Public Health England

Protecting and improving the nation's health

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

Technical briefing 17

25 June 2021

This briefing provides an update on previous briefings up to 18 June 2021

Contents

Summary

There are 4 current 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) and Lambda (C.37, VUI-21JUN-01). 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:

- the Delta variant accounted for approximately 95% of sequenced and 92% genotyped cases from 7 to 21 June 2021
- an operational issue at a sequencing facility resulted in a reduction in genome coverage for specimen dates 10 to 15 June 2021 (sequenced between 14 to 18 June) and may impact variant sequencing counts in figures and tables for this limited period; genotyping was not affected (see Note 1)
- C.37 (Lambda), previously a signal in monitoring, was designated a new Variant Under Investigation on 23 June 2021 based on global spread and a novel combination of mutations; further data is provided
- very preliminary results for live virus neutralisation of AY.1 (a lineage of Delta with K417N), with a small number of sera from vaccine recipients are reassuring, however further testing is required (data provided by Genotype to Phenotype consortium)
- PCR cycle threshold (Ct) values appear to be persistently lower in Delta than Alpha cases based on routine national testing data

The risk assessment for Delta is published separately and was last updated on 25 June 2021.

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

Note 1: From 14 to 18 June 2021 an operational issue at a sequencing site resulted in a reduction in the number of samples with sequencing data of sufficient quality for variant assignment. There were 19,502 samples reported to PHE as impacted by the incident. PHE has received approximately 10,000 sample identifiers from the list of those affected of which sequencing data has been obtained for approximately 4,300 and genotyping data for 3,300 have a reflex assay result. Approximately 9,000 samples are pending analysis and for approximately 2,400 samples variant assignment is not possible. This issue resulted in a reduction in genome coverage for specimen dates 10 to 15 June 2021 and

may impact variant counts in figures and tables for this limited period. The unusable samples were from locations distributed around the UK and the proportions of different variants by region should be correct. In addition, the genotyping results means that this has limited impact in the interpretation of the overall data.

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 from 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 briefings from 15 onwards include 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 2, case numbers are also updated online. Tables 2, 3 and 4 show hospitalisation and death data. Figure 2 shows cumulative cases of variants over time.

Table 1. Variant lineage and designation as of 21 June 2021 (provisionally extinct variants removed)

World Health Organization nomenclature as of 21 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
Lambda^	C.37	VUI-21JUN-01	VUI
	B.1.1.7 with E484K	VOC-21FEB-02	*Monitoring
Epsilon	B.1.427/B.1.429		Monitoring

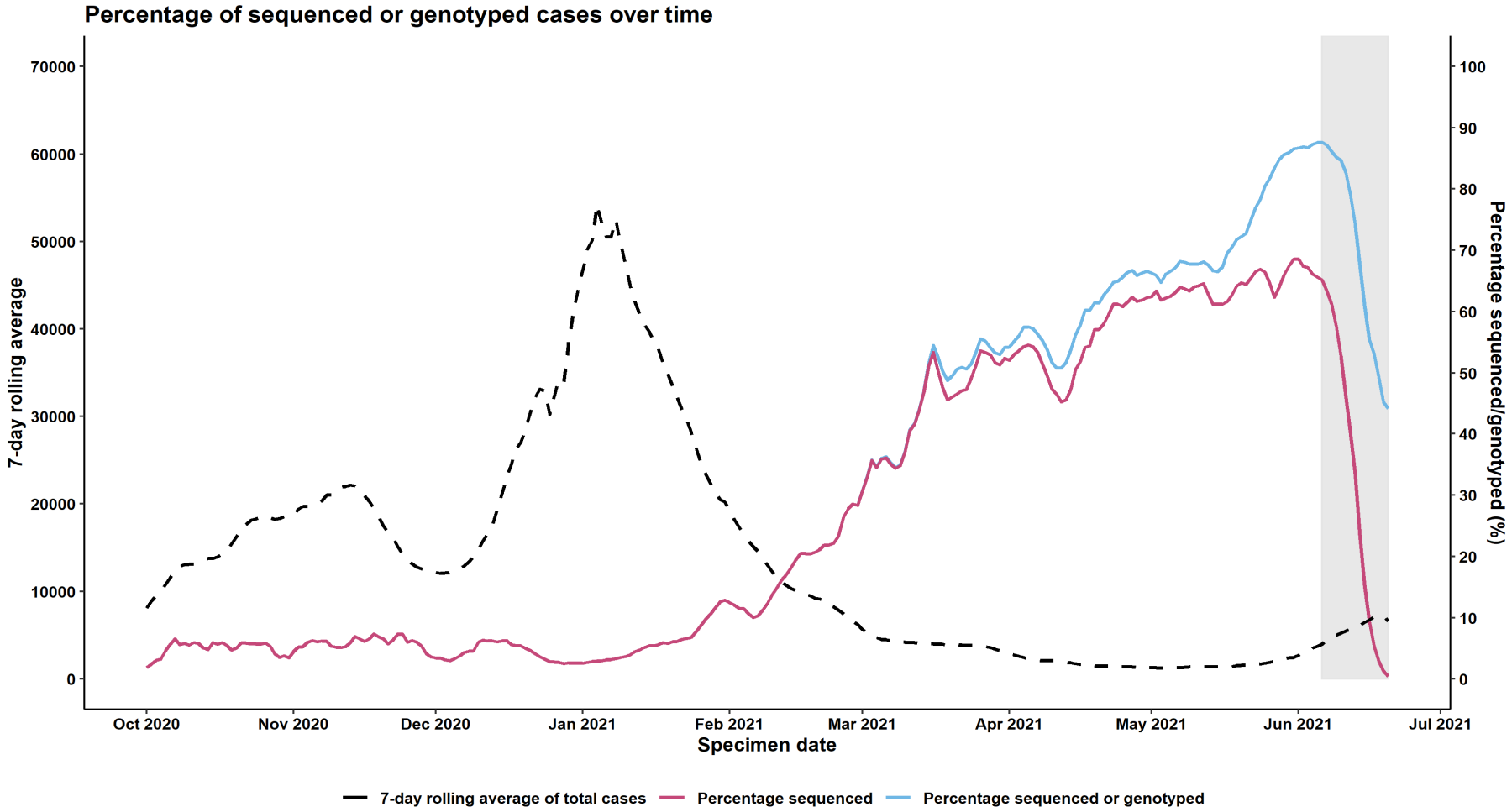
World Health Organization nomenclature as of 21 June 2021	Lineage	Designation	Status
	B.1.1.7 with S494P		Monitoring
	A.27		Monitoring
Iota	B.1.526		Monitoring
	B.1.1.7 with Q677H		Monitoring
	B.1.620		Monitoring
	B.1.214.2		Monitoring
	R.1		Monitoring
	B.1.621		Monitoring
	B.1 with 214insQAS		Monitoring
	AT.1		Monitoring
	Lineage A with R346K, T478R and E484K		Monitoring
	Delta like variant with E484A		Monitoring
	P.1 + N501T and E484Q		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 and as a variant under investigation by Public Health England on the 23 June 2021.

Sequencing coverage

Figure 1. Coverage of sequencing: percentage of SARS-CoV-2 cases sequenced over time as of 21 June 2021 (including genotyping data). (Find accessible data used in this graph in underlying data)



Data extract from 21 June 2021; data from 01 October 2020 to 20 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 or 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. Number of confirmed (sequencing) and probable (genotyping) cases by variant as of 21 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	219,570	5,515	225,085	70.3%	4,262	1.9% (1.8 - 2.0%)	219,948	4,259	1.9% (1.9 - 2.0%)
Beta	892	54	946	0.3%	13	1.4% (0.7 - 2.3%)	874	13	1.5% (0.8 - 2.5%)
Delta	50,283	41,773	92,056	28.8%	117	0.1% (0.1 - 0.2%)	11,250	32	0.3% (0.2 - 0.4%)
Eta	442	0	442	0.1%	12	2.7% (1.4 - 4.7%)	431	12	2.8% (1.4 - 4.8%)
Gamma	180	45	225	0.1%	0	0.0% (0.0 - 1.6%)	161	0	0.0% (0.0 - 2.3%)
Kappa	439	0	439	0.1%	1	0.2% (0.0 - 1.3%)	420	1	0.2% (0.0 - 1.3%)
Theta	7	0	7	0.0%	0	0.0% (0.0 - 41.0%)	5	0	0.0% (0.0 - 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
VUI-21APR-03	13	0	13	0.0%	0	0.0% (0.0 - 24.7%)	13	0	0.0% (0.0 - 24.7%)
VUI-21FEB-04	279	0	279	0.1%	1	0.4% (0.0 - 2.0%)	246	1	0.4% (0.0 - 2.2%)
VUI-21MAY-01	177	0	177	0.1%	1	0.6% (0.0 - 3.1%)	135	1	0.7% (0.0 - 4.1%)
VUI-21MAY-02	133	0	133	0.0%	0	0.0% (0.0 - 2.7%)	117	0	0.0% (0.0 - 3.1%)
Zeta	54	0	54	0.0%	1	1.9% (0.0 - 9.9%)	53	1	1.9% (0.0 - 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 (sequencing and genotyping) COVID-19 cases in England, 1 February 2021 to 21 June 2021

Variant	Age group (years)	Cases Since 1 Feb	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	<50	117,263	4,224	3.6	4,888	4.2	5,731	4.9	1,224	1.0	1,676	1.4	66	0.1
	≥50	32,289	453	1.4	3,127	9.7	4,592	14.2	1,721	5.3	2,792	8.6	1,551	4.8
Beta	<50	575	45	7.8	21	3.7	23	4.0	5	0.9	8	1.4	1	0.2
	≥50	165	11	6.7	17	10.3	25	15.2	7	4.2	15	9.1	7	4.2
Delta	<50	82,458	71,311	86.5	2,013	2.4	2,728	3.3	564	0.7	902	1.1	8	0.0
	≥50	9,571	8,025	83.8	393	4.1	732	7.6	181	1.9	418	4.4	109	1.1
Eta	<50	272	6	2.2	11	4.0	13	4.8	5	1.8	6	2.2	0	0.0
	≥50	116	-	0.0	4	3.4	7	6.0	1	0.9	3	2.6	6	5.2
Gamma	<50	207	58	28.0	7	3.4	7	3.4	1	0.5	1	0.5	0	0.0
	≥50	18	3	16.7	1	5.6	1	5.6	-	0.0	-	0.0	0	0.0
Kappa	<50	377	9	2.4	10	2.7	11	2.9	1	0.3	2	0.5	0	0.0

Variant	Age group (years)	Cases Since 1 Feb	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	%
	≥50	62	4	6.5	5	8.1	5	8.1	2	3.2	2	3.2	1	1.6
Theta	<50	4	-	0.0	1	25.0	1	25.0	-	0.0	-	0.0	0	0.0
	≥50	3	-	0.0	-	0.0	-	0.0	-	0.0	-	0.0	0	0.0
VUI-21APR-03	<50	11	-	0.0	-	0.0	-	0.0	-	0.0	-	0.0	0	0.0
	≥50	2	-	0.0	-	0.0	-	0.0	-	0.0	-	0.0	0	0.0
VUI-21FEB-04	<50	221	27	12.2	6	2.7	9	4.1	1	0.5	2	0.9	0	0.0
	≥50	51	2	3.9	1	2.0	2	3.9	-	0.0	1	2.0	1	2.0
VUI-21MAY-01	<50	154	34	22.1	1	0.6	2	1.3	-	0.0	1	0.6	0	0.0
	≥50	23	6	26.1	-	0.0	-	0.0	-	0.0	-	0.0	1	4.3
VUI-21MAY-02	<50	102	12	11.8	8	7.8	9	8.8	2	2.0	3	2.9	0	0.0
	≥50	31	1	3.2	-	0.0	-	0.0	-	0.0	-	0.0	0	0.0
Zeta	<50	16	-	0.0	-	0.0	-	0.0	-	0.0	-	0.0	0	0.0
	≥50	8	-	0.0	1	12.5	1	12.5	1	12.5	1	12.5	0	0.0

Data sources: Emergency care attendance and admissions from Emergency Care Dataset (ECDS), deaths from PHE daily death data series (deaths within 28 days). NHS trusts are required to submit emergency care attendances by the 21st of each month. As a result, the number of cases with attendances may show substantial increases in technical briefs prepared after the monthly cut-off, compared with other briefs from the same month.
¥ 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.

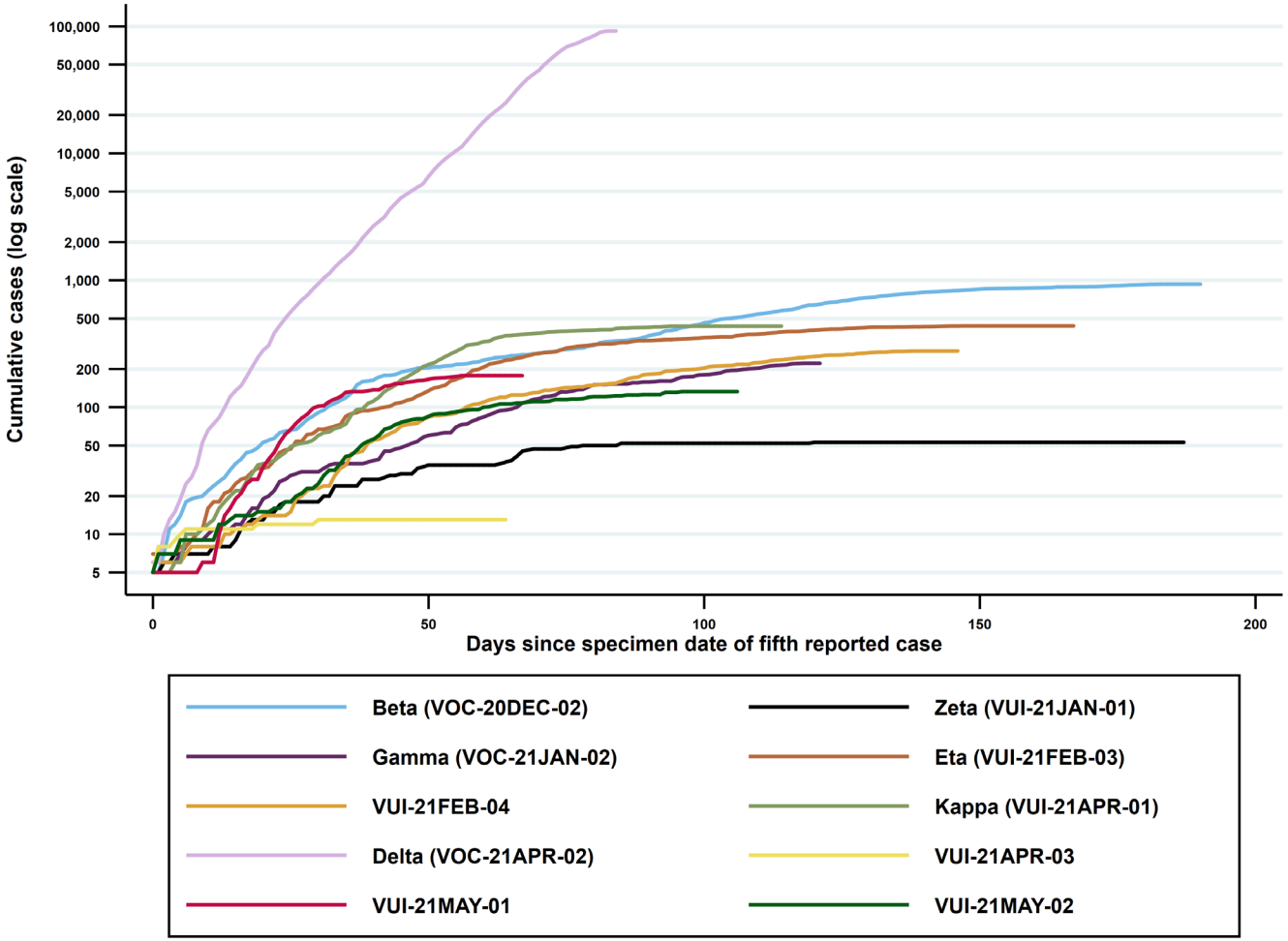
Table 4. Attendance to emergency care and deaths by vaccination status among Delta confirmed cases (sequencing and genotyping) including all confirmed Delta cases in England, 1 February 2021 to 21 June 2021

	Age group (years)	Total	Cases with specimen date in past 28 days	Unlinked	<21 days post dose 1	≥21 days post dose 1	Received 2 doses	Unvaccinated
Delta cases	All cases	92,029	79,336	11,015	6,242	13,715	7,235	53,822
	<50	82,458	71,311	9,892	6,154	9,850	3,689	52,846
	>50	9,571	8,025	1,123	88	3,865	3,546	976
Cases with an emergency care visit§ (excluding cases with the same specimen and attendance dates)‡	All cases	2,406	N/A	33	186	426	190	1,571
	<50	2,013	N/A	25	183	259	68	1,478
	>50	393	N/A	8	3	167	122	93
Cases with an emergency care visit§ (including cases with the same specimen and attendance dates)	All cases	3,460	N/A	51	249	564	348	2,248
	<50	2,728	N/A	40	238	321	94	2,035
	>50	732	N/A	11	11	243	254	213
Cases where presentation to emergency care resulted in overnight inpatient admission§ (excluding cases with the same specimen and attendance dates)‡	All cases	745	N/A	11	55	115	80	484
	<50	564	N/A	8	52	55	17	432
	>50	181	N/A	3	3	60	63	52
Cases where presentation to emergency care resulted in overnight inpatient admission§ (including cases	All cases	1,320	N/A	22	88	189	190	831
	<50	902	N/A	16	79	85	27	695
	>50	418	N/A	6	9	104	163	136

	Age group (years)	Total	Cases with specimen date in past 28 days	Unlinked	<21 days post dose 1	≥21 days post dose 1	Received 2 doses	Unvaccinated
with the same specimen and attendance dates)								
Deaths within 28 days of positive specimen date	Total	117	N/A	3	1	19	50	44
	<50	8	N/A	-	-	2	-	6
	>50	109	N/A	3	1	17	50	38

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 21 June 2021
(Find accessible data used in this graph in underlying data). Figure 2 demonstrates the rapid growth of Delta cases since its first detection relative to other variants.



