



UK Health  
Security  
Agency

# SARS-CoV-2 variant data update, England

## Version 20

14 January 2022

This edition provides an update on previous data noted within the technical [briefings and variant data updates](#) up to 10 December 2021.

# Contents

Part 1. Surveillance overview .....	3
Sequencing coverage .....	4
Part 2. Data on individual variants .....	8
Alpha – VOC-20DEC-01 (B.1.1.7) .....	8
Beta – VOC-20DEC-02 (B.1.351).....	12
Gamma – VOC-21JAN-02 (P.1).....	16
Delta – VOC-21APR-02 (B.1.617.2) with mutations at Spike:484 .....	20
VUI-21OCT-01 (AY 4.2) .....	25
Mu – VUI-21JUL-01 (B.1.621).....	28
Sources and acknowledgments .....	31
Data sources .....	31
Variant Technical Group.....	31

## Part 1. Surveillance overview

World Health Organization (WHO) nomenclature from 11 January 2022 is incorporated. Tables 1a and 1b show the current variants of concern (VOC), variants under investigation (VUI), and variants in monitoring (VIM) detected and not detected in the United Kingdom (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 under investigation	Variants in monitoring
Alpha (B.1.1.7) VOC-20DEC-01	VUI-21OCT-01 (AY.4.2) <sup>†</sup>	B.1.640
Beta (B.1.351) VOC-20DEC-02	Mu (B.1.621) VUI-21JUL-01	Delta + E484K
Gamma (P.1) VOC-21JAN-02		AY.33
Delta (B.1.617.2 and sub-lineages) VOC-21APR-02		AY.34 (Delta + Q677H)
Omicron (B.1.1.529 and sub-lineages) VOC-21NOV-01		AY.43 (N:Q9L)
		BA.2 <sup>††</sup>

<sup>†</sup> AY.4.2 is a sub-lineage within Delta that has been assigned as a distinct VUI.

<sup>††</sup> BA.2 is a sub-lineage within Omicron that has been assigned as a distinct VIM.

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

Variants of concern	Variants under investigation	Variants in monitoring
	VUI-21JAN-01 (P.2)	C.37 <sup>*</sup>
	VUI-21FEB-04 (B.1.1.318)	B.1.526
	VUI-21FEB-03 (B.1.525)	B.1 with 214insQAS
	VUI-21APR-01 (B.1.617.1)	C.1.2
	VUI-21APR-03 (B.1.617.3)	C.37 descendant (S:L5F, G75V, D614G, L452Q, E484K, P499R, N501T, H655Y, P681R)
		B.1.619
		B.1.214.2

<sup>\*</sup> Previously VUI-21JUN-01, de-escalated on 20 October 2021.

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

Enhanced analysis of Omicron VOC-21NOV-01 (B.1.1.529) is available in [Technical Briefing 34](#).

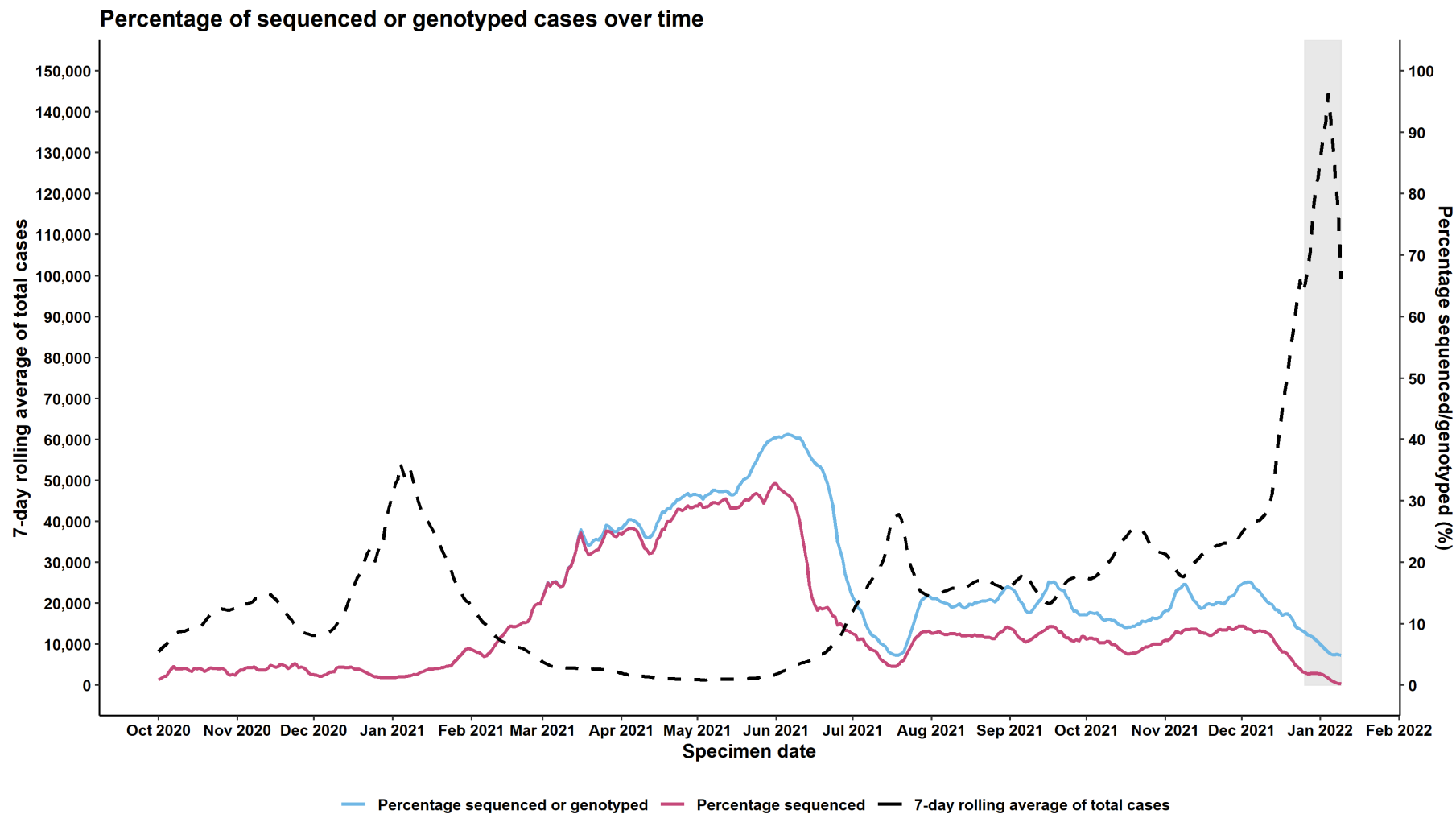
## Sequencing coverage

[Figure 1](#) shows the proportion of cases that have linked to a valid sequencing result (sequences included have 50% of the genome with sufficient read coverage) or genotyping polymerase chain reaction (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 is stable ([Figure 1](#)) and similar proportions are sequenced and genotyped across each region. Currently, the sequencing strategy for both Pillar 1 and 2 is:

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

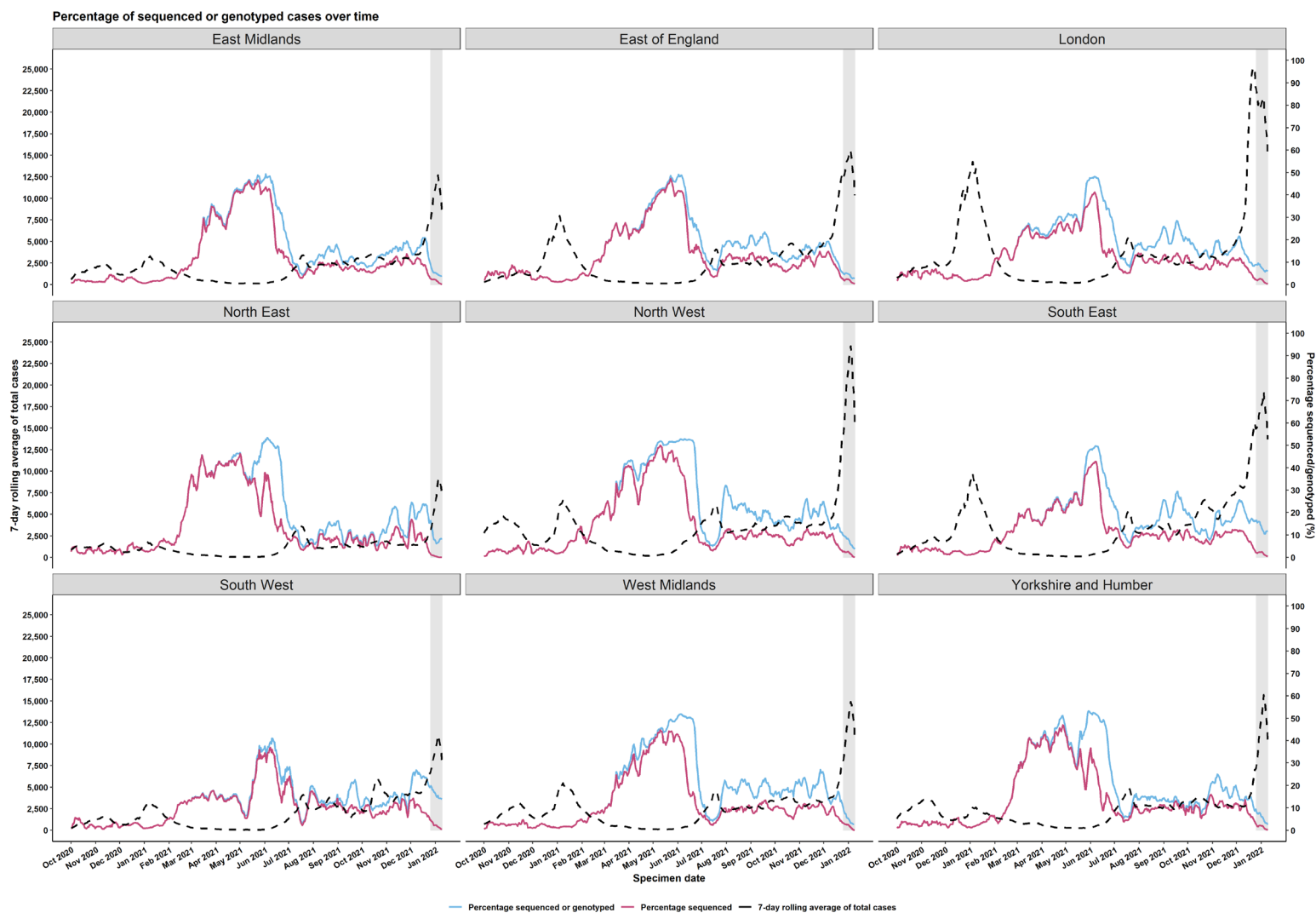
**Figure 1. Coverage of sequencing with a valid result and genotyping over time (1 October 2020 to 9 January 2022)**



Data extract from 10 January 2022; data from 01 October 2020 to 09 January 2022.  
 Grey shading was applied to the previous 14 days to account for reporting delays in sequencing data.

