UK Health Security Agency

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

Technical briefing 35

28 January 2022

This report provides an update on previous briefings up to 14 January 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 variants of concern (VOC) and variants under investigation (VUI). This specialist technical briefing contains early data and analysis on emerging variants and findings have a high level of uncertainty.

SARS-CoV-2 Routine variant data update covers surveillance data and sequencing coverage data on all other VOCs and VUIs. Unless stated otherwise, this technical briefing uses a data cut-off of 24 January 2022 to allow time for analyses. In summary:

BA.2

The Omicron variant sub-lineage BA.2 was designated a variant under investigation (VUI-22JAN-01) by the UK Health Security Agency (UKHSA) Variant Technical Group on 19 January 2022. As of 24 January 2022, 1,072 genomically confirmed cases of BA.2 have been identified in England. This is a small number of cases for characterisation analysis and BA.2 assessments are therefore preliminary. Sequencing data is complete up to 16 January, at which point 96.1% of sequences were BA.1, 3.4% were BA.2 and 0.5% were other lineages. BA.2 does not contain the deletion at S:69-70 and is S-gene target positive (SGTP) on PCR diagnostic assays with targets in this area. SGTP is now a reasonable proxy for BA.2 (accounting for 80% of sequenced SGTP cases with an increasing trend). The proportion of SGTP cases is now increasing. As of the 24 January 2022, the overall proportion of SGTP cases in England is 4.4% compared to 2.2% on the 17 January. There is geographical variation with the highest proportion in London (9.5%) and the lowest in the North-East region (0.9%).

Growth rate

BA.2 has an increased growth rate compared to BA.1 in all regions of England where there are sufficient cases present to make an assessment. Whilst growth rates can be overestimates early in the emergence of a variant, the apparent growth advantage is currently substantial.

Secondary attack rates

Analysis from routine contact tracing data indicated higher secondary attack rates amongst contacts of BA.2 cases in households (13.4%; 95% CI: 10.7%-16.8%) than those for contacts of other Omicron cases (10.3%; 95% CI: 10.1%-10.4%) in the period 27 December 2021 to 11 January 2022. These secondary attack rates are not adjusted for vaccination status and reflect overall growth advantage rather than transmissibility.

Vaccine effectiveness

A preliminary assessment did not find evidence of a difference in vaccine effectiveness against symptomatic disease for BA.2 compared to BA.1. However, numbers included in this study are relatively small and it will be iterated. The University of Oxford has reported preliminary unpublished pseudovirus neutralisation data. In this study, BA.1 and BA.2 pseudoviruses did not differ substantially in neutralisation by sera from vaccinated individuals.

Omicron B.1.1.529/ BA.1

Omicron in care homes

The VIVALDI study, investigating the epidemiology of SARS-CoV-2 infection amongst care home residents and staff in England, through collaboration with a range of Care Home Providers, finds that although there was a rapid increase in SARS-CoV-2 infections in care homes during December 2021, there has not been an associated increase in hospital admissions. More follow-up time is required to confirm findings on mortality. There were very limited numbers of BA.2 in this study and no inferences can be made regarding BA.2. Overall, findings suggest the current wave of Omicron infections is unlikely to lead to a major surge in severe disease in care home populations with high levels of vaccine coverage and/or natural immunity. Pre-printed study results can be found at Outcomes of SARS-CoV-2 Omicron infection in residents of Long-Term Care.

Updated risk assessment

A new risk assessment for VUI-22JAN-01 (BA.2) has been published.

Feedback Survey

Take our short user feedback survey. Your feedback will help us decide which features to build and what improvements could be made.

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.

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

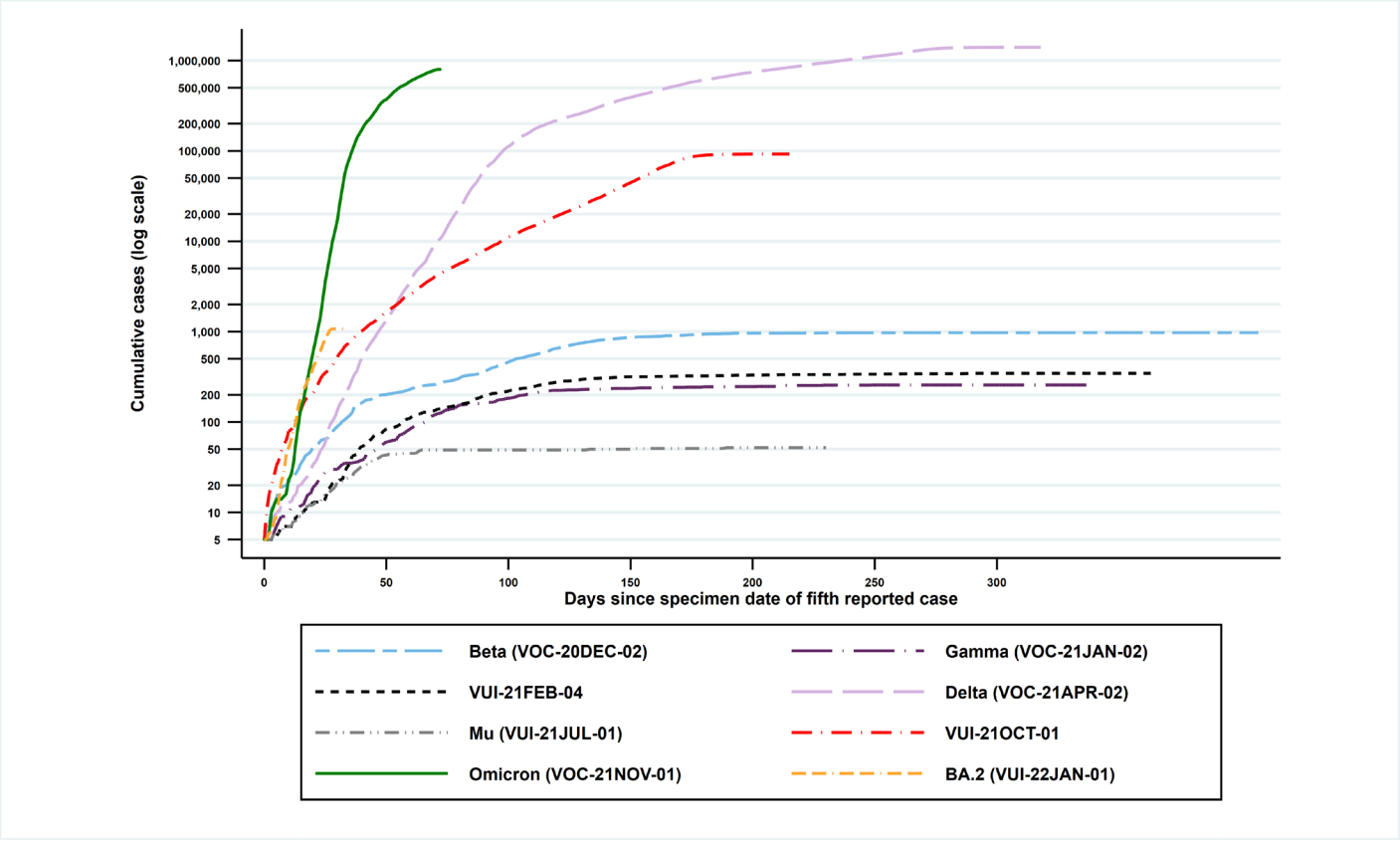
Technical briefings are published periodically. From technical briefing 15, briefings include variant diagnoses identified by whole-genome sequencing and a genotyping polymerase chain reaction (PCR) test, including the categorisation of sequenced and genotyped variant results and a rules-based decision algorithm (RBDA) to identify variant and mutation (VAM) profiles from genotype assay mutation profiles.

Part 1. Surveillance overview

1.1 VOC and VUI overview

Summary epidemiology for each variant and case numbers are updated online.
Figure 1 shows the cumulative number of cases per variant indexed by days since the first report.

Figure 1. Cumulative cases in England of variants indexed by days since the fifth reported case as of 24 January 2022



(Find accessible data used in this graph in underlying data.)

1.2 Variant prevalence

The prevalence of different variants amongst sequenced cases is presented in Figure 2.

