UK Health Security Agency

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

Technical briefing 40

8 April 2022

This report provides an update on previous briefings up to 25 March 2022

Contents

Summary

This report has been published to share the detailed variant surveillance analyses which contribute to the variant risk assessments and designation of new SARS-CoV-2 variants. This specialist technical briefing contains early data and analysis on emerging variants and findings have a high level of uncertainty.

Unless stated otherwise, this technical briefing uses a data cut-off of 4 April 2022 to allow time for analyses.

Interpreting variant data

Recent changes to testing need to be considered when interpreting all variant data; the targeting of testing at specific groups may impact the time it takes to draw conclusions about variant characteristics.

Changes to variant classification system

As of 1 April 2022, the UK Health Security Agency (UKHSA) has amended its variant classification system to give a clearer indication of which variants have potentially significant changes in biological properties compared to the current dominant variant(s). Previous variants of concern which no longer meet the criteria have been redesignated.

Under the new classification the following variants of concern (VOCs) and variants (V-date-number) in the United Kingdom (UK) retain a current designation from UKHSA:

- Omicron sub-lineage BA.1 VOC-21NOV-01
- Omicron sub-lineage BA.2 VOC-22JAN-01
- V-22APR-02 (XE)
- V-22APR-03 (Omicron sub-lineage BA.4)
- V-22APR-04 (Omicron sub-lineage BA.5)
- V-21OCT-01 (AY.4.2)
- V-20DEC-01 (Alpha, B.1.1.7) and
- V-21APR-02 (Delta, and all sub-lineages).

Newly classified variants (Vs)

V-22APR-01 (XD) and V-22APR-02 (XE)

XD and XE are recombinant lineages. On 6 April 2022, the Variant Technical Group (VTG) classified recombinant XD as V-22APR-01 and recombinant XE as V-22APR-02.

XD, which has an Omicron S gene incorporated into a Delta genome, is present primarily in France but has not been detected in the UK. Whilst the total number of genomes is still small, it

has been designated on the basis that data published from France suggests that it may be biologically distinct.

XE is a BA.1/BA.2 recombinant, with the majority of the genome including the S gene belonging to BA.2. XE shows evidence of community transmission within England, although it is currently less than 1% of total sequenced cases. As of 5 April, 1,125 cases of XE have been identified in England. XE has been designated on the basis of community transmission and possible growth in England.

Earlier published growth rates for XE were not significantly different from BA.2, but using the most recent data up to 30 March 2022, XE has a growth rate 12.6% above that of BA.2. Over the most recent 3-week period, XE growth advantage reached 20.9%. As this estimate has not remained consistent as new data have been added, it cannot yet be interpreted as an estimate of growth advantage for the recombinant. Relationship to changes in testing policy are being explored.

V-22APR-03 (Omicron sub-lineage BA.4)

Omicron sub-lineage BA.4 was classified V-22APR-03 by the VTG on 6 April 2022. BA.4 was designated on the basis of potentially biologically significant mutations in spike. V-22APR-03 (hereafter referred to as BA.4) shares all mutations/deletions with the BA.2 lineage except the following: NSP4: L438 (WT, wild type); S: 69/70 deletion, L452R, F486V, Q493 (WT); ORF 7b: L11F; N: P151S. The S gene 69/70 deletion is associated with S gene target failure (SGTF). Sequence samples have been identified in GISAID between 10 January 2022 and 30 March 2022 from South Africa (45), Denmark (3), Botswana (2), Scotland (1), and England (1).

V-22APR-04 (Omicron sub-lineage BA.5)

Omicron sub-lineage BA.5 was classified V-22APR-04 by the VTG on 6 April 2022. V-22APR-04 (referred to as BA.5) shares the same mutations/deletions as BA.4 (V-22APR-03) except the following: M: D3N; ORF 6: D61 (WT); ORF 7b: L11 (WT); N: P151 (WT); synonymous SNPs: A27038G, and C27889T. All samples submitted to GISAID are from South Africa (27) between 25 February 2022 and 25 March 2022.

VOC-22JAN-01 (BA.2)

BA.2 rarely contains the spike gene deletion at position 69/70 and is S-gene target positive (SGTP) on diagnostic assays with targets in this area. The overall proportion of SGTP amongst cases tested by the relevant assay in England on 3 April 2022 is 97.6**%** compared to 93.7% on 20 March 2022. As well as the general fall in case ascertainment, the numbers of samples processed by the assay which detects S gene target failure has fallen which will affect reliability of estimates. The proportion of BA.2 in sequenced data from 20 March to 27 March 2022 was 93.9%.

Published information on variants

On 1 April 2022 UKHSA amended its variant classification system. Further details are available in Technical Briefing 39.

SARS-CoV-2 Routine variant data update covers surveillance data and sequencing coverage data on all other VOCs and VUIs up to 25 March 2022. The latest COVID-19 variants: genomically confirmed case numbers are published on Gov.uk.

The collection page gives content on variants, including prior technical briefings. 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 to identify variant and mutation profiles from genotype assay mutation profiles.

The Public Health England repository from 5 March 2021 contains the previous genomic definitions for VOCs and variants under investigation (VUIs).

Part 1. Surveillance overview

World Health Organization (WHO) nomenclature from 24 January 2022 is incorporated. Tables 1a and 1b show the current VOCs, variants (V-date-number), and signals in monitoring detected and not detected in the UK incorporating WHO designations with Phylogenetic Assignment of Named Global Outbreak Lineages (Pangolin lineages).

Table 1a. Variants detected in the UK in the past 12 weeks

Variants of concern	Variants (Vs)	Signals in monitoring
Omicron (B.1.1.529) sub-lineage BA.1 VOC-21NOV-01	V-21OCT-01 (AY.4.2)†	B.1.640
Omicron (B.1.1.529) sub-lineage BA.2 VOC-22JAN-01	Alpha (B.1.1.7) V-20DEC-01	BA.3
	Delta (B.1.617.2 and sub-lineages) V-21APR-02	Delta and Omicron recombinant lineages (UK)
	XE Recombinant (BA.1 x BA.2) V-22APR-02	BA.1/BA.2 Recombinant (with unique mutation C3583T)
	Omicron (B.1.1.529) sub-lineage BA.4 V-22APR-03	XF Recombinant
	Omicron (B.1.1.529) sub-lineage BA.5 V-22APR-04	

† AY.4.2 is a sub-lineage within Delta that has been assigned as a distinct V-date-number.

Table 1b. Variants detected in GISAID, but not in the UK, in the past 12 weeks

Variants of concern	Variants (Vs)	Signals in monitoring
Beta (B.1.351) V-20DEC-02	Mu (B.1.621) V-21JUL-01	AY.119.2/BA.1.1 Recombinant
	(B.1.617.3) V-21APR-03	
	XD Recombinant (Delta x BA.1) V-22APR-01	

VOCs and other variants (V-date-number) 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 variant has not been observed in the UK or international data sets within the preceding 12 weeks, it is designated as provisionally extinct, but monitoring remains in place. Variants and signals in monitoring may also be removed from the grid if they show consistently low growth rates.

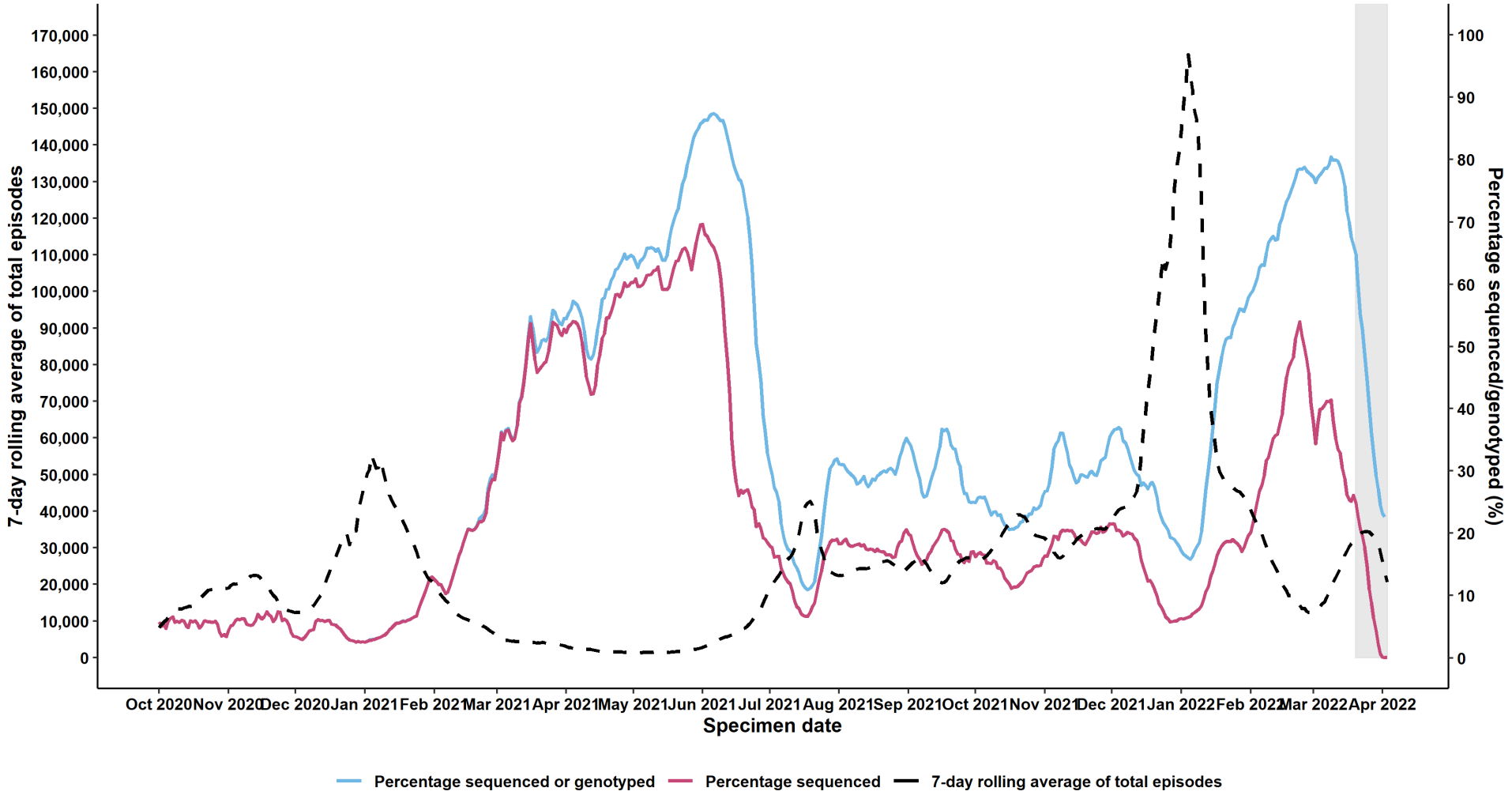
1.1 Sequencing coverage

Figure 1 shows the proportion of coronavirus (COVID-19) cases as detected by polymerase chain reaction (PCR) 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.

Sequencing coverage of PCR confirmed cases was high during March 2022 (Figure 1) however, this needs to be interpreted with care as PCR tests have declined substantially since mid-February 2022 and case ascertainment is reduced.

Currently, the sequencing strategy prioritises hospitalised cases, patients who are receiving specific antiviral therapy, and national core priority studies.

