UK Health Security Agency

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

Variant of concern: Omicron, VOC-21NOV-01 (B.1.1.529)

Technical briefing 30

3 December 2021

This briefing is an addition specific to Omicron VOC-21NOV-01 (B.1.1.529) and provides an update on the previous briefing on 26 November 2021

Contents

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.

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

Summary

This specialist technical briefing contains early data and analysis on an emerging variant of concern Omicron VOC-21NOV-01 (B.1.1.529) and findings have a high level of uncertainty.

The data cut-off for this briefing is 30 November 2021 to allow for analyses. The most recent case numbers can be found here. The technical briefing will be updated weekly at present.

In summary:

- there are 5 current VOCs and 7 VUIs (Table 1). The World Health Organization (WHO) designated B.1.1.529 as a VOC, named Omicron, on 26 November 2021
- a new risk assessment for Omicron VOC-21NOV-01 (B.1.1.529) has been published
- Delta remains the predominant variant in England accounting for approximately 99.8% of sequenced cases from 10 October to 30 November 2021
- characterisation of the variant Omicron VOC-21NOV-01 (B.1.1.529) has commenced – a complete list of deployed and planned studies is provided in Section 2.1
- Omicron VOC-21NOV-01 (B.1.1.529) can be identified through genotyping or sequencing – as of 30 November 2021, there are 22 confirmed cases of Omicron VOC-21NOV-01 (B.1.1.529) identified through sequencing or genotyping in England; none of the cases of are known to have been hospitalised or died
- of the 22 confirmed cases, there are 12 cases who have received at least 2 doses of vaccine more than 14 days ago, 2 cases more than 28 days post first dose, 6 unvaccinated cases, and 2 with no available information
- the UKHSA genomic case definition for Omicron VOC-21NOV-01 (B.1.1.529) is included and has been published for use at GitHub
- Omicron VOC-21NOV-01 (B.1.1.529) can be detected through the current genotyping panel in use in England – the current profile requires K417N must be present, and P681R, E484K, and K417T must not be present; additional targets for Omicron VOC-21NOV-01 (B.1.1.529) are being validated

- the Omicron VOC-21NOV-01 (B.1.1.529) global phylogeny shows little diversity which is compatible with a recent emergence and rapid spread – due to mixed sequence quality, requiring the masking of informative sites from the alignment, the phylogeny is not suitable for detailed cluster analysis, however it supports the epidemiological finding that there have been a number of separate introductions into England

- Omicron VOC-21NOV-01 (B.1.1.529) has a deletion at position 69/70 of the spike protein which allows it to be tracked through S gene target failure (SGTF) in some polymerase chain reaction (PCR) tests. SGTF is also observed in a very small fraction of test results from lineages lacking this deletion, including the Delta lineage and sub-lineages. The proportion of test results with SGTF has been low over the past 90 days, but in the past week has increased. The logistic growth rate of SGTF has fluctuated between approximately -50% and +50% over the past 90 days but in the past week has climbed to +141%. This finding indicates that SGTF is growing faster, and can be considered a strong early signal. However, the number cannot be interpreted as a change in transmissibility or an increase in the absolute number of cases of the variant.

- structural modelling shared by the University of Oxford indicates that the mutations present in Omicron are highly likely to affect the binding of natural and therapeutic antibodies, and to enhance binding to human Angiotensin-Converting Enzyme 2 (ACE2) to an extent greater than that seen in other variants to date. (Data not included; will be linked from here once available)

- there is very little evidence of Omicron VOC-21NOV-01 (B.1.1.529) in wastewater surveillance up to 21 November 2021; more recent data is being analysed

Part 1. Surveillance overview

1.1 Variants under surveillance

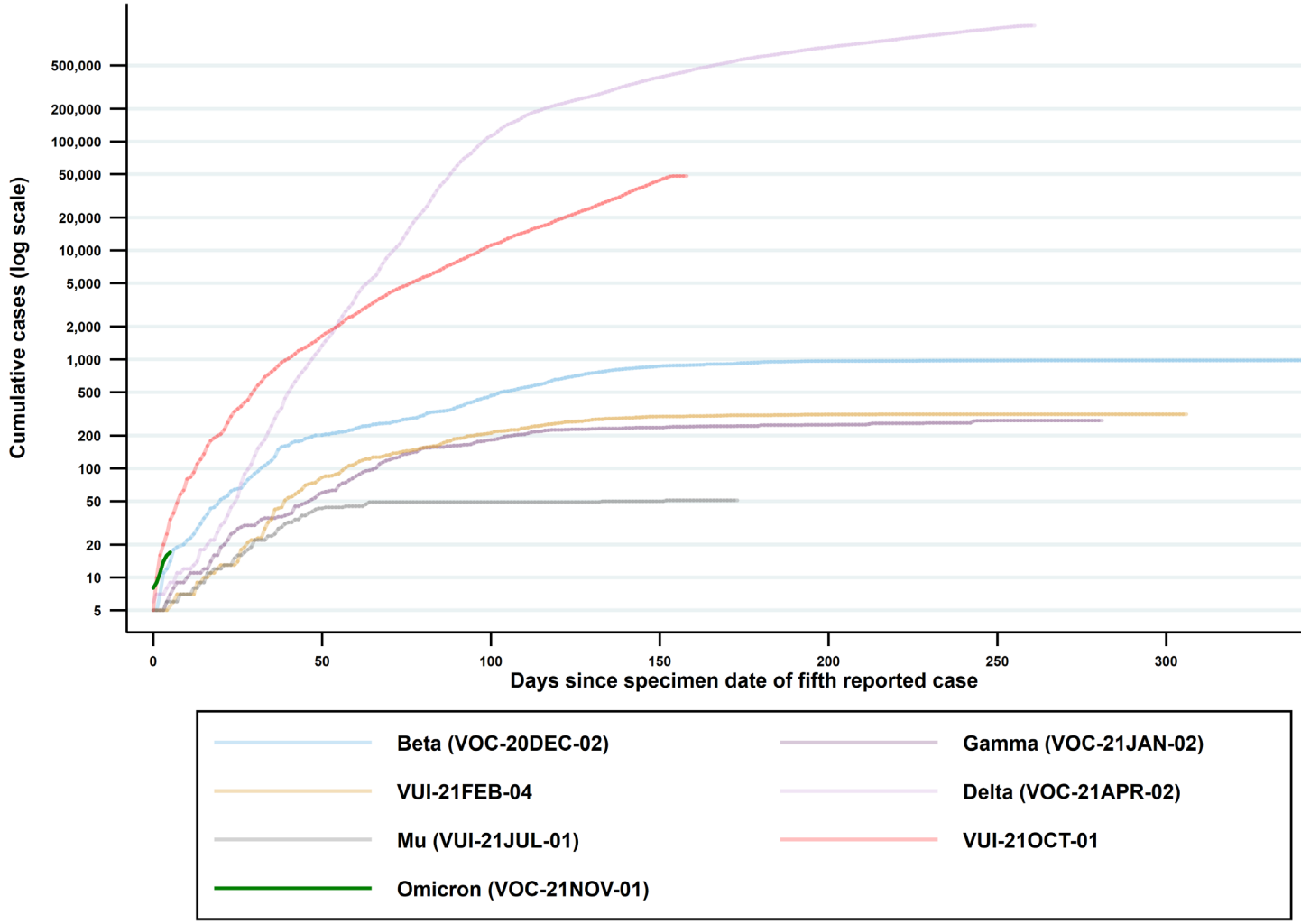
Table 1: Variants under surveillance

Variants of Concern	Variants Under Investigation	Variants in monitoring
Variants detected in the UK in the past 12 weeks		
Alpha (B.1.1.7) **VOC-20DEC-01**	VUI-21OCT-01 (AY.4.2)	B.1.640
Beta (B.1.351) **VOC-20DEC-02**	VUI-21FEB-03 (B.1.525)	B.1.617.2 + E484K
Gamma (P.1) **VOC-21JAN-02**	VUI-21APR-01 (B.1.617.1)	
Delta (B.1.617.2 and sublineages) **VOC-21APR-02**	VUI-21JUL-01 (B.1.621)	
Omicron (B.1.1.529) **VOC-21NOV-01**		
Variants detected in GISAID, but not in the UK, in the past 12 weeks		
	VUI-21APR-03 (B.1.617.3)	C.37*
	VUI-21JAN-01 (P.2)	B.1.526
	VUI-21FEB-04 (B.1.1.318)	B.1 with 214insQAS
		B.1.629
		B.1.630, B.1.631/B.1.628
		P.1.8
		P.5
		B.1.1.7 + B.1.617.2 possible recombinant
		C.37 descendant (S:L5F, G75V, D614G, L452Q, E484K, P499R, N501T, H655Y, P681R)
		C.36.3††

		B.1.427/B.1.429
		B.1.620
		R.1
		C.1.2

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 and not included in these tables. Provisionally extinct variants remain in the definitions used to scan the data and will be identified if re-emerging.

Figure 1. Cumulative cases in England of variants indexed by days since the fifth reported case as of 30 November 2021



NB. Cases without a specimen date are excluded (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 and genotyped cases in Figure 3.

The genotyping panels used were as follows:

From 29 March 2021: N501Y, K417N, K417T and E484K

From 11 May 2021: P681R, K417N, K417T and E484K

The 'Other' category in Figures 2 and 3 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.

Figure 2. Variant prevalence for all England available sequenced cases from 1 February 2021 as of 30 November 2021

(Find accessible data used in this graph in underlying data.) Dashed lines indicate period incorporating issue at a sequencing site. Black line indicates proportion of cases sequenced.

