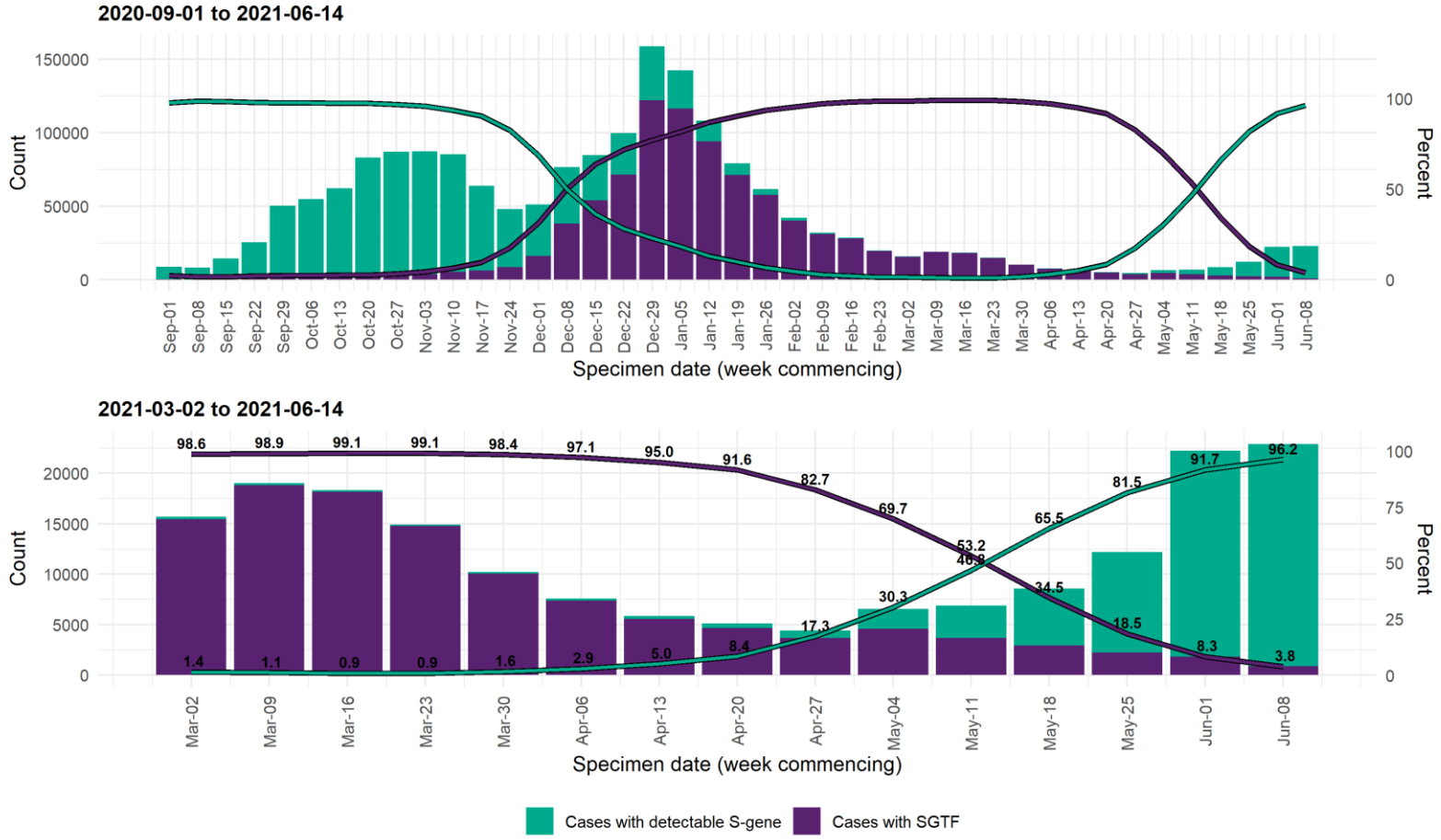
The number and proportion of S gene positive samples in England (Figure 17 and Figure 18) has also steadily increased since mid-April, with 22,003 cases reported in the week starting 1 June; 96.2% of all cases tested on the TaqPath assay and reported to PHE that week. Local authorities in the North West continue to stand out in terms of numbers of S gene positives (Figure 19). S gene analyses presented here have been reduced since the introduction of genotyping.

Figure 17. Weekly distribution of variants among sequenced S gene positive SARS-CoV-2 specimens
Specimen dates between 5 January 2021 and 7 June 2021, data as of 15 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).



