Public Health England

Protecting and improving the nation's health

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

Technical briefing 23

17 September 2021

This briefing provides an update on previous briefings up to 3 September 2021

Contents

Summary

This report has been published to continue to share the detailed variant surveillance analyses which contribute to the variant risk assessments and designation of new variants of concern (VOCs) and variants under investigation (VUIs). The specialist technical briefings contain early data and analysis on emerging variants and findings have a high level of uncertainty.

A separate report is published covering surveillance data on all other VOCs and VUIs.

In summary:

- an assessment of Delta diversity, including mutations and designated sub-lineages, is provided
- there are 4 current VOCs and 8 VUIs (Table 1)
- there are no new VOCs or VUIs since the last briefing in the UK classification.
- there has been an increase in secondary attack rates for Delta in household contacts but not non-household contacts
- 2 doses of the vaccine remain highly effective, with 60 to 85% effectiveness against infection, 90 to 99% effectiveness against hospitalisation, 90 to 95% against mortality and 65 to 99% against symptomatic disease

All risk assessments are published separately here, except for Gamma, which was published within Technical Briefing 7 and Alpha within Technical Briefing 9. As Delta is the dominant variant in the UK, epidemiological and re-infection data in the weekly surveillance report is also relevant.

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.

Public Health England (PHE) curated a repository on the 5 March 2021 containing the up-to-date genomic definitions for all VOCs and VUIs. The repository is accessible on GitHub.

World Health Organization (WHO) nomenclature from 31 May 2021 is incorporated. A table incorporating WHO and UK designations with Pango lineages is provided below (Table 1). Following the table, 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 technical briefing 15, briefings include variant diagnoses identified by whole-genome sequencing and a genotyping PCR test, including the categorisation of sequenced and genotyped 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 (or B.1.621), Delta, and Gamma. Targets were updated in mid-May 2021 to prioritise accurate identification of Delta over Alpha.

Part 1 Surveillance overview

1.1 Variants under surveillance

Table 1 shows the current VOC, VUI, and variants in monitoring as of 13 September 2021.

Table 1. Variant lineage and designation as of 13 September 2021

WHO nomenclature	Lineage	Designation	Status	UK or International (not currently detected in UK)
Alpha	B.1.1.7	VOC-20DEC-01	VOC	UK
Beta	B.1.351	VOC-20DEC-02	VOC	UK
Gamma	P.1	VOC-21JAN-02	VOC	UK
Delta	B.1.617.2, AY.1, AY.2, AY.3, and AY.4	VOC-21APR-02	VOC	UK
Eta	B.1.525	VUI-21FEB-03	VUI	UK
	B.1.1.318	VUI-21FEB-04	VUI	UK
Theta^	P.3	VUI-21MAR-02	VUI	UK
	B.1.617.3	VUI-21APR-03	VUI	International
	AV.1	VUI-21MAY-01	VUI	UK
	C.36.3	VUI-21MAY-02	VUI	UK
Lambda	C.37	VUI-21JUN-01	VUI	UK
Mu	B.1.621	VUI-21JUL-01	VUI	UK
Epsilon^	B.1.427/B.1.429		Monitoring	
	B.1.1.7 with S494P		Monitoring	
	A.27		Monitoring	
Iota	B.1.526		Monitoring	
	B.1.1.7 with Q677H		Monitoring	
	B.1.620		Monitoring	
	B.1.214.2		Monitoring	
	R.1		Monitoring	
	B.1 with 214insQAS		Monitoring	
	AT.1		Monitoring	
	A.30		Monitoring	
	P.1 + N501T and E484Q		Monitoring	
	B.1.629		Monitoring	
	B.1.619		Monitoring	
	C.1.2		Monitoring	
	B.1.630		Monitoring	
	B.1.631/B.1.628		Monitoring	
	P.1.8		Monitoring	

Provisionally extinct variants are excluded from this table.

VOCs and VUIs are monitored weekly for observations within the last 12 weeks. If variants have not been detected in the UK within this period, they are moved to international status with continued monitoring. If a VOC or VUI has not been observed in the UK or international datasets within the preceding 12 weeks, it is designated as provisionally extinct, but monitoring remains in place.

The last documented case of VUI-21APR-03 (B.1.617.3) was on the 17 May 2021 in the UK, this variant was moved to international monitoring on the 16 August 2021.

VUI-21FEB-01 (A.23.1 with E484K), VOC-21FEB-02 (B.1.1.7 with E484K), VUI-21MAR-01 (B.1.324.1 with E484K), Kappa VUI-21APR-01 (B.1.617.1) and Zeta (VUI-21JAN-01) have not been observed in the UK or within the international GISAID dataset within the last 12 weeks. These variants are no longer included in the data update.

^ Epsilon, Zeta and Theta were de-escalated by ECDC and by WHO. Mu was designated on the 30 August 2021

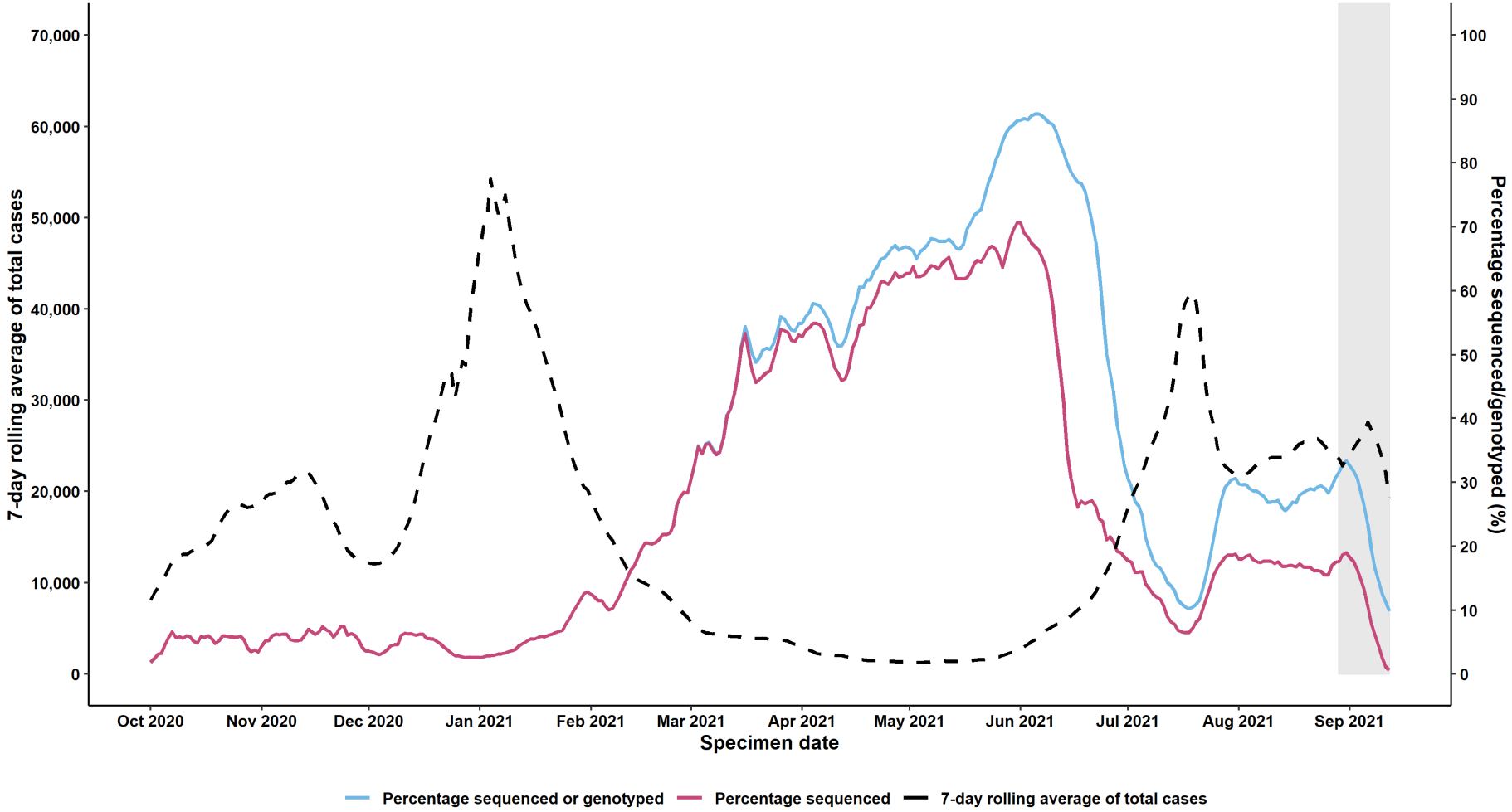
1.2 Sequencing coverage

Figure 1 shows the proportion of cases that have linked to a valid sequencing result (sequences included have 50% of the genome with sufficient read coverage) or genotyping PCR result over time. Figure 2 shows the proportion of cases sequenced and genotyped over time by regions. Figure 3 shows the proportion of cases sequenced and genotyped amongst cases who tested positive while in hospital. Figure 4 shows coverage of sequencing and genotyping for cases by age group.

Sequencing coverage is improving (Figure 1). During the current surge period, the sequencing strategy for both Pillar 1 and 2 is:

- hospitalised cases and hospital staff
- cases among international travellers
- national core priority studies
- as near random a sample as possible from each region, to the maximum coverage allowed by laboratory capacity

Figure 1. Coverage of sequencing with a valid result and genotyping over time (1 October 2020 to 12 September 2021)
(Find accessible data used in this graph in underlying data)



Data extract from 13 September 2021; data from 01 October 2020 to 12 September 2021.
Grey shading was applied to the previous 14 days to account for reporting delays in sequencing data.

Figure 2. Coverage of sequencing with a valid result and genotyping over time by region (1 October 2020 to 12 September 2021) (Find accessible data used in this graph in underlying data)

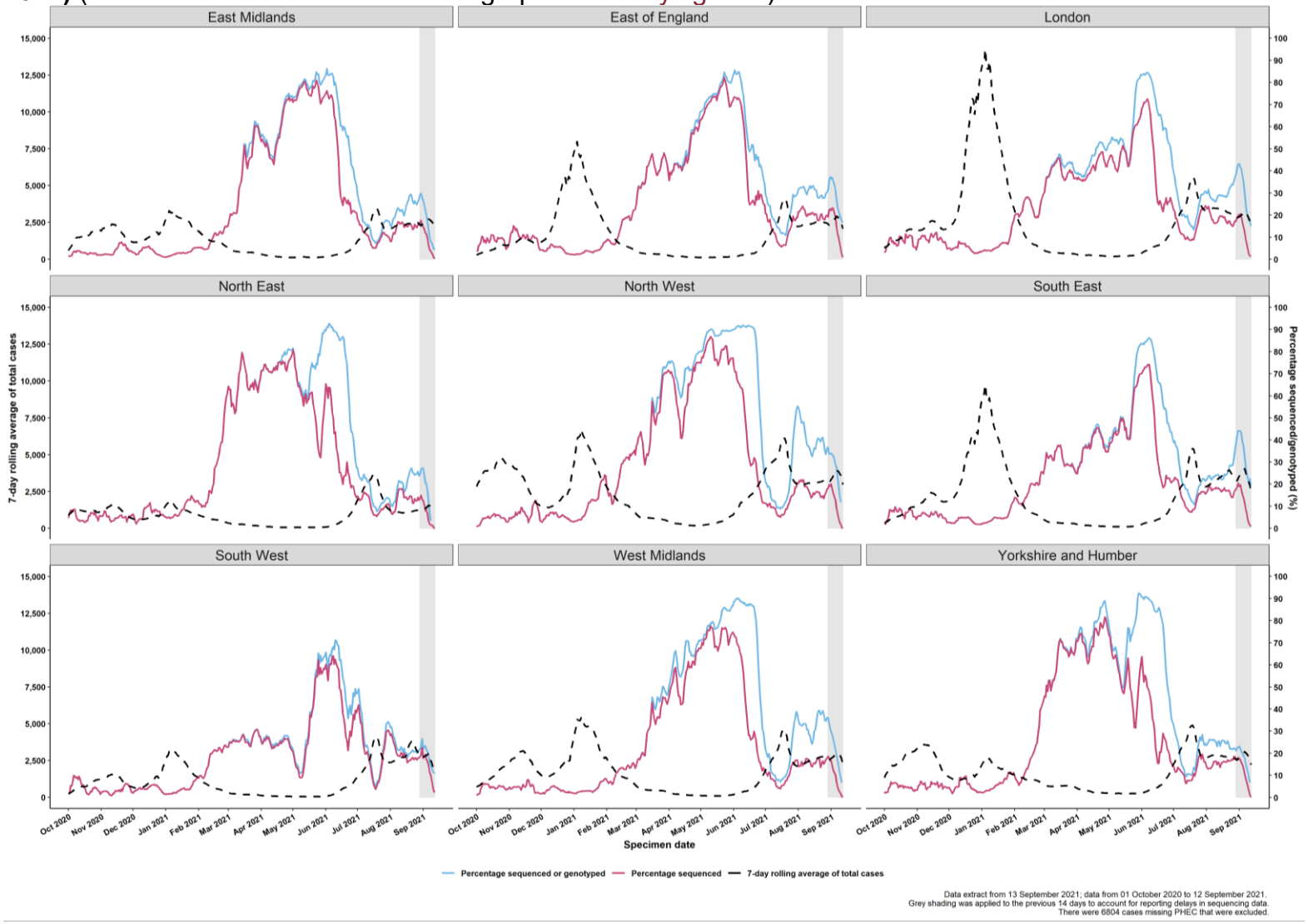
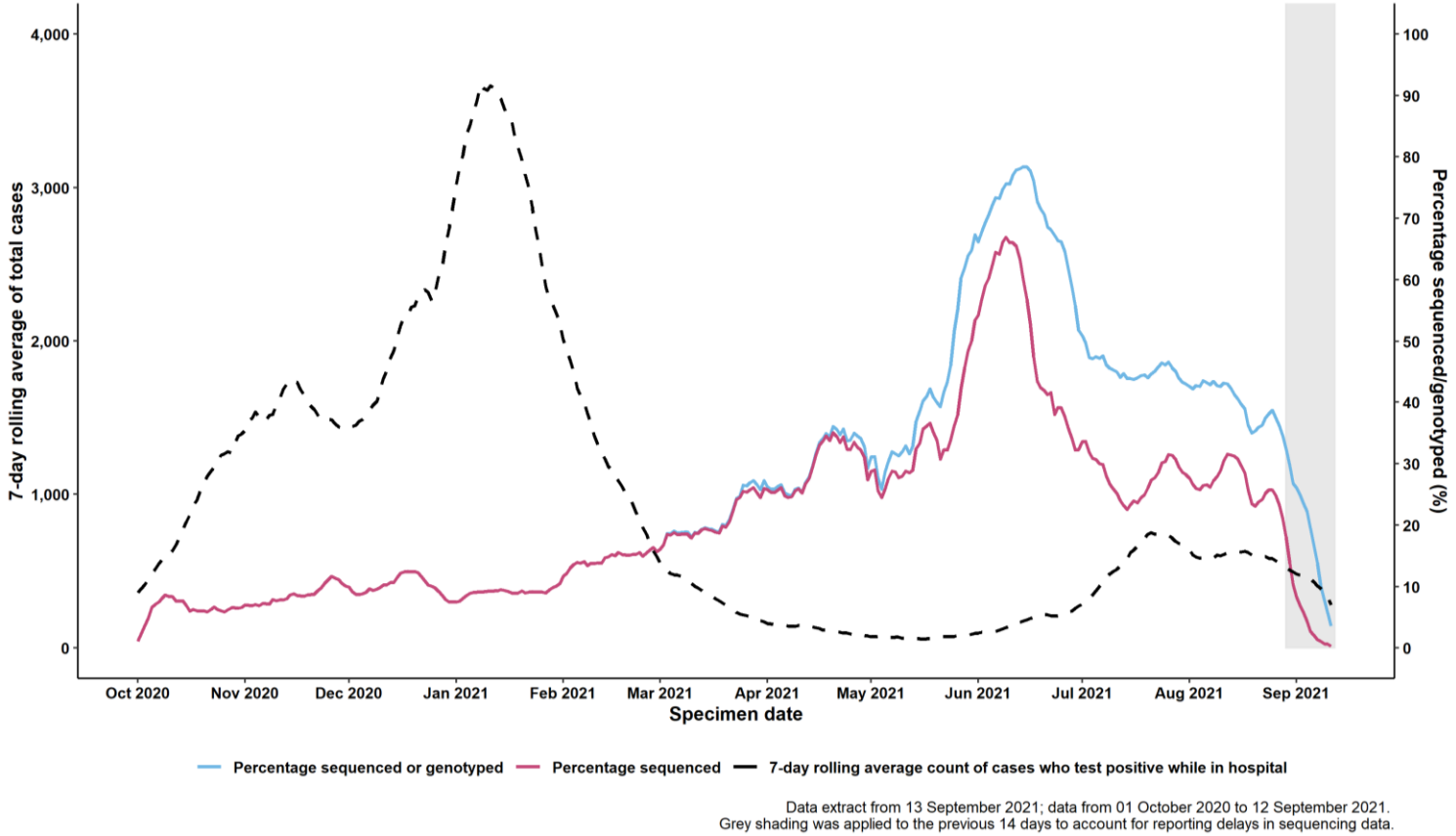


