



UK Health  
Security  
Agency

# SARS-CoV-2 variant data update, England

## Version 22

11 February 2022

This edition provides an update on previous data noted within the technical [briefings and variant data updates](#) up to 28 January 2022.

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# Part 1. Surveillance overview

World Health Organization (WHO) nomenclature from 24 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)†	B.1.640
Beta (B.1.351) VOC-20DEC-02	Mu (B.1.621) VUI-21JUL-01	BA.3
Gamma (P.1) VOC-21JAN-02	VUI-22JAN-01 BA.2††	Delta x BA.1 Recombinant
Delta (B.1.617.2 and sub-lineages) VOC-21APR-02		
Omicron (B.1.1.529, and sub-lineages) VOC-21NOV-01		

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

†† BA.2 is a sub-lineage within Omicron that has been assigned as a distinct VUI.

**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)	
	VUI-21FEB-03 (B.1.525)	
	VUI-21FEB-04 (B.1.1.318)	
	VUI-21APR-01 (B.1.617.1)	

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. VUIs and signals in monitoring may also be removed from the grid if they show consistently low growth rates.

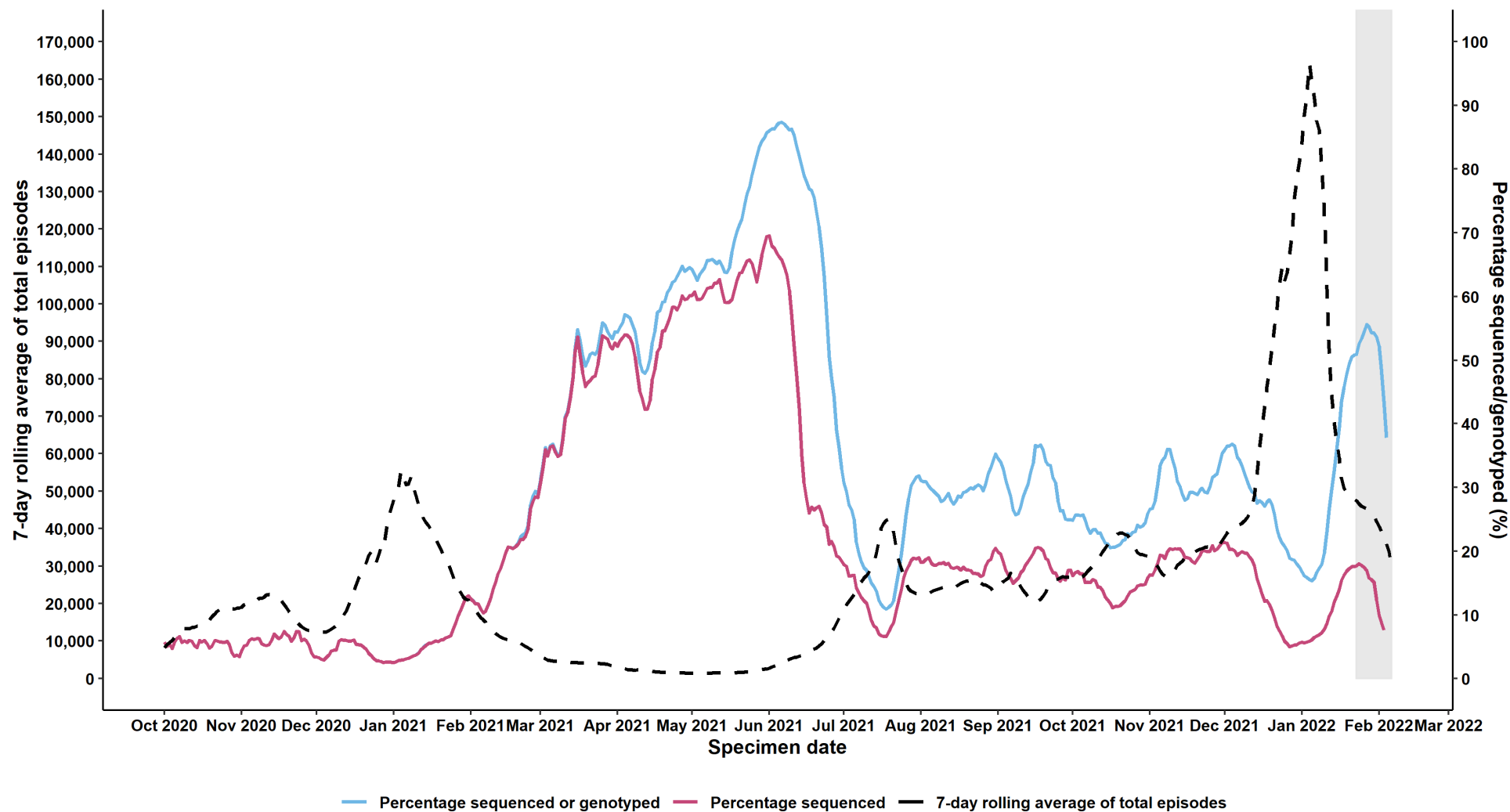
## Sequencing coverage

[Figure 1](#) shows the proportion of COVID-19 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