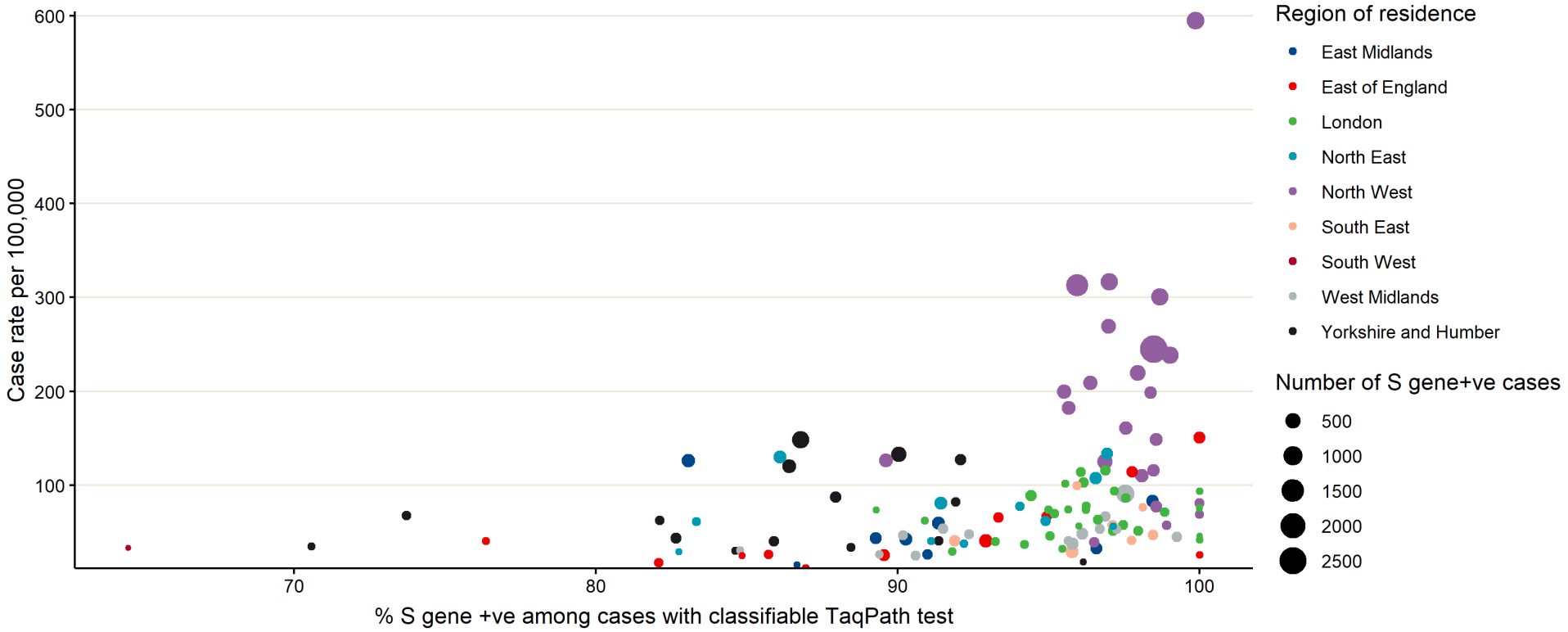
Source: SGSS and COG-UK sequencing data, restricted to sequenced positive S-gene positive tests from Newcastle, Alderley Park, Glasgow, and Milton Keynes Lighthouse Laboratories.
S gene +ve defined as positive SARS-CoV-2 test with CT values <=30 for S, N, and ORF1ab.

Figure 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 14 June 2021, data as of 15 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 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. 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 5 June 2021 and 11 June 2021, data as of 15 June 2021 (Three most recent days excluded due to reporting delay). Restricted to UTLAs with >20 cases tested on TaqPath assay. (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.