Variant prevalence

The prevalence of different variants amongst all sequenced cases is presented in Figures 3 and 4, split by region in Figures 5 and 6 and by travel status in Figures 7 and 8. Technical briefings from 15 onwards include 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. Genotyping allows shorter turnaround time (12-24h after initial confirmation of COVID-19) for a probable variant result. The initial panel of targets began trials in March 2021, using single nucleotide polymorphisms (SNPs): N501Y, E484K, K417N and K417T. Results have been reported and used for public health action since 29 March 2021. On 11 May 2021, after rapid validation of targets to allow identification of Delta variant, P681R was introduced in the panel to replace N501Y. Genotyping results have now been fully integrated into the Variant data reports and analyses. 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 8 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.

Delta variant accounted for approximately 95% of sequenced and 92% genotyped cases from 7 to 21 June 2021.

Figure 3. Variant prevalence for all England available genotyped cases from 1 February 2021 as of 21 June 2021 (excluding 1 case where the specimen date was unknown). (Find accessible data used in this graph in underlying data).

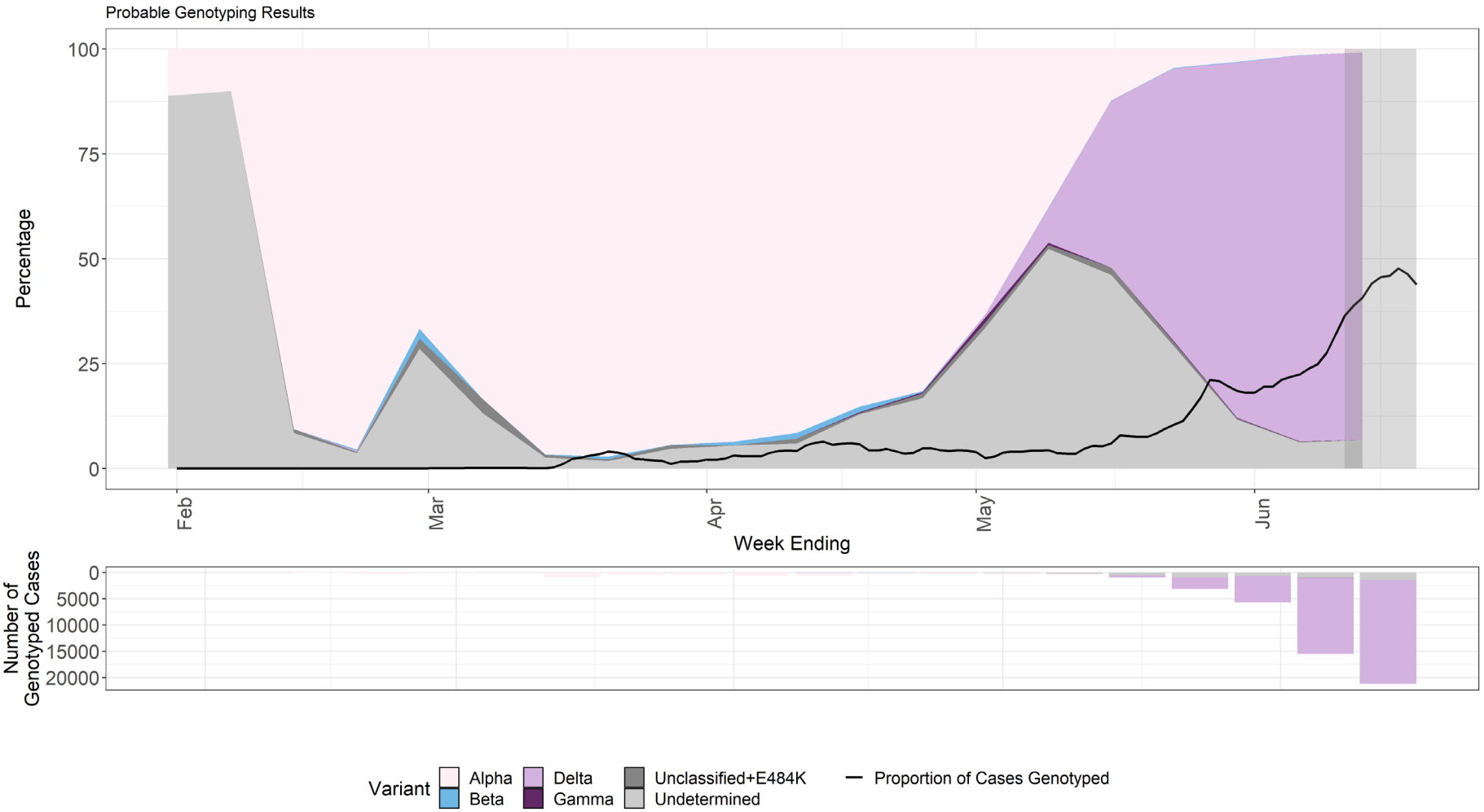


Figure 4. Variant prevalence for all England available sequenced cases from 1 February 2021 as of 21 June 2021 (excluding 1 case where the specimen date was unknown). (Find accessible data used in this graph in underlying data).

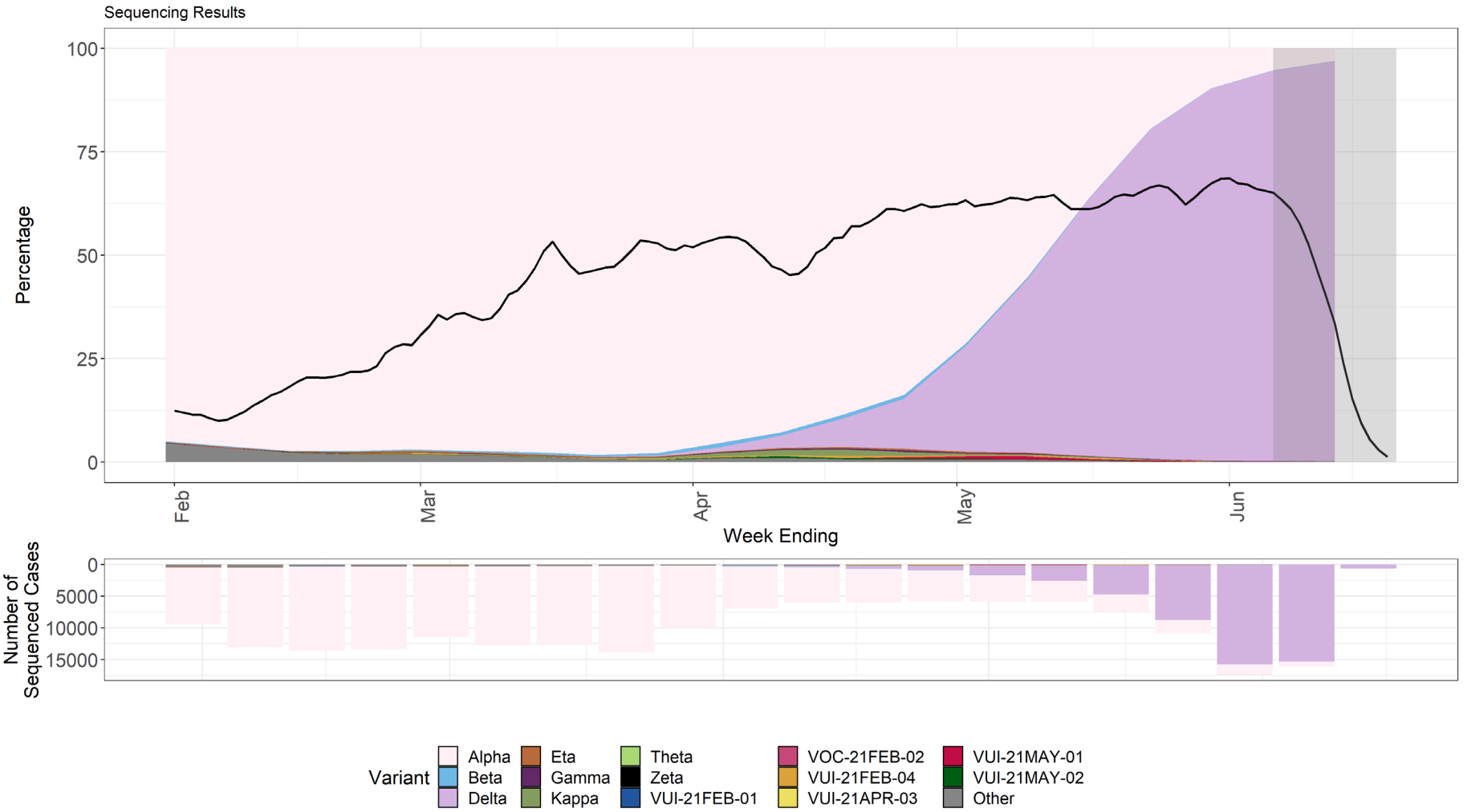


Figure 5. Variant prevalence from 1 February 2021 as of 21 June 2021 by region for all genotyped cases in England (excluding 282 cases where the region or specimen date were unknown). (Find accessible data used in this graph in underlying data).

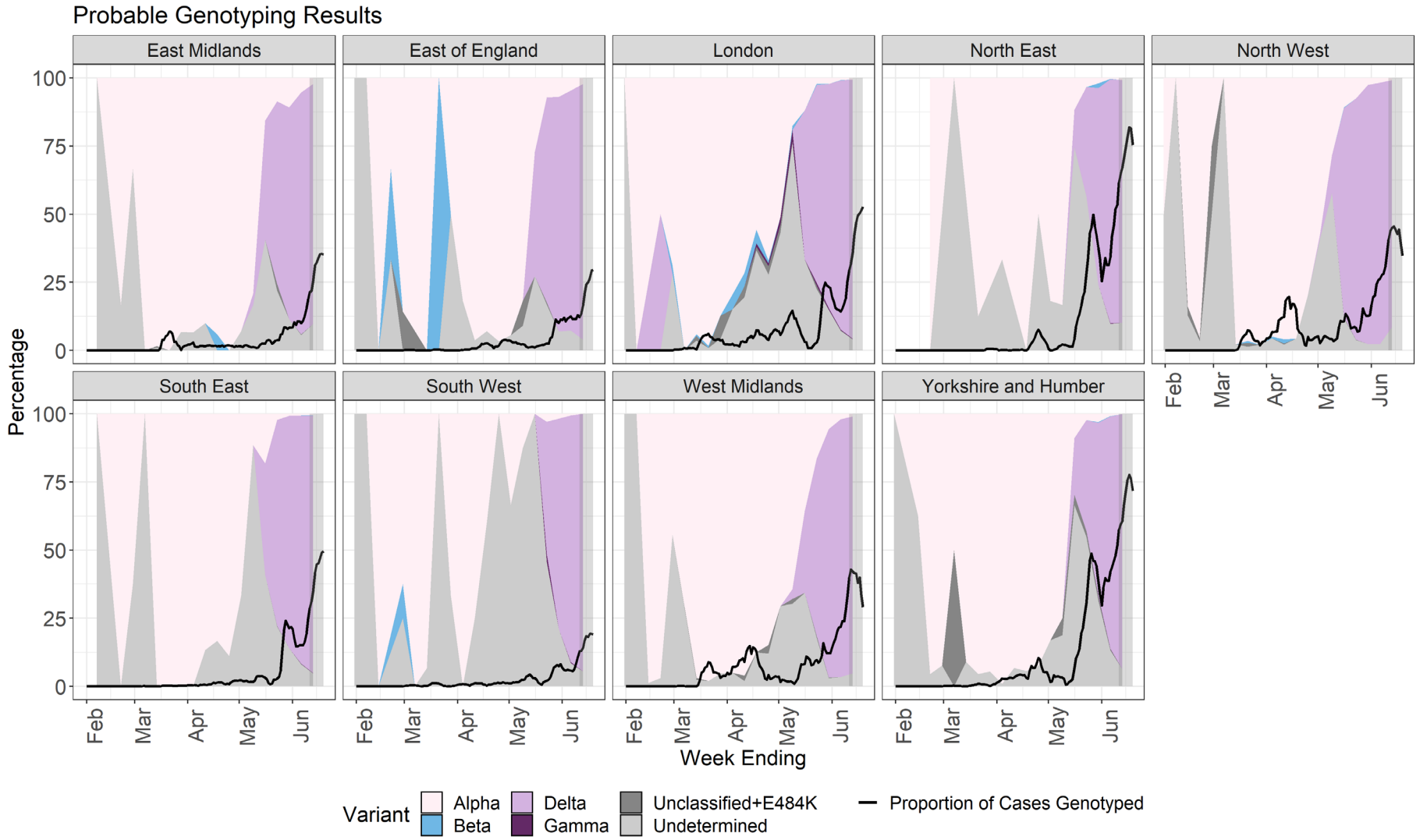


Figure 6. Variant prevalence from 1 February 2021 as of 21 June 2021 by region for all sequenced cases in England (excluding 282 cases where the region or specimen date were unknown). (Find accessible data used in this graph in underlying data).

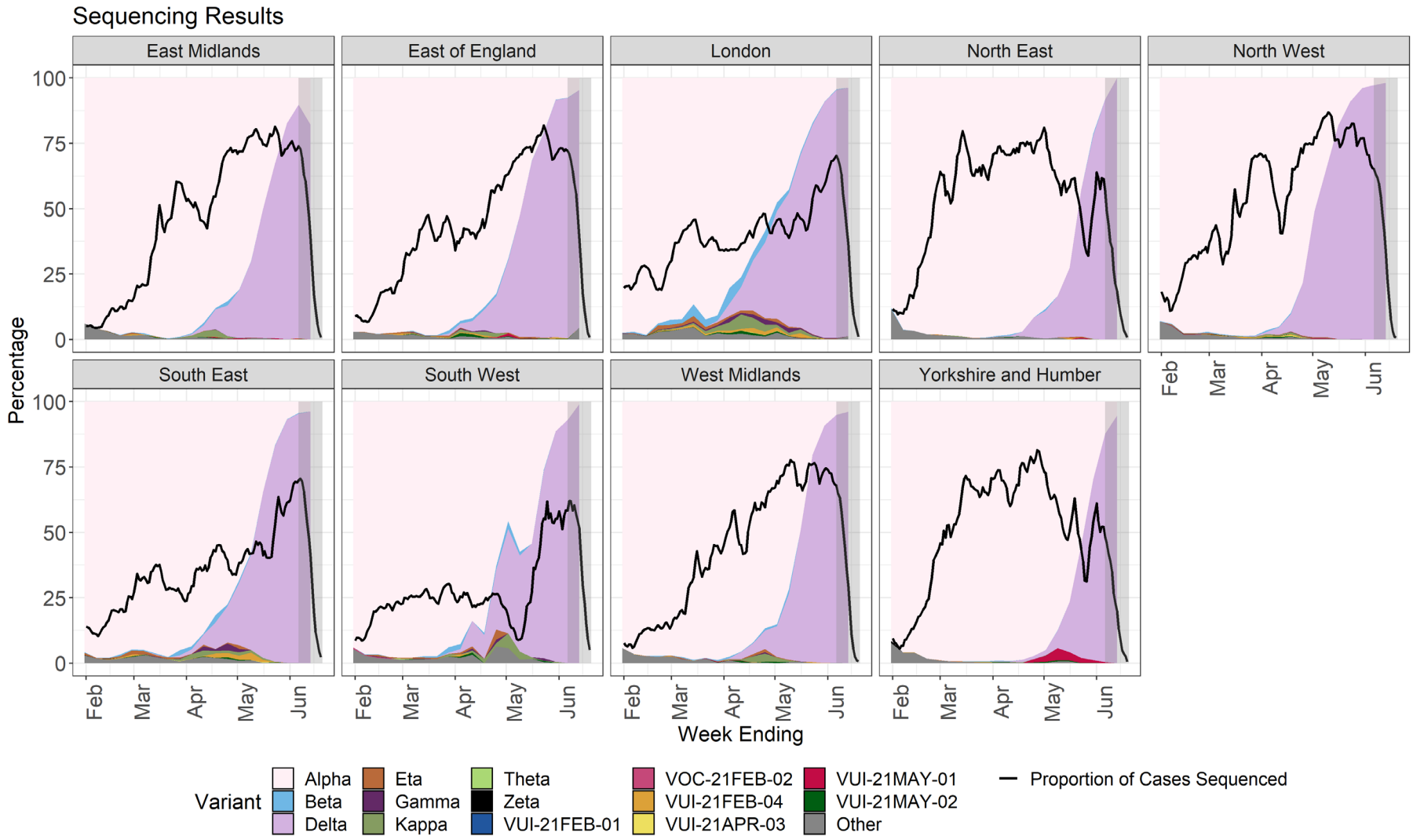


Figure 7. Prevalence of variants over time: all genotyped cases in England, split by travel status as of 21 June 2021.
Travel-linked variant data available until 13 June 2021 only. (Find accessible data used in this graph in underlying data).