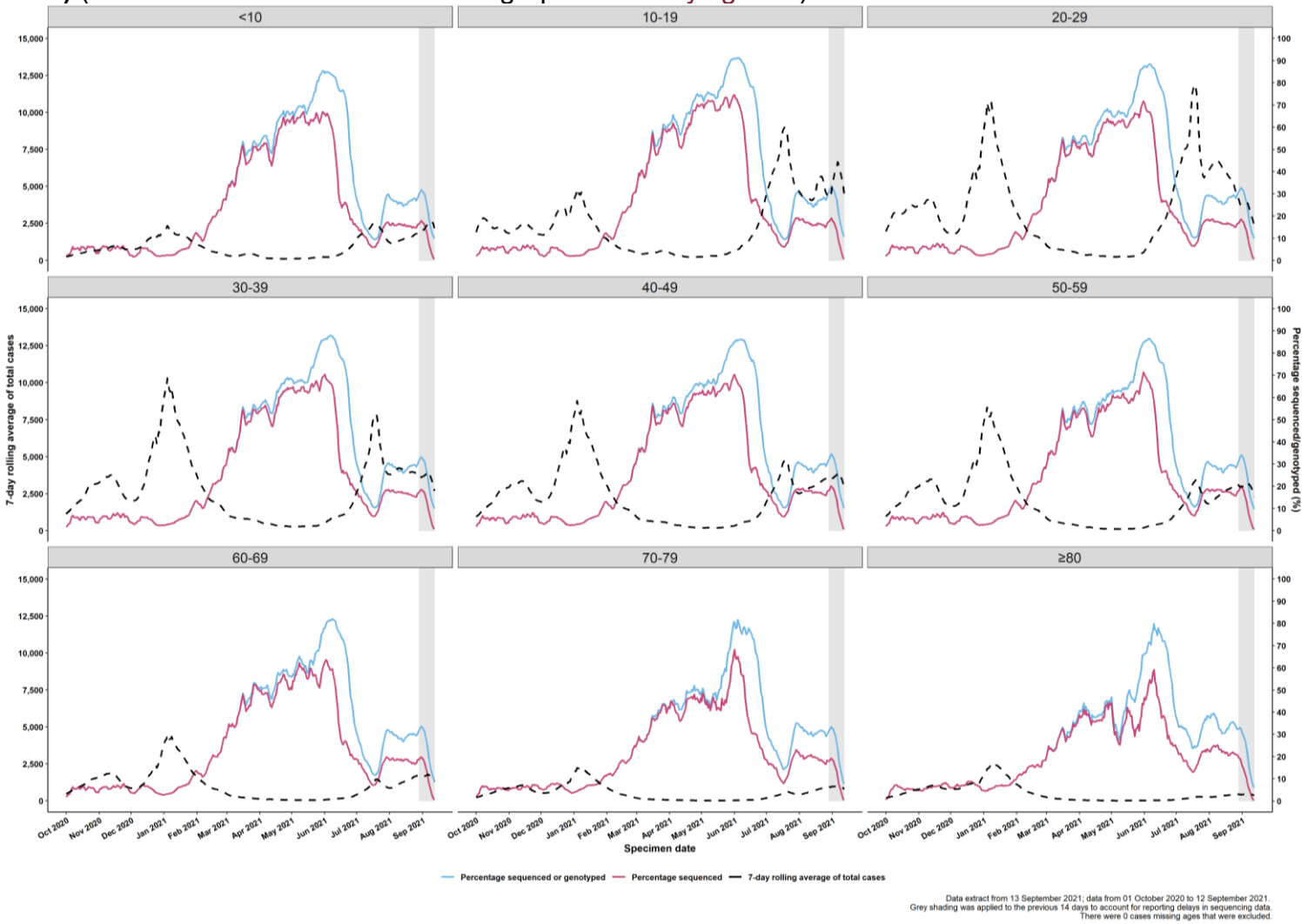
Figure 3. Coverage of sequencing with valid result and genotyping for cases who test positive in hospital (1 October 2020 to 12 September 2021) (Find accessible data used in this graph in underlying data)



Grey shading was applied to the previous 14 days to account for reporting delays in sequencing data.

[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. 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 4. Coverage of sequencing with valid result and genotyping for cases by age group (1 October 2020 to 12 September 2021) (Find accessible data used in this graph in underlying data)



Grey shading was applied to the previous 14 days to account for reporting delays in sequencing data.

1.3 VOC and VUI case numbers, proportion and deaths

Summary epidemiology on Delta is shown in Table 2 and for each variant is shown in Table 3, case numbers are also updated online. Table 3 shows the number of sequenced, genotyped, and total cases and deaths for each variant. However, case fatality rates are not comparable across variants (see Table 3 footnote). Tables 4 and 5 show the number of cases who visited an NHS Emergency Department, were admitted, and died in any setting. The data is shown from 1 February 2021 onwards to enable comparisons across variants. Figure 5 shows the cumulative number of cases per variant indexed by days since the first report.

Information on attendance to emergency care is derived from the Emergency Care Data Set (ECDS), provided by NHS Digital. These data only show whether a case has attended emergency care at an NHS hospital and was subsequently admitted as an inpatient. The data does not include cases who were directly admitted without first presenting to emergency care.

The crude analysis indicates that the proportion of Delta cases who present to emergency care is greater than that of Alpha, but a more detailed analysis of 43,338 coronavirus (COVID-19) cases indicates that the risk of hospitalisation among Delta cases is 2.26 times greater compared to Alpha (Twohig et al, 2021[1]).

ECDS reporting is lagged as NHS trusts routinely provide monthly data by the 21st of the following month. However, some trusts report daily data, and the linkage between COVID-19 cases and ECDS data is updated twice-weekly.

Data on all COVID-19 cases, hospitalisation and deaths by age and vaccination status are now published weekly in PHE's Vaccine Surveillance Report. Publication of Table 5 in the Variant Technical Report will continue for 2 more issues and then cease.

[1] Hospital admission and emergency care attendance risk for SARS-CoV-2 delta (B.1.617.2) compared with alpha (B.1.1.7) variants of concern: a cohort study

Table 2. Sequenced and genotyped Delta cases by region from 1 October 2020 as of 13 September 2021

Region	Sequenced cases	Genotyped cases[1]	Total Delta case number (1 October 2020 as of 30 August 2021)	Proportion of total Delta cases per region
East Midlands	25,119	14,382	39,501	6.7%
East of England	34,951	19,463	54,414	9.2%
London	52,357	36,081	88,438	14.9%
North East	18,022	13,091	31,113	5.2%
North West	65,652	65,709	131,361	22.1%
South East	45,293	30,643	75,936	12.8%
South West	41,483	7,819	49,302	8.3%
West Midlands	29,622	28,934	58,556	9.9%
Yorkshire and Humber	36,552	25,012	61,564	10.4%
Unknown region	1,991	1,685	3,676	0.6%
Total	351,042	242,819	593,861	-

[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. If a Genotyped specimen also has a reported sequencing result, this case is removed from the Genotyped category and added to Sequenced category once/if the sequence data is reported.

Table 3. Number of sequenced and genotyped cases by variant from 1 October 2020 as of 12 September 2021

Variant	Sequenced cases	Genotyped cases[1]	Total case number	Proportion of total cases	Deaths
Alpha	221,507	5,707	227,214	27.6%	4,353
Beta	925	71	996	0.1%	13
Gamma	207	47	254	0.0%	0
Delta	351,042	242,819	593,861	71.1%	2,547
Eta	460	0	460	0.1%	12
VUI-21FEB-04	314	0	314	0.0%	<5
Theta	7	0	7	0.0%	0
VUI-21APR-03	15	0	15	0.0%	0
VUI-21MAY-01	184	0	184	0.0%	<5
VUI-21MAY-02	147	0	147	0.0%	0
Lambda	8	0	8	0.0%	0
Mu	47	0	47	0.0%	0

[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. If a Genotyped specimen also has a reported sequencing result this case is removed from the Genotyped category and added to Sequenced category once/if the sequence data is reported.

Table 4. Attendance to emergency care and deaths of sequenced and genotyped cases in England (1 February 2021 to 12 September 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	<50	118,561	13	0.0	5,029	4.2	5,863	4.9	1,244	1.0	1,682	1.4	67	0.1
	≥50	32,373	6	0.0	3,162	9.8	4,595	14.2	1,734	5.4	2,773	8.6	1,551	4.8
	All cases	151,038	20	0.0	8,191	5.4	10,458	6.9	2,978	2.0	4,455	2.9	1,618	1.1
Beta	<50	614	<5	0.2	26	4.2	28	4.6	6	1.0	9	1.5	<5	0.2
	≥50	168	<5	0.6	18	10.7	26	15.5	7	4.2	15	8.9	7	4.2
	All cases	791	2	0.3	44	5.6	54	6.8	13	1.6	24	3.0	8	1.0
Gamma	<50	229	5	2.2	9	3.9	9	3.9	<5	0.4	<5	0.4	-	0.0
	≥50	24	<5	4.2	<5	8.3	<5	8.3	-	0.0	-	0.0	-	0.0
	All cases	253	6	2.4	11	4.3	11	4.3	<5	0.4	<5	0.4	-	0.0
Delta	<50	497,105	119,611	24.1	16,709	3.4	22,719	4.6	3,490	0.7	6,230	1.3	204	0.0

	≥50	95,587	35,596	37.2	5,445	5.7	10,102	10.6	2,784	2.9	6,167	6.5	2,336	2.4
	All cases	593,572	155,252	26.2	22,162	3.7	32,834	5.5	6,280	1.1	12,407	2.1	2,542	0.4
Zeta	<50	16	-	0.0	-	0.0	-	0.0	-	0.0	-	0.0	-	0.0
	≥50	8	-	0.0	<5	12.5	<5	12.5	<5	12.5	<5	12.5	-	0.0
	All cases	24	-	0.0	<5	4.2	<5	4.2	<5	4.2	<5	4.2	-	0.0
Eta	<50	283	-	0.0	10	3.5	12	4.2	5	1.8	6	2.1	-	0.0
	≥50	120	-	0.0	<5	3.3	7	5.8	<5	0.8	<5	2.5	6	5.0
	All cases	406	-	0.0	14	3.4	19	4.7	6	1.5	9	2.2	6	1.5
VUI-21FEB-04	<50	247	<5	0.4	6	2.4	9	3.6	<5	0.4	<5	0.8	-	0.0
	≥50	58	-	0.0	<5	1.7	2	3.4	-	0.0	<5	1.7	<5	1.7
	All cases	307	<5	0.3	7	2.3	11	3.6	<5	0.3	<5	1.0	<5	0.3
Theta	<50	<5	-	0.0	<5	25.0	<5	25.0	-	0.0	-	0.0	-	0.0
	≥50	<5	-	0.0	-	0.0	-	0.0	-	0.0	-	0.0	-	0.0
	All cases	7	-	0.0	<5	14.3	<5	14.3	-	0.0	-	0.0	-	0.0
Kappa	<50	404	-	0.0	9	2.2	10	2.5	<5	0.2	<5	0.5	-	0.0
	≥50	67	-	0.0	6	9.0	6	9.0	<5	4.5	<5	4.5	<5	3.0

	All cases	471	-	0.0	15	3.2	16	3.4	<5	0.8	5	1.1	<5	0.4
VUI-21APR-03	<50	13	-	0.0	-	0.0	-	0.0	-	0.0	-	0.0	-	0.0
	≥50	<5	-	0.0	-	0.0	-	0.0	-	0.0	-	0.0	-	0.0
	All cases	15	-	0.0	-	0.0	-	0.0	-	0.0	-	0.0	-	0.0
VUI-21MAY-01	<50	161	-	0.0	<5	0.6	<5	1.2	-	0.0	<5	0.6	-	0.0
	≥50	22	-	0.0	-	0.0	-	0.0	-	0.0	-	0.0	<5	4.5
	All cases	184	-	0.0	<5	0.5	<5	1.1	-	0.0	<5	0.5	<5	0.5
VUI-21MAY-02	<50	112	-	0.0	9	8.0	10	8.9	<5	2.7	<5	3.6	-	0.0
	≥50	33	-	0.0	-	0.0	-	0.0	-	0.0	-	0.0	-	0.0
	All cases	147	-	0.0	9	6.1	10	6.8	<5	2.0	<5	2.7	-	0.0
Lambda	<50	8	-	0.0	<5	12.5	<5	12.5	<5	12.5	<5	12.5	-	0.0
	≥50	14	-	0.0	<5	29	5	36	<5	7	<5	7	-	0.0
	All cases	8	-	0.0	<5	12.5	<5	12.5	<5	12.5	<5	12.5	-	0.0
Mu	<50	33	-	0.0	<5	3.0	<5	3.0	-	0.0	-	0.0	-	0.0
	≥50	14	-	0.0	<5	28.6	5	35.7	<5	7.1	<5	7.1	-	0.0
	All cases	47	-	0.0	5	10.6	6	12.8	<5	2.1	<5	2.1	-	0.0

Data sources: Emergency care attendance and admissions from 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 one 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.