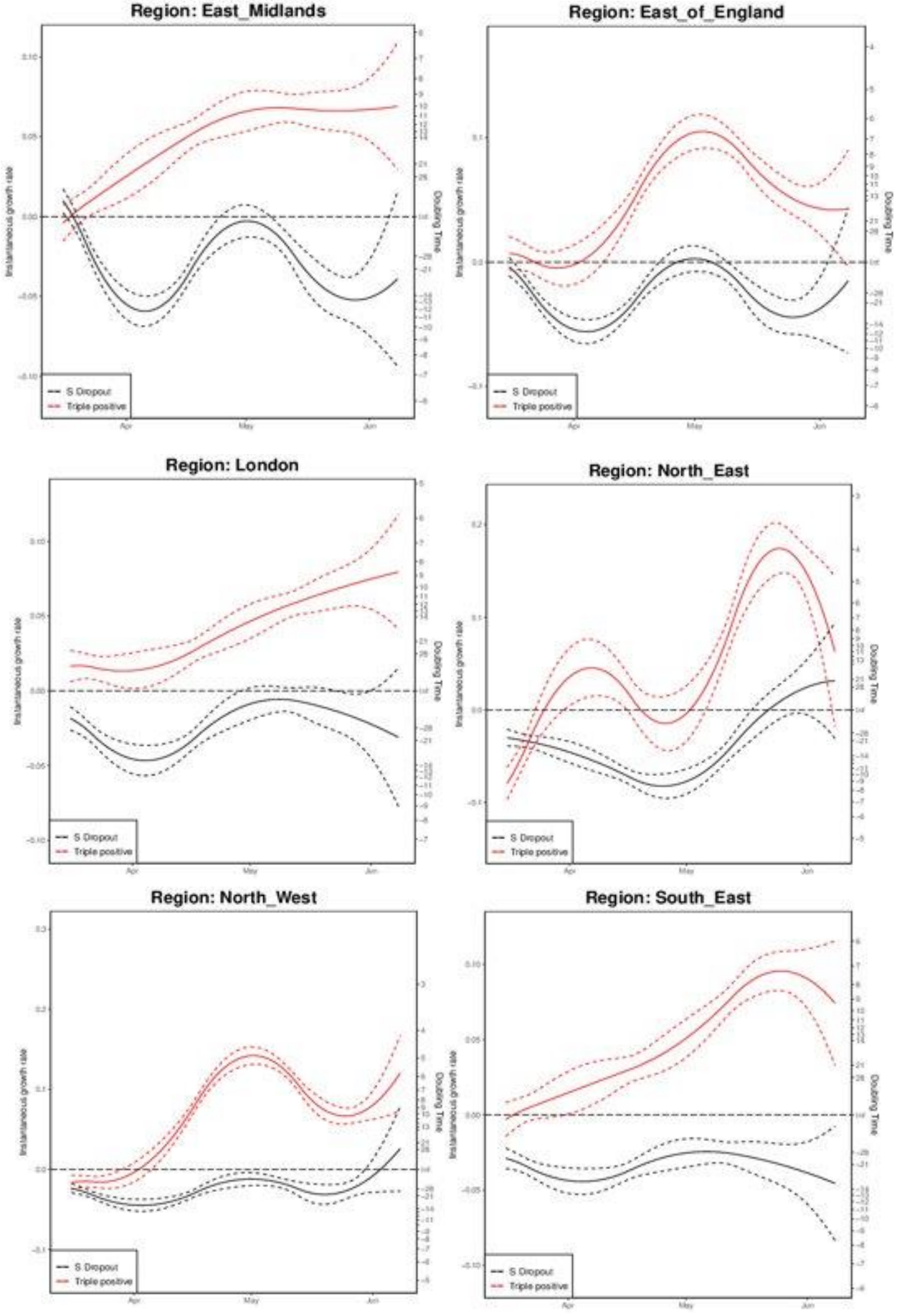
Growth rate of S gene positive and negative cases[1]

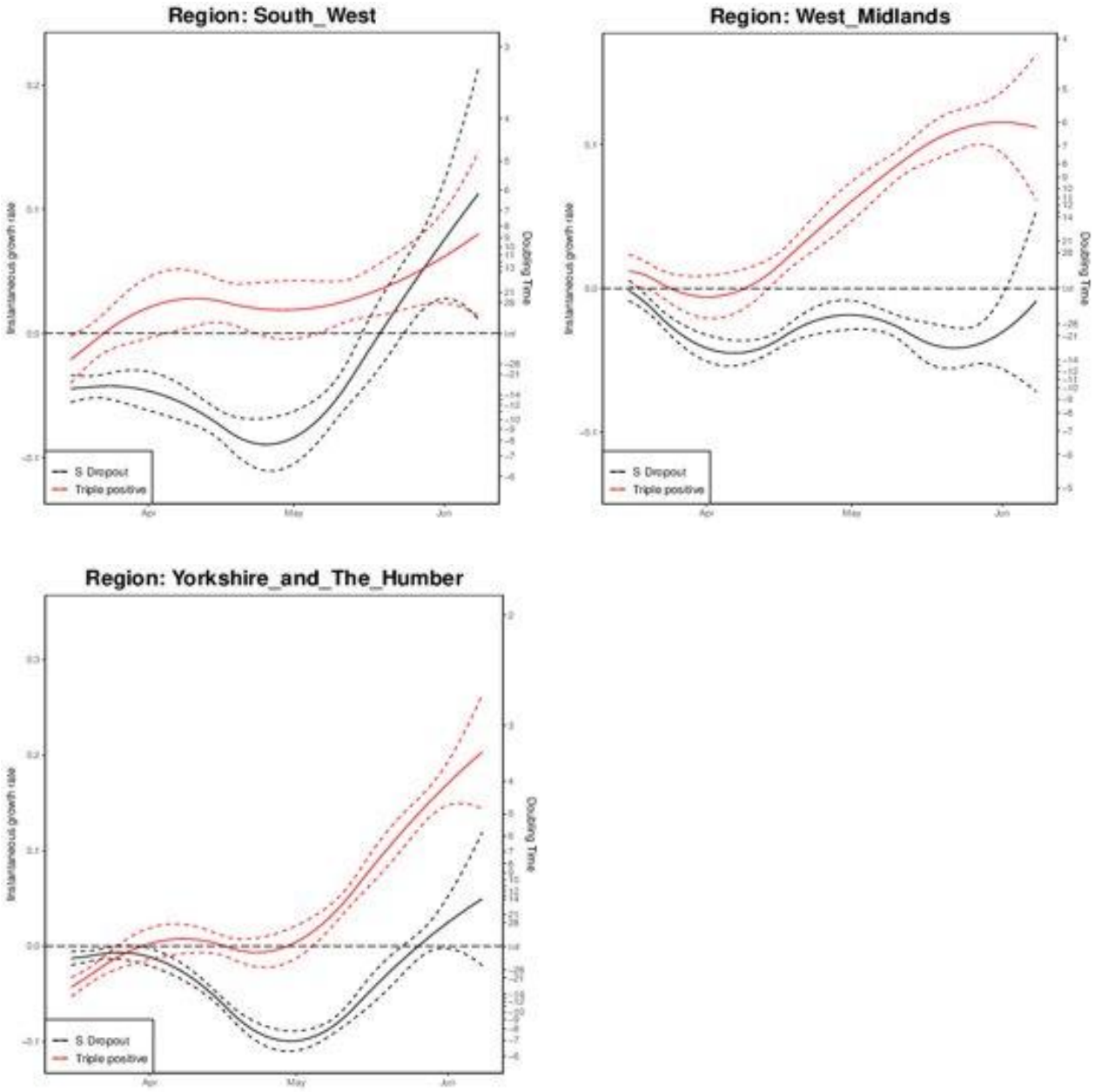
Figures 20, 21, and 22 show growth rate and doubling times of S gene positive (all 3 PCR targets positive) and negative (S gene target failure), produced by fitting a generalized additive model with a quasi-Poisson.