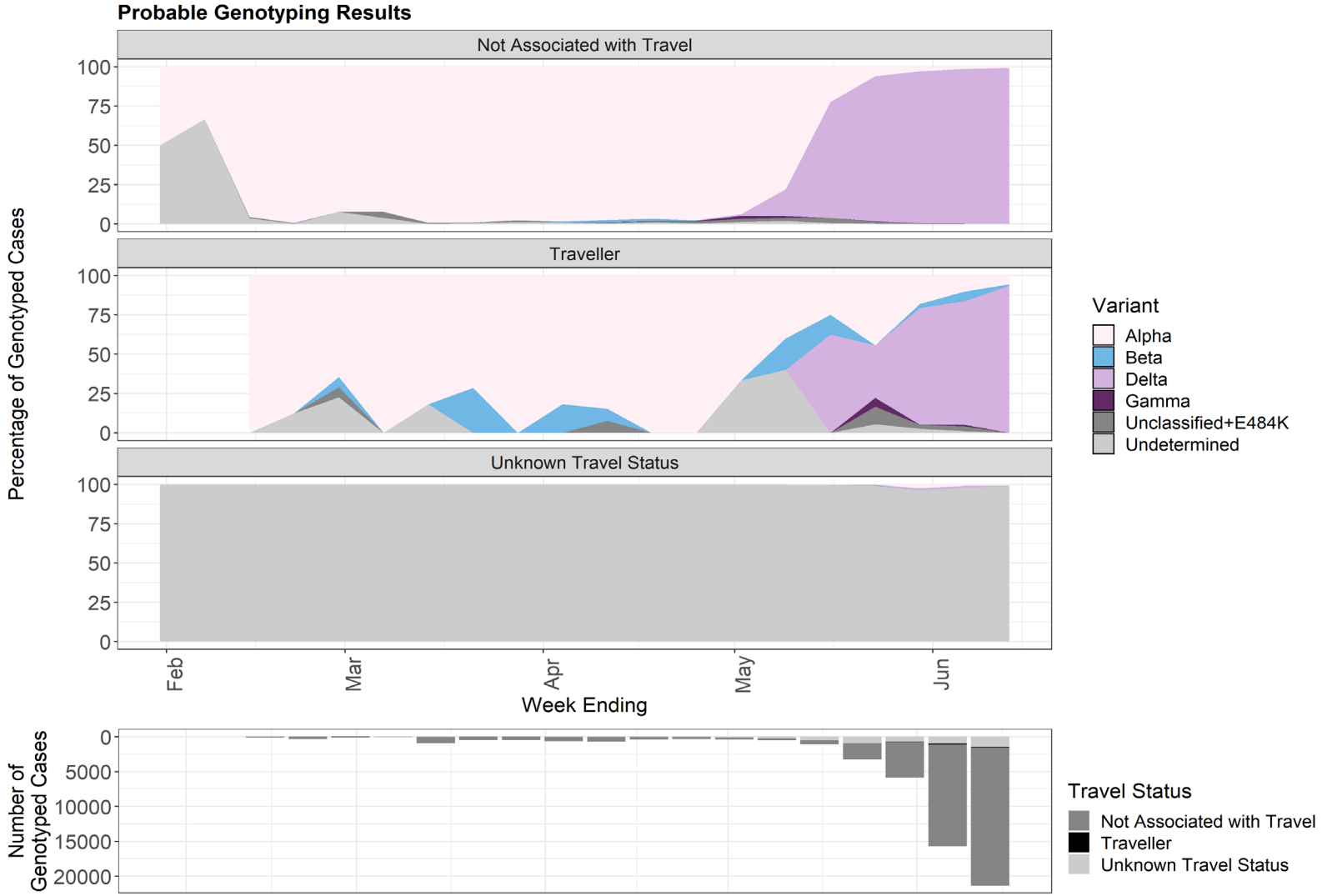
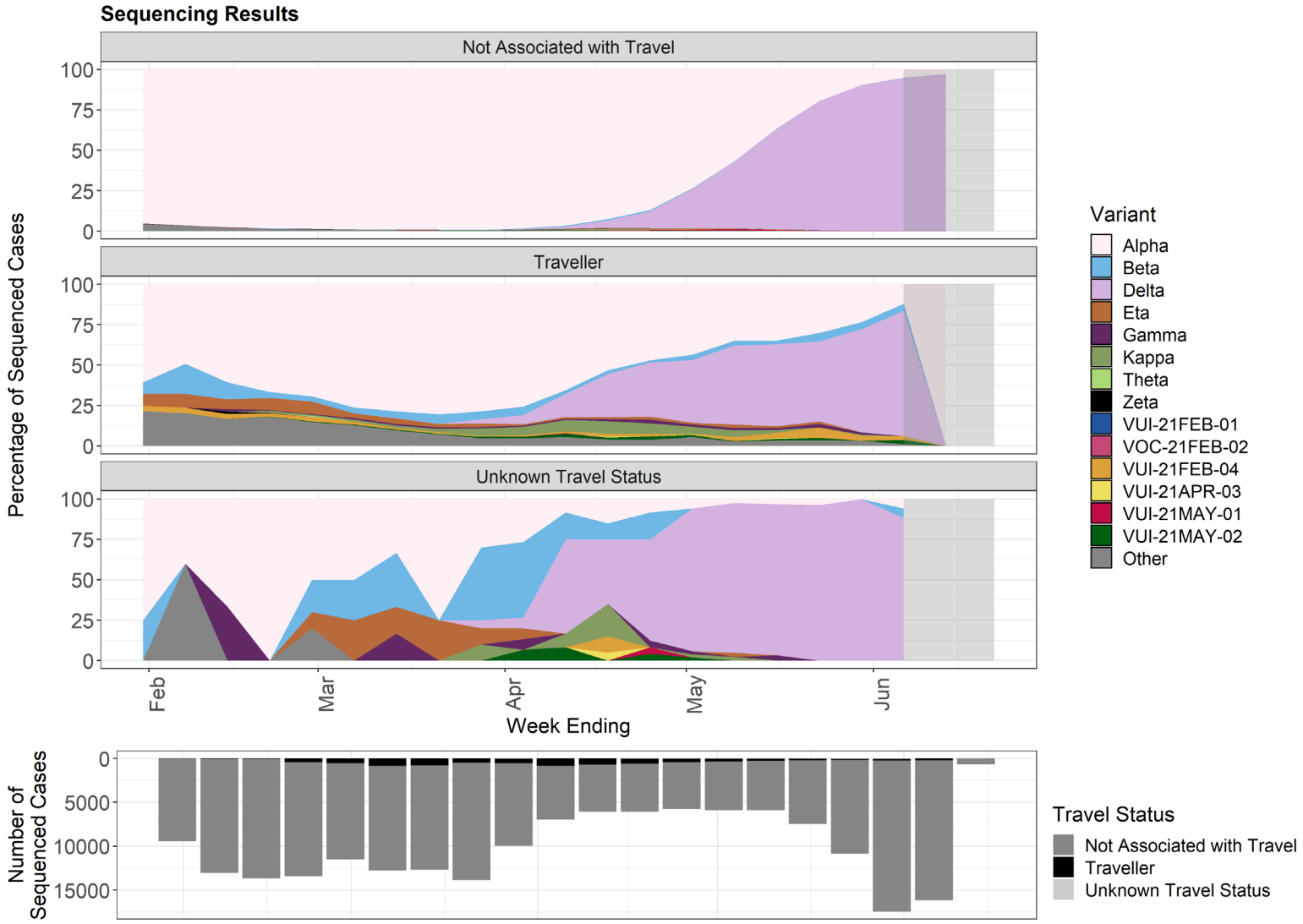


Figure 8. Prevalence of variants over time: all sequenced cases in England, split by travel status as of 21 June 2021. Travel-linked variant data available until 13 June 2021 only. (Find accessible data used in this graph in underlying data).



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 (including transit), 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 supplemented with probable (genotyping) results as of 14 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 suggests, but does not confirm, where infection of the original case may have occurred.

Table 5 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 1 June 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 6 covering 5 January 2021 to 1 June 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: 10.7% (95% CI 10.5% to 10.9%) compared to 7.9% (95% CI 7.7% to 8.0%). 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 6 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 1 June 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 7 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 1 June 2021 as in Table 5. Secondary attack rates are higher amongst household contacts than non-household contacts of non-travel cases with both variants and higher for contacts of non-travel cases with Delta than Alpha; this is consistent with Table 5.

Figure 9 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 30 May 2021, with 95% confidence intervals. The fall in secondary attack rate amongst household contacts of cases with Delta in previous weeks has now levelled, with an estimate of 12.0% (95% CI 11.6% to 12.4%) for exposure events in week commencing 24 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. Secondary attack rates amongst household contacts of cases with Alpha also peaked in week commencing 26 April, though the increase up to that week and decline since that week are modest.

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 1 June 2021, variant data as at 14 June 2021, contact tracing data as at 22 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	2,111 (69.9% with contacts)	40,364 (82.5% with contacts)	5.0%	1.4% (1.3% - 1.6%) [527/36,713]	7.9% (7.7% - 8.0%) [8,474/107,791]
Kappa	187 (75.9% with contacts)	139 (79.9% with contacts)	57.4%	2.0% (1.6% - 2.5%) [62/3107]	10.3% (7.5% - 13.9%) [36/351]
Delta	805 (69.1% with contacts)	32,376 (84.1% with contacts)	2.4%	2.2% (2.0% - 2.5%) [296/13,449]	10.7% (10.5% - 10.9%) [10,043/93,549]
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 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 1 June 2021 in order to allow time for contacts to become cases, hence case counts are lower than other sources. Cases are included in case counts if their onset or (if asymptomatic) test is during the period of study. Contacts are included in secondary attack rates if their exposure date (or onset or test of exposing case if the contact is a household contact) is during the period of study. 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 1 June 2021, variant data as of 14 June 2021, contact tracing data as of 22 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	4,307 (76.6% with contacts)	182,269 (75.0% with contacts)	2.3%	1.6% (1.5% - 1.7%) [1,256/79,820]	9.6% (9.5% - 9.7%) [37,534/389,848]
Beta	320 (71.9% with contacts)	397 (68.0% with contacts)	44.6%	2.1% (1.8% - 2.5%) [111/5,248]	8.4% (6.7% - 10.4%) [75/894]
Zeta	4 (75.0% with contacts)	27 (74.1% with contacts)	12.9%	Unavailable [0/160]	7.7% (3.0% - 18.2%) [4/52]
Gamma	69 (65.2% with contacts)	105 (72.4% with contacts)	39.7%	1.0% (0.5% - 2.0%) [9/863]	10.3% (7.0% - 14.8%) [24/234]
Eta	194 (70.1% with contacts)	198 (73.2% with contacts)	49.5%	1.1% (0.8% - 1.5%) [47/4,240]	8.4% (6.0% - 11.6%) [32/380]
VUI-21FEB-04	100 (67.0% with contacts)	145 (78.6% with contacts)	40.8%	0.5% (0.3% - 0.8%) [16/3,054]	8.2% (5.8% - 11.6%) [29/352]
Theta	5 (40.0% with contacts)	1 (100.0% with contacts)	83.3%	Unavailable [0/5]	Unavailable [0/3]
VUI-21MAY-01	2 (0.0% with contacts)	158 (84.8% with contacts)	1.2%	Unavailable [0/0]	6.8% (4.9% - 9.3%) [33/488]
VUI-21MAY-02	61 (73.8% with contacts)	50 (82.0% with contacts)	55.0%	0.9% (0.5% - 1.6%) [11/1248]	7.1% (3.6% - 13.4%) [8/113]

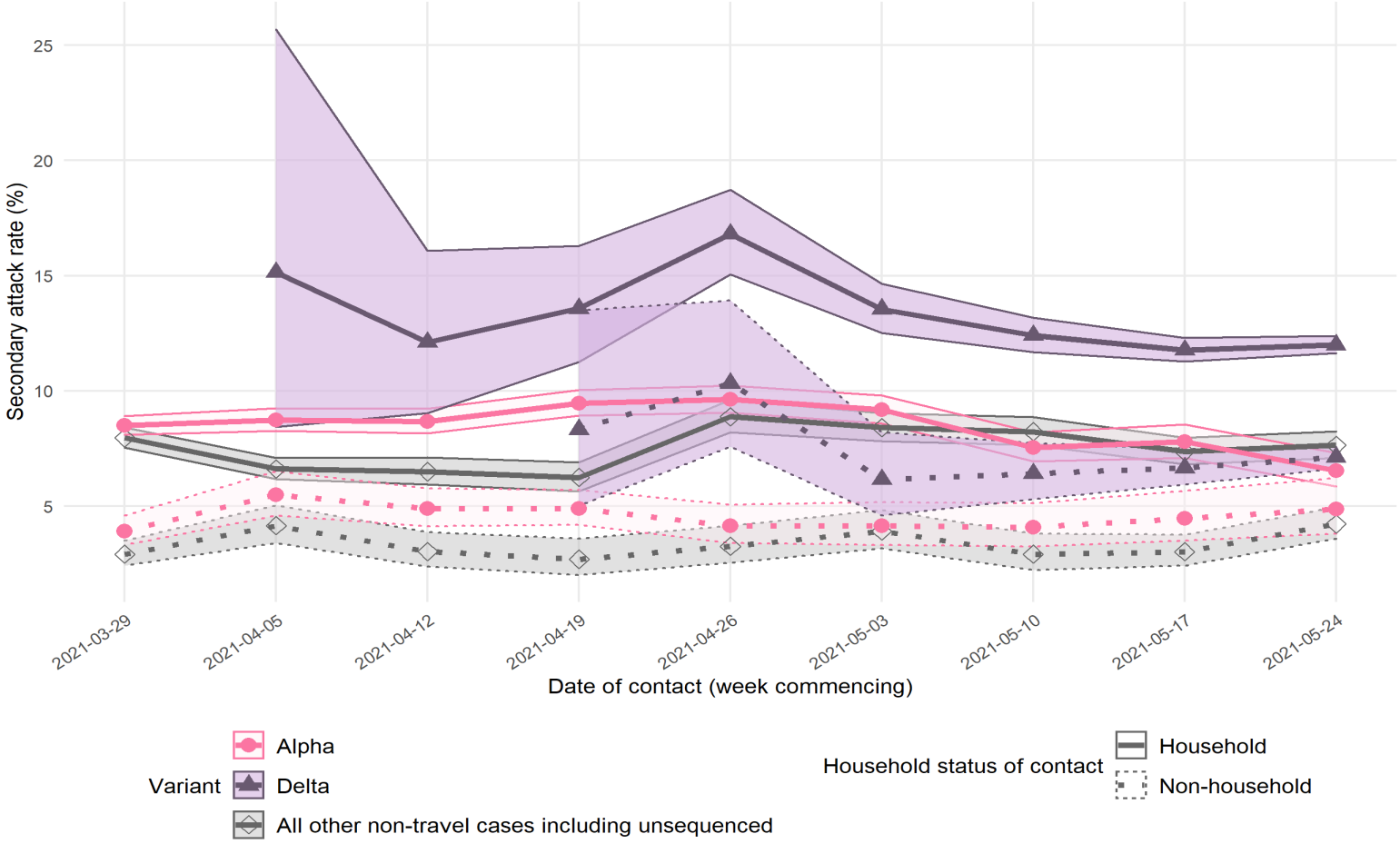
Note legend from Table 5. Data provided is for period until 1 June 2021 in order to allow time for contacts to become cases, hence case counts are lower than other sources. Probable (genotyping) results are included, low quality genomic results are not.

Table 7. Secondary attack rates for household contacts of non-travel cases of Alpha and Delta
(29 March 2021 to 1 June 2021, variant data as of 14 June 2021, contact tracing data as of 22 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	40,364 (80.4% with household, 18.4% with non-household contacts)	8.6% (8.4% - 8.8%) [7,560/87,725]	4.6% (4.3% - 4.9%) [914/20,066]
Delta	32,376 (81.6% with household, 21.1% with non-household contacts)	12.0% (11.7% - 12.2%) [8,659/72,431]	6.6% (6.2% - 6.9%) [1384/21,118]

Note legend from Table 5. Data provided is for period until 1 June 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

Figure 9. 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 30 May 2021, variant data as of 14 June 2021, contact tracing data as of 22 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 cases is less than 20. Data provided is for period until 30 May 2021 in order to allow time for contacts to become cases and complete weeks to be shown. Probable (genotyping) results are included, low quality genomic results are not.