Grey shading was applied to the previous 14 days to account for reporting delays in sequencing data. (The data used in this graph can be found in the [accompanying spreadsheet.](#))

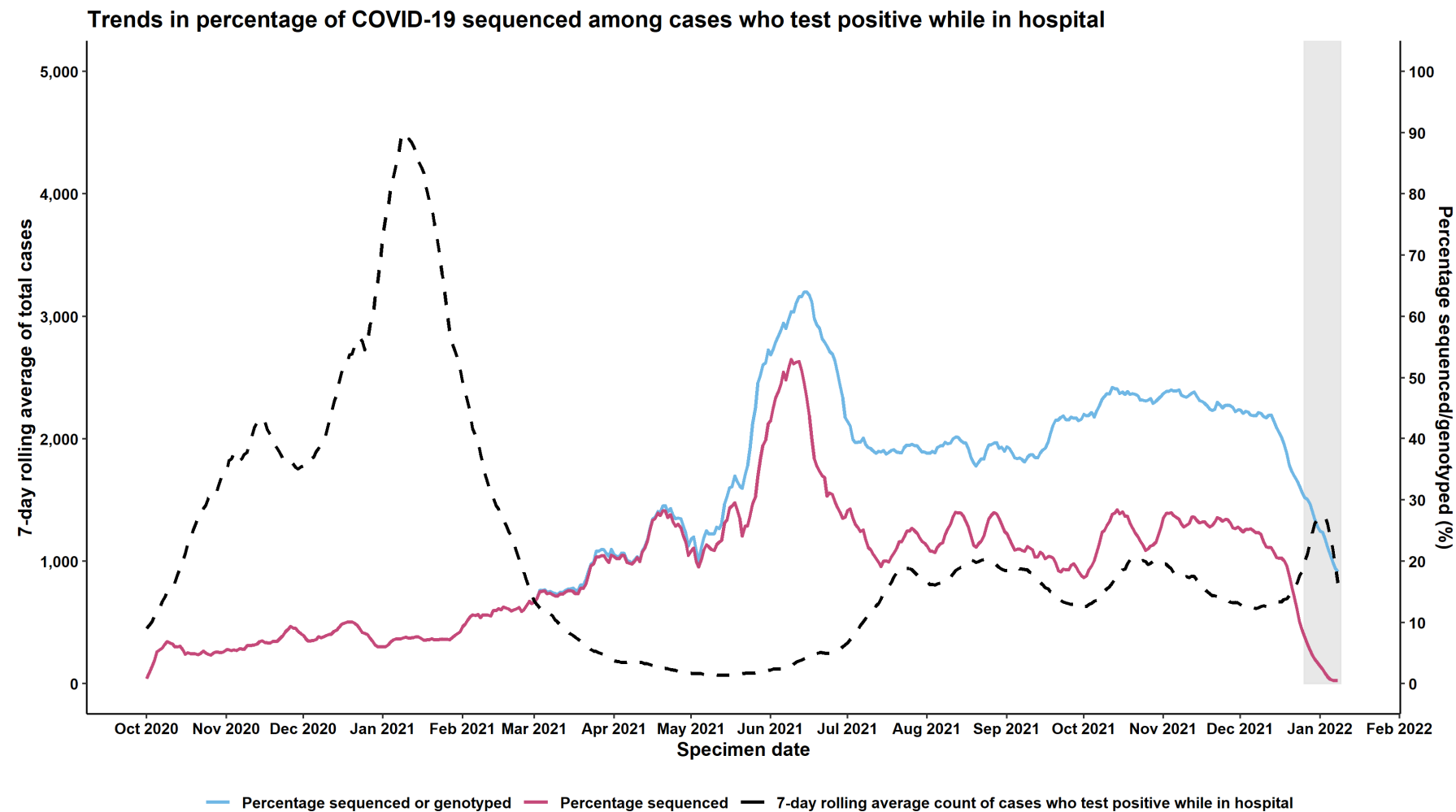
**Figure 2. Coverage of sequencing with a valid result and genotyping over time by region (1 October 2020 to 9 January 2022)**



Data extract from 10 January 2022; data from 01 October 2020 to 09 January 2022. Grey shading was applied to the previous 14 days to account for reporting delays in sequencing data. There were 15004 cases missing PHEC that were 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 9 January 2022)**



Data extract from 10 January 2022; data from 01 October 2020 to 09 January 2022.  
Grey shading was applied to the previous 14 days to account for reporting delays in sequencing data.

Grey shading was applied to the previous 14 days to account for reporting delays in sequencing data. (The data used in this graph can be found in the [accompanying spreadsheet](#).)

## Part 2. Data on individual variants

### Alpha – VOC-20DEC-01 (B.1.1.7)

This variant was designated VUI 202012/01 (B.1.1.7) on detection and on review re-designated as VOC-20DEC-01 (202012/01, B.1.1.7) on 18 December 2020. This was named Alpha by WHO on 31 May 2021.

#### Epidemiology

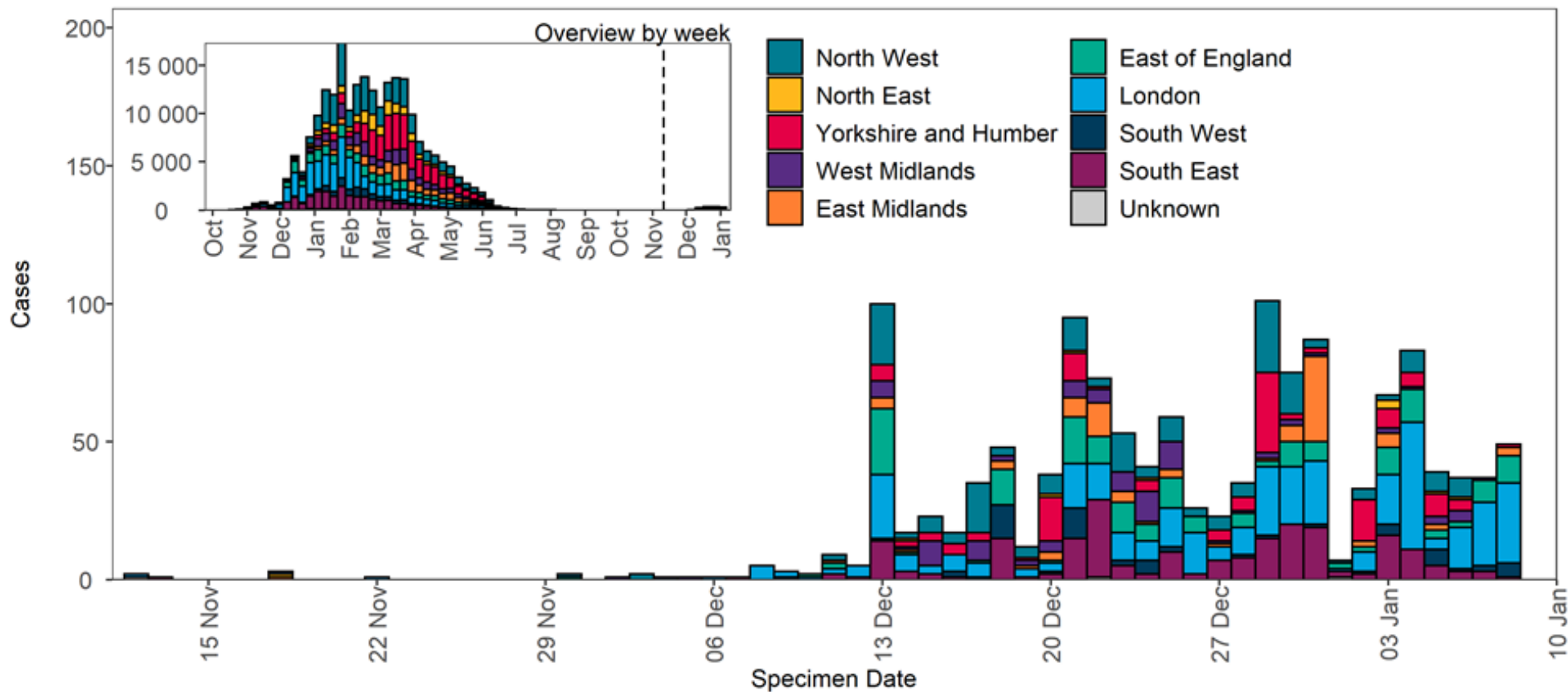
**Table 2. Number of confirmed (sequencing) and provisional (genotyping) Alpha - VOC-20DEC-01 (B.1.1.7) cases, by region of residence as of 10 January 2022**

Region	Confirmed case number	Provisional case number	Total case number	Case proportion
East Midlands	16,186	574	16,760	7.4%
East of England	19,721	359	20,080	8.8%
London	40,419	1,137	41,556	18.3%
North East	14,672	122	14,794	6.5%
North West	41,962	1,935	43,897	19.3%
South East	23,970	330	24,300	10.7%
South West	8,188	112	8,300	3.6%
West Midlands	18,309	1,388	19,697	8.7%
Yorkshire and Humber	35,931	1,020	36,951	16.2%
Unknown region	1,243	20	1,263	0.6%
Total	220,601	6,997	227,598	-