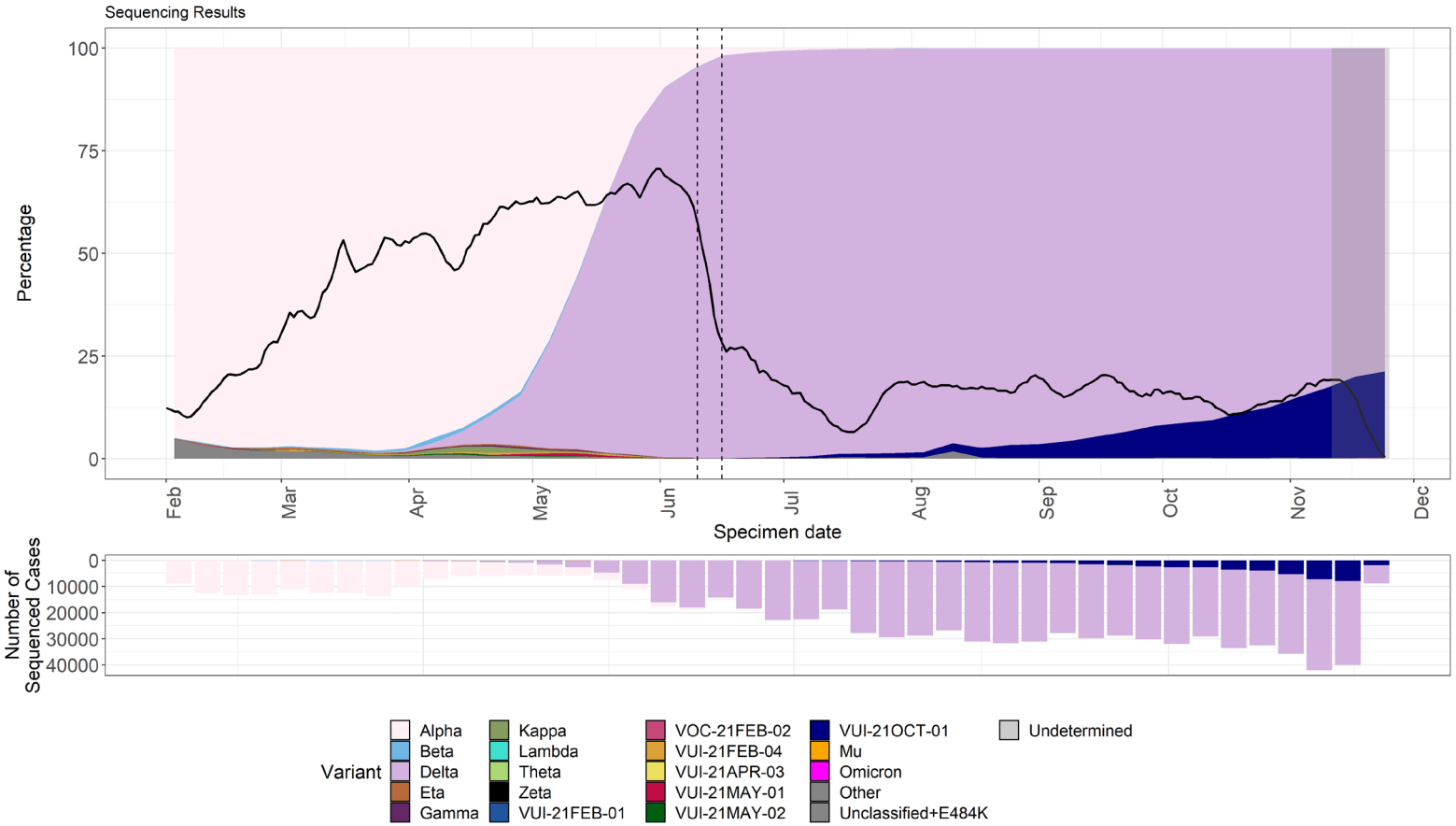
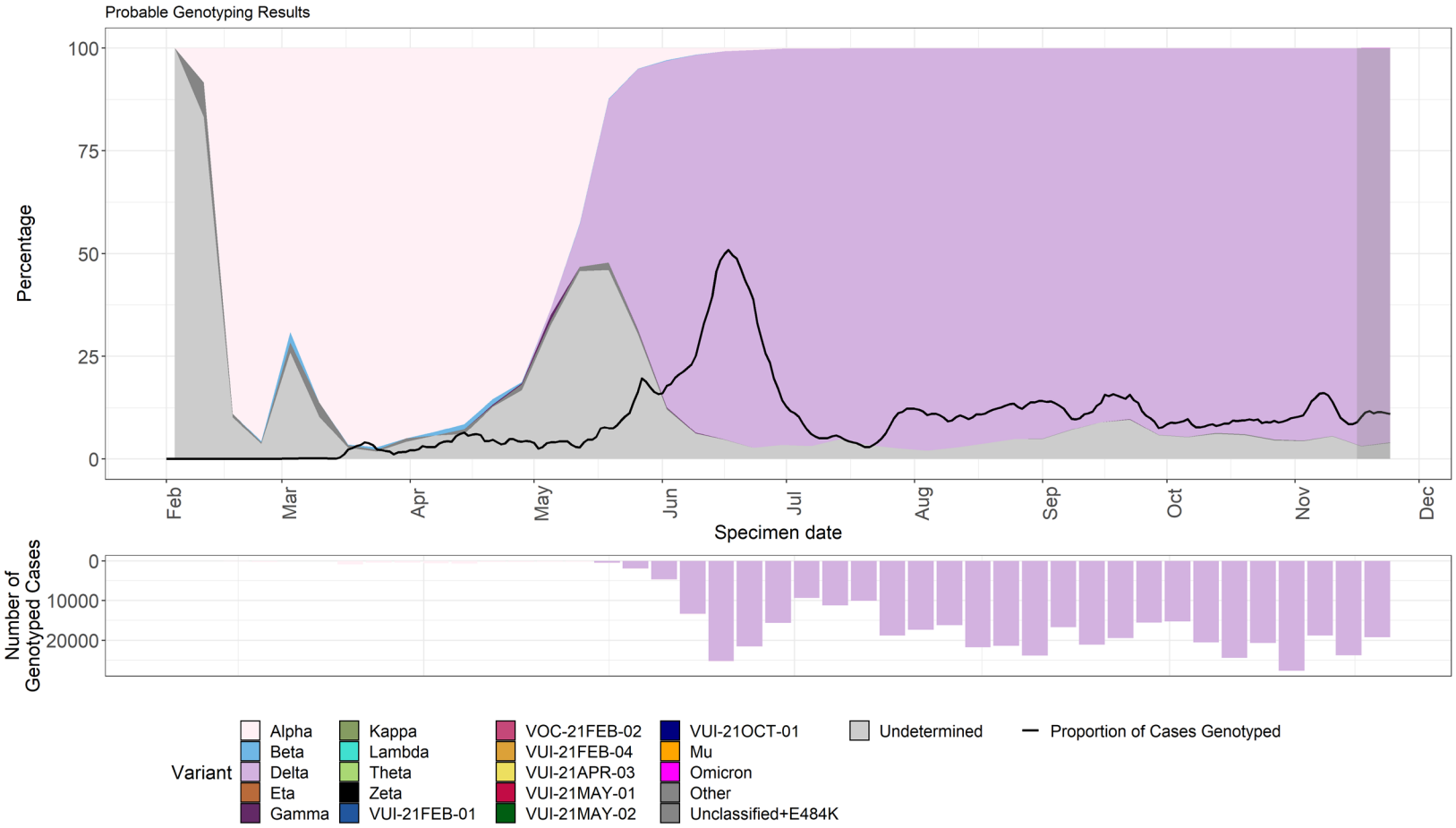


Figure 3. Variant prevalence for all England available genotyped cases from 1 February 2021 as of 30 November 2021

(Find accessible data used in this graph in underlying data.) Dashed lines indicate period incorporating issue at a sequencing site. Black line indicates proportion of cases sequenced.



Part 2. Enhanced analysis on Omicron VOC-21NOV-01 (B.1.1.529)

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

2.1 Studies for the characterisation of Omicron VOC-21NOV-01 (B.1.1.529)

Table 2 shows the studies reporting into the UKHSA Variant Technical Group for the characterisation for Omicron VOC-21NOV-01 (B.1.1.529). Some studies have commenced; others await sufficient case numbers or biological materials.

Table 2: Planned studies for the characterisation of Omicron VOC-21NOV-01 (B.1.1.529)

Transmissibility between humans	Population growth rates in sequence confirmed and SGTF (UKHSA/Imperial, SPI-M, WSI, ONS) Phylogeny (UKHSA/Edinburgh) Secondary attack rates from routine contact tracing data (UKHSA) Household transmission risk (UKHSA, ONS) Replication in vitro (G2P-UK) Population CT values (UKHSA, ONS, REACT) Incoming travel prevalence estimates and incursion risk (UKHSA) Environmental stability (UKHSA)
Infection severity and clinical characterisation	Hospitalisation and deaths cohort, including adjustment for vaccination (UKHSA/Cambridge) Severity in animal models (G2P-UK) Clinical characterisation (ISARIC)
Naturally acquired immunity	Neutralisation by convalescent sera (G2P-UK, Oxford, UKHSA) T cell epitopes (PITCH consortium) Population symptomatic reinfection risk (UKHSA, ONS) Healthcare worker all reinfection risk (UKHSA SIREN)
Vaccine-derived immunity	Predictors of being an Omicron case (REACT, Imperial) Neutralisation by vaccinee sera (G2P-UK, Oxford, UKHSA) Vaccine effectiveness against symptomatic infection and hospitalisation, using population data, 2 study designs (UKHSA) Vaccine effectiveness against infection (REACT) Vaccine effectiveness against infection and comparison with protection from previous natural infection (ONS) Vaccine effectiveness against infection in healthcare workers (UKHSA) Vaccine effectiveness in care home residents and staff (VIVALDI) Hospital admission vaccination status (UKHSA)
Therapeutics	Laboratory susceptibility testing to therapeutic monoclonals and small molecule antivirals (UKHSA, G2P)
Diagnostics	Laboratory assessment of lateral flow device performance (UKHSA Porton).

2.2 Genomic case definitions

A total of 55 mutations were identified in at least 30 of 59 initial Omicron VOC-21NOV-01 (B.1.1.529) genomes. These mutations were assessed for inclusion in the genomic definition for this variant (Table 3). Currently, insertions and deletions are not considered for inclusion in genomic definitions due to bioinformatic challenges with consistent identification. Twenty-six of the mutations were selected for the genomic definition based on the consistency of calling across the initial Omicron VOC-21NOV-01 (B.1.1.529) genomes, and their frequency in the UK and GISAID databases. Within the UK dataset, all Omicron VOC-21NOV-01 (B.1.1.529) genomes have at least 10 of the mutations selected for the genomic definition and the remaining are missing due to data quality issues. There are no non-Omicron VOC-21NOV-01 (B.1.1.529) that have more than 4 of the mutations selected for the genomic definition suggesting a high level of specificity. The genomic definition thresholds are shown in Table 4.

The number of genomes containing each mutation and their frequency in the COG UK and GISAID database are given in the table. For those that were excluded from the genomic definition, a reason for exclusion is provided. Currently, only non-synonymous mutations can be counted in the GISAID database. Insertions and deletions are not included in genomic definitions currently.