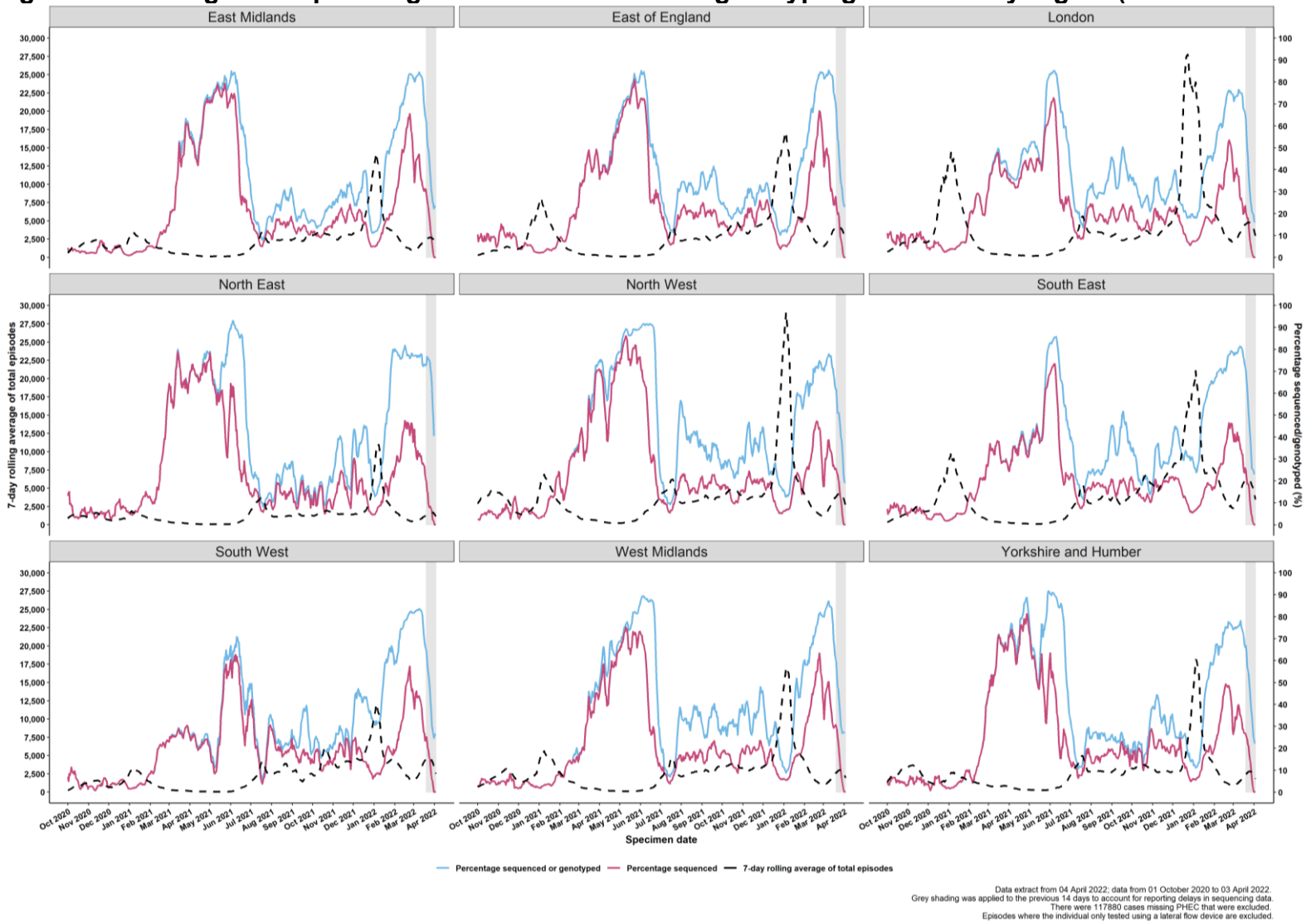
Figure 1. Coverage of sequencing with a valid result and genotyping over time (1 October 2020 to 3 April 2022)



Data extract from 04 April 2022; data from 01 October 2020 to 03 April 2022.
Grey shading was applied to the previous 14 days to account for reporting delays in sequencing data.
Episodes where the individual only tested using a lateral flow device are excluded.

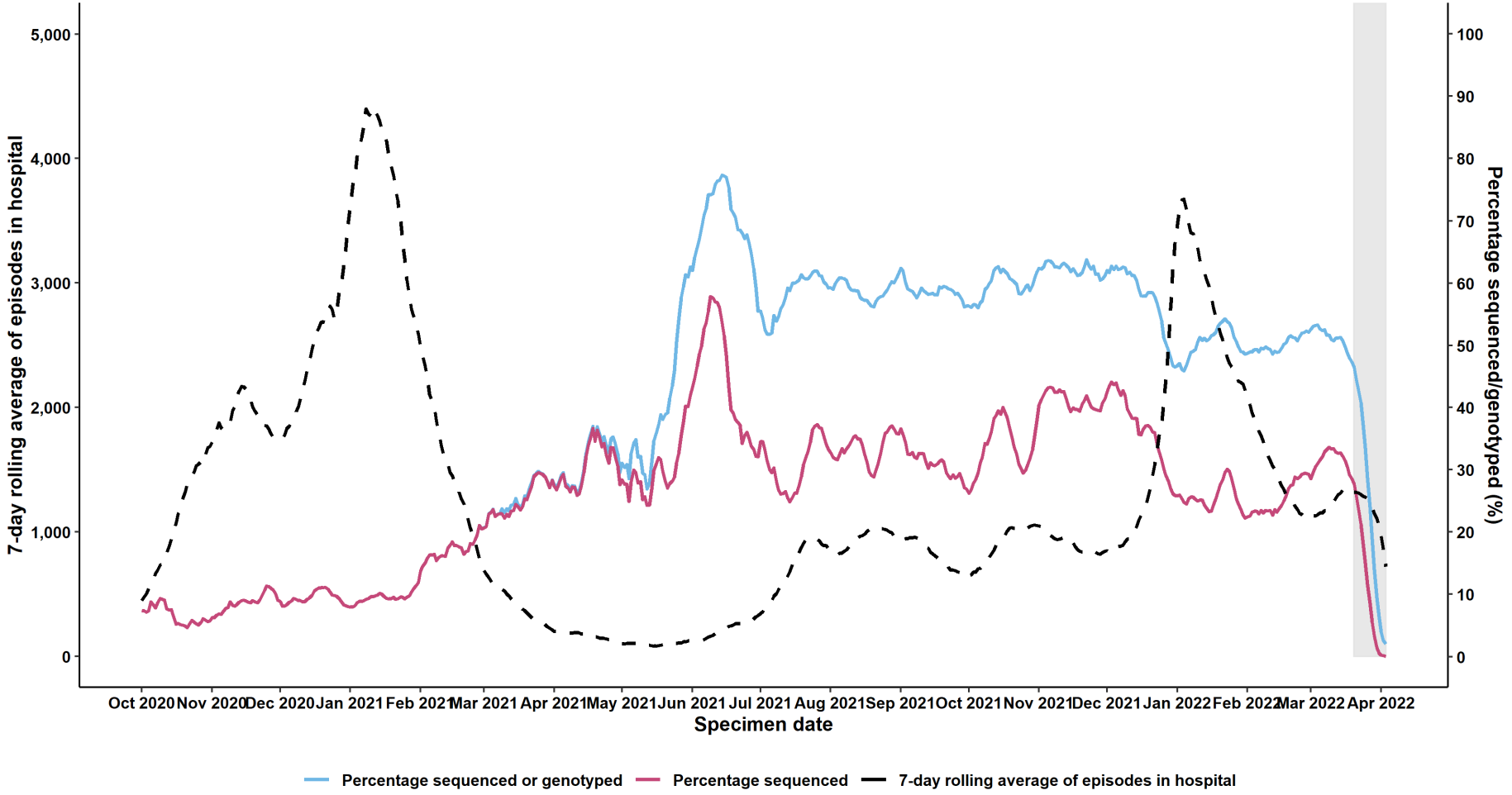
Episodes where the individual only tested using a lateral flow device are excluded. Grey shading was applied to the previous 14 days to account for reporting delays in sequencing data. (The data used in this graph can be found in the accompanying spreadsheet.)

Figure 2. Coverage of sequencing with a valid result and genotyping over time by region (1 October 2020 to 3 April 2022)



Episodes where the individual only tested positive using a lateral flow device are excluded. Grey shading was applied to the previous 14 days to account for reporting delays in sequencing data. (The data used in this graph can be found in the accompanying spreadsheet.)

Figure 3. Coverage of sequencing with valid result and genotyping for cases who test positive in hospital (1 October 2020 to 3 April 2022)

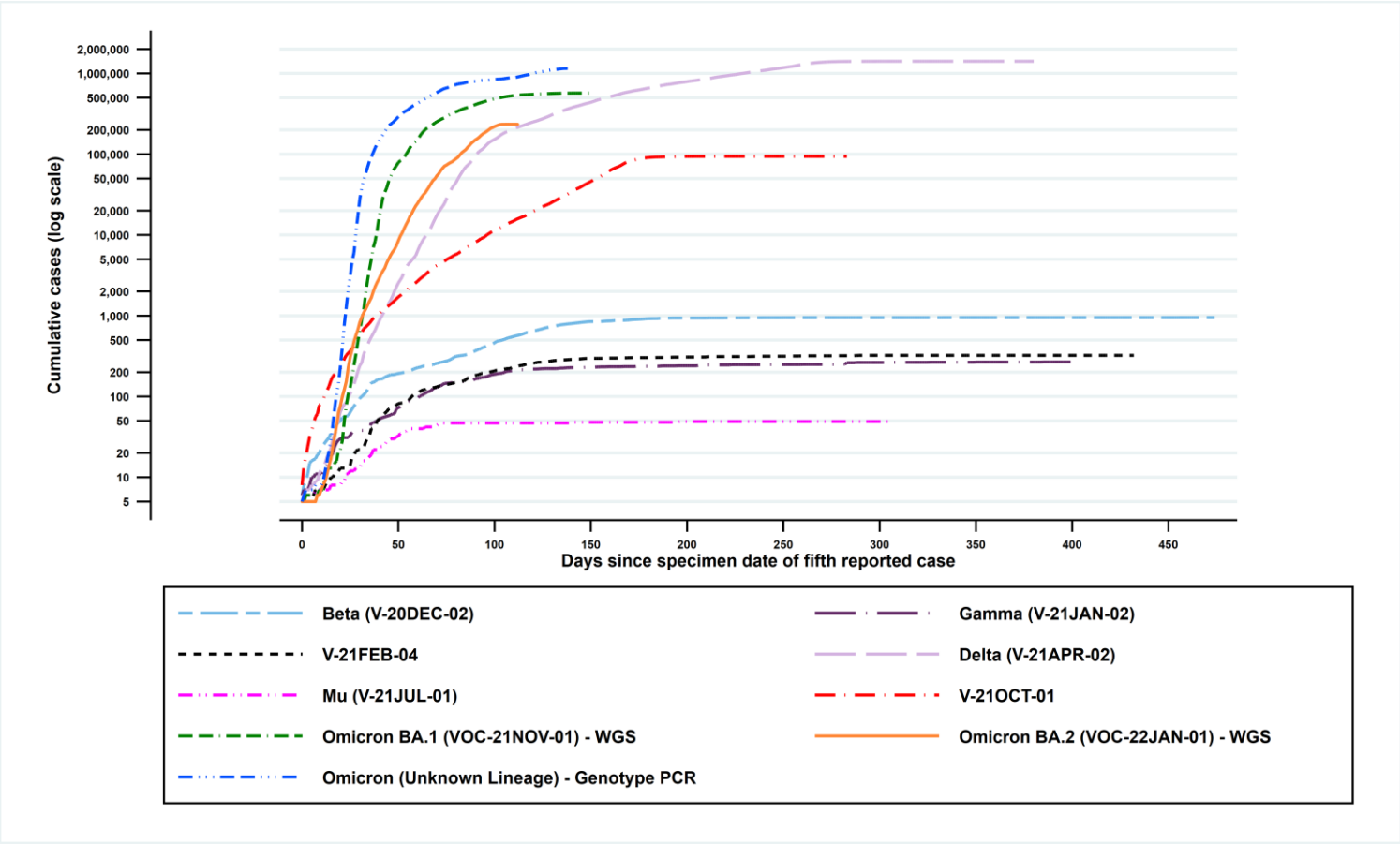


Episodes where the individual only tested positive using a lateral flow device are excluded. Grey shading was applied to the previous 14 days to account for reporting delays in sequencing data. (The data used in this graph can be found in the accompanying spreadsheet.)

1.2 VOC and variant overview

Summary epidemiology for each variant and case numbers are updated online. Figure 4 shows the cumulative number of cases per variant indexed by days since the first report.

Figure 4. Cumulative cases in England of variants indexed by days since the fifth reported case as of 3 April 2022



Find accessible data used in this graph in underlying data.