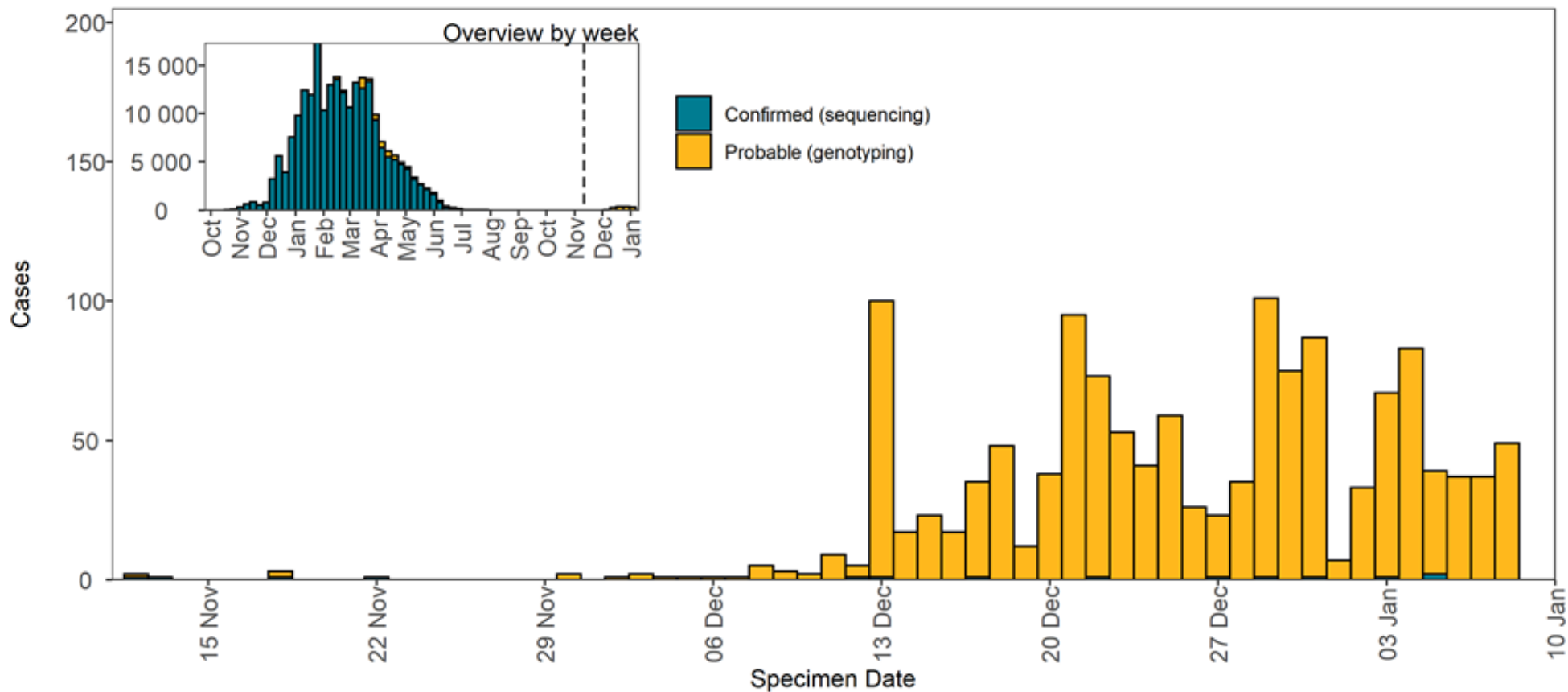
**Figure 4. Confirmed (sequencing) and provisional (genotyping) Alpha - VOC-20DEC-01 (B.1.1.7) cases by specimen date and region of residence as of 10 January 2022**

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



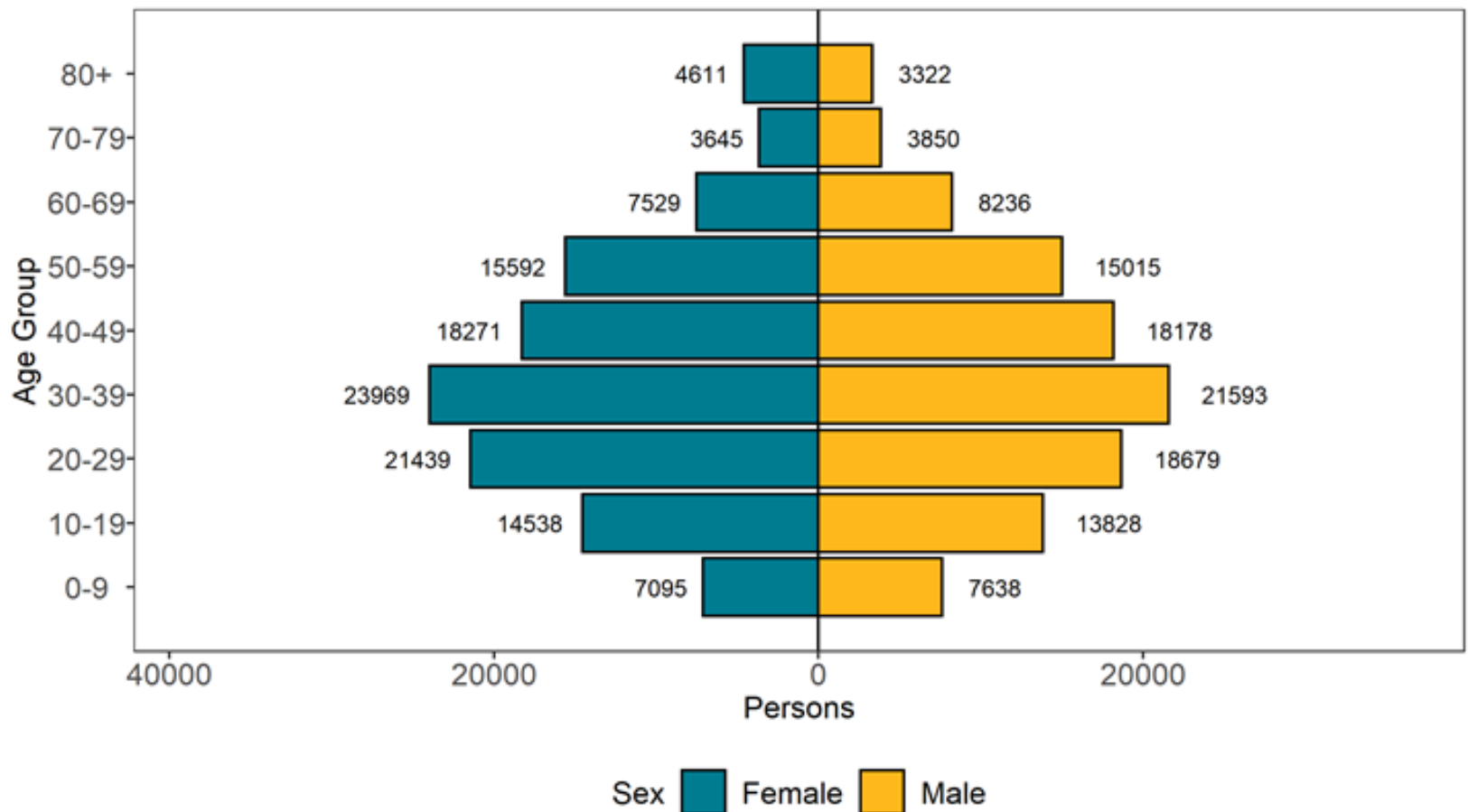
**Figure 5. Confirmed (sequencing) and provisional (genotyping) Alpha - VOC-20DEC-01 (B.1.1.7) cases by specimen date and detection method as of 10 January 2022**

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



**Figure 6. Age-sex pyramid of Alpha - VOC-20DEC-01 (B.1.1.7) cases as of 10 January 2022**

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



570 cases excluded where sex or age not reported

## Beta – VOC-20DEC-02 (B.1.351)

B.1.351 variant was designated VUI on detection and on review re-designated as VOC-20DEC-02 (B.1.351) on 24 December 2020. It was named Beta by WHO on 31 May 2021.

### Epidemiology

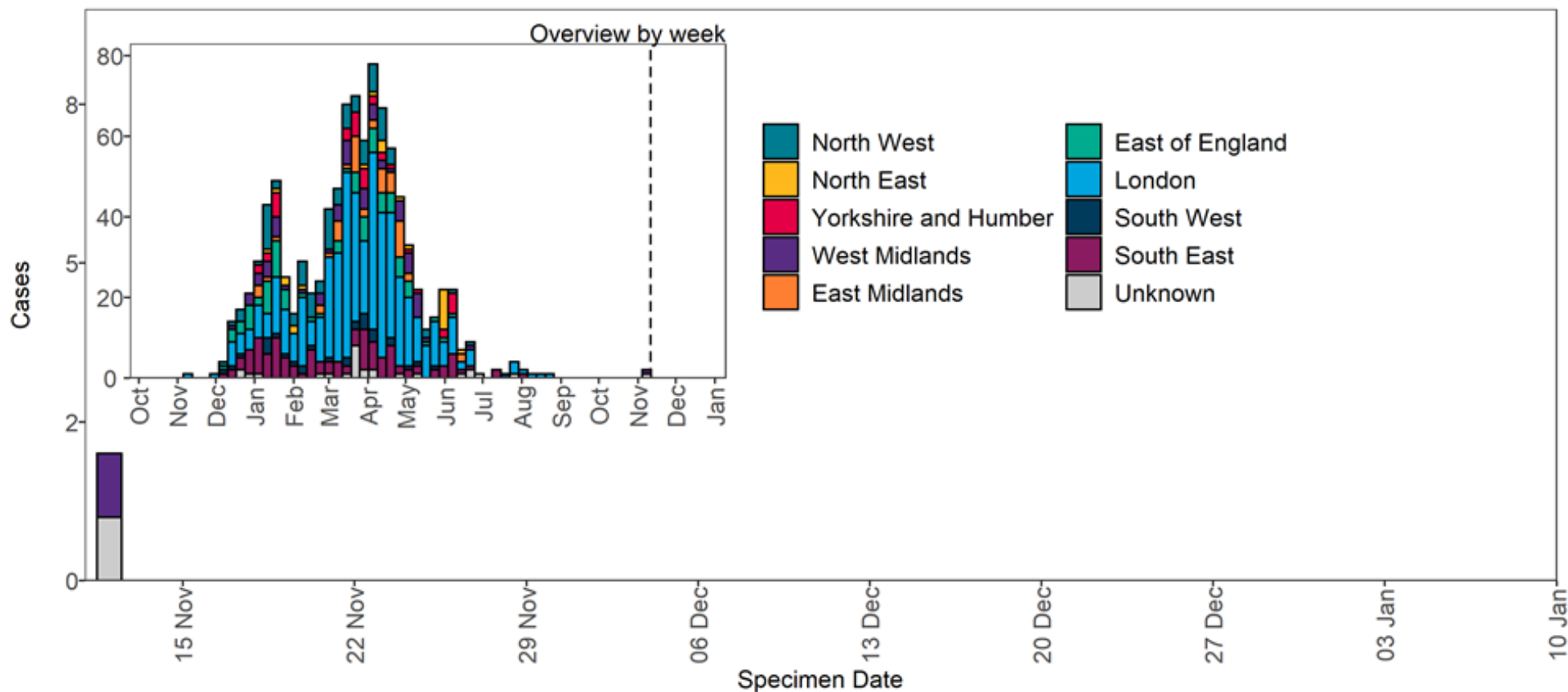
Currently there are no Beta genomes in the last 12 weeks in the UK that have been linked to individuals, however there are cases that have been confirmed as Beta through sequencing in the last 12 weeks that are in the process of being linked.