The 'Other' category in Figure 2 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 Omicron genome (lineage BA.1) contains the spike deletion at position 69-70 which is associated with SGTF in some widely used PCR tests. Such PCR tests evaluate the presence of 3 SARS-CoV-2 genes: Spike (S), N and ORF1ab. SGTF is defined as a PCR test where the N and ORF1ab genes are detected (with Ct values <=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, VUI-22JAN-01, does not contain the deletion and is S-gene target positive. The number of coronavirus (COVID-19) cases with S-gene positive/SGTF by day, among those tested in TaqPath labs is shown in Figure 4. There is significant variability across the country in SGTF varying from 90% in London to 99% in the North East.

Figure 2. Variant prevalence for all England available sequenced cases from 1 February 2021 as of 24 January 2022 (excluding 28 cases where the specimen date was unknown)
(Find accessible data used in this graph in underlying data.)

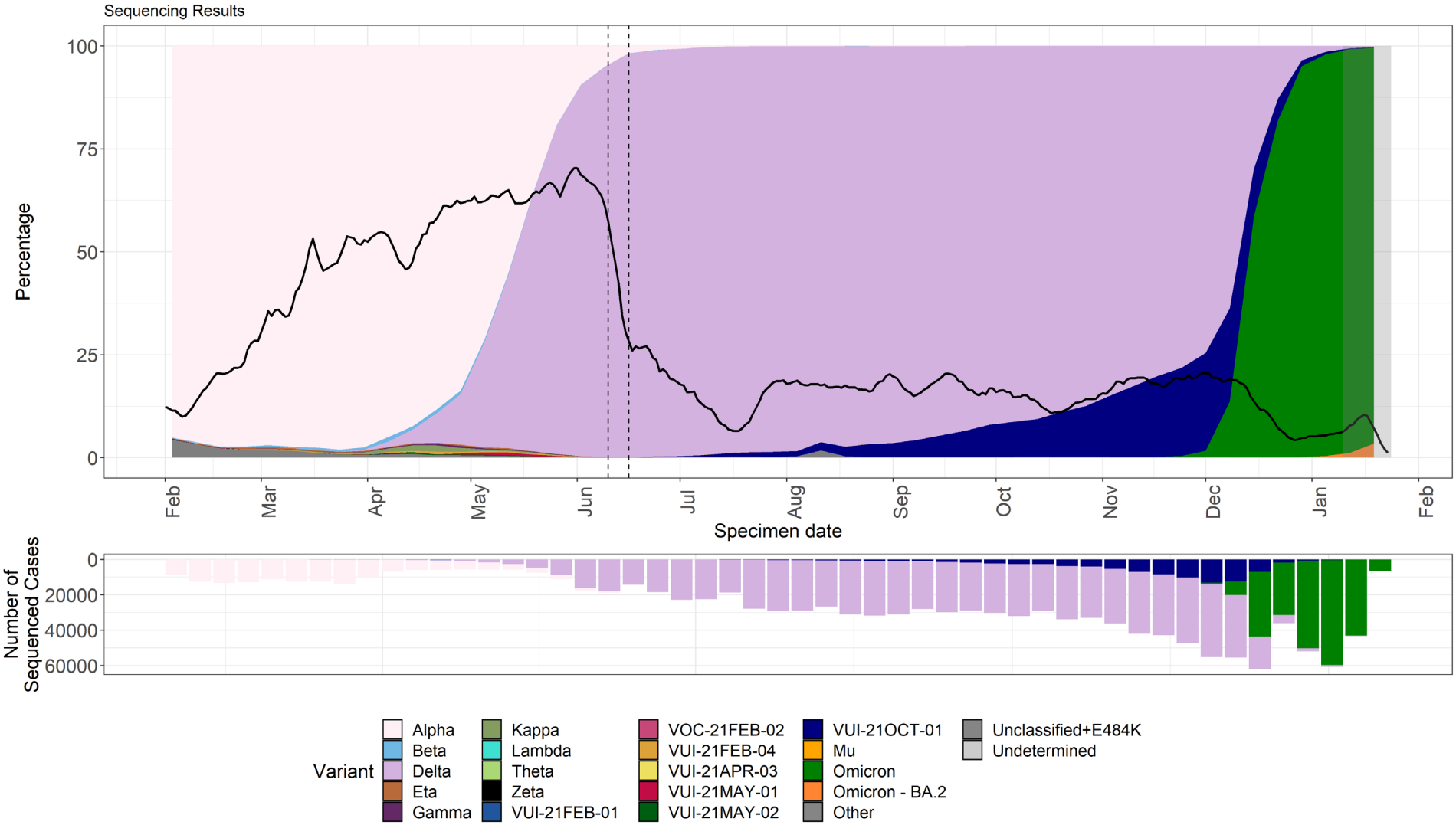


Figure 3. Number of COVID-19 cases with S-gene positive/SGTF by day, among those tested in TaqPath labs as of 24 January 2022 (95% confidence intervals indicated by grey shading. Percentages for most recent 7 days shown)

(Find accessible data used in this graph in underlying data.)