Table 3: Mutations identified in at least 30 of 59 initial Omicron VOC-21NOV-01 (B.1.1.529) genomes

Gene	Nucleotide Change	Amino Acid Change	Number of B.1.1.529 Genomes	Number of UK Genomes	Number of GISAID Genomes	Included in Genomic Definition	Reason for Exclusion
Orf1ab	2832A>G	K856R (nsp3:K38R)	58	198	882	True	
	3037C>T	-	58	1488067	-	False	Non specific
	5386T>G	-	56	39	-	False	Called as WT in more than one B.1.1.529 genomes
	6513_5del	2083_2084del (nsp3:1265_1266del)	59	-	-	-	
	8393G>A	A2710T (nsp3:A1892T)	58	48	294	True	
	10029C>T	T3255I (nsp4:T492I)	58	990212	2671361	False	Non specific
	10449C>A	P3395H (nsp5:P132H)	58	122	639	True	
	11283_11291del	3674_3677del (nsp6:105_107del)	52	-	-	-	

	11537A>G	I3758V (nsp6:I189V)	57	328	1900	False	Called as WT in one B.1.1.529 genome and present in a number of GISAID genomes
	13195T>C	-	58	186	-	True	
	14408C>T	P4715L (nsp12:P323L)	58	1477966	5392842	False	Non specific
	15240C>T	-	58	4721	-	True	
	18163A>G	I5967V (nsp14:I42V)	58	32	223	True	
S	21762C>T	A67V	54	5050		False	Non specific
	21764_21770del	69_70del	56	-	-	-	
	21846C>T	T95I	54	644590	1192955	False	Non specific
	21986_21995del	143-145del	58	-	-	-	
	22194_22196del	211del	43	-	-	-	

	221208insGCCAGAAGA	214insEPE	-	-	-	-	
	22578G>A	G339D	58	181	693	True	
	22673TC>CT	S371L	57	34	162	True	
	22679T>C	S373P	57	68	491	True	
	22687C>T	-	48	1195	-	False	Missing in a number of B.1.1.529 genomes
	22813G>T	K417N	57	1658	47142	True	
	22882T>G	N440K	58	130	9503	True	
	22898G>A	G446S	58	141	840	True	
	22992G>A	S477N	52	3980	73922	True	
	22995C>A	T478K	52	962613	2942800	False	Non specific
	23013A>C	E484A	52	75	1230	True	

	23040A>G	Q493R	52	80	444	True	
	23048G>A	G496S	52	102	654	True	
	23055A>G	Q498R	52	39	292	True	
	23063A>T	N501Y	52	286624	1339359	False	Non specific
	23075T>C	Y505H	51	43	301	False	Missing in a number of B.1.1.529 genomes
	23202C>A	T547K	59	98	824	True	
	23403A>G	D614G	58	1511816	5503009	False	Non specific
	23525C>T	H655Y	58	3152	126085	True	
	23599T>G	N679K	58	53	5380	True	
	23604C>A	P681H	58	295091	1262141	False	Non specific
	23854C>A	N764K	55	29	496	False	Missing in a number of B.1.1.529 genomes
	23948G>T	D796Y	55	959	4518	False	Missing in a number of B.1.1.529 genomes

	24130C>A	N856K	56	34	246	False	Missing in a number of B.1.1.529 genomes
	24424A>T	Q954H	55	32	212	False	Missing in a number of B.1.1.529 genomes
	24469T>A	N969K	56	33	254	False	Missing in a number of B.1.1.529 genomes
	24503C>T	L981F	55	38	225	False	Missing in a number of B.1.1.529 genomes
	25000C>T	-	58	2076	-	True	
E	26270C>T	T9I	57	1554	5525	False	Called as WT in one B.1.1.529 genome and non-specific in GISAID genomes
M	26530A>G	D3G	58	364	4358	True	
	26577C>G	Q19E	58	47	223	True	
	26709G>A	A63T	58	225	752	True	
Orf6	27259A>C	-	58	40	-	True	

Orf7b	27807C>T	-	58	217	-	True	
N	28881GG>AA	R203K	58	347261	1534994	False	Non specific
	28883G>C	G204R	58	347121	1451594	False	Non specific
	28362_28370del	31_33del	30	-	-	-	

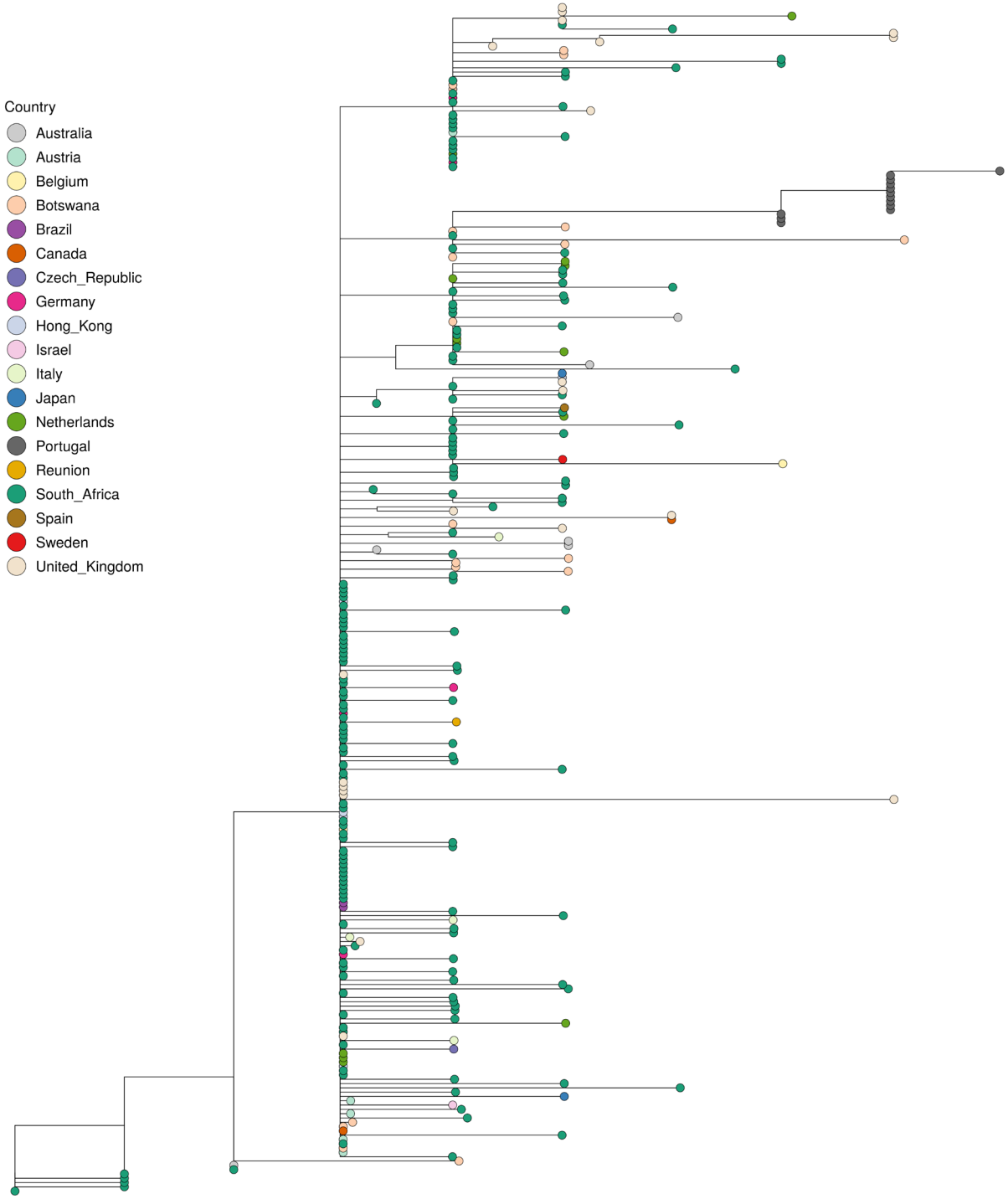
Table 4: Thresholds for genomic definition categories for Omicron VOC-21NOV-01 (B.1.1.529)

Category	Mutations Required	Wild Type Allowed	Indels Required
Confirmed	20	0	False
Probable	10	7	False
Low Quality	0	7	False

Figure 4 shows the phylogeny for Omicron VOC-21NOV-01 (B.1.1.529) genomes in GISAID (n=255) and B.1.1.529 genomes from England (n=21) up to 01 December 2021. The phylogeny shows little diversity among Omicron VOC-21NOV-01 (B.1.1.529) genomes which is compatible with a recent emergence and rapid spread. Due to mixed sequence quality, requiring the masking of informative sites from the alignment, the phylogeny is not suitable for detailed epidemiological cluster analysis. However, it supports the epidemiological data showing multiple independent introductions into England.

Figure 4: Maximum likelihood phylogeny for Omicron VOC-21NOV-01 (B.1.1.529) genomes (n=276) as of 1 December 2021

Country is indicated by tip colour. Positions masked due to data quality are provided in supplementary data. Masking was carried out using methods in Github.



2.3 Epidemiology of Omicron, VOC-21NOV-01 (B.1.1.529) in England

Confirmed Omicron VOC-21NOV-01 (B.1.1.529) cases are those which have been identified by sequencing or genotyping. Additional cases are under investigation.

The Omicron VOC-21NOV-01 (B.1.1.529) genome also 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 VOC-21NOV-01 (B.1.1.529).

Table 5. Number of confirmed (sequencing) Omicron VOC-21NOV-01 (B.1.1.529) cases, by region of residence as of 30 November 2021

Region	Number of confirmed (sequencing) cases	Proportion of cases (%)
East of England	5	23
London	14	64
North West	2	9
South East	1	5

Figure 5. Cases of Omicron VOC-21NOV-01 (B.1.1.529) in England by region as of 30 November 2021

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

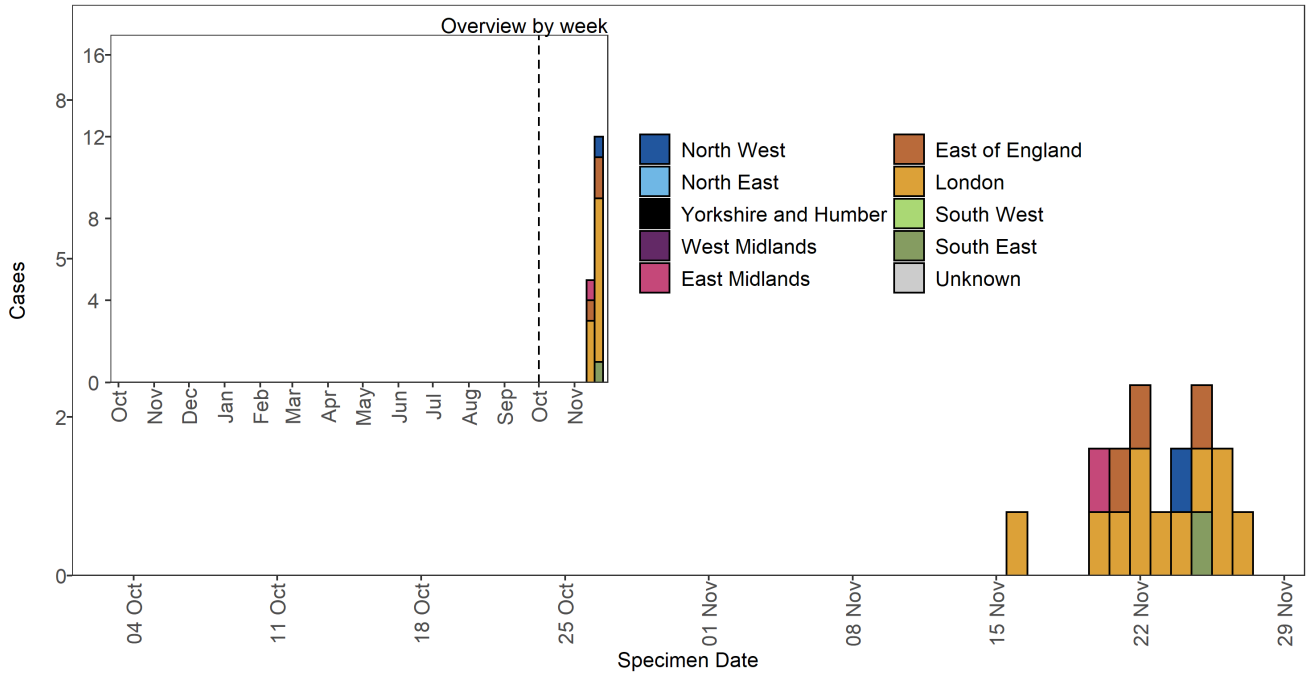


Figure 6. Cases of Omicron VOC-21NOV-01 (B.1.1.529) in England by travel status as of 30 November 2021