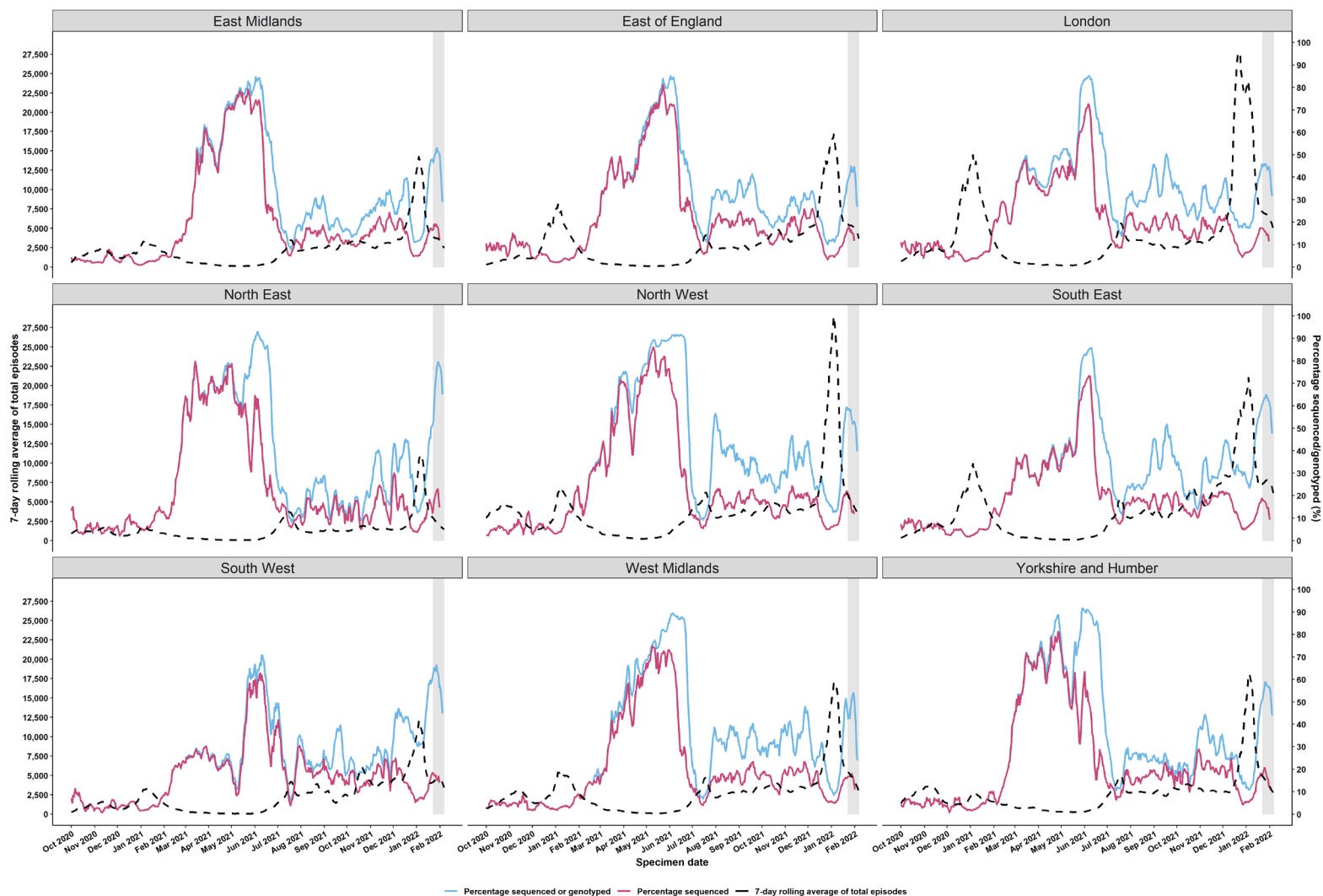
**Figure 1. Coverage of sequencing with a valid result and genotyping over time (1 October 2020 to 6 February 2022)**



Data extract from 07 February 2022; data from 01 October 2020 to 06 February 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](#).)

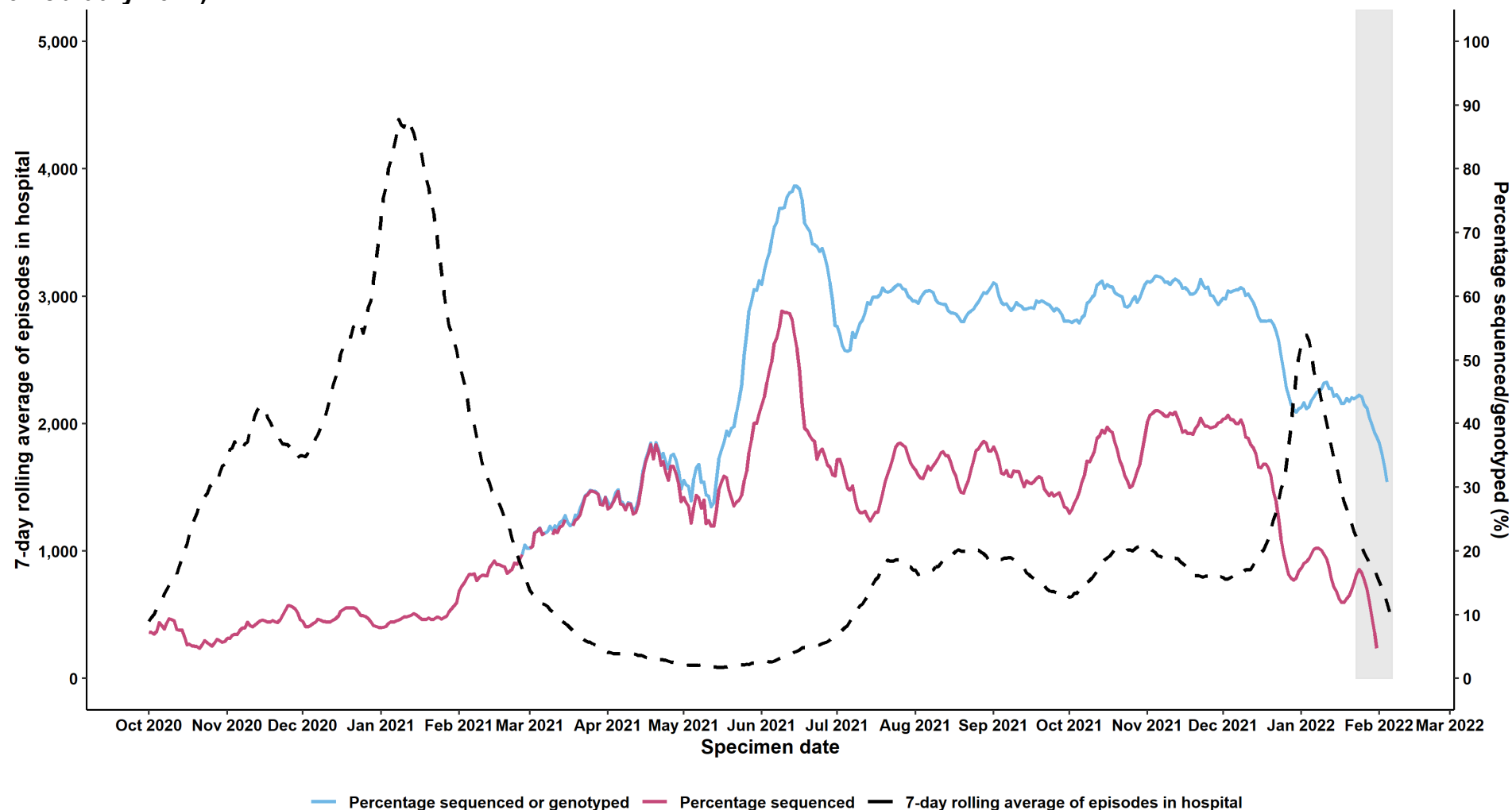
**Figure 2. Coverage of sequencing with a valid result and genotyping over time by region (1 October 2020 to 6 February 2022)**



Data extract from 07 February 2022; data from 01 October 2020 to 06 February 2022.  
 Grey shading was applied to the previous 14 days to account for reporting delays in sequencing data.  
 There were 96856 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 6 February 2022)**



Data extract from 07 February 2022; data from 01 October 2020 to 06 February 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

### Methodology note

As of 31 January 2022, COVID-19 surveillance data in England has been updated to recognise the possibility of a person being infected more than once. Positive SARS-CoV-2 tests more than 90 days apart are considered to be separate COVID-19 episodes. Consequently, in the tables and figures below, cases may be counted more than once if they have multiple episodes with sequencing or genotyping information. Figures may differ slightly from prior publications due to the changes in data processing.

