UK Health Security Agency

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

Technical briefing 25

15 October 2021

This briefing provides an update on previous briefings up to 1 October 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 VOCs and 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:

- there are 4 current variants of concern (VOCs) and 10 variants under investigation (VUIs) (Table 1)
- there are no new VOCs or VUIs since the last briefing in the UK classification. Lambda has not been identified in the UK dataset since 10 July and has been moved to international monitoring
- Delta remains the predominant variant accounting for approximately 99.8% of sequenced cases in England as of 11 October 2021
- data on diversity within Delta is included – a Delta sublineage newly designated as AY.4.2 is noted to be expanding in England. It is now a signal in monitoring and assessment has commenced; there are also small numbers of new cases of Delta with E484K and Delta with E484Q
- discrepancies between SARS-COV-2 lineages in the population and mutations detected in wastewater have been identified and exploratory analyses have been initiated

All risk assessments are published separately, 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 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) (now UKHSA) 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 and 2 show the current VOC, VUI, and variants in monitoring detected and not detected in the UK as of 13 October 21.

Table 1. SARS-CoV-2 variants of public health interest: variants detected in the UK

WHO nomenclature	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 and sub-lineages	VOC-21APR-02	VOC
	B.1.1.318	VUI-21FEB-04	VUI
Kappa	B.1.617.1	VUI-21APR-01	VUI
Mu	B.1.621	VUI-21JUL-01	VUI
Epsilon^	B.1.427/B.1.429		Monitoring
	B.1.620		Monitoring
	R.1		Monitoring
	P.5		Monitoring
	C.1.2		Monitoring
	AY.4.2		Monitoring

Table 2. SARS-CoV-2 variants of public health interest: variants present in GISAID but not detected in the UK

WHO nomenclature	Lineage	Designation	Status
Eta	B.1.525	VUI-21FEB-03	VUI
Theta^	P.3	VUI-21MAR-02	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
Zeta	P.2	VUI-21JAN-01	VUI

	A.27		Monitoring
Iota	B.1.526		Monitoring
	B.1.1.7 with Q677H		Monitoring
	B.1 with 214insQAS		Monitoring
	AT.1		Monitoring
	B.1.629		Monitoring
	B.1.619		Monitoring
	B.1.630		Monitoring
	B.1.631/B.1.628		Monitoring
	P.1.8		Monitoring

Provisionally extinct variants are excluded from these tables.

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 UK cases of VUI-21JAN-01 was on 14 April 2021, VUI-21APR-03 on 17 May 2021, VUI-21FEB-03 on 19 June 2021, VUI-21MAR-02 on 25 May 2021, VUI-21MAY-01 on 21 June 2021, VUI-21MAY-02 on 26 June 2021 and are in International monitoring. Following the prior technical briefing VUI-21JUN-01 has been moved to international monitoring with the last documented case on 10 July 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), A.30, B.1.633, B.1.214.2 and B.1.1.7 with S494P 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.

^ Zeta and Theta were de-escalated by WHO and are no longer WHO variants under monitoring. Kappa, Iota, Eta and Epsilon were de-escalated by WHO to WHO variants under monitoring.

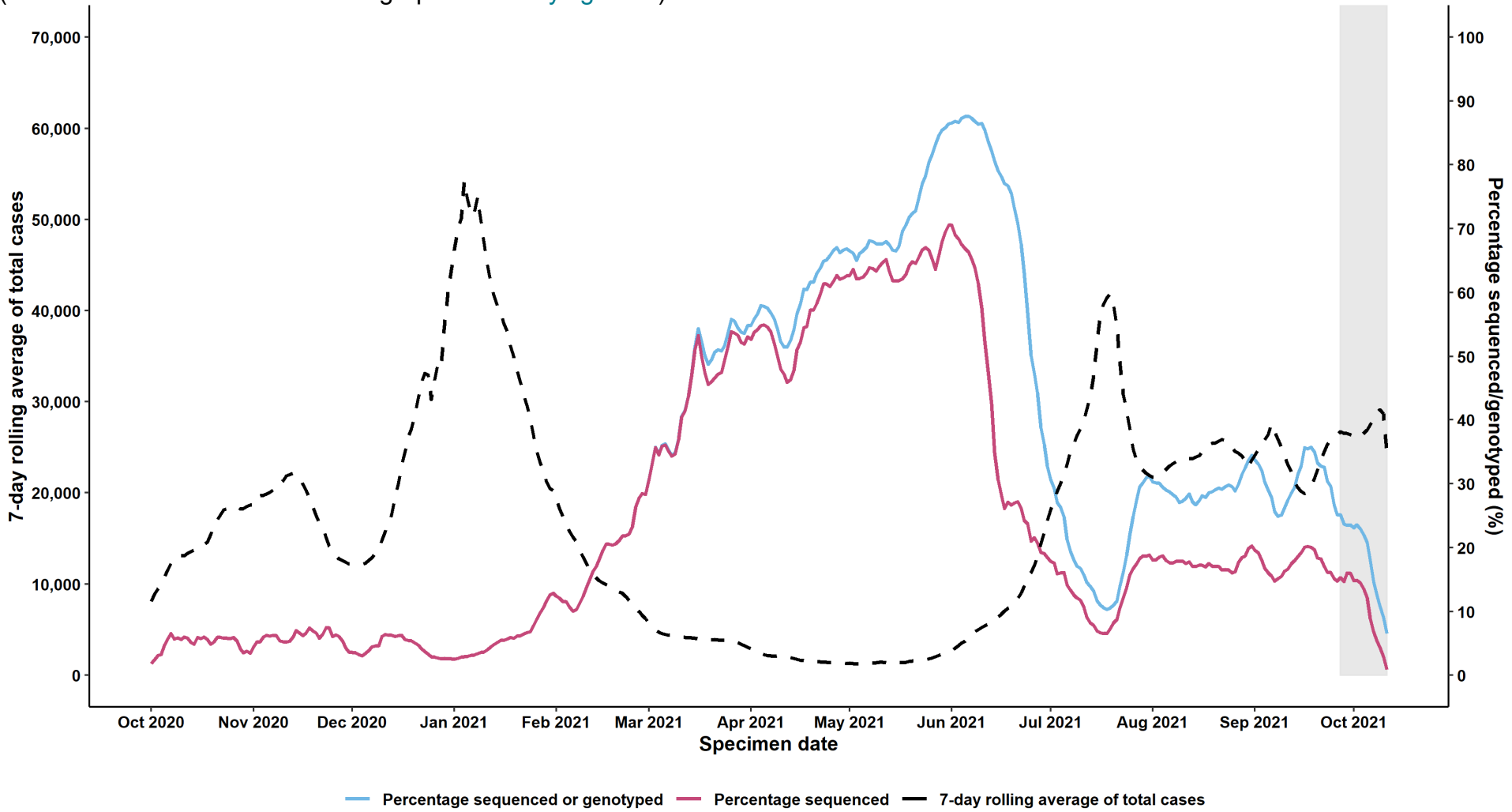
1.2 Sequencing coverage

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 among 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

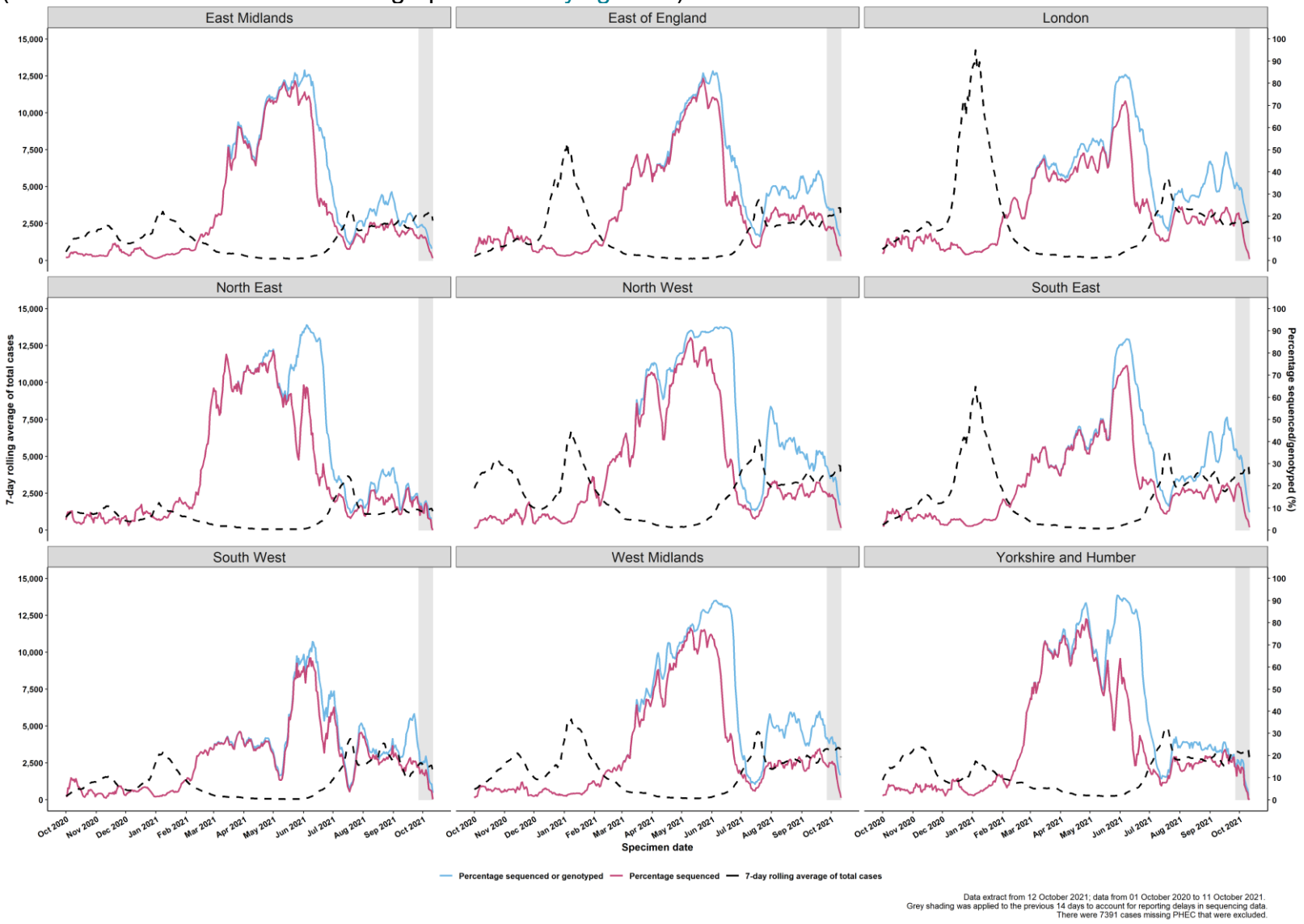
Figure 1. Coverage of sequencing with a valid result and genotyping over time (1 October 2020 to 11 October 2021)
(Find accessible data used in this graph in underlying data.)



Data extract from 12 October 2021; data from 01 October 2020 to 11 October 2021.
Grey shading was applied to the previous 14 days to account for reporting delays in sequencing data.