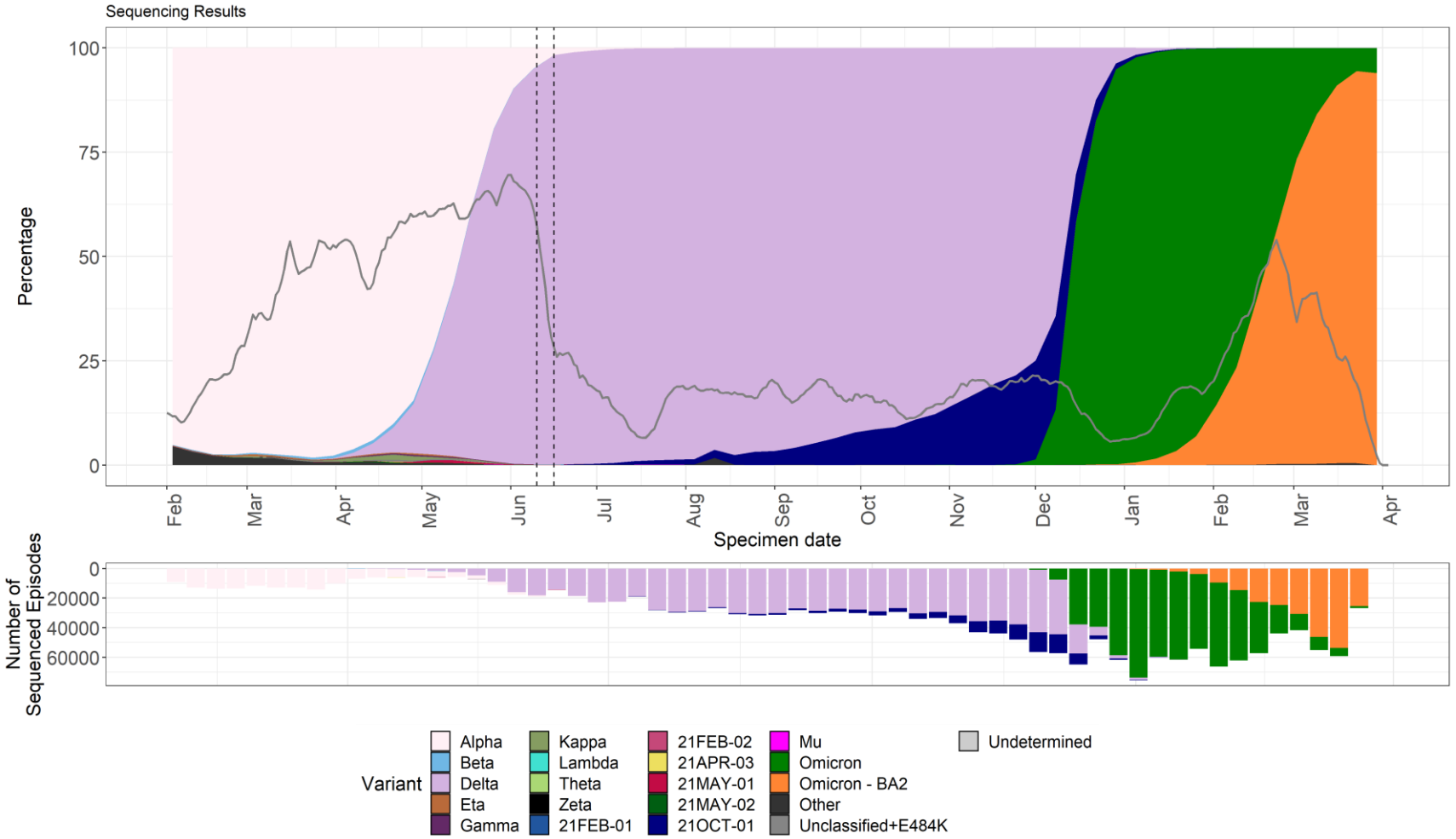
1.3 Variant prevalence

The prevalence of different variants amongst sequenced episodes is presented in Figure 5. Of the sequenced episodes from 27 March to 3 April 2022, 88.5% were Omicron lineage BA.2 (VOC-22JAN-01), 11.0% were Omicron lineage BA.1 (VOC-21NOV-01), and 0.5% were other variants.

The Omicron genome (lineage BA.1) contains the spike deletion at position 69/70 which is associated with S-gene target failure (SGTF) in some widely used PCR tests. Such PCR tests evaluate the presence of 3 SARS-CoV-2 genes: Spike (S), nucleocapsid (N) and ORF1ab. SGTF is defined as a PCR test where the N and ORF1ab genes are detected (with Ct values less than or equal to 30) but the S-gene is not. SGTF patterns can be used to assess the spread of Omicron lineage BA.1. The Omicron lineage BA.2, VOC-22JAN-01, does not generally contain the spike gene deletion and is S-gene target positive (SGTP).

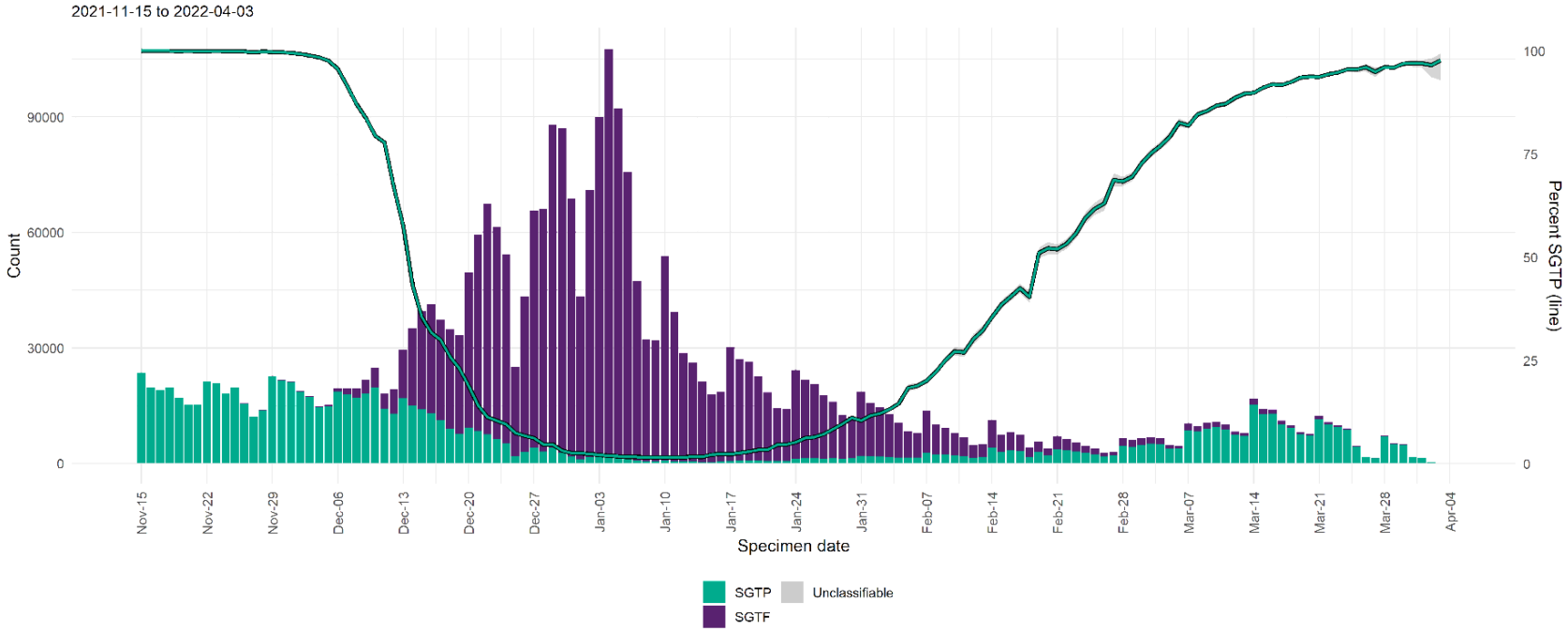
The number of COVID-19 cases with SGTP/SGTF by day, among those tested in TaqPath labs is shown in Figure 6. From 28 March to 3 April 2022 there have been 20,952 tests that have been tested for S-gene. In line with the Government's 'Living with COVID-19' plan, access to free community COVID-19 testing (under Pillar 2), covering PCR tests for symptomatic infections and lateral flow tests for asymptomatic infections, ended on 1 April 2022 with a resulting decrease in the number of specimens tested Between 1 and 3 April 2022, 1,899 samples were tested for S-gene.

Figure 5. Variant prevalence of available sequenced cases for England from 1 February 2021 as of 5 April 2022



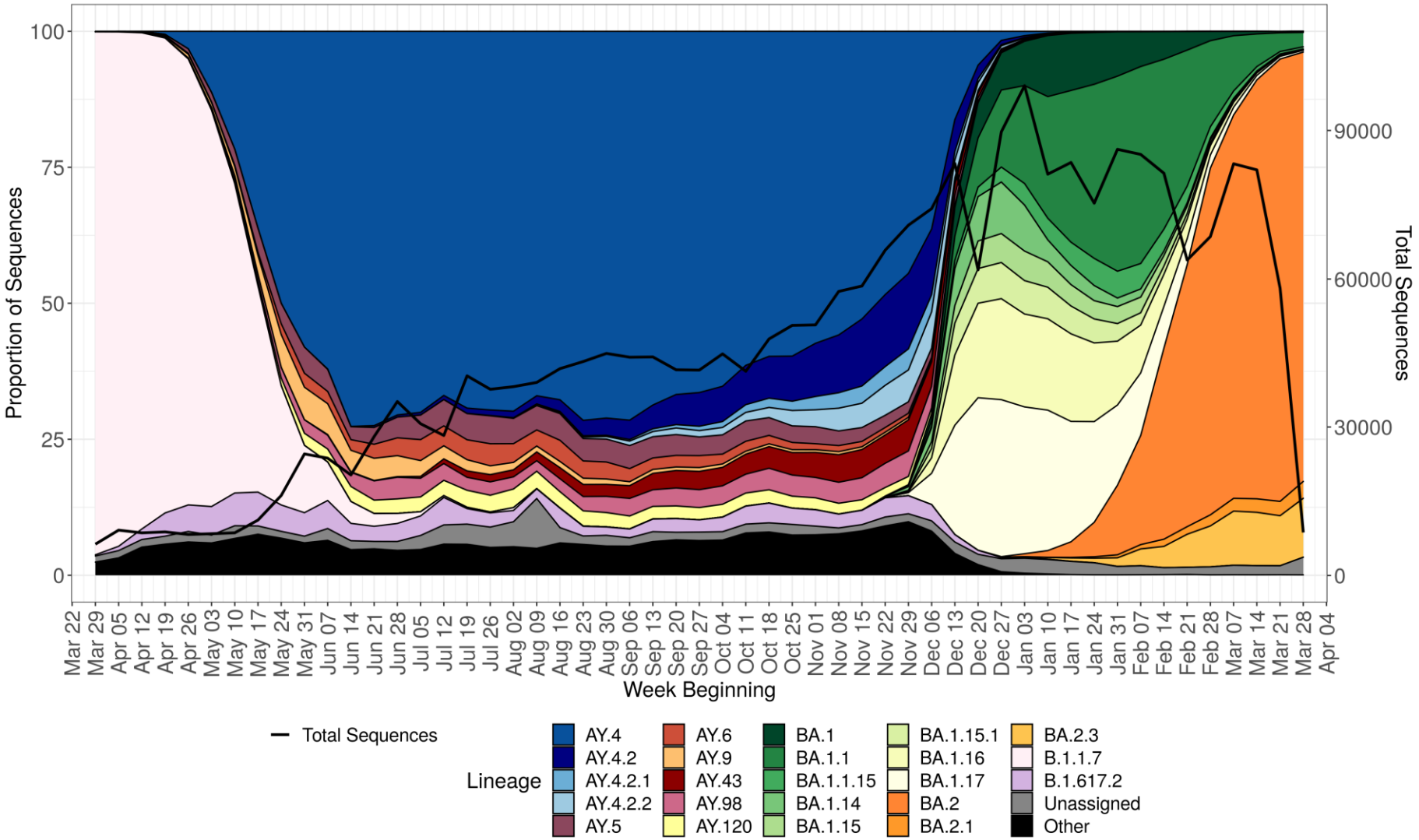
Find accessible data used in this graph in underlying data. Dashed lines indicate period incorporating issue at a sequencing site. Grey line indicates proportion of cases sequenced. Note recombinants, such as XE, are not specified but are largely within the 'other' group currently as numbers are too small.

Figure 6. Number of COVID-19 cases with SGTP/SGTF by day, among those tested in TaqPath labs as of 5 April 2022



Ninety-five percent confidence intervals indicated by grey shading. Percentage for most recent day shown.
Find accessible data used in this graph in underlying data.

Figure 7. Prevalence of Pangolin lineages in the United Kingdom (UK) with sequence data from 1 April 2021 to 3 April 2022



The ‘Other’ category in Figure 7 includes genomes where the quality is insufficient to determine variant status and genomes that do not meet the current definition for a variant or VOC.

The total number of valid sequence results per week is shown by the black line. Only lineages with more than 5,000 sequences and accounts for >=2% of sequences within at least one week 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’. Sequences where Pangolin could not assign a lineage due to poor quality data are assigned ‘None’ in this plot. XE is not currently is not currently at a high enough proportion so is included in Other in this plot. Find accessible data used in this graph in underlying data.

Part 2. Newly designated variants

2.1 BA.4 and BA.5 variants within the Omicron lineage

Two new variants were identified as part of horizon scanning on 4 April 2022. Work is underway to precisely define the phylogeny of these variants. These have been designated as lineages BA.4 and BA.5 and classified by the VTG on 6 April 2022, as V-22APR-03 and V-22APR-04, respectively.