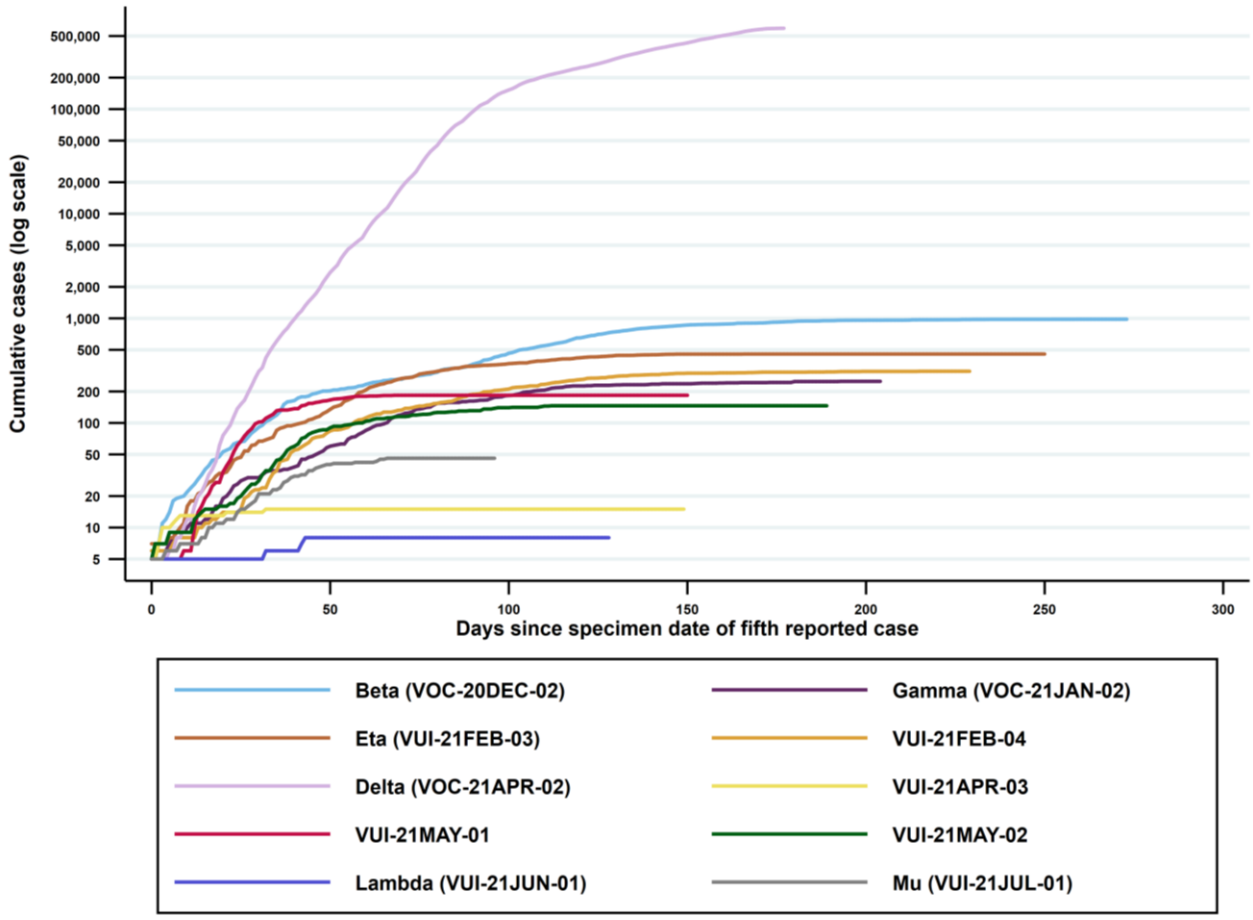
Table 5. Attendance to emergency care and deaths of sequenced and genotyped Delta cases in England by vaccination status (1 February 2021 to 12 September 2021)

Variant	Age group (years)**	Total	Cases with specimen date in past 28 days	Unlinked	<21 days post dose 1	≥21 days post dose 1	≥14 days post dose 2	Un-vaccinated
Delta cases	<50	497,105	119,611	49,527	30,359	83,009	85,407	248,803
	≥50	95,587	35,596	7,602	314	7,129	71,991	8,551
	All cases	593,572	155,252	58,003	30,674	90,138	157,400	257,357
Cases with an emergency care visit§ (exclusion‡)	<50	16,709	N/A	167	1,051	2,494	2,518	10,479
	≥50	5,445	N/A	21	30	448	3,747	1,199
	All cases	22,162	N/A	196	1,081	2,942	6,265	11,678
Cases with an emergency care visit§ (inclusion#)	<50	22,719	N/A	273	1,364	3,060	3,162	14,860
	≥50	10,102	N/A	50	64	755	6,532	2,701
	All cases	32,834	N/A	336	1,428	3,815	9,694	17,561
Cases where presentation to emergency care resulted in overnight inpatient admission§ ((exclusion‡)	<50	3,490	N/A	95	174	352	453	2,416
	≥50	2,784	N/A	10	18	184	1,908	664
	All cases	6,280	N/A	111	192	536	2,361	3,080
Cases where presentation to emergency care resulted in overnight inpatient admission§ (inclusion#)	<50	6,230	N/A	144	283	565	721	4,517
	≥50	6,167	N/A	33	42	393	3,913	1,786
	All cases	12,407	N/A	187	325	958	4,634	6,303

Deaths within 28 days of positive specimen date	<50	204	N/A	7	6	11	48	132
	≥50	2,336	N/A	32	11	138	1,565	590
	All cases	2,542	N/A	41	17	149	1,613	722

Data sources: Emergency care attendance and admissions from 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 one 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

Figure 5. Cumulative cases in England of variants indexed by days since the fifth reported case as of 12 September 2021
(Find accessible data used in this graph in underlying data)



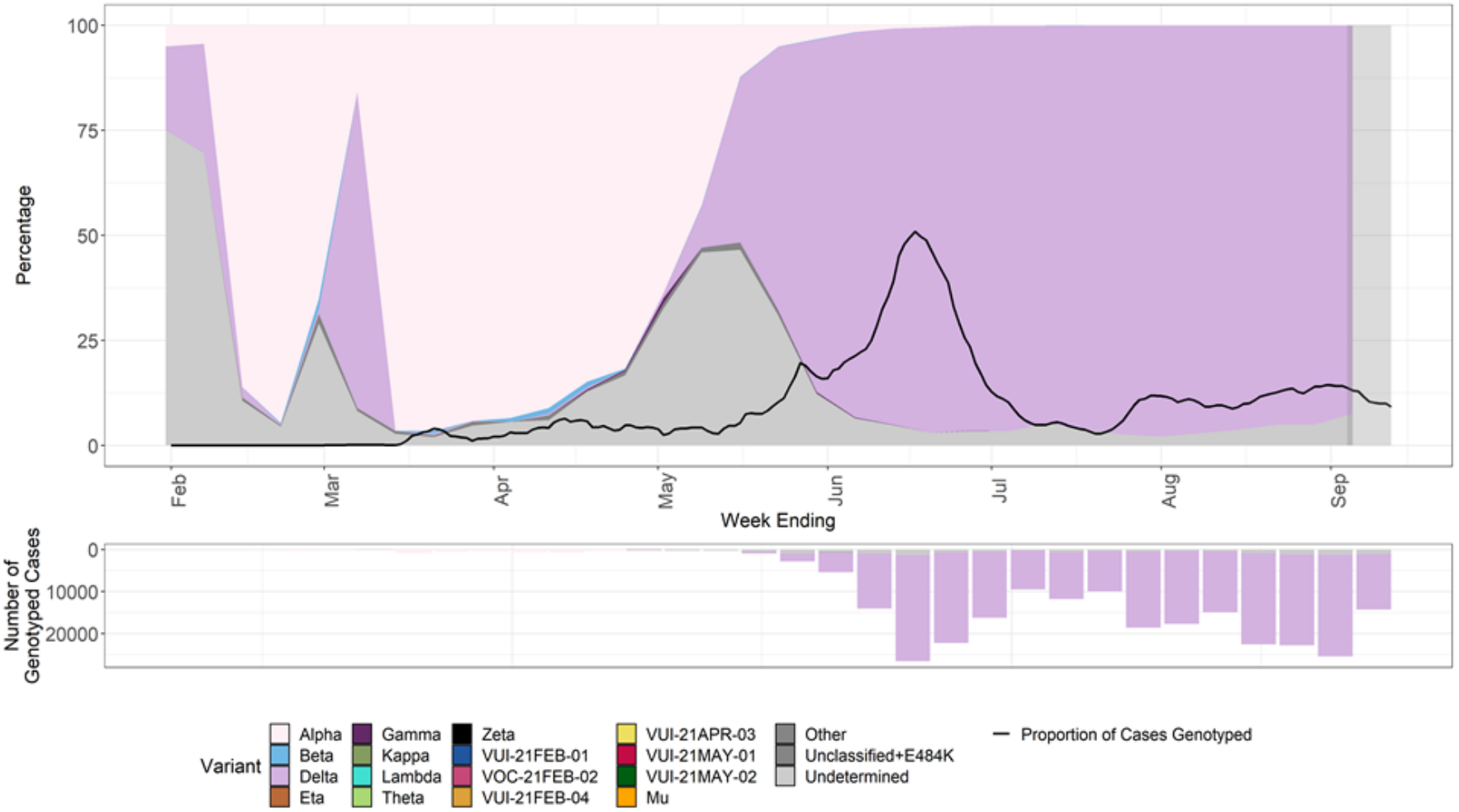
1.4 Variant prevalence

The prevalence of different variants amongst genotyped and sequenced cases is presented in Figure 6 and Figure 7 and split by region in Figure 8 and Figure 9. Genotyping provides a provisional variant identification with a shorter turnaround time of 12 to 24 hours after initial confirmation of COVID-19. The initial panel of targets began trials in March 2021, using single nucleotide polymorphisms that included 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. Changes in the use of genotyping over time should be considered when interpreting prevalence from genotyped data.

The ‘Other’ category in Figures 7 and 9 includes genomes where the quality is insufficient to determine variant status and genomes that do not meet the current definition for a VUI or VOC. The supplementary data for figures are available.

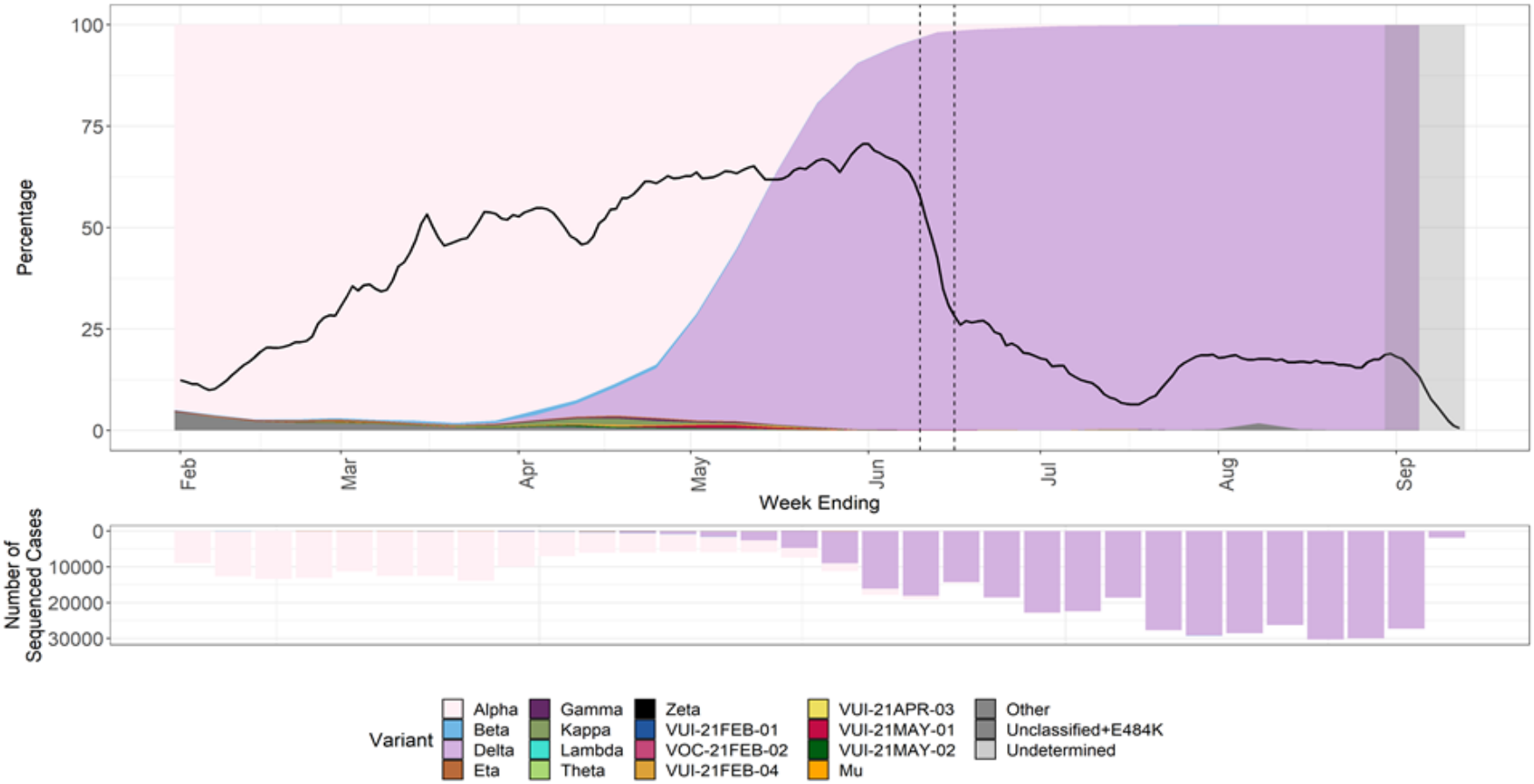
Delta variant accounted for approximately 99.7% of sequenced and 94.9% genotyped cases from 15 August 2021 as of 13 September 2021.

Figure 6. Variant prevalence for all England available genotyped cases from 1 February 2021 as of 13 September 2021
(Find accessible data used in this graph in underlying data)



A small number of cases identified as Beta (B.1.351) on genotyping since May 2021 without confirmatory sequencing may be VUI-21JUL-01 (B.1.621) with an additional K417N mutation.

Figure 7. Variant prevalence for all England available sequenced cases from 1 February 2021 as of 13 September 2021 (excluding 288 case where the specimen date was unknown). (Find accessible data used in this graph in underlying data).



Dashed lines indicate period incorporating issue at a sequencing site.