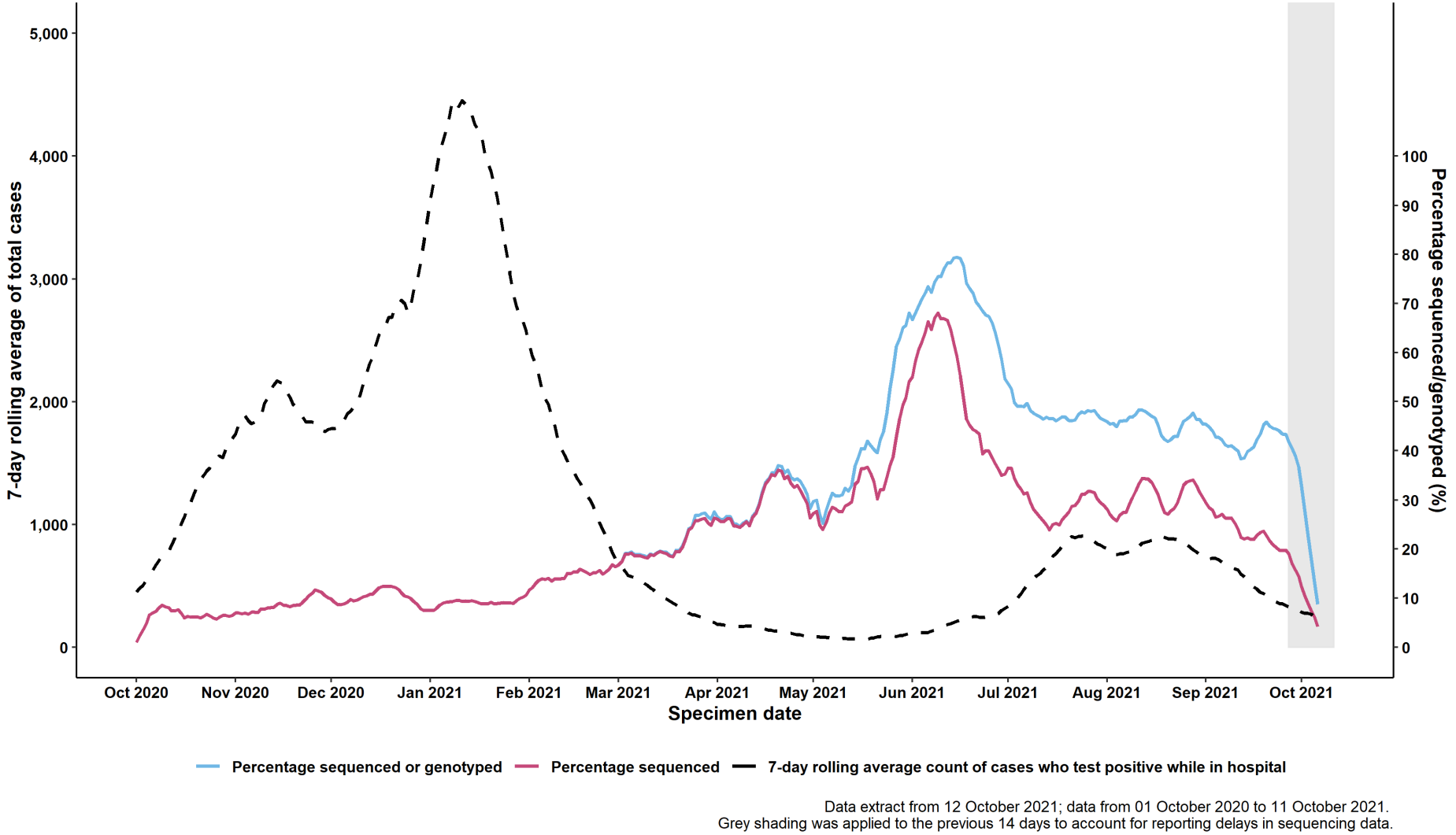
Grey shading was applied to the previous 14 days to account for reporting delays in sequencing data.

Figure 2. Coverage of sequencing with a valid result and genotyping over time by region (1 October 2020 to 11 October 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.

Figure 3. Coverage of sequencing with valid result and genotyping for cases who test positive in hospital (1 October 2020 to 11 October 2021) (Find accessible data used in this graph in underlying data.)



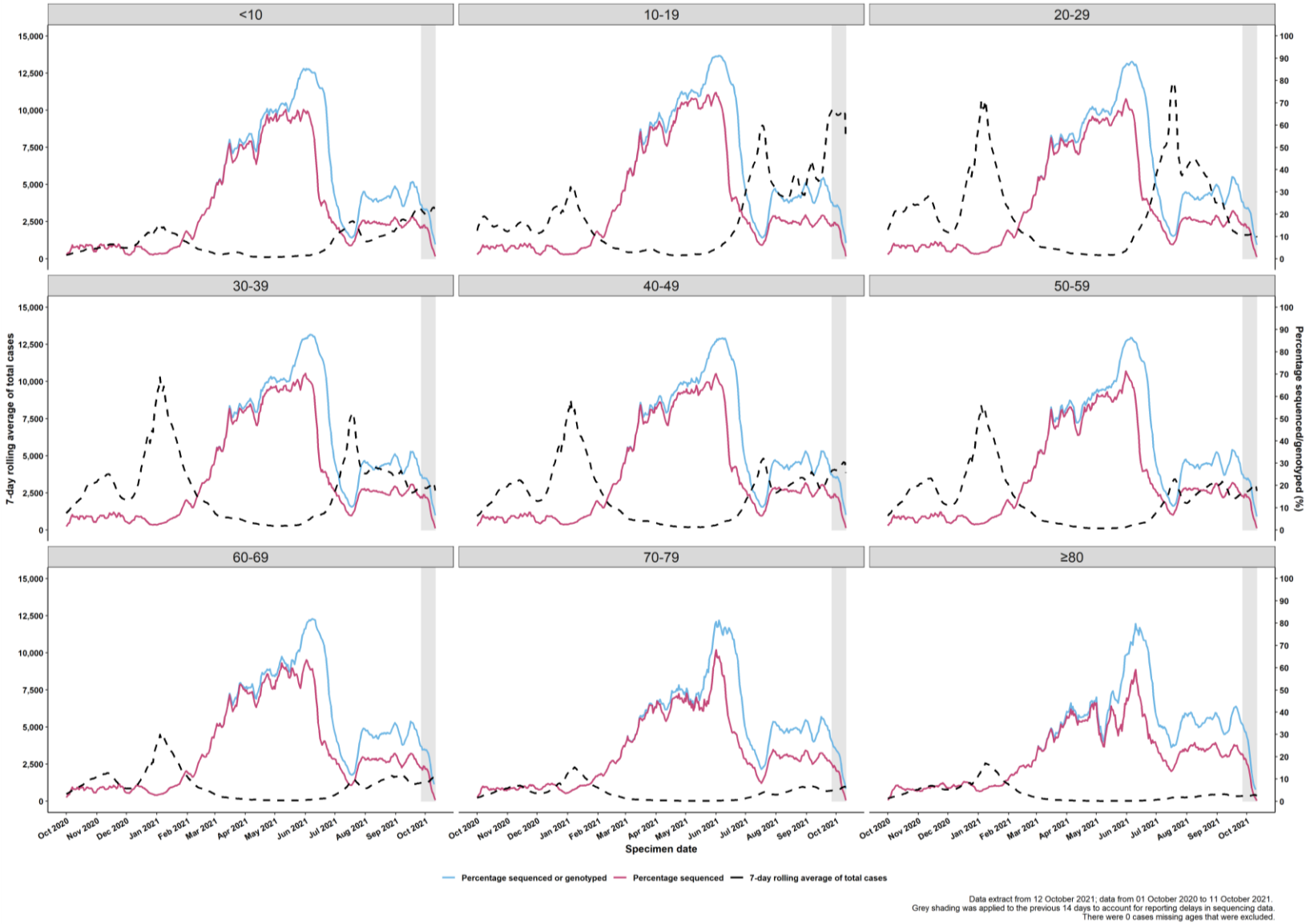
Grey shading was applied to the previous 14 days to account for reporting delays in sequencing data.

Notes to Figure 3

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

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 11 October 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 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 2 footnote). Figure 5 shows the cumulative number of cases per variant indexed by days since the first report.

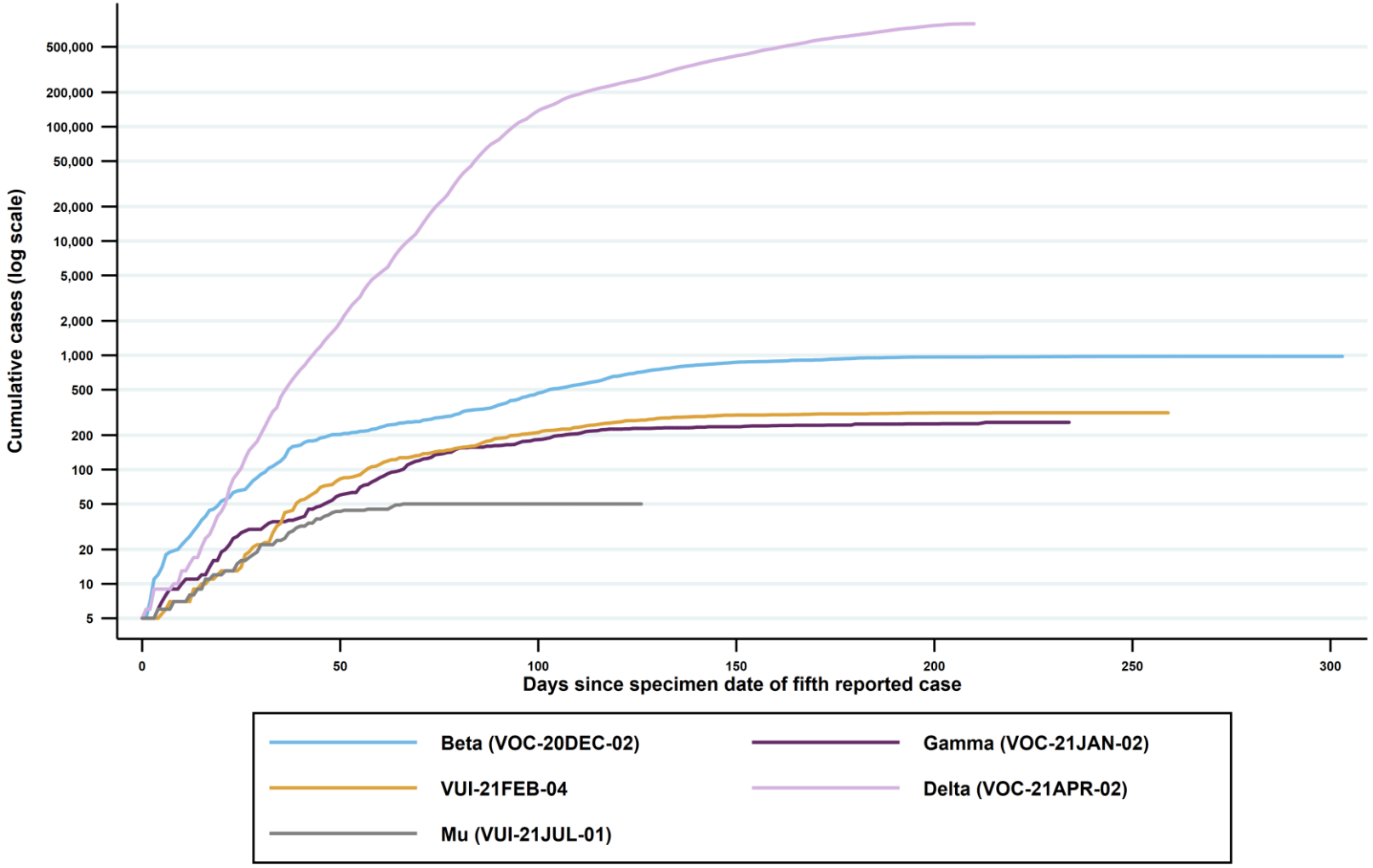
Cases, hospitalisation, attendance and deaths by vaccination status are now presented in the covid-19-vaccine-surveillance-report, therefore this data will not be produced in future editions of the variant technical briefing. These tables will be reinstated in the technical briefing if new variants of concern arise.