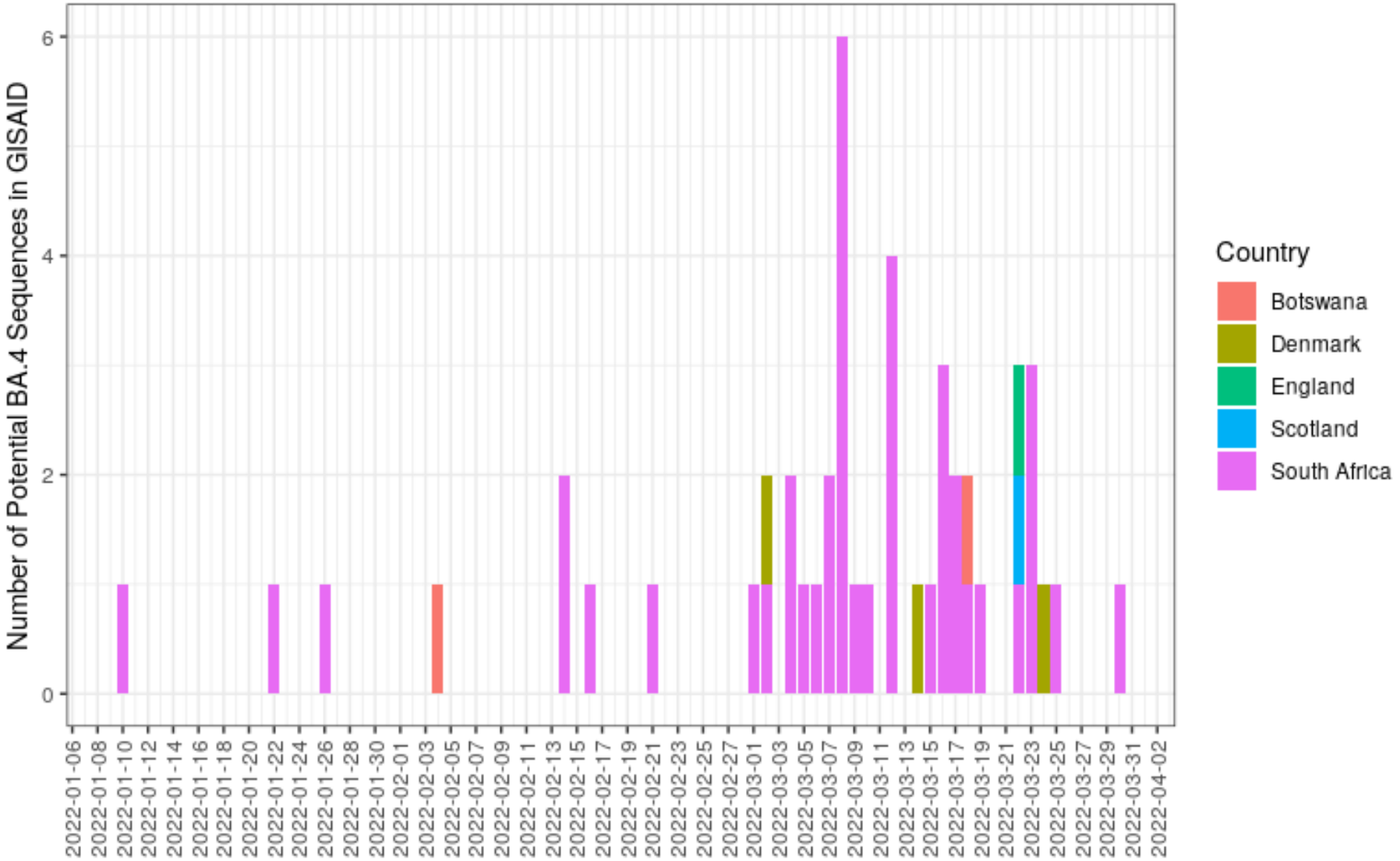
V-22APR-03 shares all mutations/deletions with the BA.2 lineage except the following: NSP4: L438F reverted to WT (wild type); S: 69/70 deletion, L452R, F486V, Q493 (WT); ORF 6: D61 (WT); ORF 7b: L11F; N: P151S. The spike 69/70 deletion will result in an undetectable S-gene target (S-gene target failure) in the Taqpath assay.

The earliest BA.4 sample in GISAID was from South Africa with a sample collection date of 10 January 2022. However, Figure 8 shows the accumulation of genomes and geographic spread is more recent. Countries reporting BA.4 genomes via GISAID now include South Africa (41 genomes), Denmark (3), Botswana (2) and England and Scotland reporting one each. Although the number of total genomes is small, the apparent geographic spread suggests that the variant is transmitting successfully.

BA.5 shares the same mutations/deletions as BA.4 except the following: M: D3N; ORF 7b: L11 (WT); N: P151 (WT); synonymous SNPs: A27038G, and C27889T.

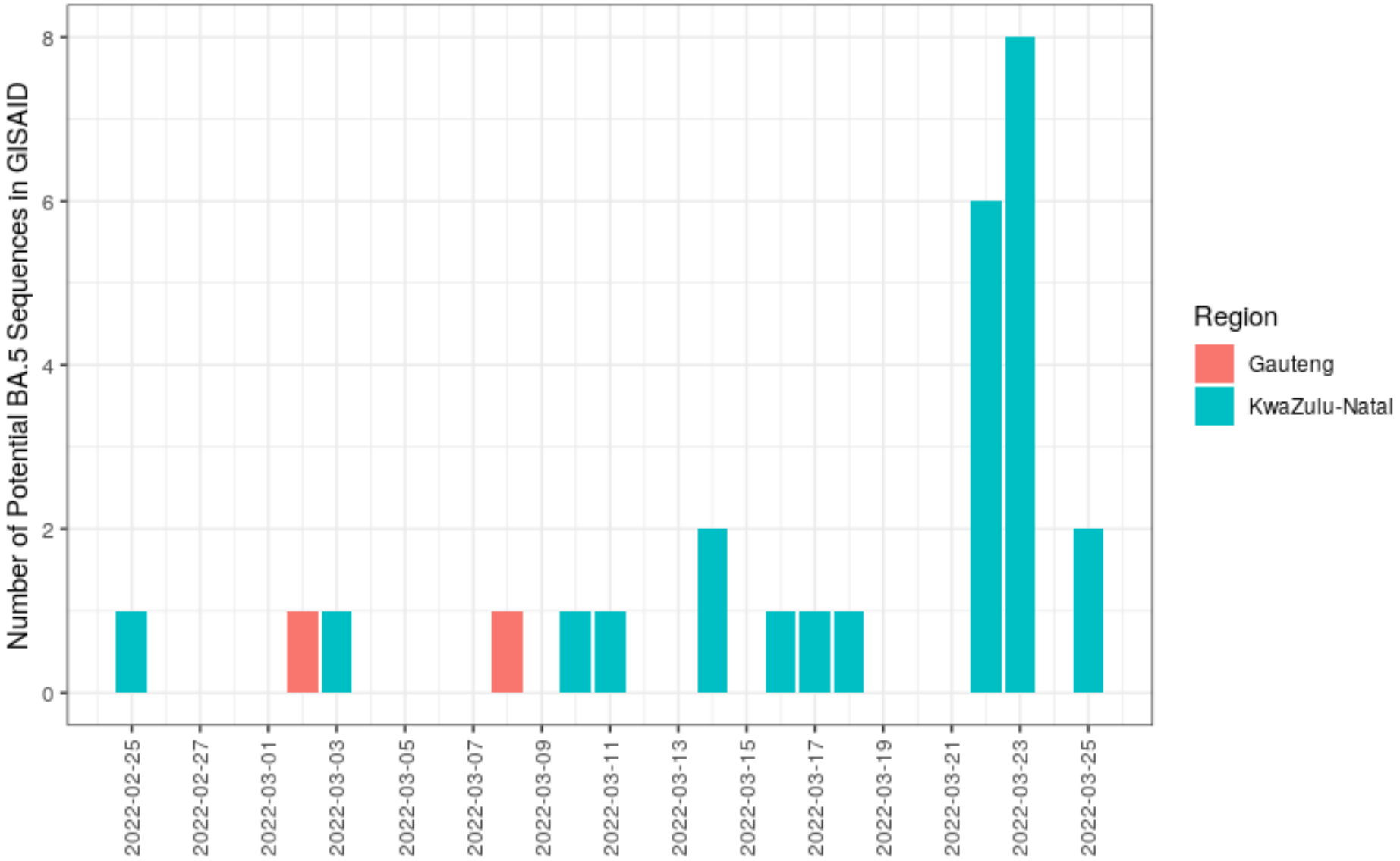
Currently there are 27 sequences reported with this lineage, all from South Africa. This lineage shows sample dates between 25 February and 25 March 2022 (Figure 9).

Figure 8. BA.4 (V-22APR-03) sequences by date of sample collection, from GISAID



Find accessible data used in this graph in underlying data.

Figure 9. BA.5 (V-22APR-04) sequences by date of sample collection, from GISAID



Find accessible data used in this graph in underlying data.

2.2 Designated recombinant lineages

Whilst recombinant lineages generally are monitored through horizon scanning, UKHSA has classified XD and XE recombinant lineages as variants V-22APR-01 and V-22APR-02, respectively. XD has been classified a variant (V) on the basis of the data published from France, suggesting that it may be biologically distinct. XE has been classified a variant (V) based on apparent continued growth within the UK.

XD has an Omicron BA.1 S gene incorporated into a Delta AY.4 genome with break points at approximate nucleotide positions 21,643 and 25,581. XD also contains the unique mutation NSP2: E172D. In total, 68 XD samples were identified on 1 April 2022 in GISAID, of which 66 were from France and one each from The Netherlands and Belgium. To date no samples have been assigned to the XD lineage in the UK.

XE is a BA.1 and BA.2 recombinant (containing BA.1 mutations for NSP1-6 and BA.2 mutations for the rest of the genome). It also has 3 mutations that are not present in all BA.1 or BA.2 sequences: NSP3 V1069I (non-synonymous) and C3241T (synonymous), and NSP12 C14599T (synonymous).

As of 5 April 2022, there are 1,179 XE sequences in the UK data with 1,125 XE cases in England.

2.3 Epidemiology of XE (V-22APR-02)

Cases are geographically distributed across England and increasing in number, with the first case detected via sequencing on 19 January 2022, and most cases in East of England, London, and the South East.

Figure 10. Age-sex pyramid of Recombinant XE (BA.1 and BA.2) cases as of 5 April 2022