**Table 3. Number of confirmed (sequencing) and probable (genotyping) Beta - VOC-20DEC-02 (B.1.351) cases, by region of residence as of 10 January 2022**

Region	Confirmed case number	Provisional case number	Total case number	Case proportion
East Midlands	48	3	51	5.1%
East of England	84	3	87	8.8%
London	431	26	457	46.0%
North East	19	6	25	2.5%
North West	80	10	90	9.1%
South East	117	4	121	12.2%
South West	31	1	32	3.2%
West Midlands	64	2	66	6.6%
Yorkshire and Humber	32	6	38	3.8%
Unknown region	23	4	27	2.7%
Total	929	65	994	-

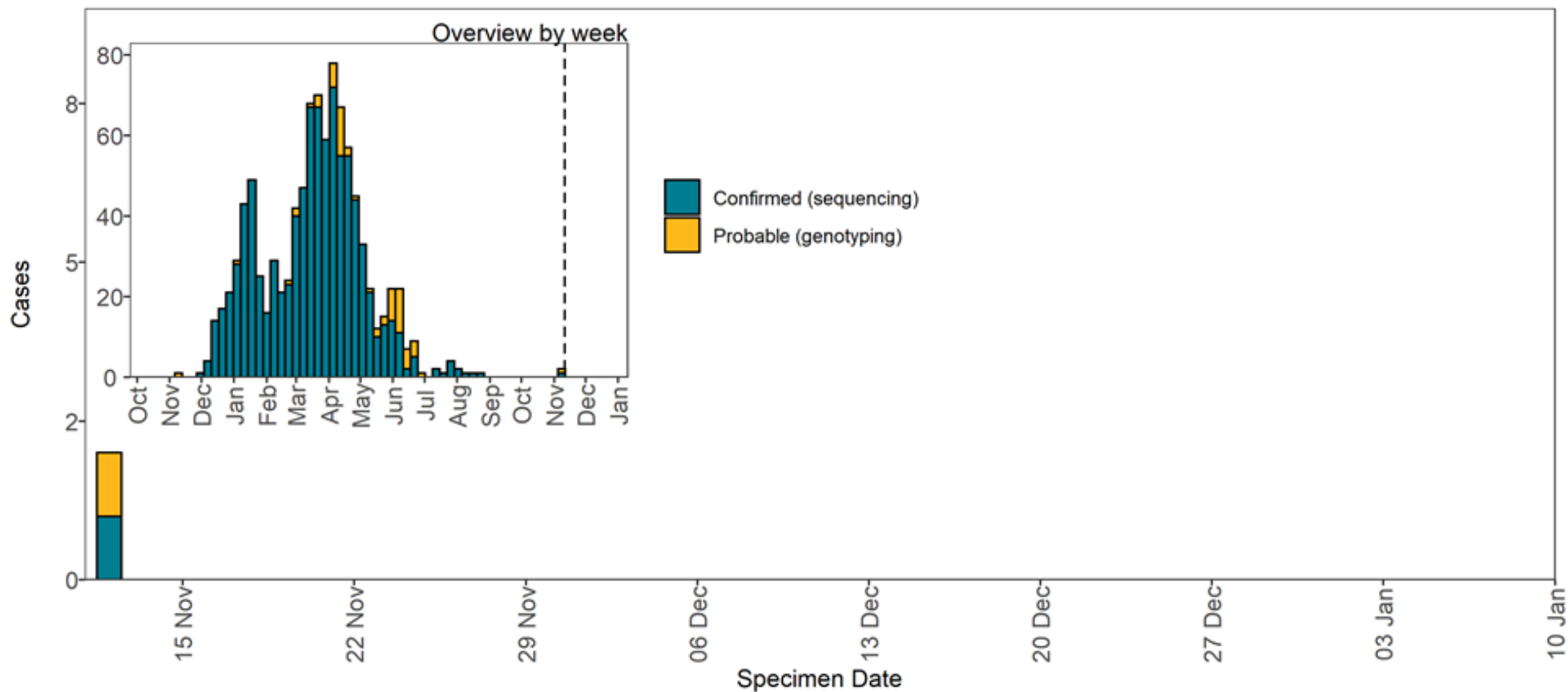
**Figure 7. Confirmed (sequencing) and probable (genotyping) Beta - VOC-20DEC-02 (B.1.351) cases by specimen date and region of residence as of 10 January 2022**

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



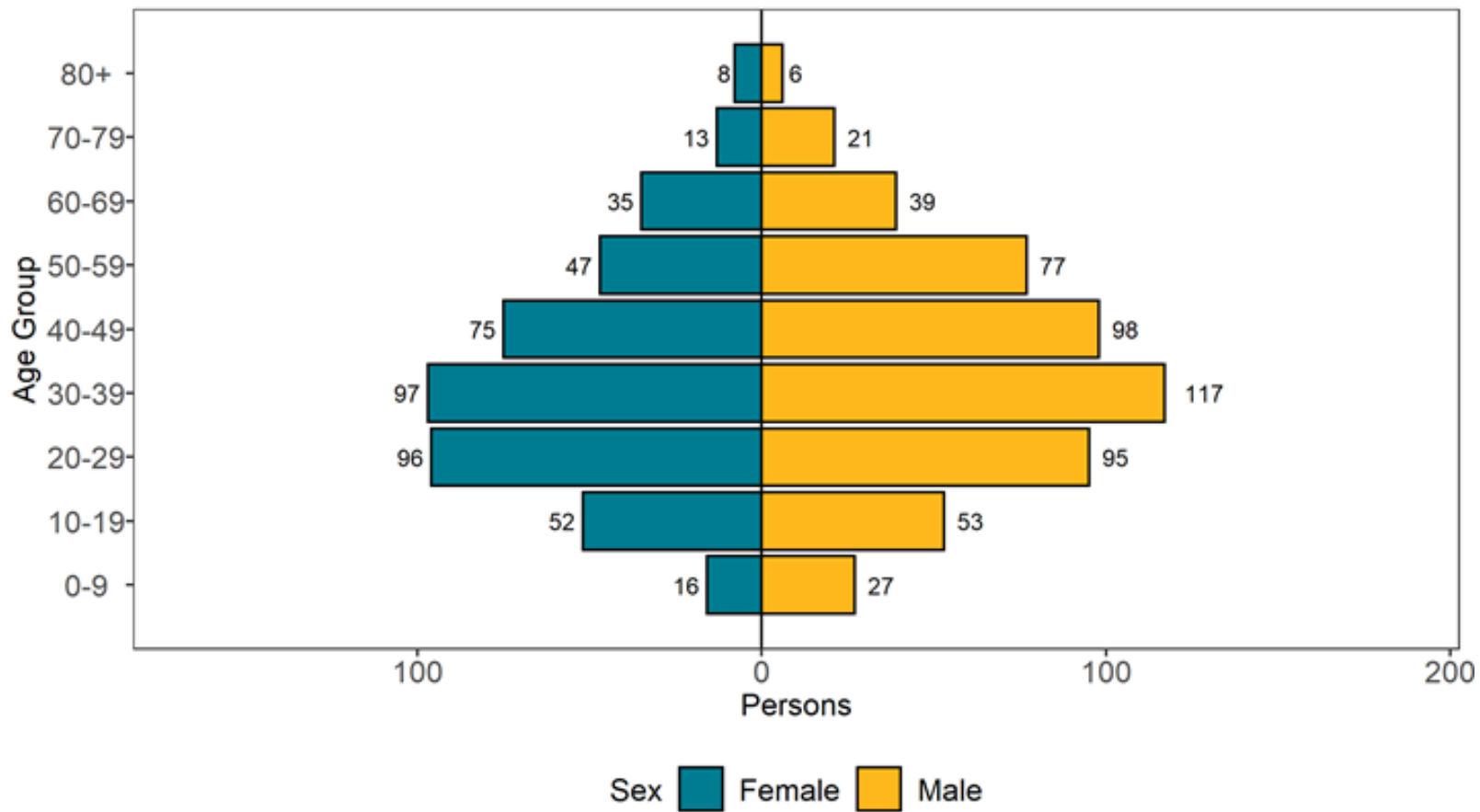
**Figure 8. Confirmed (sequencing) and probable (genotyping) Beta - VOC-20DEC-02 (B.1.351) cases by specimen date and detection method as of 10 January 2022**

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



**Figure 9. Age-sex pyramid of Beta - VOC-20DEC-02 (B.1.351) cases as of 10 January 2022**

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



22 cases excluded where sex or age not reported

## Gamma – VOC-21JAN-02 (P.1)

The P.1 lineage is a descendant of B.1.1.28. This variant was designated VUI on detection and on review re-designated as VOC-21JAN-02 (P.1) on 13 January 2021. This was named Gamma by WHO on 31 May 2021.