Table 3. Number of confirmed and probable cases by variant as of 11 October 2021

Variant	Confirmed (sequencing) case number	Probable (genotyping) case number[1]	Total case number	Case proportion	Deaths
Alpha	221,704	5,686	227,390	22.5%	4,369
Beta[2]	930	61	991	0.1%	12
Delta	467,335	313,268	780,603	77.2%	3,897
Eta	461	0	461	0.0%	12
Gamma	209	54	263	0.0%	0
Kappa	474	0	474	0.0%	2
Lambda	8	0	8	0.0%	0
Mu[2]	50	0	50	0.0%	0
Theta	7	0	7	0.0%	0
VOC-21FEB-02	45	0	45	0.0%	1
VUI-21APR-03	15	0	15	0.0%	0
VUI-21FEB-01	79	0	79	0.0%	2
VUI-21FEB-04	315	0	315	0.0%	1
VUI-21MAR-01	2	0	2	0.0%	0
VUI-21MAY-01	184	0	184	0.0%	1
VUI-21MAY-02	148	0	148	0.0%	0
Zeta	54	0	54	0.0%	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]Due to having identical genotyping profiles, since 1 July 2021 Beta and Mu cases identified by genotyping have been categorised as ‘Beta or Mu'. In addition to the above numbers, a further 12 ‘Beta or Mu’ provisional genotyping cases have been identified.

Figure 5. Cumulative cases in England of variants indexed by days since the fifth reported case as of 11 October 2021
(Find accessible data used in this graph in underlying data.)



1.4 Variant prevalence

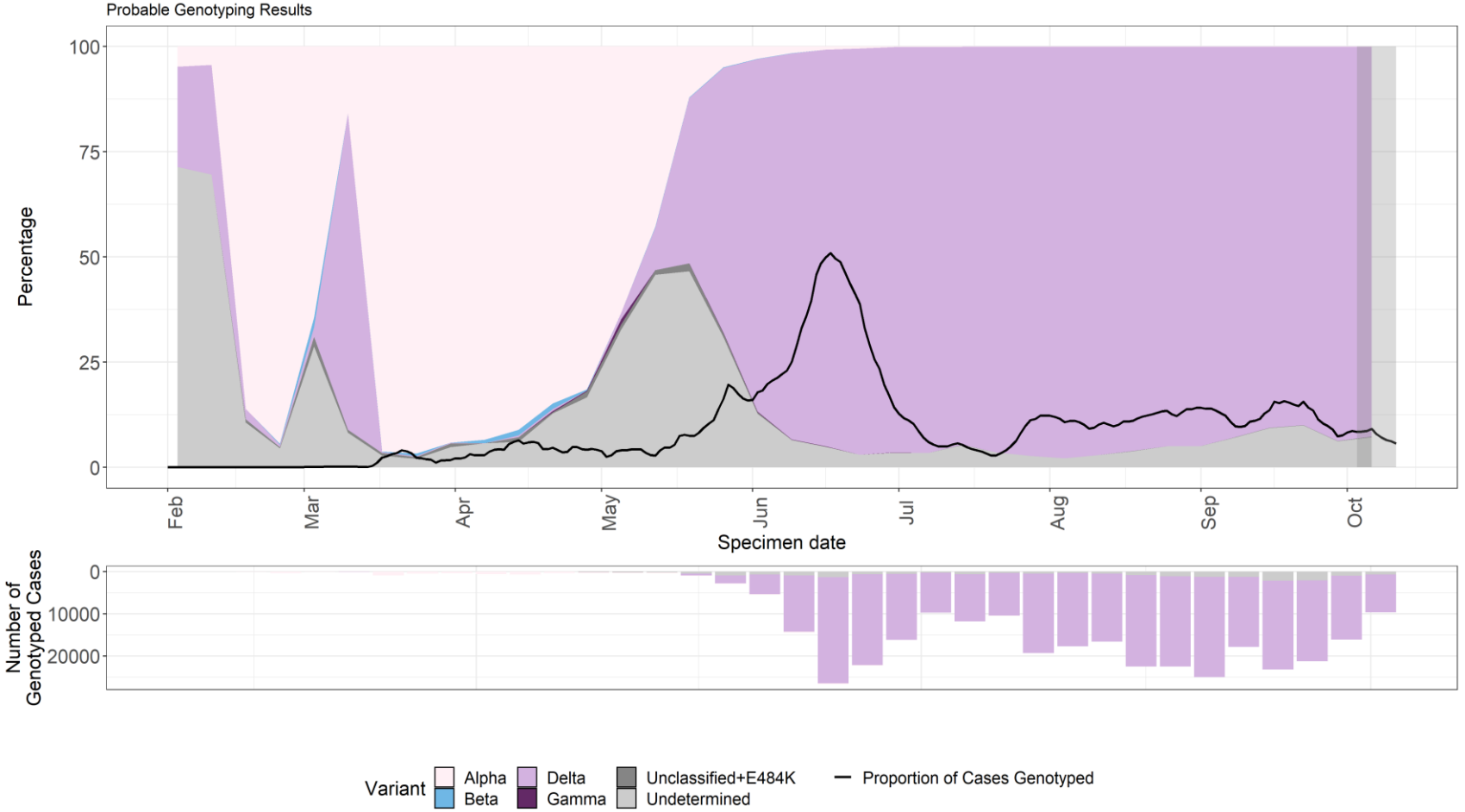
The prevalence of different variants amongst genotyped and sequenced cases is presented in Figure 6 and Figure 7 and split by region in Figure 8 and Figure 9.

Genotyping provides probable variant results 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 Figure 7 and Figure 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 99.8% of sequenced and 91.4% genotyped cases from 12 September 2021 as of 11 October 2021.

Figure 6. Variant prevalence for all England available genotyped cases from 1 February 2021 as of 12 October 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 12 October 2021 (excluding 254 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.

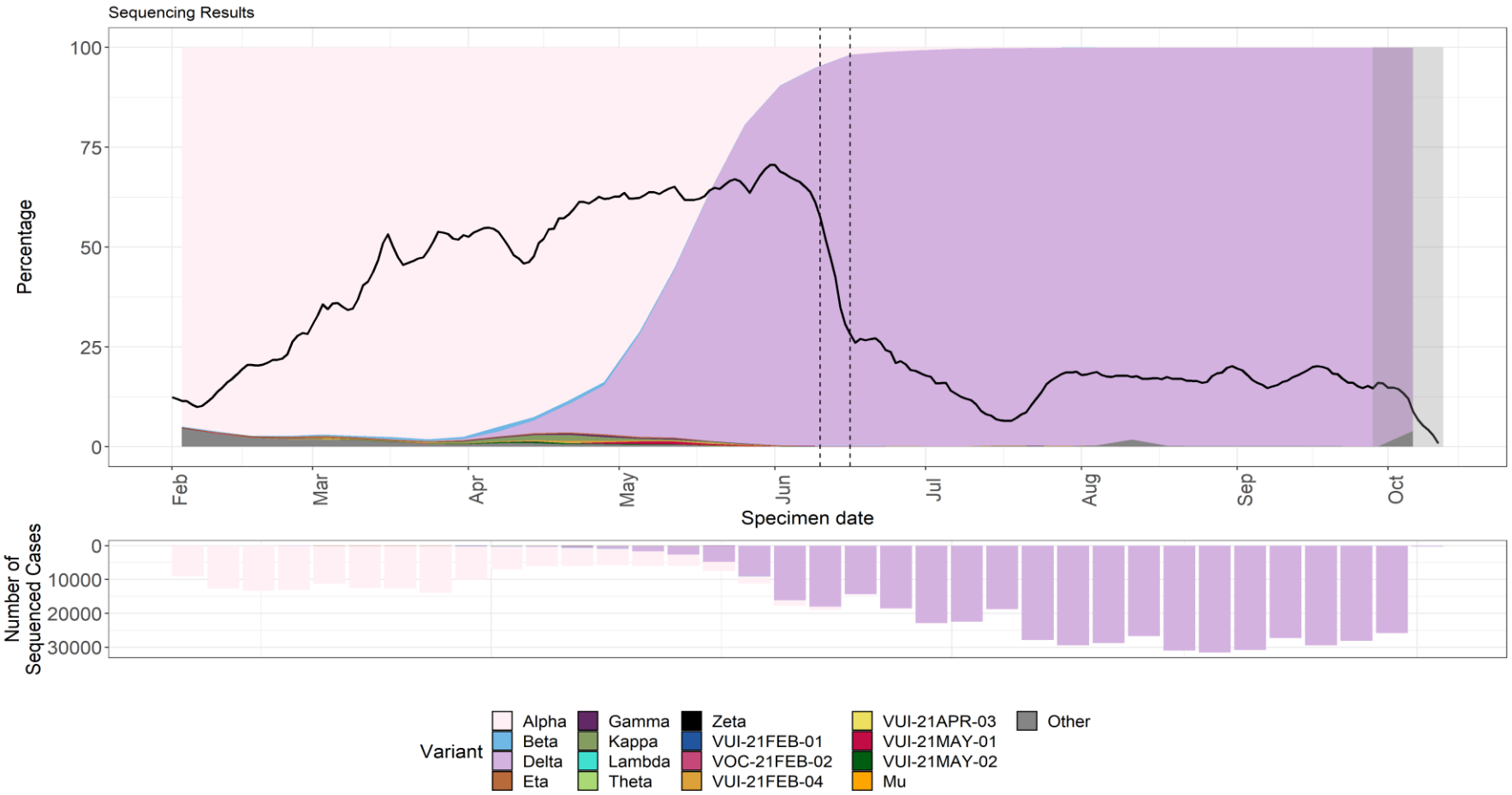


Figure 8. Variant prevalence from 1 February 2021 as of 12 October 2021 by region for all genotyped cases in England (excluding 2,345 cases where the region or specimen date were unknown)
(Find accessible data used in this graph in underlying data.)