Figure 8. Variant prevalence from 1 February 2021 as of 13 September 2021 by region for all genotyped cases in England (excluding 2,163 cases where the region or specimen date were unknown). (Find accessible data used in this graph in underlying data)

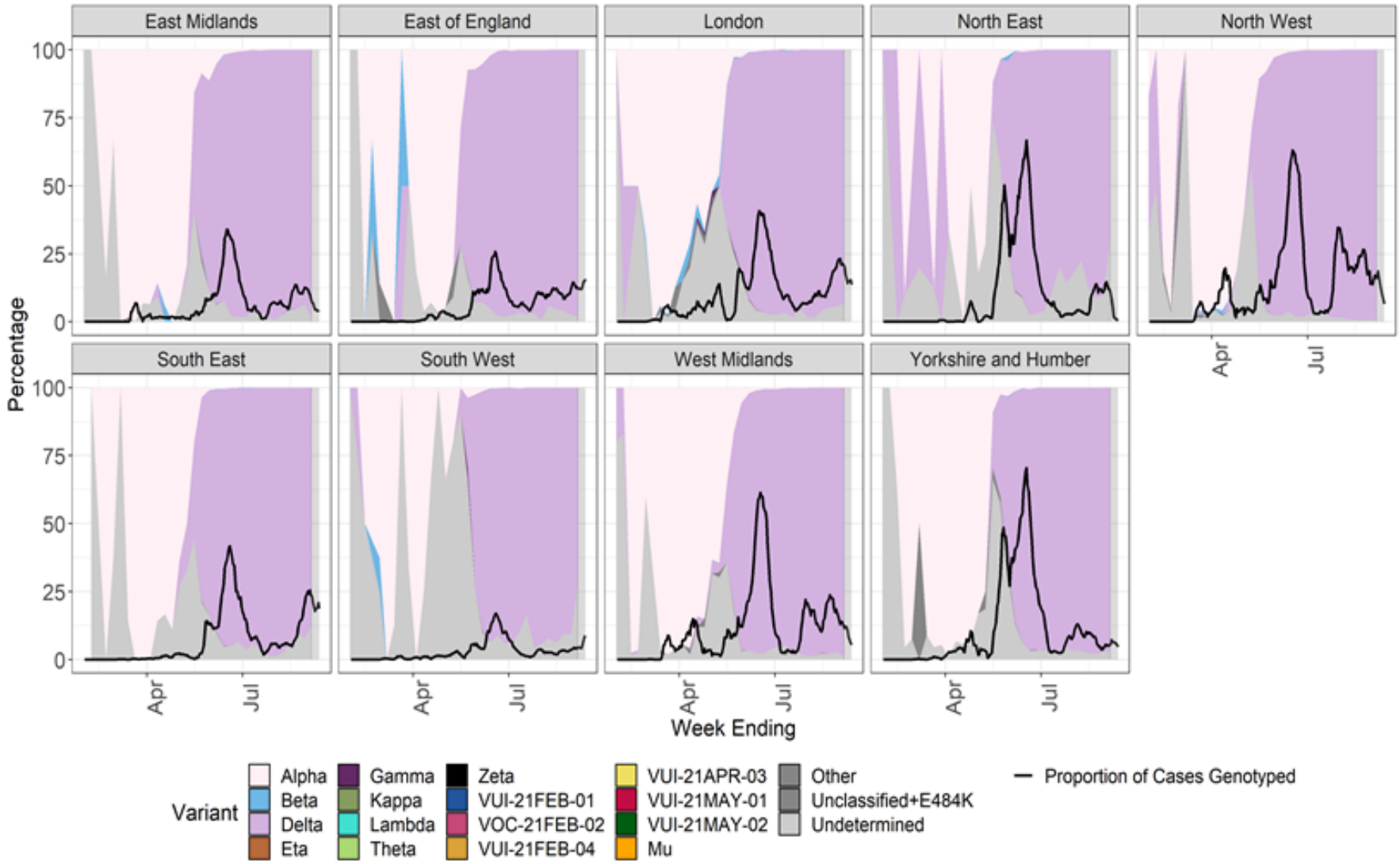
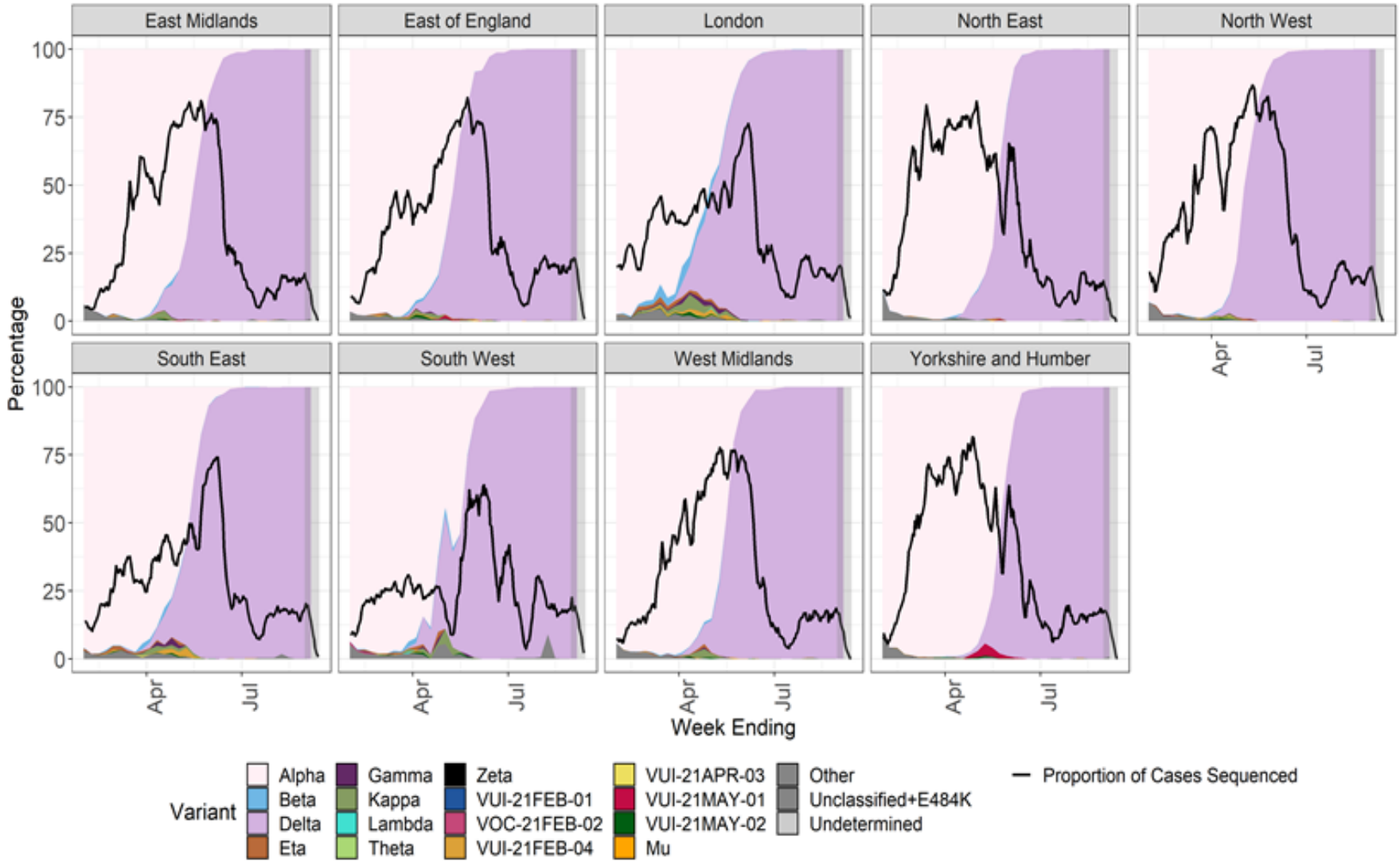


Figure 9. Variant prevalence from 1 February 2021 as of 13 September 2021 by region for all sequenced cases in England (excluding 2,918 cases where the region or specimen date were unknown). (Find accessible data used in this graph in underlying data)



1.5 Monitoring GISAID data diversity of antigenic mutations within variants

A list of mutations of potential antigenic significance has been compiled using the available published evidence. The full list of mutations of potential antigenic significance is compiled and continuously 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 14 September 2021 (excluding UK data). The increase in the number of antigenic mutations over time is illustrated for all variants in Figure 10 and for variants excluding VOCs and VUIs in Figure 11.

The plots in Figures 10 and 11 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 31 August 2021. All non-synonymous mutations at positions in the spike protein that have been associated with antigenicity were considered antigenic. VOCs or VUIs were identified by analysing their spike mutation profile to deal with low-quality and partial sequences.

Figure 10. Prevalence of antigenic mutations over time for all genomes in GISAID (excluding UK data) as of 14 September 2021 (Find accessible data used in this graph in underlying data)

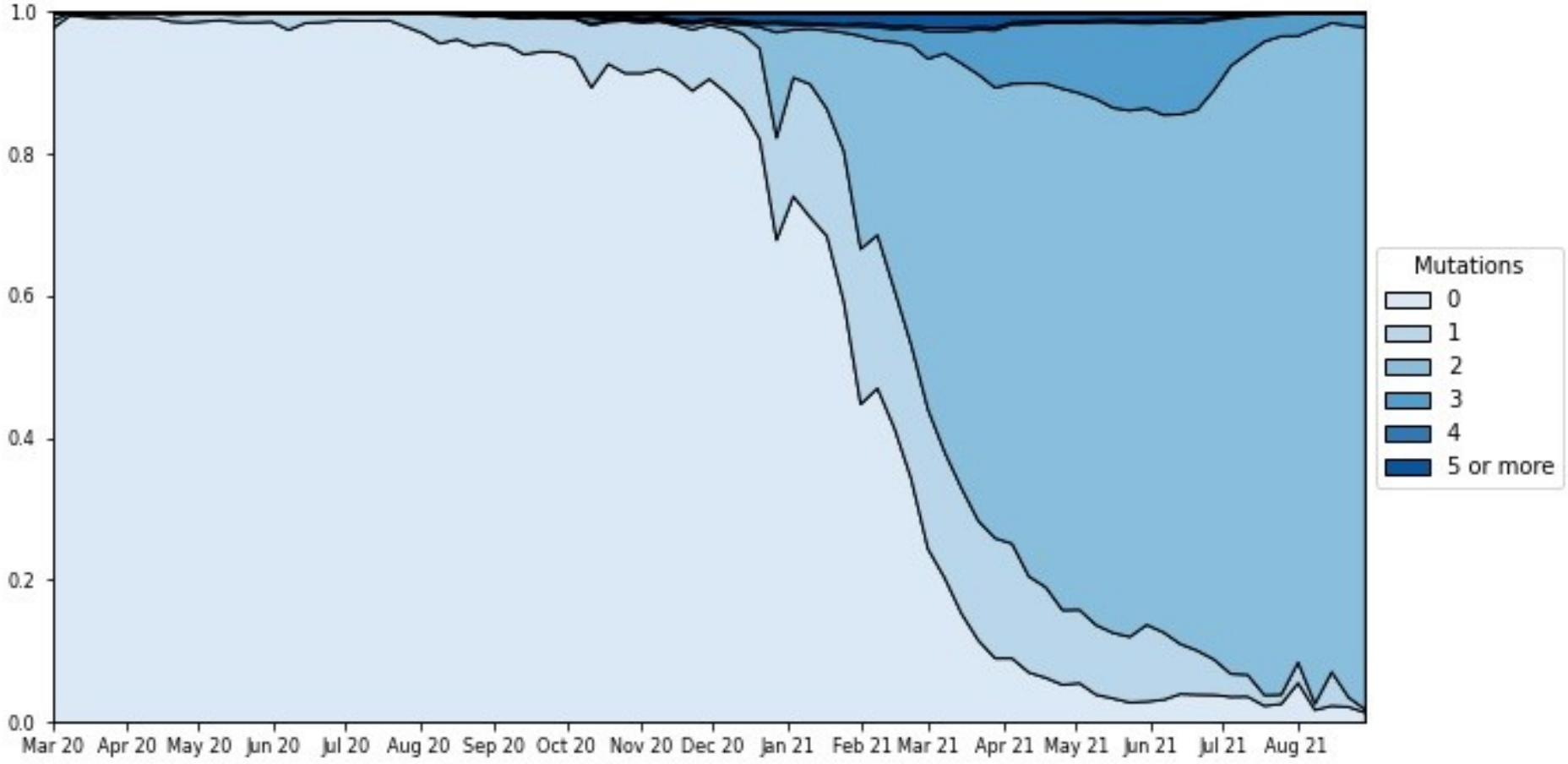
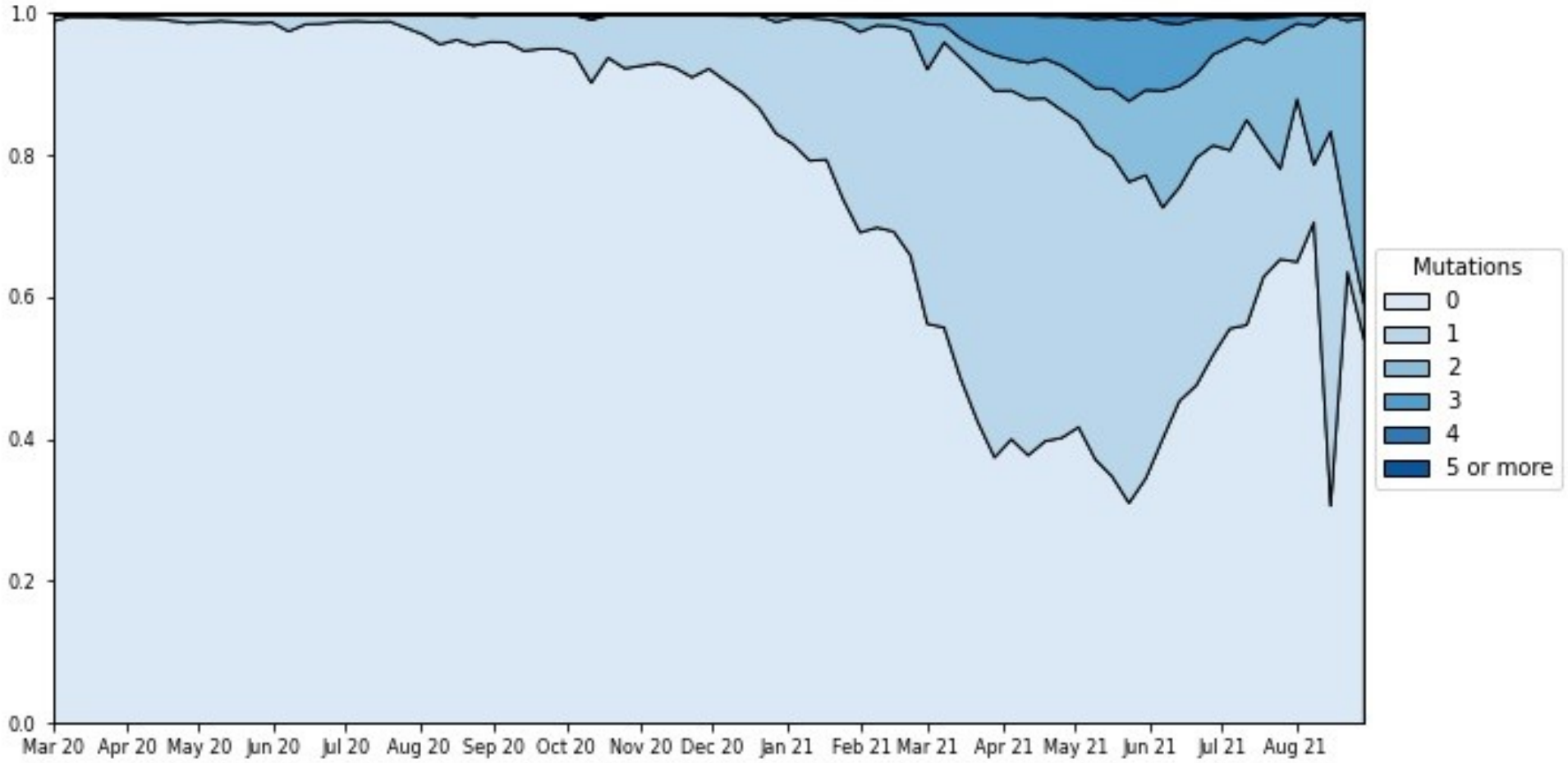


Figure 11. Prevalence of antigenic mutations over time for all genomes in GISAID (excluding UK data), excluding VOCs and VUIs, as of 14 September 2021 (Find accessible data used in this graph in underlying data)



1.6 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 sequenced or genotyped VOC or VUI. Variant cases are identified using sequencing results supplemented with genotyping results and exclude low-quality results.

