Public Health England

Protecting and improving the nation's health

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

Technical briefing 18

9 July 2021

This briefing provides an update on previous briefings up to 25 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 sharing 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. The specialist technical briefings contain early data and analysis on emerging variants and findings have a high level of uncertainty.

Principal changes and findings this week are:

- Delta variant accounted for approximately 99% of sequenced and 97% genotyped cases from 27 June to 3 July 2021
- the number of genome sequence results available is maintained but the coverage has fallen with the increasing case numbers
- secondary attack rates have fallen but remain higher for Delta than for Alpha. New data is included on the prevalence of mutations of predicted antigenic significance in the global dataset – there is an increase in mutations of predicted antigenic significance over time, even outside the designated variants of concern and variants under investigation
- additional spike mutations are occurring on Delta but are present at relatively low frequencies both in the UK and global datasets
- there is an increase in PCR positivity in the SIREN (national healthcare worker) cohort and a small but increasing number of possible reinfections
- two new variants in monitoring have been designated (B.1.619 and B.1.629, Table 1)

The risk assessment for Delta is published separately and was last updated on 9 July 2021.

The risk assessment for Lambda is published separately for the first time.

As Delta is now the dominant variant in the UK, epidemiological data in the weekly surveillance report is highly relevant and 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 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 are published periodically, from 15 onwards they 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), variants under investigation (VUI) and those in monitoring. Figure 1 shows the proportion of cases sequenced over time. Summary epidemiology on Delta is shown in Table 2 and for each variant is shown in Table 3, case numbers are also updated online.

Figure 3 shows cumulative cases of variants over time.

Table 1. Variant lineage and designation as of 5 July 2021 (provisionally extinct variants removed)

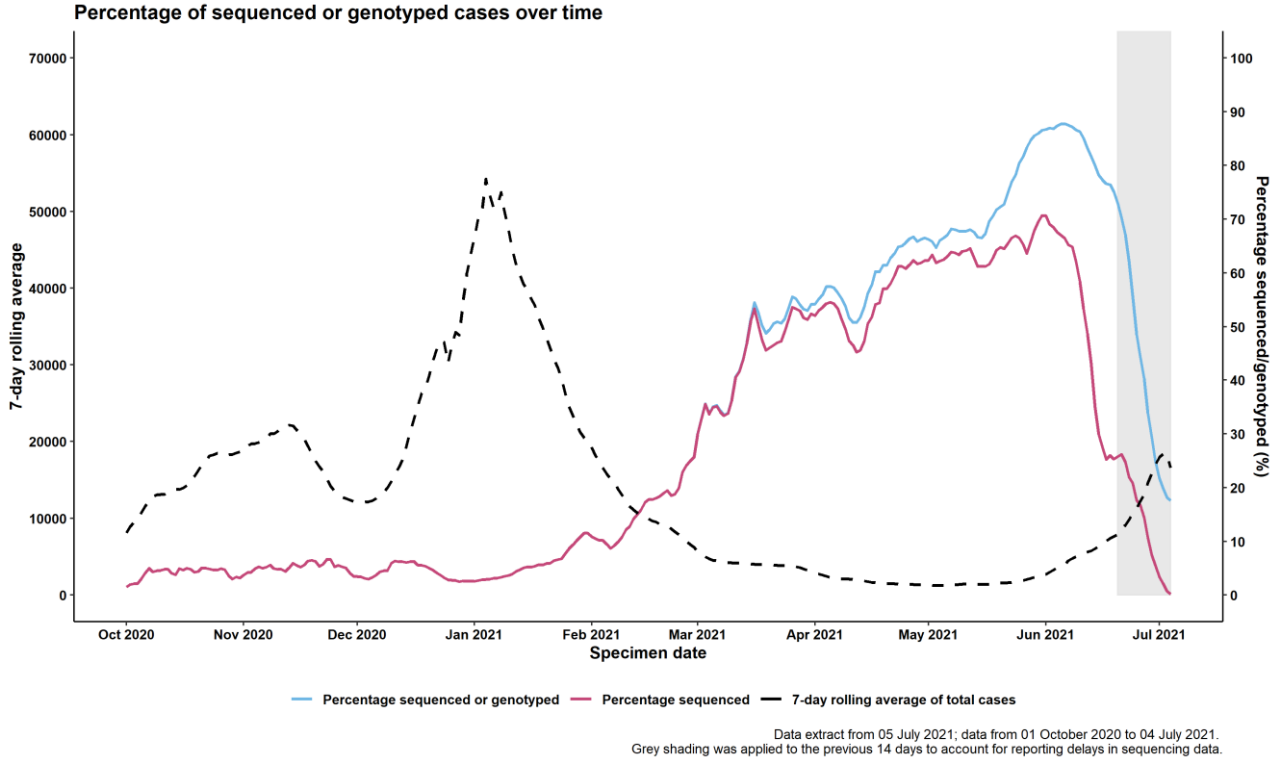
World Health Organization nomenclature as of 5 July 2021	Lineage	Designation	Status
Alpha	B.1.1.7	VOC-20DEC-01	VOC
Beta	B.1.351	VOC-20DEC-02	VOC
Gamma	P.1	VOC-21JAN-02	VOC
Delta	B.1.617.2, AY.1 and AY.2	VOC-21APR-02	VOC
Zeta	P.2	VUI-21JAN-01	VUI
Eta	B.1.525	VUI-21FEB-03	VUI
	B.1.1.318	VUI-21FEB-04	VUI
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 5 July 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
	B.1.629		Monitoring
	B.1.619		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.

Sequencing coverage

Figure 1. Coverage of sequencing: percentage of SARS-CoV-2 cases sequenced over time as of 5 July 2021 (including genotyping data) (Find accessible data used in this graph in underlying data)[1]



[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.

Figure 2. Coverage of sequencing: percentage of SARS-CoV-2 cases sequenced over time by region as of 5 July 2021 (including genotyping data) (Find accessible data used in this graph in underlying data)

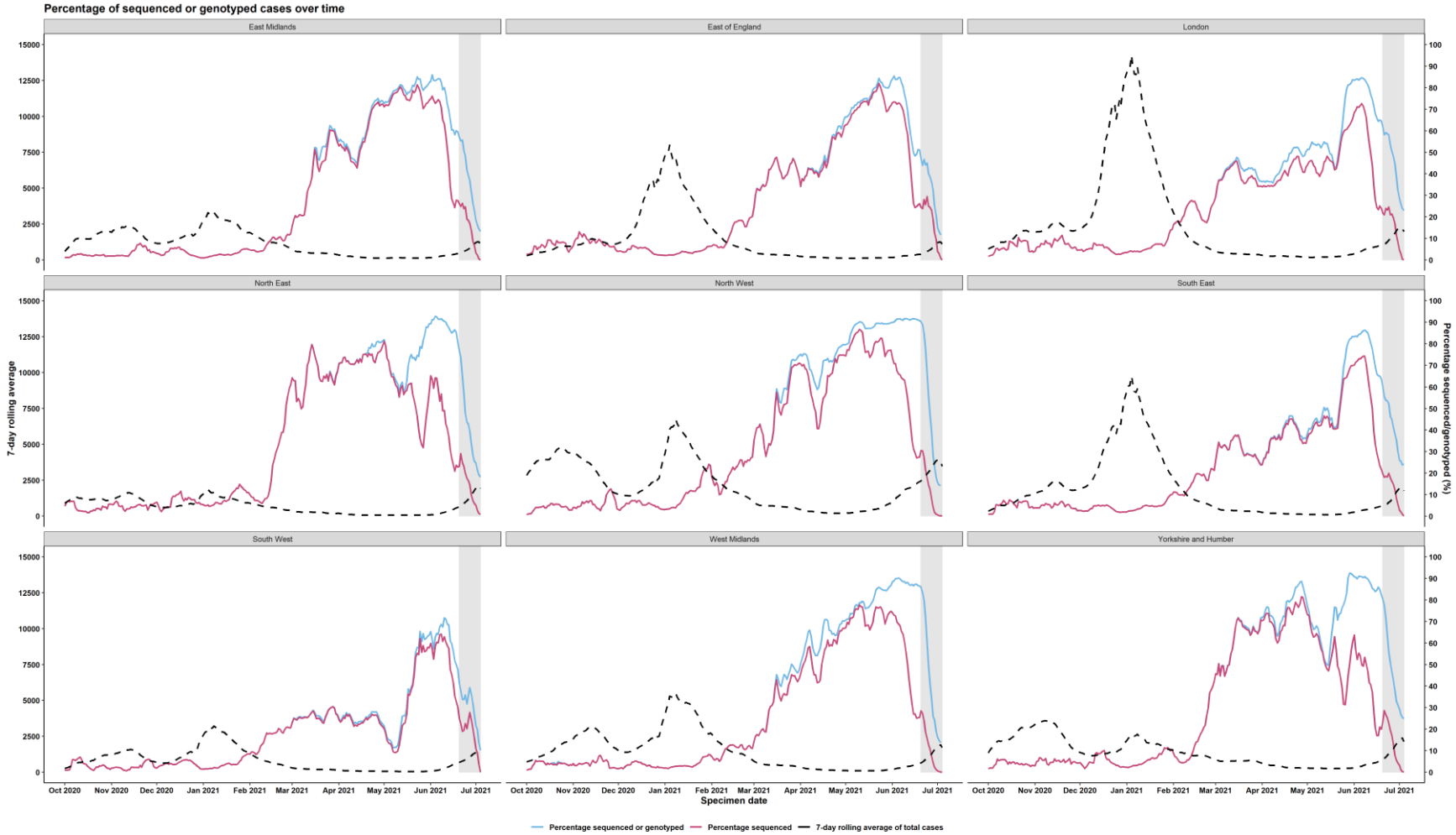


Table 2. Number of confirmed and probable Delta cases, by region of residence as of 5 July 2021

Region	Confirmed case number	Probable case number	Total case number	Proportion of total cases
East Midlands	5,159	3,630	8,789	5.2%
East of England	5,788	2,513	8,301	4.9%
London	12,329	10,980	23,309	13.7%
North East	4,117	7,912	12,029	7.1%
North West	29,236	30,223	59,459	35.0%
South East	7,631	7,975	15,606	9.2%
South West	5,612	2,680	8,292	4.9%
West Midlands	5,733	8,319	14,052	8.3%
Yorkshire and Humber	6,401	13,005	19,406	11.4%
Unknown region	444	376	820	0.5%
Total	82,450	87,613	170,063	-

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

Table 3 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. Note case fatality rates are not comparable across variants (see Table 3 footnote). Table 4 and 5 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 3 shows the cumulative number of cases per variant indexed by days since first report.

Table 3. Number of confirmed (sequencing) and probable (genotyping) cases by variant as of 5 July 2021

	All cases					Cases with at least 28-day follow-up[2]		
Variant	**Confirmed (sequencing) case number[1]**	**Probable (genotyping) case number**	**Total case number**	**Proportion of total cases**	**Deaths**	**Cases**	**Deaths**	**Case Fatality Rate** (95% confidence interval)[2]
Alpha	220,173	5,691	225,864	56.6%	4,264	224,131	4,264	1.9% (1.8 to 2.0%)
Beta	898	62	960	0.2%	13	905	13	1.4% (0.8 to 2.4%)
Delta	82,450	87,613	170,063	42.6%	259	45,136	112	0.2% (0.2 to 0.3%)
Eta	443	0	443	0.1%	12	425	12	2.8% (1.5 to 4.9%)
Gamma	186	45	231	0.1%	0	199	0	0.0% (0.0 to 1.8%)
Kappa	446	0	446	0.1%	1	443	1	0.2% (0.0 to 1.3%)
Lambda	8	0	8	0.0%	0	5	0	0.0% (0.0 to 52.2%)
Theta	7	0	7	0.0%	0	6	0	0.0% (0.0 to 45.9%)
VOC-21FEB-02	45	0	45	0.0%	1	44	1	2.3% (0.1 to 12.0%)
VUI-21APR-03	13	0	13	0.0%	0	13	0	0.0% (0.0 to 24.7%)
VUI-21FEB-01	79	0	79	0.0%	2	78	1	1.3% (0.0 to 6.9%)
VUI-21FEB-04	289	0	289	0.1%	1	270	1	0.4% (0.0 to 2.0%)
VUI-21MAR-01	2	0	2	0.0%	0	2	0	0.0% (0.0 to 84.2%)
VUI-21MAY-01	185	0	185	0.0%	1	171	1	0.6% (0.0 to 3.2%)
VUI-21MAY-02	140	0	140	0.0%	0	124	0	0.0% (0.0 to 2.9%)
Zeta	54	0	54	0.0%	1	53	1	1.9% (0.0 to 10.1%)

[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.