Surveillance of reinfections

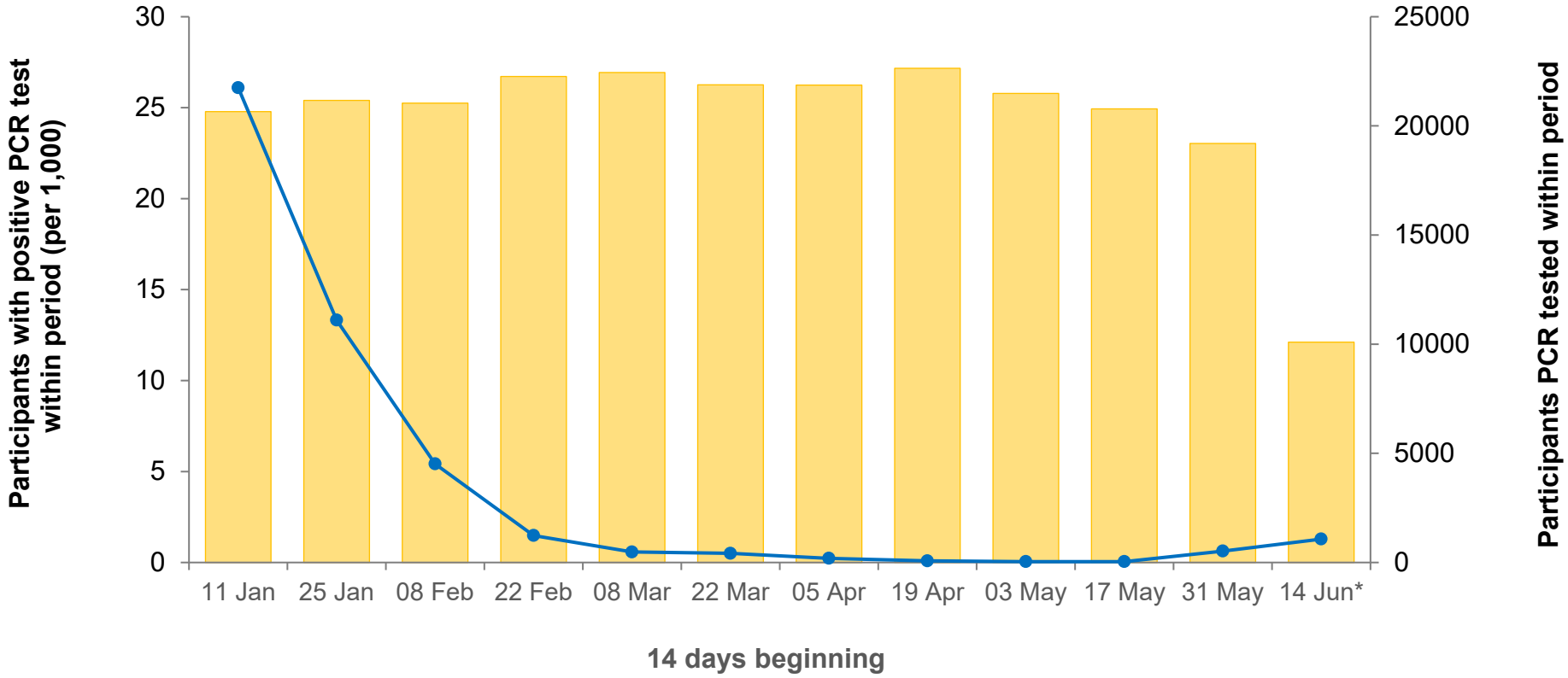
The COVID-19 reinfection surveillance programme aims to look at how long immunity lasts, protection against clinical disease (disease with symptoms) and protection against more severe disease. It is also important to understand whether those who become reinfected can pass the virus on to other people.

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, 35,704* 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. The frequency of PCR positivity in the SIREN cohort overall has increased in June, after very low levels March-May, but remains low (Figure 10). Of the 35 participants with a new PCR positive since April 2021 in the SIREN cohort overall, 28 (80%) occurred 14 days or more following their second vaccine dose. Reinfections remain at very low numbers in individuals previously either PCR positive or seropositive (Figure 11).

*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.

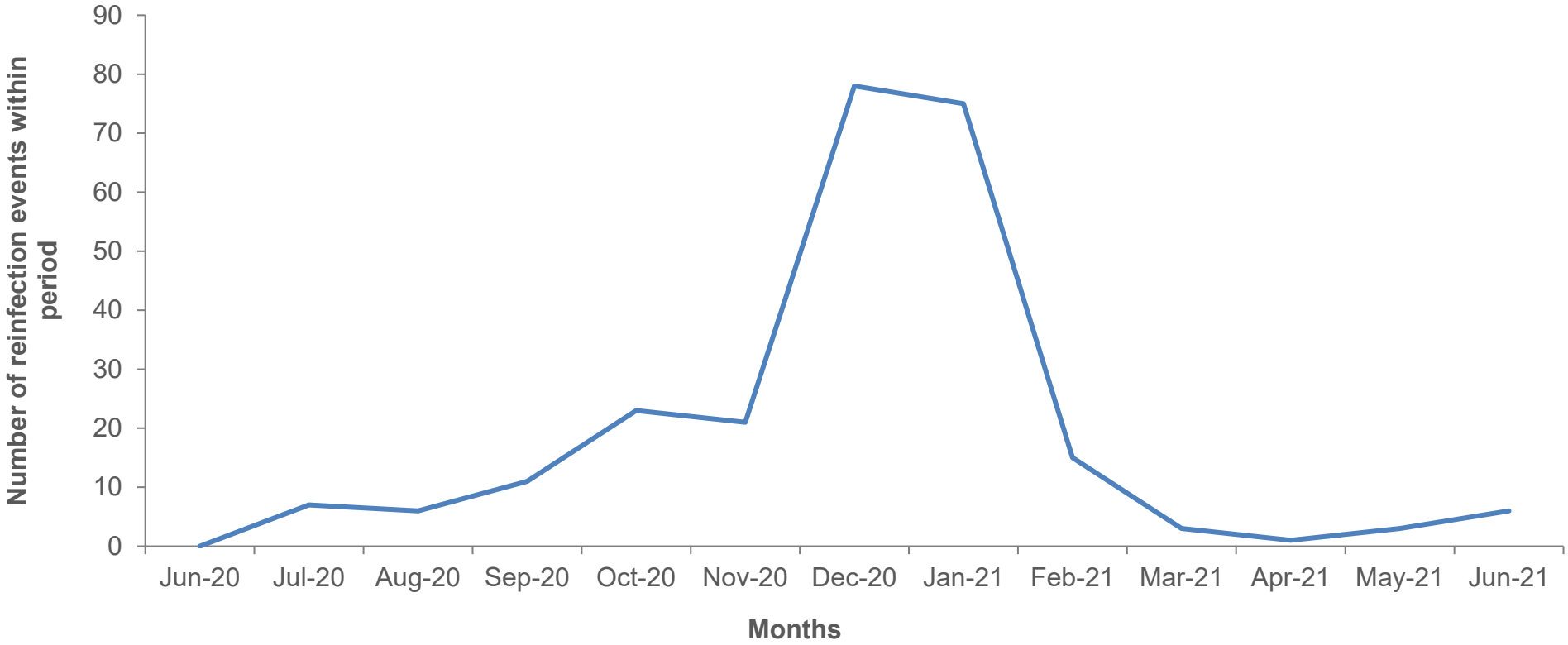
Figure 10. PCR positivity within the SIREN study for all regions, England (fortnightly testing interval) Data up to 20 June 2021. Yellow bars indicate participants PCR-tested within period (right axis), Blue line indicates participants with positive PCR within period (per 1,000) (left axis). (Find accessible data used in this graph in underlying data).



*Incomplete week (14 June to 20 June 2021).

Please note that Figure 9 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. Data has not been restricted by antibody status nor vaccination status; includes only participants from trusts in England.

Figure 11. Monthly frequency of potential reinfection events within SIREN. Data up to 13 June 2021.
(Find accessible data used in this graph in underlying data).



Of the SIREN cohort, 9,813 (31%) 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 13 June 2021, there were 249 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. There were 10 potential reinfection events from April to 13 June 2021, 9 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 and COVID-19 surveillance report.

This section includes information on a subset of these incidents – those suspected SARS-CoV-2 clusters and outbreaks that have at least one confirmed 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. Alpha and Delta variant incidents are not included here because these outbreaks have not been recorded in an equivalent way during the period that these variants are dominant so 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. To track Delta variant incidents it is best to refer to the total number of outbreaks by setting which are reported in the weekly influenza and COVID-19 surveillance report.

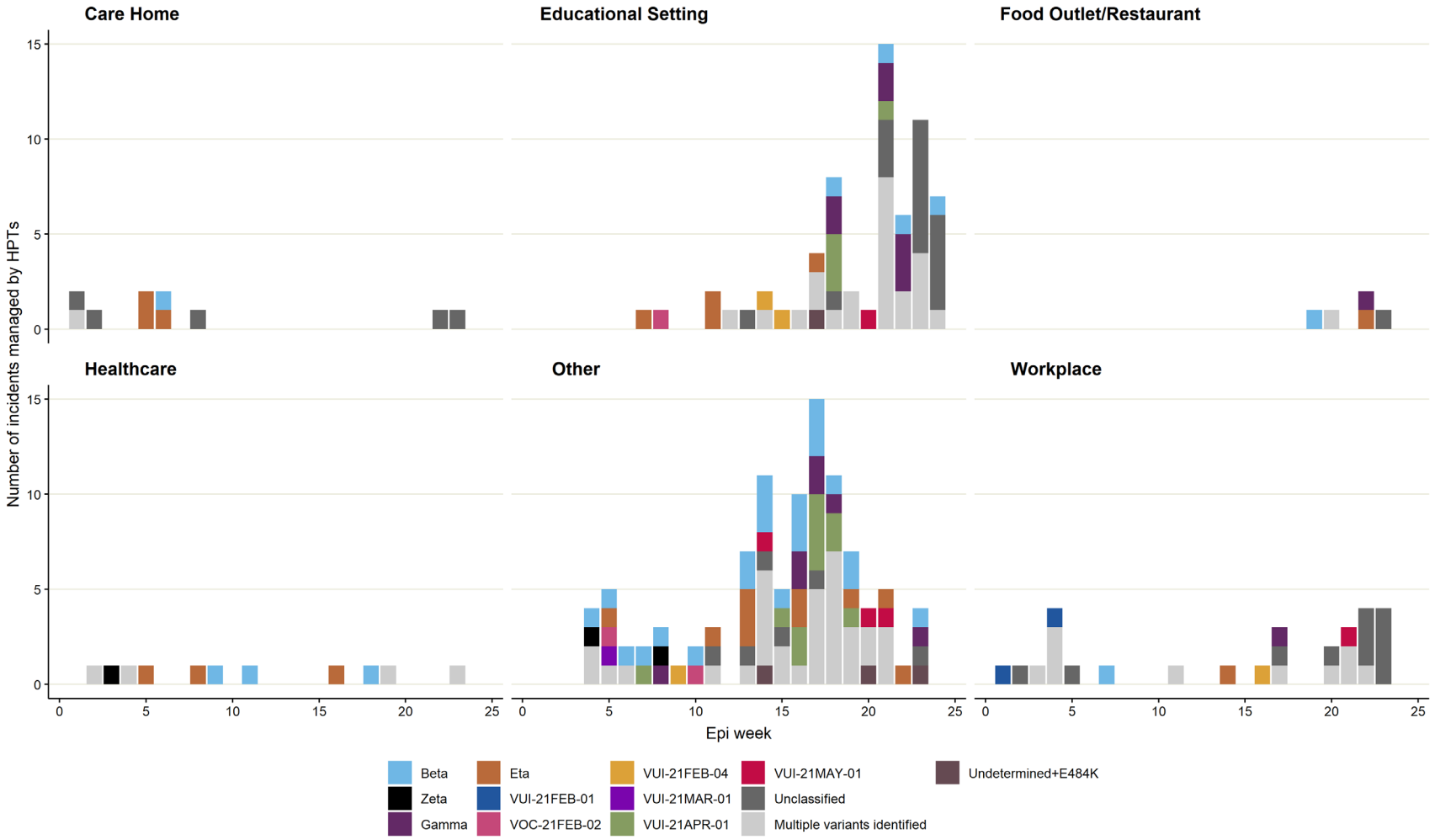
It is important to note that there is a time lag from the suspected outbreak being reported to PHE to genotyping and sequencing being undertaken and variant cases identified so data are provisional and likely to change in subsequent technical briefings.

The data for this chart is available in underlying data.

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 and Delta variant 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 12. Incidents managed by Health Protection Teams involving SARS-CoV-2 variants (excluding Delta) by iso-week, by outbreak setting (4 January 2021 up to 20 June 2021). (Find accessible and auxiliary data used in this graph in underlying data).



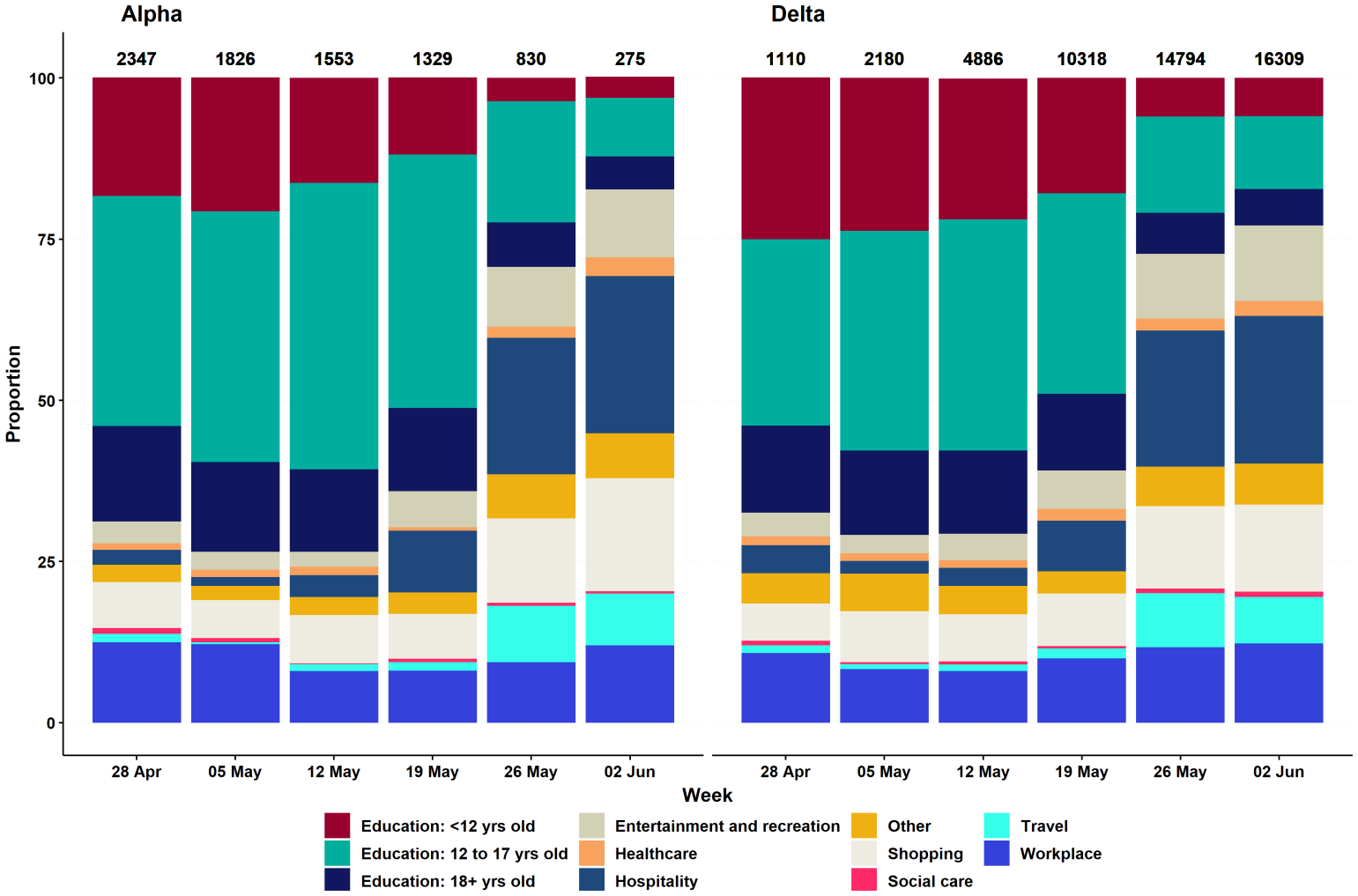
Common exposures derived from contact tracing data

Figure 13 shows the number of common exposure events reported per week, by setting, from week commencing 28 April to week of 2 June 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 settings, for both Alpha and Delta variants, in the first 4 weeks presented in Figure 13. The most recent 2 weeks presented, beginning 26 May and 2 June, include the bank holiday weekend and school half term week. In these most recent 2 weeks, 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 28 April 2021 to week commencing 2 June 2021. Variant data as of 21 June 2021, contact tracing data as of 23 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). These analyses have been reported in technical briefings 15 and 16. 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 21 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 2.4).

Monitoring of vaccine effectiveness

Analysis of routine testing data up to the 13 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 14% absolute reduction in vaccine effectiveness against symptomatic disease with Delta compared to Alpha, and a smaller 10% reduction in effectiveness after 2 doses (Table 8).

Table 8. Vaccine effectiveness against symptomatic disease for Alpha and Delta variants

Vaccination status	Vaccine effectiveness (%)	
	Alpha	Delta
Dose 1	49 (46 to 52)	35 (32 to 38)
Dose 2	89 (87 to 90)	79 (78 to 80)

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 analysis used available data from linkage of symptomatic cases, 12 April to the 10 June 2021 (updated from the previous analysis to 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 9).