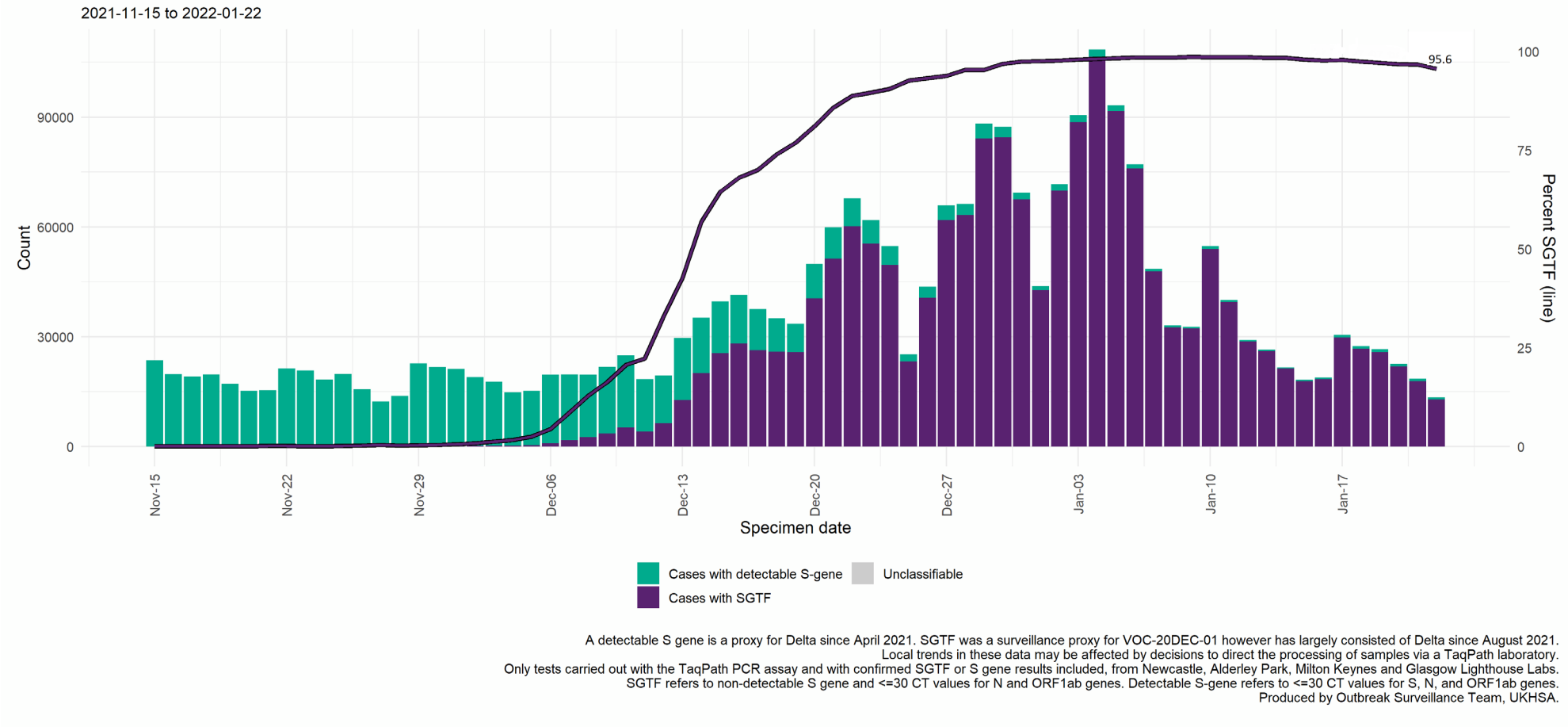
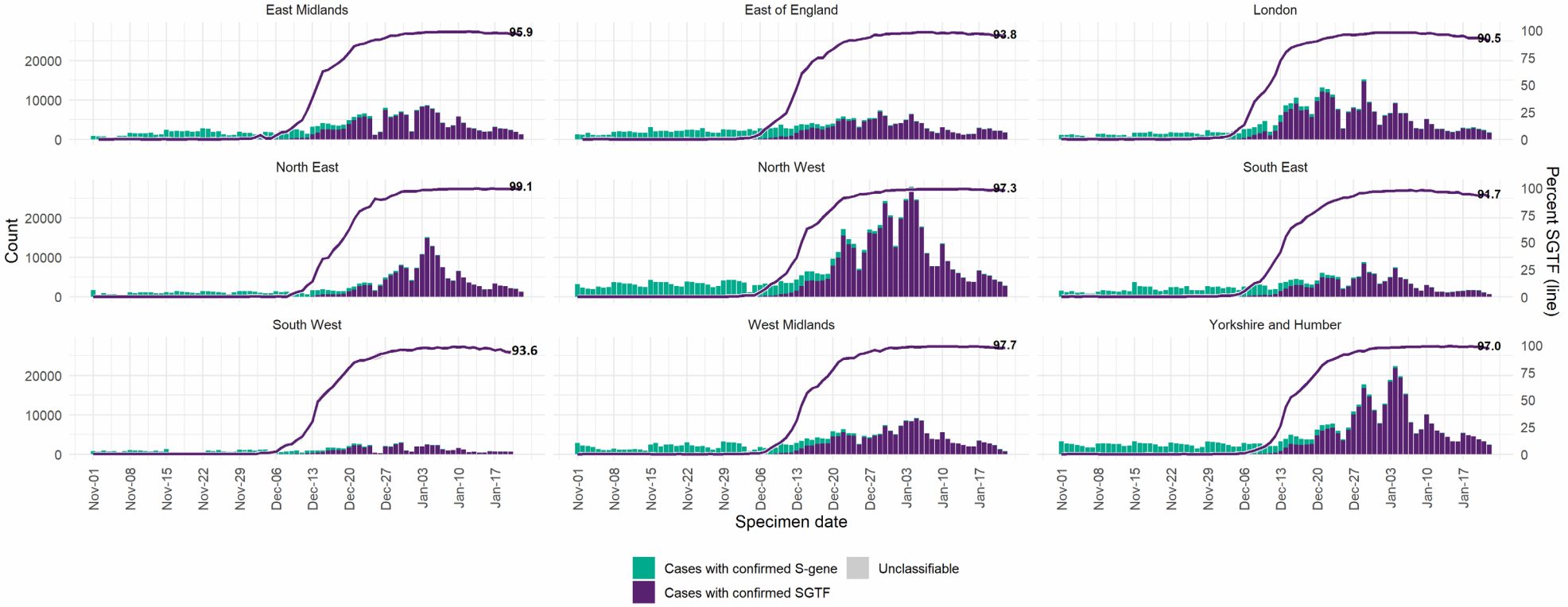
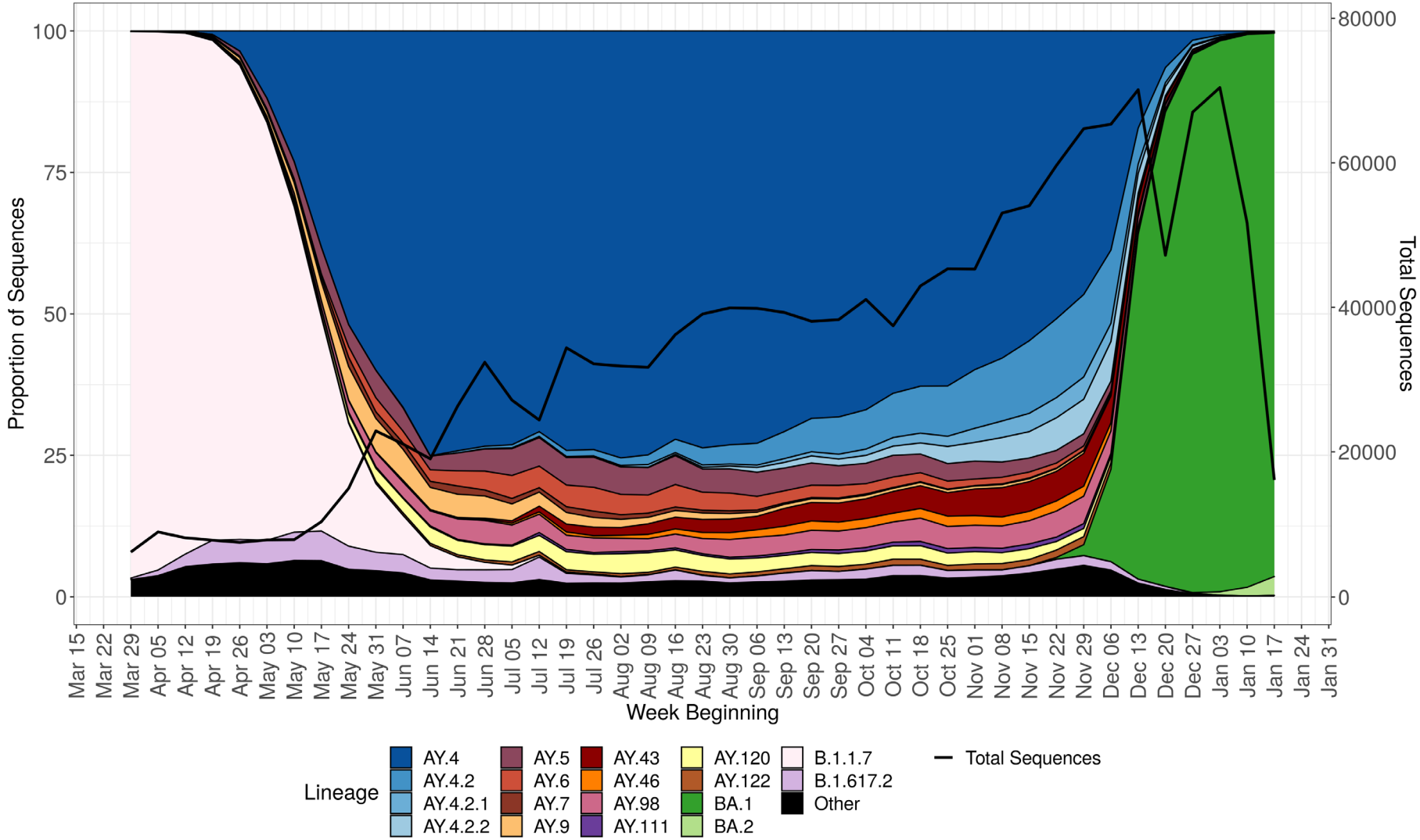


Figure 4. Number of COVID-19 cases with S-gene positive/SGTF by day, among those tested in TaqPath labs by region of residence as of 24 January 2022 (95% confidence intervals indicated by grey shading. Percentages for most recent 7 days shown)



A detectable S gene is a proxy for Delta since April 2021. SGTF was a surveillance proxy for VOC-20DEC-01 however has largely consisted of Delta since August 2021.
Local trends in these data may be affected by decisions to direct the processing of samples via a TaqPath laboratory.
Only tests carried out with the TaqPath PCR assay and with confirmed SGTF or S gene results included, from Newcastle, Alderley Park, Milton Keynes and Glasgow Lighthouse Labs.
SGTF refers to non-detectable S gene and <=30 CT values for N and ORF1ab genes. Detectable S-gene refers to <=30 CT values for S, N, and ORF1ab genes.
Produced by Outbreak Surveillance Team, UKHSA.

Figure 5. Prevalence of Pangolin lineages in UK with sequence data from 1 April 2021 to 23 January 2022
The total number of valid sequence results per week is shown by the black line. Only lineages with more than 5,000 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'.
(Find accessible data used in this graph in underlying data.)



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

This variant is a sub-lineage of Omicron (VOC-21NOV-01) that was designated by Pangolin on 6 December 2021. This sub-lineage does not have the spike gene deletion at 69-70 that causes SGTF. An increase in the number of sequences of the Omicron sub-lineage BA.2 was noted from both the UK and Denmark in the week starting 3 January 2022. The spike profile of BA.2 contains 28 mutations and a deletion at 25-27. The comparison of the Omicron sub-lineages was previously reported in Technical Briefing 31.

BA.2 was designated VUI-22JAN-01 (BA.2) by the UKHSA Variant Technical Group on 19 January 2022.