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

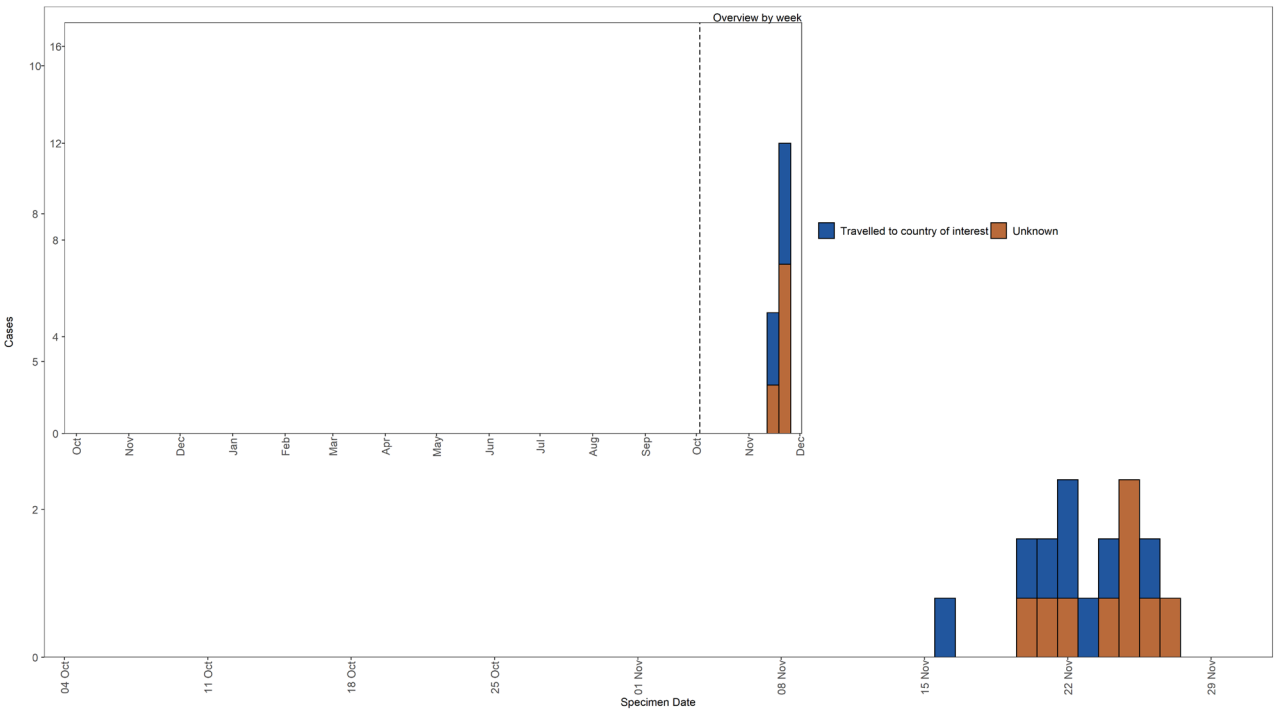


Figure 7. Cases of Omicron VOC-21NOV-01 (B.1.1.529) in England by age and sex as of 30 November 2021

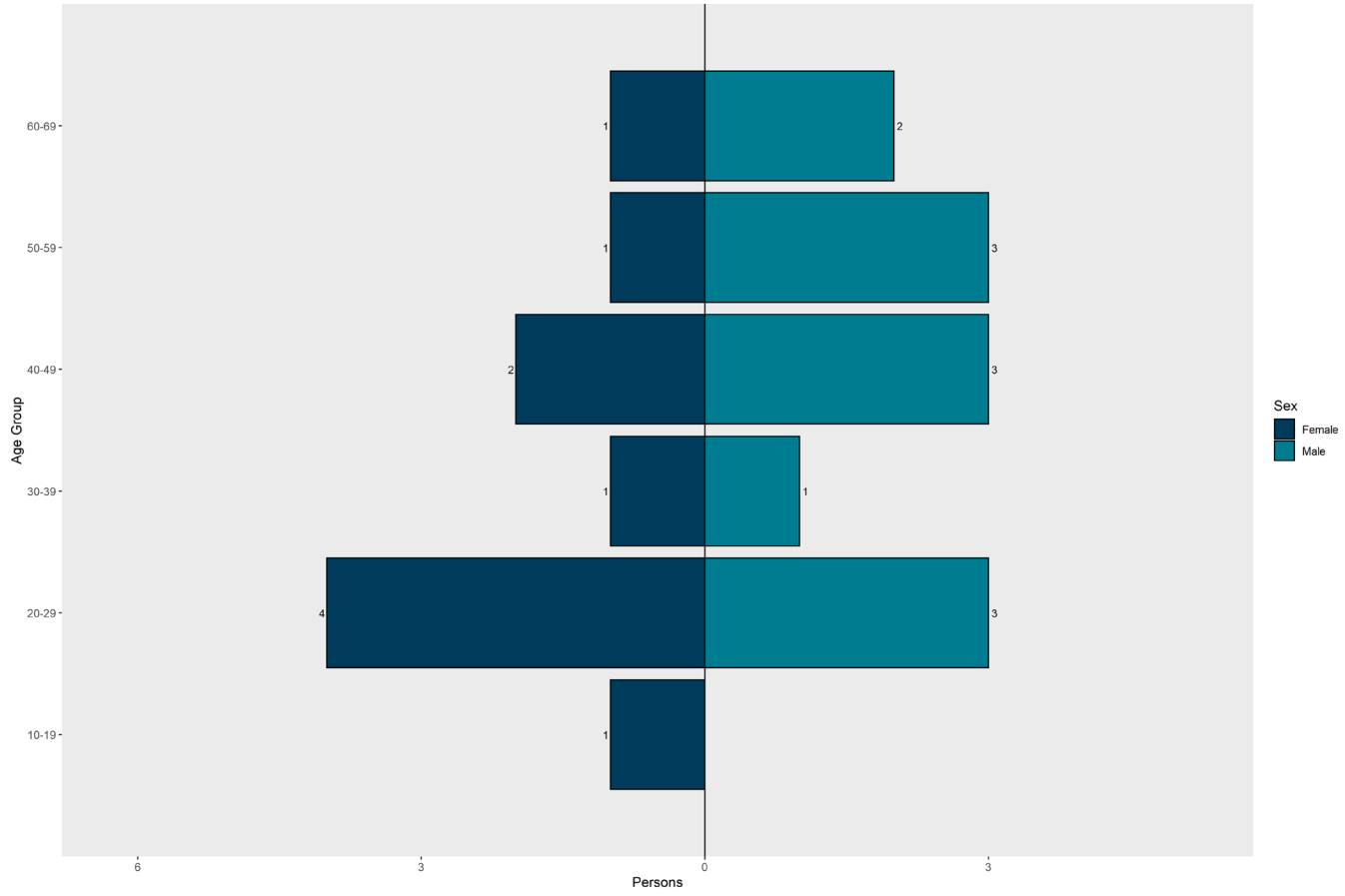


Table 6. Number of confirmed Omicron VOC-21NOV-01 (B.1.1.529) cases by vaccine status

Vaccine Status	Number of confirmed cases
> 14 Days post second dose	12
> 28 Days post first dose	2
Unvaccinated	6
Unknown	2
Total	22

Severity outcomes

To date, none of the cases of Omicron VOC-21NOV-01 (B.1.1.529) are known to have been hospitalised or died. As a result, it is not possible to compare the risk of hospitalisation or death with other variants. However, it should be noted that most of the cases have a specimen date that is very recent and that there is a lag between onset of infection and hospitalisation and death.

Future updates will assess severe outcomes from Omicron VOC-21NOV-01 (B.1.1.529) cases against Delta cases from the same time period.

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

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

2.4 Epidemiology of S gene target failure

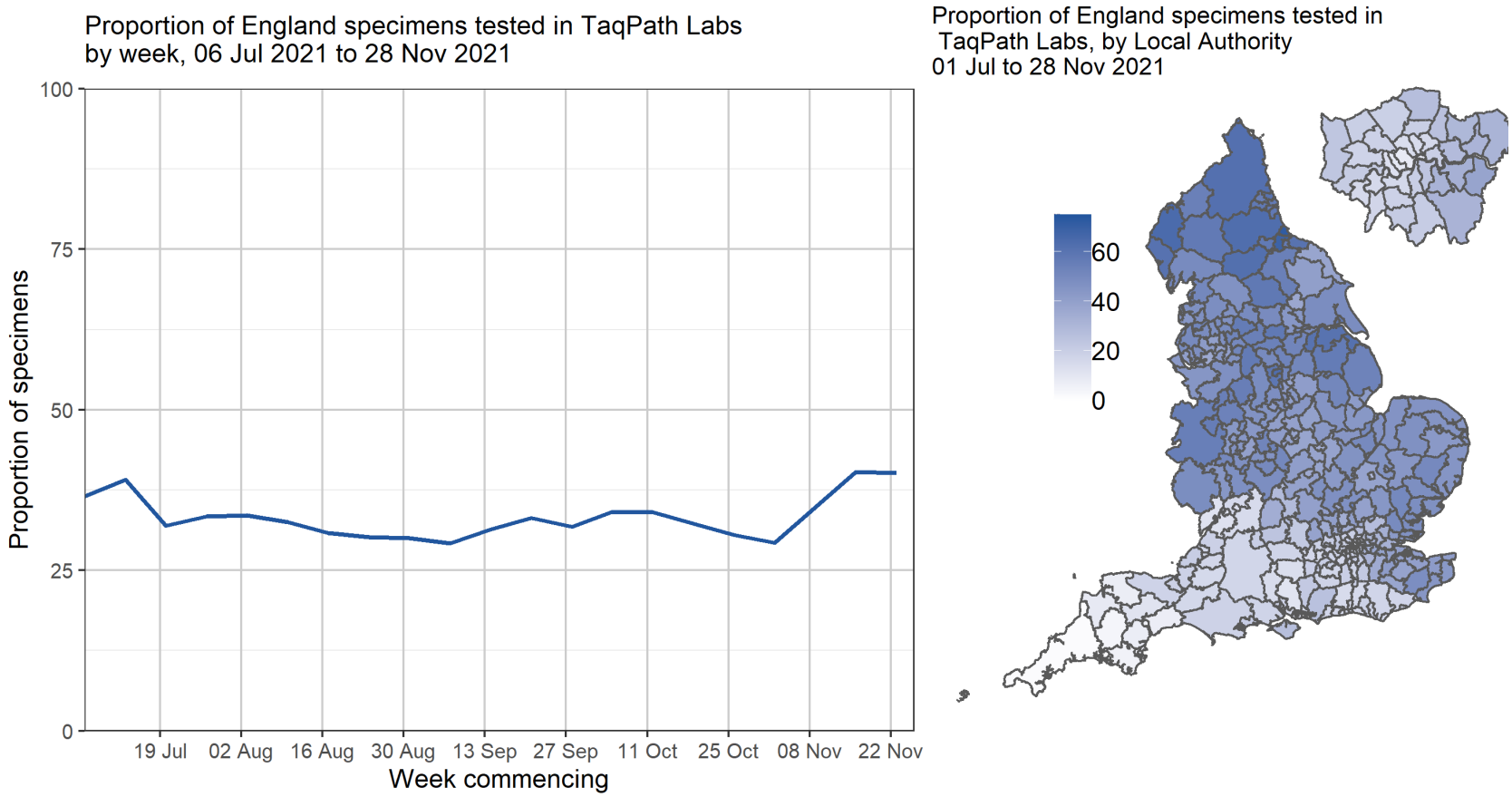
The proportion of England specimens tested in the lighthouse laboratories using the assay which produces the S gene target failure, and which report to UKHSA surveillance systems, has been relatively constant over time at 30 to 35% (Figure 8). This however varies by geography, with lower coverage since July 2021 in local authorities in the South West of England.