### Epidemiology

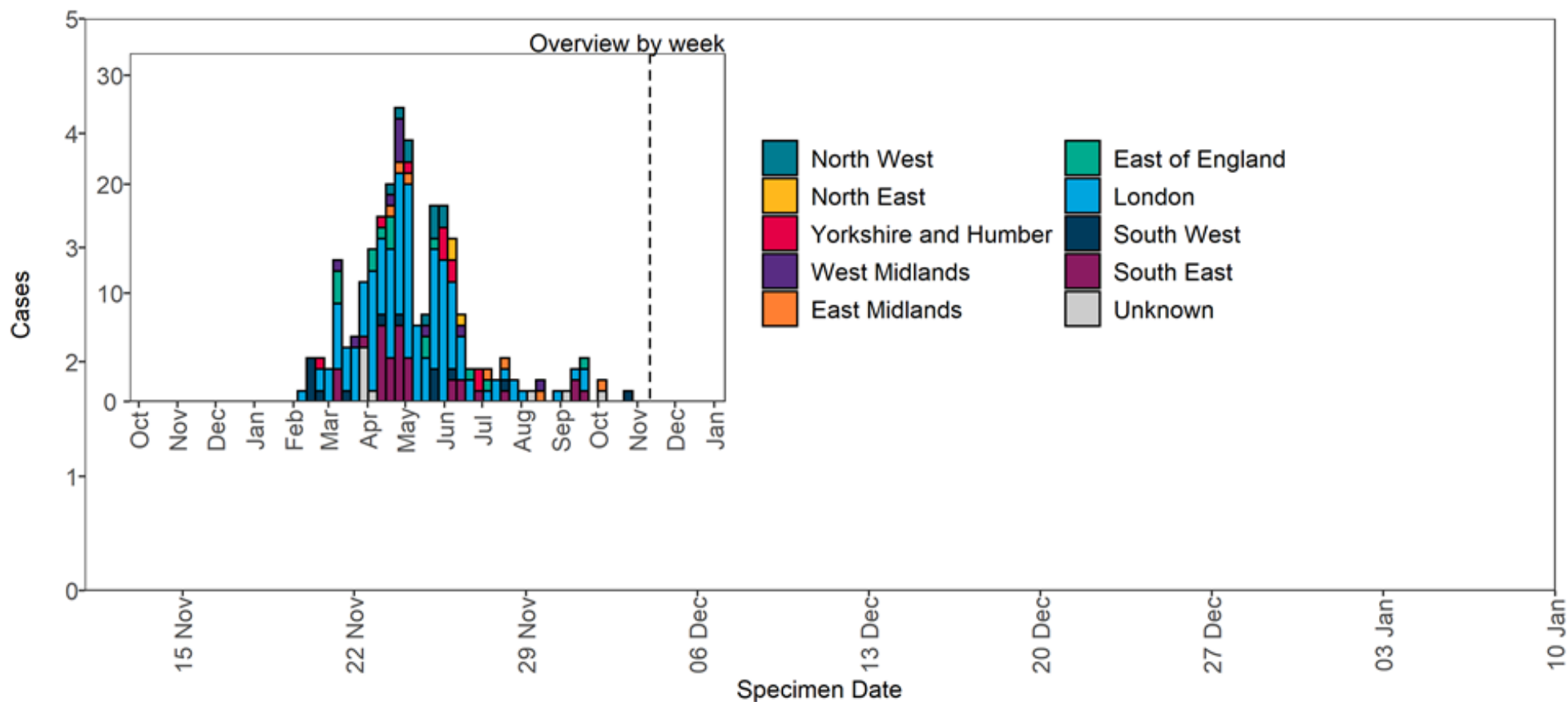
**Table 4. Number of confirmed (sequencing) and probable (genotyping) Gamma - VOC-21JAN-02 (P.1) cases, by region of residence as of 10 January 2022**

Region	Confirmed case number	Provisional case number	Total case number	Case proportion
East Midlands	7	1	8	3.1%
East of England	14	1	15	5.8%
London	121	23	144	55.6%
North East	0	3	3	1.2%
North West	9	1	10	3.9%
South East	29	7	36	13.9%
South West	11	3	14	5.4%
West Midlands	8	2	10	3.9%
Yorkshire and Humber	3	7	10	3.9%
Unknown region	9	0	9	3.5%
Total	211	48	259	-



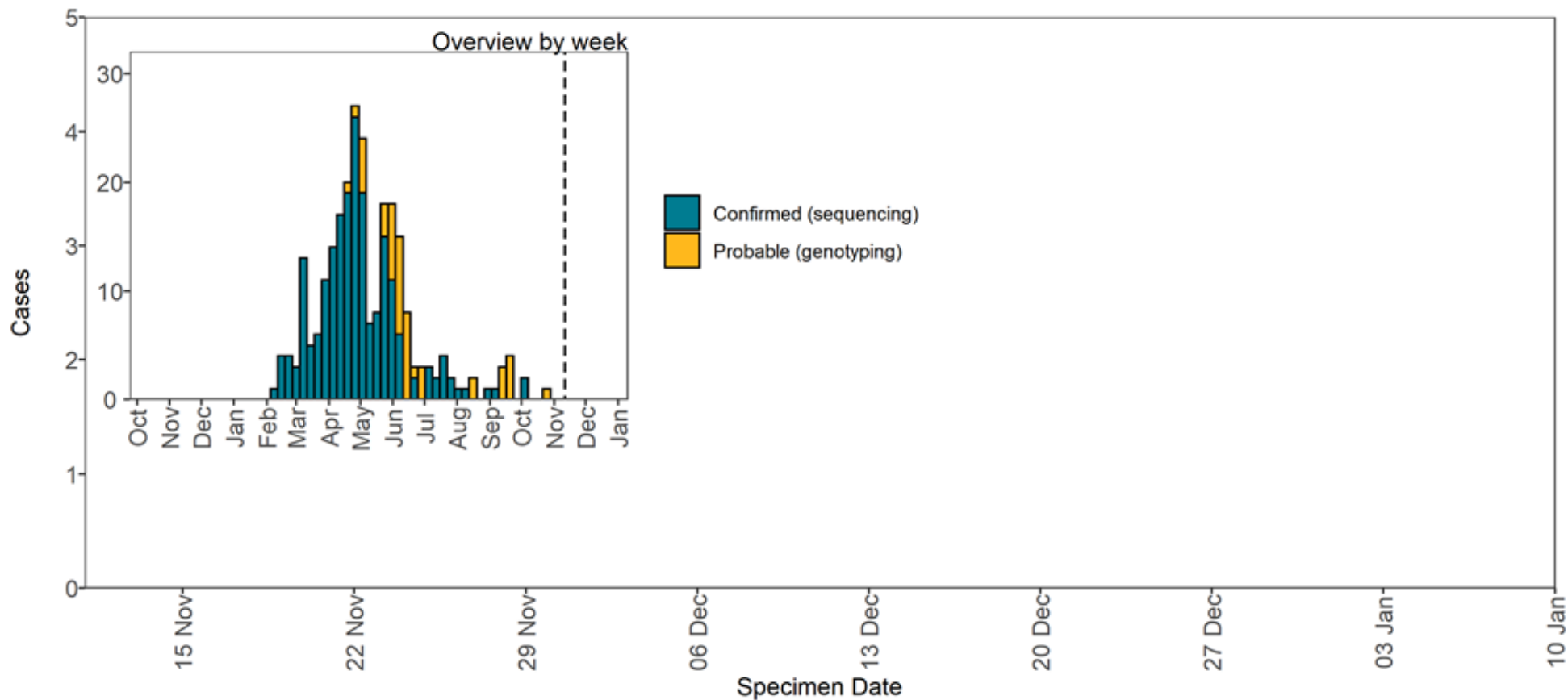
**Figure 10. Confirmed (sequencing) and probable (genotyping) Gamma - VOC-21JAN-02 (P.1) cases by specimen date and region of residence as of 10 January 2022**

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



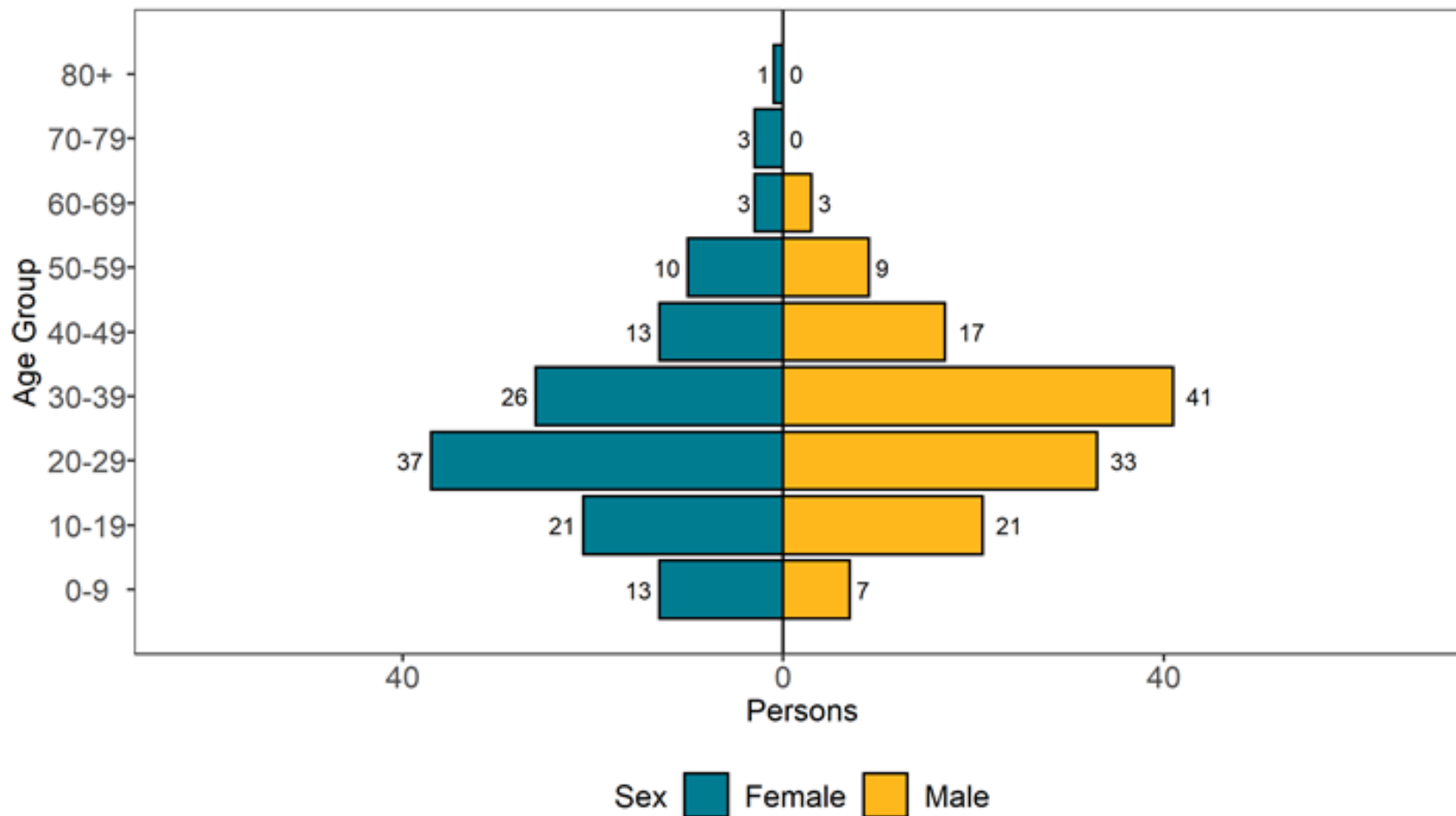
**Figure 11. Confirmed (sequencing) and probable (genotyping) Gamma - VOC-21JAN-02 (P.1) cases by specimen date and detection method as of 10 January 2022**

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



**Figure 12. Age-sex pyramid of Gamma - VOC-21JAN-02 (P.1) cases as of 10 January 2022**

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



1 cases excluded where sex or age not reported

## Delta – VOC-21APR-02 (B.1.617.2) with mutations at Spike:484

The lineage B.1.617.2 was escalated to a VOC in the UK on 6 May 2021 (VOC-21APR-02). This variant was named Delta by WHO on 31 May 2021. Changes at position 484 in spike are potentially antigenically significant and so are monitored in the UK genomes.