2.1 Epidemiology

As of 24 January 2022, 1,072 sequences of VUI-22JAN-01 (BA.2) have been identified in the UK. VUI-22JAN-01 (BA.2) accounts for an increasing proportion of SGTP tests. Caution is required when interpreting comparative analyses which use S-gene target results as the only determinant of Omicron and Delta. As VUI-22JAN-01 (BA.2) is designated by sequencing results only there is a known time lag of 11 days (interquartile range: 9 to 14) from obtaining a sample to reporting of VUI-22JAN-01 (BA.2) as the cause of infection. This will be reflected in case numbers presented.

Table 1. Number of confirmed and provisional VUI-22JAN-01 (BA.2) cases, by region of residence as of 24 January 2022

Region	Total case number	Confirmed (sequenced) case number	Percentage of sequences from England that are in this region
East Midlands	60	60	5.6%
East of England	116	116	10.8%
London	364	364	34.0%
North East	18	18	1.7%
North West	71	71	6.6%
South East	282	282	26.3%
South West	71	71	6.6%
West Midlands	31	31	2.9%
Yorkshire and Humber	46	46	4.3%
Unknown region	13	13	1.2%
Total	1,072	1,072	-

Figure 6. Confirmed VUI-22JAN-01 (BA.2) cases by specimen date and region of residence as of 24 January 2022
(Find accessible data used in this graph in underlying data.)

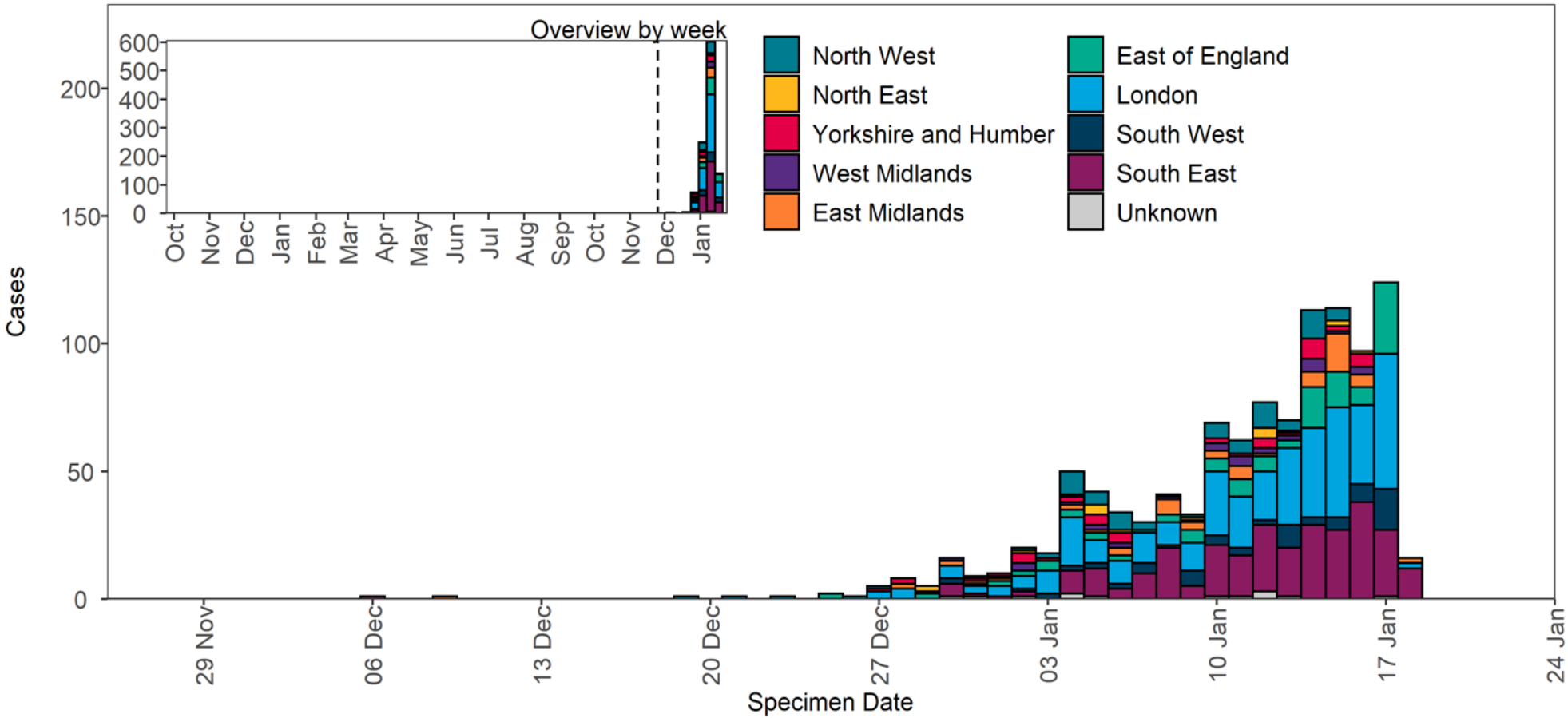
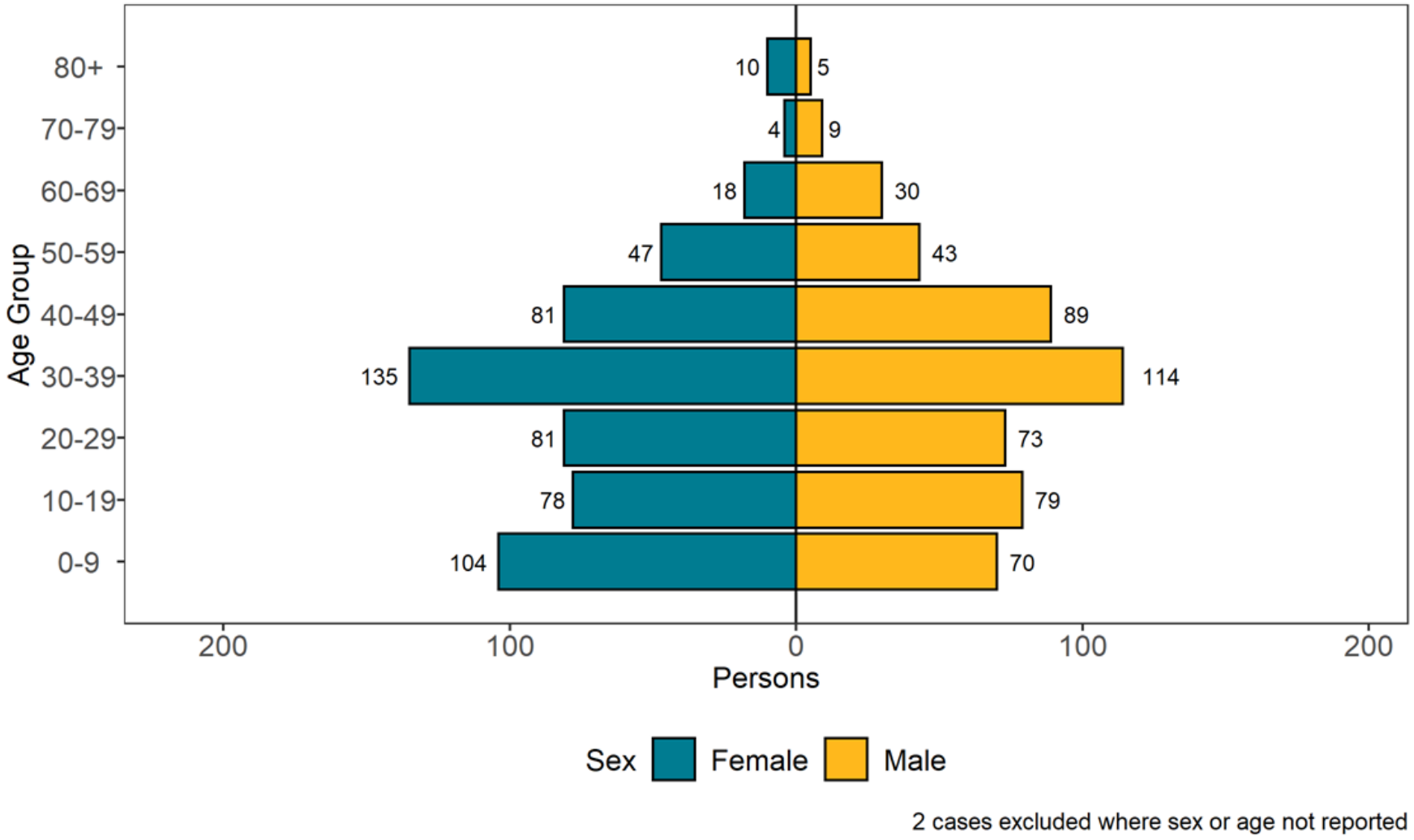