The left vertical axis in the figures describe the daily growth rates; 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 when the number of data points used for the estimation is 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 20. Growth rate and doubling time of S gene positive and negative cases by region as of 9 June 2021





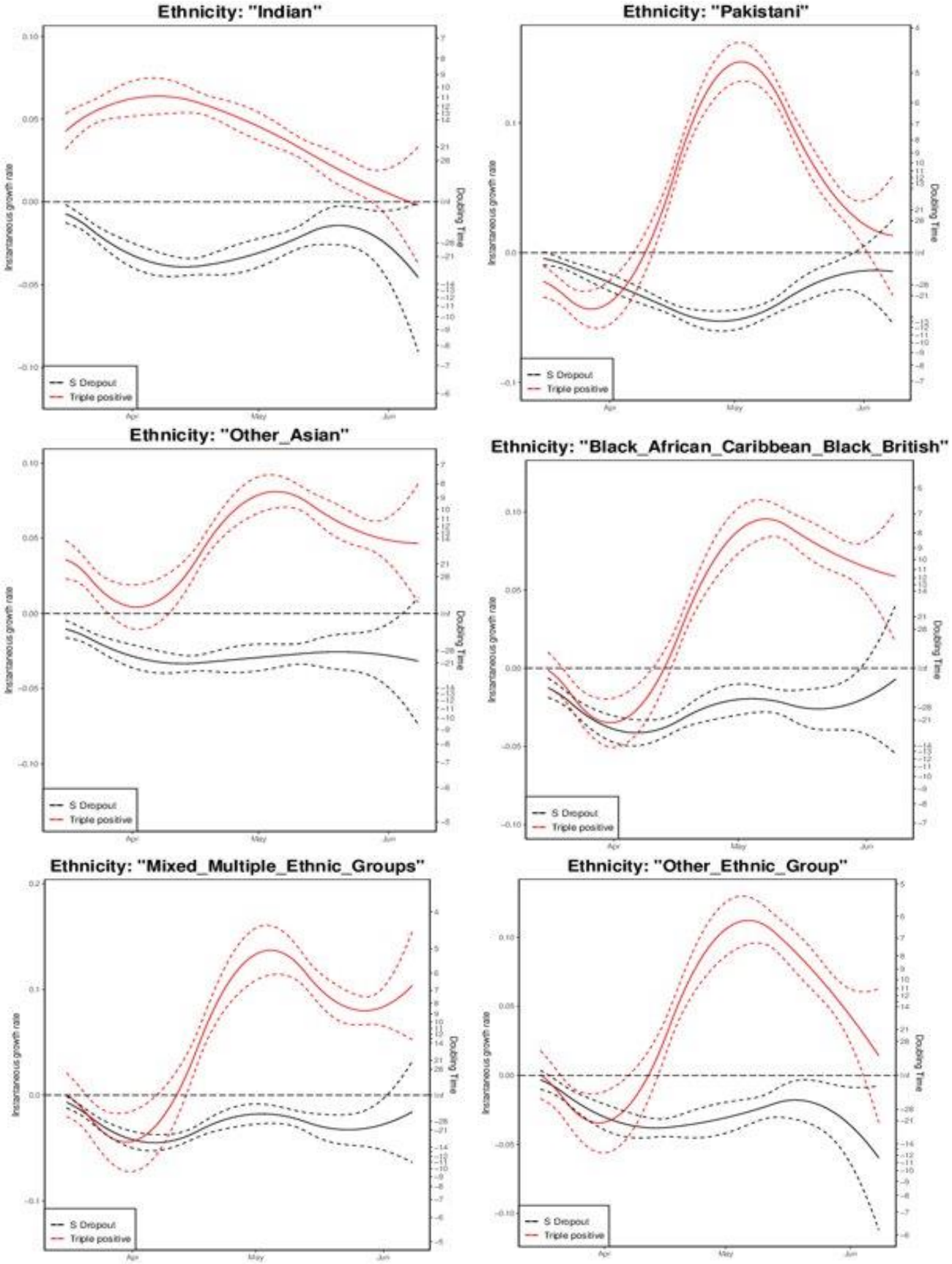
Cases with S gene positive (all 3 PCR targets positive) have been increasing since April in all regions. Regional doubling times range from 3.5 days to 16 days; shortest in Yorkshire and the Humber, longest in the East of England, although there is uncertainty around these estimates, and PCR target data coverage is low in Yorkshire and the Humber, as noted below.