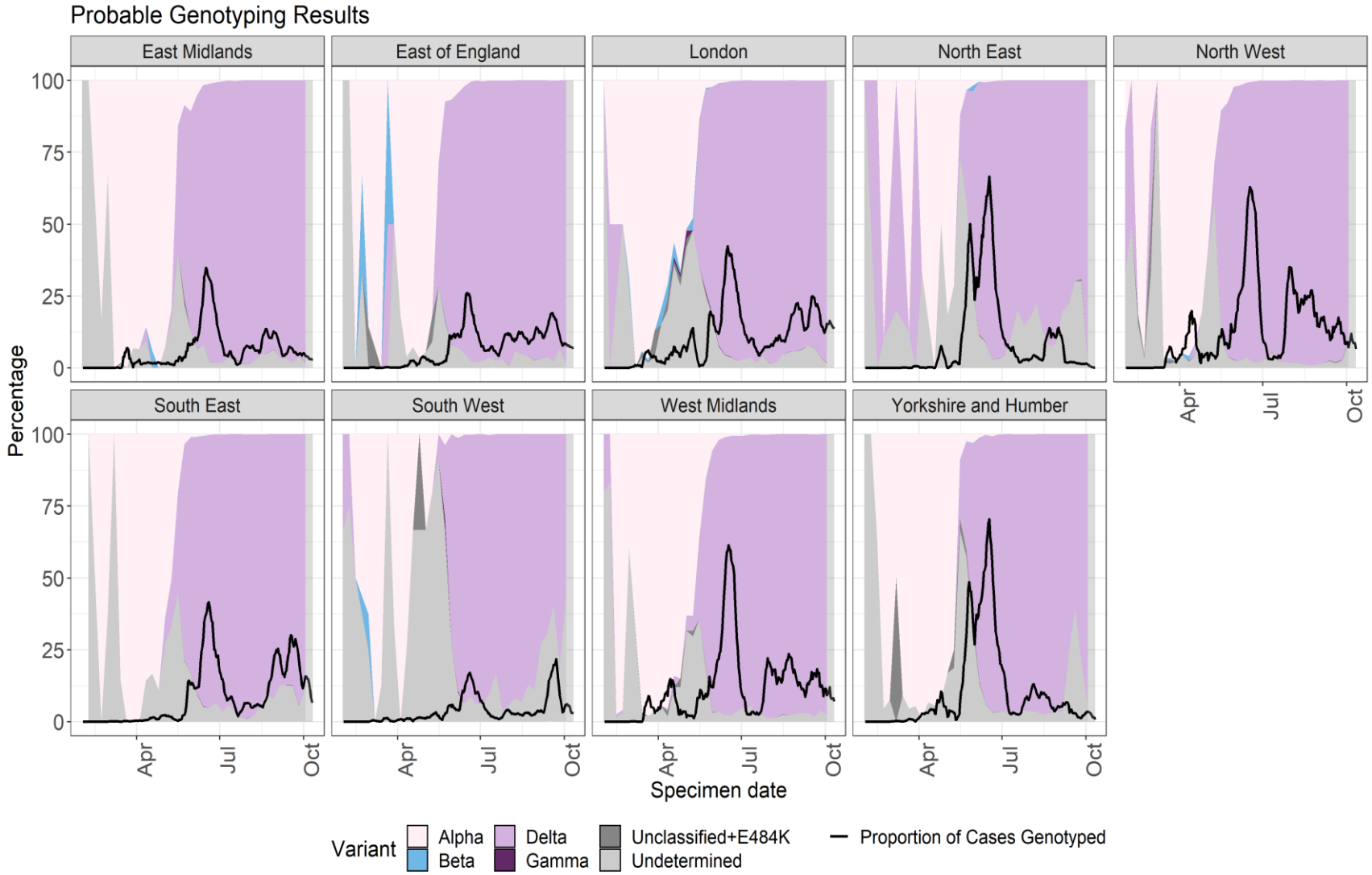
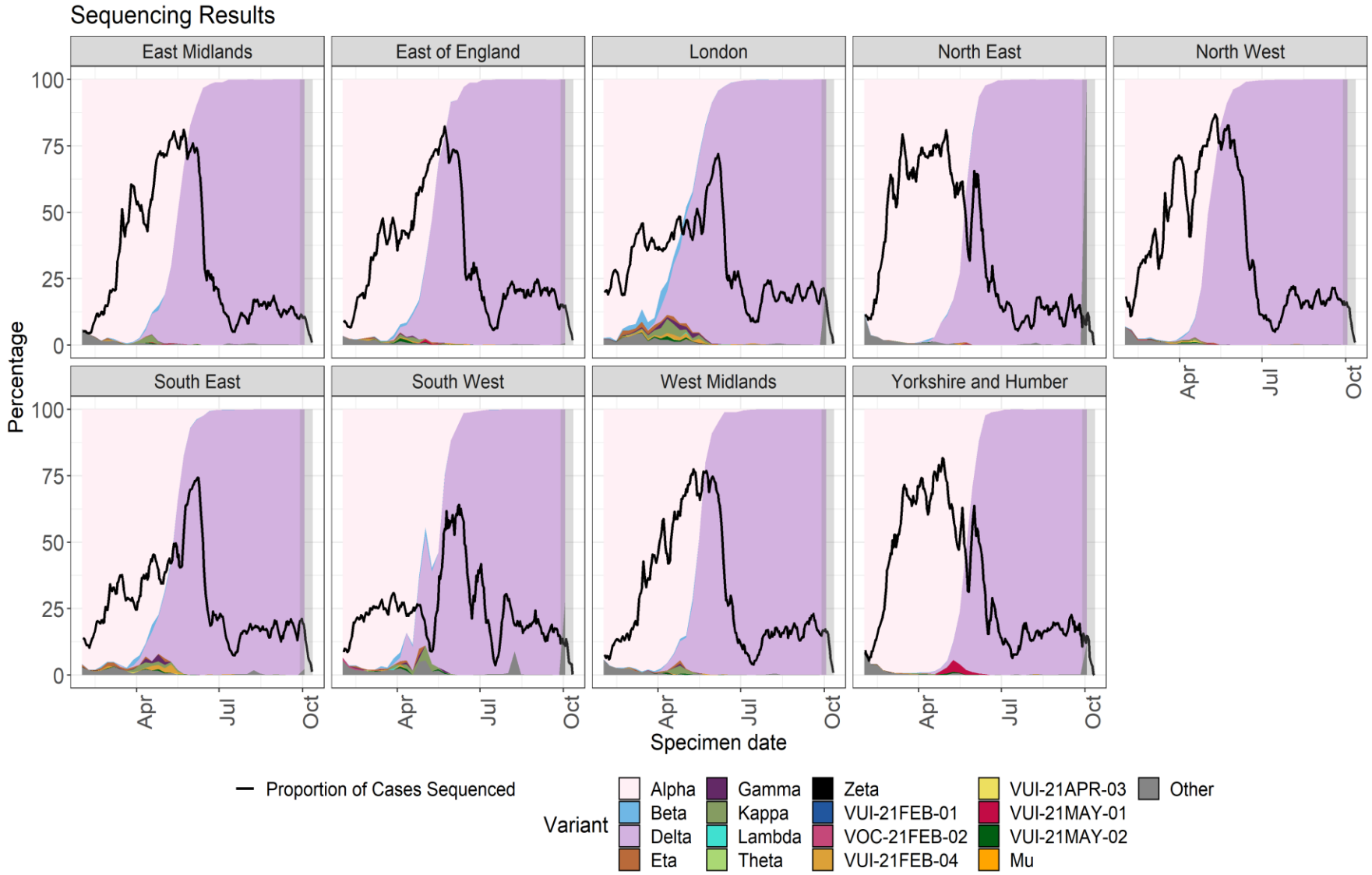


Figure 9. Variant prevalence from 1 February 2021 as of 12 October 2021 by region for all sequenced cases in England (excluding 3,776 cases where the region or specimen date were unknown). (Find accessible data used in this graph in underlying data.)



Wastewater investigation

Environmental monitoring of wastewater samples for the presence of SARS-CoV-2 variants is being undertaken across England and is in early stages of validation as a surveillance system. Wastewater is monitored for SARS-CoV-2 RNA at over 450 sites including sewage treatment works and local sewer networks. Sampling is undertaken multiple times per week. This sampling framework is estimated to cover approximately 70% of the English population. It is possible to look for mutations from variants in the wastewater, but detection of variants can be transient and the correlation between population prevalence and wastewater variant detection has not been established. Wastewater is currently considered as supplementary data in variant monitoring and is unvalidated as an independent variant surveillance system.

The wastewater routine analysis is to look for the presence of pre-defined sets of single nucleotide polymorphisms (SNPs) that identify known variants of concern, variants under investigation, and signals in monitoring. Since June 2021, 5 of the SNPs that contribute to the Beta variant definition, 5 SNPs contributing to the Gamma definition and one SNP that is shared between the Beta and Gamma definitions have been consistently detected in the North West area and sporadically elsewhere. Despite adequate sequencing coverage of the SARS-CoV-2 genome in the wastewater, the remaining SNPs that define either Beta or Gamma have been consistently absent from samples. Corresponding Beta and Gamma human infections were not detected in those areas over the relevant period through routine surveillance without lapses in coverage. Delta has been consistently detected in the wastewater in the same areas, however, relative abundance of SNPs making the Delta definition has declined, whilst the 5 SNPs from both Beta and Gamma and the shared SNP have increased. These anomalous findings have triggered further investigation.

Analysis shows the presence of additional novel SNPs not associated with the SARS-CoV-2 variants known to be circulating in humans, including some at biologically significant sites in the viral genome. This has also been noted in at least one international report from wastewater in another country[1]. An investigation is being undertaken to understand whether there may be technical artefacts contributing to this finding, or whether it may reflect mutations in human or animal SARS-COV-2 infections. Updates will be provided in future technical briefings.

[1] Tracking Cryptic SARS-CoV-2 Lineages Detected in NYC Wastewater | medRxiv

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 – overview

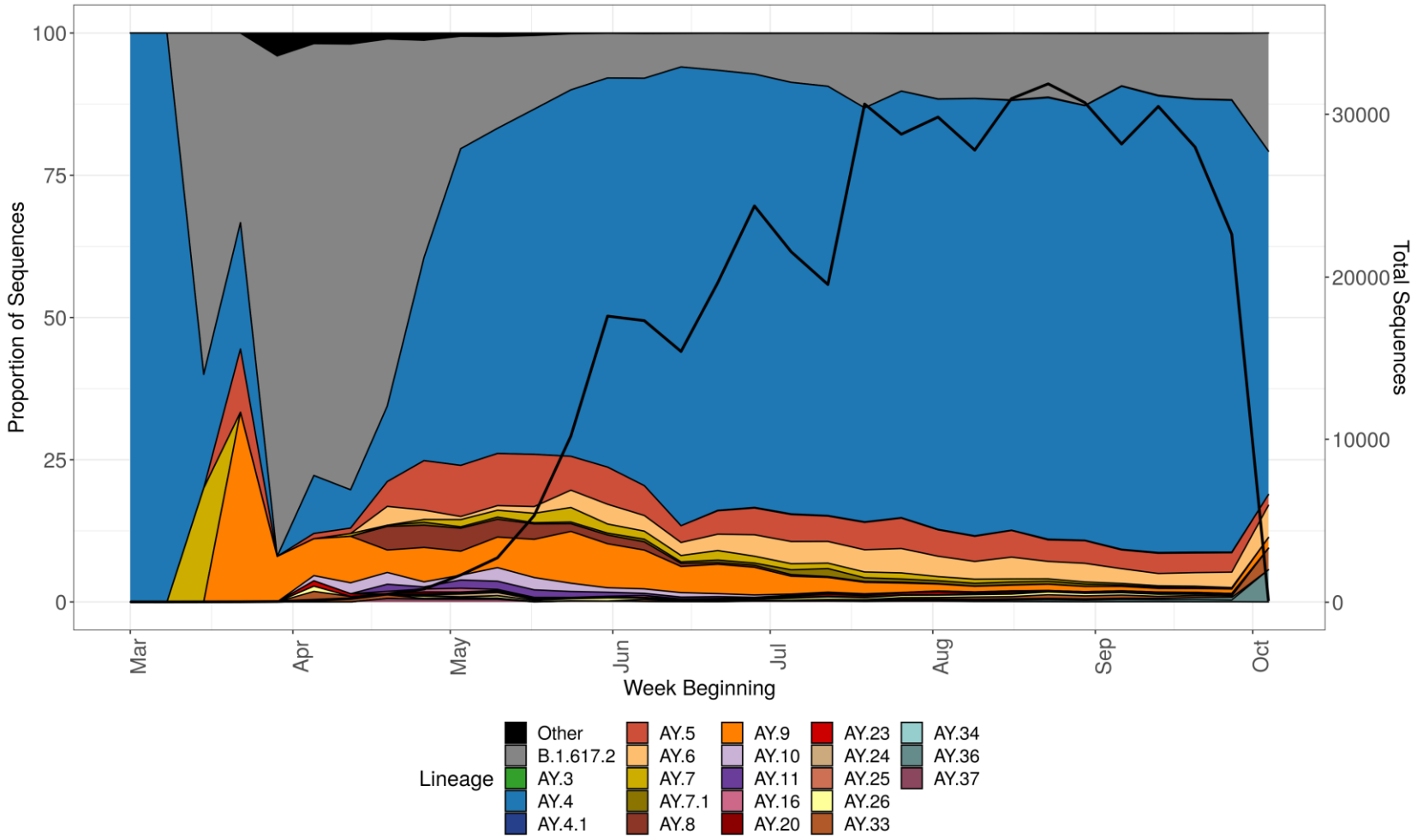
Diversity within Delta is monitored through lineages and through individual mutations.