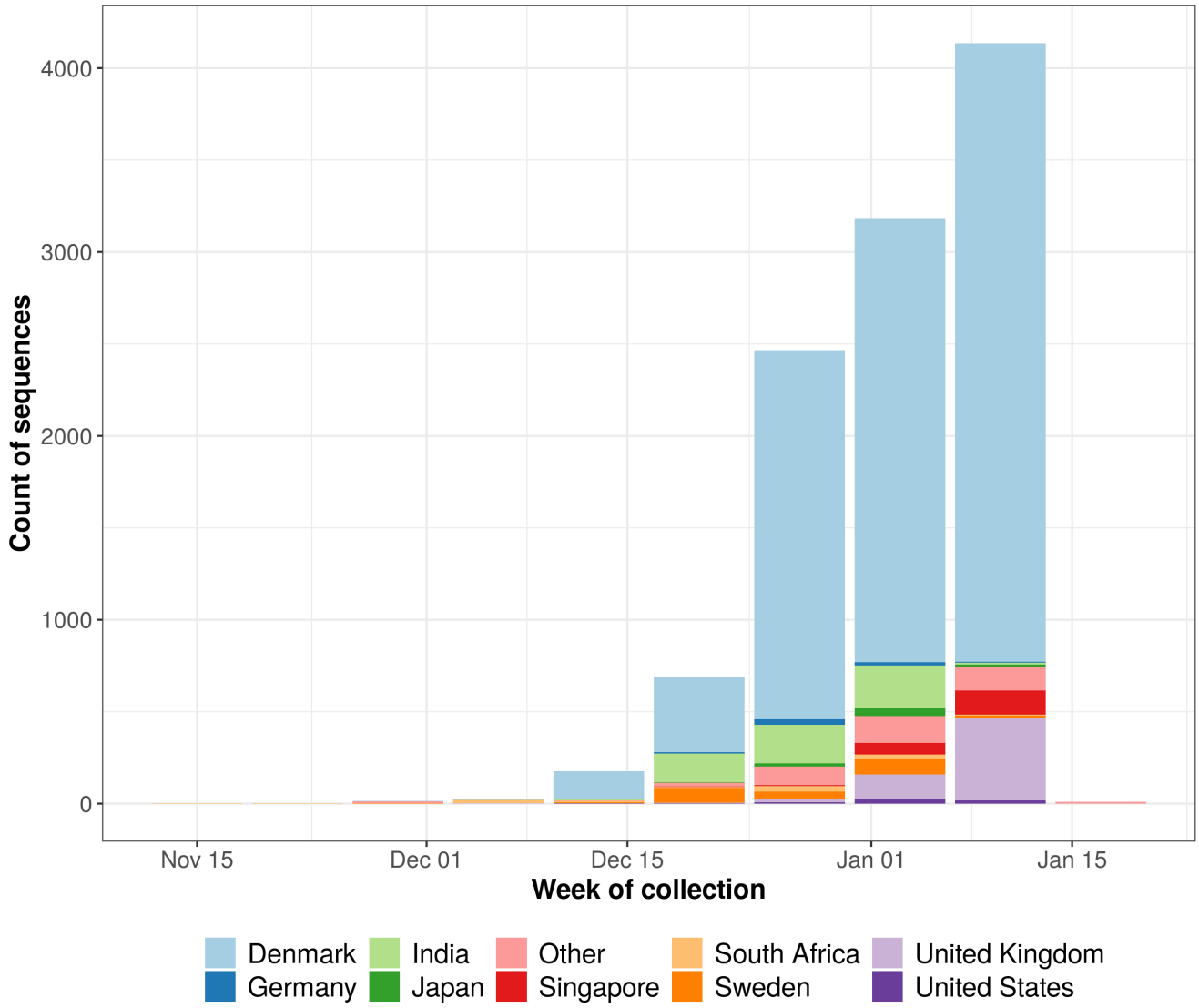
Figure 7. Age-sex pyramid of VUI-22JAN-01 (BA.2) cases as of 24 January 2022
(Find accessible data used in this graph in underlying data.)



2.2 International epidemiology

As of 24 January 2022, 10,873 sequences on GISAID meet the VUI-22JAN-01 (BA.2) Pangolin definition from 49 countries including the UK. Figure 9 shows an increasing number of VUI-22JAN-01 (BA.2) sequences in recent weeks, many from Denmark. The most recent week will be affected by data lags.

Figure 8. Count of VUI-22JAN-01 (BA.2) classified sequences by week of collection (with valid dates) uploaded to GISAID by week as of 24 January 2022
Countries with 50 or fewer sequences have been grouped together as 'Other'. Of the submitted sequences, 10,703 had valid collection dates.
(Find accessible data used in this graph in underlying data)

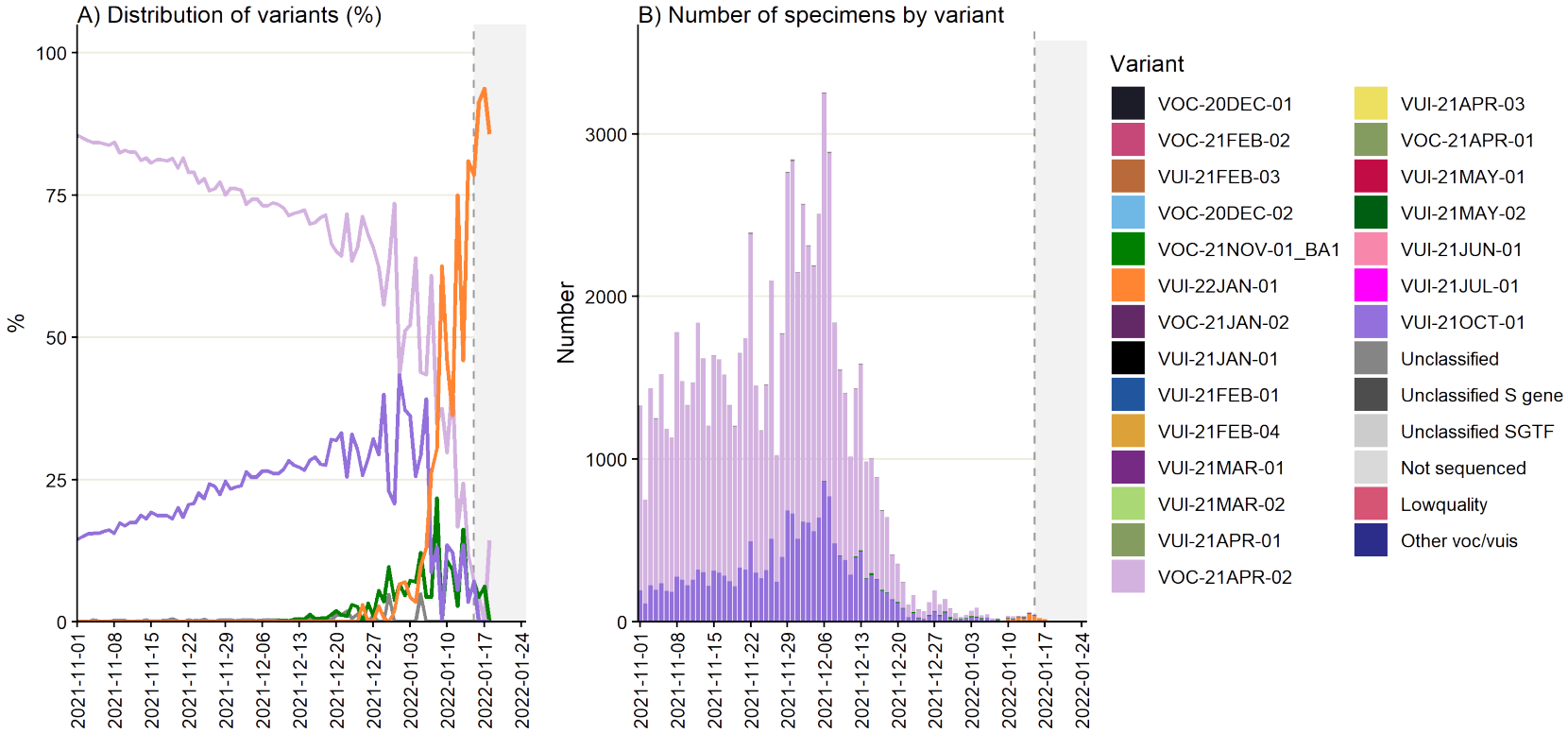


2.3 Epidemiology of SGTP

The Omicron lineage VUI-22JAN-01 (BA.2) does not contain the spike deletion and therefore is S-gene target positive (SGTP). By 24 January 2022, VUI-22JAN-01 (BA.2) accounted for 80% of sequenced SGTP and this proportion is increasing, however, overall numbers remain low. Therefore, SGTF is no longer sufficient to assess the spread of Omicron as a whole.