[2] Case fatality rate is only calculated for those with at least 28 days since specimen date. Case fatality is not comparable across variants as they have peaked at different points in the pandemic, and so vary in background hospital pressure, vaccination availability and rates and case profiles, treatment options, and impact of reporting delay, among other factors.

Data presented in tables 4 and 5 are affected by an interruption to the data on hospitalisation provided to PHE by NHS Digital. This interruption means that it was not possible to provide data for the most recent weeks and have therefore updated previously reported data covering cases up until 21 June 2021.

Table 4. 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§ (exclusion‡)		Cases with an A&E visit§ (inclusion#)		Cases where presentation to A&E resulted in overnight inpatient admission§ (exclusion‡)		Cases where presentation to A&E resulted in overnight inpatient admission§ (inclusion#)		Deaths^	
			n	%	n	%	n	%	n	%	n	%	n	%
Alpha (VOC-20DEC-01)	<50	117,737	730	0.6	4,940	4.2	5,786	4.9	1,230	1.0	1,680	1.4	66	0.1
	≥50	32,238	88	0.3	3,130	9.7	4,584	14.2	1,721	5.3	2,782	8.6	1,550	4.8
	All cases	150,059	818	0.5	8,070	5.4	10,370	6.9	2,951	2.0	4,462	3.0	1,616	1.1
Beta (VOC-20DEC-02)	<50	572	14	2.4	24	4.2	26	4.5	5	0.9	8	1.4	1	0.2
	≥50	159	5	3.1	17	10.7	25	15.7	7	4.4	15	9.4	7	4.4
	All cases	735	20	2.7	41	5.6	51	6.9	12	1.6	23	3.1	8	1.1
Gamma (VOC-21JAN-02)	<50	203	17	8.4	8	3.9	8	3.9	1	0.5	1	0.5	-	0.0
	≥50	18	2	11.1	1	5.6	1	5.6	-	0.0	-	0.0	-	0.0

Variant	Age group (years)	Cases Since 1 Feb	Cases with specimen date in past 28 days		Cases with an A&E visit§ (exclusion‡)		Cases with an A&E visit§ (inclusion#)		Cases where presentation to A&E resulted in overnight inpatient admission§ (exclusion‡)		Cases where presentation to A&E resulted in overnight inpatient admission§ (inclusion#)		Deaths^	
			n	%	n	%	n	%	n	%	n	%	n	%
	All cases	221	19	8.6	9	4.1	9	4.1	1	0.5	1	0.5	-	0.0
Delta (VOC-21APR-02)	<50	111,008	57,673	52.0	3,487	3.1	4,410	4.0	852	0.8	1,283	1.2	26	0.0
	≥50	12,404	5,957	48.0	646	5.2	1,079	8.7	307	2.5	615	5.0	231	1.9
	All cases	123,620	63,707	51.5	4,141	3.3	5,497	4.4	1,165	0.9	1,904	1.5	257	0.2
Eta (VUI-21FEB-03)	<50	270	1	0.4	11	4.1	13	4.8	5	1.9	6	2.2	-	0.0
	≥50	114	-	0.0	4	3.5	7	6.1	1	0.9	3	2.6	6	5.3
	All cases	385	1	0.3	15	3.9	20	5.2	6	1.6	9	2.3	6	1.6
VUI-21FEB-04	<50	227	9	4.0	6	2.6	9	4.0	1	0.4	2	0.9	-	0.0
	≥50	54	3	5.6	1	1.9	2	3.7	-	0.0	1	1.9	1	1.9
	All cases	281	12	4.3	7	2.5	11	3.9	1	0.4	3	1.1	1	0.4
Theta (VUI-21MAR-02)	<50	3	-	0.0	1	33.3	1	33.3	-	0.0	-	0.0	-	0.0

Variant	Age group (years)	Cases Since 1 Feb	Cases with specimen date in past 28 days		Cases with an A&E visit§ (exclusion‡)		Cases with an A&E visit§ (inclusion#)		Cases where presentation to A&E resulted in overnight inpatient admission§ (exclusion‡)		Cases where presentation to A&E resulted in overnight inpatient admission§ (inclusion#)		Deaths^	
			n	%	n	%	n	%	n	%	n	%	n	%
	≥50	3	-	0.0	-	0.0	-	0.0	-	0.0	-	0.0	-	0.0
	All cases	6	-	0.0	1	16.7	1	16.7	-	0.0	-	0.0	-	0.0
Kappa (VUI-21APR-01)	<50	380	-	0.0	10	2.6	11	2.9	1	0.3	2	0.5	-	0.0
	≥50	63	-	0.0	5	7.9	5	7.9	2	3.2	2	3.2	1	1.6
	All cases	443	-	0.0	15	3.4	16	3.6	3	0.7	4	0.9	1	0.2
VUI-21APR-03	<50	11	-	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
	All cases	13	-	0.0	-	0.0	-	0.0	-	0.0	-	0.0	-	0.0
VUI-21MAY-01	<50	161	7	4.3	1	0.6	2	1.2	-	0.0	1	0.6	-	0.0
	≥50	23	-	0.0	-	0.0	-	0.0	-	0.0	-	0.0	1	4.3
	All cases	184	7	3.8	1	0.5	2	1.1	-	0.0	1	0.5	1	0.5

Variant	Age group (years)	Cases Since 1 Feb	Cases with specimen date in past 28 days		Cases with an A&E visit§ (exclusion‡)		Cases with an A&E visit§ (inclusion#)		Cases where presentation to A&E resulted in overnight inpatient admission§ (exclusion‡)		Cases where presentation to A&E resulted in overnight inpatient admission§ (inclusion#)		Deaths^	
			n	%	n	%	n	%	n	%	n	%	n	%
VUI-21MAY-02	<50	104	5	4.8	8	7.7	9	8.7	2	1.9	3	2.9	-	0.0
	≥50	30	-	0.0	-	0.0	-	0.0	-	0.0	-	0.0	-	0.0
	All cases	134	5	3.7	8	6.0	9	6.7	2	1.5	3	2.2	-	0.0
Lambda (VUI-21JUN-01)	<50	8	2	25.0	1	12.5	1	12.5	1	12.5	1	12.5	-	0.0
	≥50	-	-	-	-	-	-	-	-	-	-	-	-	-
	All cases	8	2	25.0	1	12.5	1	12.5	1	12.5	1	12.5	-	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

Inclusion: Including cases with the same specimen and attendance dates

‡ Exclusion: Excluding cases with the same specimen and attendance dates. 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 5. 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	Vaccination status unknown	<21 days post dose 1	≥21 days post dose 1	Received 2 doses	Unvaccinated
Delta cases	All cases	123,620	63,707	14,359	8,562	17,933	10,834	71,932
	<50	111,008	57,673	12,900	8,453	13,391	5,600	70,664
	≥50	12,404	5,957	1,252	109	4,542	5,234	1,267
Cases with an emergency care visit§ (exclusion‡)	All cases	4,141	N/A	49	301	667	437	2,687
	<50	3,487	N/A	40	296	435	173	2,543
	≥50	646	N/A	1	5	232	264	144
Cases with an emergency care visit§ (inclusion#)	All cases	5,497	N/A	70	383	837	641	3,566
	<50	4,410	N/A	57	369	511	208	3,265
	≥50	1,079	N/A	5	14	326	433	301

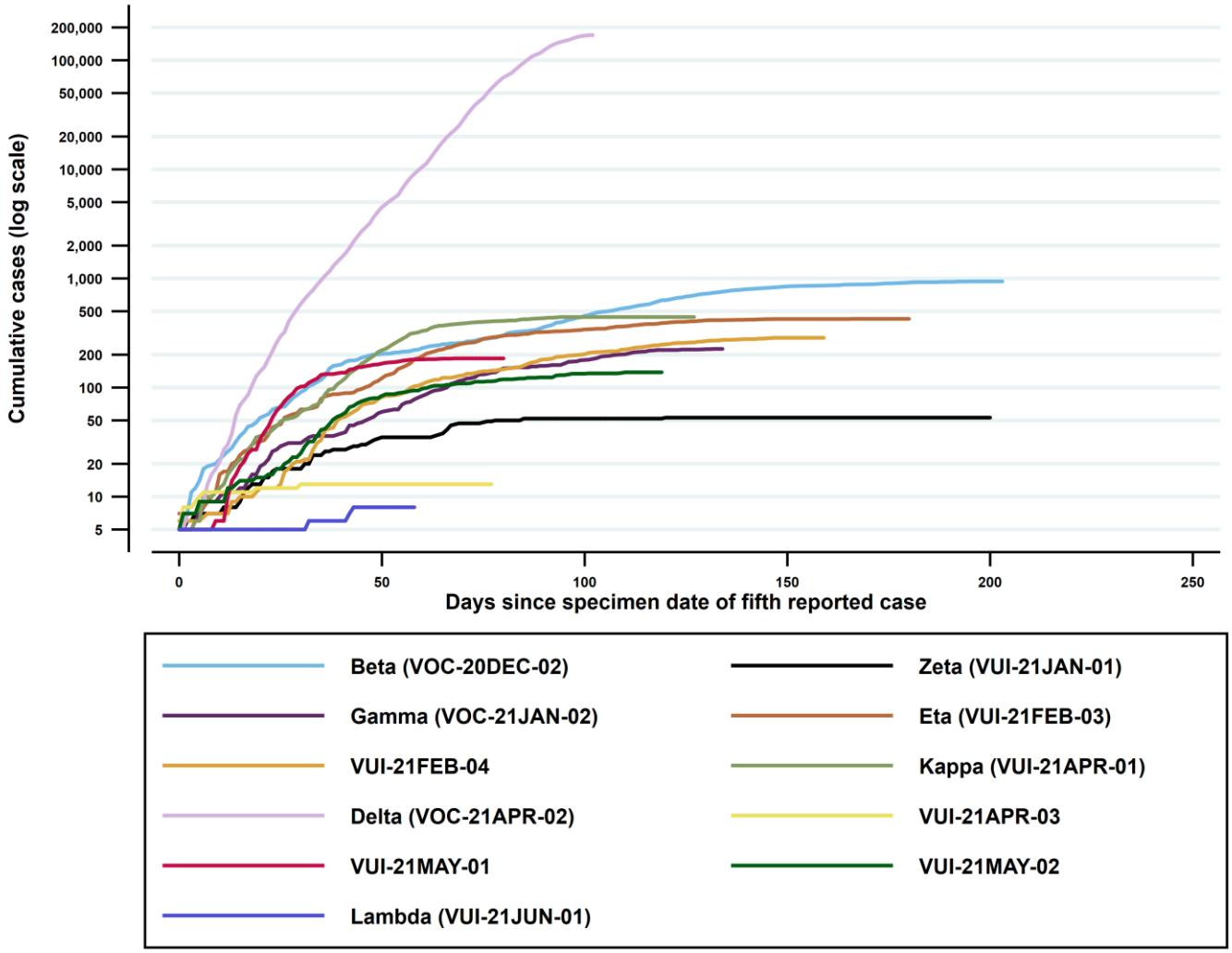
	Age group (years)**	Total	Cases with specimen date in past 28 days	Vaccination status unknown	<21 days post dose 1	≥21 days post dose 1	Received 2 doses	Unvaccinated
Cases where presentation to emergency care resulted in overnight inpatient admission§ (exclusion‡)	All cases	1,165	N/A	23	74	162	173	733
	<50	852	N/A	17	71	80	33	651
	≥50	307	N/A	-	3	82	140	82
Cases where presentation to emergency care resulted in overnight inpatient admission§ (inclusion#)	All cases	1,904	N/A	34	117	258	313	1,182
	<50	1,283	N/A	24	106	118	48	987
	≥50	615	N/A	4	11	140	265	195
Deaths within 28 days of positive specimen date	All cases	257	N/A	2	1	44	118	92
	<50	26	N/A	-	-	3	2	21
	≥50	231	N/A	2	1	41	116	71

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
# Inclusion: Including cases with the same specimen and attendance dates
‡ Exclusion: Excluding cases with the same specimen and attendance dates. 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.
** Age <50 + >50 do not total ‘all cases’ per category as some cases lack reported age data

Hospitalisation data are subject to reporting delays as, although trusts may update daily data, they are only obliged to submit data on a monthly basis. Different organisations may have different reporting patterns. These data show only cases who have been hospitalised and do not show those who are currently in hospital with COVID-19. As such, it is not appropriate for use for surveillance of those currently hospitalised with COVID-19. In addition, these data will not show cases who were directly admitted as inpatients without presenting to emergency care.