### 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

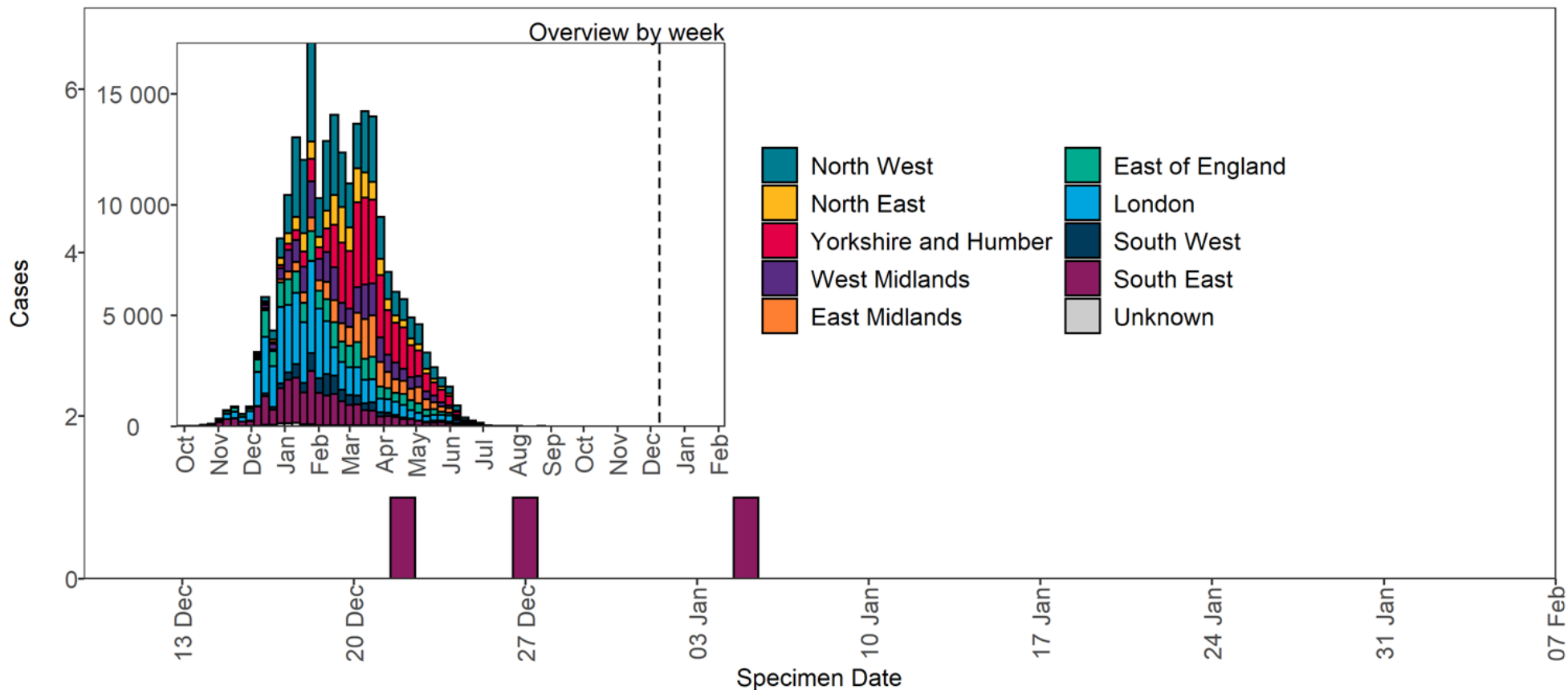
**Table 2. Number of confirmed (sequencing) and probable (genotyping) Alpha - VOC-20DEC-01 (B.1.1.7) cases, by region of residence as of 7 February 2022**

Region	Confirmed case number	Probable case number	Total case number	Case proportion
East Midlands	16,438	484	16,922	7.3%
East of England	20,078	189	20,267	8.8%
London	40,151	813	40,964	17.8%
North East	15,153	109	15,262	6.6%
North West	43,044	1,729	44,773	19.4%
South East	24,937	122	25,059	10.9%
South West	8,098	51	8,149	3.5%
West Midlands	19,538	1,315	20,853	9.0%
Yorkshire and Humber	35,997	892	36,889	16.0%
Unknown region	1,313	32	1,345	0.6%
Total	224,747	5,736	230,483	-



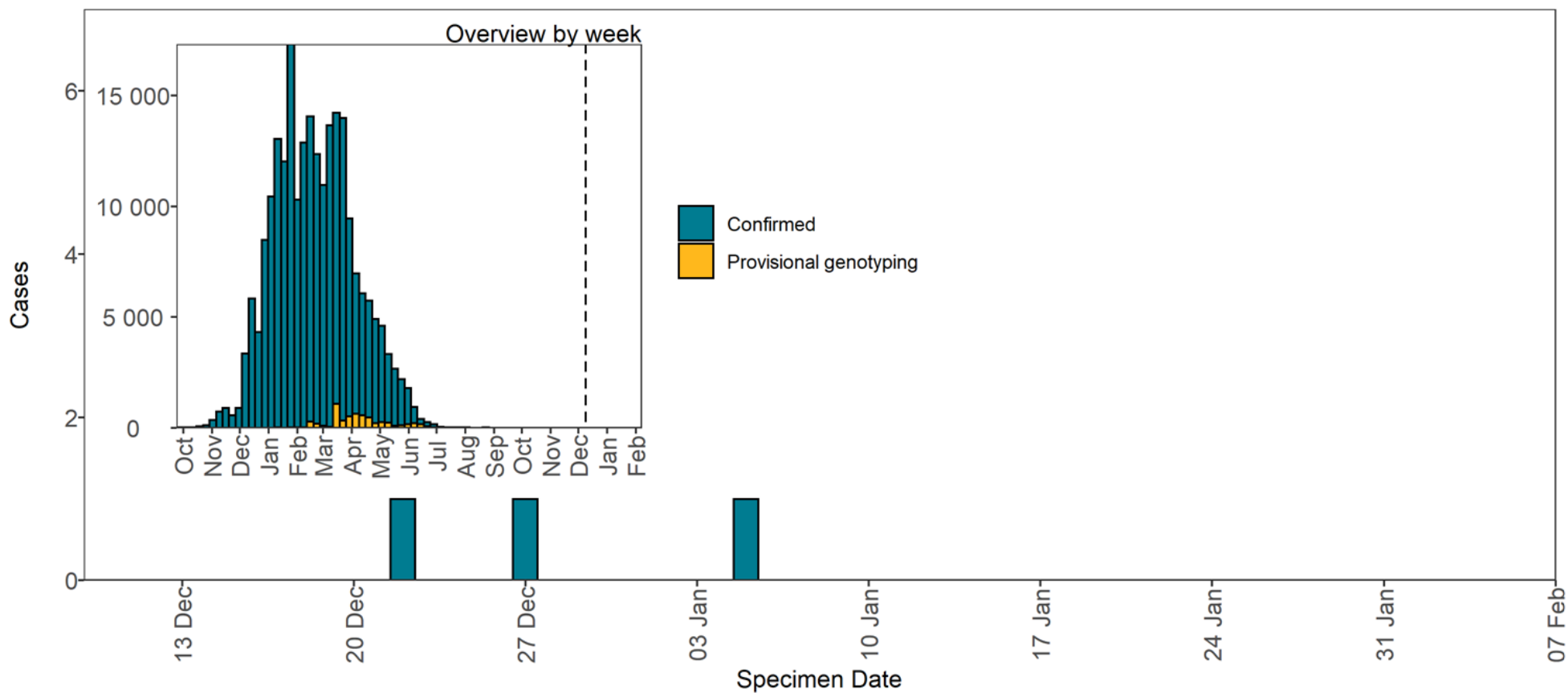
**Figure 4. Confirmed (sequencing) and probable (genotyping) Alpha – VOC-20DEC-01 (B.1.1.7) cases by specimen date and region of residence as of 7 February 2022**