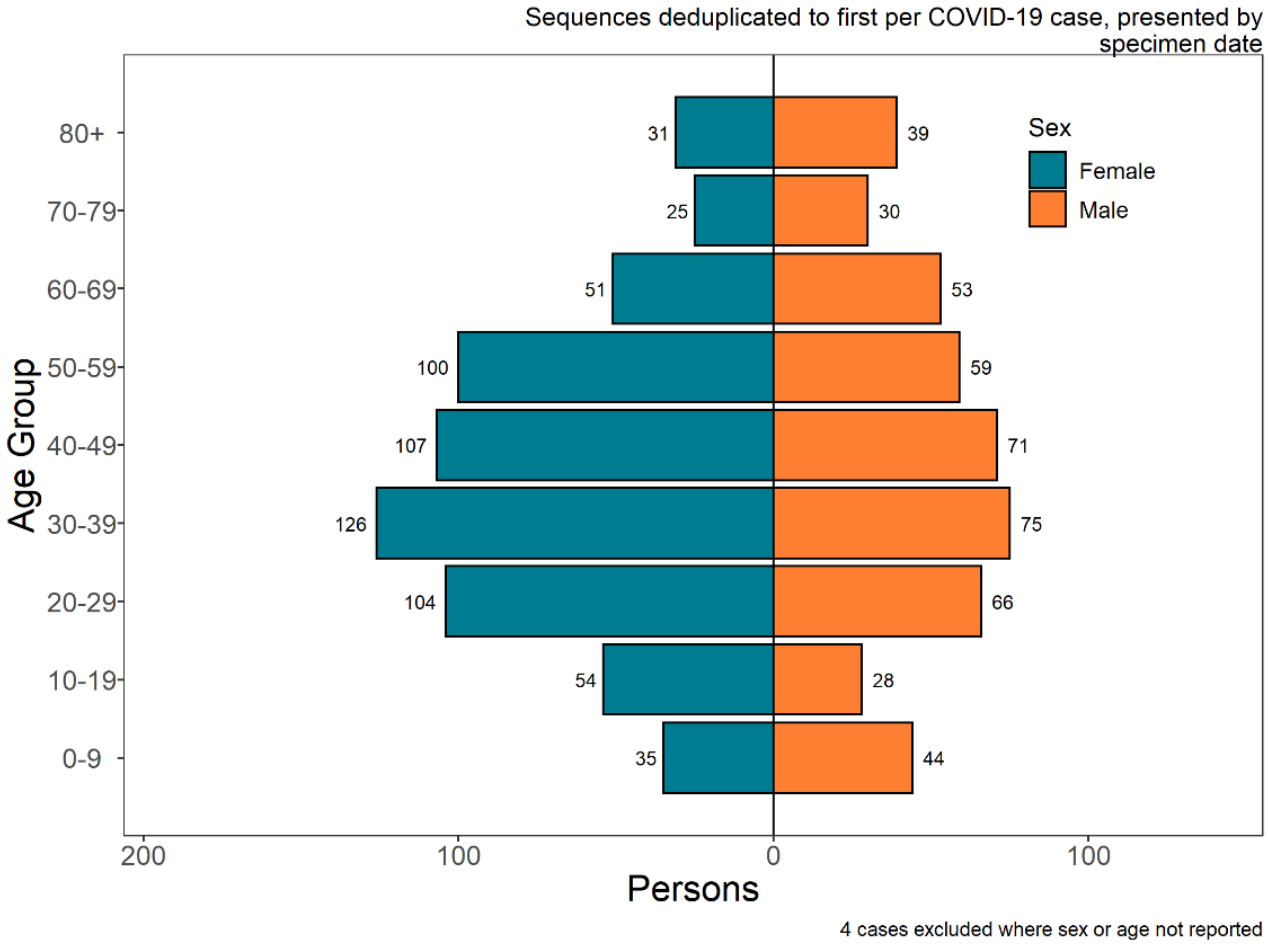
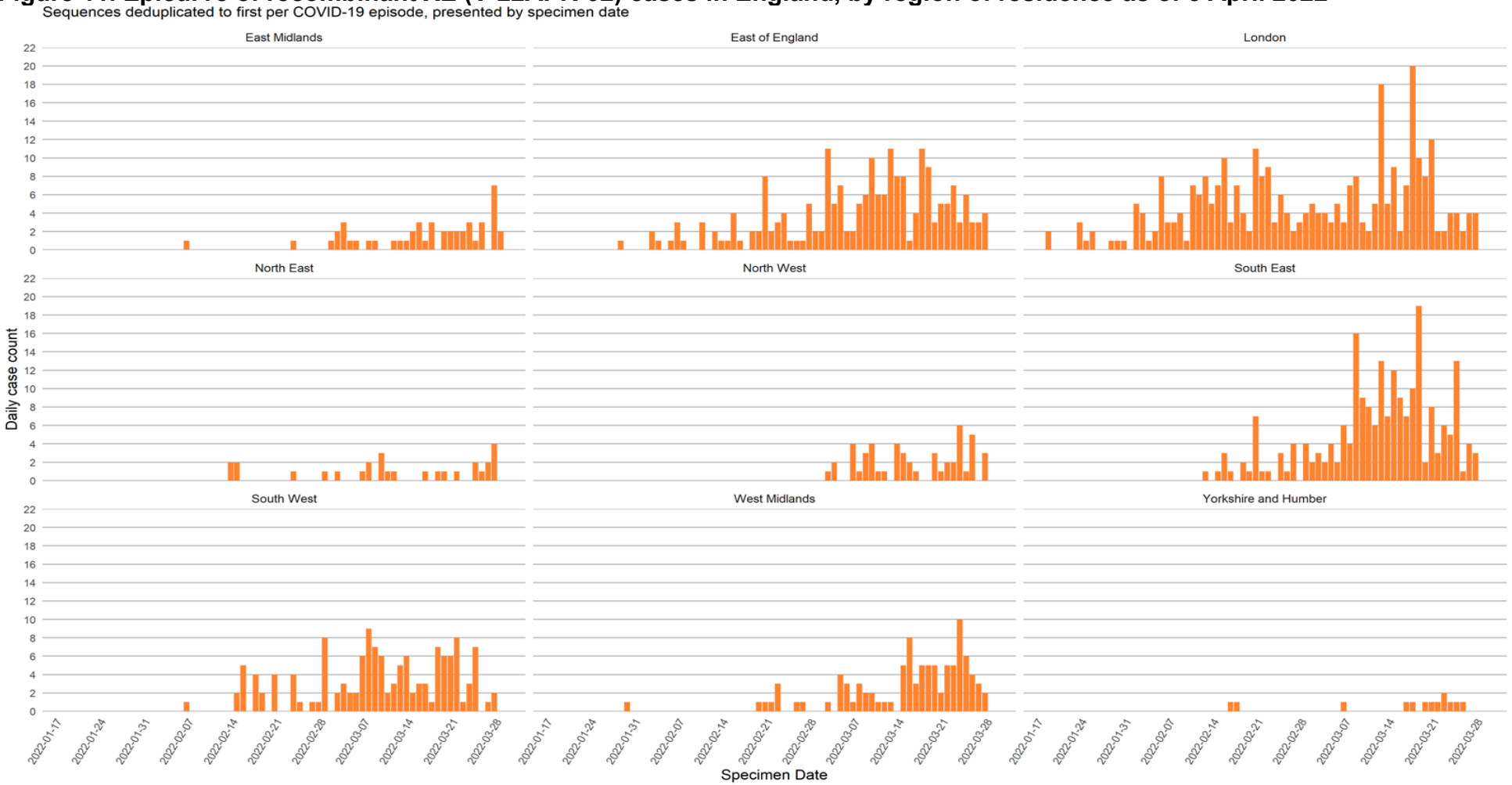


Figure 11. Epicurve of recombinant XE (V-22APR-02) cases in England, by region of residence as of 5 April 2022



Find accessible data used in this graph in underlying data. Twenty-six cases not included due to missing linkage data.

2.4 Growth rate for XE (V-22APR-02)

The growth rate of a novel variant is calculated relative to a matched control. Matched controls are samples of other circulating variants selected from the same time and location. For XE, genomes identified as XE using a draft mutation-based definition are compared to co-circulating BA.2 only.

We run a statistical model to calculate the probability of a sampled genome being from the novel variant vs from the control over time. Growth rates are calculated per week or per day and are expressed on a log scale. A logistic growth rate of 0.5 per week indicates that the variant is increasing by a multiplicative factor of exp (0.5) =1.65 per week in comparison to the control. A logistic growth rate of zero would indicate no difference in growth rates between the 2 variants.

Using a control adjusts for geographic and temporal variation in case numbers, but despite these adjustments, differences in growth rates can be due to epidemiological factors such as founder effects and sampling, especially early on. Over time, the growth rate of a variant will converge towards an estimate of the variant's inherent transmissibility in comparison to other circulating variants.

The growth rate is estimated by logistic regression of the number of genomes sampled with the XE and BA.2 lineages on time of sample collection. Only Pillar 2 testing (community testing) samples are included. To adjust for geographic variation in case growth rates, XE growth rates were estimated relative to a geographically matched sample of BA.2 genomes.

Data sampled between 15 January 2021 and 30 March 2022 were included. The relative frequency of genomes from the BA.2 lineage is shown in Figure 12. The median growth rate is +12.6% per week over that time period, but in the last 3 weeks, the growth rate was +20.9% (Figures 12 and 13). Patterns across regions are inconsistent and not reported.

Figure 12. Sample frequency of XE (V-22APR-02) relative to Omicron (BA.2) over time sampled through Pillar 2 testing

Supplementary data is not available for this figure.

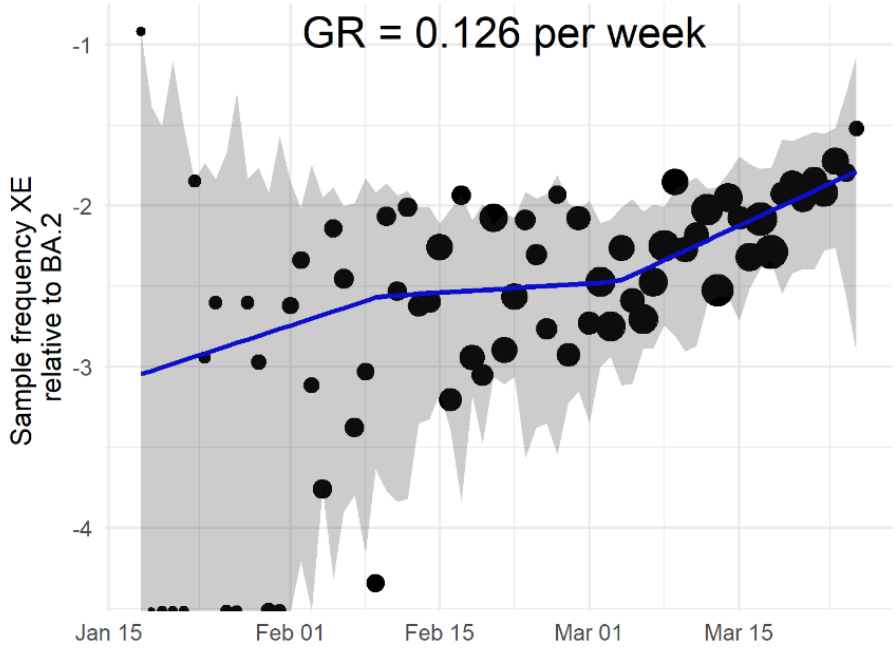
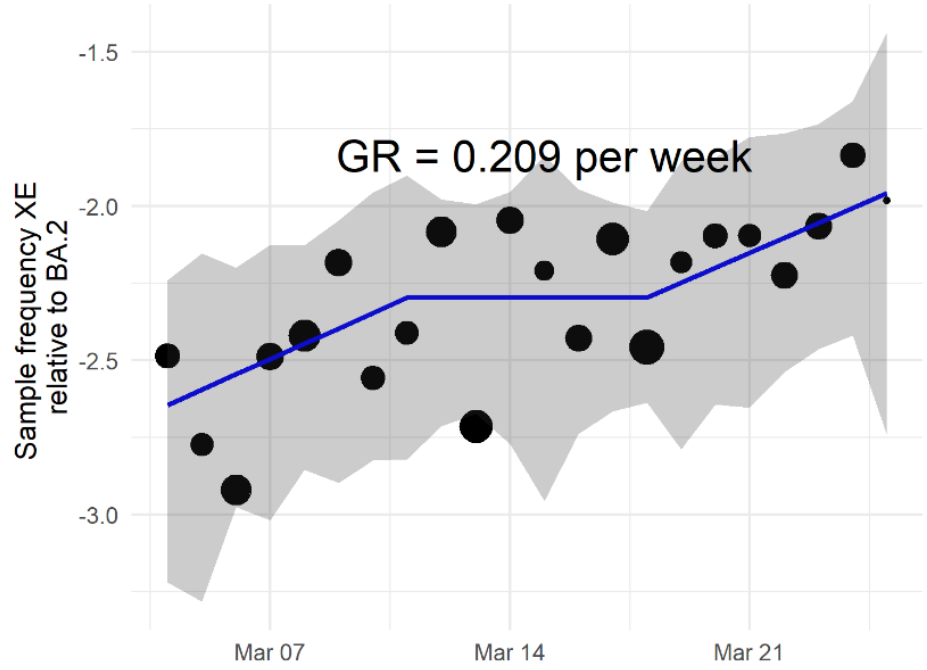


Figure 13. Sample frequency of XE (V-22APR-02) relative to Omicron (BA.2) sampled through Pillar 2 testing over the 3 weeks leading to 30 March 2022

Supplementary data is not available for this figure.



Part 3. Enhanced analysis of VOC-22JAN-01 (BA.2)

The mutation profile of the Omicron sub-lineages was previously reported in Technical Briefing 31.

BA.2 has been reclassified as a VOC under the new classification on 1 April 2022.