Secondary attack rates are shown for cases with and without travel history. In non-travel settings, only close contacts named by the original case are included, that is, household members, face-to-face contact, people within one metre of the case for one minute or longer, or people within 2 metres for 15 minutes. 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. This likely deflates 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 where infection of the original case may have occurred.

Table 6 shows secondary attack rates for all variants between 5 January 2021 and 24 August 2021, which was a period chosen to capture data for all variants. Direct comparisons between variants are not valid as vaccination levels and social restrictions in England have varied over this period. Estimates of secondary attack rates for travel-related contacts with VOCs or VUIS were considerably lower than non-travel cases due to differences in contact definitions.

Figure 12 shows the secondary attack rates amongst household and non-household contacts of non-travel cases with Delta and Alpha between 29 March 2021 to 22 August 2021. Secondary attack rates amongst household contacts of cases with Delta have risen over the most recent weeks reported, with estimate of 11.4% (95% CI: 11.2% to 11.6%) for household contacts in week commencing 16 August 2021. Secondary attack rates among non-household contacts have remained steady: 4.9% (95% CI: 4.6% to 5.2%) in that week. Secondary attack rate estimates for contacts of cases with Alpha have not been produced for recent weeks due to low case numbers.

Table 6. Secondary attack rates for all variants
(5 January 2021 to 24 August 2021, variant data as of 13 September 2021, and contact tracing data as of 14 September 2021)

Variant	Travel-related cases (with contacts)	Non-travel cases (with contacts)	Travel-related case proportions	Secondary attack rate in contacts of travel-related cases (95% CI) [secondary cases/contacts]	Secondary attack rate in household contacts of non-travel or unknown cases (95% CI) [secondary cases/contacts]	Secondary attack rate in non-household contacts of non-travel or unknown cases (95% CI) [secondary cases/contacts]
Alpha	4,868 (75.1% with contacts)	185,166 (75.0% with contacts)	2.6%	1.5% (1.4% - 1.6%) [1,344/89,204]	10.2% (10.1% - 10.3%) [34,623/338,558]	5.6% (5.4% - 5.8%) [3,306/58,686]
Beta	358 (69.6% with contacts)	432 (67.6% with contacts)	45.3%	1.8% (1.5% - 2.2%) [112/6,202]	9.9% (8.0% - 12.2%) [75/757]	2.9% (1.3% - 6.2%) [6/206]
Gamma	87 (62.1% with contacts)	153 (72.5% with contacts)	36.2%	1.1% (0.6% - 1.9%) [12/1,123]	10.7% (7.4% - 15.1%) [27/253]	3.3% (1.1% - 9.2%) [3/91]
Eta	211 (67.8% with contacts)	197 (73.1% with contacts)	51.7%	1.1% (0.8% - 1.4%) [47/4,339]	9.9% (7.2% - 13.6%) [33/332]	Unavailable [1/43]
VUI-21FEB-04	135 (66.7% with contacts)	157 (79.6% with contacts)	46.2%	0.5% (0.3% - 0.8%) [18/3,429]	8.6% (5.9% - 12.3%) [26/303]	6.5% (3.0% - 13.4%) [6/93]
Theta	5 (40.0% with contacts)	1 (100.0% with contacts)	83.3%	Unavailable [0/5]	Unavailable [0/3]	Unavailable [0/0]
Delta	11,059 (63.2% with contacts)	471,476 (72.6% with contacts)	2.3%	1.8% (1.8% - 1.9%) [2,454/133,378]	10.4% (10.4% - 10.5%) [81,552/781,192]	5.4% (5.3% - 5.5%) [13,956/259,671]
VOC-21APR-02+K417N	0 (0 with contacts)	31 (71.0% with contacts)	0.0%	Unavailable [0/0]	20.0% (12.1% - 31.3%) [13/65]	Unavailable [2/9]
VUI-21APR-03	9 (22.2% with contacts)	5 (100.0% with contacts)	64.3%	Unavailable [2/204]	Unavailable [1/12]	Unavailable [0/0]
VUI-21MAY-01	2 (0.0% with contacts)	176 (84.7% with contacts)	1.1%	Unavailable [0/0]	8.0% (5.8% - 11.1%) [33/411]	2.4% (0.8% - 6.9%) [3/124]
VUI-21MAY-02	76 (75.0% with contacts)	51 (82.4% with contacts)	59.8%	1.0% (0.6% - 1.6%) [14/1,439]	8.4% (4.5% - 15.2%) [9/107]	Unavailable [0/13]
Lambda	9 (66.7% with contacts)	0 (0 with contacts)	100.0%	Unavailable [1/196]	Unavailable [0/0]	Unavailable [0/0]

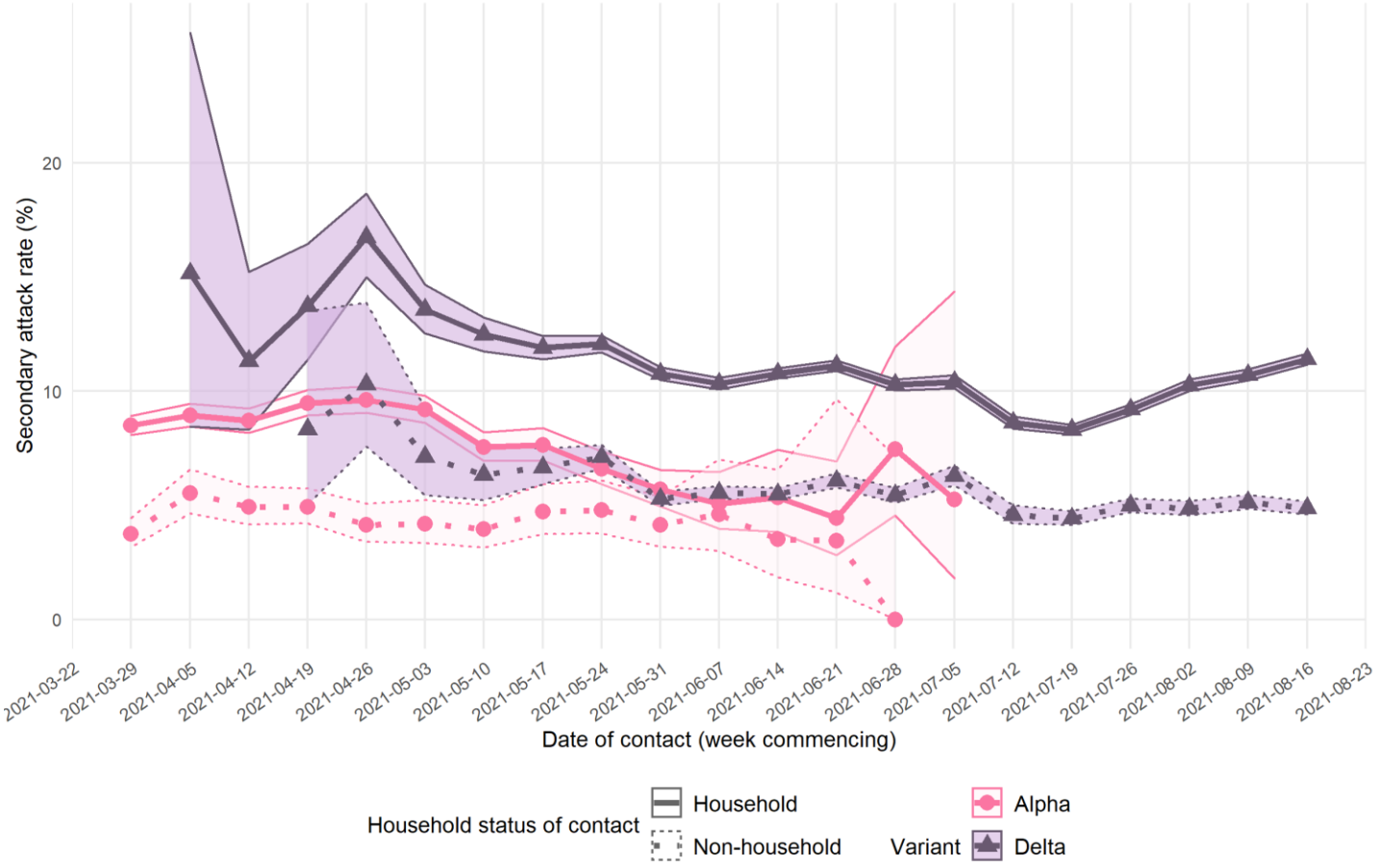
Mu	20 (50.0% with contacts)	22 (68.2% with contacts)	47.6%	Unavailable [10/297]	Unavailable [2/30]	Unavailable [1/9]

Secondary attack rates are marked as ‘Unavailable’ when count of contacts is fewer than 50 or count of cases is fewer 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 International Health Regulations National Focal Point, 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 24 August 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. Secondary attack rates are suppressed when count of contacts is less than 50 or count of cases is less than 20. Probable (genotyping) results are included, low quality genomic results are not.

Figure 12. Secondary attack rates in household and non-household contacts of non-travel Alpha and Delta cases, with 95% confidence intervals

29 March 2021 to 22 August 2021, variant data as of 13 September 2021 and contact tracing data as of 14 September 2021 (Find accessible data used in this graph in underlying data)



Please see footnote from Table 6. Data provided is for period until 22 August 2021 in order to allow time for contacts to become cases and complete weeks to be shown.

1.7 Monitoring of vaccine effectiveness

The COVID-19 vaccine surveillance reports – GOV.UK (www.gov.uk) was published 16 September 2021 including further details on vaccine effectiveness. Recent data is available in Table 7 and Vaccine effectiveness and duration of protection (khub.net). Table 7 includes analysis of routine testing data up to 3 September 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 (including data on 3 vaccines).

Table 7. Summary of evidence on vaccine effectiveness against different outcomes for the Delta variant

Outcome	Vaccine effectiveness*			
	Pfizer-BioNTech Cominarty	AstraZeneca Vaxzevria	Moderna Spikevax	All
Infection	75 to 85%	60 to 70%		60 to 85%
Symptomatic disease	80 to 90%	65 to 75%	90 to 99%	65 to 99%
Hospitalisation	95 to 99%	90 to 99%	95 to 99%	90 to 99%
Mortality	90 to 99%	90 to 95%		90 to 95%

*Estimates of initial vaccine effectiveness in the general population after a 2-dose course. This typically applies for at least the first 3-4 months after vaccination. For some outcomes there may be waning of effectiveness beyond this point.

Part 2: Enhanced analysis on specific variants. Delta (B.1.617.2)

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.

2.1 Monitoring diversity within Delta – mutation scan

Table 8 shows spike mutations with a potential impact on antigenicity, avidity, or the furin cleavage site significance acquired by Delta in the UK. This data uses the numbers of genomes in the national genomic data set rather than case numbers. Only mutations associated with antigenic change are presented here, such as those identified by published research. The unlinked sequences represent the number of sequences not present within the English surveillance system. These sequences include those samples from the Devolved Administrations and cannot be associated with a date by PHE.

Table 8. Additional spike mutations of interest detected in Delta genomes in the UK as of 14 September 2021

Amino acid change	Delta sequences in UK dataset	Delta sequences outside UK (GISAID)	Delta sequences 15 June to 14 July 2021		Delta sequences 15 July to 14 August 2021		Delta sequences 15 August to 14 September 2021	
			England	Outside UK	England	Outside UK	England	Outside UK
P251L	2,714	7,957	251	1,642	592	4,551	349	1,555
G446V	1,541	1,128	141	200	261	575	272	252
Q613H	580	12,564	62	814	162	7,184	212	4,204
V483F	547	252	34	24	103	125	98	73
Q493E	326	137	24	41	134	61	112	10
S494L	204	188	15	25	73	98	91	46
K417N	150	6,548	2	2,230	50	2,794	32	474
E484Q	144	1,026	8	241	53	529	51	174
L455F	132	394	20	40	58	236	35	70
V445I	99	20	10	2	57	9	17	6
F490L	91	207	8	9	37	72	33	108
K444N	76	270	3	46	28	122	17	62
N501Y	58	508	12	138	20	325	11	8
S494P	53	155	8	20	21	78	4	39
P681H	40	186	1	19	19	114	4	30
R246I	39	57	3	3	21	20	7	25
K458N	37	36	21	5	9	21	7	5
A475V	32	23	3	4	9	14	16	3
K444R	25	32	3	3	12	19	5	10
F490S	22	56	1	9	11	29	8	15
E484K	20	188	1	35	5	102	12	43

L452Q	20	53	1	7	5	31	8	14
P499L	18	21	2	5	7	7	3	8
N439K	17	2	0	0	7	0	8	2
N501T	16	11	0	3	4	4	0	2
E484A	14	51	2	14	2	13	4	14
V445F	11	26	2	5	5	10	4	9
E484G	10	14	3	10	4	9	0	2
Q493L	10	84	3	28	4	46	0	10
D80N	8	23	2	1	3	12	0	8
E484V	8	17	1	9	1	6	3	1
S494A	7	17	0	10	0	10	4	6
V445A	6	18	2	13	3	10	1	5
E484D	6	50	3	4	2	32	0	10
F486L	5	1	5	0	0	1	0	0
G446D	5	10	1	6	2	5	2	3
V483A	5	21	0	2	3	11	2	6
Q498R	3	15	1	3	0	11	0	0
D80A	3	113	0	72	1	34	1	1
Q493H	3	8	2	1	0	2	0	1
G485D	3	1	1	1	0	0	1	0
K444E	3	3	0	0	2	3	0	0
I472V	2	2	0	1	0	0	0	0
T478I	2	6	0	0	1	3	0	3
K417E	2	8	2	0	0	2	0	6
V483G	1	3	0	0	1	3	0	0
V503L	1	1	0	0	0	0	0	1
Y144N	1	2	0	1	1	1	0	0

K458Q	1	2	0	0	0	0	1	2
R246G	1	20	0	0	1	15	0	4
K417T	1	9	0	2	0	2	1	4
N501H	1	2	1	0	0	2	0	0
Y453F	1	3	0	0	0	1	1	1
Total of Delta sequences	466,153	675,172	87,059	122,199	122,783	355,518	93,055	148,693

2.2 Monitoring diversity within Delta – AY Lineages

Sub-lineages of B.1.617.2 are given the alias of AY. These lineages have been recently designated to monitor diversity within Delta and improve the identification of newly emerging clades (Table 9). They are phylogenetically defined and they do not necessarily have any biological differences between them. Data on the sub-lineages will not be published routinely unless there is evidence of biologically significant change.

Figure 13 shows the prevalence of the AY lineages within all Delta sequences in the UK. AY.4 is the dominant lineage in the UK, but smaller lineages have also persisted over time. Table 10 shows the non-synonymous mutations present in at least 50% of the sequences for a given AY lineage that are not present in >50% of the sequences designated as B.1.617.2 in the UK.

Figure 15 shows a phylogenetic tree of a subset of Delta sequences from the UK, coloured by lineage. To generate the subset of data, the Delta sequences that could be matched to case data were grouped by their week of sample and lineage. Where the group was <4 sequences, all sequences were included in the subset. For larger groups, 25% of the group was included. In total, 79,944 of 406,346 sequences were included in the tree.