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



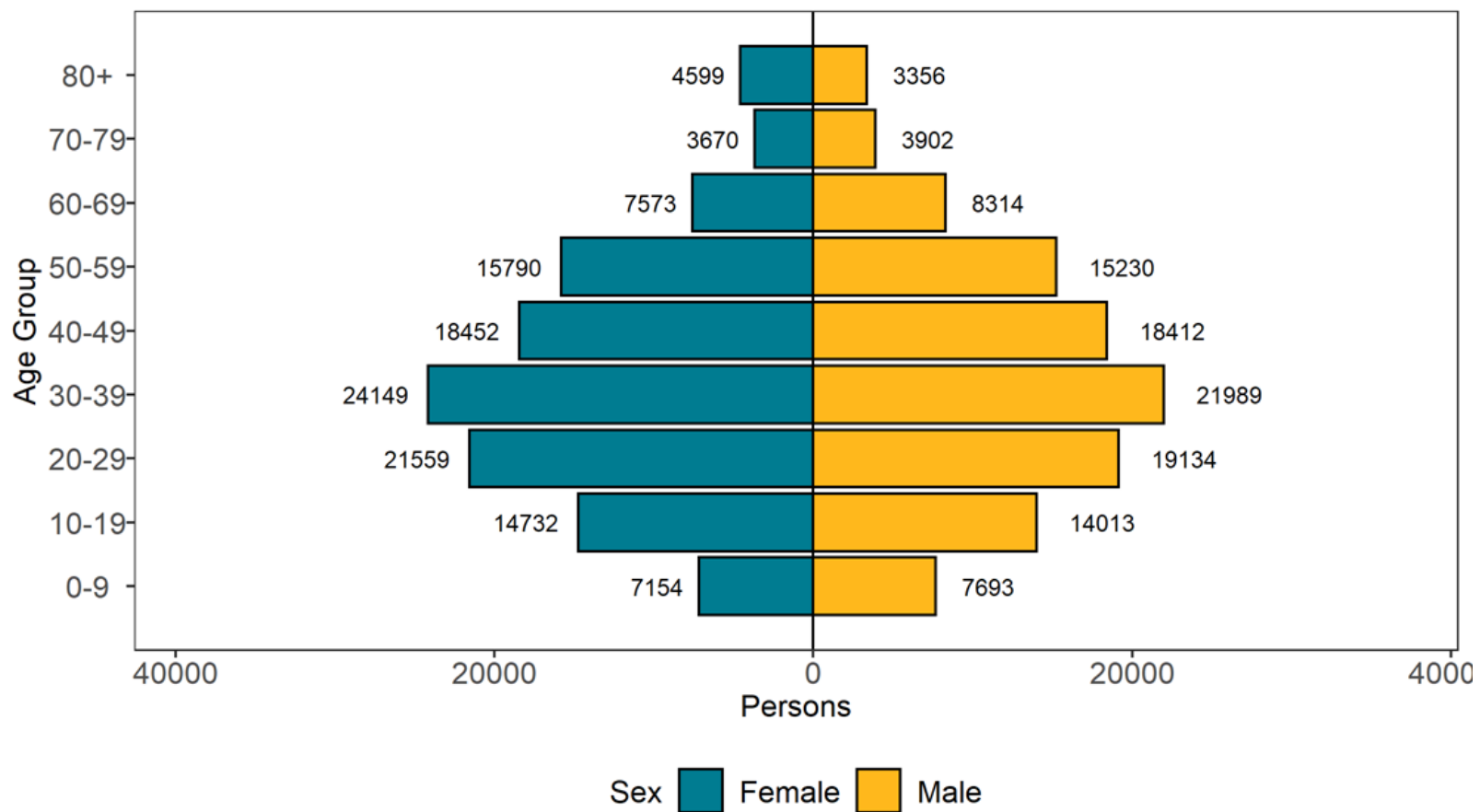
**Figure 5. Confirmed (sequencing) and probable (genotyping) Alpha - VOC-20DEC-01 (B.1.1.7) cases by specimen date and detection method as of 7 February 2022**

(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 7 February 2022**

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



666 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.