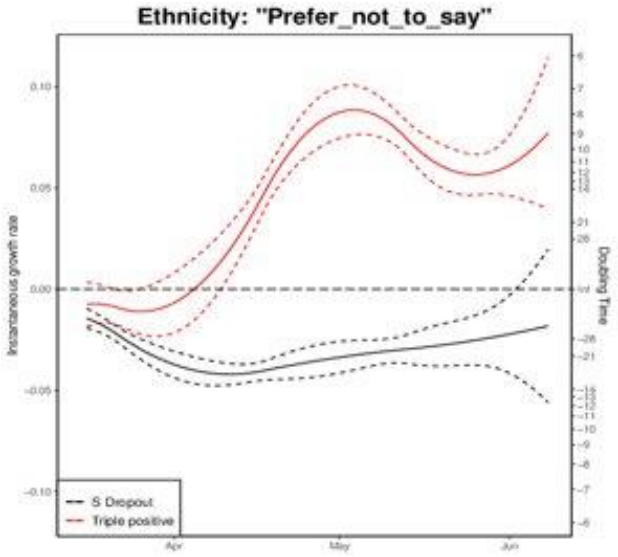
There is very rapid growth (doubling times 6 days) in S gene positive in the North West and West Midlands, where PCR target data coverage is good. There is also rapid growth in S gene positive in London, the East Midlands, and South East (doubling times around 8 to 10 days). There is rapid growth in S gene positive the South West but slowing in the North East. PCR target data coverage is lower in these regions, as for Yorkshire and the Humber, and has some variability. This may lead to artificial increases or decreases in growth rates.

There is apparent slowing of decline and/or increase in growth in cases with S gene target failure in several regions, but uncertainty is increased in the most recent estimates, and variability in PCR target data coverage, particularly where numbers are low, can lead to artificial increases or decreases in growth rates. Find accessible data used in this graph in underlying data.

Figure 21. Growth rate and doubling time of S gene positive and negative cases by ethnicity as of 9 June 2021