Figure 9. Number and distribution of variants per week among sequenced SGTP specimens as of 24 January 2022

Specimen dates between 2021-11-01 and 2022-01-18. Data as of 2022-01-24.
Specimen dates within last 11 days shaded in gray due to associated reporting delay; 10 days is median turn-around-time for sequencing.



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

2.4 Growth rates

The growth rate is estimated by logistic regression of the number of genomes sampled with the BA.1 and VUI-22JAN-01 (BA.2) lineages on time of sample collection. Sample inclusion criteria are: 1) a non-traveller as determined by matching each case against passenger locator forms and managed quarantine service test codes, and 2) collected from Pillar 2 testing. To adjust for geographic variation in case growth rates, VUI-22JAN-01 (BA.2) growth rates were estimated relative to a geographically matched sample of BA.1 genomes. A logistic growth rate of zero would indicate no difference in growth rates between BA.1 and VUI-22JAN-01 (BA.2).

Data sampled between 27 December 2021 and 19 January 2022 were included. The estimated and empirical proportion of genomes from the VUI-22JAN-01 (BA.2) lineage are shown in Figure 10. The median growth rate in the most recent 7-day period is +126% per week. The analysis was repeated on data from each region of England with at least 40 BA.2 genomes and is shown in Figure 11. Current logistic growth rates range from 53% to 159% per week.

Figure 10. Sample frequency of VUI-22JAN-01 (BA.2) relative to other Omicron over time
Supplementary data is not available for this figure.

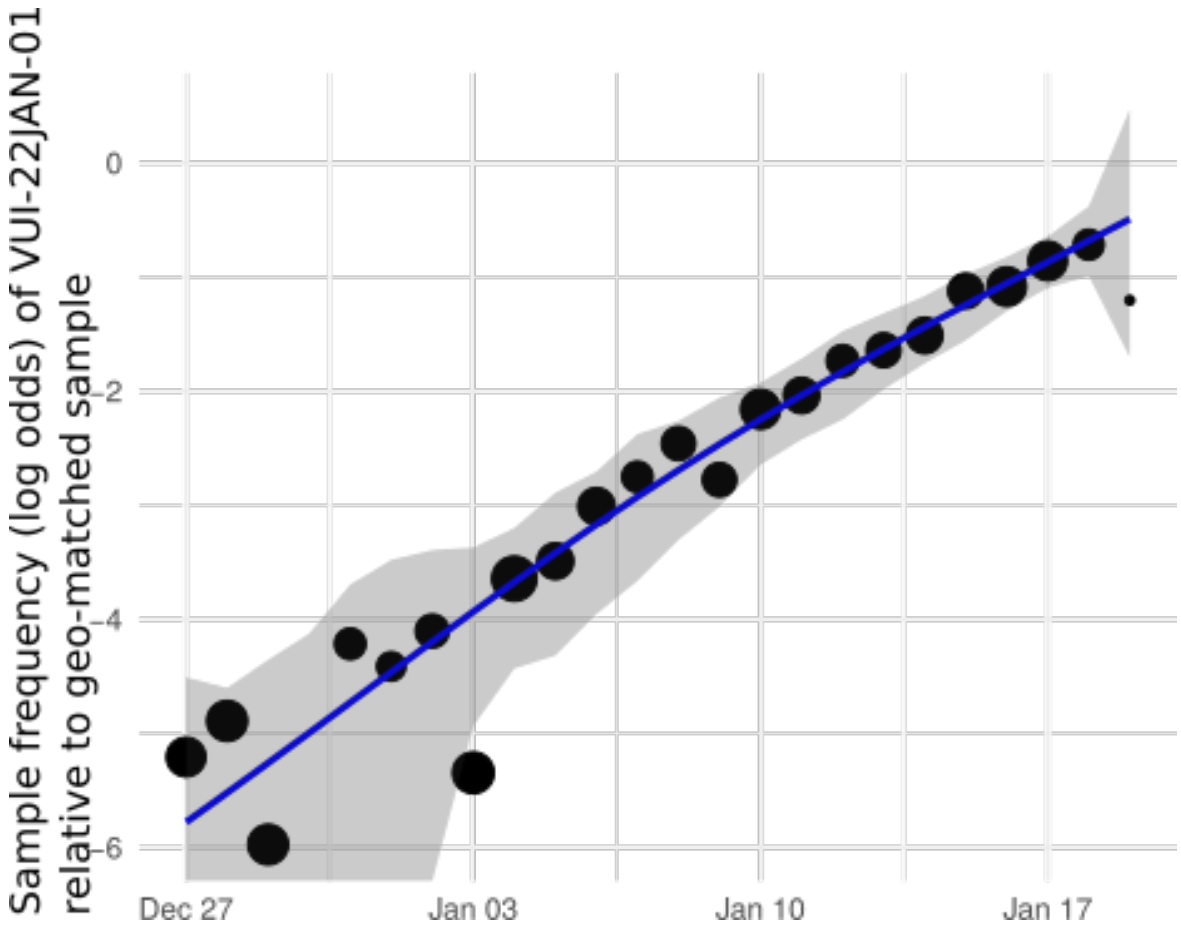
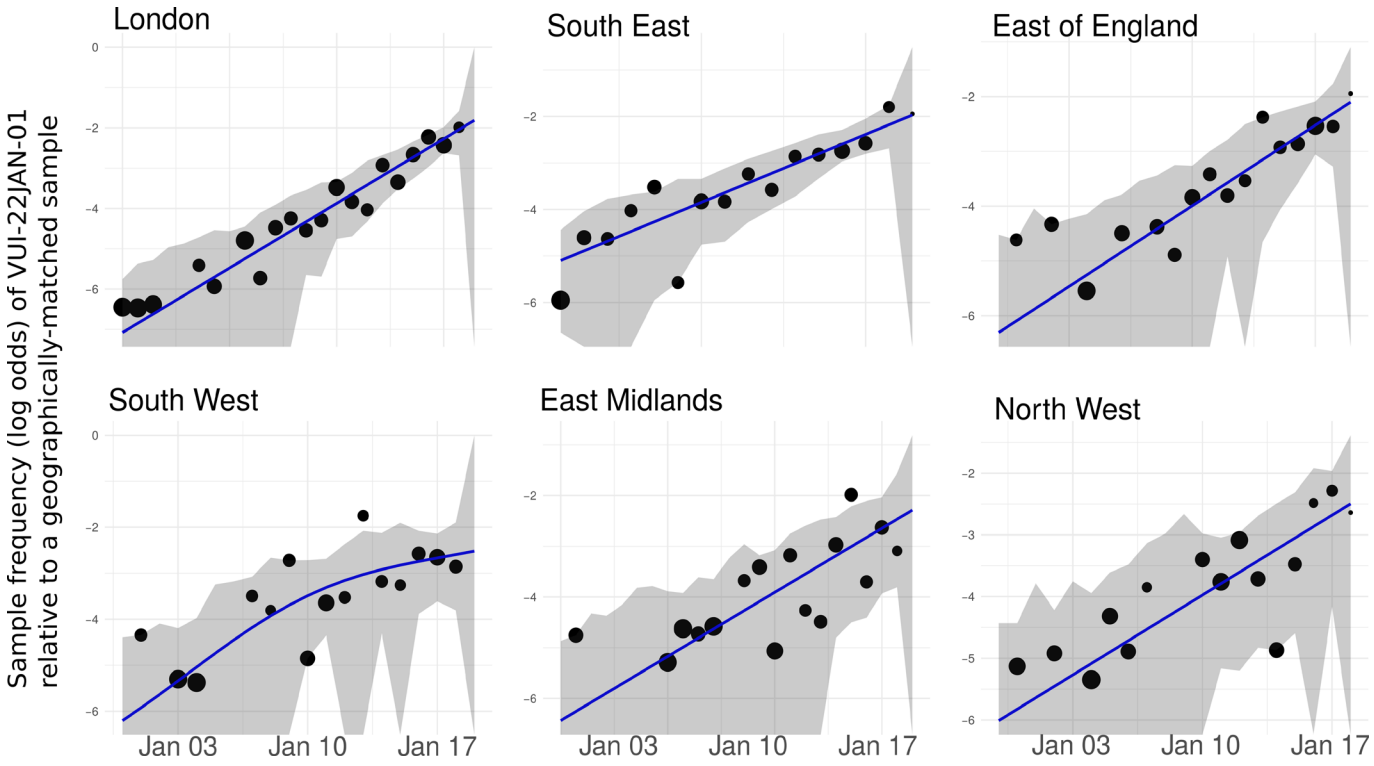
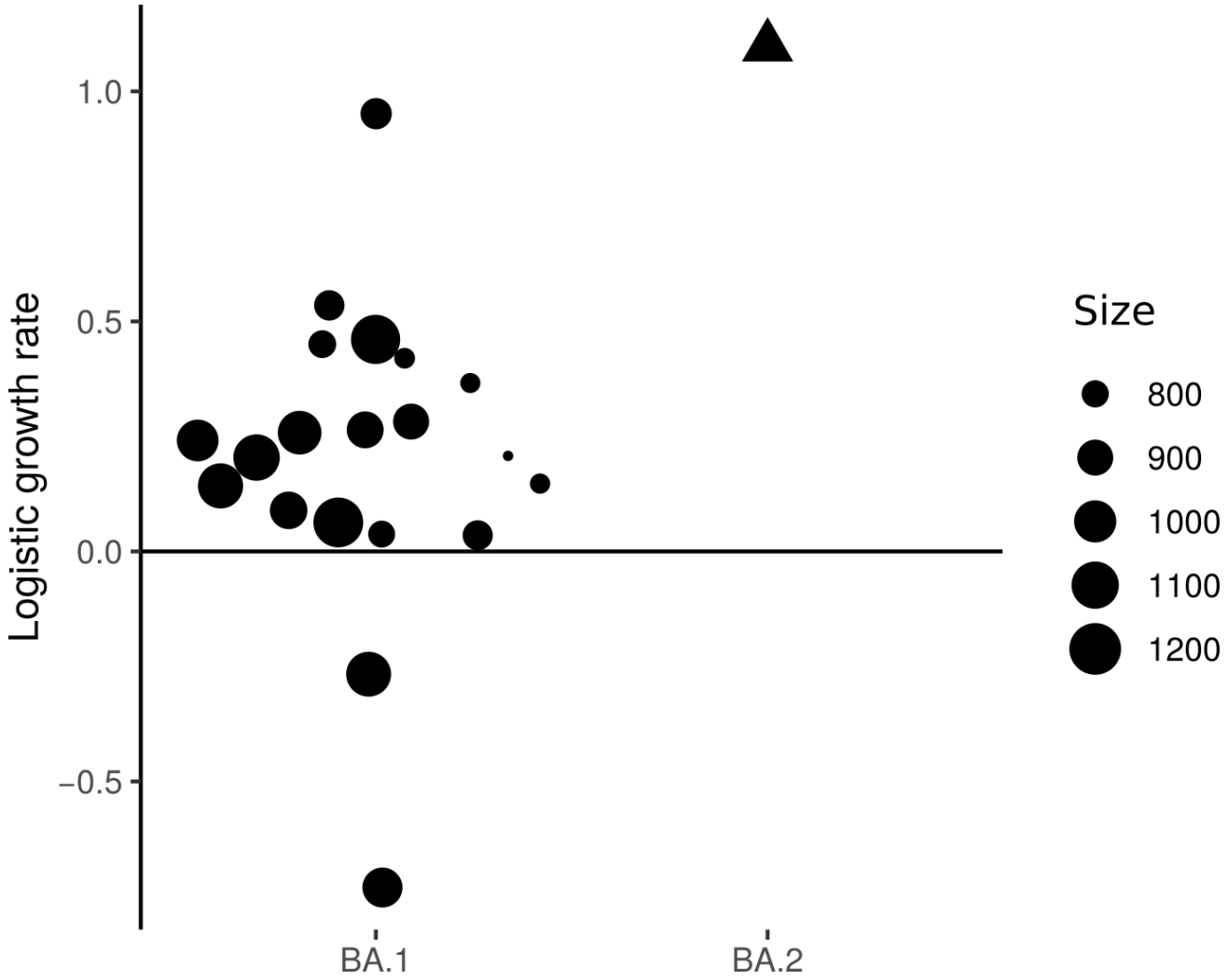