Presented to emergency care are those cases who have a record in the Emergency Care Data Set showing that they presented to emergency care 1 to 28 days after the specimen date. The Emergency Care Data Set is updated weekly, and sequence data are linked to these data daily.

Figure 3. Cumulative cases in England of variants indexed by days since the fifth reported case, data as of 5 July 2021
(Find accessible data used in this graph in underlying data)



Variant prevalence

The prevalence of different variants amongst all sequenced cases is presented in Figures 4 and 5, split by region in Figures 6 and 7 and by travel status in Figures 8 and 9. 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 4 to 9 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 99% of sequenced and 97% genotyped cases from 27 June to 3 July 2021.

Figure 4. Variant prevalence for all England available genotyped cases from 1 February 2021 as of 5 July 2021
(Find accessible data used in this graph in underlying data)

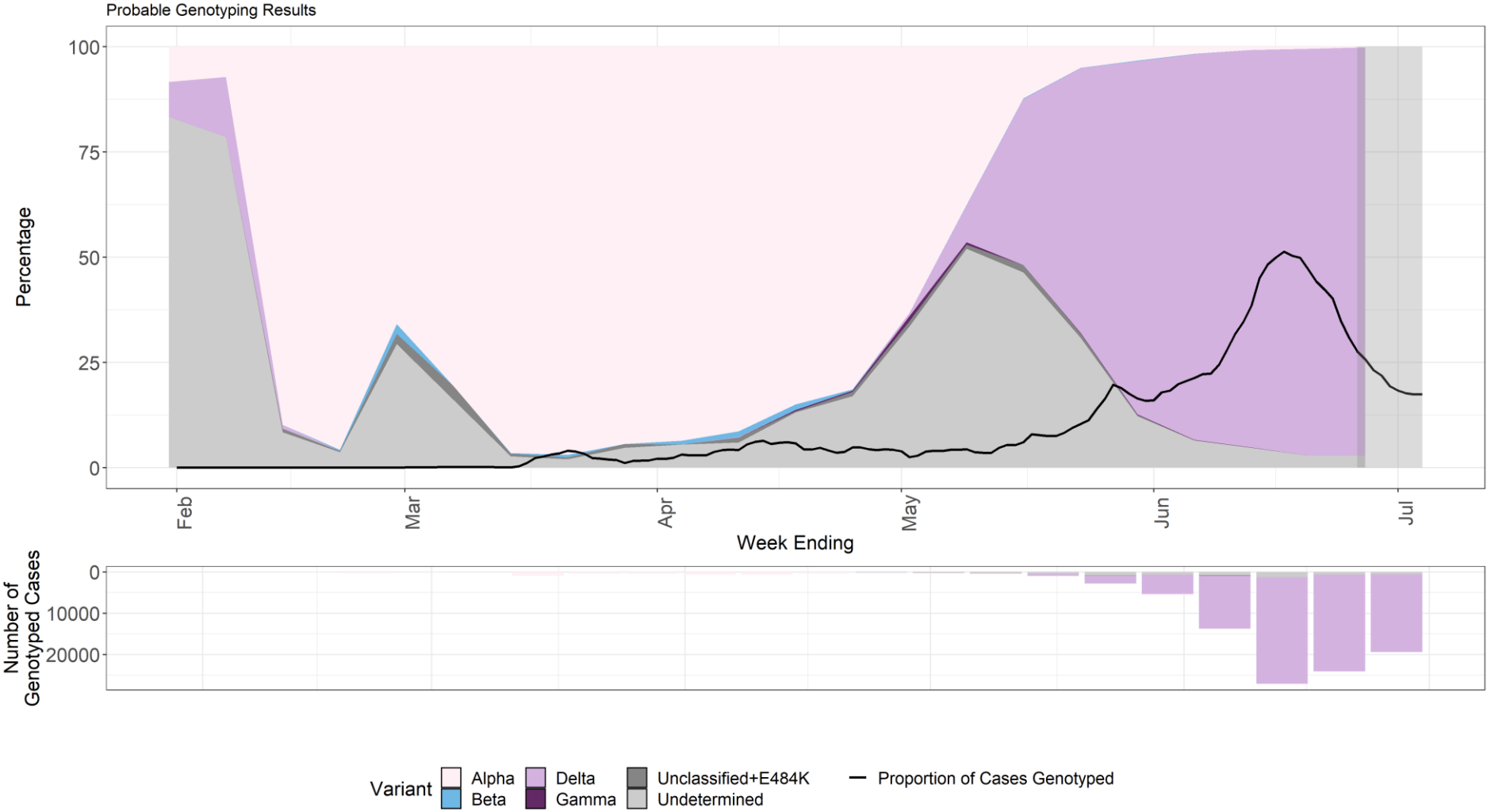


Figure 5. Variant prevalence for all England available sequenced cases from 1 February 2021 as of 5 July 2021
(Find accessible data used in this graph in underlying data). Dashed lines indicate period incorporating issue at a sequencing site.

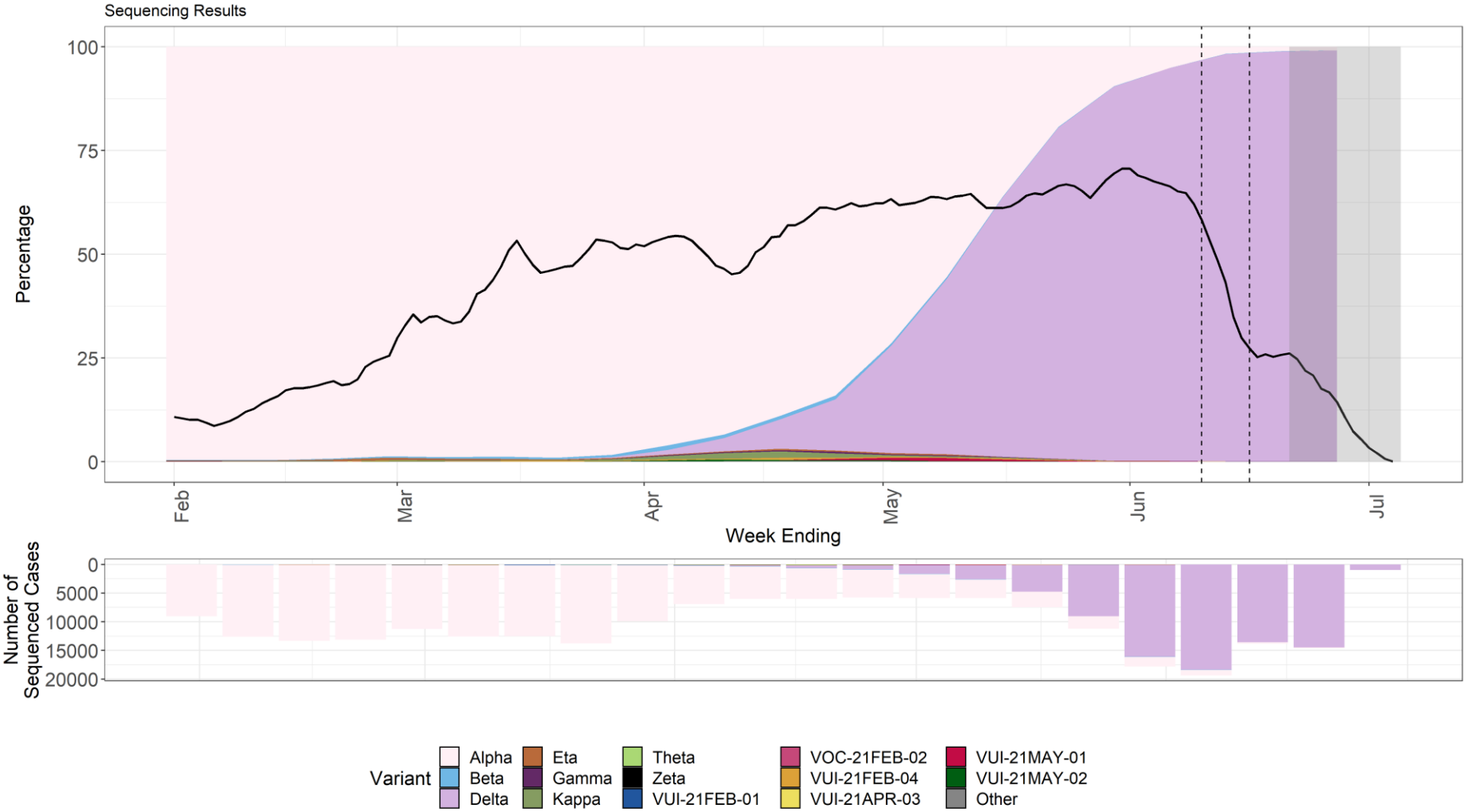


Figure 6. Variant prevalence from 1 February 2021 as of 5 July 2021 by region for all genotyped cases in England (excluding 497 cases where the region or specimen date were unknown). (Find accessible data used in this graph in underlying data)

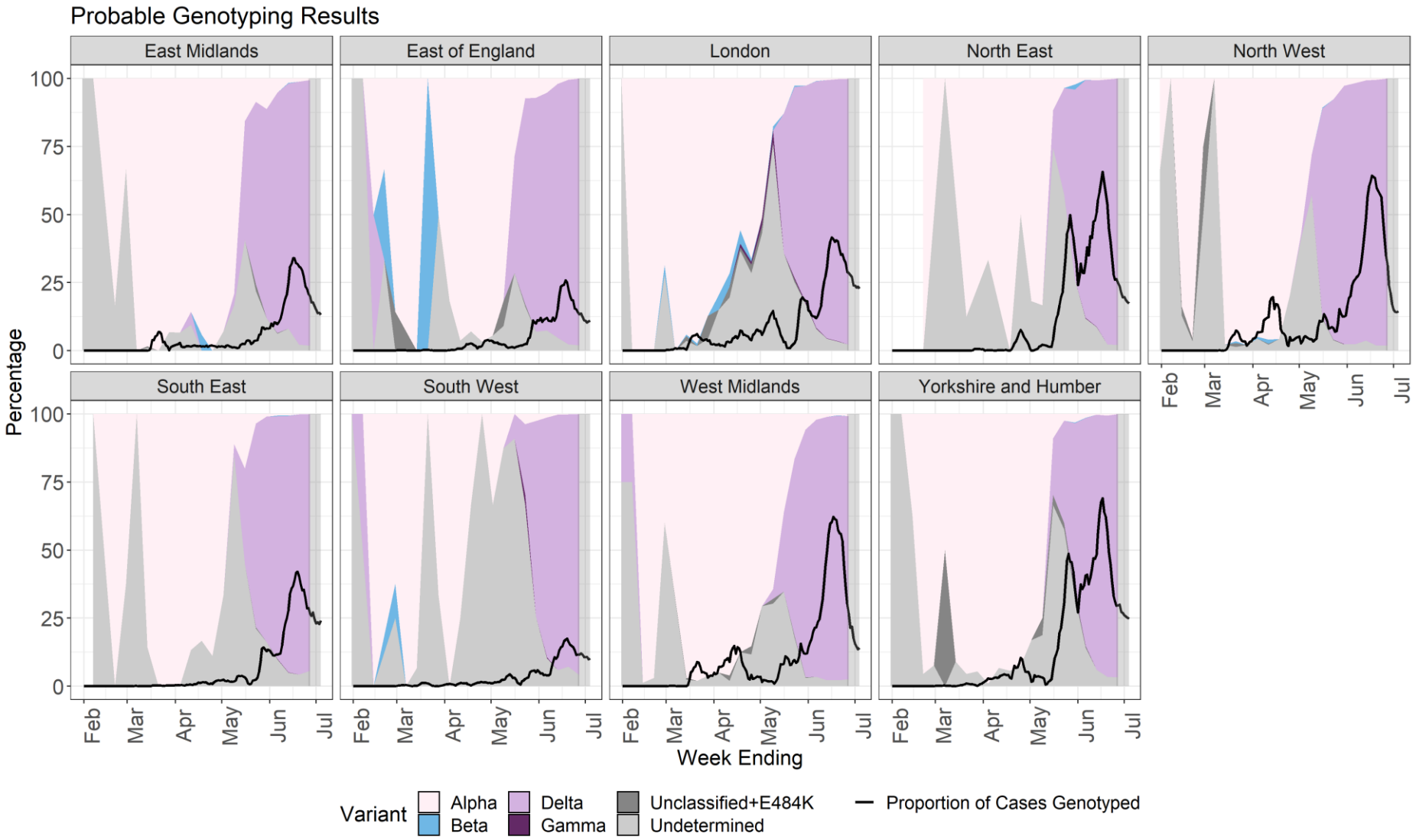


Figure 7. Variant prevalence from 1 February 2021 as of 5 July 2021 by region for all sequenced cases in England (excluding 1030 cases where the region or specimen date were unknown). (Find accessible data used in this graph in underlying data)