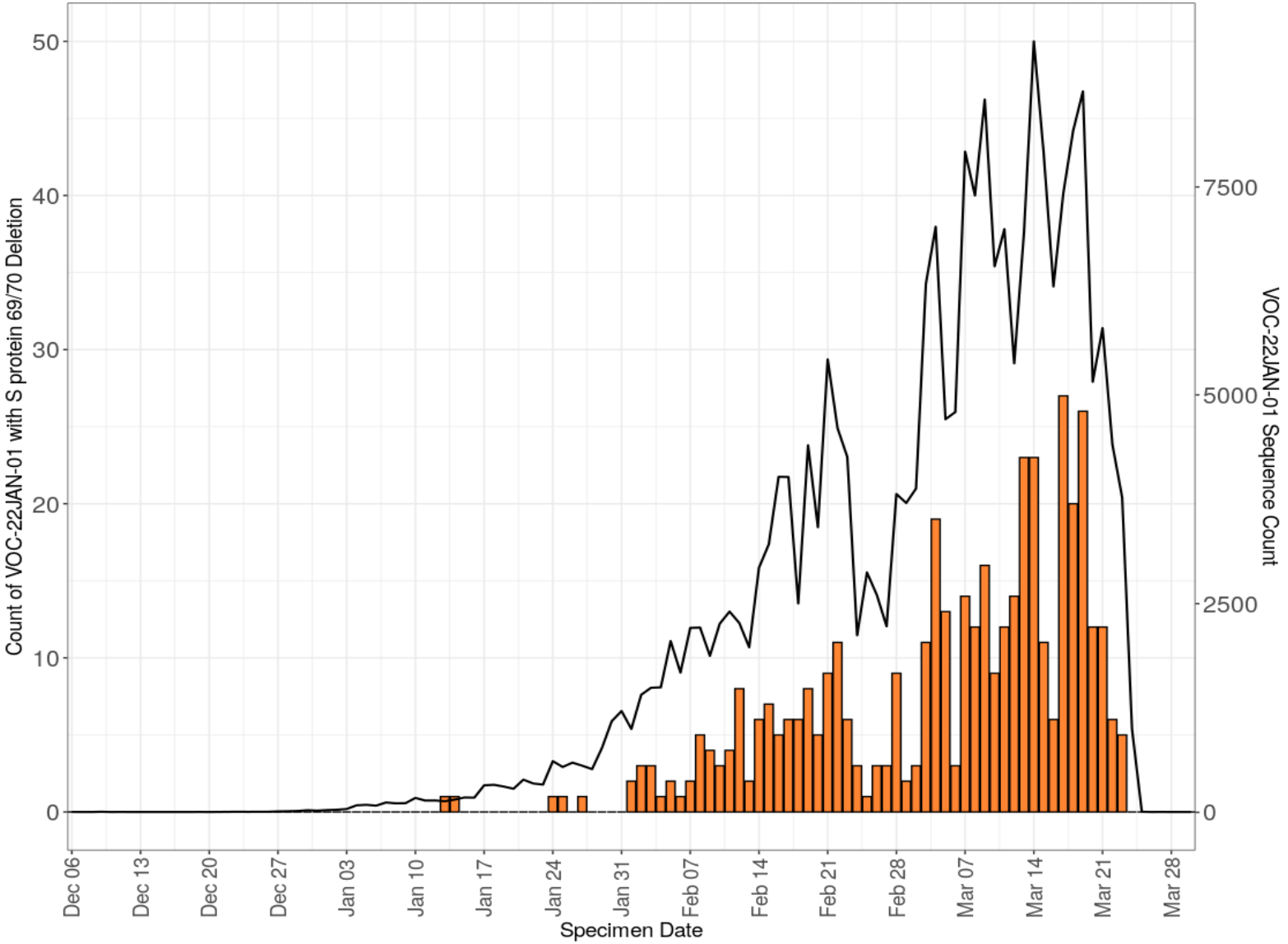
3.1 Genomic diversity

S-gene 69/70 deletion

Currently, SGTF is a suitable proxy for the VOC-21NOV-01 (BA.1) variant due to the deletion of amino acids at position 69 and 70 of the S protein for laboratories using the specific assays. The deletion is not present in the VOC-22JAN-01 (BA.2) definition, although recently a number of VOC-22JAN-01 (BA.2) sequences containing the deletion have been identified. As of 30 March 2022, a total of 516 VOC-22JAN-01 (BA.2) sequences were detected with the deletion in the UK genome data, out of a total of 320,144 confirmed or probable VOC-22JAN-01 (BA.2) sequences.

This represents 0.16% of the VOC-22JAN-01 (BA.2) sequences. A graph of English sequences, where specimen date is available is shown in Figure 14. The frequency of detections of VOC-22JAN-01 (BA.2) sequences with 69/70 deletion tracks the total number of sequences available. The correlation between the S-gene target results, deletion and Omicron lineages will be monitored. Of the 516 sequences most are concentrated in the East Midlands, East of England and South East.

Figure 14. Daily count of confirmed VOC-22JAN-01 (BA.2) sequences in England containing S-gene 69/70 deletion that can be called (bar), alongside the number of England VOC-22-JAN-01 sequences (line), where specimen dates are available



Find accessible data used in this graph in underlying data.

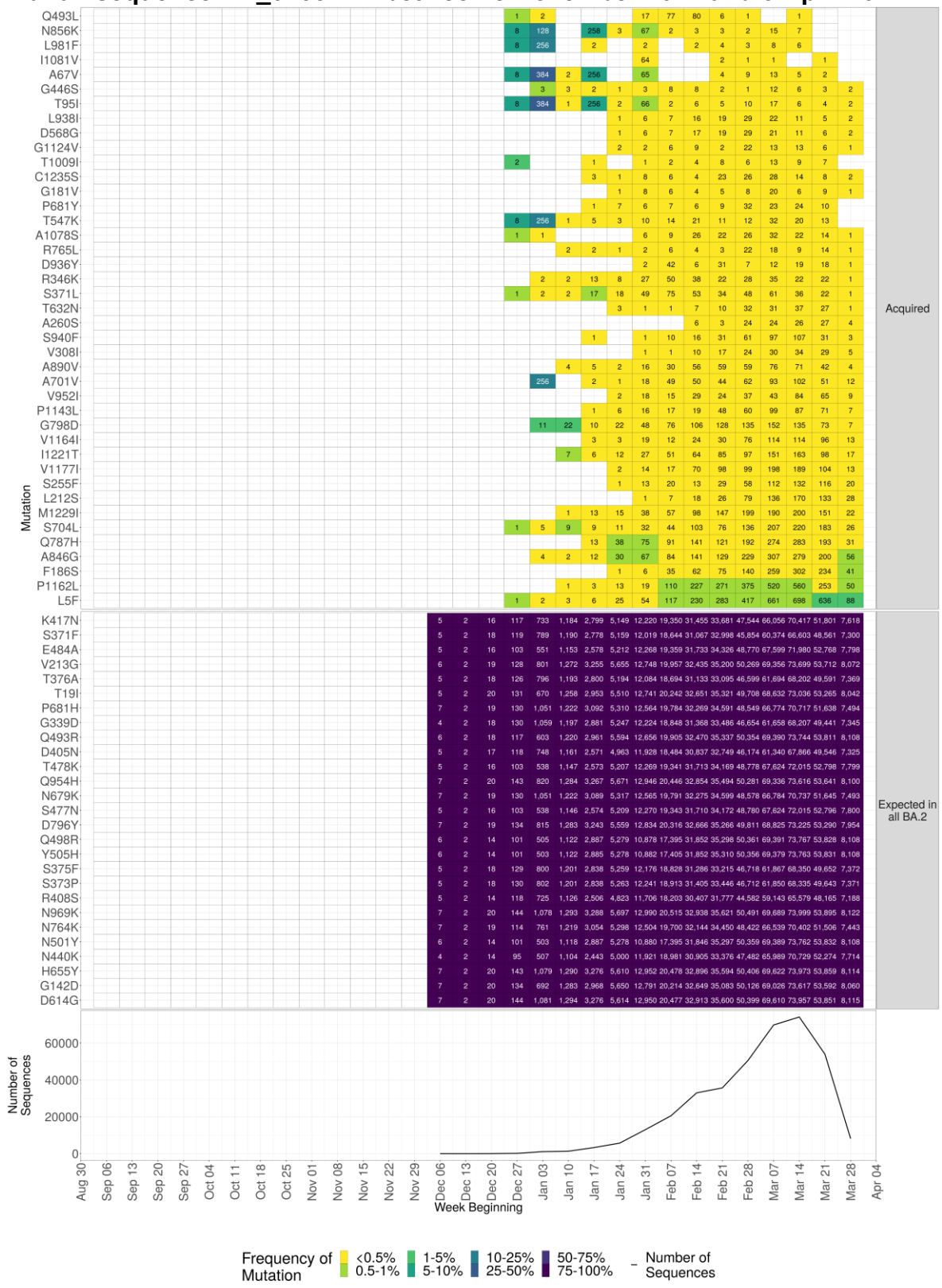
Diversity in Spike

Spike mutations are monitored within BA.2 using 4 criteria (Table 2). A mutation is investigated further if it meets more than one of these criteria and is present in at least 10 sequences. Forty-one additional mutations have been observed in BA.2 sequences according to the criteria in Table 2 (Figure 15). The criteria for mutation monitoring are currently being reviewed and amended.

Table 2. Criteria used to assess emerging mutations

Criteria	Threshold
Cumulative count	Running total for the number of sequences containing mutation is at least 50
Proportion	1% of sequences classified as this variant contain this mutation within a single week
Difference in proportion	The difference in the proportion of sequences in 2 consecutive weeks is at least 0.25%
Percentage change in the number of sequences	The percentage change between the number of sequences containing the mutation in 2 consecutive weeks is at least 5%

Figure 15. Spike mutations found in BA.2 genomes in the UK dataset relative to the Wuhan sequence NC_045512.2 between 8 November 2021 and 3 April 2022

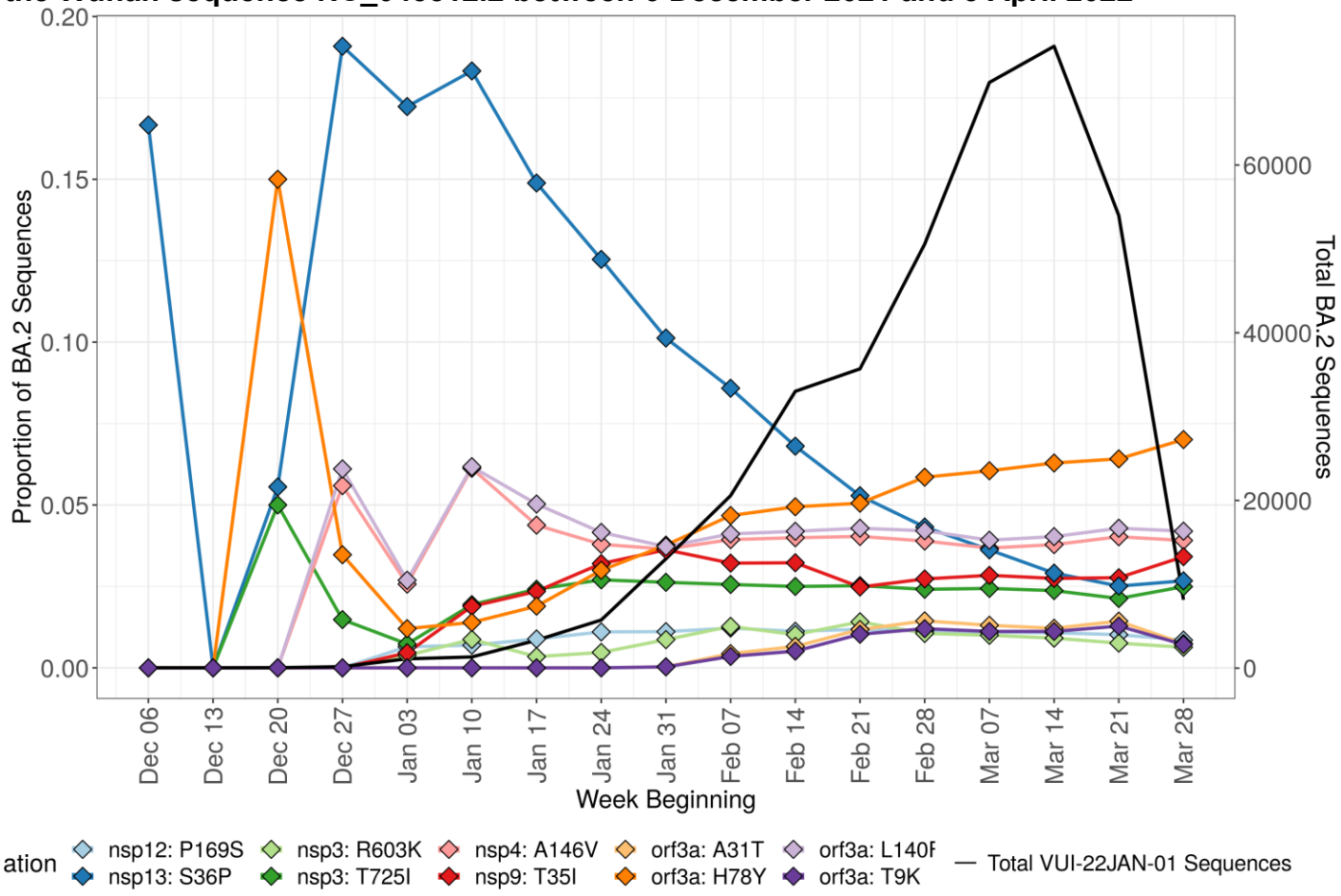


Find accessible data used in this graph in underlying data.

It should be noted all mutations in the sequence alignment are reported in these plots for review purposes.

Outside of Spike, there are 10 mutations that are present in at least 1% of BA.2 sequences for 3 consecutive weeks (Figure 16). One of these (nsp13: S36P) has been declining since December 2021.