### Delta with E484Q

Delta with E484Q was first identified through horizon scanning on the 3 August 2021 after being detected in 6 samples between 22 and 28 July 2021.

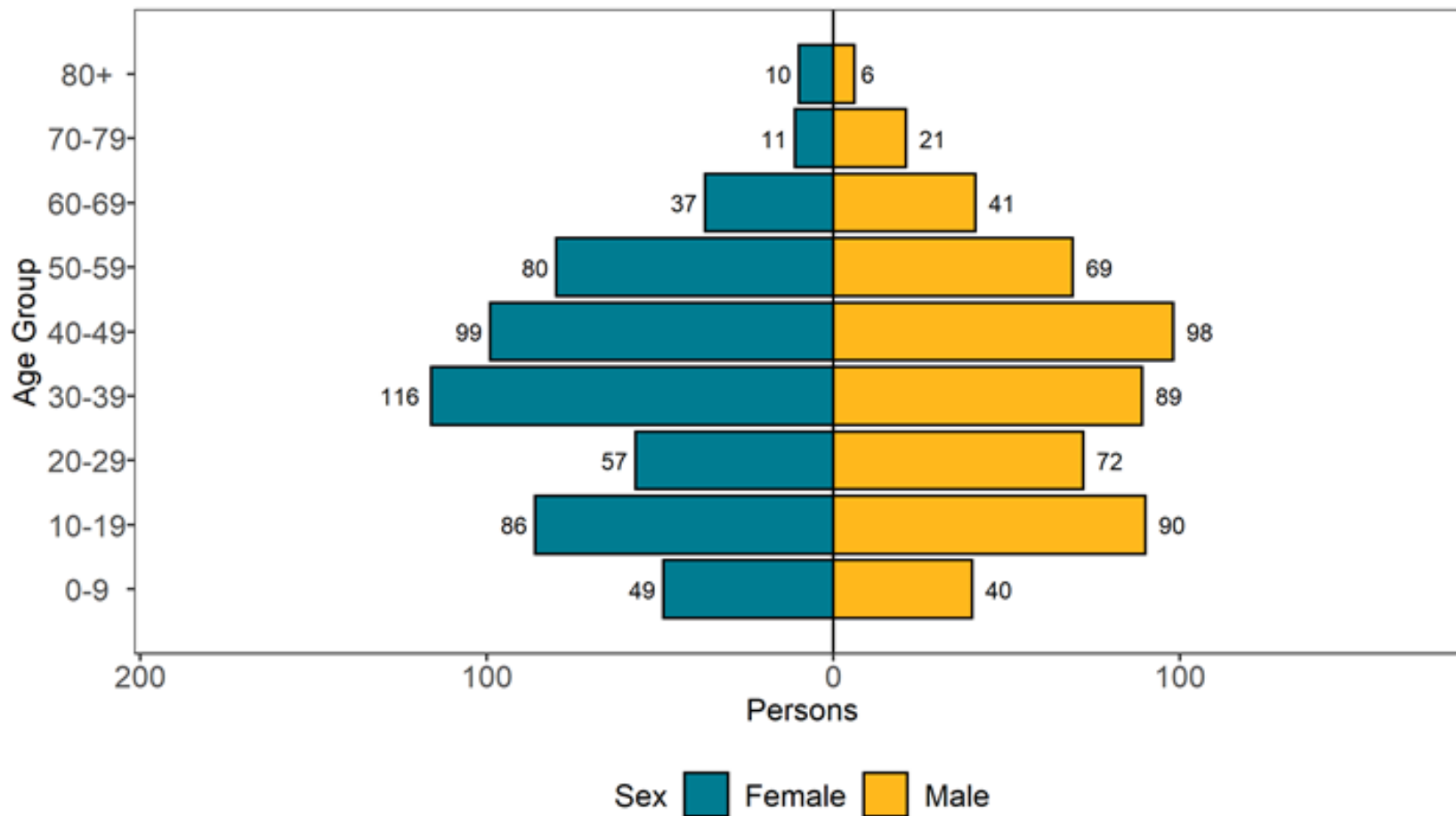
### Epidemiology

**Table 5. Number of confirmed (sequencing) Delta cases with E484Q mutation, by region of residence as of 10 January 2022**

Region	Total case number	Case proportion
East Midlands	47	4.4%
East of England	103	9.6%
London	289	26.8%
North East	99	9.2%
North West	159	14.7%
South East	195	18.1%
South West	28	2.6%
West Midlands	64	5.9%
Yorkshire and Humber	67	6.2%
Unknown region	27	2.5%
Total	1,078	-

1,078 of the 1,293 Delta + E484Q sequences linked to a case.

**Figure 13. Age-sex pyramid of confirmed (sequencing) Delta with E484Q mutation cases as of 10 January 2022**  
 (The data used in this graph can be found in the [accompanying spreadsheet.](#))



7 cases excluded where sex or age not reported

## Delta with E484K

Delta with E484K was first detected on 8 July 2021 in a UK sequence with a collection date of 28 June 2021.

## Epidemiology in England

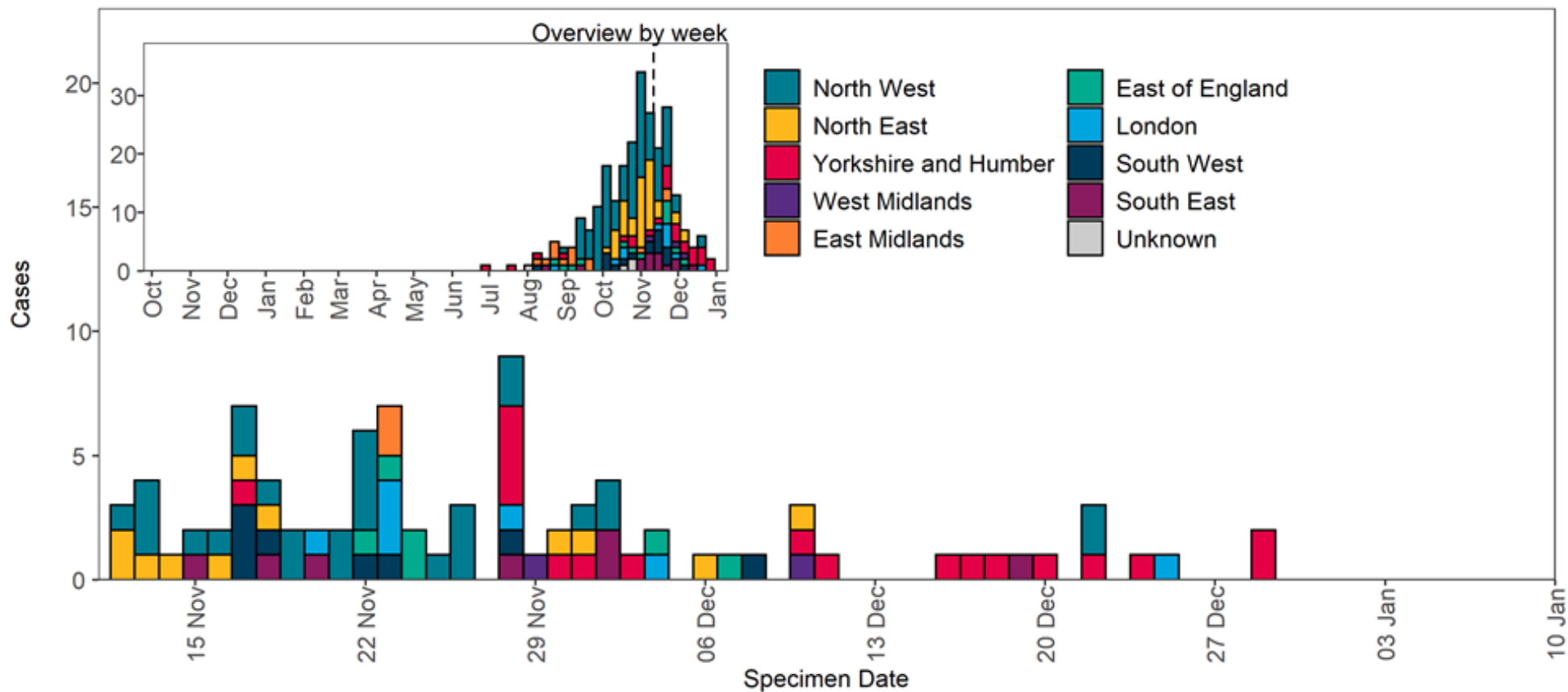
**Table 6. Number of confirmed (sequencing) Delta cases with E484K mutation, by region of residence as of 10 January 2022**

Region	Total case number	Case proportion
East Midlands	14	5.4%
East of England	13	5.0%
London	11	4.2%
North East	46	17.7%
North West	112	43.1%
South East	14	5.4%
South West	17	6.5%
West Midlands	3	1.2%
Yorkshire and Humber	26	10.0%
Unknown region	4	1.5%
Total	260	-

260 of the 352 Delta + E484K sequences linked to a case.