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

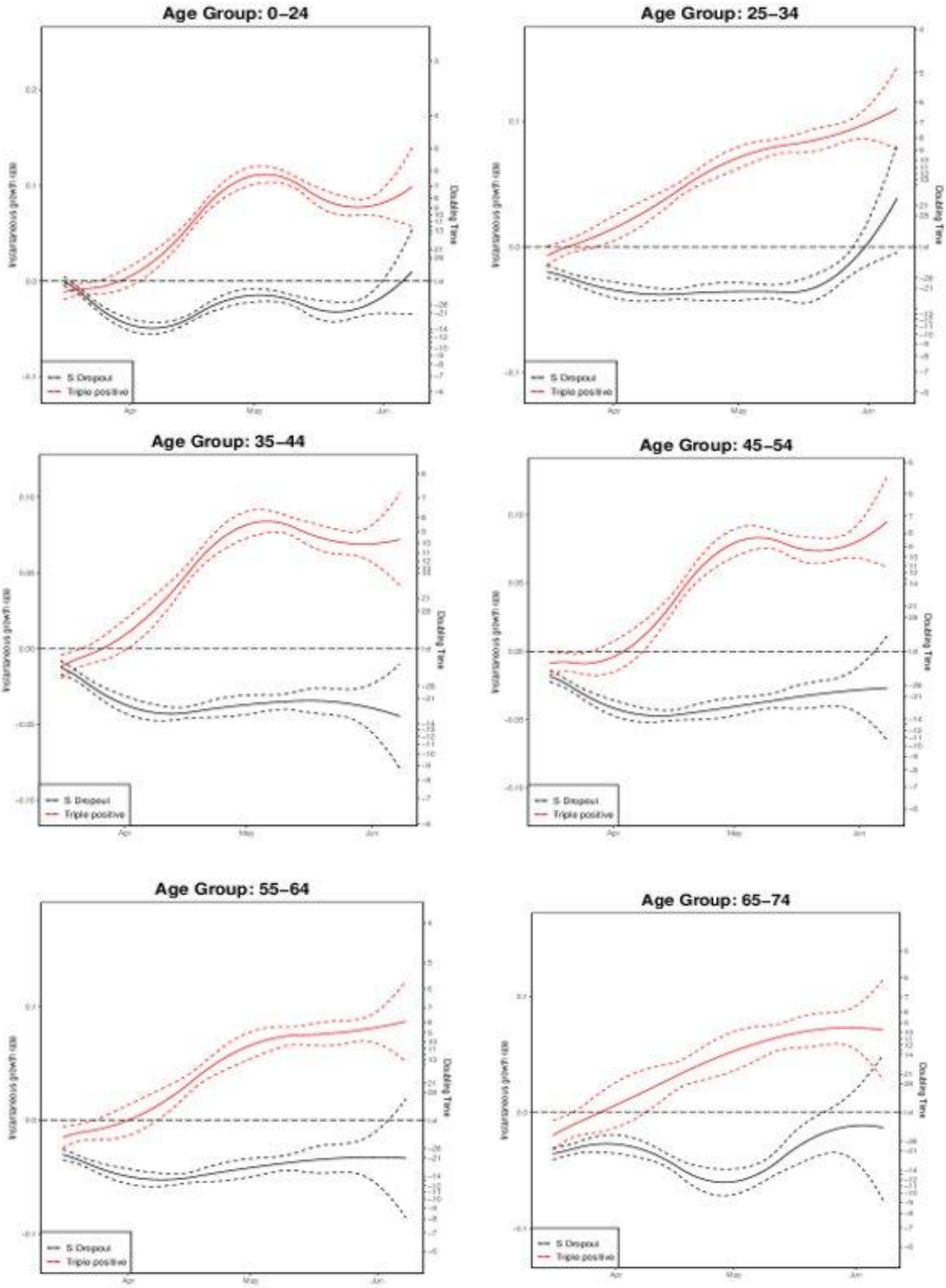


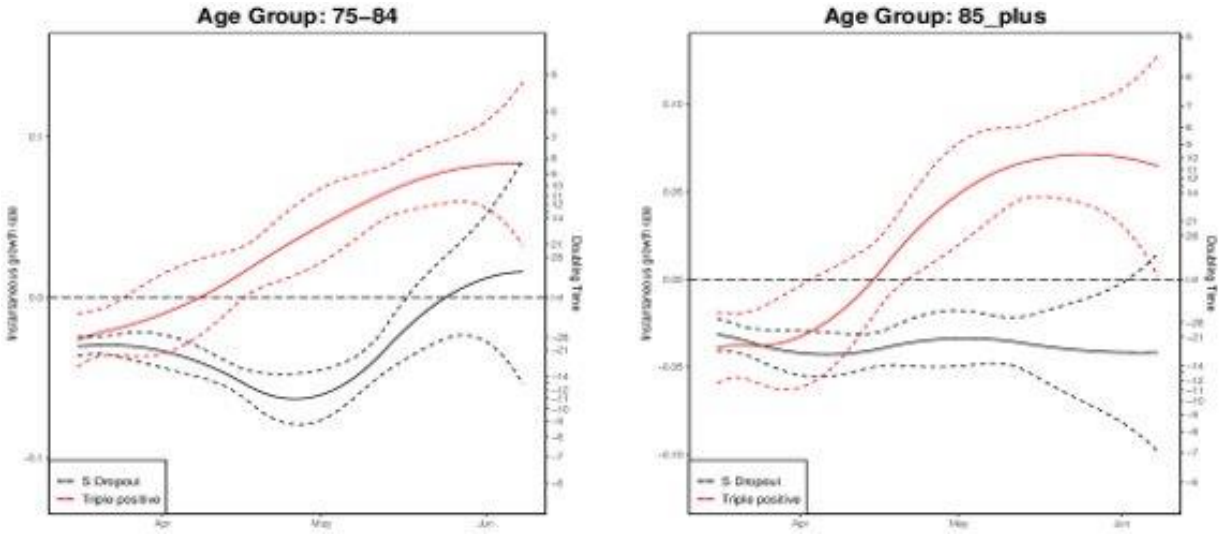


Cases with S gene positive (in addition to N and Orf1a PCR targets positive) have been increasing over the course of April and May. White ethnicity, Mixed Multiple Ethnic Groups and people who prefer not to state their ethnicity with S gene positive cases are increasing (doubling time around 5 days, 7 days and 9 days respectively). Growth rates of S gene positive have slowed in most other ethnic groups. Confidence intervals are wide, and data on PCR targets is variable. (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 age as of 9 June 2021.