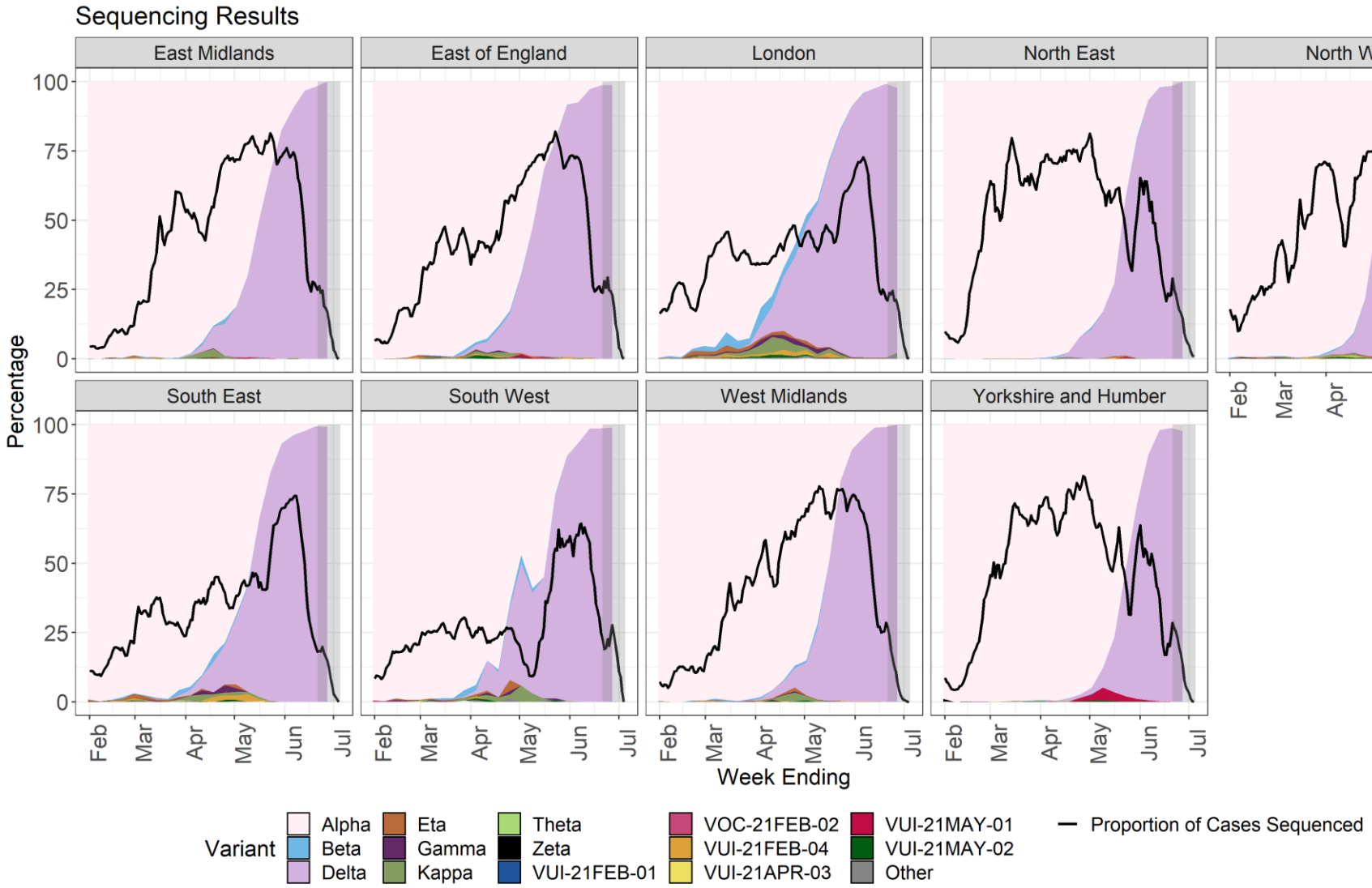


Figure 8. Prevalence of variants over time: all genotyped cases in England, split by travel status as of 5 July 2021
(Find accessible data used in this graph in underlying data)

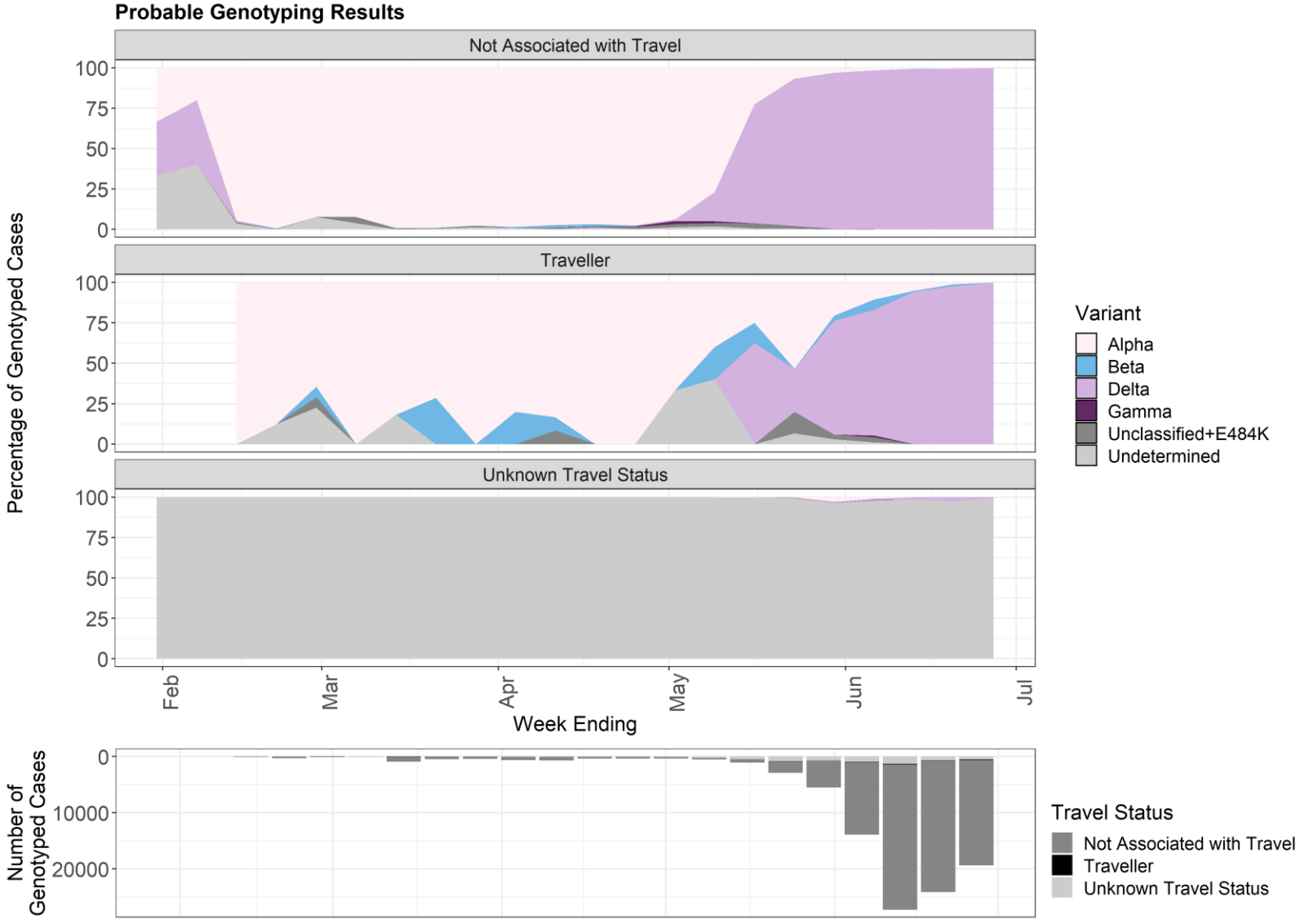
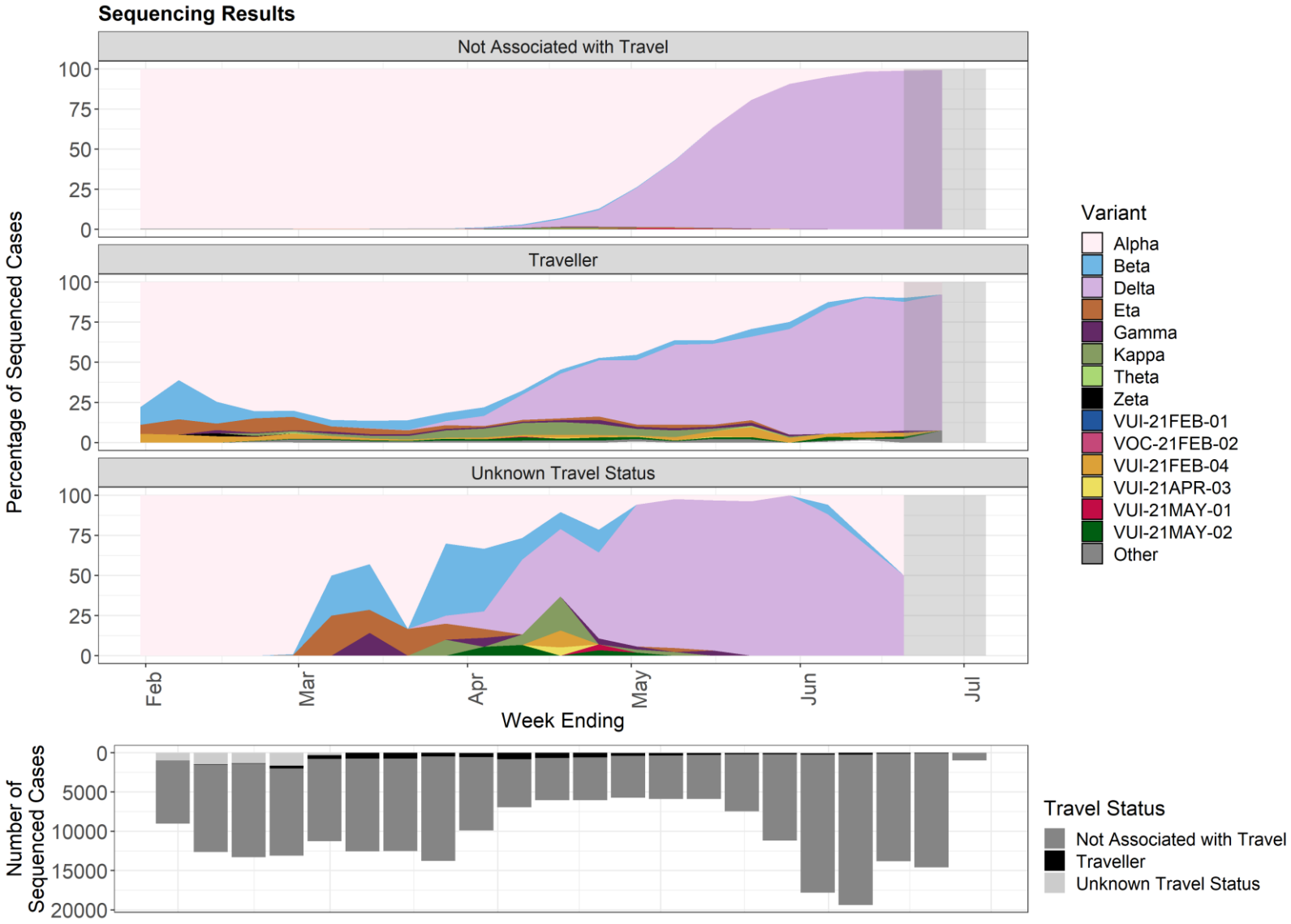


Figure 9. Prevalence of variants over time: all sequenced cases in England, split by travel status as of 5 July 2021
(Find accessible data used in this graph in underlying data)



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).