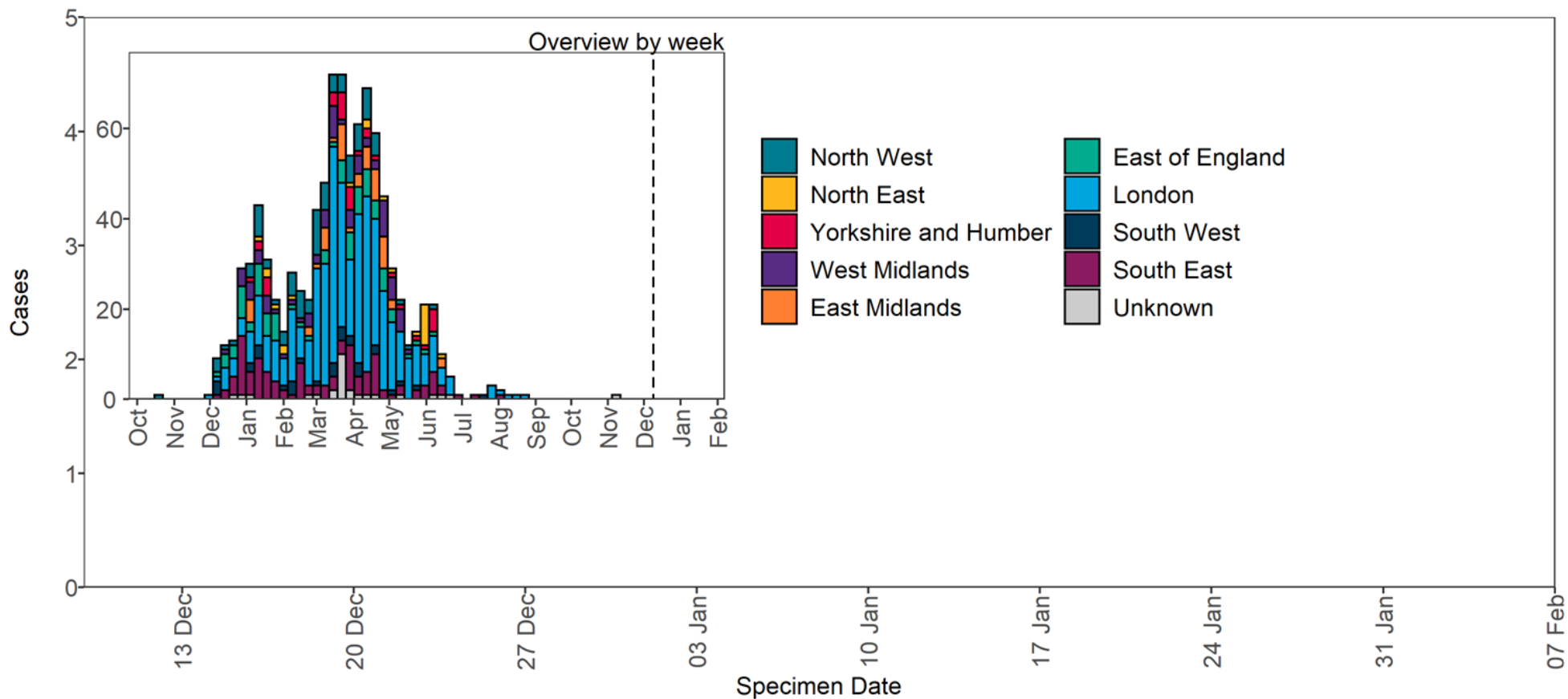
### Epidemiology

**Table 3. Number of confirmed (sequencing) and probable (genotyping) Beta - VOC-20DEC-02 (B.1.351) cases, by region of residence as of 7 February 2022**

Region	Confirmed case number	Probable case number	Total case number	Case proportion
East Midlands	46	3	49	5.2%
East of England	78	2	80	8.4%
London	406	28	434	45.7%
North East	17	6	23	2.4%
North West	78	9	87	9.2%
South East	112	4	116	12.2%
South West	30	1	31	3.3%
West Midlands	67	1	68	7.2%
Yorkshire and Humber	28	6	34	3.6%
Unknown region	24	3	27	2.8%
Total	886	63	949	-

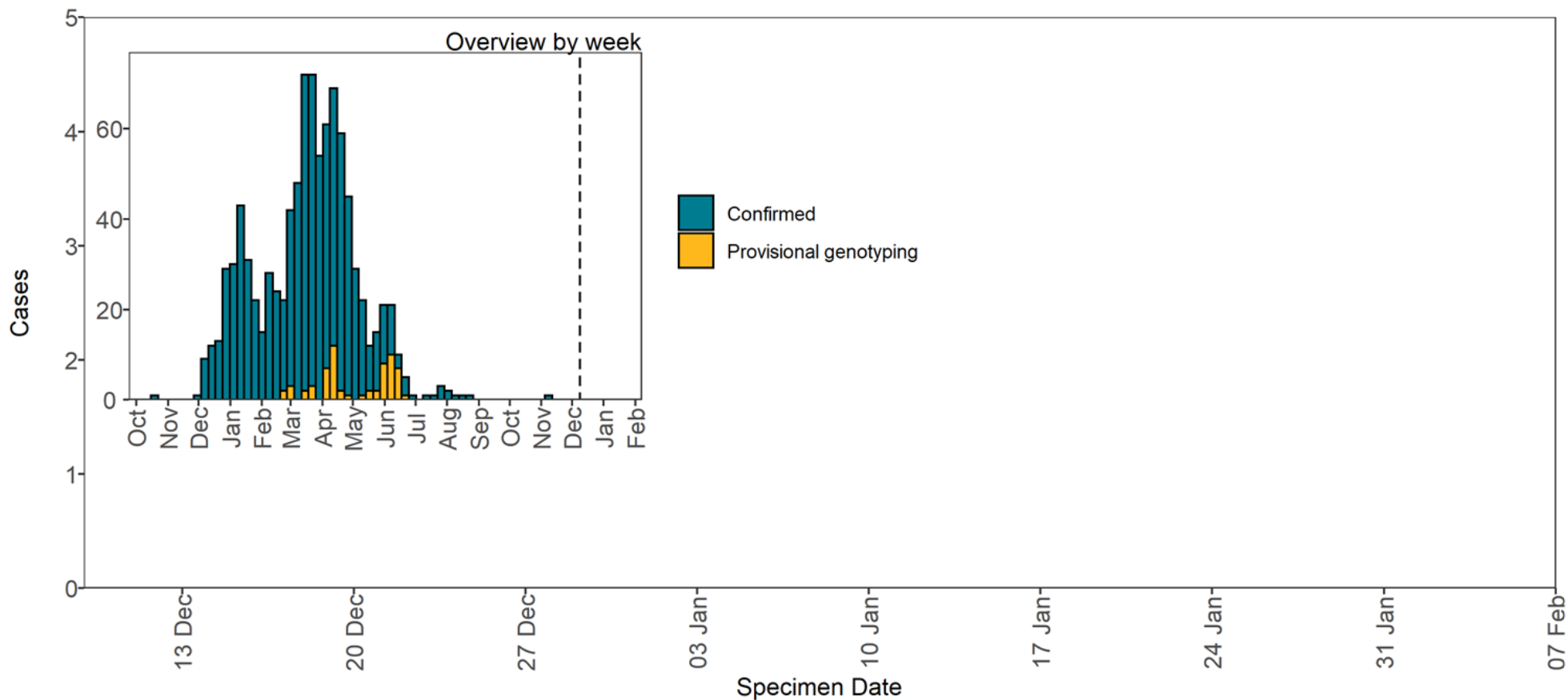
**Figure 7. Confirmed (sequencing) and probable (genotyping) Beta - VOC-20DEC-02 (B.1.351) cases by specimen date and region of residence as of 7 February 2022**