The numbers of SGTF cases are now increasing, although the absolute numbers are very small (Figure 9,10 and 12). Figure 11 shows the proportion of Omicron VOC-21NOV-01 (B.1.1.529) positive tests with SGTF as tested in Alderley Park, Glasgow and Milton Keynes.

The likelihood of SGTF depends on the whether the Spike 69/70 deletion is common in circulating lineages. The dominant lineage in the UK is Delta, accounting for 99.8% of cases. Since the beginning of July, 0.15% of sequenced Delta lineages have the Spike 69/70 deletion. This proportion has decreased over time (Figure 13). Over the last 8 weeks (6 October onwards), only 0.056% of sequenced Delta genomes had the deletion.

Figure 8. Coverage of TaqPath laboratories over time and by local authority, England as of 30 November 2021

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



TaqPath Labs = Newcastle, Alderley Park, Milton Keynes and Glasgow Lighthouse Labs
Includes both positive and negative SARS-CoV specimens from Pillar 1 and 2.
Excludes lateral flow device tests and does not account for use of other assays in these laboratories. Data source: USD

Figure 9. Number of COVID-19 cases with S gene positive/SGTF and proportion SGTF among those tested in TaqPath Labs by week as of 30 November 2021

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

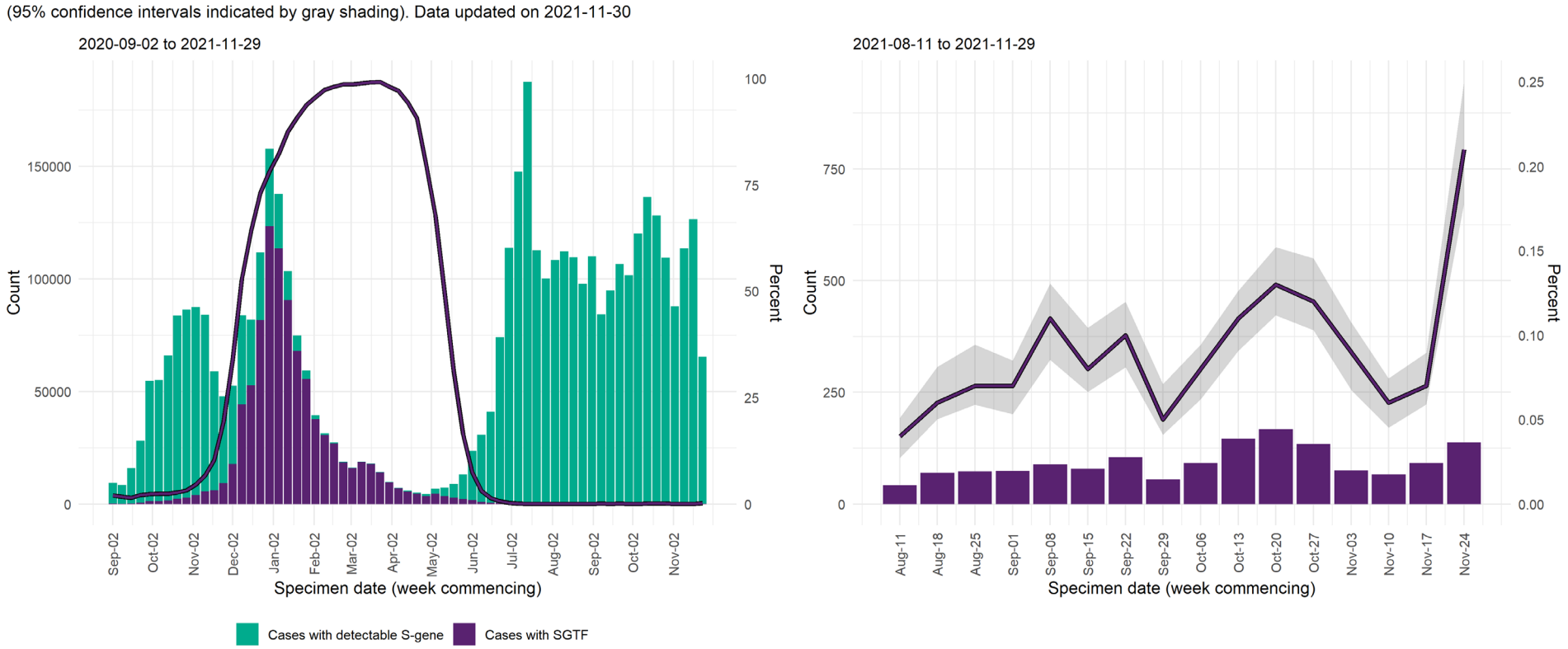
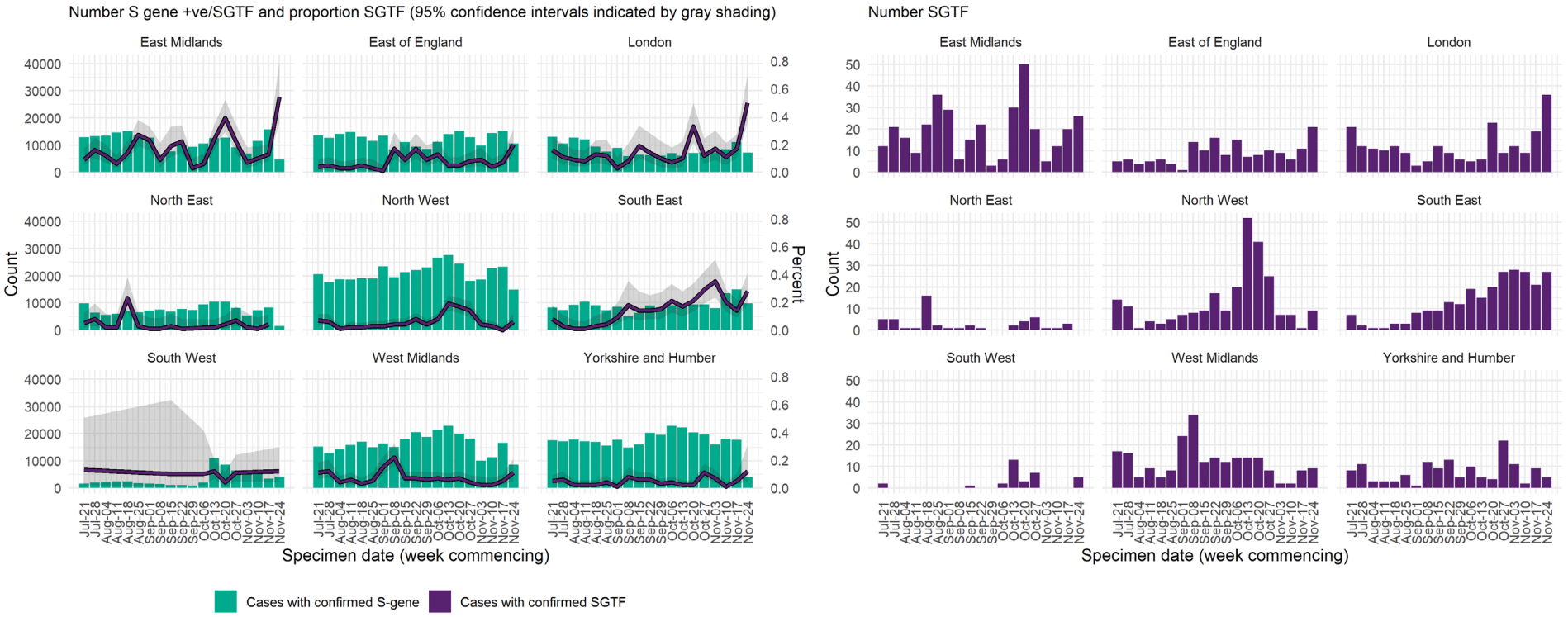


Figure 10. Weekly COVID-19 cases with detectable S gene or SGTF among those tested in TaqPath Labs, by region of residence as of 30 November 2021 (21 July 2021 to 29 November 2021)

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



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 11 shows the proportion of Omicron VOC-21NOV-01 (B.1.1.529) positive tests with SGTF as tested in Alderley Park, Glasgow and Milton Keynes. The vertical dashed line shows date of most recent Omicron VOC-21NOV-01 (B.1.1.529) sequences – samples to the right of this line are currently being sequenced.

Figure 11. Timing of SGTF and sequencing data: proportion of positive Omicron VOC-21NOV-01 (B.1.1.529) tests with SGTF tested in selected lighthouse laboratories as of 1 December 2021

Supplementary data are not available for this figure.