Antigenic change of variants over time

A list of mutations of potential antigenic significance has been compiled using the available published evidence. The comprehensive list of mutations of potential antigenic significance is compiled and continues to be updated by an expert group comprising members of the variant technical group, COG-UK and UK-G2P using literature searches and data mining from publicly available datasets. Data analysis includes GISAID data uploaded before the 6 July 2021 (excluding UK data). The increase in the number of antigenic mutations over time is illustrated for all variants in Figure 10 and for all variants excluding variants of concern and under investigation in Figure 11.

The plots were obtained by first counting the number of high confidence antigenic mutations for each sequence. The sequences were then grouped and the prevalence for each number of mutations was estimated weekly from March 2020 until the beginning of June 2021. All non-synonymous mutations at positions in the Spike protein that have been associated with antigenicity were considered antigenic. Variant of concern or under investigation were identified by analysing their Spike mutation profile in order to deal with low-quality and partial sequences.

Figure 10. Prevalence of antigenic mutations over time for all variants within GISAID as of 6 July 2021, excluding UK data
(Find accessible data used in this graph in underlying data)

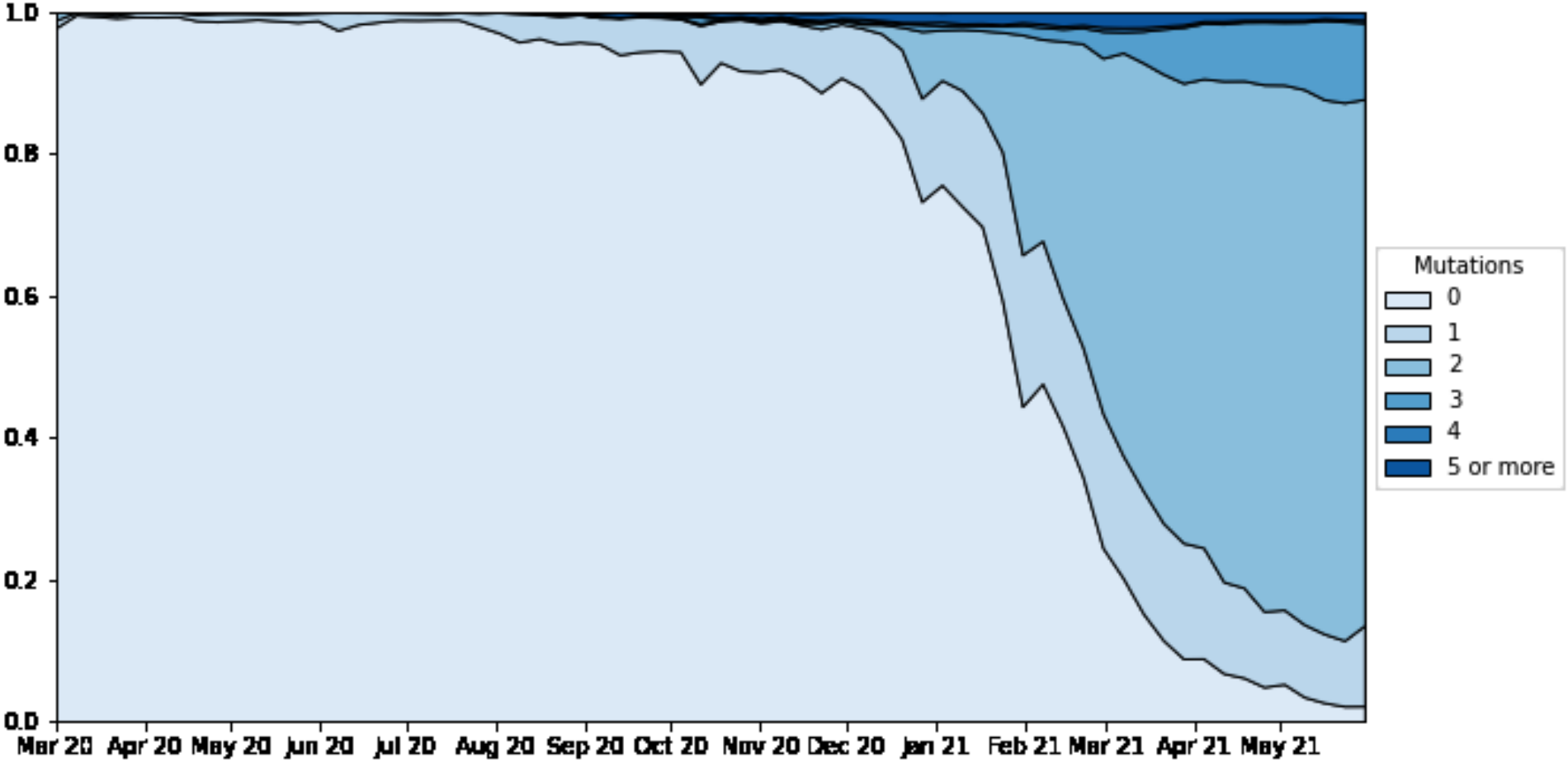
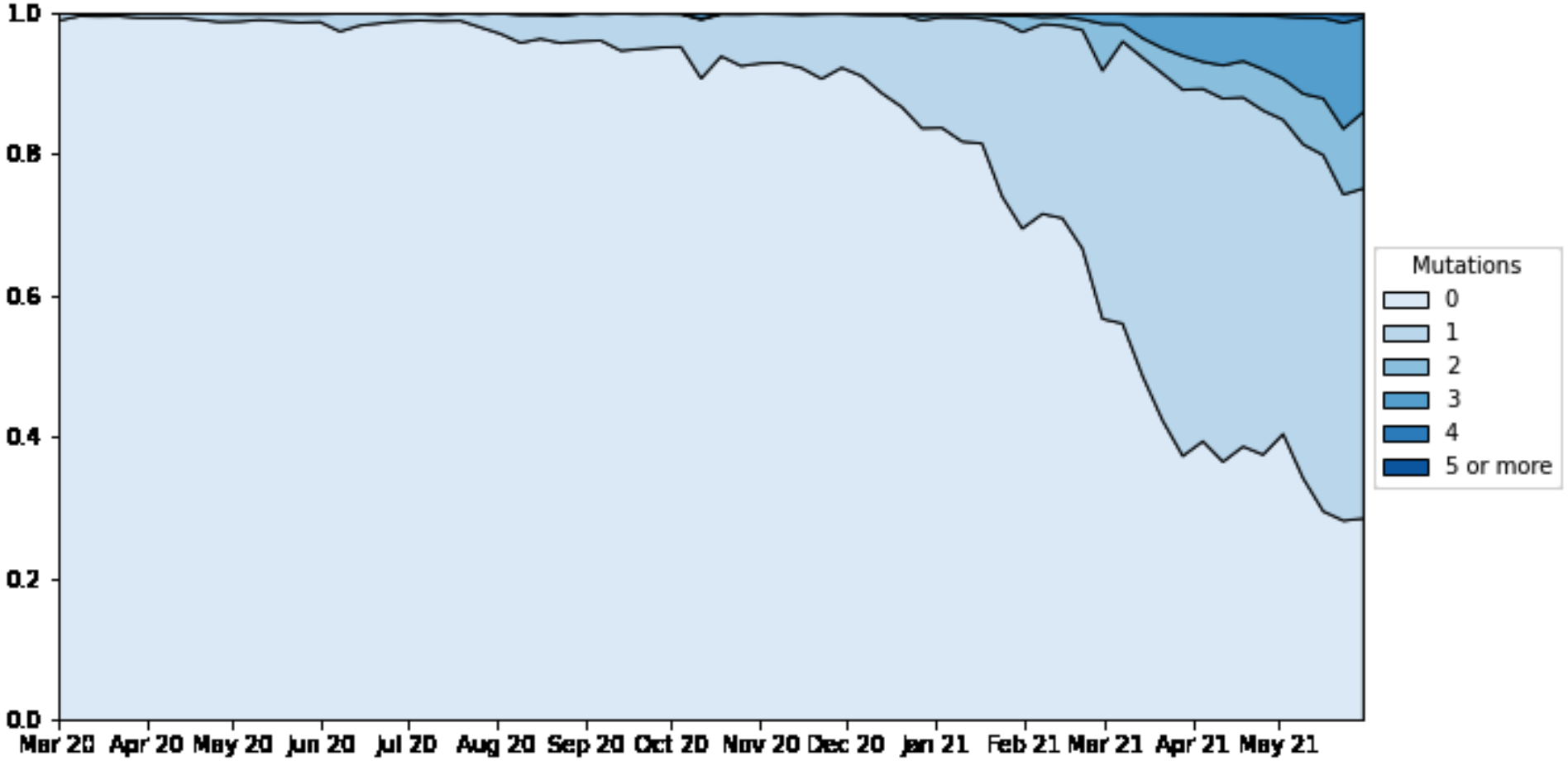


Figure 11. Prevalence of antigenic mutations over time for all variants excluding variants of concern and variants of interest as of 6 July 2021, excluding UK data (Find accessible data used in this graph in underlying data)



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 5 July 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 6 shows secondary attack rates for all variants. The time period of study for secondary attack rate to the period 5 January 2021 to 16 June 2021, to capture data for all variants. Vaccination levels and social restrictions in England have varied over this period, so comparisons between variants prevalent during different periods are not valid. 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.

Figure 12 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 13 June 2021, with 95% confidence intervals. The fall in secondary attack rate amongst household contacts of cases with Delta in previous weeks has continued, with an estimate of 10.3% (95% CI 10.1% to 10.6%) for exposure events in week commencing 7 June 2021. Over the period presented, secondary attack rates for both household and non-household contacts of cases respectively with Delta remain higher than for Alpha (or other cases).