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



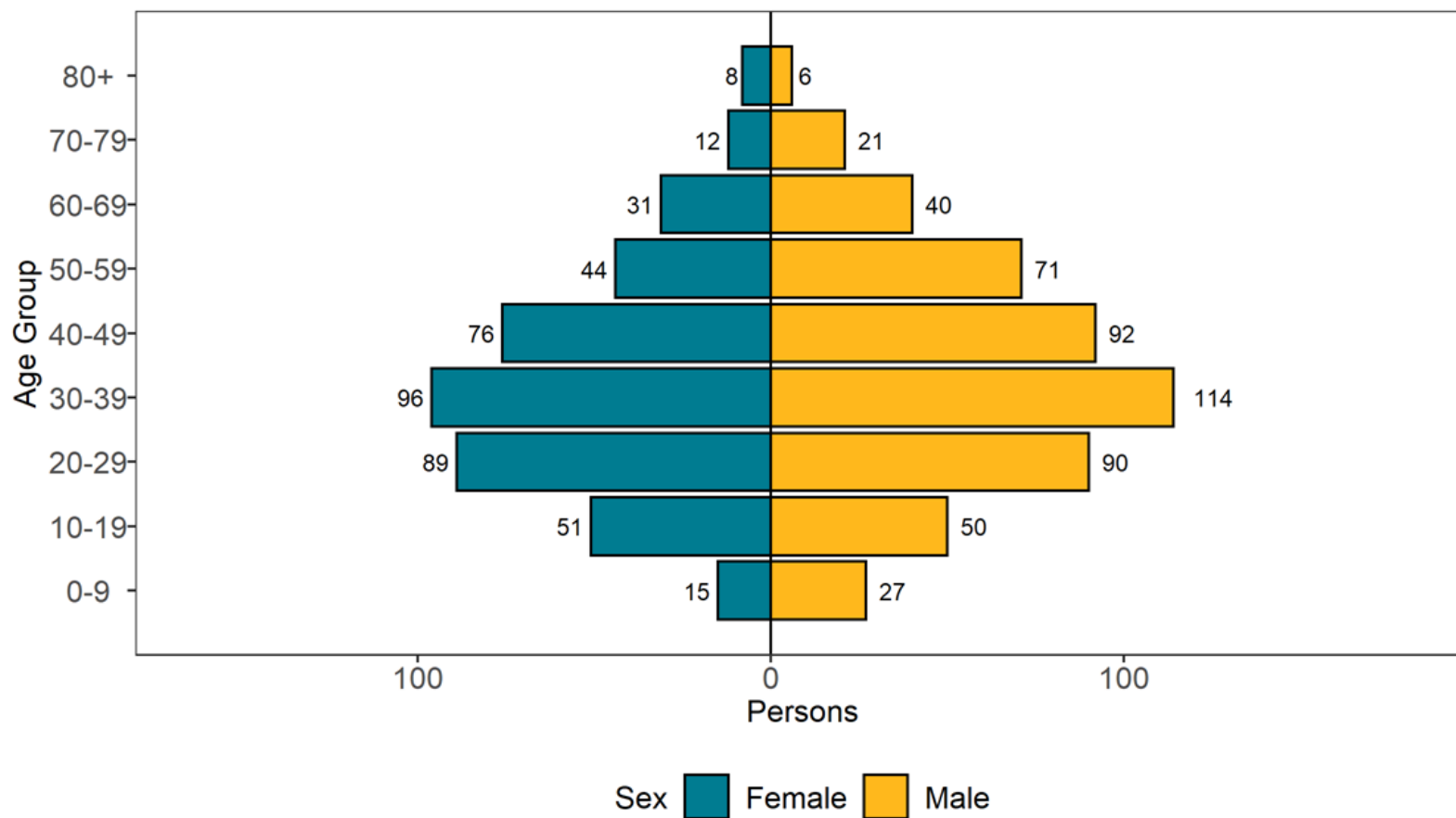
**Figure 8. Confirmed (sequencing) and probable (genotyping) Beta - VOC-20DEC-02 (B.1.351) cases by specimen date and detection method as of 7 February 2022**

(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 7 February 2022**

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



15 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

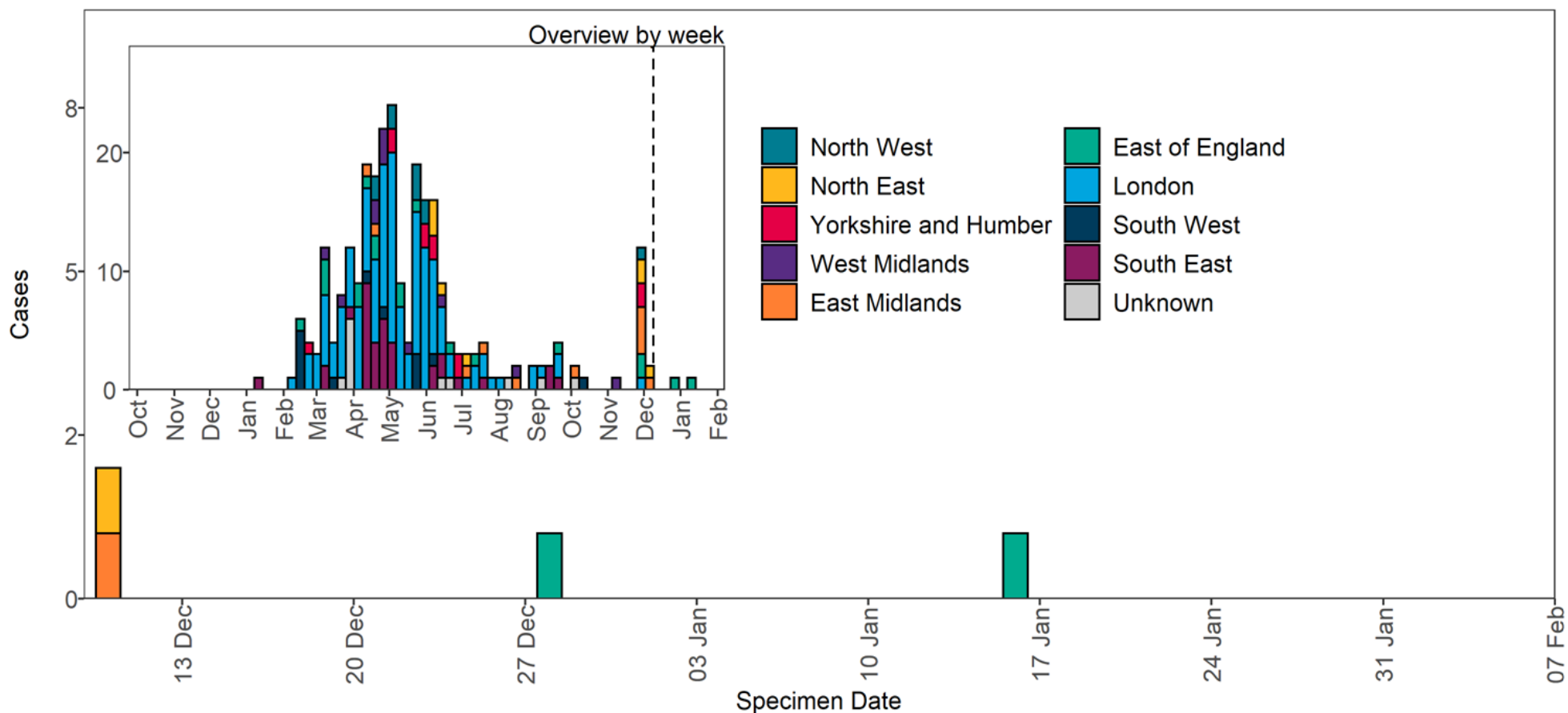
**Table 4. Number of confirmed (sequencing) and probable (genotyping) Gamma - VOC-21JAN-02 (P.1) cases, by region of residence as of 7 February 2022**