Figure 16. Proportion of sequences containing mutations found in BA.2 genomes that are present in at least 1% of sequence for 3 consecutive weeks in the UK dataset relative to the Wuhan sequence NC_045512.2 between 6 December 2021 and 3 April 2022

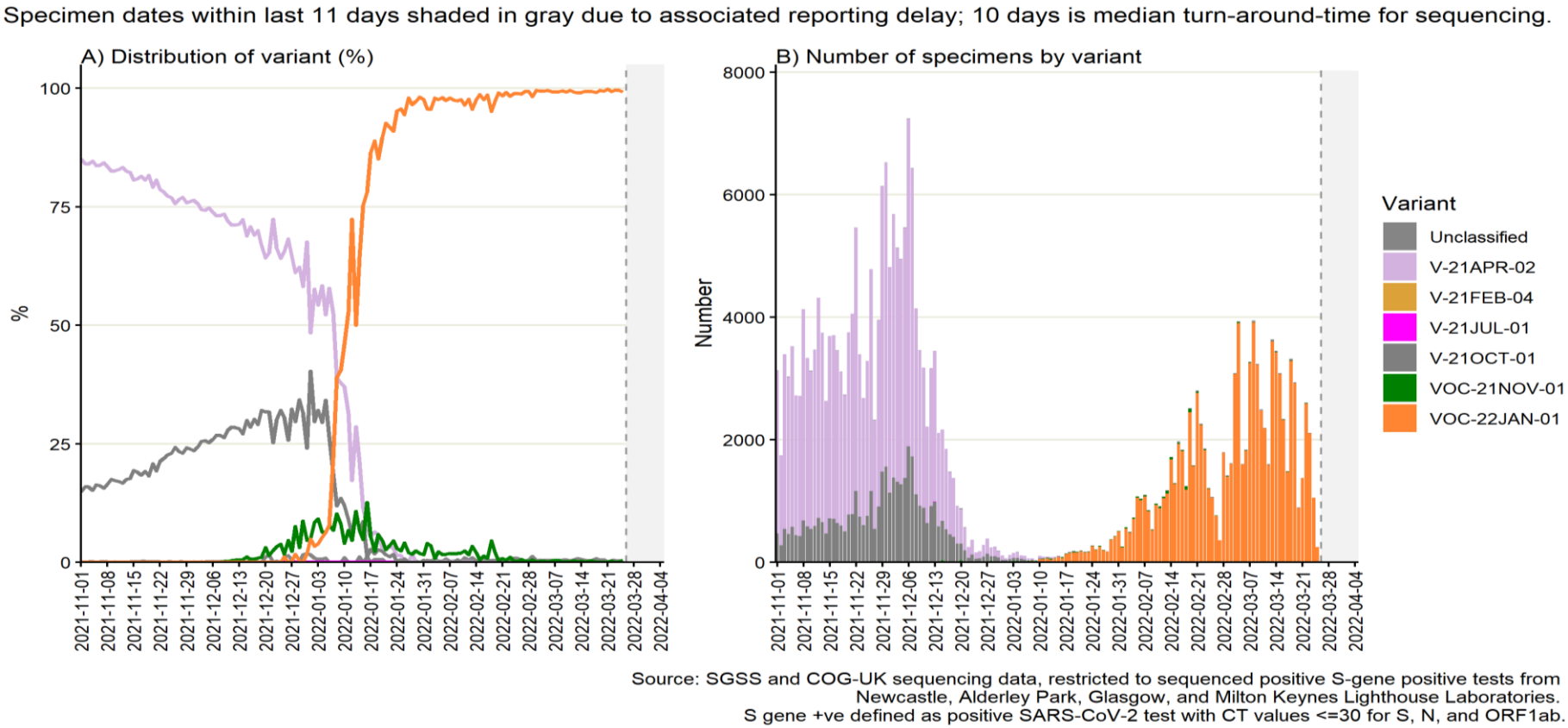


The total number of BA.2 mutations per week are indicated by the black line.
(Find accessible data used in this graph in underlying data.)

Epidemiology of SGTP

The Omicron sub-lineage VOC-22JAN-01 (BA.2) rarely contains the spike deletion and therefore is SGTP. VOC-22JAN-01 (BA.2) has accounted for more than 95% of sequenced SGTP from 27 January to 25 March 2022.

Figure 17. Number and distribution of variants per week among sequenced SGTP specimens as of 5 April 2022
Find accessible data used in this graph in underlying data.



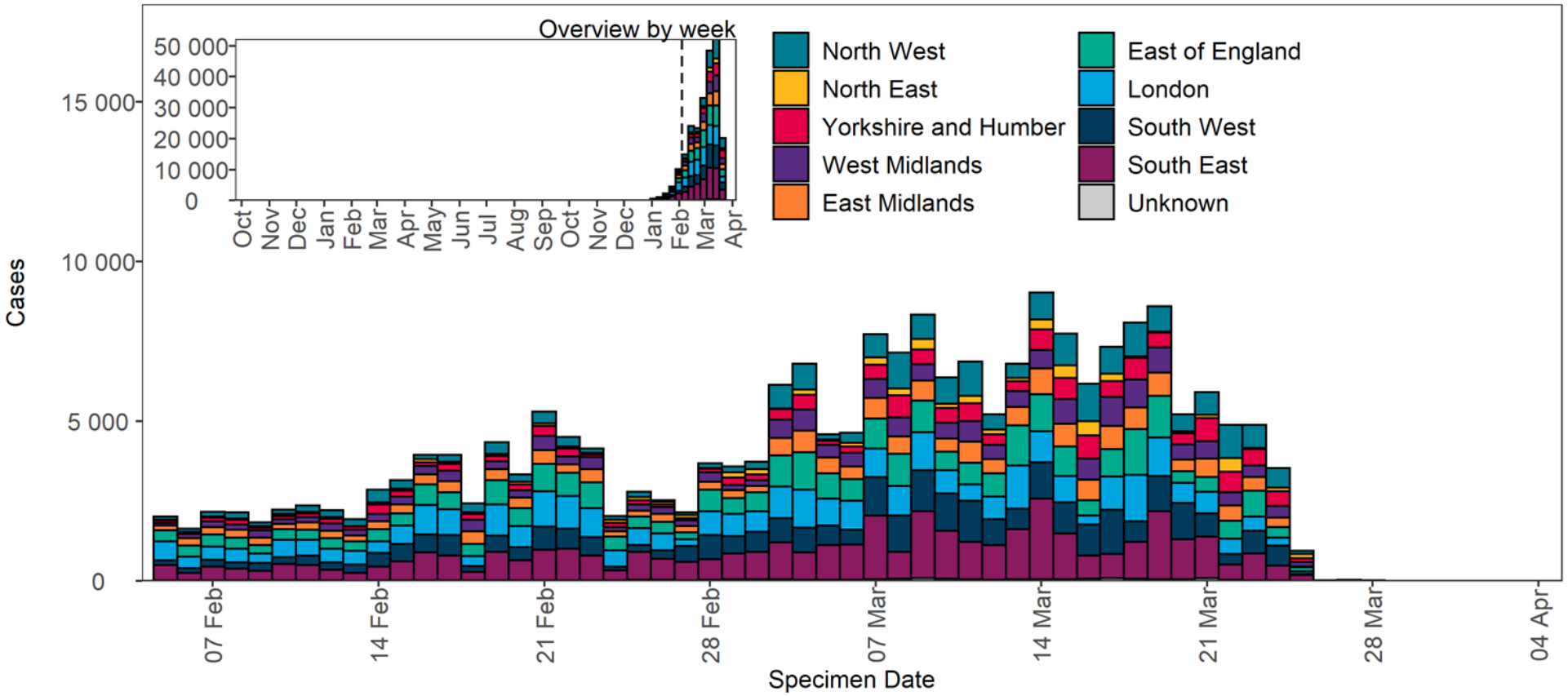
3.2 Epidemiology

As of 5 April 2022, 234,650 sequences of VOC-22JAN-01 (BA.2) have been identified by sequencing in England. Therefore, there is a known time lag of 11 days (interquartile range: 9 to 18) from obtaining a sample to reporting of VOC-22JAN-01 (BA.2) as the cause of infection. This will be reflected in the case numbers presented.

Table 3. Number of confirmed VOC-22JAN-01 (BA.2) cases, by region of residence as of 5 April 2022

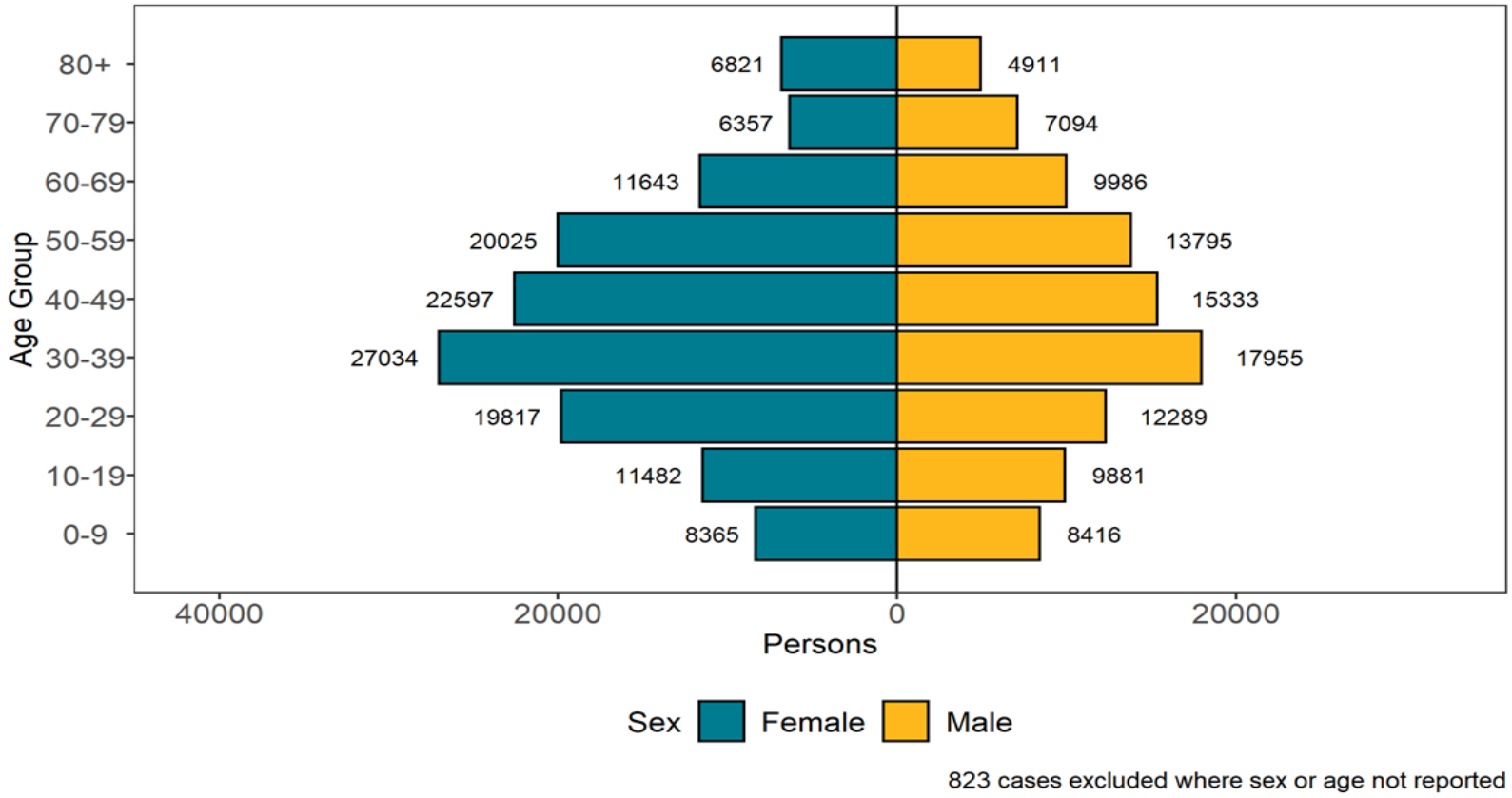
Region	Total case number	Case proportion
East Midlands	20,406	8.7%
East of England	32,518	13.9%
London	37,925	16.2%
North East	6,018	2.6%
North West	23,009	9.8%
South East	46,492	19.8%
South West	31,526	13.4%
West Midlands	19,521	8.3%
Yorkshire and Humber	15,417	6.6%
Unknown region	1,818	0.8%
Total	**234,650**	**-**

Figure 18. Confirmed VOC-22JAN-01 (BA.2) cases by specimen date and region of residence as of 5 April 2022



Find accessible data used in this graph in underlying data.

Figure 19. Age-sex pyramid of VOC-22JAN-01 (BA.2) cases as of 5 April 2022



Find accessible data used in this graph in underlying data.