Table 9. Vaccine effectiveness against hospitalisation for Alpha and Delta variants

Vaccination status	Vaccine Effectiveness (%)	
	Alpha	Delta
Dose 1	78 (64 to 87)	80 (69 to 88)
Dose 2	93 (80 to 97)	96 (91 to 98)

International surveillance

GISAID includes data on sequences available internationally. As of 22 June 2021, sequences from 71 countries (excluding UK) have been identified in GISAID of Delta: In total 14,606 sequences from: Angola (4), Anguilla (1), Argentina (1), Aruba (3), Australia (183), Austria (22), Bahrain (15), Bangladesh (84), Barbados (3), Belgium (346), Brazil (3), Bulgaria (1), Cambodia (1), Canada (739), China (2), Czech Republic (21), Democratic Republic of the Congo (6), Denmark (94), Finland (2), France (181), Georgia (4), Germany (707), Ghana (1), Greece (4), Guadeloupe (3), Hong Kong (8), India (5427), Indonesia (216), Iran (9), Ireland (211), Israel (64), Italy (221), Japan (206), Jordan (1), Kenya (37), Lithuania (2), Luxembourg (52), Malawi (6), Malaysia (19), Malta (1), Mauritius (2), Mexico (65), Morocco (1), Nepal (45), Netherlands (126), New Zealand (13), Norway (80), Pakistan (6), Peru (1), Philippines (11), Poland (71), Portugal (273), Qatar (26), Reunion (2), Romania (8), Russia (286), Saint Martin (1), Senegal (2), Singapore (818), Slovenia (4), South Africa (20), South Korea (20), Spain (307), Sri Lanka (4), Sweden (161), Switzerland (145), Thailand (89), Turkey (1), USA (3036), Uganda (3), Vietnam (68).

Surveillance through genomic data

Table 10. Number of confirmed (sequencing) and probable (genotyping) cases, by region of residence as of 21 June 2021

Region	Confirmed case number	Provisional case number	Total case number	Proportion of all cases[1]
East Midlands	3,209	1,497	4,706	5.1%
East of England	3,767	1,235	5,002	5.4%
London	7,829	6,070	13,899	15.1%
North East	1,224	4,139	5,363	5.8%
North West	20,846	14,044	34,890	37.9%
South East	4,756	3,790	8,546	9.3%
South West	2,226	1,173	3,399	3.7%
West Midlands	3,554	2,772	6,326	6.9%
Yorkshire and Humber	2,649	6,865	9,514	10.3%
Unknown region	223	188	411	0.4%
Total	50,283	41,773	92,056	-

[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 21 June 2021 (Find accessible data used in this graph in underlying data.).

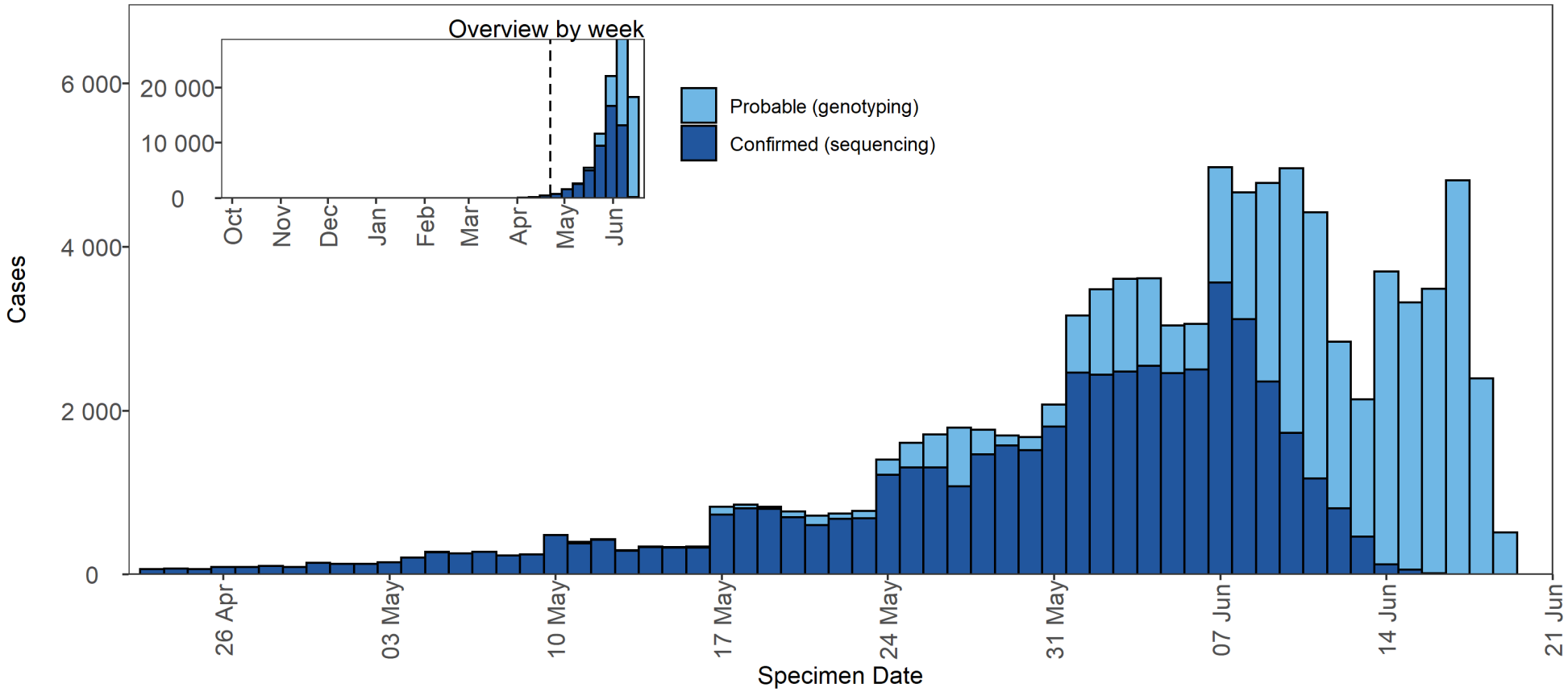


Figure 15. Confirmed (sequencing) and probable (genotyping) Delta cases by specimen date and region of residence as of 21 June 2021 (Find accessible data used in this graph in underlying data.).

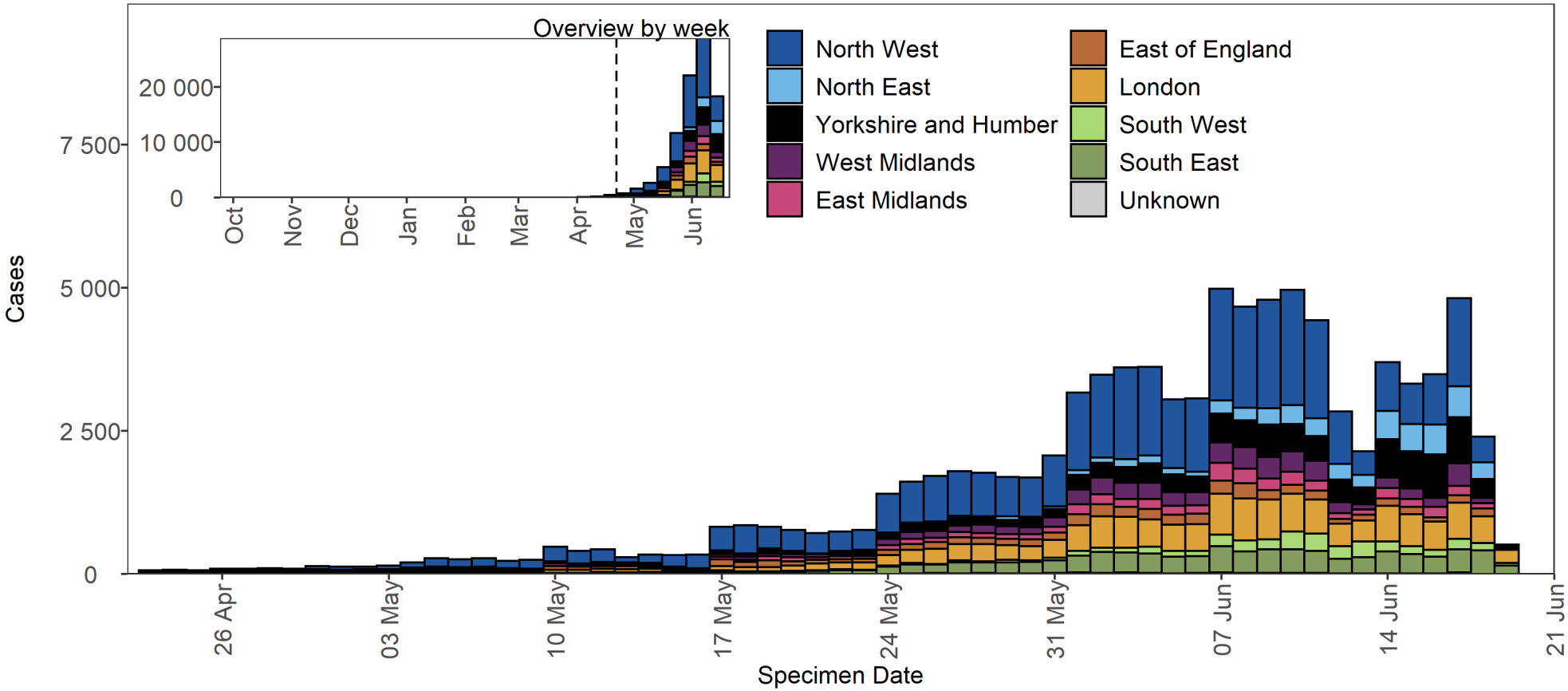


Figure 16. Age-sex pyramid of confirmed (sequencing) and probable (genotyping) Delta cases as of 21 June 2021 (Find accessible data used in this graph in underlying data.).

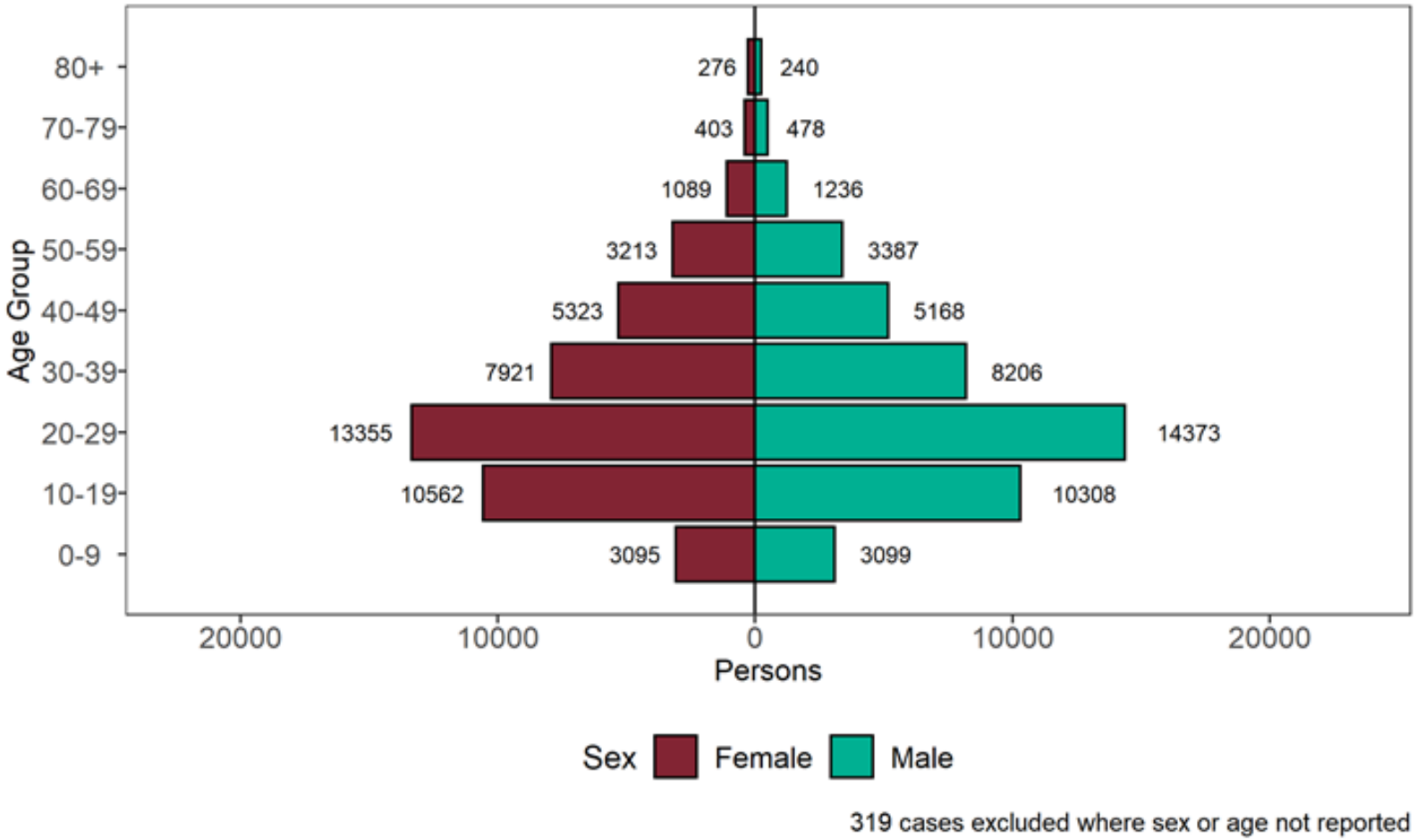


Table 11. Additional spike mutations of interest detected in Delta genomes in the UK, as of 23 June 2021

Amino acid change	Nucleotide change	Total number of sequences (UK)	Number of unlinked sequences	Number of sequences 23 March to 22 April 2021	Number of sequences 23 April to 22 May 2021	Number of sequences 23 May to 22 June 2021
P681R	C23604G	68,778	11,708	646	10,512	45,912
L452R	T22917G	65,312	11,304	645	10,259	43,104
G142D	G21987A	40,821	6,682	445	6,849	26,845
P251L	C22314T	424	399	0	1	24
G446V	G22899T	171	76	0	5	90
R158G	A22034G	77	3	0	10	64
L452R	G22918A	60	2	0	24	34
K417N	G22813T	51	8	0	36	7
R683Q	G23610A	47	4	0	1	42
Q677H	G23593T	33	1	7	3	22
S255F	C22326T	19	0	1	5	13
V503I	G23069A	17	5	0	8	4
T716I	C23709T	16	7	0	0	9
K444N	G22894T	11	7	0	0	4
S477I	G22992T	11	3	0	1	7
D215G	A22206G	10	0	0	0	10

Amino acid change	Nucleotide change	Total number of sequences (UK)	Number of unlinked sequences	Number of sequences 23 March to 22 April 2021	Number of sequences 23 April to 22 May 2021	Number of sequences 23 May to 22 June 2021
L18F	C21614T	10	1	0	1	8
P479S	C22997T	9	2	0	1	6
L244S	T22293C	9	3	0	6	0
P681L	C23604T	8	0	0	0	8
P384S	C22712T	7	1	0	0	6
S494L	C23043T	7	1	0	3	3
V483F	G23009T	5	1	1	0	3
R683L	G23610T	5	0	0	1	4
E484A	A23013C	5	0	0	4	1
Q677H	G23593C	4	4	0	0	0
F490L	T23030C	4	4	0	0	0
P384L	C22713T	4	1	0	0	3
P499L	C23058T	3	1	0	0	2
S494A	T23042G	3	0	0	1	2
P479L	C22998T	3	0	0	0	3
A701V	C23664T	3	1	1	0	1
K378N	G22696T	3	0	0	0	3

Amino acid change	Nucleotide change	Total number of sequences (UK)	Number of unlinked sequences	Number of sequences 23 March to 22 April 2021	Number of sequences 23 April to 22 May 2021	Number of sequences 23 May to 22 June 2021
S477G	A22991G	3	0	0	0	3
L455F	G22927T	3	0	1	0	2
D253G	A22320G	3	0	0	0	3
D405Y	G22775T	3	2	0	0	1