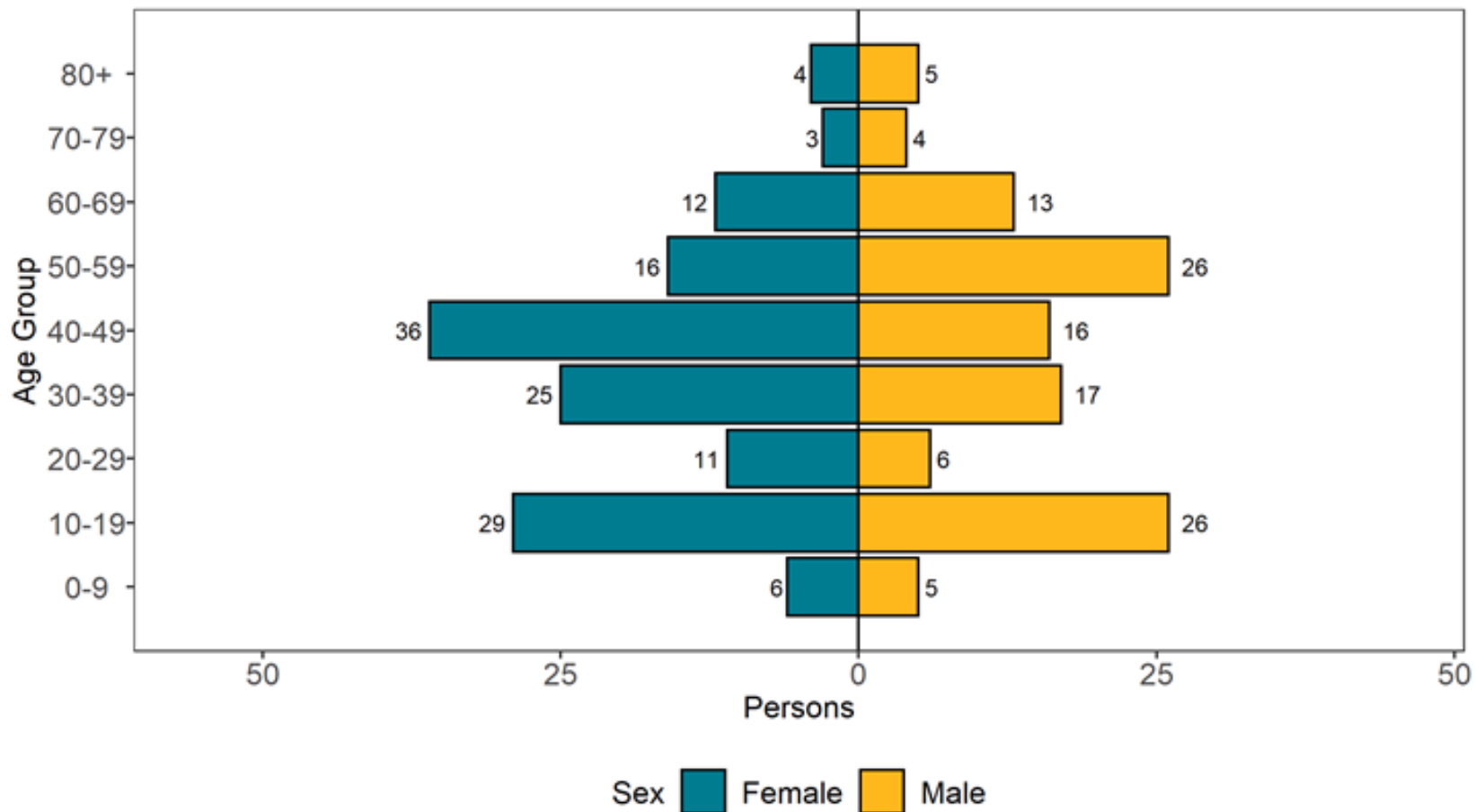
**Figure 14. Confirmed (sequencing) Delta with E484K mutation cases by specimen date and region of residence as of 10 January 2022**

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



**Figure 15. Age-sex pyramid of confirmed (sequencing) Delta with E484K mutation cases as of 10 January 2022**

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



0 cases excluded where sex or age not reported



## VUI-21OCT-01 (AY 4.2)

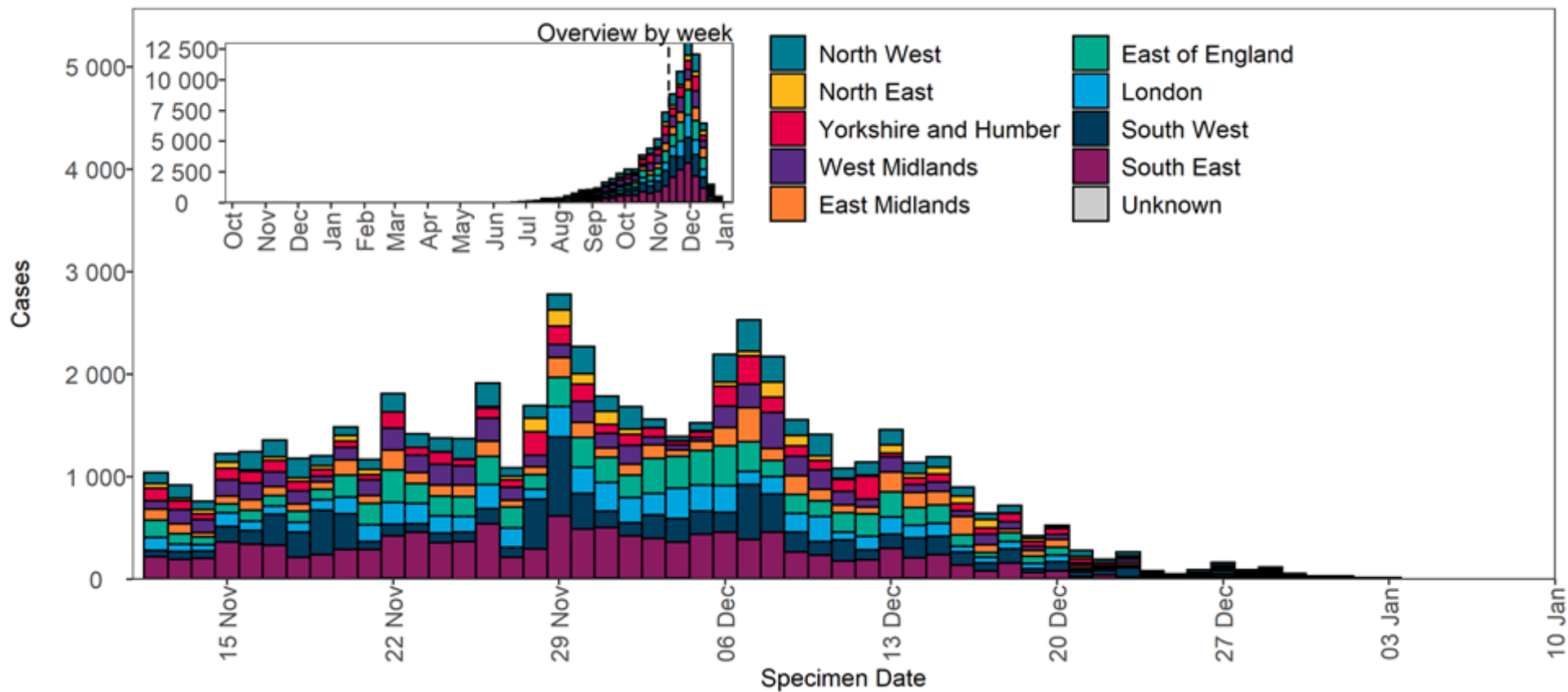
New sub-lineages of Delta are regularly identified and designated. The Delta sublineage AY.4.2 was designated VUI-21OCT-01 on 20 October 2021.

### Epidemiology

**Table 7. Number of confirmed (sequencing) VUI-21OCT-01 cases, by region of residence as of 10 January 2022**

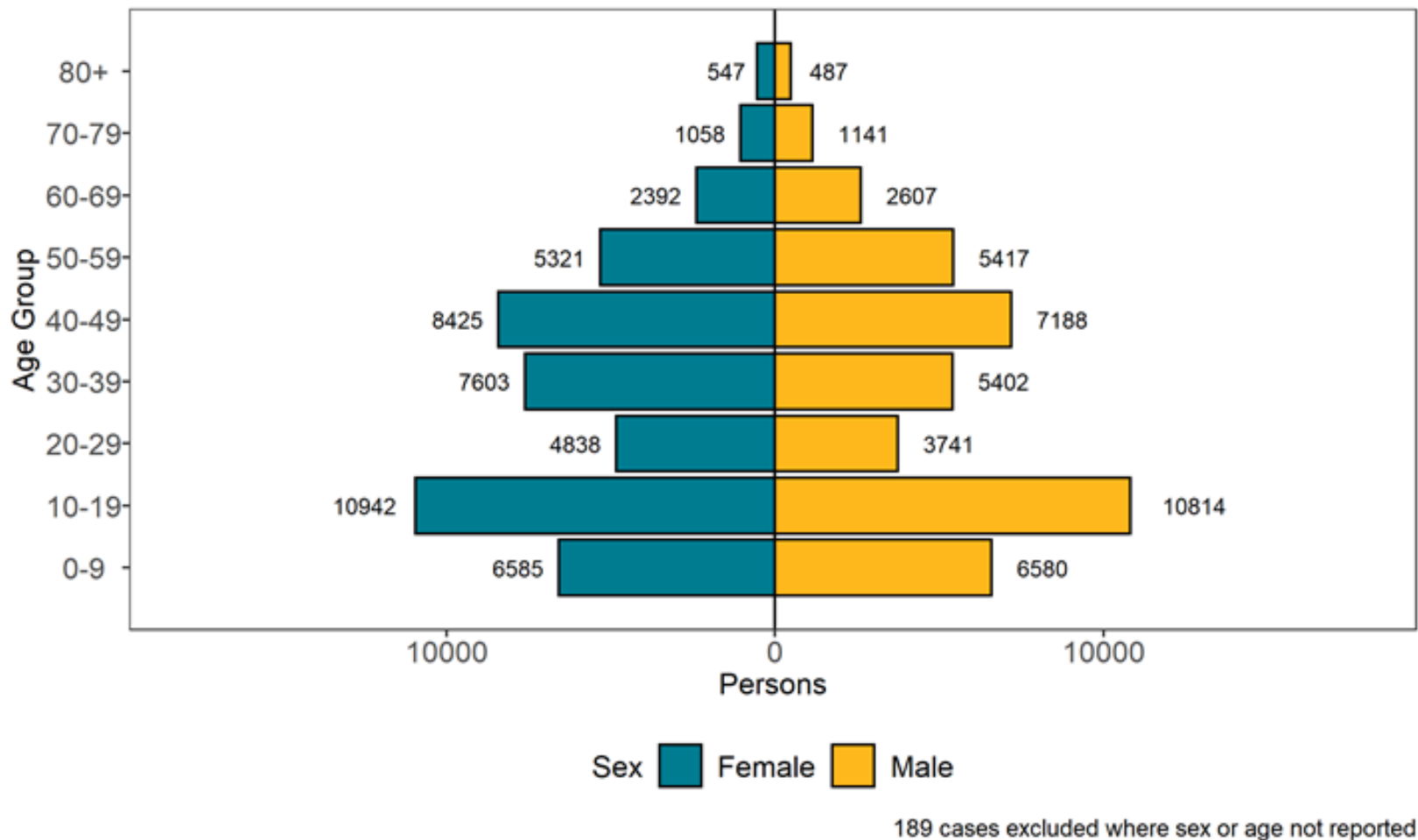
Region	Total case number	Case proportion
East Midlands	7,123	7.8%
East of England	11,587	12.7%
London	10,321	11.3%
North East	2,845	3.1%
North West	9,329	10.2%
South East	18,644	20.4%
South West	13,324	14.6%
West Midlands	10,067	11.0%
Yorkshire and Humber	7,746	8.5%
Unknown region	291	0.3%
Total	91,277	-

**Figure 16. Confirmed (sequencing) VUI-21OCT-01 (AY 4.2) cases by specimen date and region of residence as of 10 January 2022**  
 (The data used in this graph can be found in the [accompanying spreadsheet.](#))



**Figure 17. Age-sex pyramid of VUI-21OCT-01 (AY 4.2) cases as of 10 January 2022**

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



## Mu – VUI-21JUL-01 (B.1.621)

VUI-21JUL-01 was identified through international variant horizon scanning and was made a signal in monitoring in the UK on 7 June 2021 (lineage B.1.621 at the time). On 21 July 2021, B.1.621 was designated as VUI-21JUL-01, based on apparent spread into multiple countries, importation to the UK and mutations of concern. B.1.621 was designated as Mu by WHO on the 30 August 2021.