AY.4 represents a large proportion of the tree. The other lineages that are predominantly UK based generally form a single clade within the tree. Some clusters of apparent B.1.617.2 sequences can be seen spread throughout the tree. This is likely because those sequences are missing mutations that define the AY lineages due to a lower sequence quality.

Table 9. Date of lineage designation and pangoLEARN release for new AY lineages

Lineage	Pango Designation Version	Date of Designation	pangoLEARN Release	Date of Release
AY.1	v1.2.12	2021-06-04	2021-06-05	2021-06-07
AY.2	V1.2.13	2021-06-14	2021-06-15	2021-06-16
AY.3	V1.2.28	2021-06-30	2021-07-07	2021-07-09
AY.3.1	V1.2.42	2021-07-23	2021-07-28	2021-07-29
AY.4	V1.2.50	2021-07-30	2021-08-09	2021-08-12
AY.5	V1.2.50	2021-07-30	2021-08-09	2021-08-12
AY.5.1	V1.2.60	2021-08-16	2021-08-24	2021-08-27
AY.5.2	V1.2.60	2021-08-16	2021-08-24	2021-08-27
AY.6	V1.2.50	2021-07-30	2021-08-09	2021-08-12
AY.7	V1.2.50	2021-07-30	2021-08-09	2021-08-12
AY.7.1	V1.2.60	2021-08-16	2021-08-24	2021-08-27
AY.7.2	V1.2.60	2021-08-16	2021-08-24	2021-08-27
AY.8	V1.2.50	2021-07-30	2021-08-09	2021-08-12
AY.9	V1.2.50	2021-07-30	2021-08-09	2021-08-12
AY.10	V1.2.50	2021-07-30	2021-08-09	2021-08-12
AY.11	V1.2.56	2021-08-09	2021-08-09	2021-08-12
AY.12	V1.2.56	2021-08-09	2021-08-09	2021-08-12
AY.13	V1.2.60	2021-08-16	2021-08-24	2021-08-27
AY.14	V1.2.60	2021-08-16	2021-08-24	2021-08-27
AY.15	V1.2.60	2021-08-16	2021-08-24	2021-08-27
AY.16	V1.2.60	2021-08-16	2021-08-24	2021-08-27
AY.17	V1.2.60	2021-08-16	2021-08-24	2021-08-27

AY.18	V1.2.60	2021-08-16	2021-08-24	2021-08-27
AY.19	V1.2.60	2021-08-16	2021-08-24	2021-08-27
AY.20	V1.2.60	2021-08-16	2021-08-24	2021-08-27
AY.21	V1.2.60	2021-08-16	2021-08-24	2021-08-27
AY.22	V1.2.60	2021-08-16	2021-08-24	2021-08-27
AY.23	V1.2.61	2021-08-17	2021-08-24	2021-08-27
AY.24	V1.2.61	2021-08-17	2021-08-24	2021-08-27
AY.25	V1.2.62	2021-08-18	2021-08-24	2021-08-27
AY.26	v1.2.68	2021-08-21	Not yet released	
AY.27	v1.2.68	2021-08-21	Not yet released	
AY.28	v1.2.68	2021-08-21	Not yet released	
AY.29	V1.2.74	2021-09-02	Not yet released	
AY.30	V1.2.75	2021-09-02	Not yet released	
AY.31	V1.2.75	2021-09-02	Not yet released	
AY.32	V1.2.76	2021-09-03	Not yet released	

Data analysed before the pangoLEARN release will not include newer AY lineages unless the sequences have been specifically designated as part of the Pango Designation release. Data in this analysis uses Pango Designation v1.2.76 and pangoLEARN release 2021-08-24. Pangolin releases can be found at the relevant GitHub repositories: cov-lineages/pango-designation and cov-lineages/pangoLEARN

Figure 13. Prevalence of AY lineages among Delta sequences in the UK from 1 March 2021 as of 6 September 2021
Total number of Delta sequences per week is indicated by the black line.

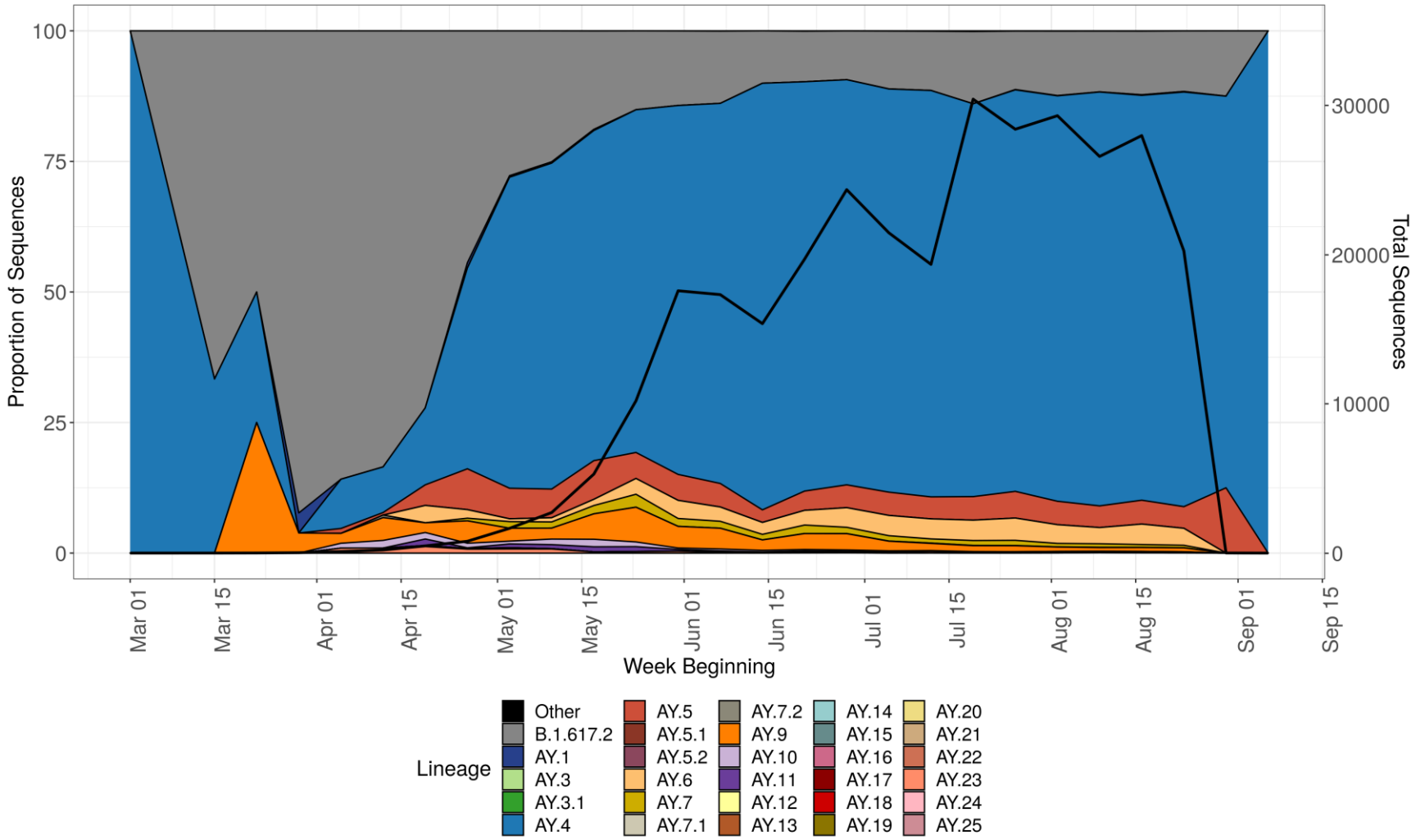


Figure 14. Prevalence of AY lineages among Delta sequences in the UK from 1 March 2021 as of 6 September 2021

Total number of Delta sequences for that region is indicated by the black line.

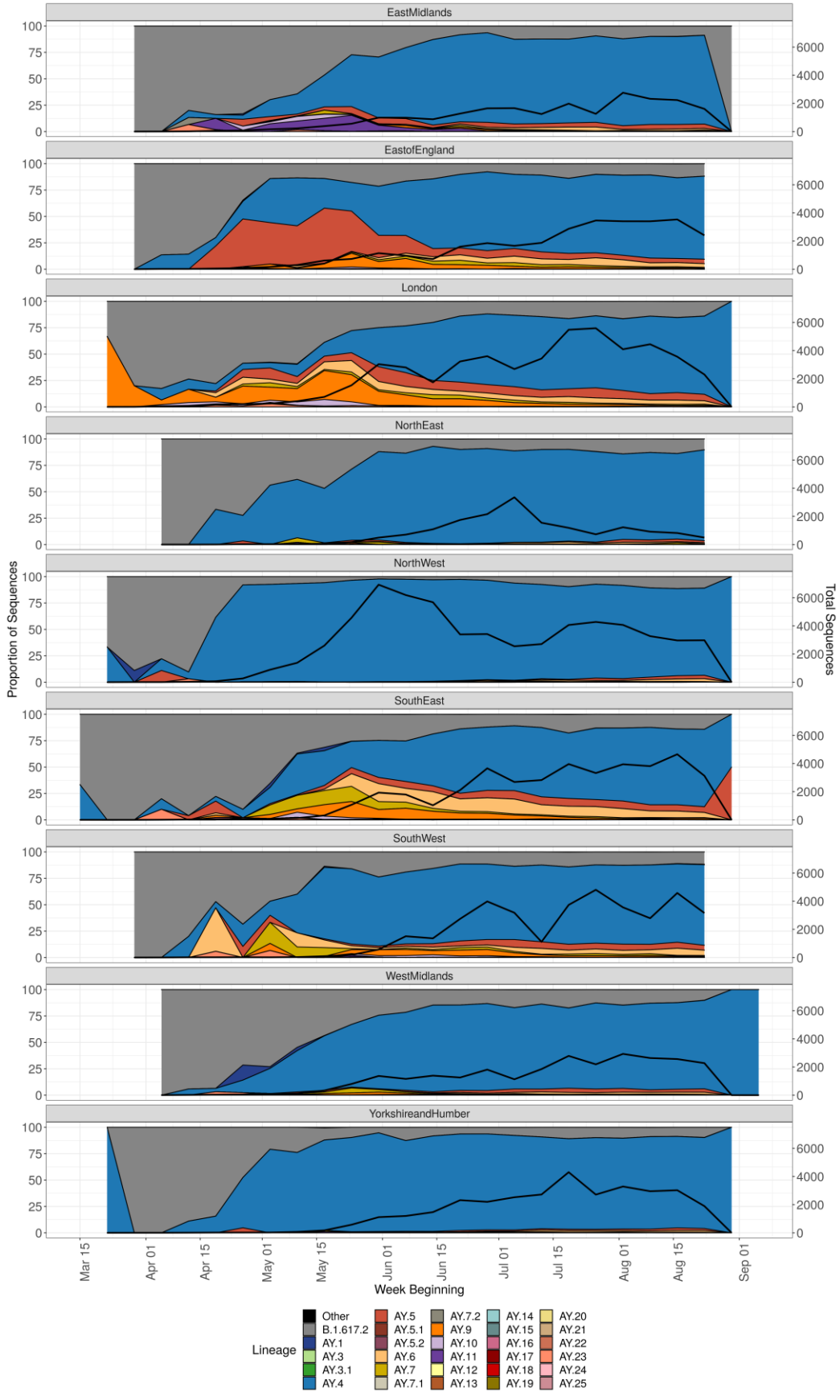


Table 10: Non-synonymous mutations present in at least 50% of each lineage that are not present in more than 50% of the B.1.617.2 designated sequences within the UK Delta sequences

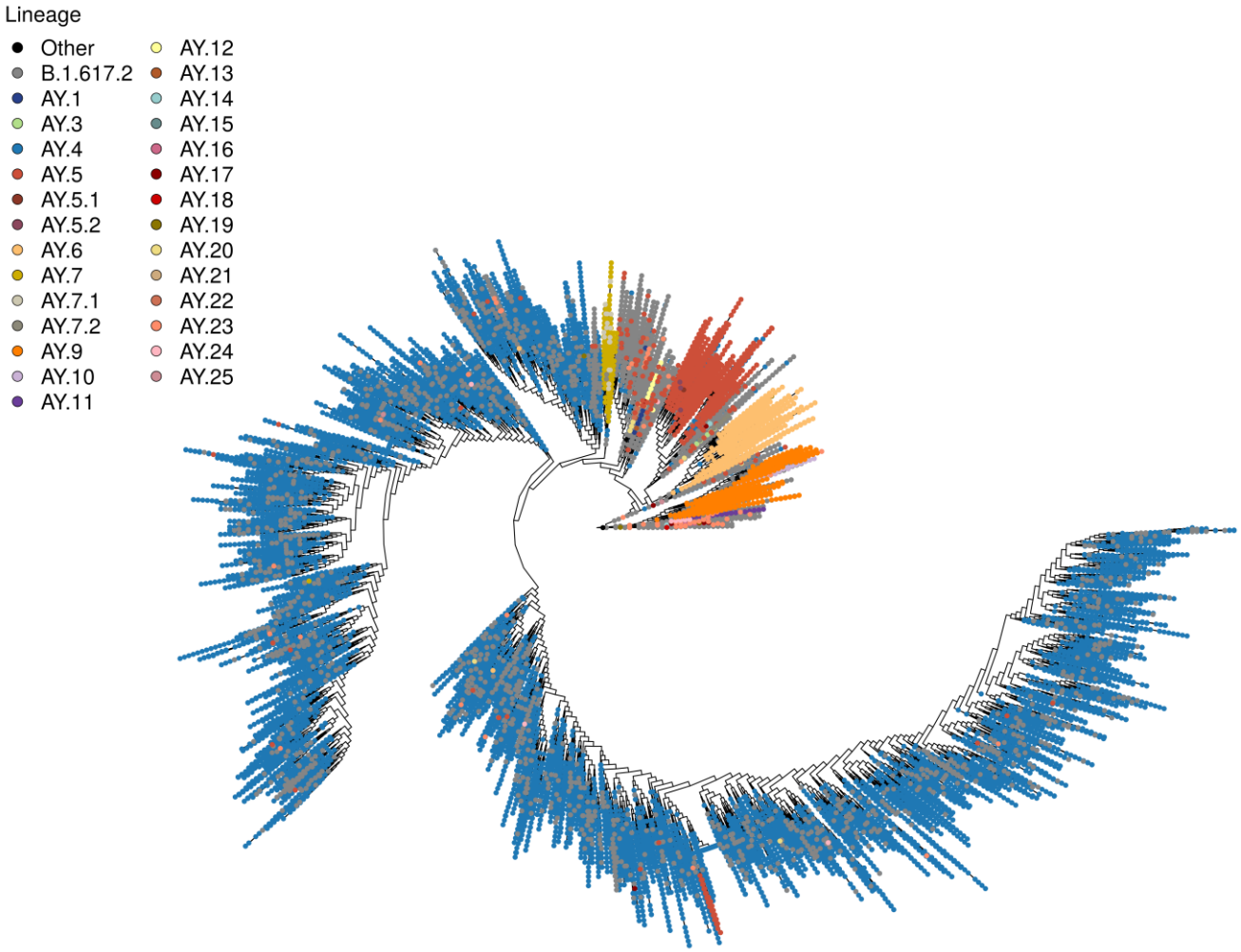
AY lineages that are not seen in the UK data are not included in this table.