Table 6. Secondary attack rates for all variants (5 January 2021 to 16 June 2021, variant data as of 5 July 2021, contact tracing data as of 7 July 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 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 (VOC-20DEC-01)	4,373 (76.6% with contacts)	184,585 (73.0% with household, 14.0% with non-household contacts)	2.3%	1.5% (1.4% - 1.6%) [1,243/81,647]	10.2% (10.1% - 10.3%) [34,547/337,506]	5.6% (5.5% - 5.8%) [3293/58,387]
Beta (VOC-20DEC-02)	336 (70.5% with contacts)	408 (65.0% with household, 15.0% with non-household contacts)	45.2%	1.9% (1.6% - 2.2%) [112/5,978]	9.7% (7.7% - 12.1%) [70/722]	3.0% (1.4% - 6.3%) [6/202]
Zeta (VUI-21JAN-01)	4 (75.0% with contacts)	27 (70.4% with household, 3.7% with non-household contacts)	12.9%	Unavailable [0/159]	Unavailable [4/51]	Unavailable [0/1]

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 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]
Gamma (VOC-21JAN-02)	71 (64.8% with contacts)	140 (72.1% with household, 15.0% with non-household contacts)	33.6%	1.0% (0.5% - 1.9%) [9/889]	9.9% (6.7% - 14.4%) [23/233]	3.5% (1.2% - 9.8%) [3/86]
VUI-21FEB-01	0 (0 with contacts)	63 (57.1% with household, 12.7% with non-household contacts)	0.0%	Unavailable [0/0]	9.9% (5.1% - 18.3%) [8/81]	Unavailable [1/12]
Eta (VUI-21FEB-03)	190 (69.5% with contacts)	191 (70.7% with household, 13.1% with non-	49.9%	1.0% (0.8% - 1.4%) [43/4,231]	8.9% (6.2% - 12.4%) [29/327]	Unavailable [1/43]

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 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]
		household contacts)				
VUI-21FEB-04	108 (67.6% with contacts)	154 (77.3% with household, 20.1% with non-household contacts)	41.2%	0.5% (0.3% - 0.8%) [16/3,067]	8.8% (6.0% - 12.5%) [26/297]	5.6% (2.4% - 12.5%) [5/89]
VUI-21MAR-01	1 (100.0% with contacts)	0 (0 with household, 0 with non-household contacts)	100.0%	Unavailable [0/7]	Unavailable [0/0]	Unavailable [0/0]

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 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]
Theta (VUI-21MAR-02)	5 (40.0% with contacts)	1 (100.0% with household, 0.0% with non-household contacts)	83.3%	Unavailable [0/4]	Unavailable [0/3]	Unavailable [0/0]
Kappa (VUI-21APR-01)	233 (77.3% with contacts)	173 (74.6% with household, 13.3% with non-household contacts)	57.4%	1.9% (1.5% - 2.3%) [83/4,449]	9.7% (7.1% - 13.0%) [38/392]	Unavailable [3/45]
Delta (VOC-21APR-02)	1172 (70.6% with contacts)	99192 (78.7% with household, 23.5% with non-	1.2%	1.7% (1.6% - 1.9%) [382/22,060]	10.9% (10.8% - 11.0%) [21,929/201142]	5.7% (5.5% - 5.9%) [4,149/72,808]

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 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]
		household contacts)				
VUI-21APR-03	7 (14.3% with contacts)	5 (100.0% with household, 0.0% with non-household contacts)	58.3%	Unavailable [1/201]	Unavailable [1/12]	Unavailable [0/0]
VUI-21MAY-01	2 (0.0% with contacts)	174 (83.3% with household, 17.8% with non-household contacts)	1.1%	Unavailable [0/0]	8.1% (5.8% - 11.1%) [33/409]	2.4% (0.8% - 6.9%) [3/124]
VUI-21MAY-02	66 (74.2% with contacts)	52 (82.7% with household, 9.6% with non-	55.9%	0.9% (0.5% - 1.5%) [11/1,275]	8.3% (4.4% - 15.0%) [9/109]	Unavailable [0/13]

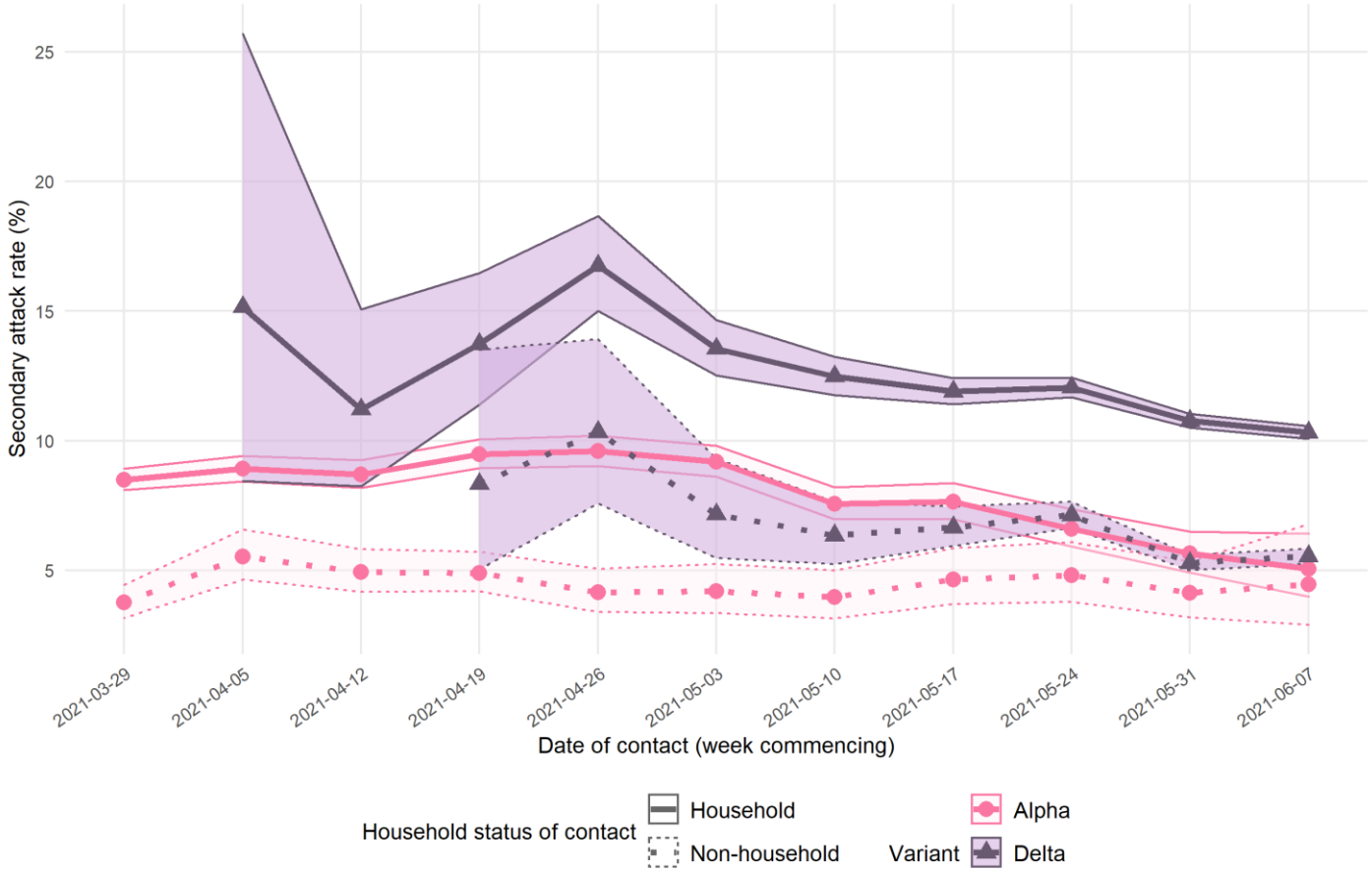
Variant	Cases in those that have travelled (with contacts)	Cases in those that have not travelled or unknown (with contacts)	Case proportion that have travelled	Secondary attack rate among contacts of cases that have travelled (95% CI) [secondary cases/contacts]	Secondary Attack Rate among household 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]
		household contacts)				
Lambda (VUI-21JUN-01)	6 (66.7% with contacts)	0 (0 with household, 0 with non-household contacts)	100.0%	Unavailable [0/159]	Unavailable [0/0]	Unavailable [0/0]

Table 6 legend: 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 16 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.

Figure 12. Secondary attack rates amongst household and non-household contacts of non-travel cases of Alpha and Delta, with 95% confidence intervals (29 March 2021 to 13 June 2021, variant data as of 5 July 2021, contact tracing data as of 7 July 2021)
(Find accessible data used in this graph in underlying data)



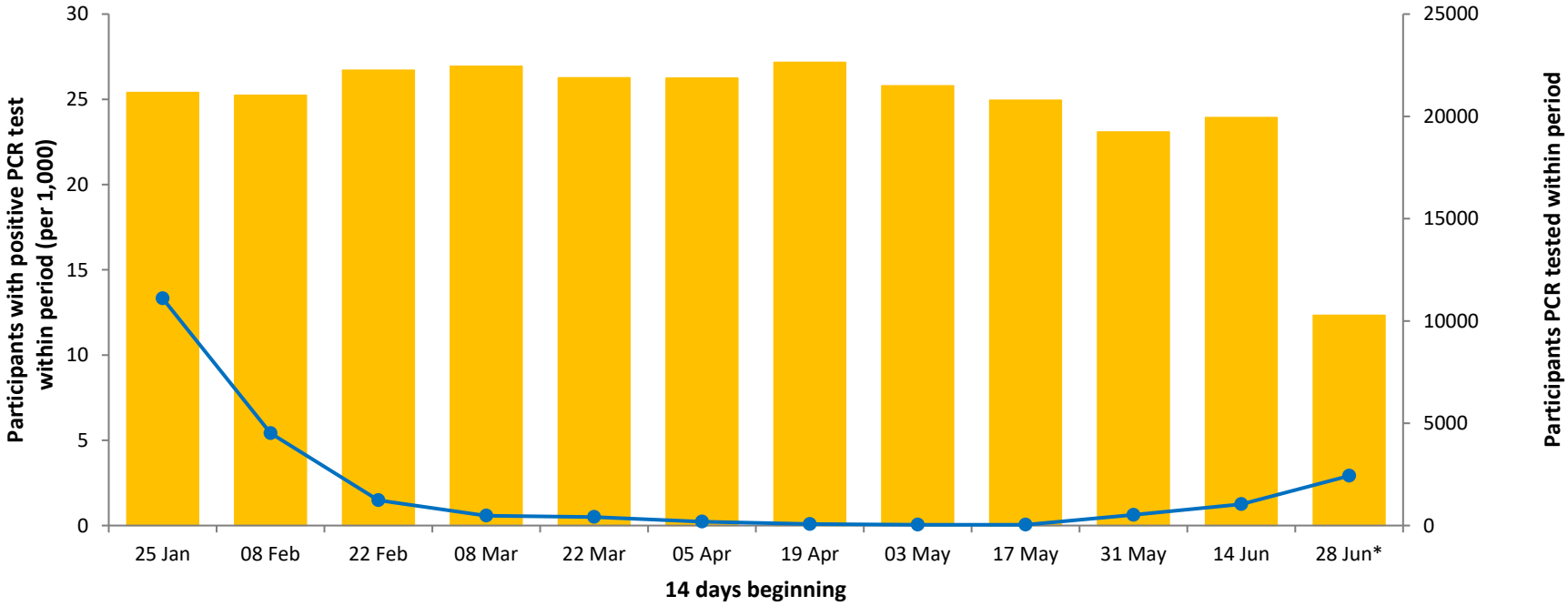
Note legend from Table 6. Secondary attack rates are suppressed when count of contacts is less than 50 or count of cases is less than 20. Data provided is for period until 13 June 2021 in order to allow time for contacts to become cases and complete weeks to be shown. Probable (genotyping) results are included, low quality genomic results are not.

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, 35,693* 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 (Figure 13). Of the 77 participants with a PCR positive sample since April 2021 in the SIREN cohort overall, 66 (81%) 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 14).

*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.