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





Cases with S gene positive (in addition to other PCR targets) have been increasing over the course of April and May in all age groups. Growth is most rapid in the younger age groups, with doubling times of around a week in those aged under 34. Growth is occurring least quickly in the oldest age group (85 years and older), but doubling times are still around 11 days, although there is wide uncertainty around this estimate. Confidence intervals are wide, and data on PCR targets is variable. (Find accessible data used in this graph in underlying data

Delta with K417N

Through routine scanning of variation in Delta a small number of sequences were detected which had acquired the spike protein mutation K417N.

Information suggests that there are at least 2 separate clades of Delta with K417N. One clade is large and internationally distributed with PANGO lineage designation AY.1. A second clade found in sequences uploaded to GISAID from the USA, now designated AY.2.

International epidemiology

As of 16 June 2021, 161 genomes of Delta-AY.1 have been identified on GISAID. from Canada (1), India (8), Japan (15), Nepal (3), Poland (9), Portugal (22), Russia (1), Switzerland (18), Turkey (1), USA (83).

Epidemiology

There are currently 38 cases of Delta-AY.1 in England (36 confirmed sequencing and 2 probable genotyping). Cases have been detected in 6 different regions in England (Table 14, Figure 23). Delta-AY.2 has not been detected in England.

Delta with K417N can be detected by genotyping assay, which means that rapid case identification and response activities can be undertaken. Until laboratory characterisation has been undertaken, Health Protection Teams will respond with high priority to case finding and control measures for cases of Delta with K417N. Neutralisation assays are now underway for Delta-AY.1

Table 14. Number of confirmed (sequencing) and probable (genotyping) Delta-AY.1 cases, by region of residence as of 14 June 2021

Region	Confirmed case number	Probable case number	Total case number	Proportion of all cases[1]
East Midlands	1	0	1	2.6%
East of England	0	0	0	0.0%
London	4	2	6	15.8%
North East	0	0	0	0.0%
North West	3	0	3	7.9%
South East	15	0	15	39.5%
South West	2	0	2	5.3%
West Midlands	10	0	10	26.3%
Yorkshire and Humber	0	0	0	0.0%
Unknown region	1	0	1	2.6%
Total	**36**	**2**	**38**	-

[1] Genotyping is used to identify variants Alpha, Beta, Delta and Gamma; targets were updated in mid-May 2021 to prioritise accurate identification of Delta over Alpha

Figure 23. Delta-AY.1 cases (confirmed sequencing and probable genotyping) by region of residence and specimen date as of 14 June 2021. Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data).