Figure 10 shows the prevalence of Delta lineages over time in sequences in England, as defined using Pangolin. AY.4 remains dominant but other lineages introduced to the UK early have persisted over time.

New sublineages of Delta are regularly identified and designated. One recently designated sublineage, AY.4.2, is not yet assigned by the Pangolin tool and therefore is not represented in Figure 10. This sublineage is currently increasing in frequency. It includes spike mutations A222V and Y145H. In the week beginning 27 September 2021 (the last week with complete sequencing data), this sublineage accounted for approximately 6% of all sequences generated, on an increasing trajectory. This estimate may be imprecise due to known sequencing issues affecting position S:145. Further assessment is underway.

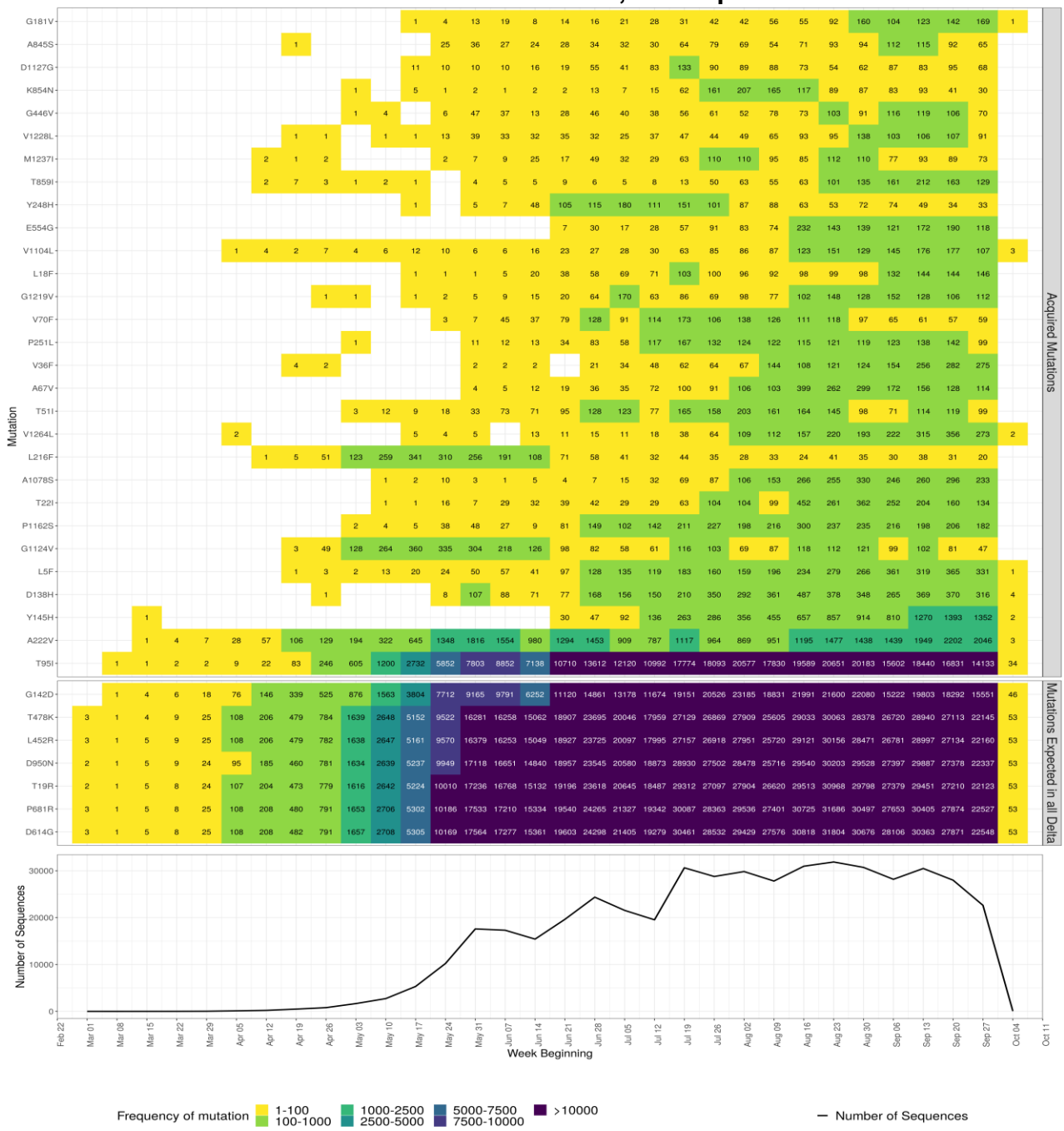
Mutations arising on Delta are shown in Figure 11 (heatmap of mutation frequency in S gene for any mutation seen in at least 1000 genomes), and Table 3 (limited to S gene mutations with evidence for impact on antigenicity, avidity or furin cleavage site).

Figure 10. Prevalence of Pangolin lineages within Delta from 1 March 2021 to 9 October 2021
(Find accessible data used in this graph in underlying data.)



The plot excludes 29,373 sequences that were not linked to date information and a further 219 that were not assigned a lineage by Pangolin due to sequence quality. The total number of sequences per week is shown by the black line. Only lineages with more than 100 sequences are shown. Smaller lineages are either merged with parent lineages (for example AY.3.1 is included in AY.3) or are included in 'Other'. AY.4.2 is not included as it is not yet called by Pangolin.

Figure 11. Number of UK Delta sequences containing mutations in spike, restricted to those mutations which are observed in at least 1,000 sequences



The total number of Delta sequences per week are shown in the bottom panel. The number of sequences with each mutation is shown in each cell. Sequences with no date information (n=29,373) and those that are not of sufficient quality (n=219) are excluded. Mutations are split into those that are expected in all Delta sequences and those acquired subsequently (right hand axis label). Those present in all Delta are not limited to those used in the UKHSA variant definition for this VOC as the definition excludes some due to sequencing issues (for example G142D) or because they are shared with other lineages (for example D950N). This figure shows raw counts and is not adjusted for genome areas that are differentially affected by sequencing issues so mutations in some areas will be underrepresented.

Table 4*. Additional spike mutations of possible functional significance detected in Delta genomes in the UK as of 11 October 2021

Amino Acid Change	Delta sequences in UK dataset	Delta sequences outside UK (GISAID)	Delta sequences 14 July to 13 August		Delta sequences 14 August to 13 September		Delta sequences 14 September to 13 October	
			England	Outside UK	England	Outside UK	England	Outside UK
P251L	3,591	13,176	584	5,770	542	4,566	432	1,029
G446V	2,381	2,027	252	693	413	803	318	211
Q613H	1,130	16,573	148	5,094	320	9,681	393	1,171
V483F	871	496	94	139	133	221	68	70
Q493E	396	198	125	84	143	44	42	5
S494L	315	489	62	143	126	262	77	29
E484Q	263	1,653	52	675	80	521	67	124
K417N	192	4,413	42	1,942	56	714	16	58
L455F	192	384	54	131	48	152	38	45
V445I	107	44	55	10	22	25	6	4
F490L	107	193	34	29	43	139	5	11
K444N	98	233	28	71	21	96	15	21
S494P	77	295	21	91	9	133	11	30
N501Y	74	545	17	329	17	38	13	1
F490S	71	124	11	34	20	65	28	13
A475V	55	58	6	24	19	26	17	3
K458N	44	61	8	29	9	19	4	2
R246I	61	116	20	31	7	64	15	8
P681H	43	280	11	127	5	89	3	19

E484K	62	334	4	130	16	117	34	39
K444R	57	96	12	20	7	43	26	22
L452Q	32	111	3	32	13	59	8	10
E484A	38	168	1	18	9	62	17	62
P499L	25	42	5	10	7	19	4	6
V445F	26	52	3	13	10	28	11	4
N439K	18	3	5	1	11	1	0	0
S494A	21	20	0	12	9	8	9	0
N501T	18	40	4	4	0	16	1	13
E484G	15	39	4	15	2	16	1	5
E484V	11	39	1	10	5	15	0	4
Q493L	10	59	3	30	2	12	0	4
D80N	9	45	3	15	1	22	0	5
V483A	6	45	3	16	2	20	1	5
F486L	6	4	0	2	1	0	0	2
V445A	11	41	4	20	1	12	4	7
E484D	11	55	2	18	0	26	0	6
G446D	5	15	2	5	2	6	0	2
G485D	4	2	0	0	2	0	0	1
T478I	3	13	1	3	0	8	0	2
Y453F	3	11	0	2	1	7	2	1
Q498R	6	32	0	12	0	11	1	4
Q493H	3	13	0	2	0	5	0	1
D80A	4	151	1	40	1	14	1	3
K444E	3	3	2	3	0	0	0	0
I472V	2	4	0	0	0	1	0	1
R246G	9	23	1	13	0	9	5	0
Q493R	1	4	0	0	0	2	0	1
Q493K	2	1	0	1	1	0	1	0

N450K	1	7	0	3	1	2	0	1
K458Q	1	3	0	0	1	2	0	1
K417T	3	15	1	4	1	6	0	2
K417E	6	16	3	4	0	12	1	0
V483G	1	11	1	9	0	1	0	1
V503L	32	1	1	0	6	1	1	0
Y144N	1	3	1	2	0	0	0	0
N501H	1	6	0	3	0	3	0	0
Total of Delta sequences	639,610	1,126,058	121,163	437,861	132,105	431,350	92,039	81,169

*This data uses the numbers of genomes in the national genomic data set rather than case numbers. 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 UKHSA.