Clade	Gene							
	orf1ab	**S**	**orf3a**	**M**	**orf6**	**orf7a**	**orf8**	**N**
AY.1		T95I, W258L, K417N						
AY.3	I3731V							
AY.3.1	D1127Y, I3731V, T3857I, V5550L, H5951Y, T6564I							
AY.4	A2529V	T95I						
AY.5								S327L
AY.5.1	K4552N			N207K				S327L
AY.5.2							S54L	S327L
AY.6	D691N, E5689D							
AY.7	Q4151H					C58F, A79D		
AY.7.1	Q4151H					C58F, A79D		
AY.7.2			G18V					
AY.9	P1640L, A3209V, V3718A, T3750I	A222V						

AY.10	P1640L, M2796V, M3087I, A3209V, V3718A, T3750I, T4164I	A222V						
AY.11	A1074V, P1640L, A3209V, V3718A, T3750I, R6088C	A222V		A2S				
AY.12	S443F, K3353R, P7013T	T95I			E59*			
AY.13	P309L, P1640L, A3209V, V3718A, P5971L	T95I				L116F		
AY.14	K261N, G519S, S538P, E940D, L3606F, K6958R					P45L		
AY.15	T78I, P1640L, A3209V, D6249Y				D61L			
AY.16	P309L, P1640L, A3209V, V3718A, P5971L					L116F		
AY.17	P309L, I659V, P1640L, A3209V, V3718A, A4815V, P5971L		Q57R			L116F		
AY.18	S212L, P309L, P1640L, P1921Q, D2980N, F3138S, H3580Q, K6711R	K77T, A694V				Q94L		
AY.19			Q185H					
AY.20	A599V	T95I, V1104L						
AY.21	A3571V, T5102I							D402Y

AY.22	L3606F, V4649F, M4993I	T95I, M177I, Q218H, V1104L	G224C					
AY.24	P1640L, A3209V, V3718A, T3750I	A222V	P104S					
AY.25			E239Q					

Figure 15: Phylogenetic tree of a subset of Delta sequences coloured by lineage
Supplementary data is not available for this figure.



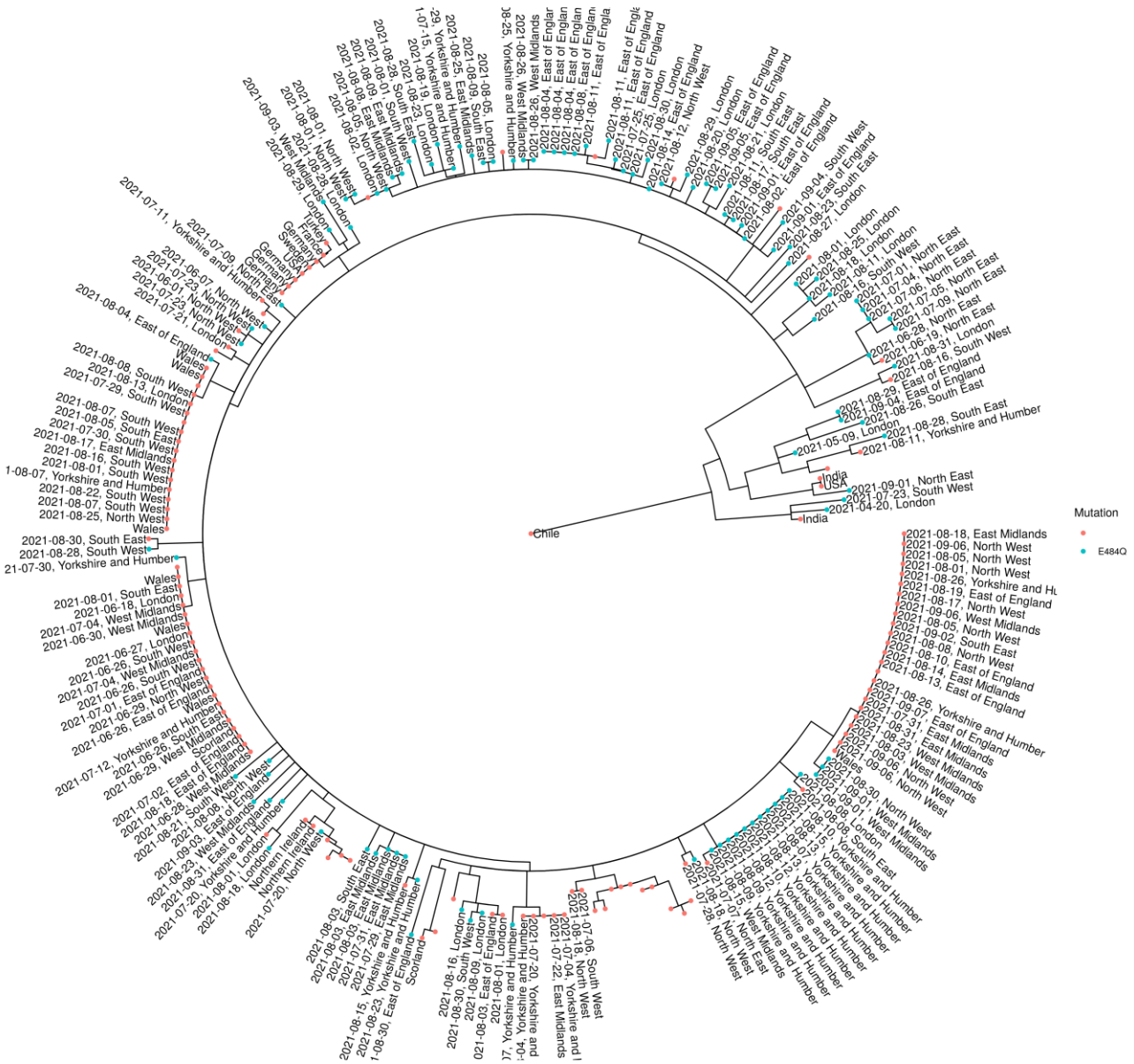
2.3 Monitoring diversity within Delta – Delta with E484Q

Changes at position 484 in spike are potentially antigenically significant. Delta with E484Q was first detailed as a signal under investigation on the 3 August 2021 after being detected in 6 Scottish samples between 22 and 28 July 2021. 144 sequences have been identified as of the 13 September 2021, with 126 from England, 12 from Scotland, and 6 from Wales.

The phylogenetic tree of UK Delta with E484Q cases is shown in Figure 16, which includes a cluster of 11 genetically indistinguishable samples from Yorkshire and Humber (10) and West Midlands (1), a node of 4 samples (3 genetically indistinguishable) from the East Midlands, a large node of diverse (genetically and geographically) samples that are predominantly annotated with the E484Q mutation, and an additional cluster of 5 samples from the North East.

Figure 16. Phylogenetic tree of UK Delta (B.1.617.2) with E484Q cases with a down-sampled international background dataset

The tree is generated using Civet which down-samples UK and international samples for background context. Presence of the E484Q mutation is indicated by the tip colour (blue indicates E484Q annotated, red indicates E484Q not annotated). Sample date and location of case is shown in the label for each tip (note 11 samples excluded from the tree by Civet due to a technical issue). Supplementary data is not available for this figure.



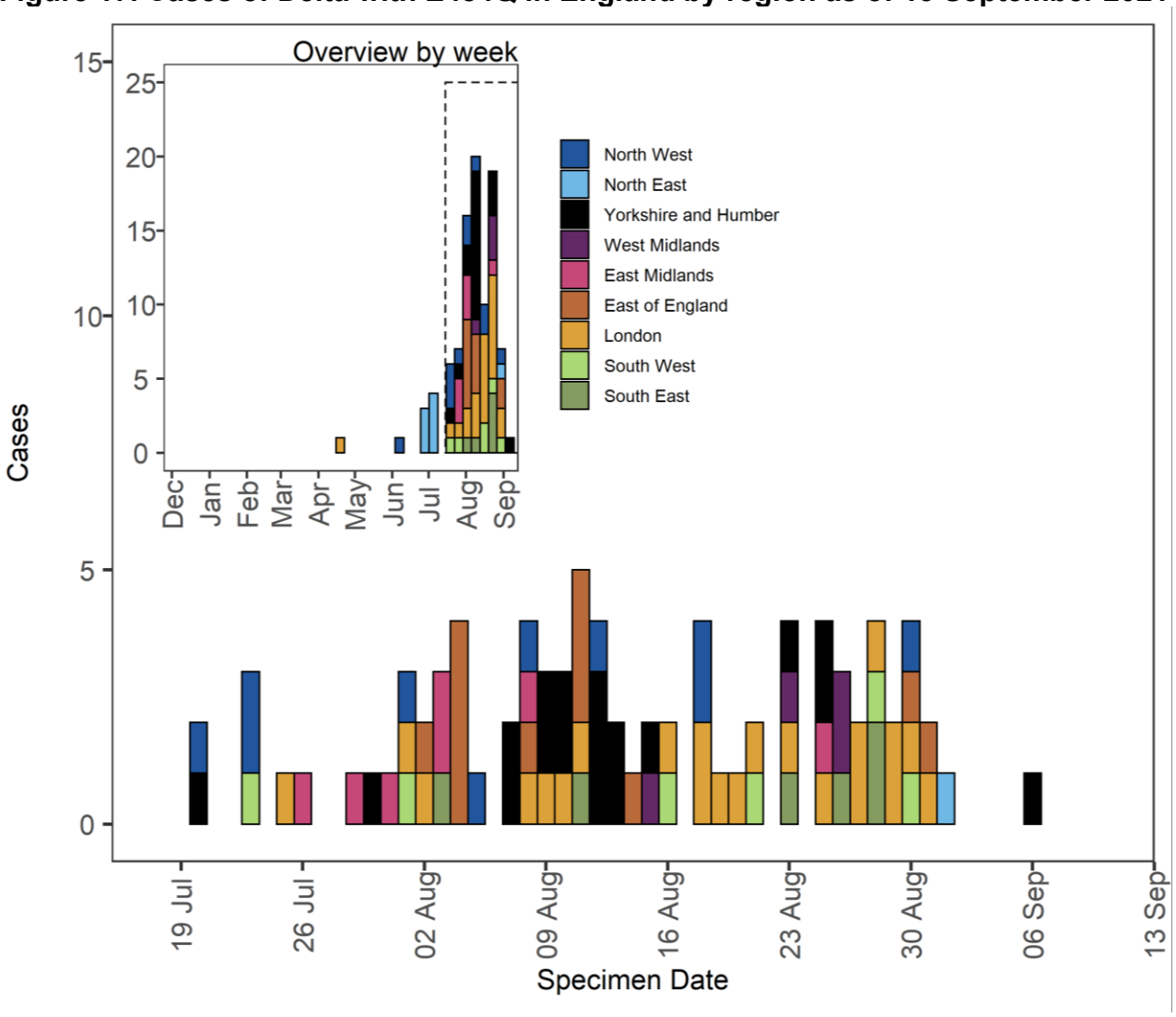
Epidemiology in England

As of 13 September 2021, there are 126 Delta with E484Q cases in England, 99 of which were linked to epidemiological data. Cases have been detected across all 9 English regions, with most cases in the London (23, 23.2%) as shown in Table 11 and cases by region in Figure 17. The most frequent age group was the 20 to 29 age group, with 18 cases. 14 of the 126 cases have history of travel which includes travel from or transit through Spain (1), Nigeria (10), and India (3).

Table 11. Confirmed and provisional Delta with E484Q cases in England by region as of 13 September 2021

Region	Total case number	Proportion of Delta with E484Q cases in England with epidemiological data
East Midlands	7	7.0%
East of England	12	12.1%
London	23	23.2%
North East	8	8.0%
North West	11	11.1%
South East	6	6.1%
South West	6	6.1%
West Midlands	4	4.0%
Yorkshire and Humber	18	18.2%
Unknown region	4	4.0%
Total	99	-

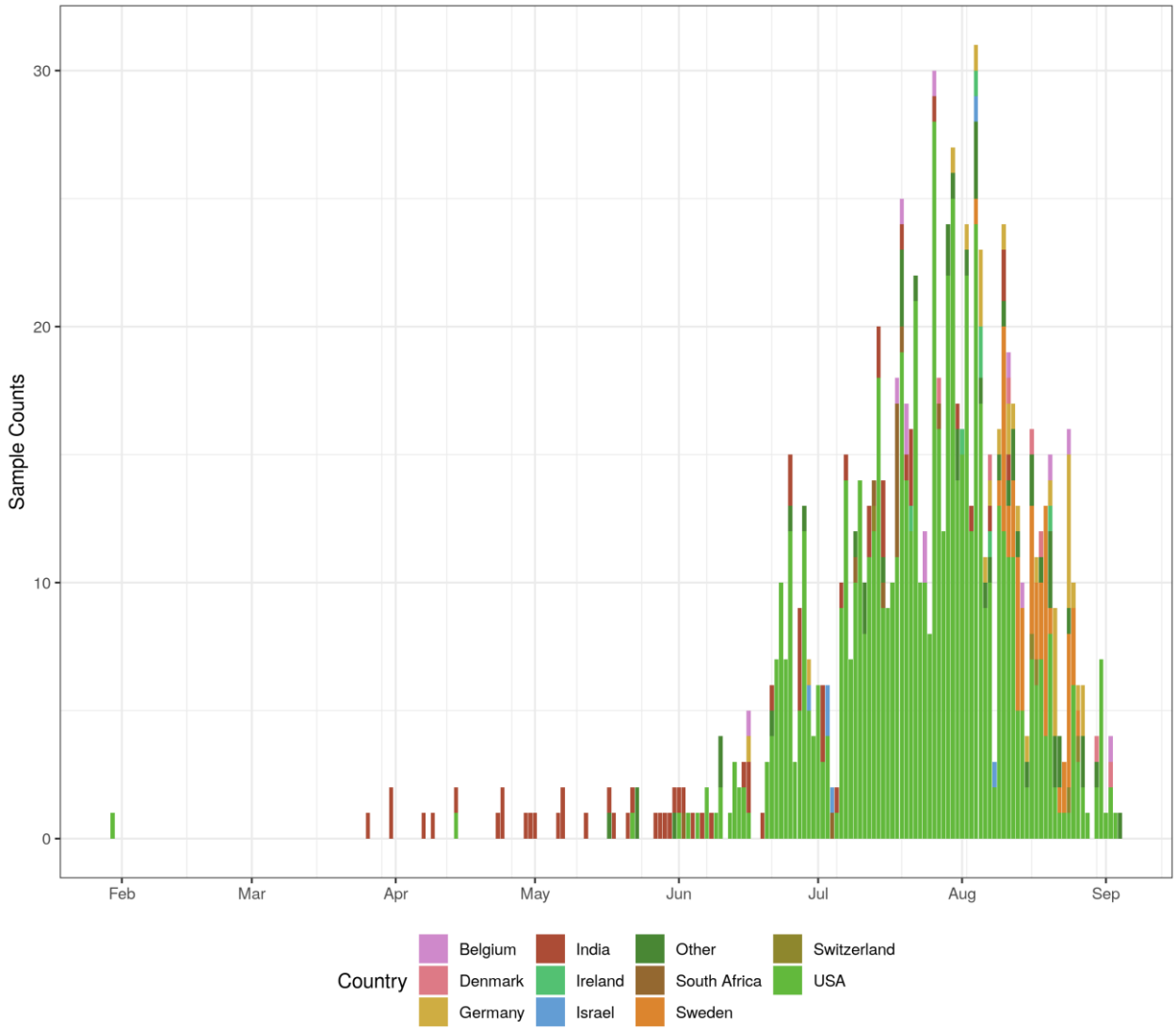
Figure 17. Cases of Delta with E484Q in England by region as of 13 September 2021



International epidemiology

As of 13 September 2021, 999 GISAID sequences have been assigned to the B.1.617.2 lineage with the additional E484Q mutation, of those 952 sequences had appropriate date information. Sequences have been uploaded from USA (691), India (66), Sweden (59), Germany (34), Belgium (13), South Africa (13), Denmark (7), Ireland (7), Israel (6), Switzerland (5) and 30 other countries with less than 5 samples. Figure 18 shows the distribution of cases per country over time, based on GISAID data, indicating an increase in observations of Delta with E484Q from July through to September.