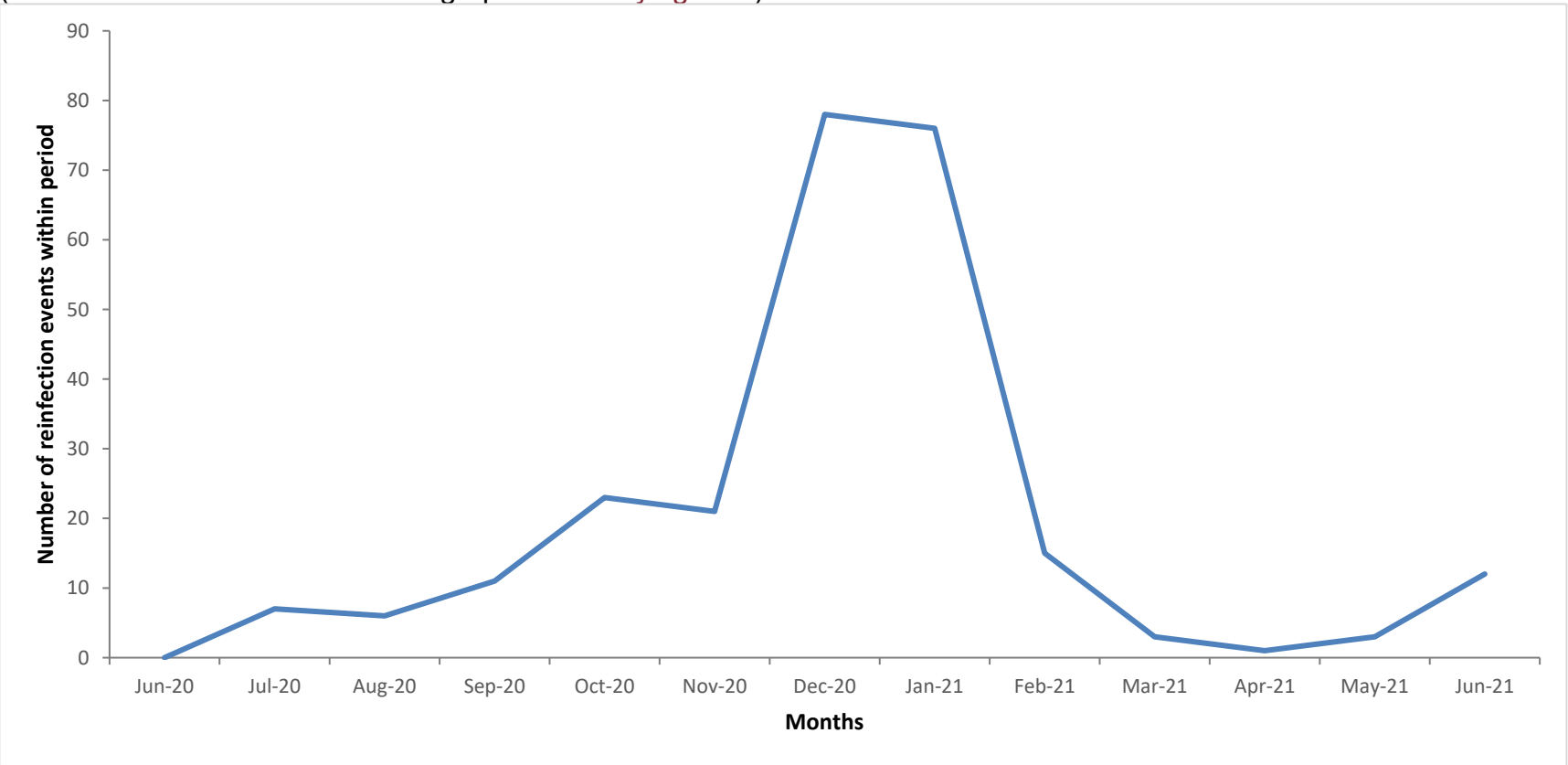
Figure 13. PCR positivity within the SIREN study for all regions, England (fortnightly testing interval) Data up to 4 July 2021
Yellow bars indicate participants PCR-tested within period (right axis), Blue line indicates participants with positive PCR within period (per 1,000) (left axis). (Find accessible data used in this graph in underlying data)



*Incomplete week commencing 28 June 2021

Please note that Figure 11 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 14. Monthly frequency of potential reinfection events within SIREN. Data up to 27 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. Up to the 27 June 2021, there were 256 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 16 potential reinfection events from April to 27 June 2021, 15 (93%) of which occurred at least 14 days after participants received their second vaccine dose.

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.

Surveillance through genomic data

Figure 15. Confirmed (sequencing) and probable (genotyping) Delta cases by specimen date and detection method as of 5 July 2021 (Find accessible data used in this graph in underlying data)

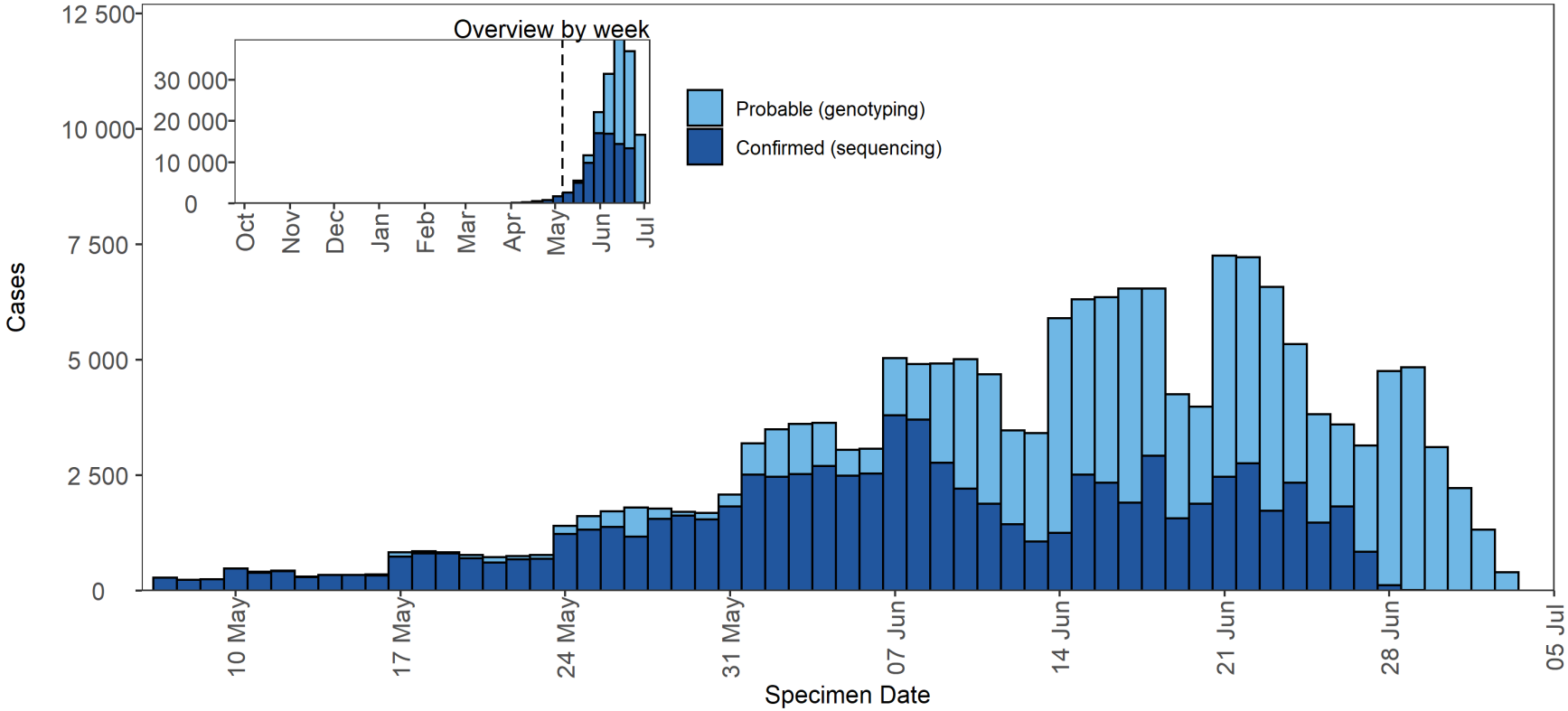


Figure 16. Confirmed (sequencing) and probable (genotyping) Delta cases by specimen date and region of residence as of 5 July 2021 (Find accessible data used in this graph in underlying data)

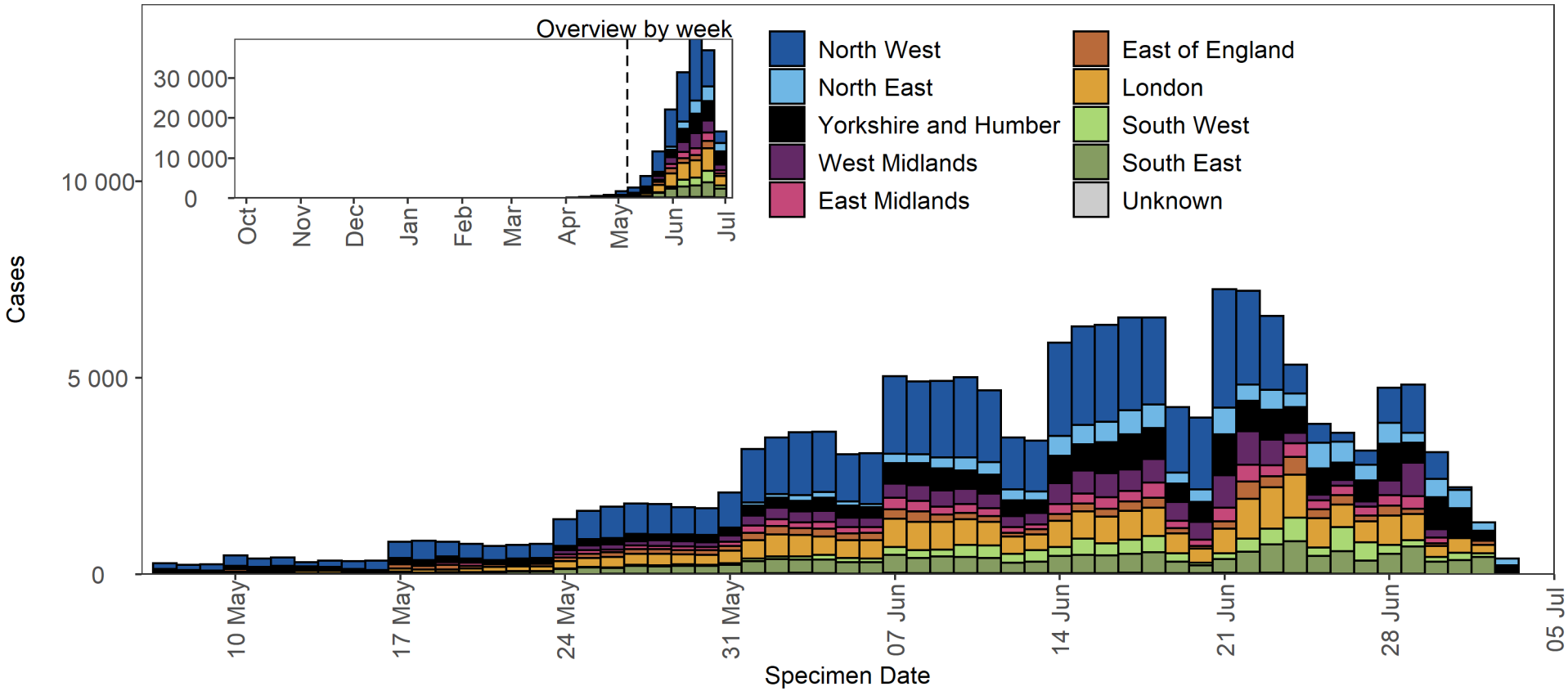


Table 7. Additional spike mutations of interest detected in Delta genomes in the UK and globally excluding the UK (GISAID), as of 6 July 2021

Amino acid change	Number of Delta sequences with mutation (England)	Number of Delta sequences with mutation Global (outside UK)	Number of Delta sequences with mutation 7 April to 6 May 2021		Number of Delta sequences with mutation 7 May to 6 June 2021		Number of Delta sequences with mutation 7 June to 6 July 2021	
			England	Global	England	Global	England	Global
Total number of Delta sequences (England and outside UK, GISAID data)	90,813	31,446	2,684	7,519	40,042	11,709	48,013	10,388
G446V	136	59	1	21	68	29	67	8
P251L	70	100	0	12	15	40	55	48
K417N	44	448	14	40	28	228	2	175
S494L	14	17	0	3	6	5	8	9
V483F	11	17	1	5	2	4	8	3
K458N	11	3	0	0	0	0	11	3

N501Y	7	37	2	10	0	13	5	14
L455F	6	12	0	4	0	7	5	1
E484A	6	6	4	0	1	1	1	5
K444N	4	8	0	0	3	7	1	1
S494P	4	10	0	1	0	8	4	0
Q493E	4	23	0	5	0	10	4	8
P681H	2	5	0	0	1	3	1	2
F490L	2	2	0	0	0	2	0	0
D80N	2	2	0	2	0	0	2	0
P499L	2	1	0	1	0	0	2	0
E484Q	2	21	0	4	2	8	0	9
E484V	2	1	0	0	0	0	2	1
D80A	1	29	0	10	1	12	0	4

This data uses the numbers of genomes in the national genomic dataset and international dataset (GISAID), excluding UK sequences (GISAID), rather than case numbers. Only antigenic variants on the Delta genome are presented. The total number of sequences from the COG dataset is generated using sequences from 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.

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

GISAID includes data on sequences available internationally. As of 6 July 2021, 448 genomes of Delta-with K417N have been identified in GISAID internationally, excluding the UK: USA (253), Portugal (55), Japan (47), Switzerland (41), India (16), Nepal (11), Poland (11), France (8), Canada (1), Denmark (1), Germany (1), Romania (1), Russia (1), Spain (1).