Figure 11. Sample frequency of VUI-22JAN-01 (BA.2) relative to other Omicron over time in regions of England with at least 40 BA.2 genomes sampled through Pillar 2 testing
Supplementary data is not available for this figure.



To provide context surrounding the high growth rate of BA.2 lineage, a comparison was made to cocirculating BA.1 clades in England. Clades were selected which were sampled between 1 December 2021 and 19 January 2022 and which have a cumulative number of samples within 25% of the number of BA.2 genomes sampled in England. Growth rates for each clade were computed by simple logistic regression on time. Figure 12 shows that the BA.2 lineage has the largest growth rate in comparison to similar BA.1 clades.

Figure 12. Omicron sub-lineage growth rates in England including BA.2 and a selection of BA.1 clades matched by time and number of samples



2.5 Secondary attack rates

This analysis is based on original cases with test dates from 27 December 2021 to 11 January 2022. Secondary attack rates and odds ratios are based on positive tests amongst contacts named to NHS Test and Trace by an original case identified with sequenced confirmed VUI-22JAN-01 (BA.2) or other sequenced confirmed Omicron, with date of symptom onset or positive test of the secondary case occurring 2 to 7 days after original exposure. This shortened follow up period was used to expedite analysis on VUI-22JAN-01 (BA.2), in the context of limited data so far.

Only close contacts named by the original case to NHS Test and Trace 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. Contacts not named by the case but identified as part of contact tracing of international travellers on flights are excluded. The use of

sequenced confirmed cases only may lead to bias: certain groups such as international travellers and those in hospital are more likely to be selected for sequencing and may not represent all community transmission.

Table 2 shows the secondary attack rates (for contacts becoming cases within 2 to 7 days of exposure) split by type of contact. With limited data and limited follow-up so far, secondary attack rates amongst contacts of VUI-22JAN-01 (BA.2) cases in households (13.4%; 95% CI: 10.7%-16.8%) are higher than those for other Omicron cases (10.3%; 95% CI: 10.1%-10.4%). There is not yet enough data for analysis of secondary attack rates amongst non-household contacts of cases with genomically confirmed VUI-22JAN-01 (BA.2). Note that a similar analysis reported in Technical Briefing 32 showed secondary attack rate amongst contacts of sequenced Omicron cases to be 15.8% (95% CI: 14.3%-17.5%). Some variation in transmission is observed over time as new variants are identified so these early findings on VUI-22JAN-01 (BA.2) should be interpreted with caution.

Table 2. Secondary attack rates (within 2 to 7 days of exposure) for contacts of cases with sequenced confirmed VUI-22JAN-01 (BA.2) and all other sequenced confirmed Omicron

(Case test dates 27 December 2021 to 11 January 2022, variant data as of 24 January 2022 and contact tracing data as of 24 January 2022)

Variant	Household contacts becoming cases / all household contacts	Secondary attack rate amongst household contacts (95% CI)	Non-household contacts becoming cases / all non-household contacts	Secondary attack rate amongst non-household contacts (95% CI)
VUI-22JAN-01 (BA.2)	64 / 476	13.4% (10.7%-16.8%)	1 / 42	Unavailable
Omicron excluding VUI-22JAN-01	10,444 / 101,773	10.3% (10.1%-10.4%)	1,299 / 23,665	5.5% (5.2%-5.8%)

Secondary attack rates are marked as 'Unavailable' when count of contacts is fewer than 50 or count of cases is fewer than 20. Secondary attack rates from NHS Test and Trace should generally be considered lower bounds due to the nature of contact tracing and testing, and specifically so here because of the restricted time period for secondary case detection.

2.6 Vaccine effectiveness

The latest vaccine effectiveness estimates from UKHSA are published in the weekly vaccine surveillance report.