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

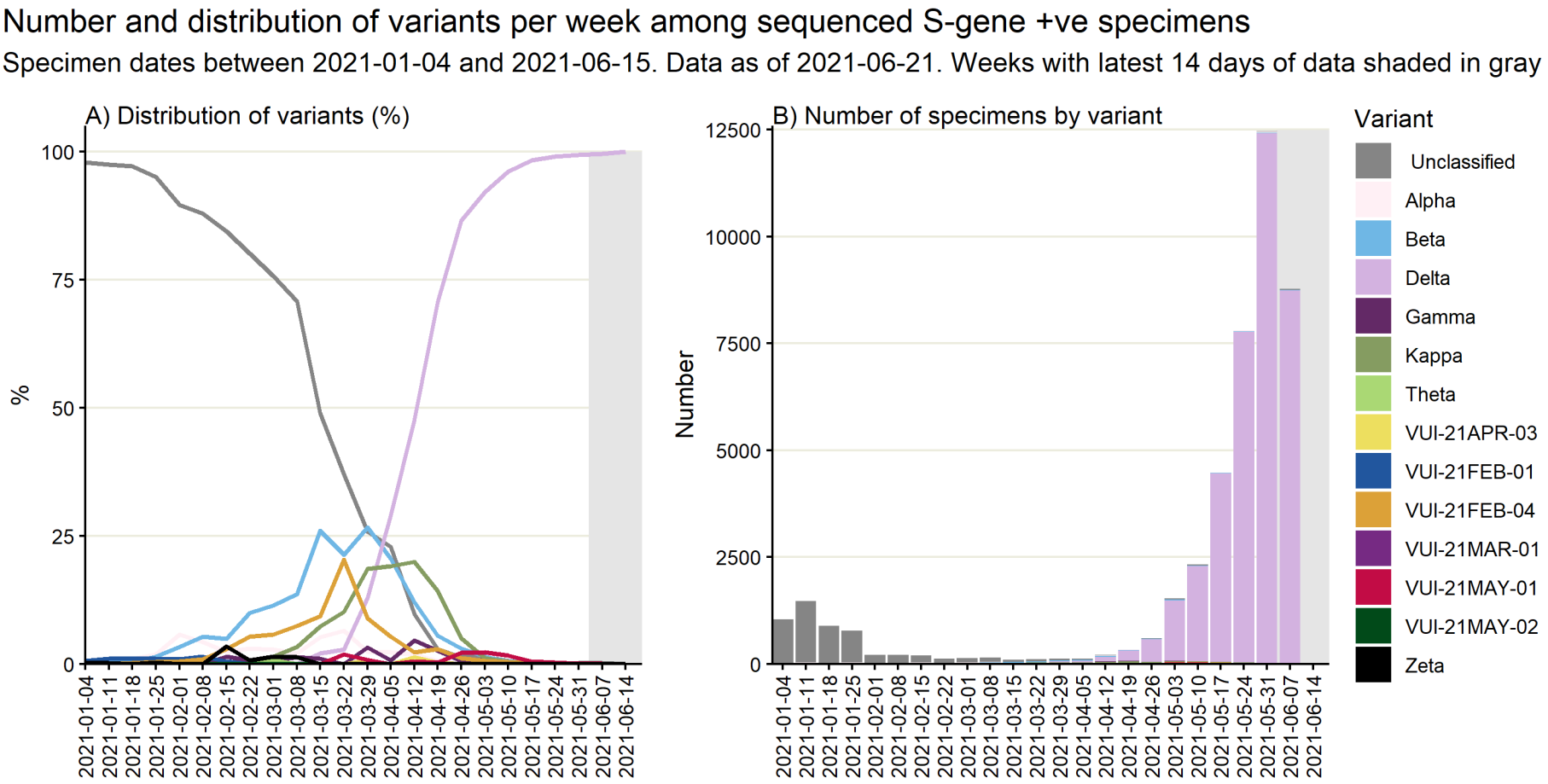
The S gene target in a 3-target assay (S, N and ORF1ab) used in some Lighthouse Laboratories is not detected in Alpha. However, this S gene is also detected in Beta, Kappa, Delta, VUI-21APR-03 (B.1.617.3) and other variants. Specimens with a detectable S gene (also referred to as S gene positive) are 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 6 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 33,101 cases reported in the week starting 14 June; 98.2% 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.

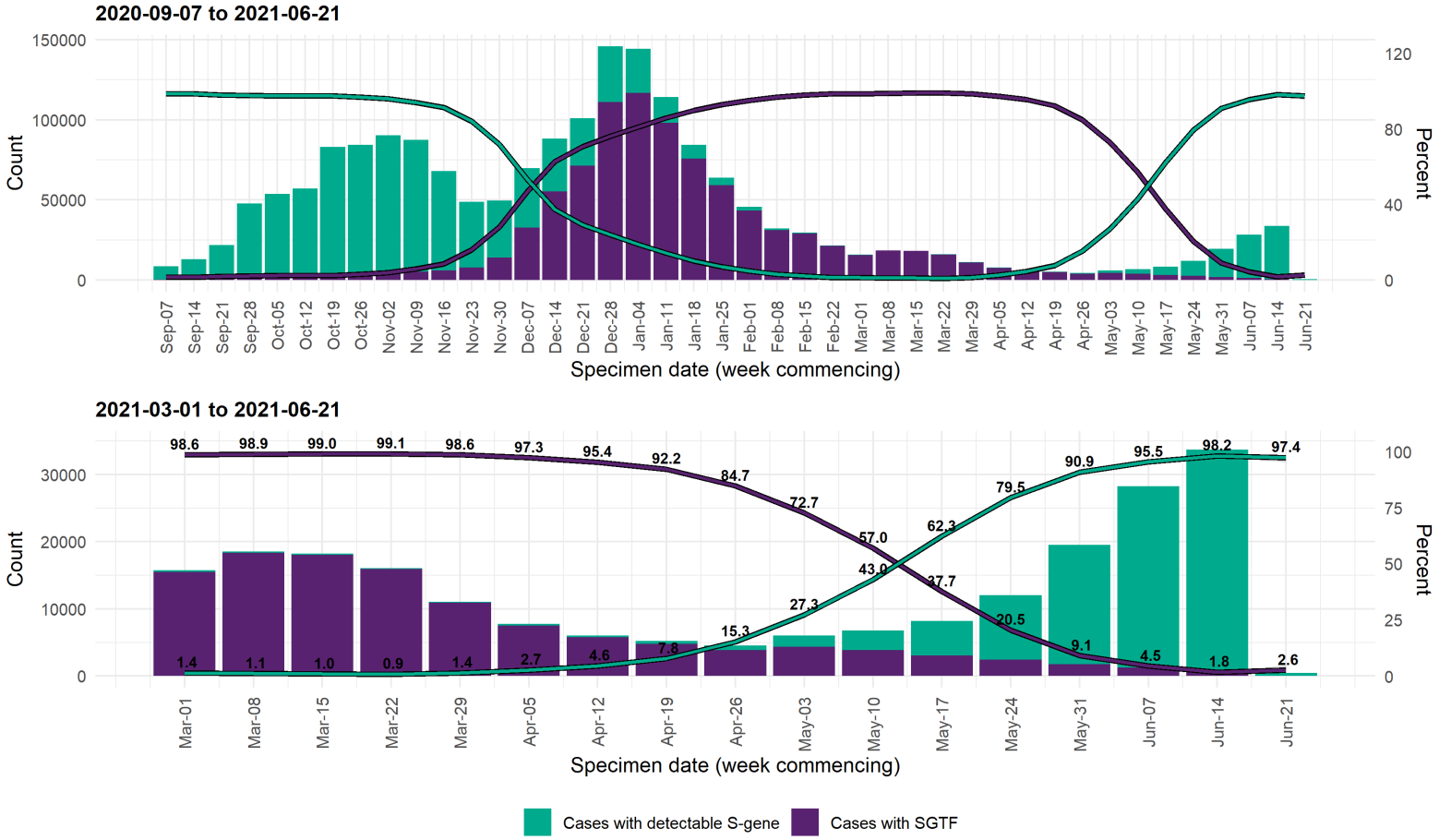
Figure 17. Weekly distribution of variants among sequenced S gene positive SARS-CoV-2 specimens

Specimen dates between 5 January 2021 and 14 June 2021, data as of 21 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).



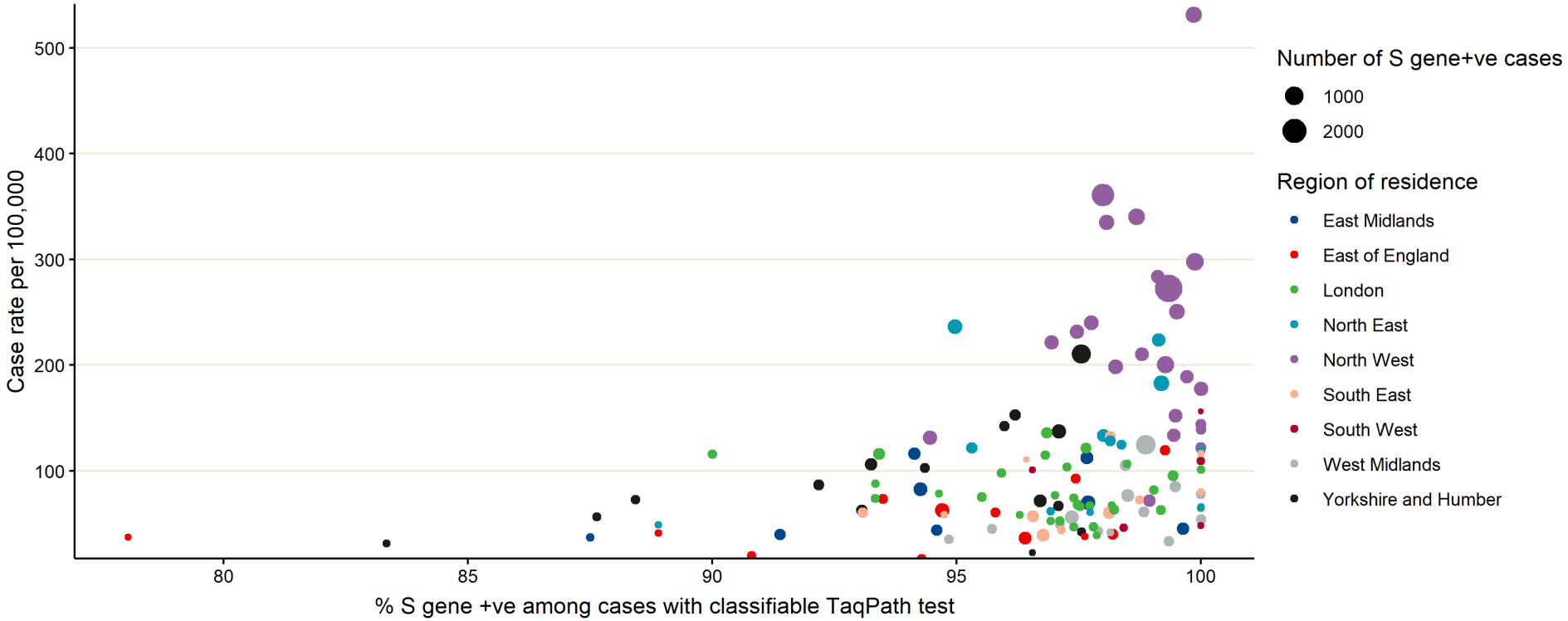
Source: SGSS and COG-UK sequencing data, restricted to sequenced positive S-gene positive tests from Newcastle, Alderley Park, Glasgow, and Milton Keynes Lighthouse Laboratories.
S gene +ve defined as positive SARS-CoV-2 test with CT values <=30 for S, N, and ORF1ab.

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 21 June 2021, data as of 21 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 18 June 2021, data as of 21 June 2021 (3 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.

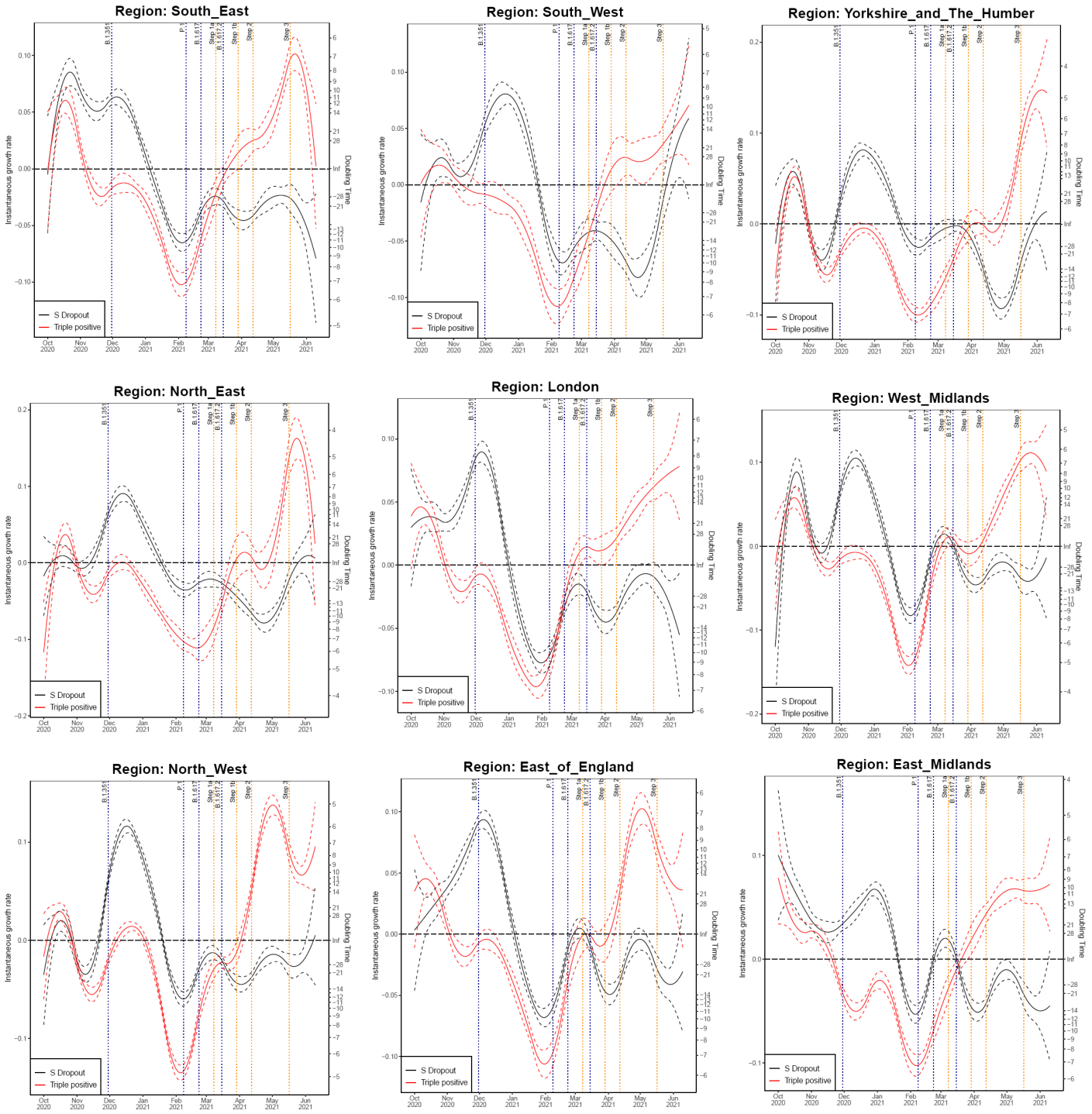
Growth rate of S gene positive and negative cases[1]

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 18 June 2021



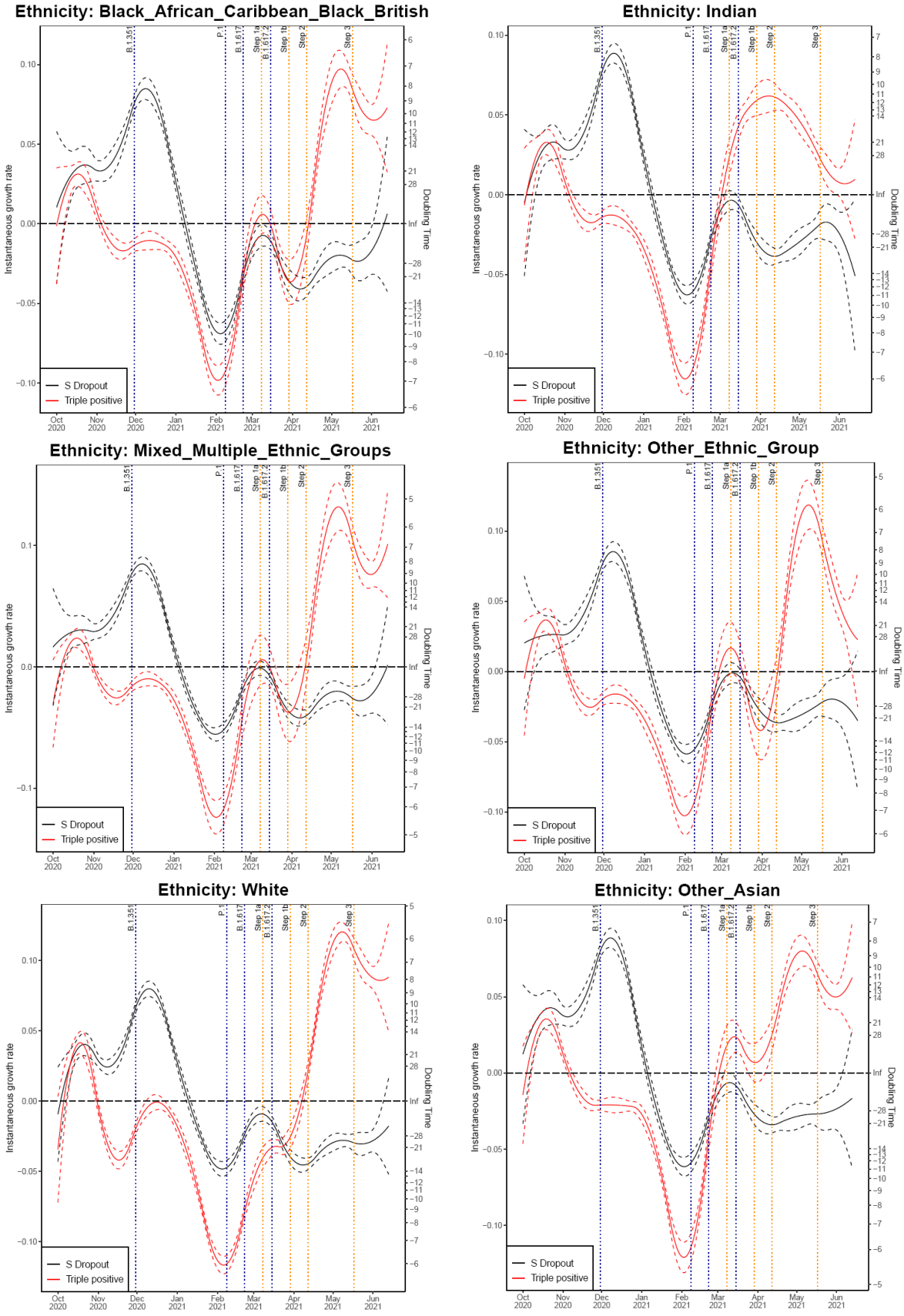
Case rate doubling times for S gene positive cases in England have plateaued and show signs of a decline in recent weeks. This may be partially due to decreases in coverage of CT data in the East Midlands, East of England, South East, Yorkshire and the Humber. Trends in the North West are currently unclear, despite good coverage of CT data. Case data is presented until the 18 June 2021