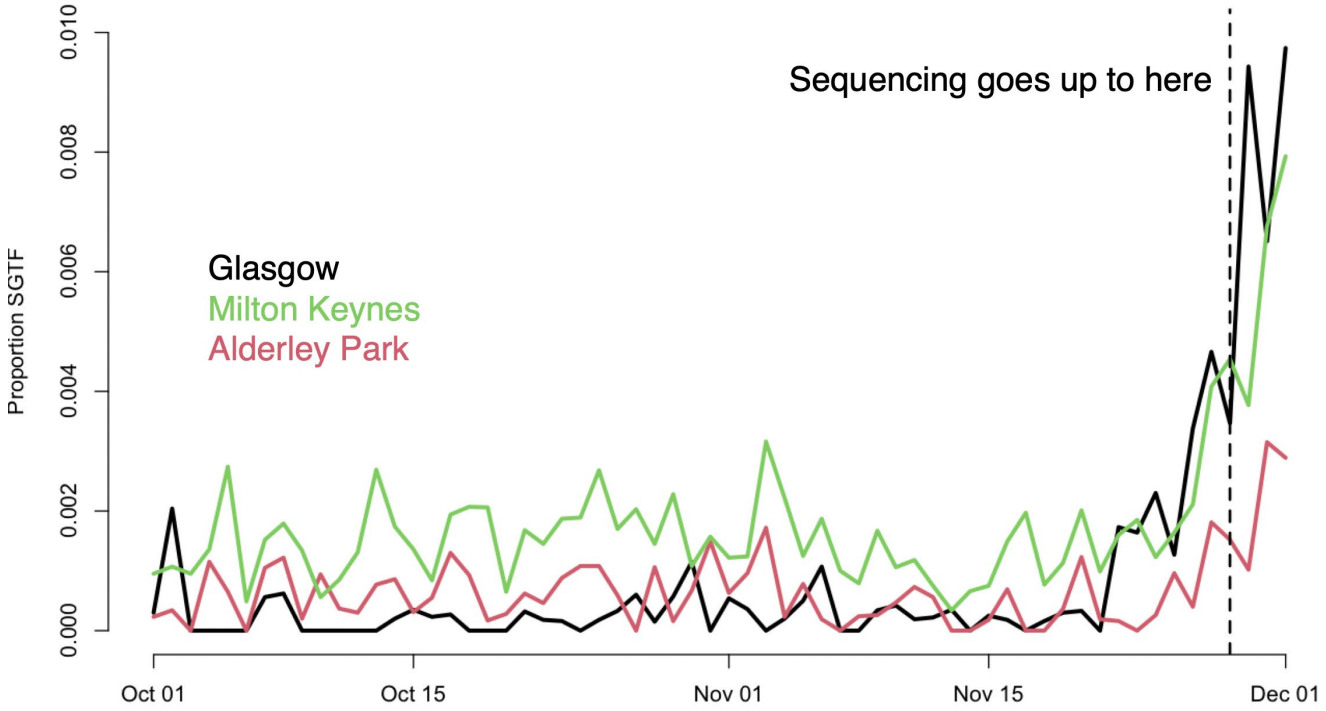


Figure 12. Number and distribution of variants per week among sequenced SGTF specimens as of 30 November 2021 (6 January 2021 to 24 November 2021)

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

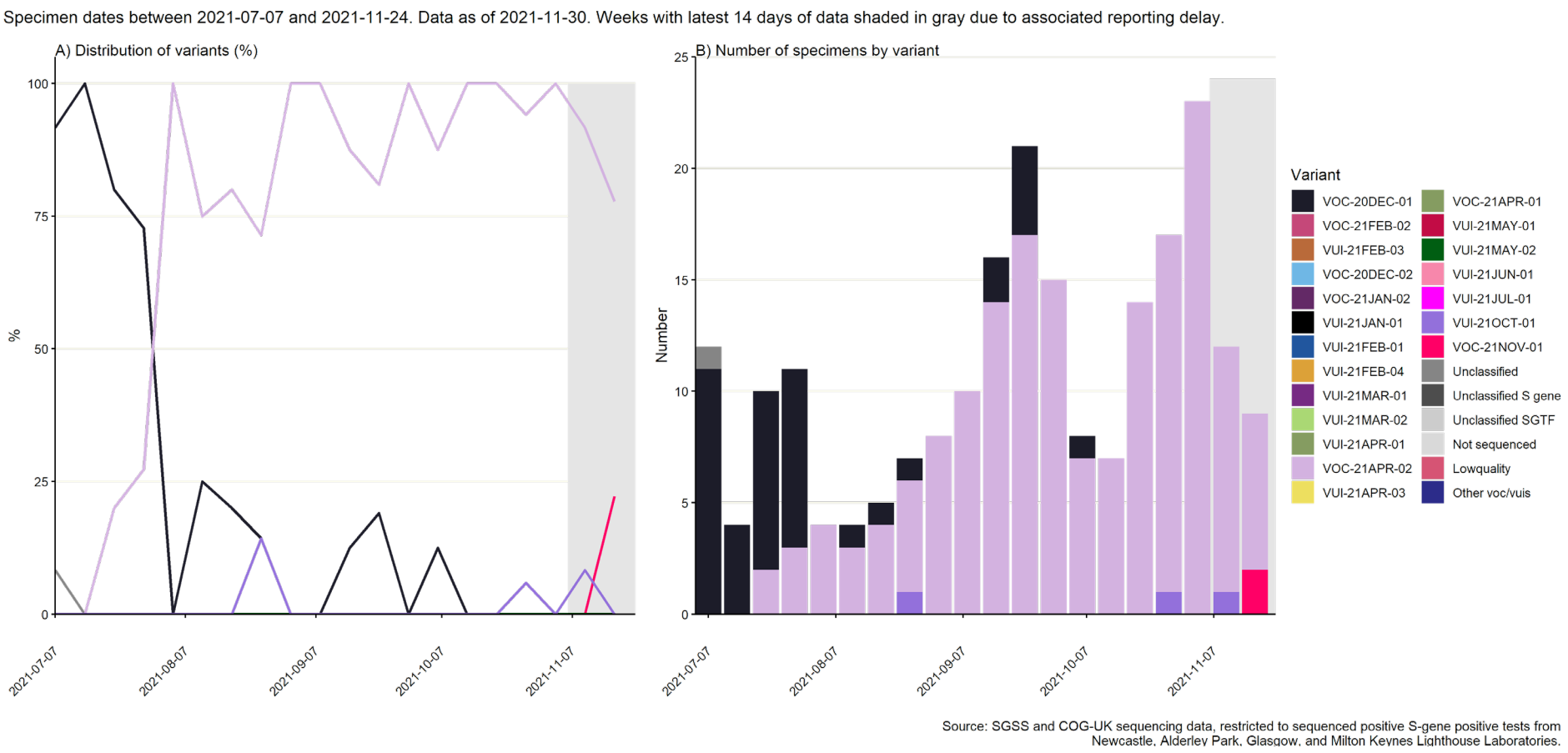
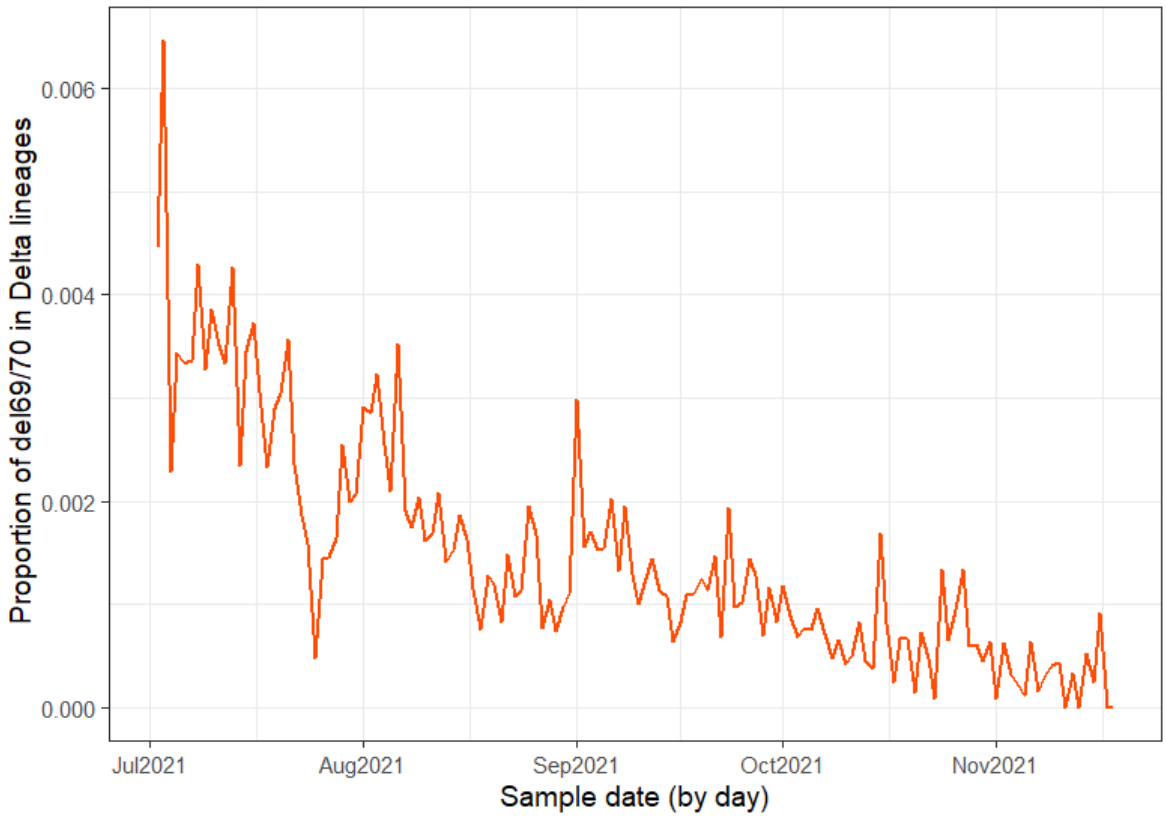


Figure 13 shows the proportion of sequenced Delta genomes (B1.617.2 and all AY sublineages) with a deletion at Spike 69/70. For the time period shown (1 July to end of November), 0.15% of sequenced Delta genomes had the deletion. Over the last 8 weeks (6 October onwards), only 0.056% of sequenced Delta genomes had the deletion.

Figure 13. Proportion of sequenced Delta lineages with a deletion in Spike at amino acid positions 69/70