Region	Confirmed case number	Probable case number	Total case number	Case proportion
East Midlands	5	6	11	4.1%
East of England	14	5	19	7.1%
London	111	26	137	51.1%
North East	1	7	8	3.0%
North West	8	2	10	3.7%
South East	29	7	36	13.4%
South West	10	3	13	4.9%
West Midlands	8	3	11	4.1%
Yorkshire and Humber	2	9	11	4.1%
Unknown region	9	3	12	4.5%
Total	197	71	268	-



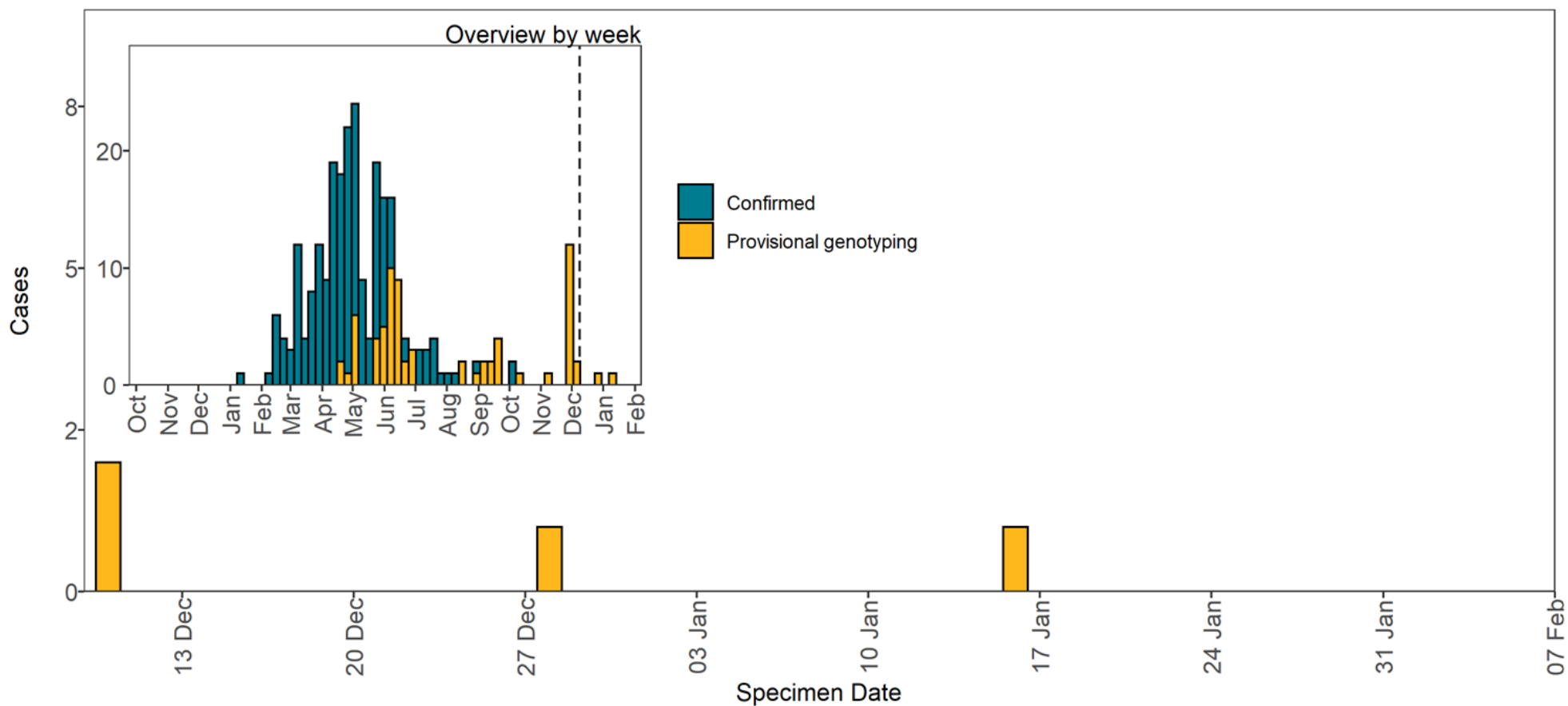
**Figure 10. Confirmed (sequencing) and probable (genotyping) Gamma - VOC-21JAN-02 (P.1) cases by specimen date and region of residence as of 7 February 2022**

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



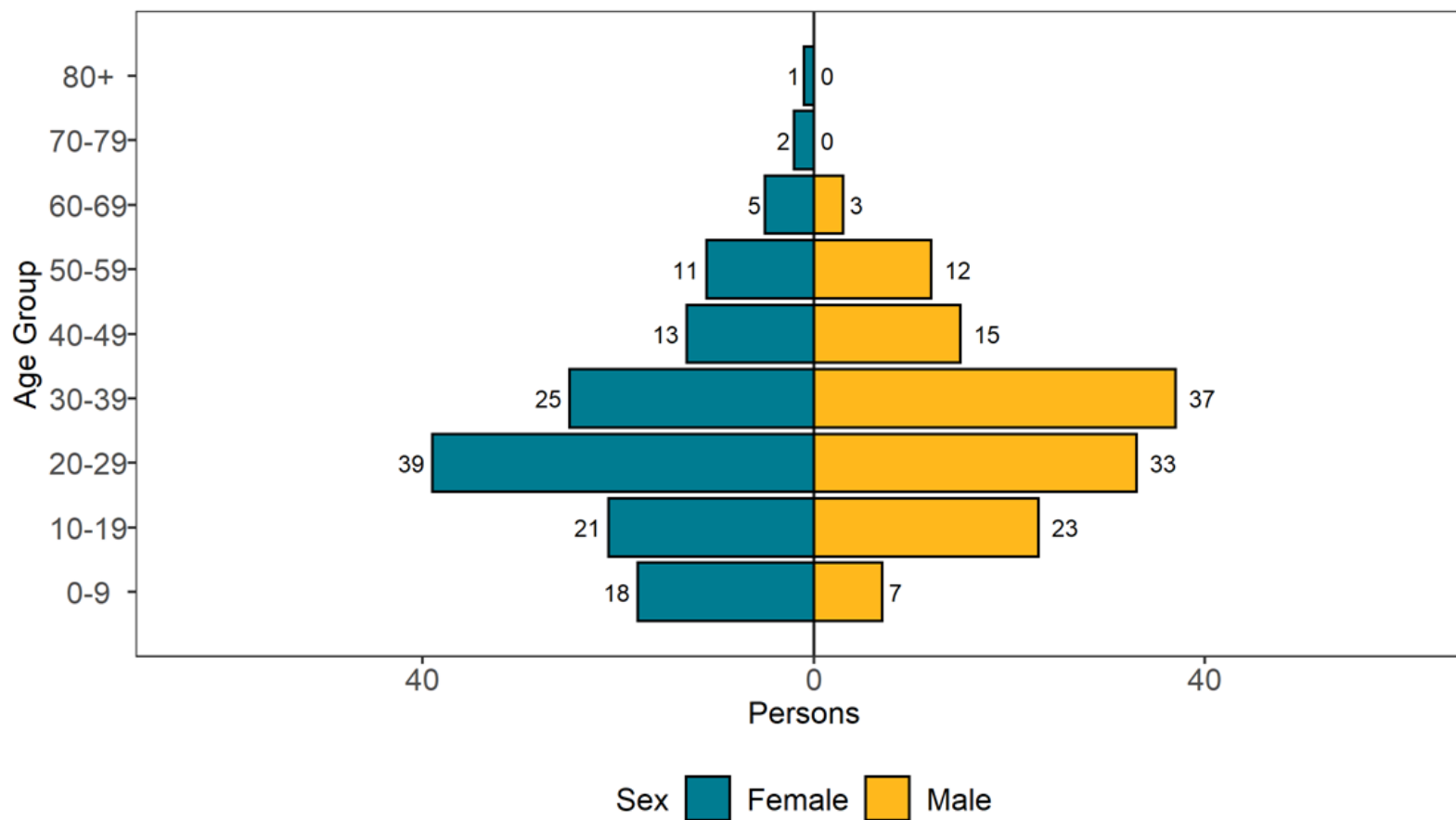
**Figure 11. Confirmed (sequencing) and probable (genotyping) Gamma - VOC-21JAN-02 (P.1) cases by specimen date and detection method as of 7 February 2022**