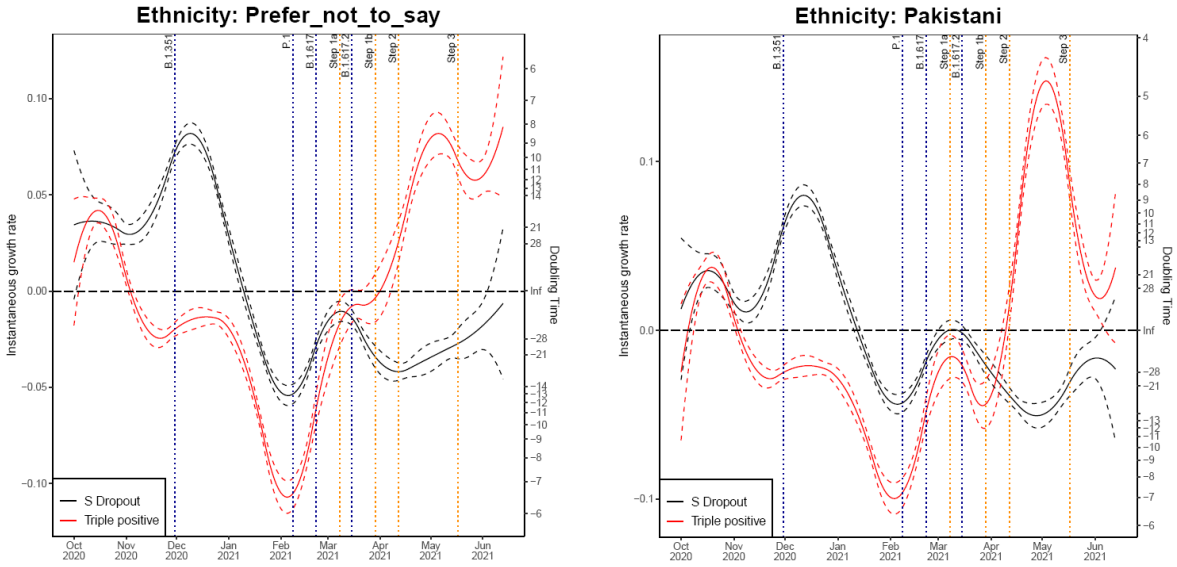
The growth rate for the all 3 positive count has plateaued or decreased in late May and

early June for all age groups, with most rapid growth in the 25 to 34 year age group and the 75 to 84 year old age group.

Doubling times are low in Pakistani and Indian Ethnicity, whilst growth rates are around 8 days in White ethnicity, 10 in Black ethnicity, 11 in other Asian ethnicity, 8 amongst those who prefer not to say. Find accessible data used in this graph in underlying data.

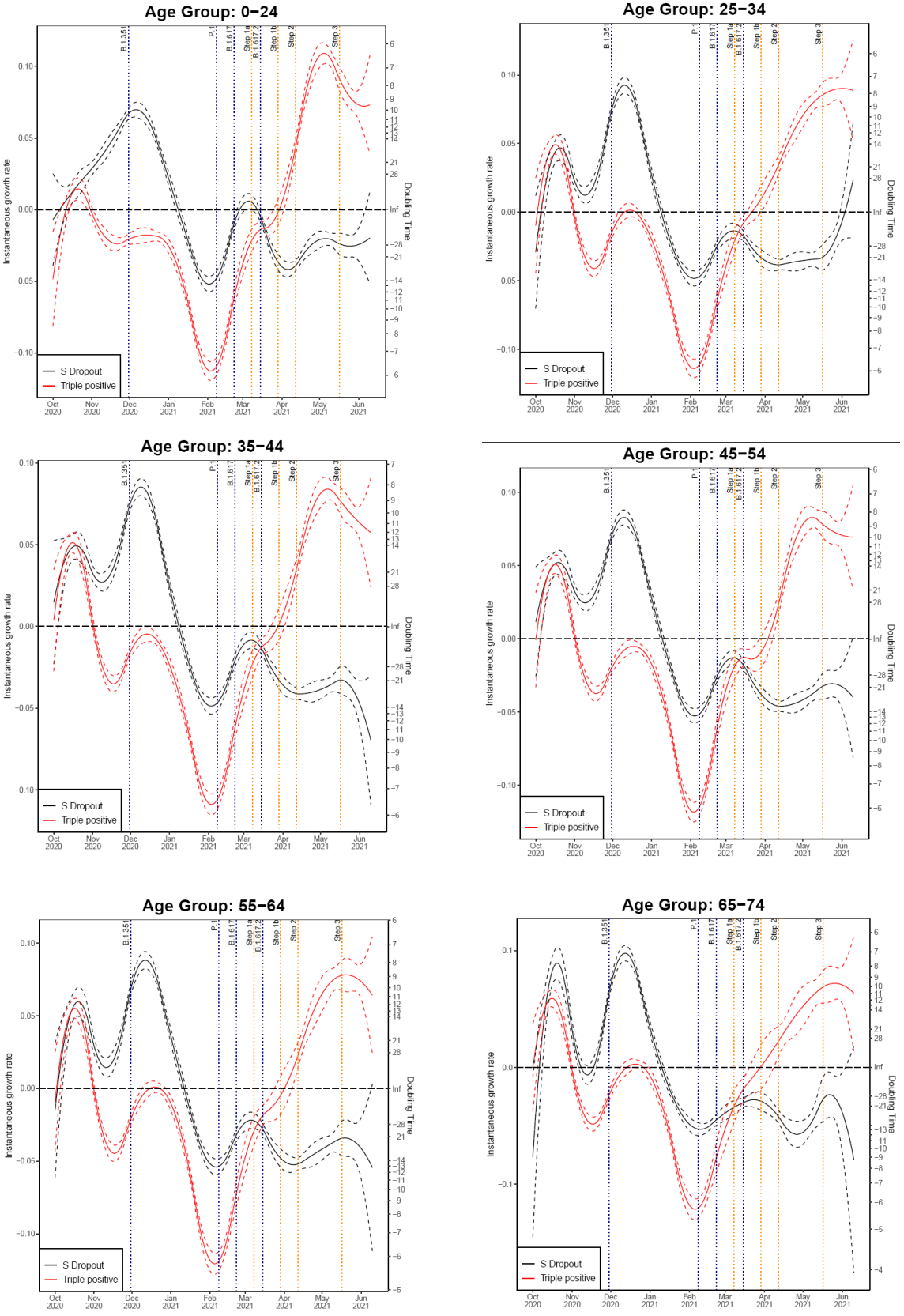
Figure 21. Growth rate and doubling time of S gene positive and negative cases by ethnicity as of 18 June 2021

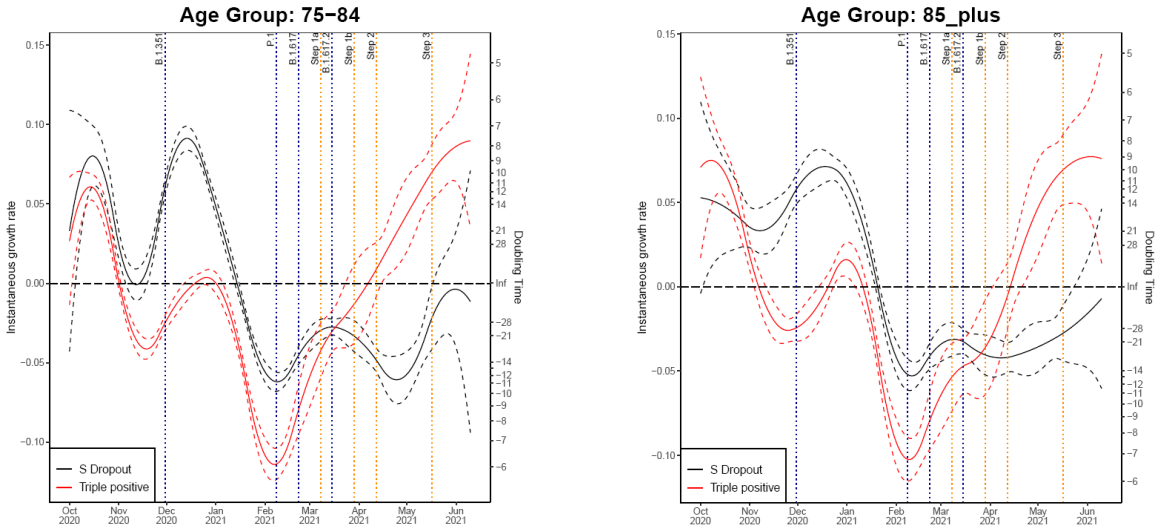




Doubling times are low in Pakistani and Indian Ethnicity, whilst growth rates are around 8 days in White ethnicity, 10 in Black ethnicity, 11 in other Asian ethnicity, 8 amongst those who prefer not to say. (Find accessible data used in this graph in underlying data).

Figure 22. Growth rate and doubling time of S gene positive and negative cases by age as of 18 June 2021.
(Find accessible data used in this graph in underlying data).





The growth rate for the all 3 positive count has plateaued or decreased in late May and early June for all age groups, with most rapid growth in the 25 to 34 year age group and the 75 to 84 year old age group.

PCR cycle threshold data

PCR cycle threshold (Ct) values appear to be persistently lower in Delta than Alpha cases based on test and trace surveillance data (Figure 23 and Figure 24).

Figure 23. Average Cycle threshold values for S gene positive samples (all 3 PCR targets positive)
Average Ct values for S+ (all 3 PCR targets positive) are currently below 20, significantly lower than the average Ct values for SGTF, which have been increasing since late May 2021, and are now around 30. There has been a drop in recent average OR-dropout Ct values though this is in a very small number of cases, and has since stabilised.

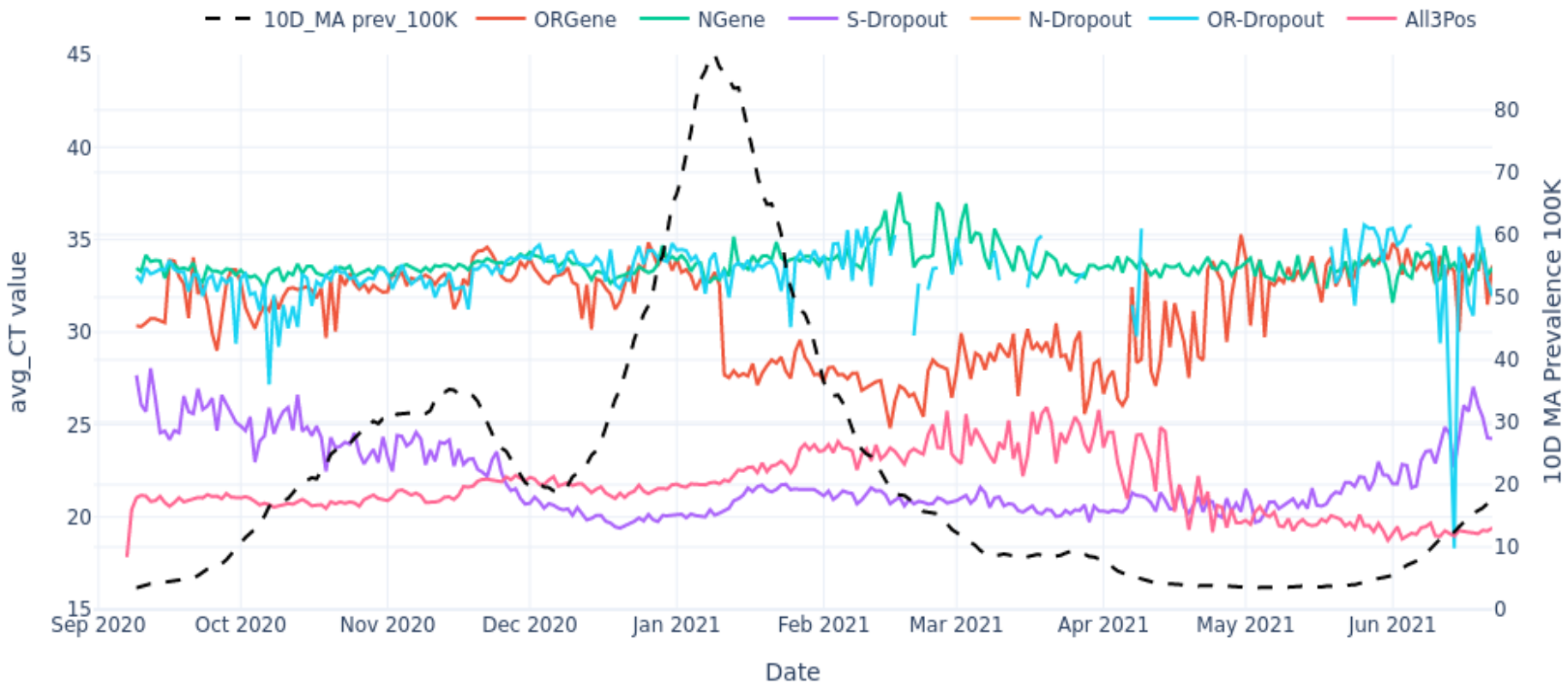
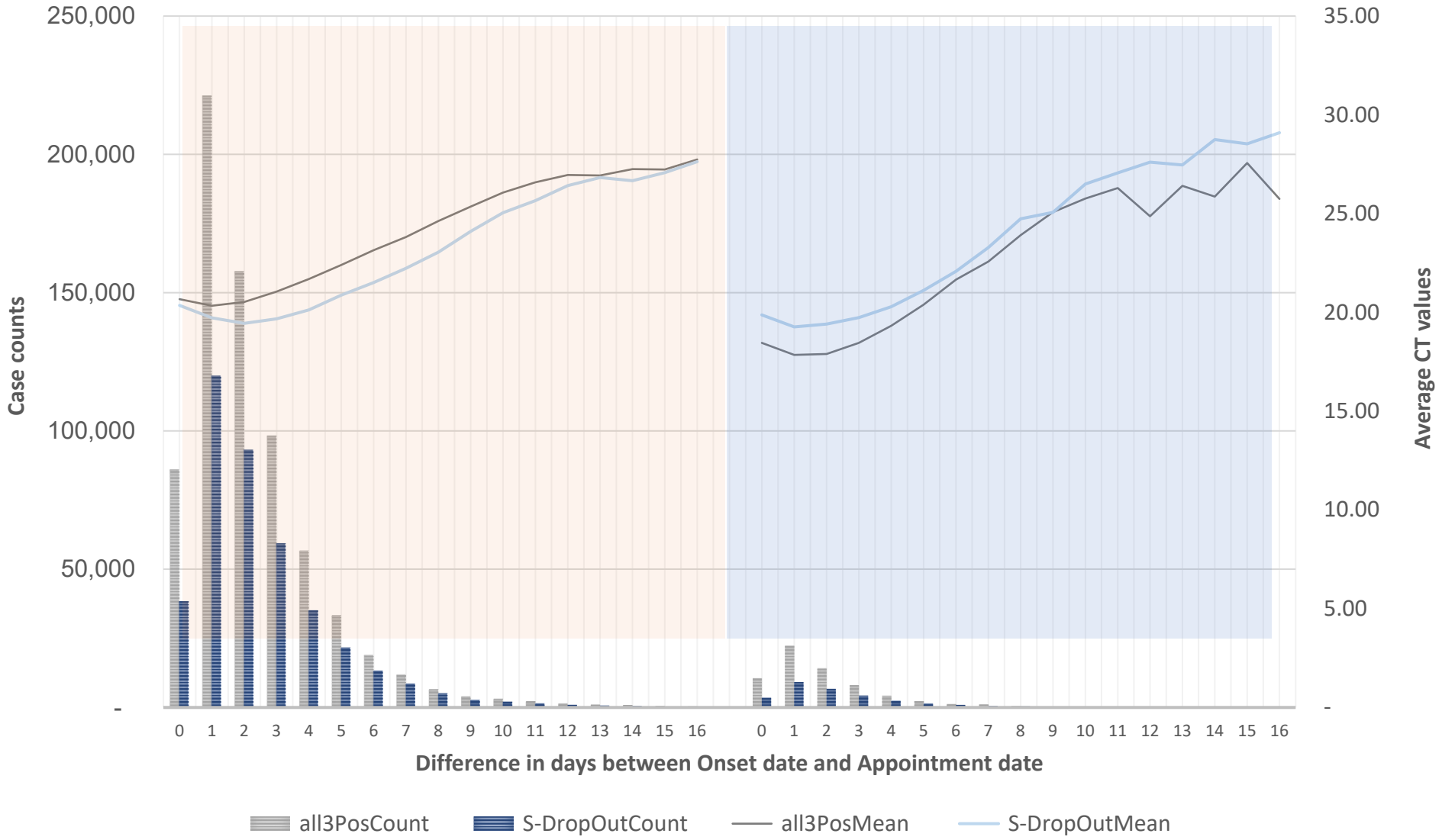


Figure 24 shows the count of cases by gene target, and the mean cycle threshold (Ct) value by the number of days since symptom onset (Symptom onset date – appointment date). This figures shows the average Ct values between 2 periods, 1 September 2020 to 15 January 2021, when Alpha was on the increase with 1 April 2021 onwards when Delta was on the increase. The data is limited to these periods to account for the fact that Ct values may reflect the dynamics of the epidemic, rather than infectivity at a moment in time. For each period, the mean SGTF cases (proxy for the Alpha variant) and S+ cases (proxy for the wild type in 1 September 2020 to 15 January 2021 period, left pane Figure 24 and Delta variant in 1 April 2021 onwards period, right pane Figure 24) since date of onset of symptoms are compared. During 1 September 2020 to 15 January 2021 period, the mean Ct values for SGTF/Alpha cases is slightly lower than S+/wild type from day 1 onwards. At day 3 the mean lowest Ct for SGTF/Alpha is 19.7 which is 1.4 lower than S+/wild type cases. During 1 April 2021 onwards period, the mean Ct values for S+/Delta cases is slightly lower from day 0 onwards, with convergence around day 9 which may be due to low numbers. At day 3 the mean lowest Ct for S+/Delta is 18.5 which is 1.3 lower than SGTF/Alpha at 19.7, almost identical to the difference at day 3 in 1 September 2020 to 15 January 2021 period, indicating the difference may be a true difference and not related to the dynamics of the epidemic at the time.