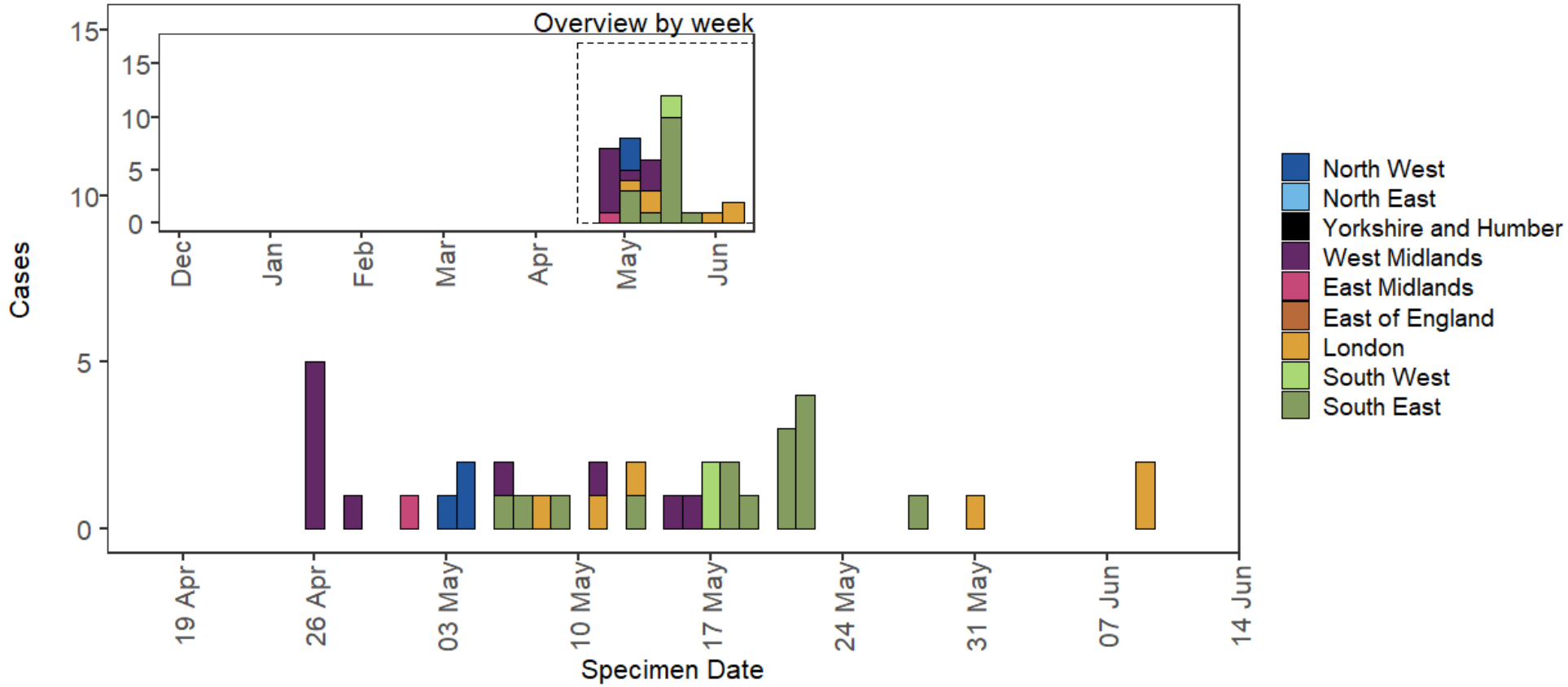
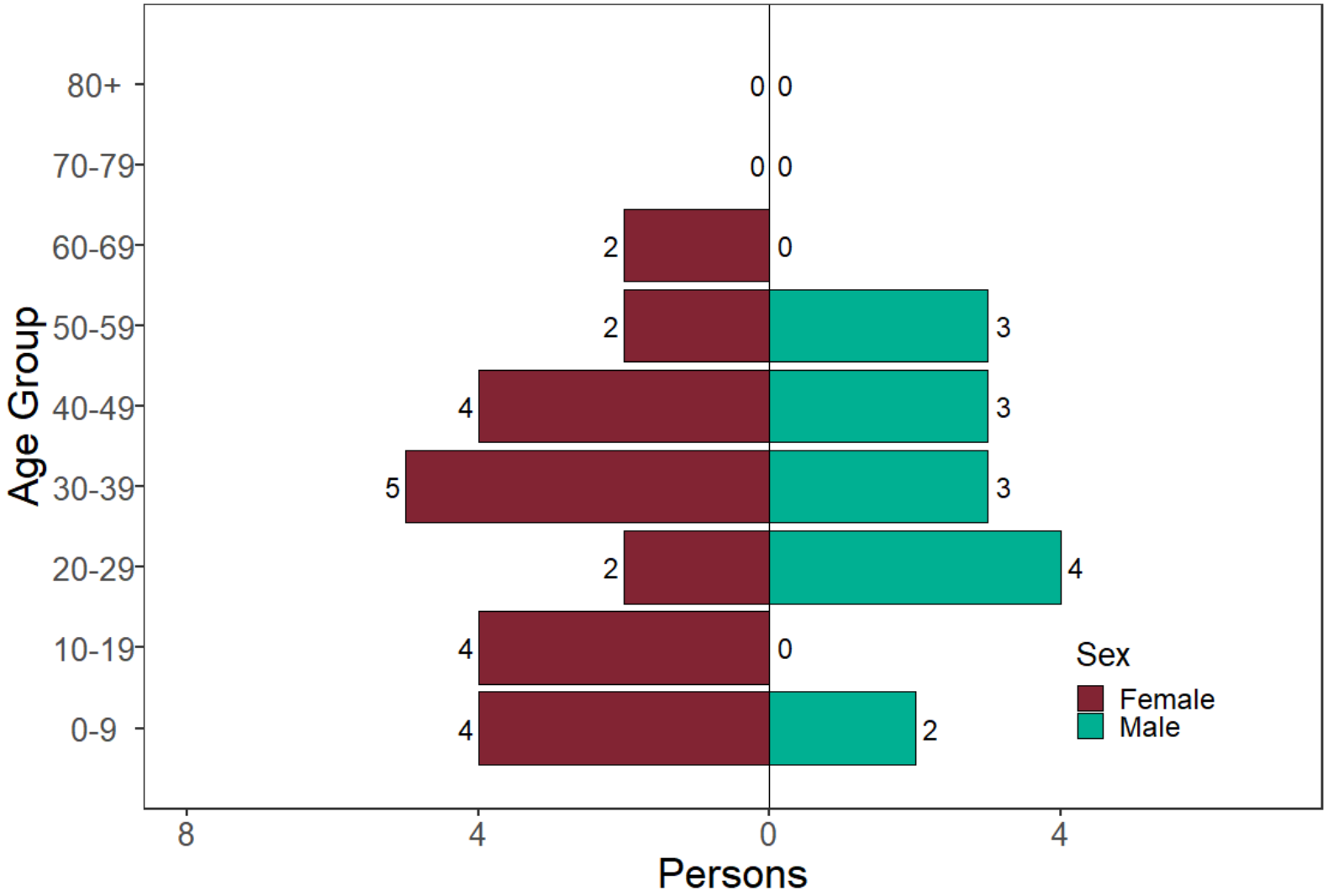


Figure 24. Age-sex pyramid of confirmed (sequencing) and probable (genotyping) Delta-AY.1 cases as of 14 June 2021
(Find accessible data used in this graph in underlying data)



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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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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