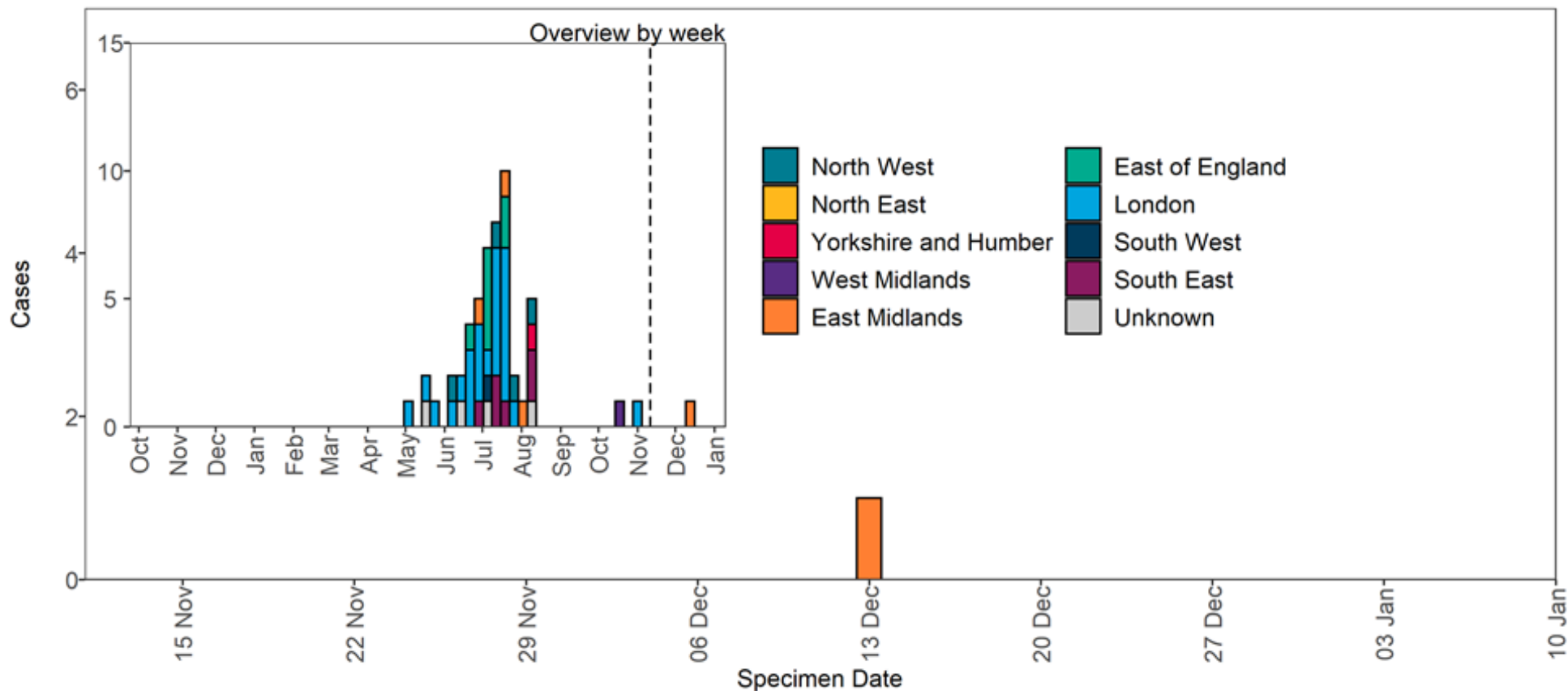
### Epidemiology

**Table 8. Number of confirmed (sequencing) Mu-VUI-21JUL-01 (B.1.621) cases, by region of residence as of 10 January 2022**

Region	Total case number	Case proportion
East Midlands	4	7.5%
East of England	7	13.2%
London	25	47.2%
North East	0	0.0%
North West	4	7.5%
South East	6	11.3%
South West	1	1.9%
West Midlands	1	1.9%
Yorkshire and Humber	1	1.9%
Unknown region	4	7.5%
Total	53	-

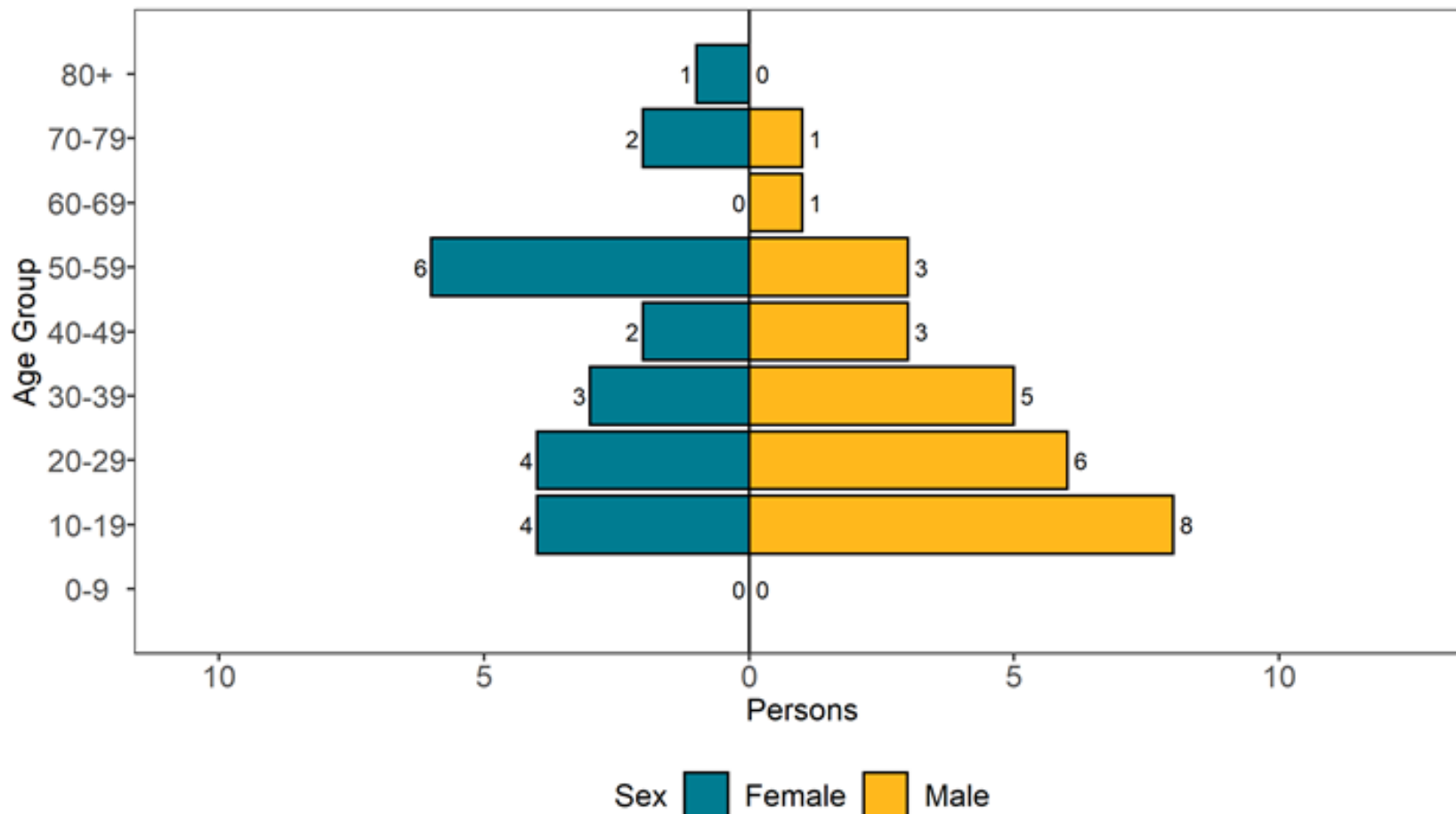
**Figure 18. Confirmed (sequencing) Mu-VUI-21JUL-01 (B.1.621) cases by specimen date and region of residence as of 10 January 2022**

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



**Figure 19. Age-sex pyramid of Mu-VUI-21JUL-01 (B.1.621) cases as of 10 January 2022**

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



4 cases excluded where sex or age not reported

# Sources and acknowledgments

## Data sources

Data used in this investigation is derived from the COG-UK data set, the UK Health Security Agency (UKHSA) Second Generation Surveillance System (SGSS), NHS Test and Trace, the Secondary Uses Service (SUS) data set and Emergency Care Data Set (ECDS). Data on international cases are derived from reports in GISAID.

## Repository of human and machine-readable genomic case definitions

A repository containing the up-to-date genomic definitions for all VOC and VUI as curated by Public Health England was created on 5 March 2021. The repository can be accessed on GitHub. They are provided 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 Cell Data Team  
UKHSA International Cell

The UKHSA Variant Technical Group includes representation from the following organisations: UKHSA, Department of Health and Social Care, Department for Business Energy and Industrial Strategy, Public Health Wales, Public Health Scotland, Public Health Agency Northern Ireland, Imperial College London, London School of Hygiene and Tropical Medicine, University of Birmingham, University of Cambridge, University of Edinburgh, University of Liverpool, the Wellcome Sanger Institute.

## Acknowledgements

The authors are grateful to those teams and groups providing data for this analysis including: the Lighthouse Laboratories, COG-UK, the Wellcome Sanger Institute, UKHSA Epidemiology Cell, Contact Tracing, Genomics and Outbreak Surveillance Teams.

# About the UK Health Security Agency

The [UK Health Security Agency](#) is an executive agency, sponsored by the [Department of Health and Social Care](#).

© Crown copyright 2022  
Version 1

Published: January 2022  
Publishing reference: GOV-10925



You may re-use this information (excluding logos) free of charge in any format or medium, under the terms of the Open Government Licence v3.0. To view this licence, visit [OGL](#). Where we have identified any third party copyright information you will need to obtain permission from the copyright holders concerned.



UKHSA supports the  
Sustainable Development Goals