Figure 24. Cycle threshold values following date of symptom onset



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.

Preliminary results for live virus neutralisation of AY.1 with a small number of sera from vaccine recipients are reassuring, however further testing is required (data provided by Genotype to Phenotype consortium).

International Epidemiology

As of 22 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 41 cases of Delta-AY.1 in England (39 confirmed sequencing and 2 probable genotyping). Cases have been detected in 7 different regions in England (Table 12, Figure 25). 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 12. Number of confirmed (sequencing) and probable (genotyping) Delta-AY.1 cases, by region of residence as of 21 June 2021

Region	Confirmed (sequencing) case number	Probable (genotyping) case number[1]	Total case number	Proportion of all cases
East Midlands	1	0	1	2.4%
East of England	0		0	0.0%
London	7	1	8	19.5%
North East	0	1	1	2.4%
North West	3	0	3	7.3%
South East	15	0	15	36.6%
South West	2	0	2	4.9%
West Midlands	10	0	10	24.4%
Yorkshire and Humber	0		0	0.0%
Unknown region	1	0	1	2.4%
Total	39	2	41	-

[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 25. Delta-AY.1 cases (confirmed sequencing and probable genotyping) by region of residence and specimen date as of 21 June 2021. Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data).

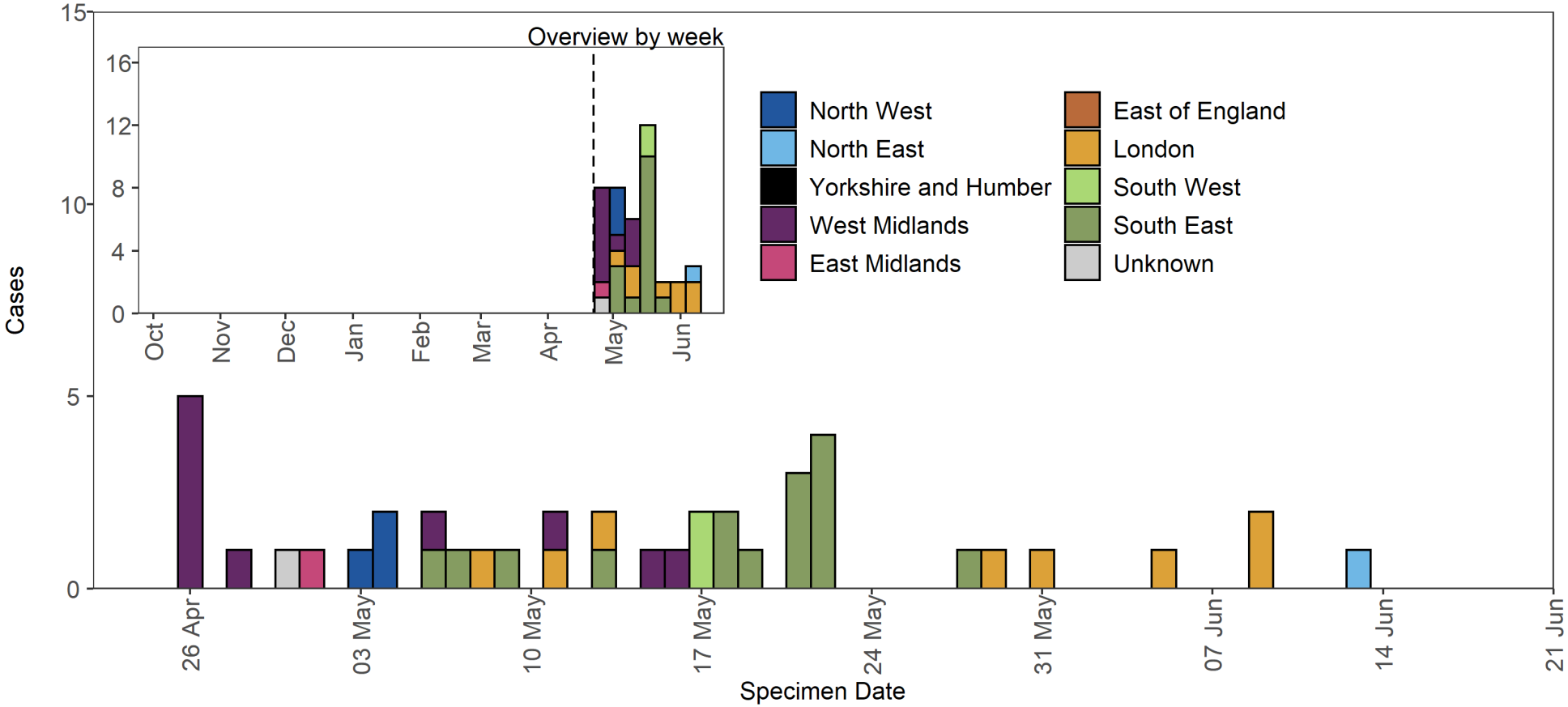


Figure 26. Confirmed (sequencing) and probable (genotyping) Delta-AY.1 cases by specimen date and detection method as of 21 June 2021 (Find accessible data used in this graph in underlying data.)

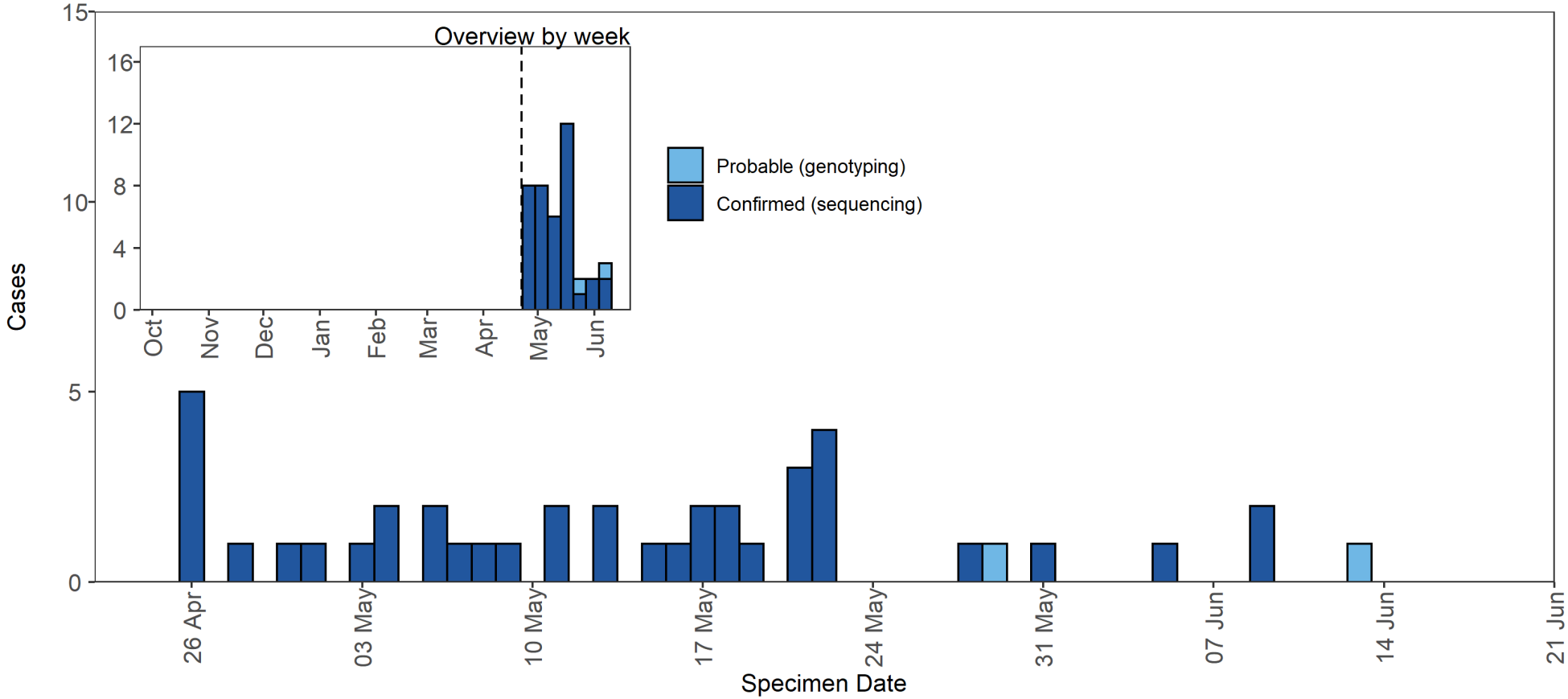
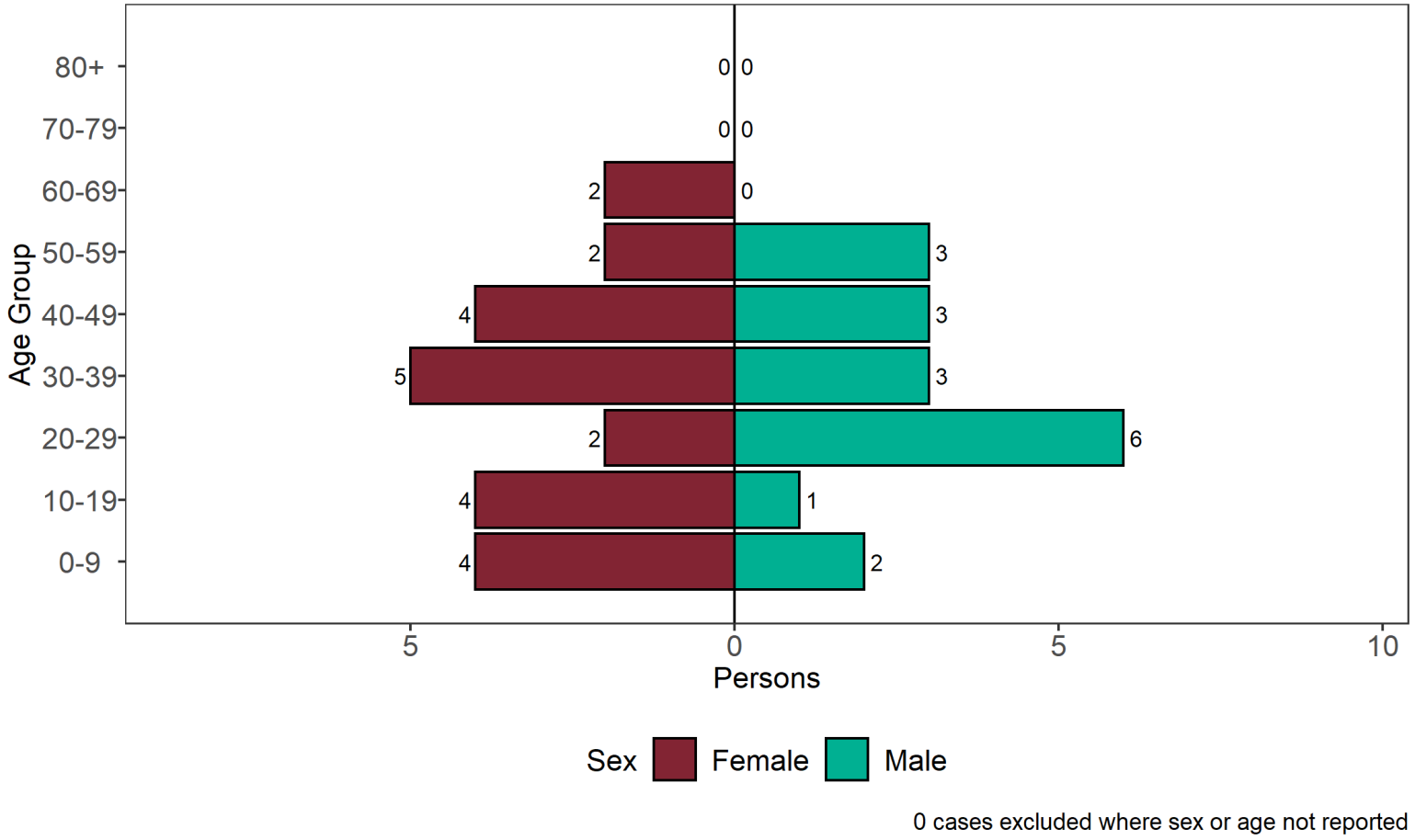


Figure 27. Age-sex pyramid of confirmed (sequencing) and probable (genotyping) Delta-AY.1 cases as of 21 June 2021.
(Find accessible data used in this graph in underlying data.).



0 cases excluded where sex or age not reported

Lambda (C.37, VUI-21JUN-01)

Lambda was identified through international variant horizon scanning and was made a signal in monitoring by PHE on 14 April 2021 (lineage B.1.1.1 at the time). On 14 June 2021, WHO designated lineage C.37 as a new variant of interest, Lambda based on evidence of continued emergence and suspected phenotypic implications. Lambda was designated a variant under investigation (VUI-21JUN-01) by PHE on the 23 June 2021.

Lambda carries a number of mutations with suspected phenotypic implications, such as a potential increased transmissibility or possible increased resistance to neutralizing antibodies[2]. It is characterised by mutations in the spike protein, including G75V, T76I, del247/253, L452Q, F490S, D614G and T859N; however, there is currently limited evidence on the full extent of the impact associated with these genomic changes, and further robust studies into the phenotypic impacts are needed to better understand the impact on countermeasures and to control the spread. Further studies are also required to validate the continued effectiveness of vaccines.[3]

International Epidemiology

As of 24 June 2021, 1,845 sequences on GISAID have been assigned to the C.37 lineage. C.37 sequences have been uploaded from Chile (707), USA (525), Peru (222), Germany (87), Argentina (86), Mexico (57), Spain (43), Ecuador (30), Israel (19), Colombia (15), France (13), Egypt (8), Switzerland (7), United Kingdom (6), Italy (5), Brazil (3), Canada (3), Netherlands (1), Aruba (1), Portugal (1), Denmark (1), Czech Republic (1), Turkey (1), Australia (1), Curacao (1), and Zimbabwe (1).

Epidemiology

There have been a small number of cases, primarily imports, of Lambda (C.37) in the United Kingdom (UK). As of the 22 June 2021, there have been 6 cases of Lambda in the UK between 23 February and 7 June 2021. Four cases were from London, one from the South West and one from West Midlands. Five cases have history of travel overseas, for one case travel status is unknown.

No deaths have been reported within 28 days.

Cases are managed in line with the approach for emerging variants with review of contact tracing, additional data collection, testing of identified contacts, and consideration of targeted case finding as required where there is evidence of community transmission.

[2] Romero PE and others (2021). Novel sublineage within B.1.1.1 currently expanding in Peru and Chile, with a convergent deletion in the ORF1a gene.
(Δ3675-3677) and a novel deletion in the Spike gene (Δ246-252, G75V, T76I, L452Q, F490S, T859N). Virologica.org, 24 Apr 2021.
[3] Weekly epidemiological update on COVID-19 to 15 June 2021

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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PHE Epidemiology Cell
PHE Contact Tracing Data Team
PHE Health Protection Data Science Team
PHE International Cell
PHE Joint Modelling Team
NHS Test and Trace Joint Biosecurity Centre
Public Health Scotland and EAVE group
Contributions from the Variant Technical Group Members

Variant Technical Group members and contributors

The PHE Variant Technical Group includes members and contributors from the following organisations: Public Health England, Public Health Wales, Public Health Scotland, Public Health Agency Northern Ireland, the Department of Health and Social Care, Imperial College London, London School of Hygiene and Tropical Medicine, University of Birmingham, University of Cambridge (including the MRC Biostatistics Unit), University of Edinburgh, University of Liverpool, the Wellcome Sanger Institute, the NHS Test and Trace Joint Biosecurity Centre, Genotype to Phenotype Consortium, SPI-M

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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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