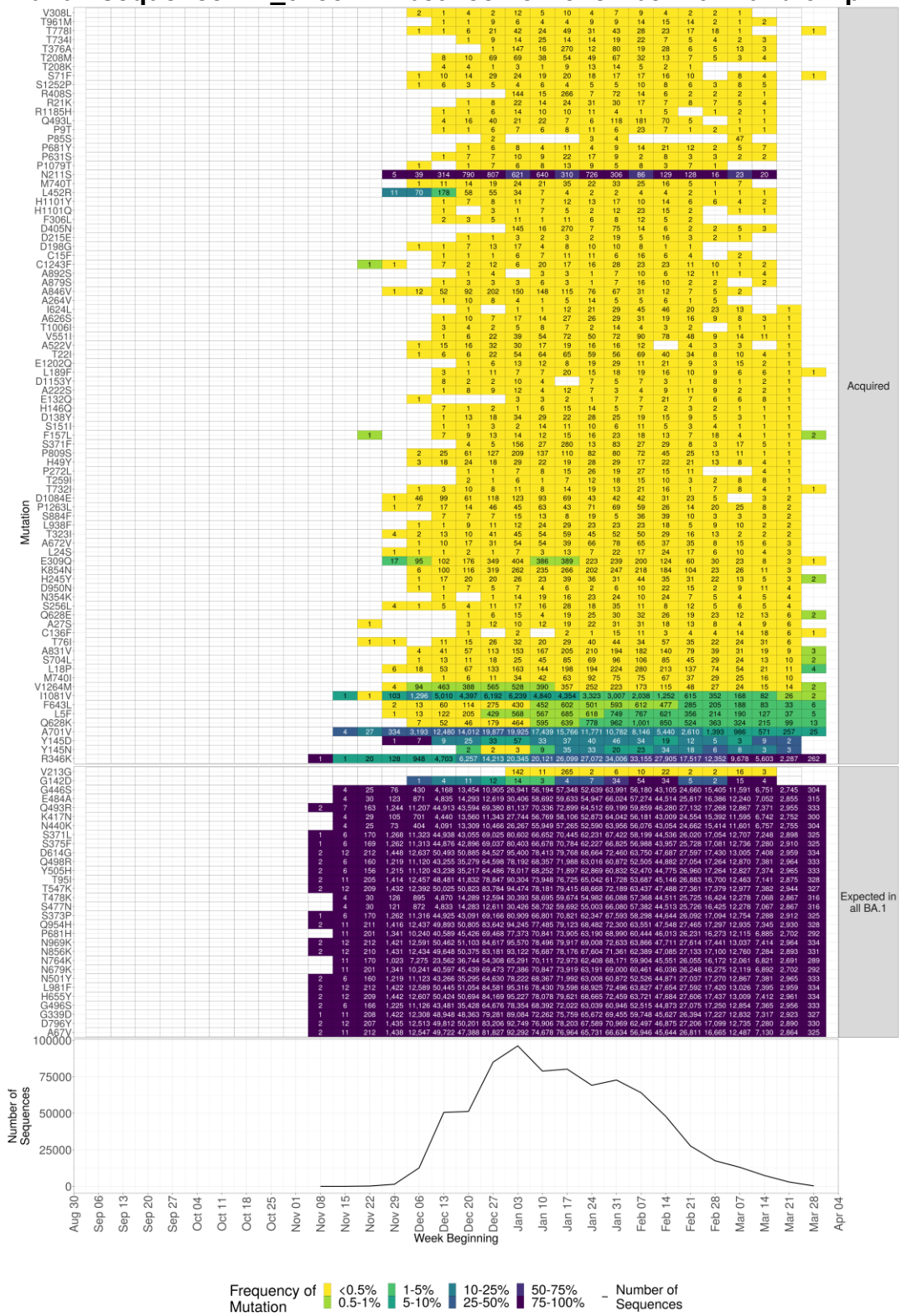
Part 4. Enhanced analyses of Omicron VOC-21NOV-01 (BA.1)

This variant was detected on GISAID on 23 November 2021 and designated B.1.1.529 on 24 November 2021. It was designated VUI-21NOV-01 by the UKHSA Variant Technical Group and on review re-designated as VOC-21NOV-01 on 27 November 2021.

4.1 Genomic diversity within Omicron VOC-21NOV-01 (BA.1)

Spike mutations are monitored within BA.1 using 4 criteria (Table 2). Eighty-four additional mutations have been observed in BA.1 sequences according to the criteria in Table 2 (Figure 20). The presence of Y145D/N, L452R and N211S may be artefactual. L452R may be due to low level contamination with Delta sequence. The mutations at position 211 and 145 are an alignment artefact caused by the deletions at these positions in Spike. These deletions also reduce the number of sequences where the positions can be called therefore artificially increasing the proportion of sequences where these mutations are present.

Figure 20. Spike mutations found in BA.1 genomes in the UK dataset relative to the Wuhan sequence NC_045512.2 between 8 November 2021 and 3 April 2022



Find accessible data used in this graph in underlying data. It should be noted all mutations in the sequence alignment are reported in these plots for review purposes. Those reported here at positions 145 and 211 arise due to base deletions affecting the sequence alignment and are artefactual.

4.2 Epidemiology

VOC-21NOV-01 currently refers specifically to the Omicron BA.1 lineage, as the BA.2 lineage is now recognized as VOC-22JAN-01. However, as genotyping cannot distinguish between BA.1 and BA.2, genotyped figures presented here may include BA.2 cases.

Epidemiology

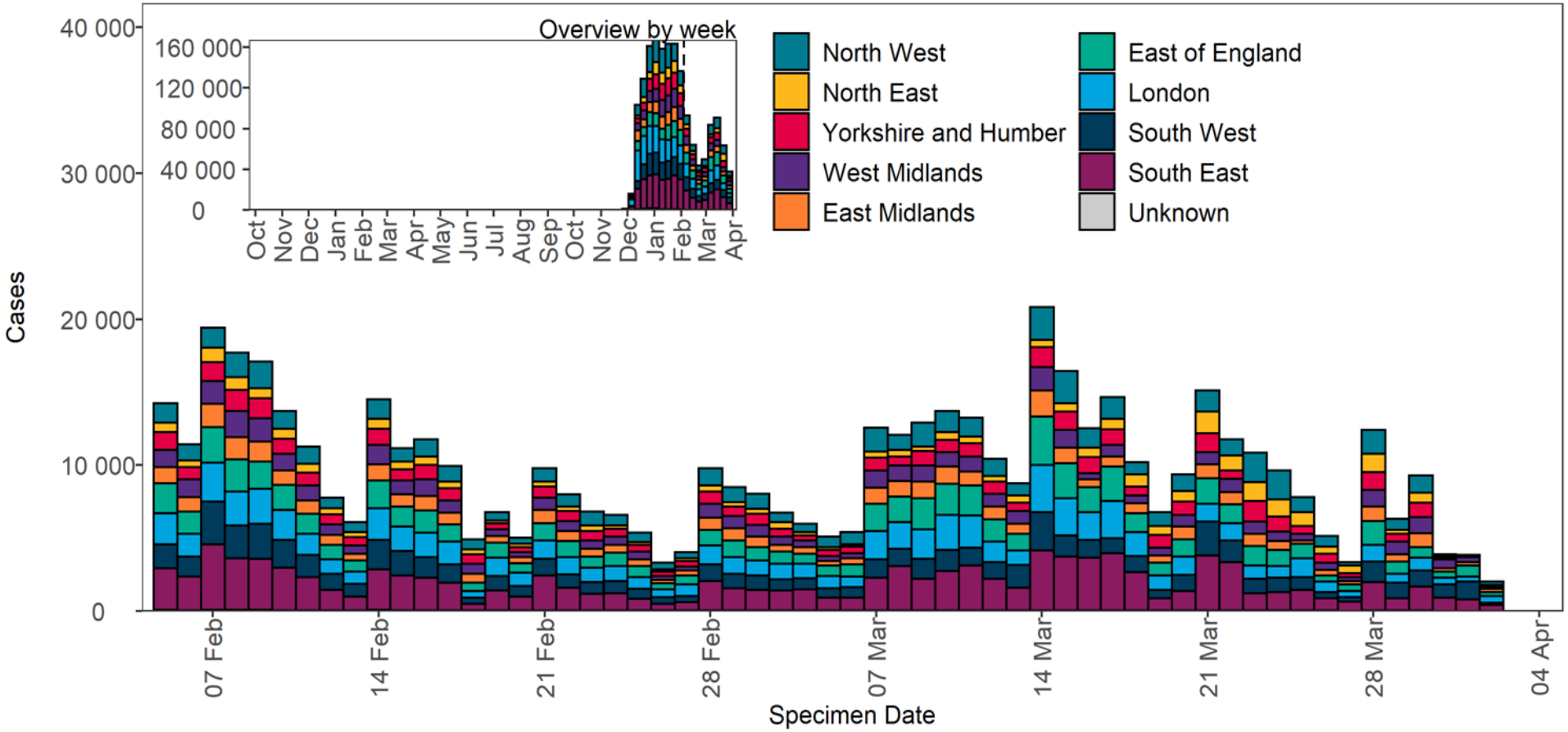
Table 6. Number of confirmed (sequenced) and probable (genotyping*) Omicron (B.1.1.529) sub-lineage BA.1 VOC-21NOV-01 cases, by region of residence as of 5 April 2022

Region	Total case number	Case proportion
East Midlands	129,922	7.5%
East of England	171,930	10.0%
London	273,899	15.9%
North East	94,646	5.5%
North West	212,893	12.3%
South East	343,564	19.9%
South West	197,776	11.5%
West Midlands	147,519	8.5%
Yorkshire and Humber	143,197	8.3%
Unknown region	10,409	0.6%
Total	**1,725,755**	**-**

* Genotyped Omicron figures may include BA.2.

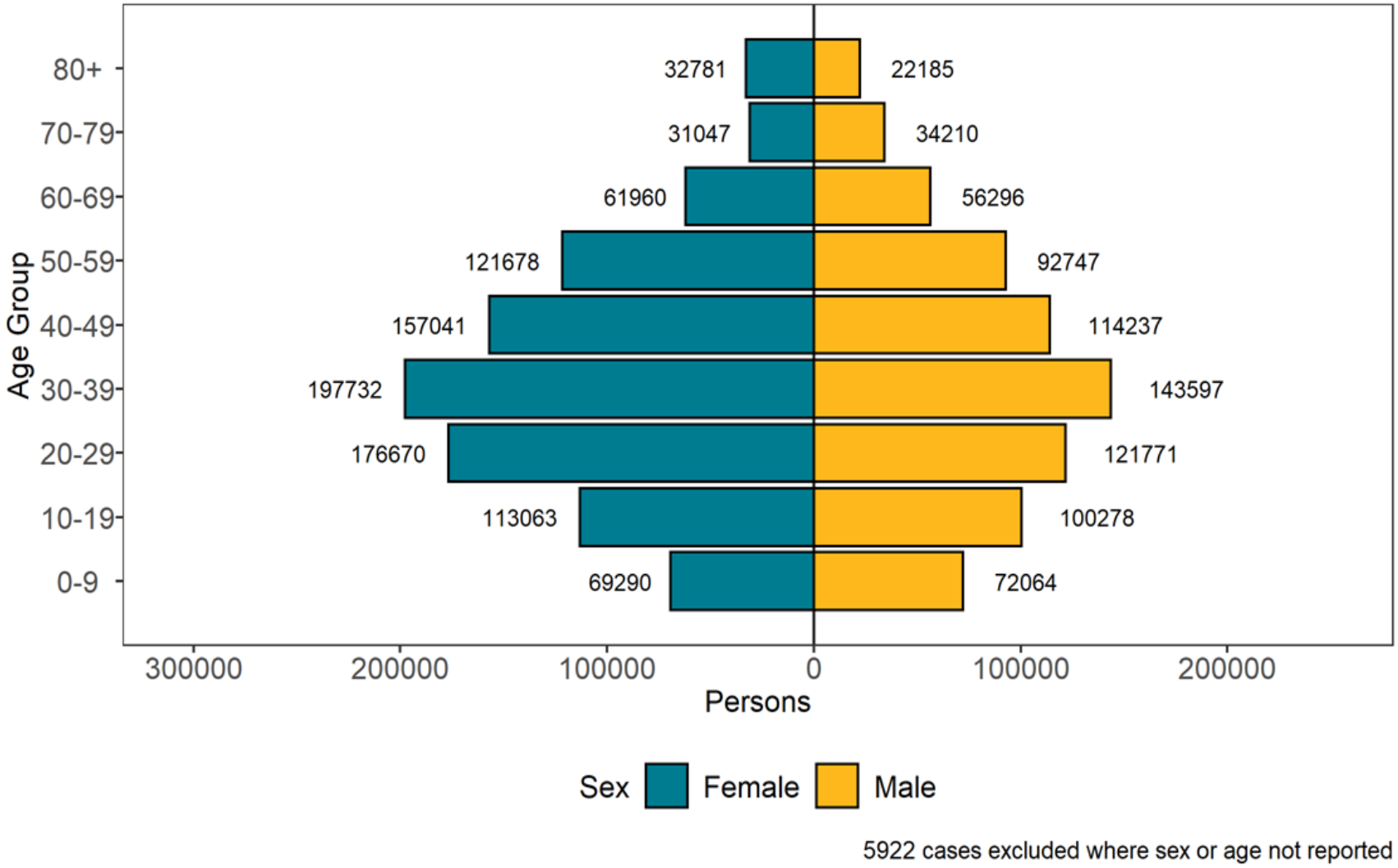
Figure 21. Confirmed (sequencing) and probable (genotyping*) Omicron (B.1.1.529) sub-lineage BA.1 VOC-21NOV-01 cases by specimen date and region of residence as of 5 April 2022

(The data used in this graph can be found in the accompanying spreadsheet.)



* Genotyped Omicron figures include BA.2.

Figure 22. Age-sex pyramid of Omicron (B.1.1.529) sub-lineage BA.1 VOC-21NOV-01 cases as of 5 April 2022*
(The data used in this graph can be found in the accompanying spreadsheet.)



* Genotyped Omicron figures include BA.2

Sources and acknowledgments

Data sources

Data used in this investigation is derived from the COG-UK and UKHSA genomic programme data set, the UKHSA Second Generation Surveillance System, the Secondary Uses Service data set, Emergency Care Data Set and the UKHSA Case and Incident Management System.

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