Figure 18. Count of Delta with E484Q classified sequences by week of collection uploaded to GISAID by week as of 13 September 2021



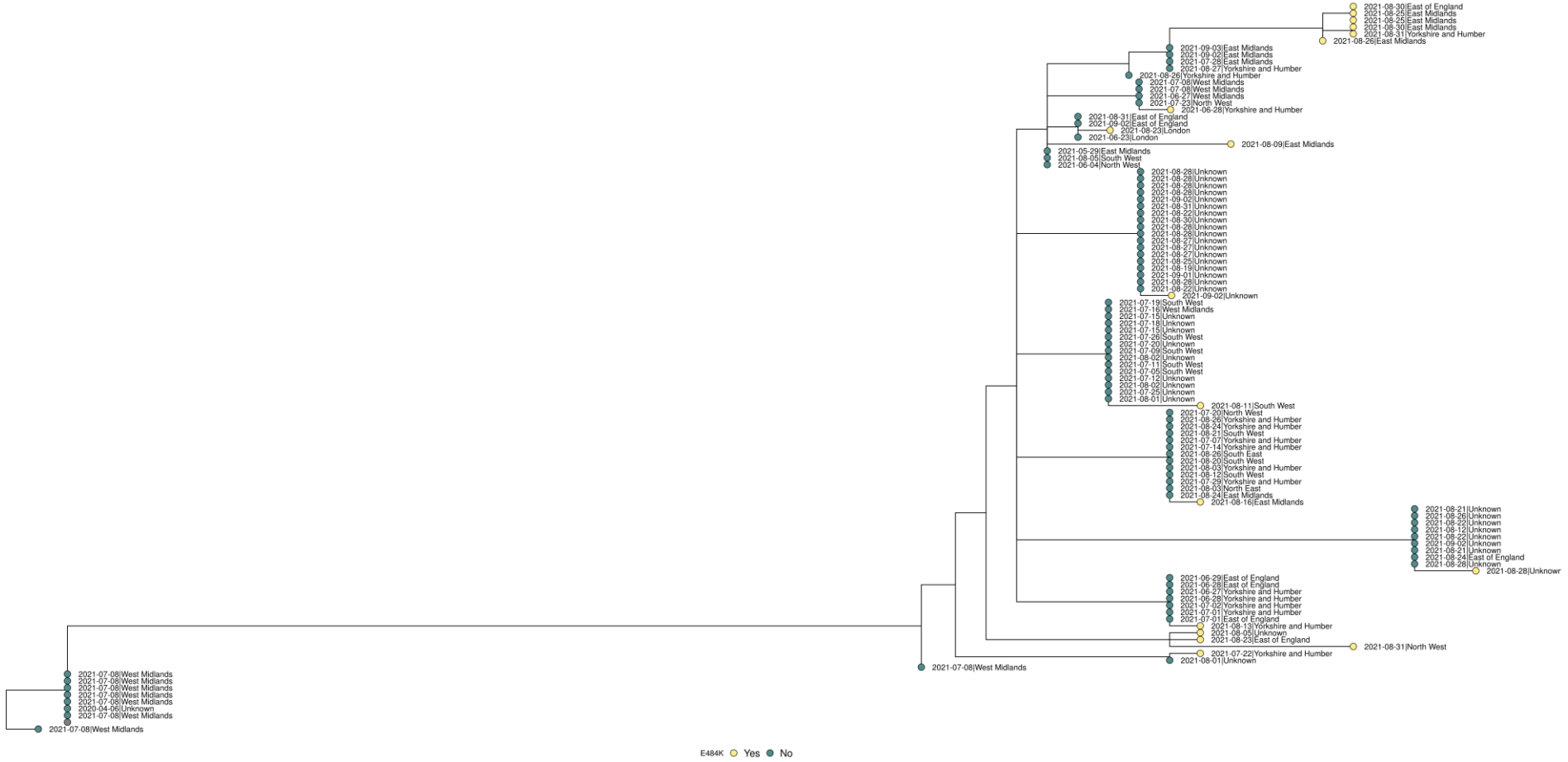
2.4 Monitoring diversity within Delta – Delta with E484K

Changes at position 484 in spike are potentially antigenically significant. Delta with E484K was detailed as a signal under investigation on 8 September 2021 and was first detected on 22 July 2021 in UK sequences. Both Delta and Delta with E484K are routinely monitored. 19 sequences have been identified as of the 13 September, with 17 from England and 2 from Scotland.

The phylogenetic tree of UK Delta with E484K cases is shown in Figure 19, which includes one small cluster and multiple independent occurrences of the mutation (Delta with E484K is shown in yellow on Figure 19).

Figure 19. Maximum likelihood tree of UK Delta (B.1.617.2) with E484K cases

Presence of the E484K mutation is indicated by the tip colour (Yellow indicates E484K cases). Sample date and location of case is shown in the label for each tip. Supplementary data is not available for this figure.



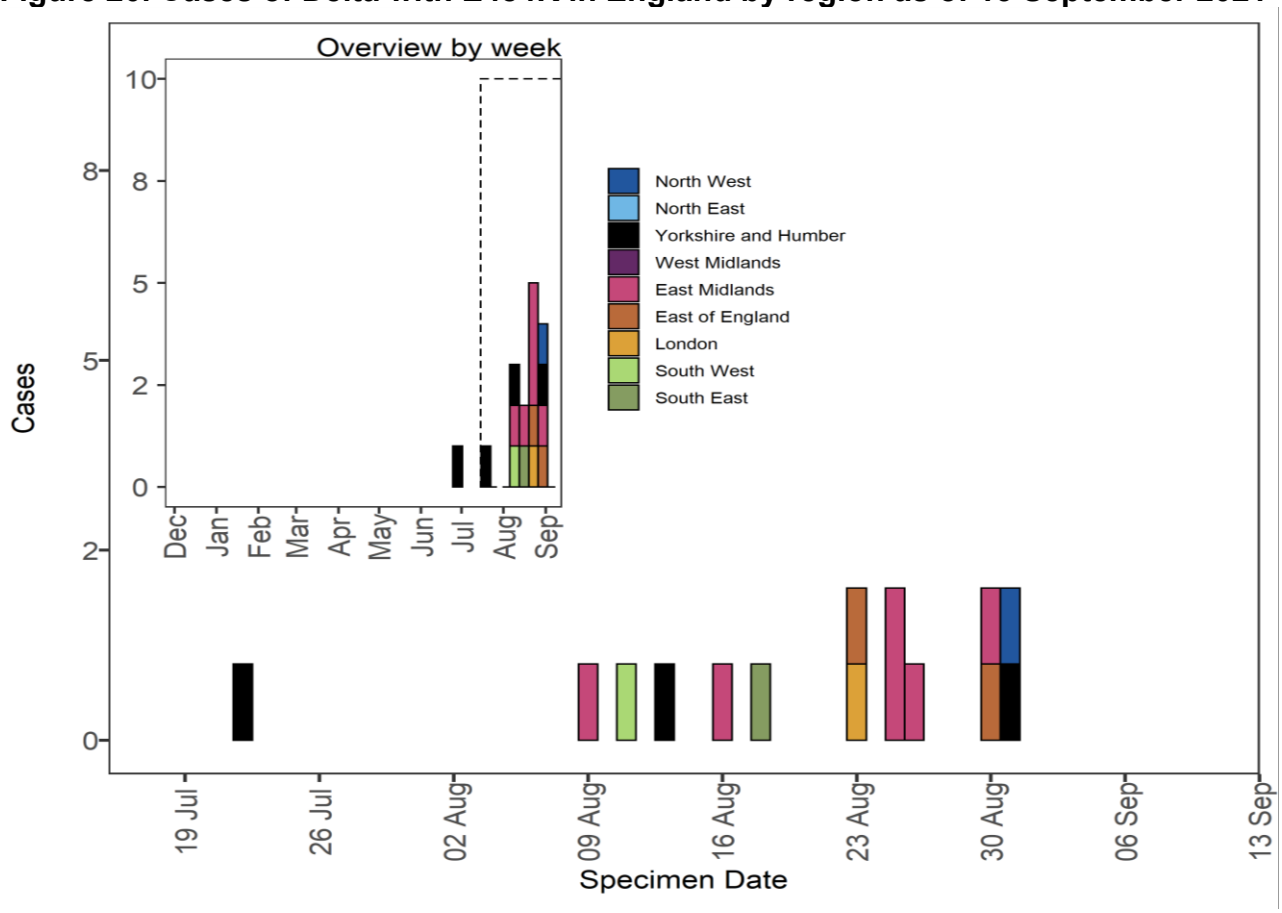
Epidemiology in England

As of 13 September 2021, there are 17 Delta with E484K cases in England. Cases have been detected across 7 English regions, with most cases in the East Midlands (6, 35.3%) as shown in Table 12 and cases by region in Figure 20. The most frequent age group was the 30 to 39 age group, with 5 cases. Three of the 17 cases have history of travel which includes travel from or transit through Latvia and Nigeria.

Table 12. Confirmed and provisional Delta with E484K cases in England by region as of 13 September 2021

Region	Total case number	Proportion of Delta with E484K cases in England with epidemiological data
East Midlands	6	35.3 %
East of England	2	11.8 %
London	1	5.9 %
North West	1	5.9 %
South East	1	5.9 %
South West	1	5.9 %
Yorkshire and Humber	4	23.5 %
Unknown region	1	5.9
Total	17	-

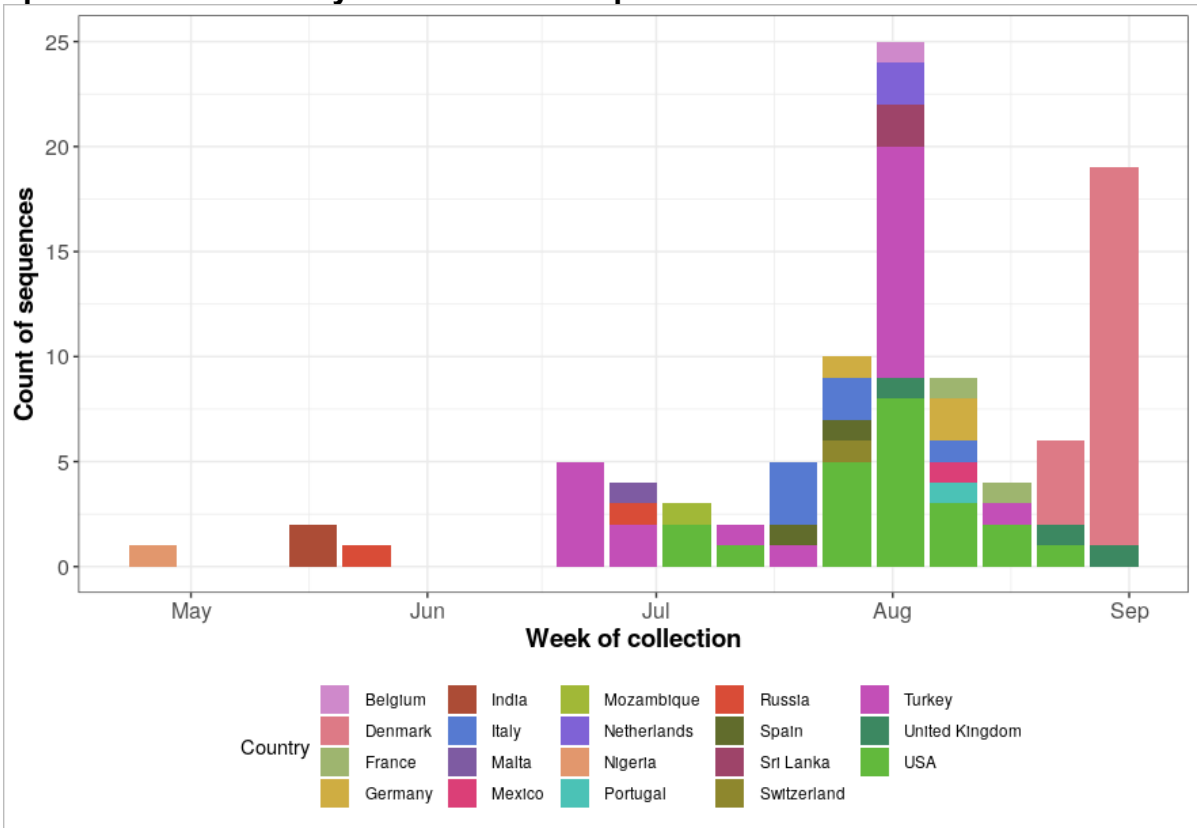
Figure 20. Cases of Delta with E484K in England by region as of 13 September 2021



International epidemiology

As of 13 September 2021, 99 sequences on GISAID have been assigned to the B.1.617.2 lineage with the additional E484K mutation. Sequences have been uploaded from USA (25), Denmark (22), Turkey (21), Italy (6), Germany (3), France (2), India (2), Netherlands (2), Russia (2), Spain (2), Sri Lanka (2), Belgium (1), Malta (1), Mexico (1), Mozambique (1), Nigeria (1), Portugal (1), Switzerland (1). Figure 21 shows the distribution of cases per country over time, based on GISAID data, indicating an increase in observations of Delta with E484K in August and September.

Figure 21. Count of Delta with E484K classified sequences by week of collection uploaded to GISAID by week as of 13 September 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

Genomic definitions for all VOC and VUI 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 PHE. Definition files are provided in YAML format so are compatible with a range of computational platforms. The repository will be regularly updated. The genomic and biological profiles of VOC and VUI are also detailed on first description in prior technical briefings.

Variant Technical Group

Authors of this report

PHE Genomics Cell
PHE Outbreak Surveillance Team
PHE Epidemiology Cell
PHE Immunisations Team
PHE Contact Tracing Data Team
PHE International Cell
JBC Public Health Science Team
Contributions from the Variant Technical Group Members including the Genotype to Phenotype Consortium

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

Acknowledgements

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

About Public Health England

Public Health England exists to protect and improve the nation's health and wellbeing, and reduce health inequalities. We do this through world-leading science, research, knowledge and intelligence, advocacy, partnerships and the delivery of specialist public health services. We are an executive agency of the Department of Health and Social Care, and a distinct delivery organisation with operational autonomy. We provide government, local government, the NHS, Parliament, industry and the public with evidence-based professional, scientific and delivery expertise and support.

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

Twitter: @PHE_uk
www.facebook.com/PublicHealthEngland

Published: September 2021
PHE gateway number: GOV-9722

PHE supports the UN Sustainable Development Goals

SUSTAINABLE DEVELOPMENT GOALS