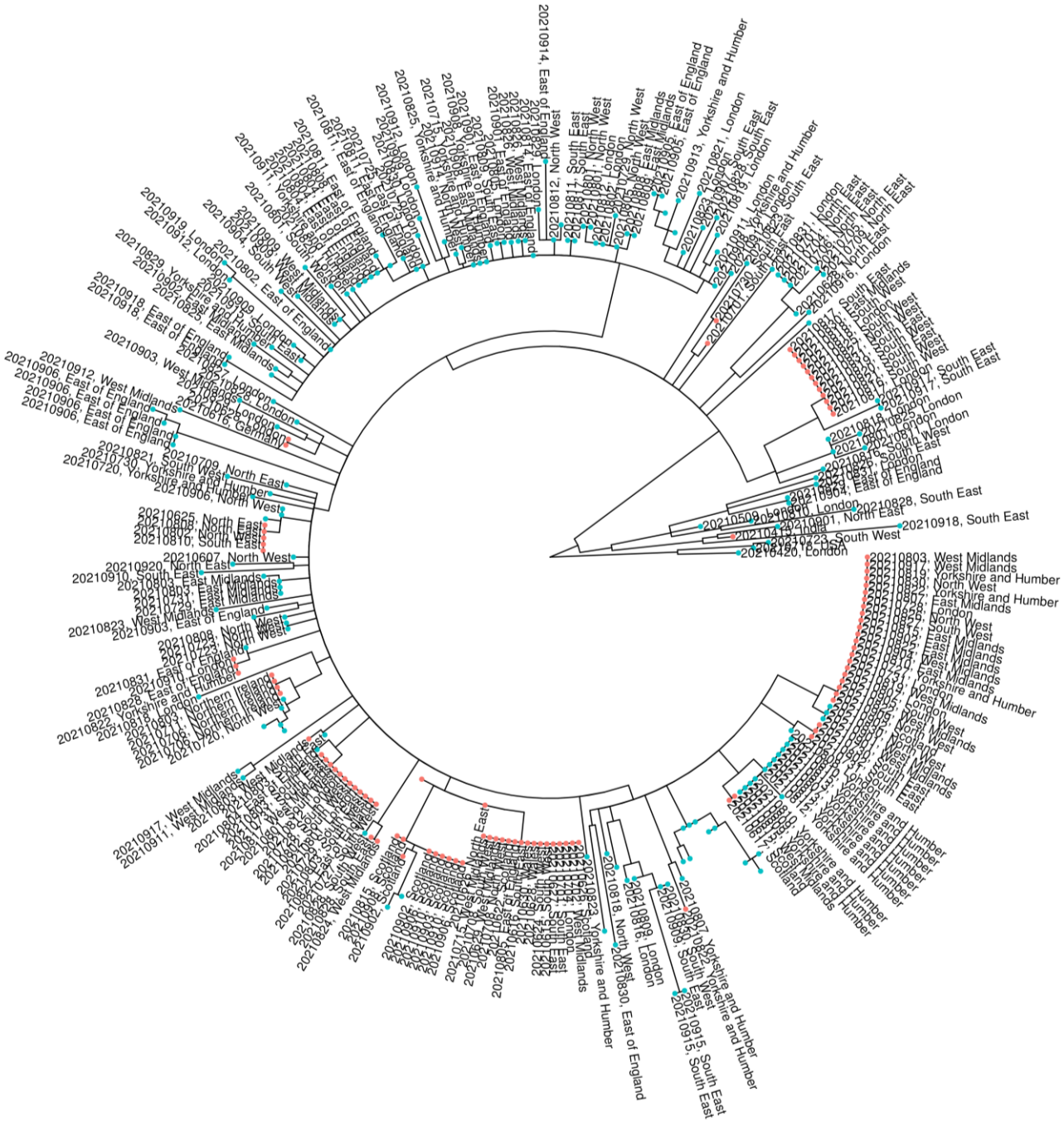
2.2 Monitoring diversity within Delta – Delta with E484Q

Changes at position 484 in spike are potentially antigenically significant. Delta with E484Q was first identified through horizon scanning on the 3 August 2021 after being detected in 6 Scottish samples between 22 and 28 July 2021. Two hundred and fifty seven sequences have been identified as of the 11 October 2021, with 231 from England, 18 from Scotland, and 8 from Wales.

The phylogenetic tree of UK Delta with E484Q cases is shown in Figure 12, which includes a cluster of 11 genetically indistinguishable samples from Yorkshire and Humber (10) and the West Midlands (1) (no change), a cluster of 5 samples from the North East (no change), a node of 4 samples (3 genetically indistinguishable) from the East Midlands (no change), a node of 6 genetically indistinguishable samples including an additional 4 London samples annotated with E484Q (the 2 pre-existing samples have ambiguous bases in at amino acid position 484).

The tree also contains a large node of diverse (genetically and geographically) samples that are predominantly annotated with the E484Q mutation; 34 samples were added to this node this week. This large node contains a cluster of 4 genetically indistinguishable samples from East of England (no change), and an additional cluster of 5 genetically indistinguishable samples from London (3) and Yorkshire and Humber (2).

Figure 12. Phylogenetic tree of UK Delta (B.1.617.2) with E484Q cases with a down-sampled international background dataset as of 15 October 2021

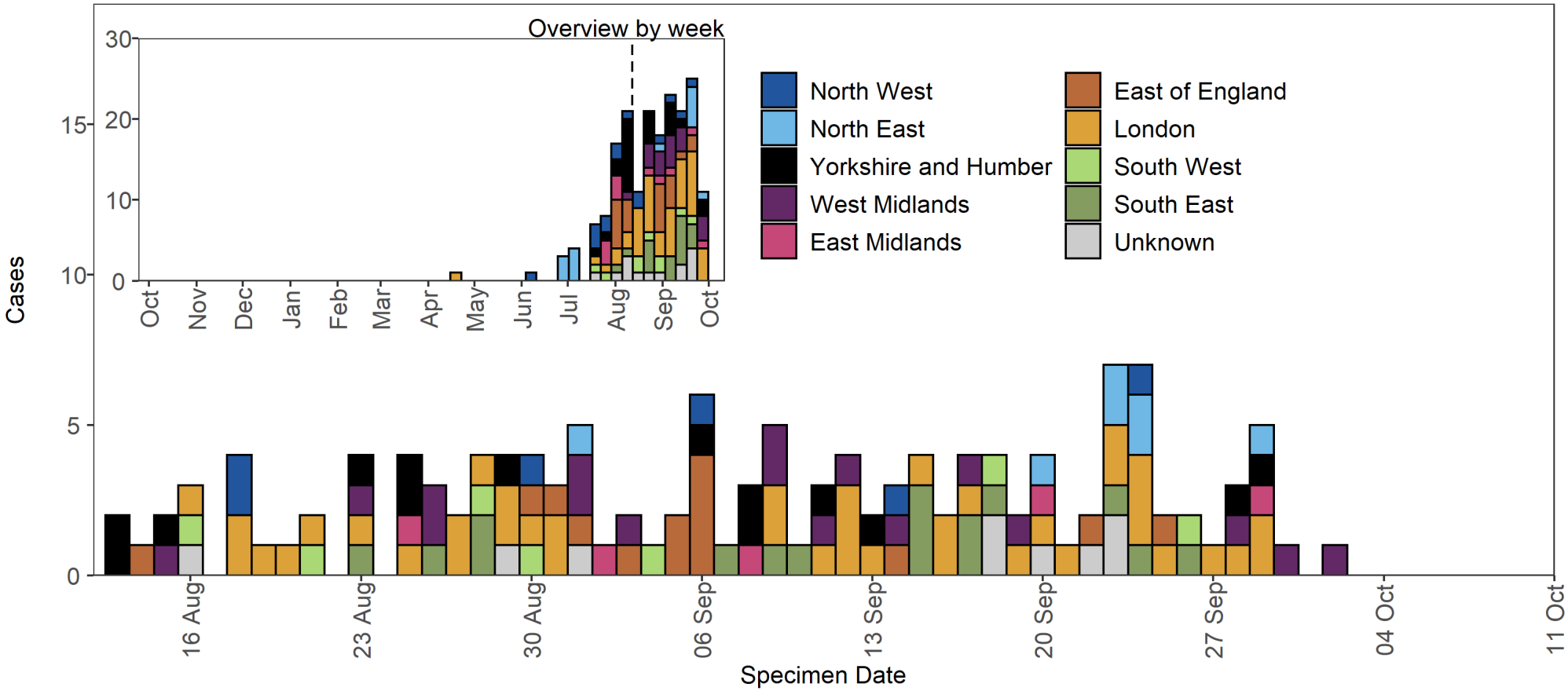


The tree is generated using Civet which down-samples UK and international samples for background context. Presence of the E484Q mutation is indicated by the tip colour (blue indicates E484Q annotated, red indicates E484Q not annotated). Sample date and location of case is shown in the label for each 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 11 October 2021, there are 257 Delta with E484Q sequences in England, 192 of which were linked to epidemiological data in England. This is an increase of 62 since the briefing of 1 October 2021. Cases have been detected across all 9 English regions, with most cases in the London (47, 24.5%) as shown by region in Figure 13. 78 of the 192 cases have history of travel.

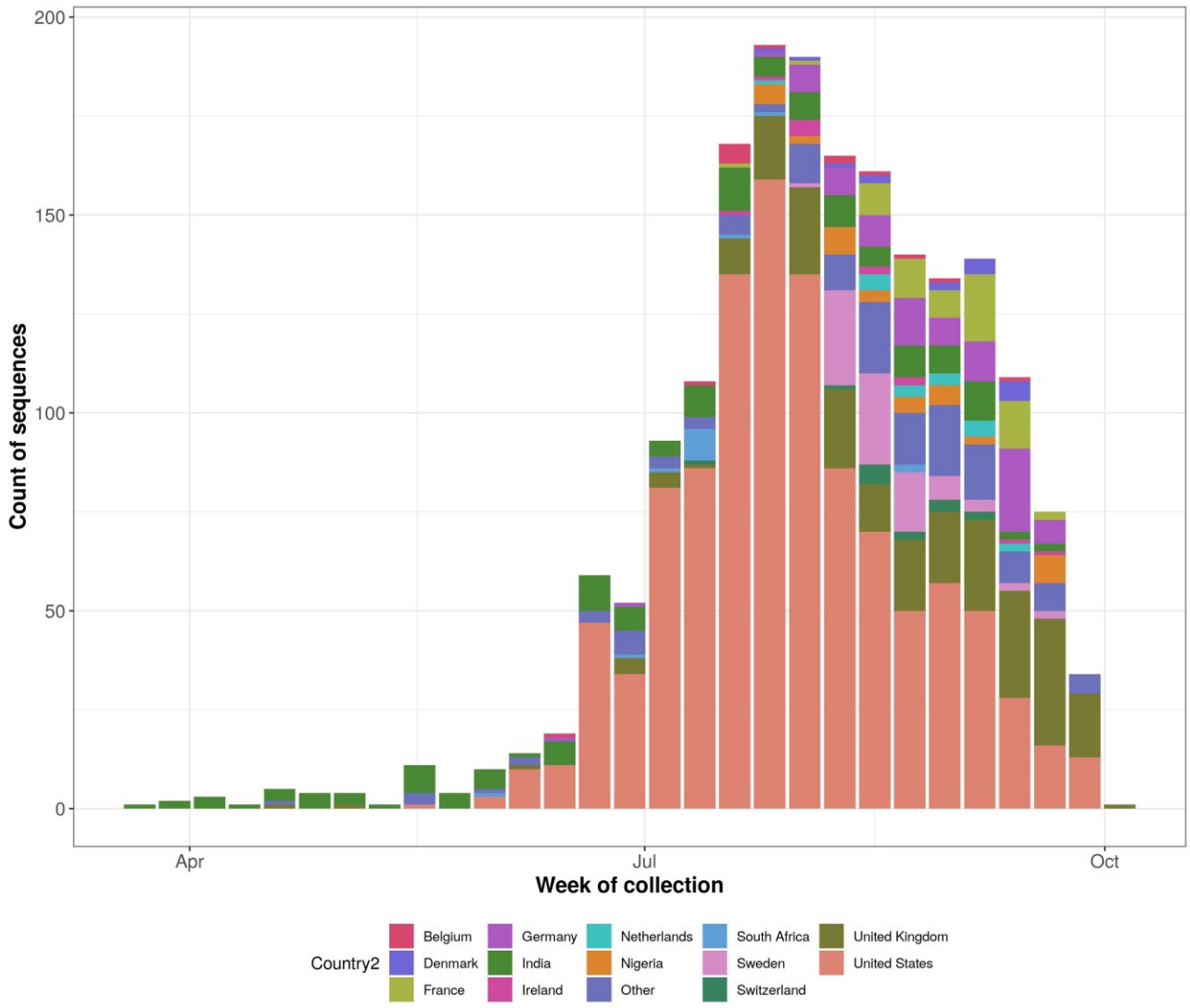
Figure 13. Confirmed (sequencing) and probable (genotyping) Delta cases with E484Q mutation cases by specimen date and region of residence as of 11 October 2021 (Find accessible data used in this graph in underlying data.)