Vaccine effectiveness against symptomatic disease following VUI-22JAN-01 (BA.2) infection was analysed in a test-negative case control design, as compared to the Omicron BA.1 sub-lineage. Pillar 2 testing data from symptomatic cases tested between 27 December 2021 and 21 January 2022 were included. Analysis combined all vaccines (Table 4). Vaccine effectiveness against symptomatic disease was similar for BA.1 and VUI-22JAN-01 (BA.2) sub-lineages of Omicron. After 2 doses effectiveness was 9% (7 to 10%) and 13% (-26 to 40%) respectively for BA.1 and VUI-22JAN-01 (BA.2), after 25+ weeks. This increased to 63% (63 to 64%) for BA.1 and 70% (58 to 79%) for VUI-22JAN-01 (BA.2) at 2 weeks following a booster vaccine. There is no statistical difference in the vaccine effectiveness for BA.1 and BA.2 at present; this analysis will be iterated.

Table 4. Vaccine effectiveness against symptomatic disease (all vaccine brands combined) for BA.1 and VUI-22JAN-01 (BA.2). OR = odds ratio, VE = vaccine effectiveness

Dose	Interval after dose	BA.1 (VE (95% CI))	BA.2 (VE (95% CI))
2	25+ weeks	9% (7-10)	13% (-26-40)
3	2+ weeks	63% (63-64)	70% (58-79)

Part 3. Enhanced analyses of Omicron VOC-21NOV-01 (B.1.1.529)

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

3.1 Severity and hospitalisation

Cases, hospitalisation, attendance and deaths by vaccination status are now presented in the COVID-19 vaccine surveillance report.

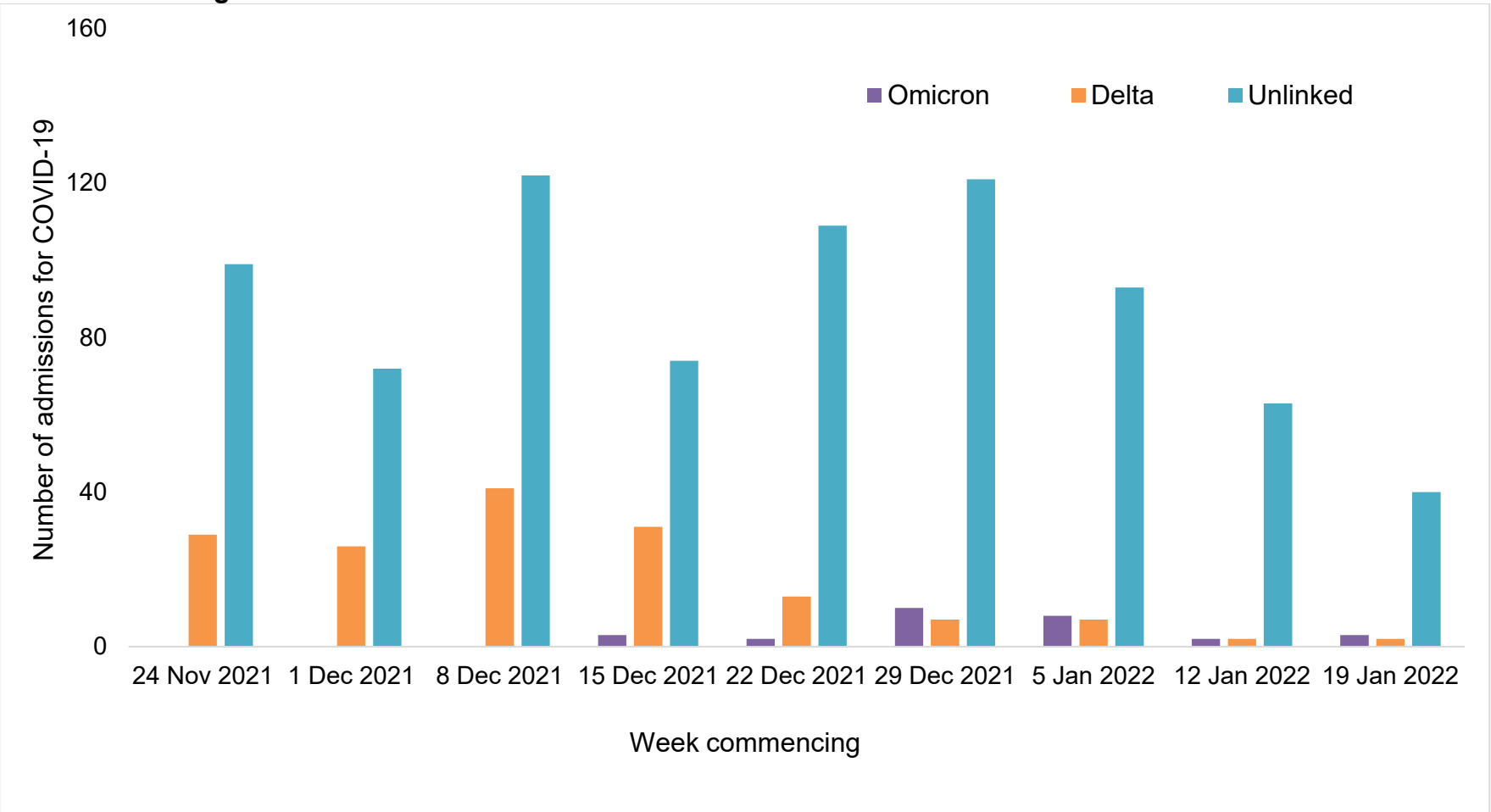
Analyses on the risk of hospitalisation were reported in Technical Briefing 33. These analyses indicated that relative to Delta, the risk of hospitalisation following infection with Omicron is lower in adults. Studies to further investigate the severity of Omicron infection compared to Delta in children are underway.

Severe Acute Respiratory Infection (SARI) Watch surveillance system – Intensive Care Unit (ICU)/High Dependency Unit (HDU) admissions

SARI-Watch monitors hospitalisations and ICU/HDU admissions with laboratory confirmed SARS-CoV-2 in acute NHS Trusts in England. Patient level data on ICU/HDU admissions, linked to variants and mutations (VAM), is reported from around 40 trusts (around one third of trusts). The weekly proportion of Delta versus Omicron ICU/HDU admissions from 24 November 2021 to 24 January 2022 are shown below in Figure 13. A linkable sample was available for 19% of critical care admissions in this time period. Overall, the majority of admissions in this subset of critical care patients had Delta infection. However, towards the end of December, Omicron infection was detected while overall numbers of critical care admissions decreased. From cases where there was a valid sequencing result, those admitted to ICU that were Omicron increased from 9% week commencing 15 December 2021 to 50% on week commencing 12 January 2022. Individuals admitted to ICU/HDU are often late in their course of infection and therefore lower yields from sequencing is expected. However, hospitals should endeavour to locate and send prior positive COVID-19 samples from individuals admitted to ICU for sequencing and genotyping, where these samples are available, in order to understand the differences in severity between variants.

SARI-Watch data is also presented in the weekly combined flu and COVID-19 surveillance report.

Figure 13. Distribution of sequence confirmed variants (or SGTF status) among ICU-HDU admission for COVID-19 in acute NHS trusts in England



Notes to chart:
1. To ensure sequence-confirmed cases were closely related to the admission, only those with test 28 days before admission and 1 day post admission are included in the variant analysis
2. Delta was defined by VOC-21APR-0 or VUI-21OCT-01 from VAM list, or SGTF status (No) prior to 27 November if variant data unavailable in variant and mutations (VAM) list.
3. Omicron was defined by VOC-21NOV-01_BA1 or VUI-22JAN-01 in VAM list, or SGTF status (Yes)
4. The majority of unlinked records (769 of 793) did not have sequence data in VAM (coded as NULL). A small minority of unlinked records had sequence confirmation but were outside the testing window – see point 1

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 (SGSS), the Secondary Uses Service (SUS) data set, Emergency Care Data Set (ECDS), the UKHSA Case and Incident Management System (CIMS) and the Severe Acute Respiratory Infection (SARI) Watch surveillance.

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.

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UKHSA Contact Tracing Data Team

UKHSA Environmental Monitoring for Health Protection Team

UKHSA Public Health Incident Directors

UKHSA Data, Analytics and Surveillance

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About the UK Health Security Agency

UKHSA is responsible for protecting every member of every community from the impact of infectious diseases, chemical, biological, radiological and nuclear incidents and other health threats. We provide intellectual, scientific and operational leadership at national and local level, as well as on the global stage, to make the nation health secure.

UKHSA is an executive agency, sponsored by the Department of Health and Social Care.

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