Supplementary data are not available for this figure



Growth modelling

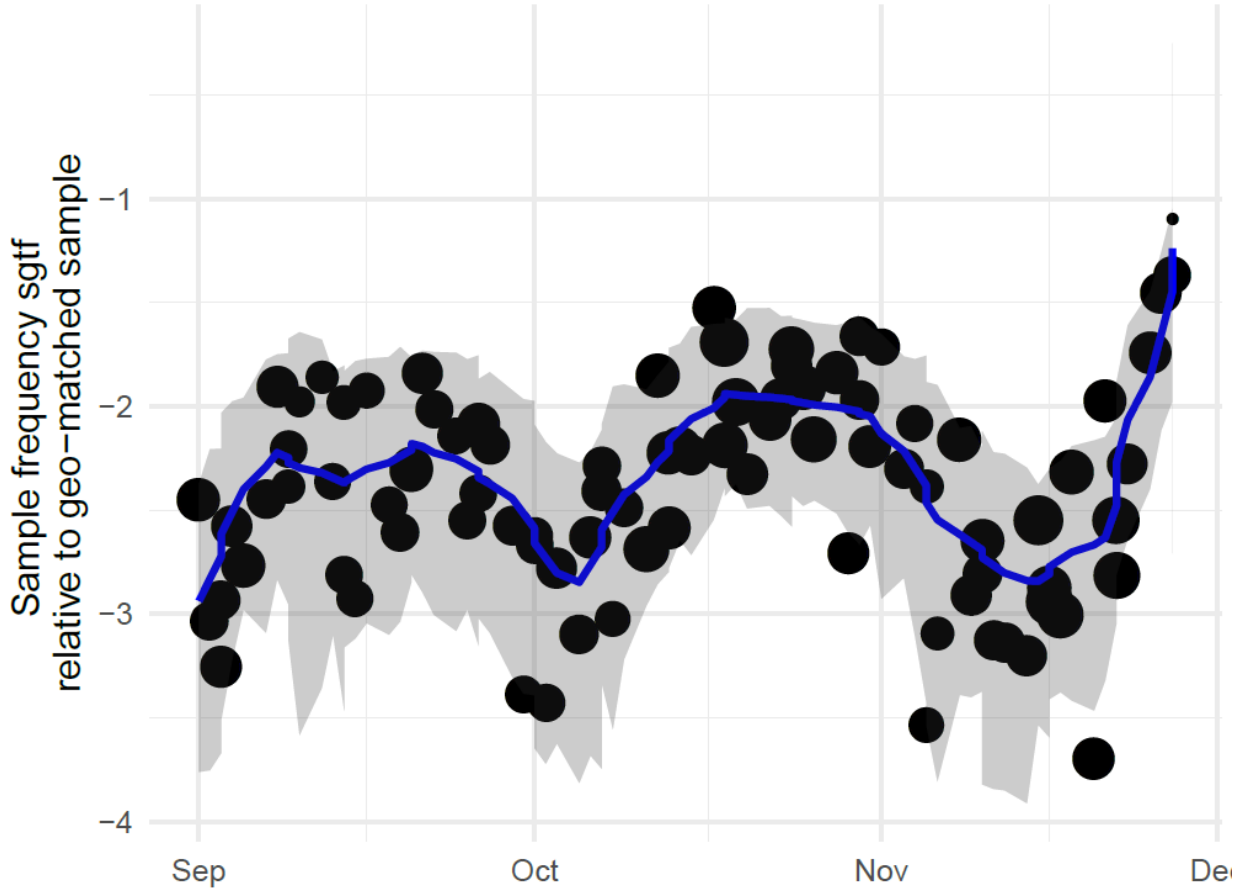
Logistic growth rates for the number of SGTF for the country as a whole and for each UK region are shown in Figures 14, 15 and 16. Growth rates are computed relative to the number of S gene positive cases circulating in the same region (geo-matched sample). Sample inclusion criteria are: 1) A non-traveller as determined by matching each case against passenger locator forms and managed quarantine service test codes 2) Collected from Pillar 2 testing. The growth rate is estimated by logistic regression of the number of SGTF on time of sample collection. A growth rate of 0 would indicate parity with S gene positive cases. Based

on a logistic growth model, the country-wide analysis yields a growth rate of 141% per week for SGTF in the most recent week.

The sample frequency of SGTF cases across the UK has increased above its usual range in the last week.

Figure 14. Sample frequency of SGTF cases as compared to S gene positive cases

Supplementary data is not available for this figure.



The frequency of SGTF cases and the logistic growth rate of SGTF cases changes over time but the change in the last week is pronounced, with a growth rate of 141%. Logistic growth rate is a metric for showing if SGTF is growing compared to S gene target positive (SGTP) variants circulating at the same time in the same place. It is calculated using cases which are not in travellers, as far as can be ascertained. If SGTF and SGTP variants were growing at the same rate, the LGR would be 0. The finding of 141% indicates that SGTF is growing faster,

and can be considered a strong early signal. However, the number cannot be interpreted as a change in transmissibility or an increase in the absolute number of cases of the variant.

Figure 15. Estimated logistic growth rate for SGTF cases per week over the last 12 weeks

Supplementary data is not available for this figure.

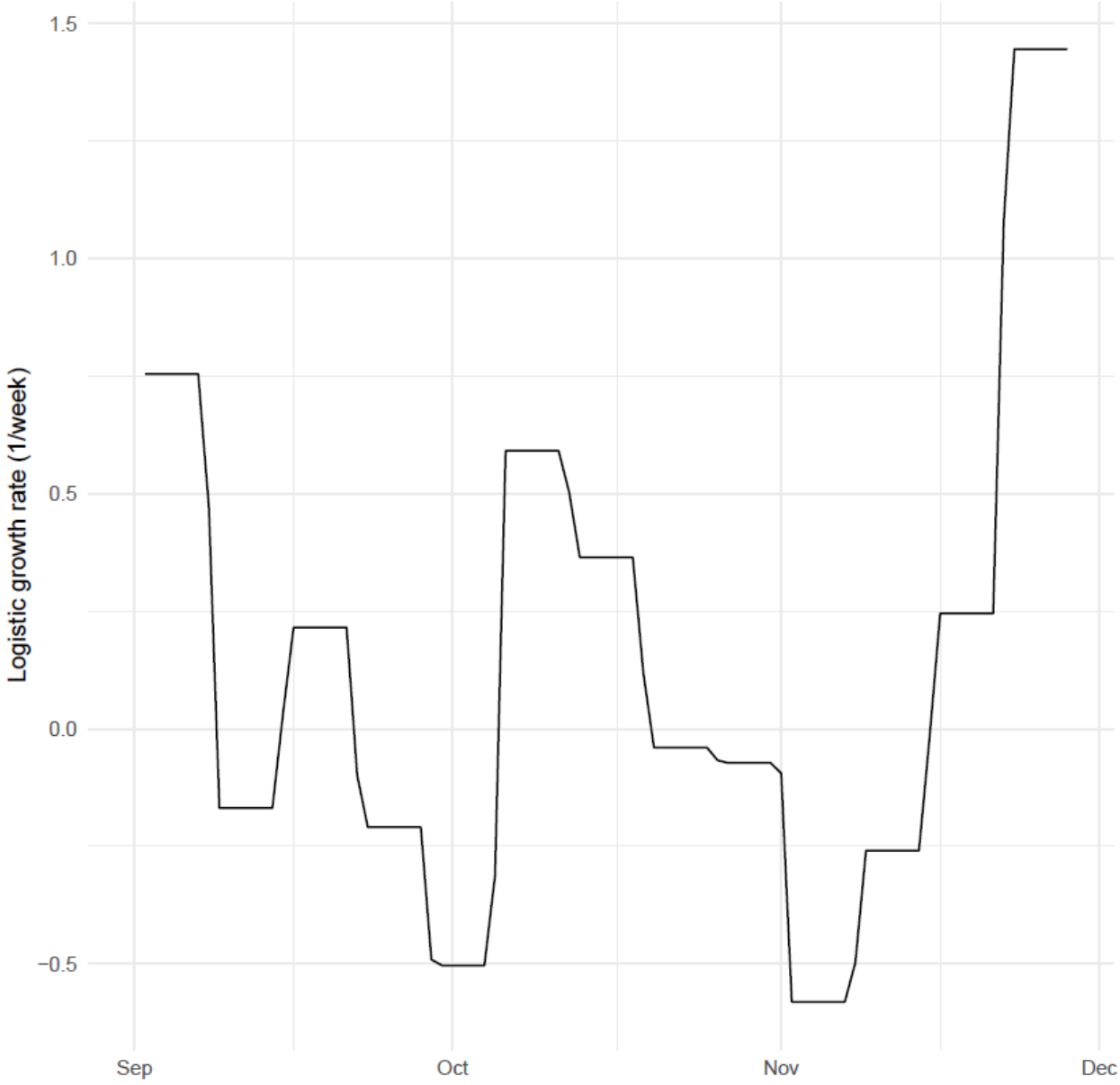
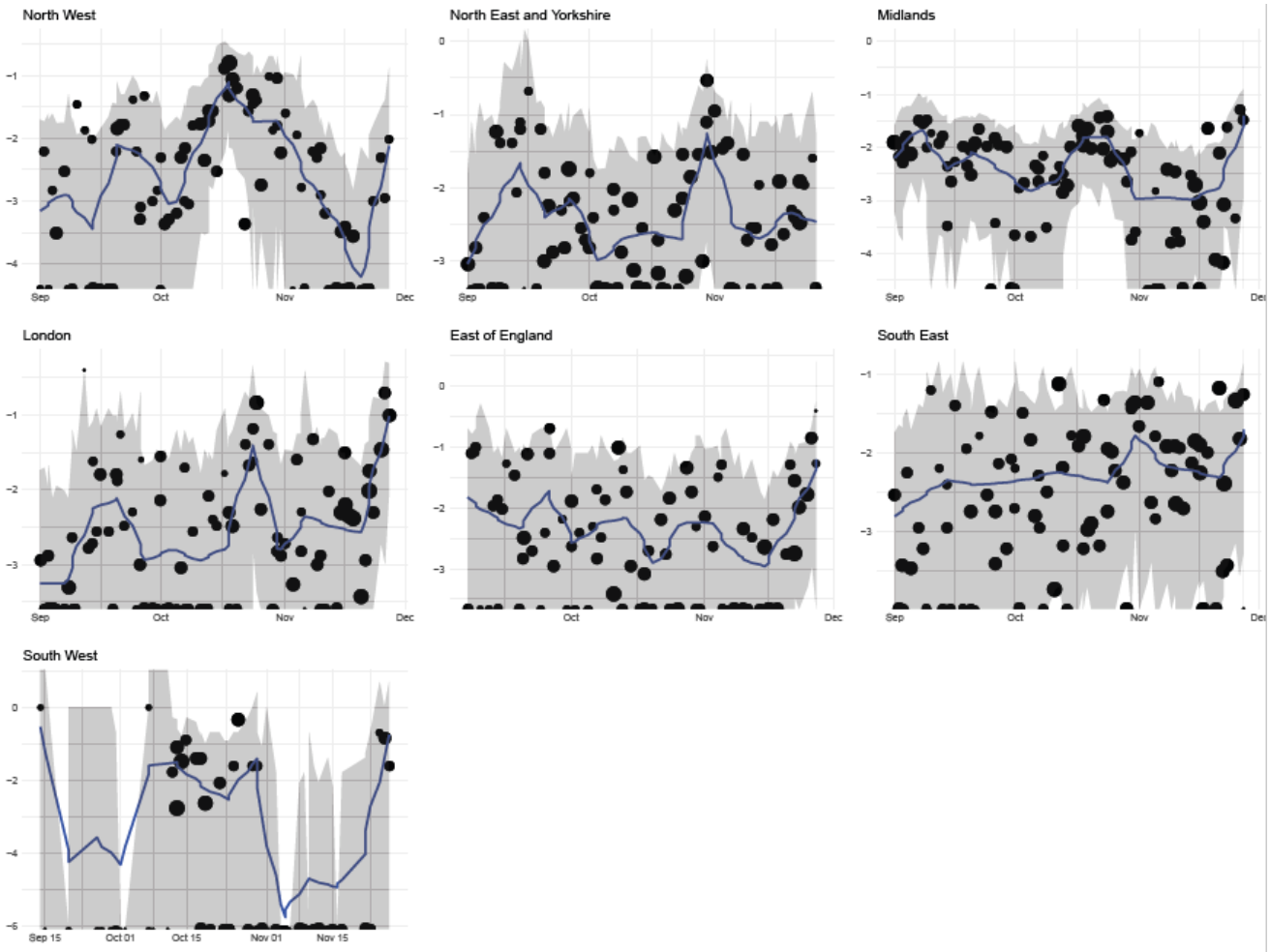


Figure 16. Sample frequency of SGTF cases as compared to geography-matched sample of S gene positive cases for each UK region

Supplementary data is not available for this figure.