International epidemiology

As of 11 October 2021, 1,981 GISAID sequences have been assigned to the B.1.617.2 and AY sub-lineages with the additional E484Q mutation, of those 1,900 sequences had appropriate date information. Sequences have been uploaded from USA (1072), India (133), Germany (81), Sweden (76), France (58), Nigeria (35), Netherlands (17), Denmark (16), South Africa (15), Belgium (14), Switzerland (14), Ireland (12) and 36 other countries with 10 or fewer samples. Figure 14 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 October 2021.

Figure 14. Count of Delta with E484Q classified sequences by week of collection uploaded to GISAID by week as of 11 October 2021 (Find accessible data used in this graph in underlying data.)



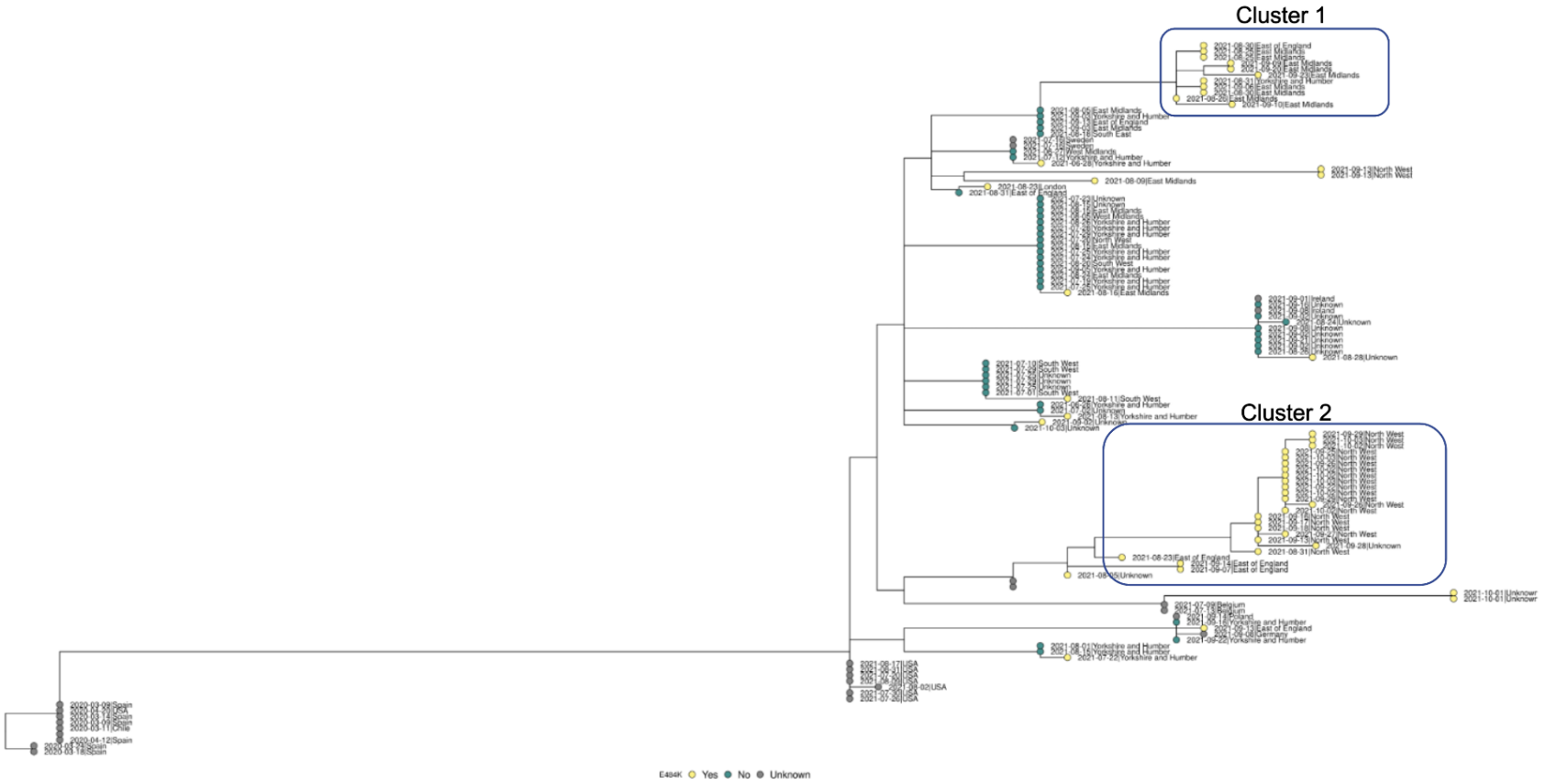
Countries with 10 or fewer sequences have been grouped together as Other.

2.3 Monitoring diversity within Delta – Delta with E484K

Changes at position 484 in spike are potentially antigenically significant. Delta with E484K was first detected on 22 July 2021 in UK sequences. 56 sequences have been identified as of the 11 October, with 54 from England and 2 from Scotland, an increase of 23 since the briefing of 1 October 2021.

The phylogenetic tree of UK Delta with E484K cases is shown in Figure 15, which includes 2 small clusters and multiple independent occurrences of the mutation (Delta with E484K is shown in yellow on Figure 15).

Figure 15. Maximum likelihood tree of UK Delta (B.1.617.2) with E484K cases



Maximum likelihood tree was built using CIVET3 with default settings of 2 SNP distance to the query sequences (Delta with E484K) and sub-sampling of the tree to 121 sequences. 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. Two clusters of Delta with E484K have been identified with 4 or more sequences, cluster 1 and 2 which are highlighted on the tree. Cluster 1 has grown by one sequence and cluster 2 by 16 sequences since the last report. No additional sequences with E484K have been added to the tree outside these clusters. Six sequences were excluded from the tree due to a technical issue with CIVET. Supplementary data is not available for this figure.

Epidemiology in England

As of 11 October 2021, there are 56 Delta with E484K sequences in England, of which 43 could be linked to epidemiological data. Cases have been detected across 9 English regions, with most cases in the North West (19, 44.2%) as shown by region in Figure 16 and by cluster in Figure 17. Three of the 43 cases have history of travel.

Figure 16. Cases of Delta with E484K in England by region as of 11 October 2021
(Find accessible data used in this graph in underlying data.)

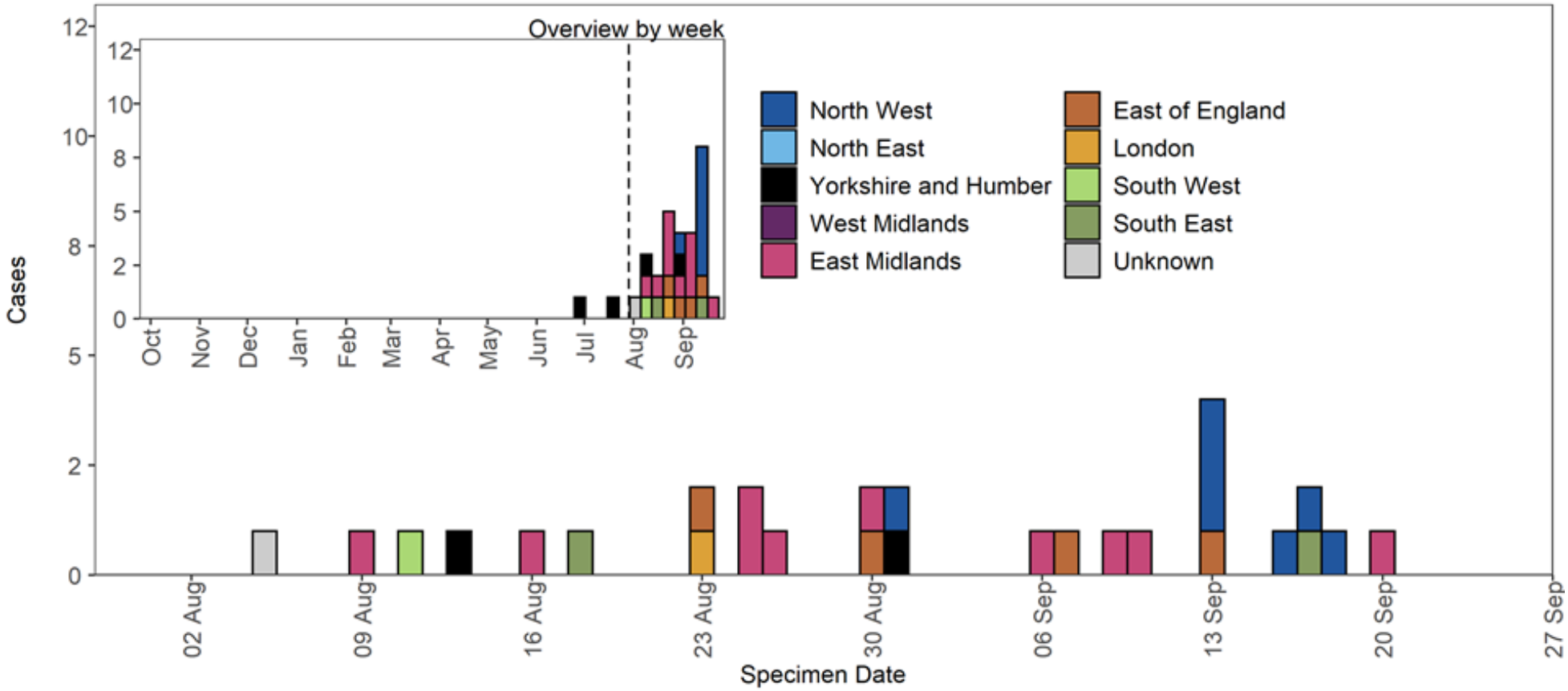
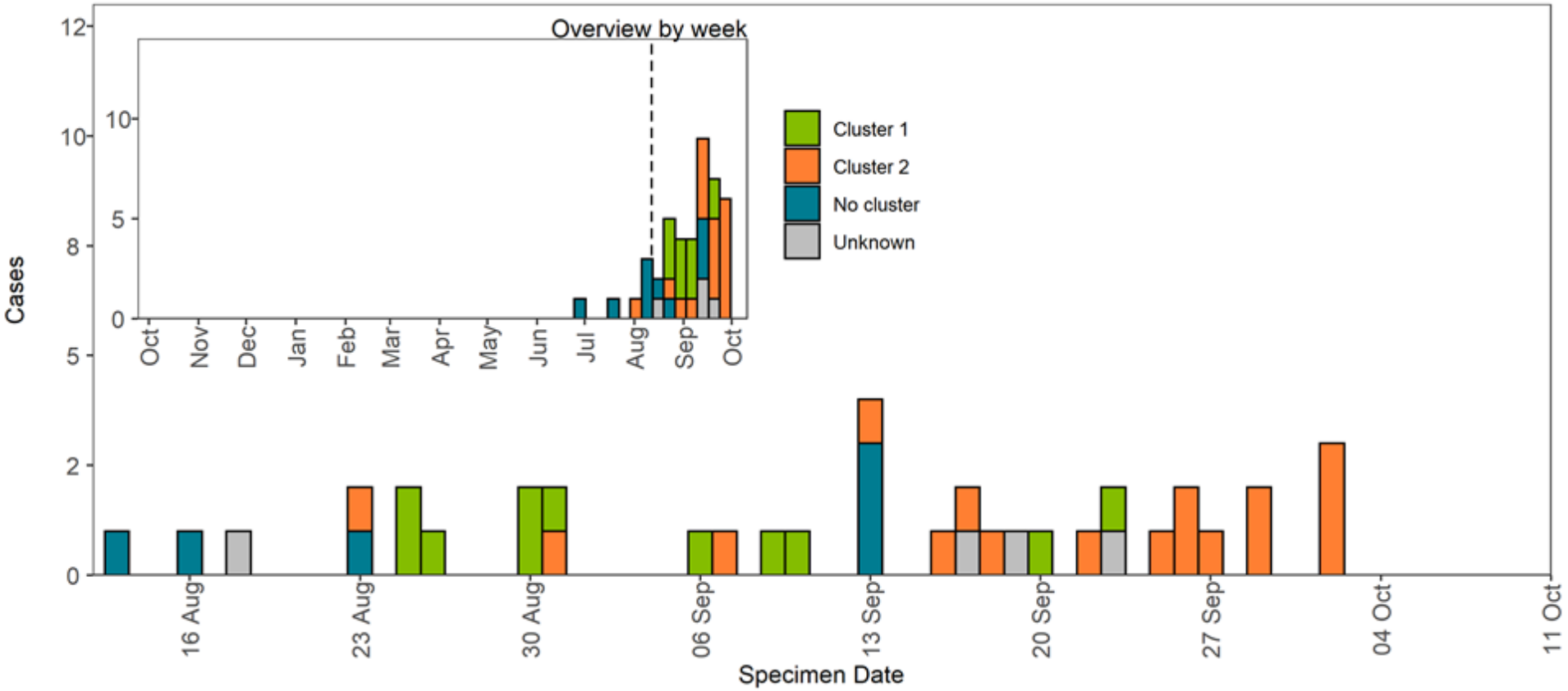