Epidemiology

There are currently 42 cases of Delta with K417N in England (39 confirmed sequencing and 3 probable genotyping). Cases have been detected in 7 different regions in England (Table 10, Figure 15).

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 underway for Delta-AY.1

Table 8. Number of confirmed (sequencing) and probable (genotyping) Delta-with K417N cases, by region of residence as of 5 July 2021

Region	Confirmed (sequencing) case number	Probable (genotyping) case number[1]	Total case number	Case Proportion
East Midlands	1	0	1	2.4%
East of England	0	0	0	0.0%
London	7	1	8	19.0%
North East	0	2	2	4.8%
North West	3	0	3	7.1%
South East	15	0	15	35.7%
South West	2	0	2	4.8%
West Midlands	10	0	10	23.8%
Yorkshire and Humber	0	0	0	0.0%
Unknown region	1	0	1	2.4%
Total	39	3	42	-

[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 17. Delta with K417N cases (confirmed sequencing and probable genotyping) by region of residence and specimen date as of 5 July 2021 Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data)

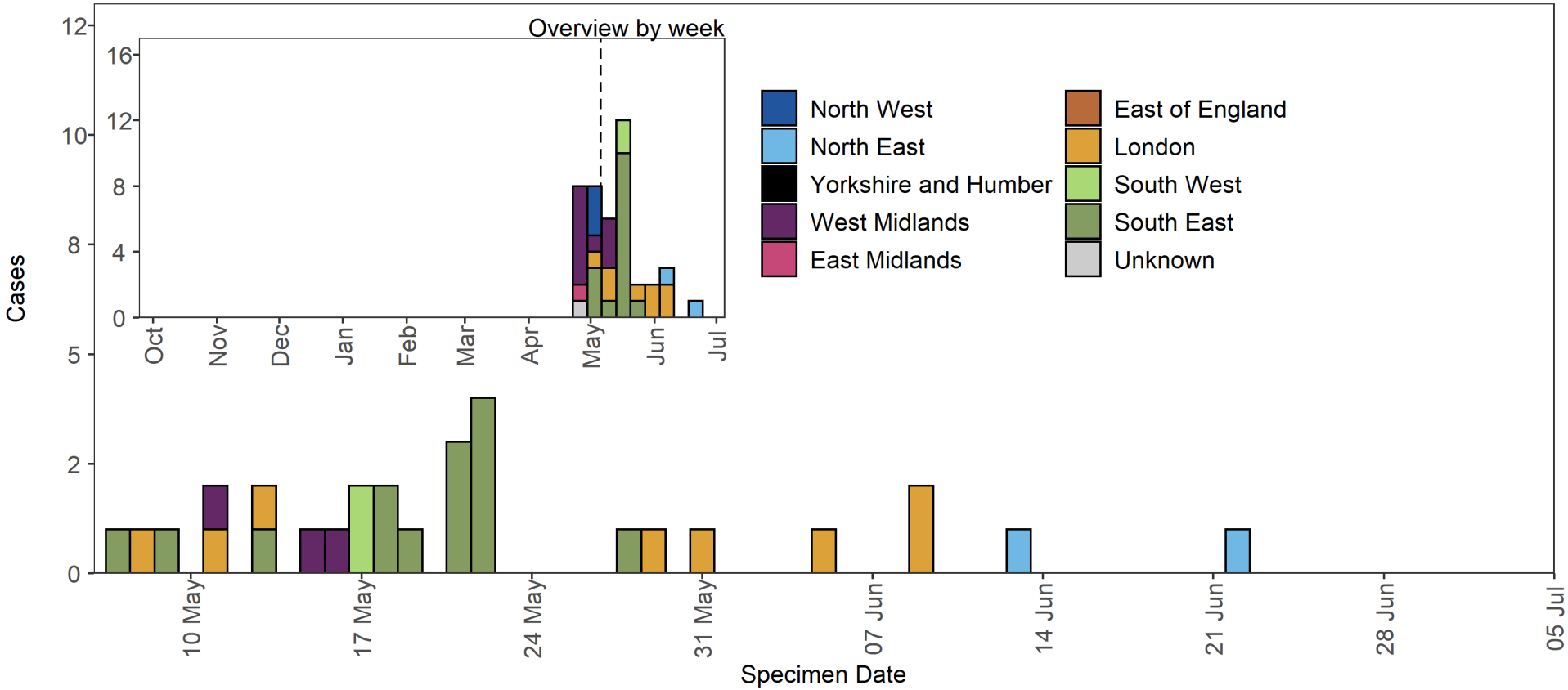


Figure 18. Confirmed (sequencing) and probable (genotyping) Delta with K417N cases by specimen date and detection method as of 5 July 2021 (Find accessible data used in this graph in underlying data)

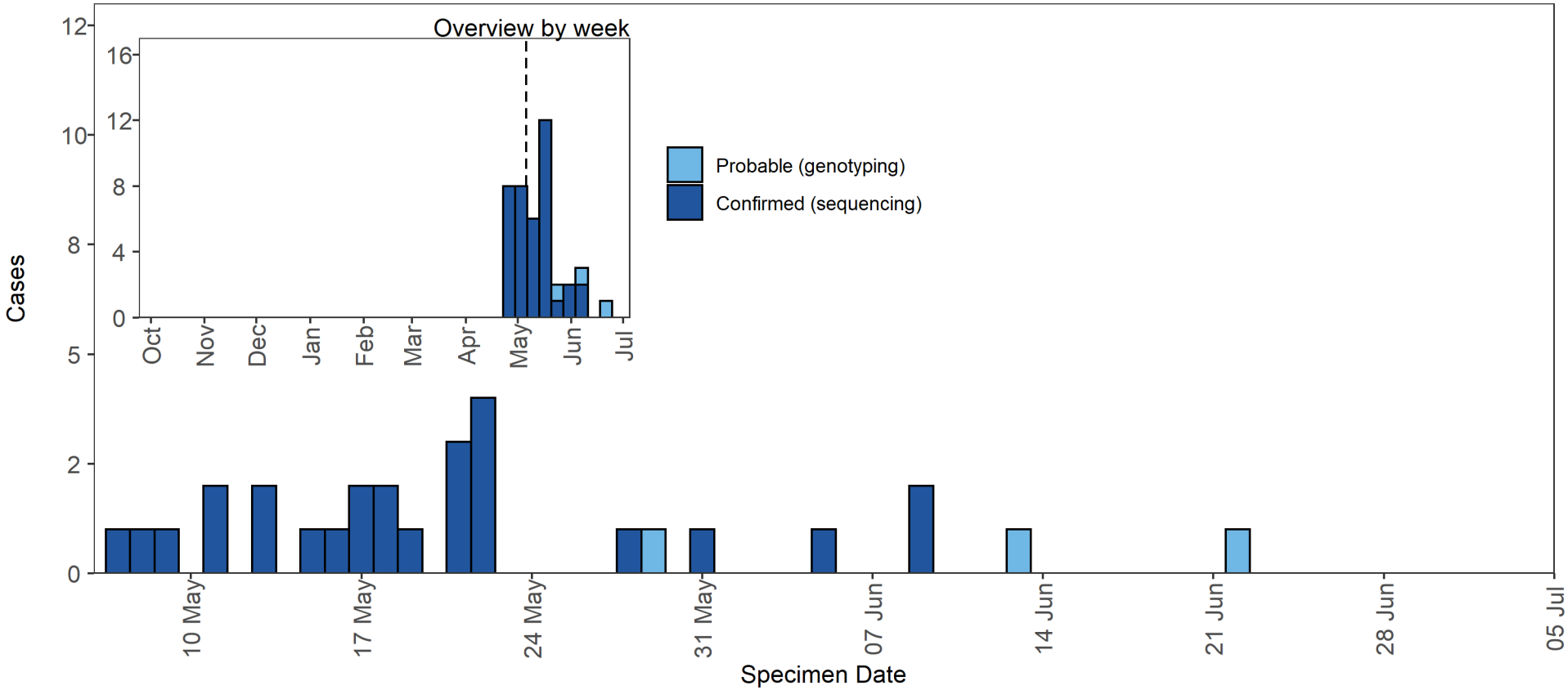
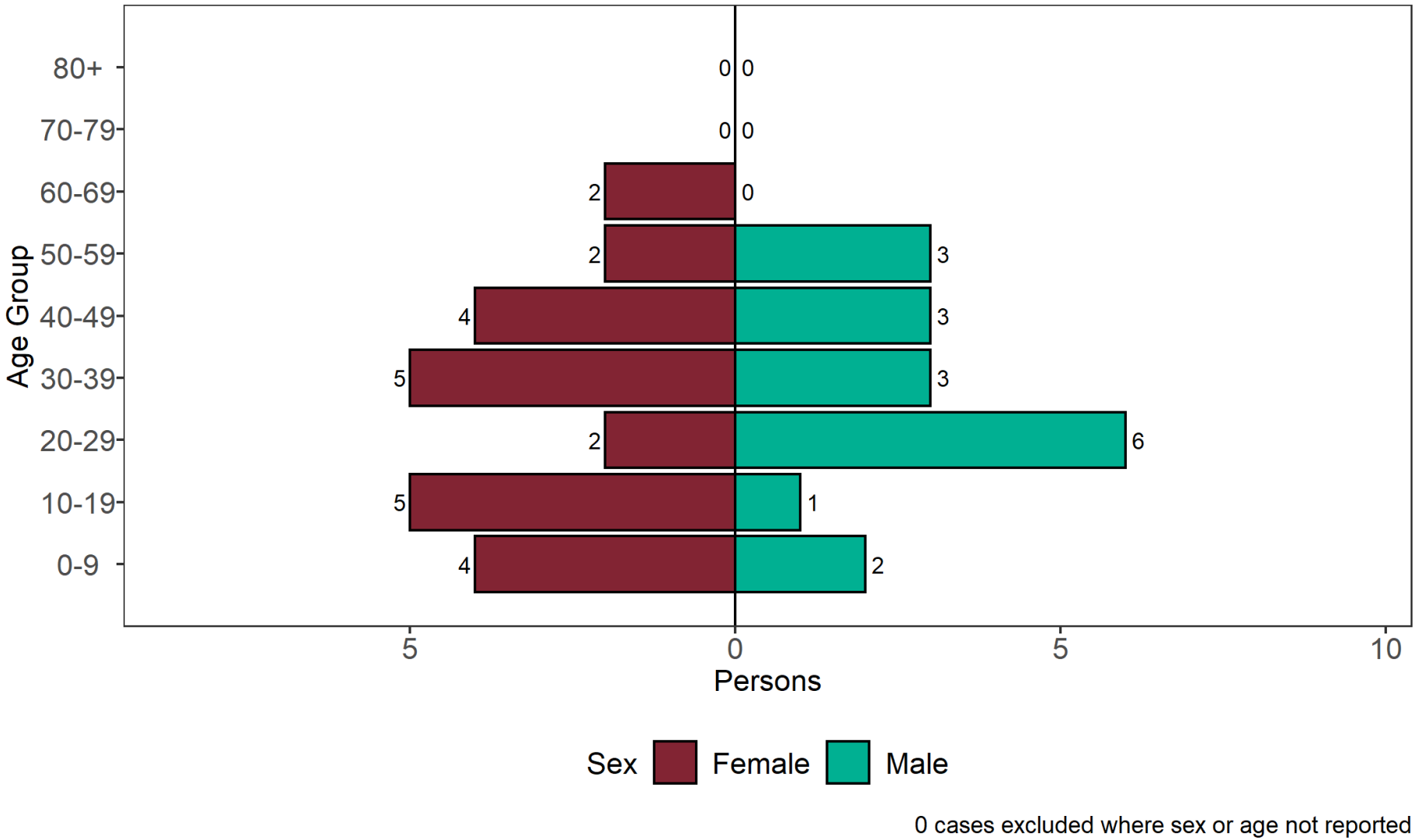


Figure 19. Age-sex pyramid of confirmed (sequencing) and probable (genotyping) Delta with K417N cases as of 5 July 2021
(Find accessible data used in this graph in underlying data)



0 cases excluded where sex or age not reported

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
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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

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