In contrast to previous briefings, data from the East and West Midlands, and from the North East and Yorkshire, respectively, has been amalgamated because SGTF numbers were low.



2.5 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 (Figure 17). 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. For the detection of Omicron VOC-21NOV-01 (B.1.1.529) in wastewater, the following definition is based on the detection of a number of SNPs from the list in the official definition is noted below. No distinction is made between SNPs which can be used to define wastewater detections.

Confirmed – ≥ 16 of 22 signature SNPs detected, ≥ 9 of 20 unique SNPs detected and co-occurrence detected on at least 7. If ≥ 16 signature SNPs and ≥ 9 unique SNPs are present, but those co-occurring are not covered, confirmed presence can also be assigned.

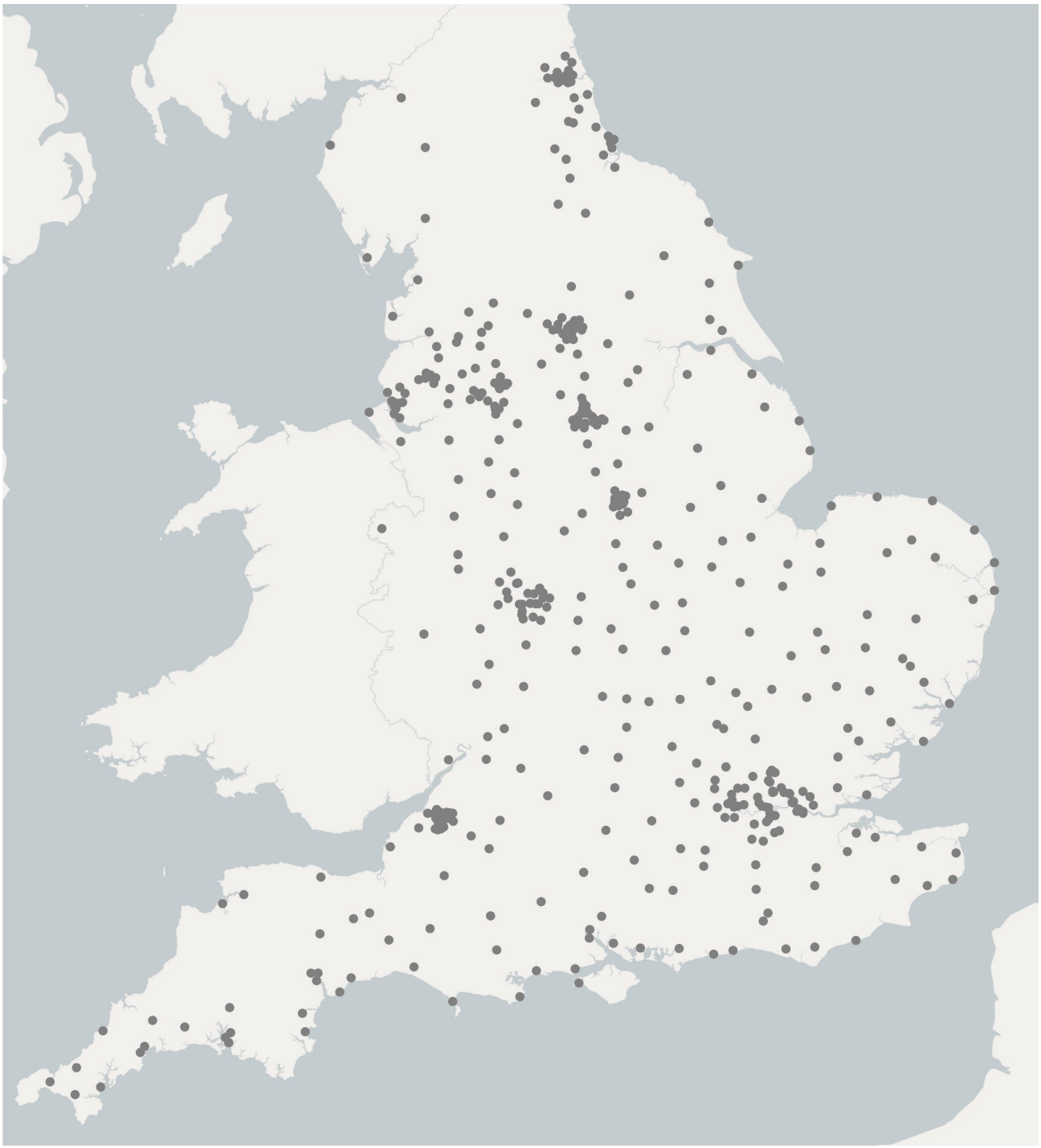
Possible – ≥ 10 of 22 signature SNPs detected and ≥ 6 of 20 unique SNPs detected. If < 10 signature SNPs and ≥ 6 unique SNPs are detected, but ≥ 9 SNPs are not covered possible presence can be assigned if those not covered are present across 2 dates from the same site, but in the same sequencing run.

Not detected - < 7 of 22 signature SNPs detected.

Applying this definition, wastewater samples collected from sites across England between 1 and 21 November have been re-analysed. There was no robust evidence for the presence of Omicron VOC-21NOV-01 (B.1.1.529) in these samples. Wastewater samples will continue to be sequenced and results reported to public health teams.

Figure 17. Existing wastewater monitoring coverage across England

Supplementary data is not available for this figure.

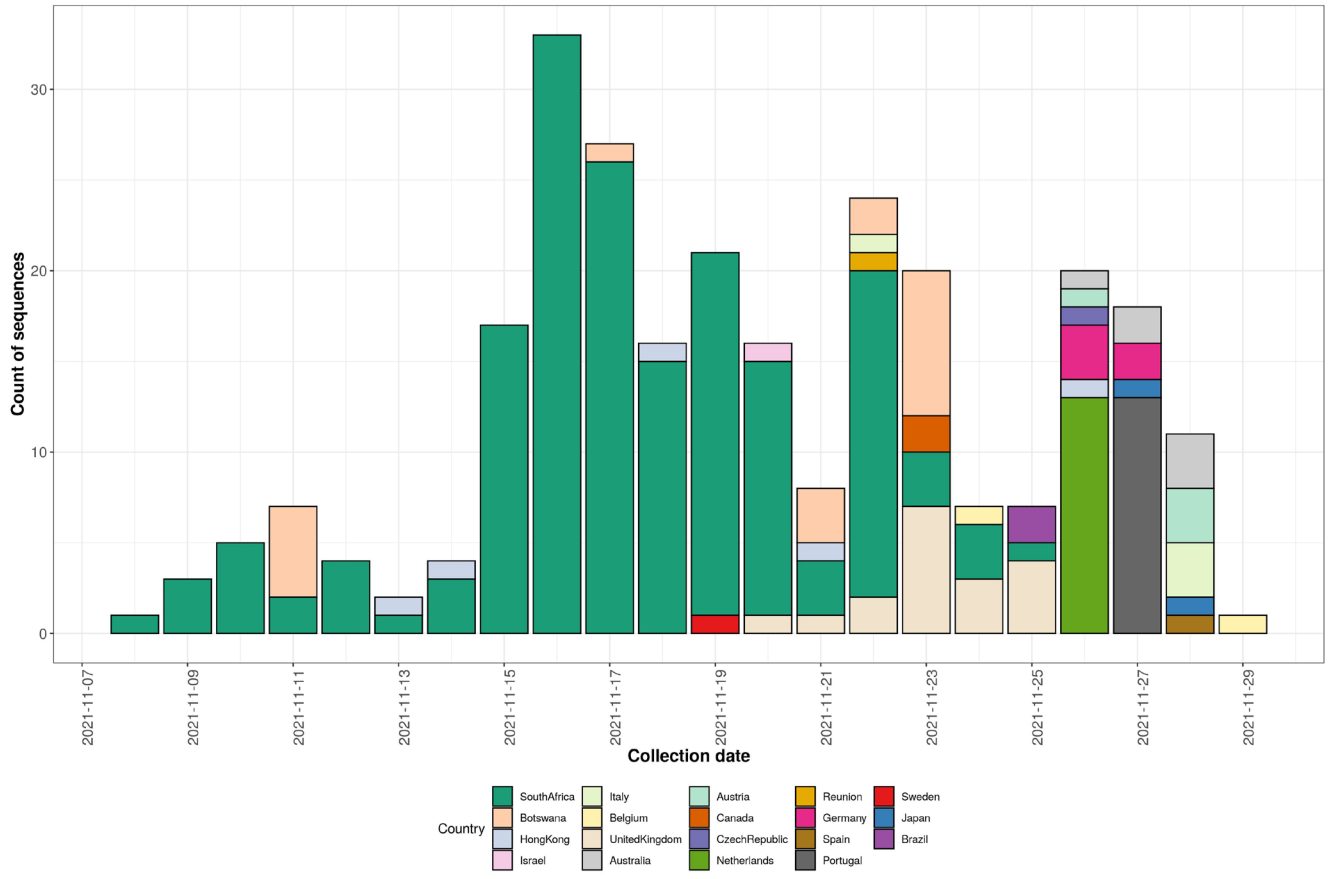


2.6 International epidemiology

As of 1 December 2021, 272 sequences on GISAID meet the pangolin B.1.1.529 definition for the Omicron variant, from 19 countries including the United Kingdom as shown in (Figure 18). The first upload was by Hong Kong on the 22 November 2021 with a collection date of 13 November 2021. The earliest known sequence (based on collection date) was uploaded by South Africa with a collection date of 8 November 2021.

Figure 18. Count of Omicron VOC-21NOV-01 (B.1.1.529) classified sequences by date of collection uploaded to GISAID as of 1 December 2021

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



Sources and acknowledgments

Data sources

Data used in this briefing 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), and the UKHSA Case and Incident Management System (CIMS). Data on international cases is derived from reports in GISAID.

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

Authors of this report

UKHSA Genomics Cell

UKHSA Outbreak Surveillance Team

UKHSA Epidemiology Cell

UKHSA Contact Tracing Data Team

UKHSA International Cell

UKHSA Environmental Monitoring for Health Protection Team

Contributions from the Variant Technical Group Members

Variant Technical Group members and contributors

The UK Health Security Agency Variant Technical Group includes members and contributors from the following organisations: UKHSA, Public Health Wales, Public Health Scotland,

Public Health Agency Northern Ireland, the Department of Health and Social Care, Imperial College London, London School of Hygiene and Tropical Medicine, University of Birmingham, University of Cambridge (including the MRC Biostatistics Unit), University of Edinburgh, University of Liverpool, the Wellcome Sanger Institute, Genotype to Phenotype Consortium, SPI-M.

Acknowledgements

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

About the UK Health Security Agency

The UK Health Security Agency is an executive agency, sponsored by the Department of Health and Social Care.

Version 1.0

Published: December 2021

Publishing reference: GOV-10547

UKHSA supports the UN Sustainable Development Goals