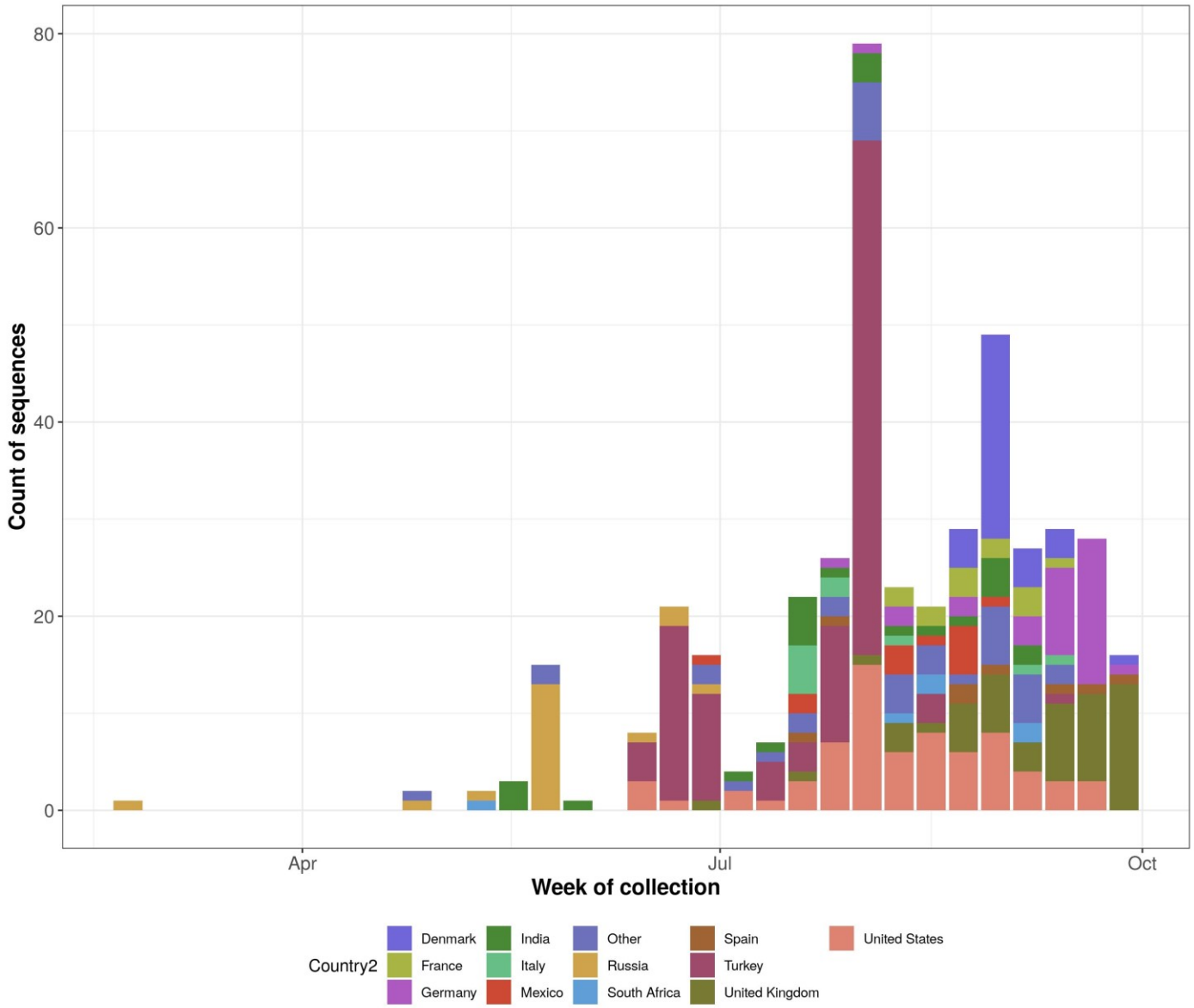
Figure 17. Cases of Delta cases with E484K mutation by detected cluster as of 11 October 2021
(Find accessible data used in this graph in underlying data.)



International epidemiology

As of 11 October 2021, 454 sequences on GISAID have been assigned to the B.1.617.2 and AY sub-lineages with the additional E484K mutation, of those 429 had appropriate date information. Sequences have been uploaded from Turkey (109), USA (73), Denmark (33), Germany (34), France (30), India (25), Russia (20), Mexico (13), Italy (11), Spain (9), South Africa (6), Japan (5), Belgium (3), Nigeria (3), Indonesia (3), Switzerland (3), Kenya (2), Netherlands (2), Poland (2), Sri Lanka (2), Australia (1), Brazil (1), Botswana (1), Canada (1), Ecuador (1), Lebanon (1), Lithuania (1), Luxembourg (1), Malta (1), Mozambique (1), Pakistan (1), Paraguay (1), Portugal (1), Ukraine (1). Figure 18 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 2021, which are continuing into October 2021.

Figure 18. Count of Delta with E484K classified sequences by week of collection uploaded to GISAID by week as of 11 October 2021 (Find accessible data used in this graph in underlying data.)

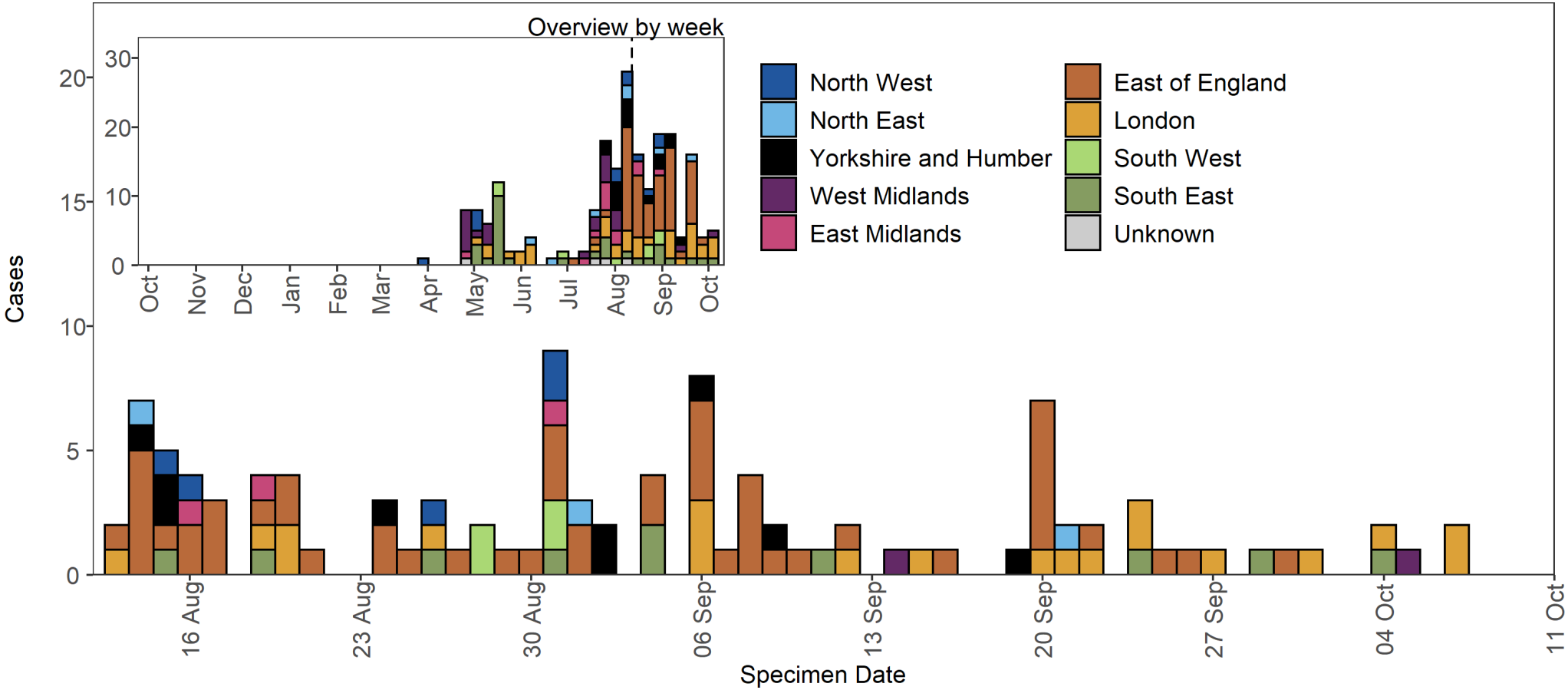


Countries with 5 or fewer sequences have been grouped together as Other.

2.4 Monitoring diversity within Delta – Delta with K417N mutation

As of 11 October 2021, there are 151 Delta with K417N sequences in England. Cases have been detected across 9 English regions, with most cases in the East of England (29.9%) as shown in Figure 19.

Figure 19. Confirmed (sequencing) and probable (genotyping) Delta cases with K417N mutation cases by specimen date and region of residence as of 11 October 2021 (Find accessible data used in this graph in underlying data.)



Sources and acknowledgments

Data sources

Data used in this investigation is derived from the COG-UK and UKHSA genomic programme dataset, the UKHSA Second Generation Surveillance System (SGSS), the Secondary Uses Service (SUS) dataset, Emergency Care Data Set (ECDS), and the UKHSA 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 UKHSA. 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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