(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 7 February 2022**

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



3 cases excluded where sex or age not reported

## Omicron – VOC-21NOV-01 (B.1.1.529/BA.1)

A new 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. This variant was designated VUI-21NOV-01 by the UK Health Security Agency (UKHSA) Variant Technical Group and on review re-designated as VOC-21NOV-01 on 27 November 2021.

VOC-21NOV-01 currently refers specifically to the Omicron BA.1 lineage, as the BA.2 lineage is now recognized as VUI-22JAN-02. However, as genotyping cannot distinguish between BA.1 and BA.2, genotyped figures presented here will include BA.2 cases.

### Epidemiology

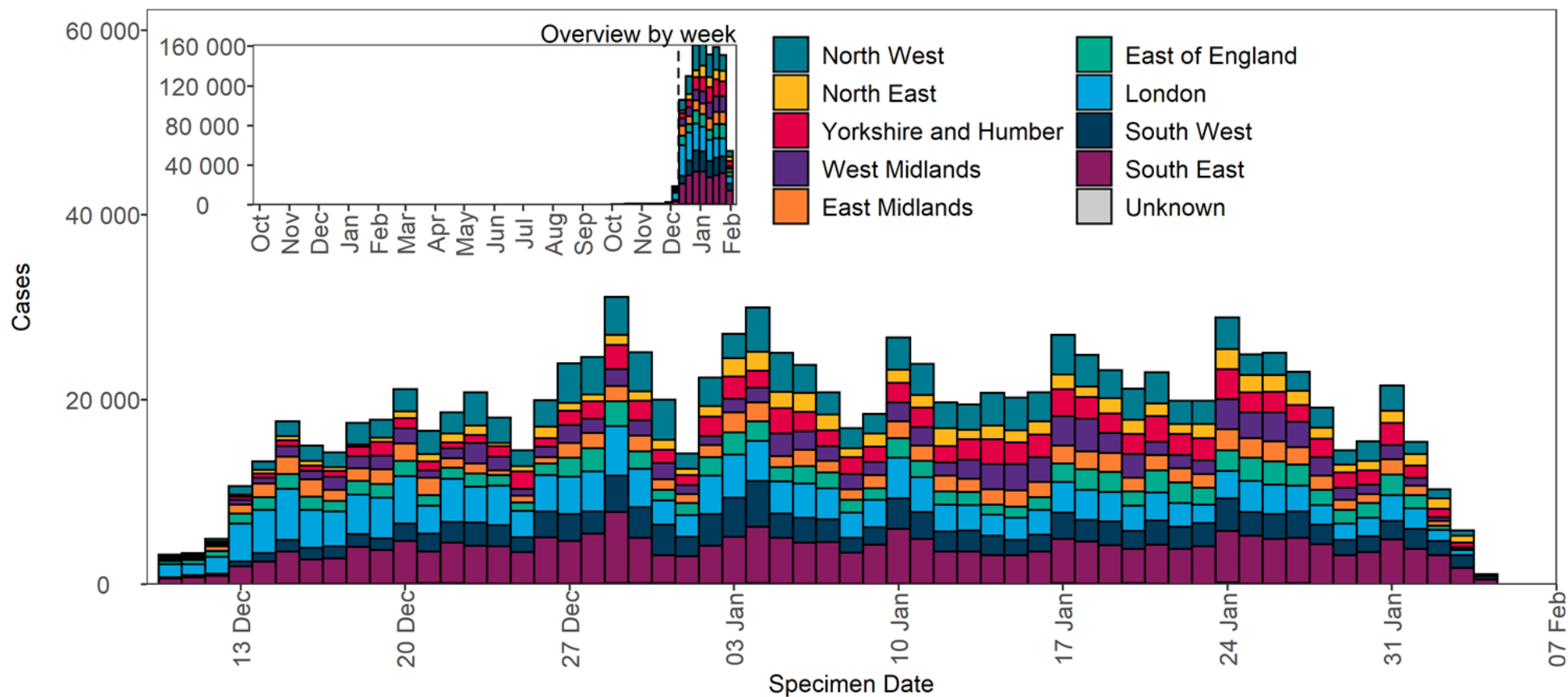
**Table 5. Number of confirmed (sequenced) and probable (genotyping) Omicron VOC-21NOV-01 (B.1.1.529/BA.1) cases, by region of residence as of 7 February 2022**

Region	Confirmed case number	Probable* case number	Total case number	Case proportion
East Midlands	29,409	51,088	80,497	7.3%
East of England	36,676	54,184	90,860	8.2%
London	66,116	120,407	186,523	16.9%
North East	19,135	43,812	62,947	5.7%
North West	52,999	92,228	145,227	13.1%
South East	54,741	169,248	223,989	20.3%
South West	29,326	96,164	125,490	11.4%
West Midlands	35,502	56,302	91,804	8.3%
Yorkshire and Humber	34,715	58,818	93,533	8.5%
Unknown region	2,486	1,786	4,272	0.4%
Total	361,105	744,037	1,105,142	-

\* Genotyped Omicron figures include BA.2.

**Figure 13. Confirmed (sequencing) and probable (genotyping\*) Omicron VOC-21NOV-01 (B.1.1.529/BA.1) cases by specimen date and region of residence as of 7 February 2022**

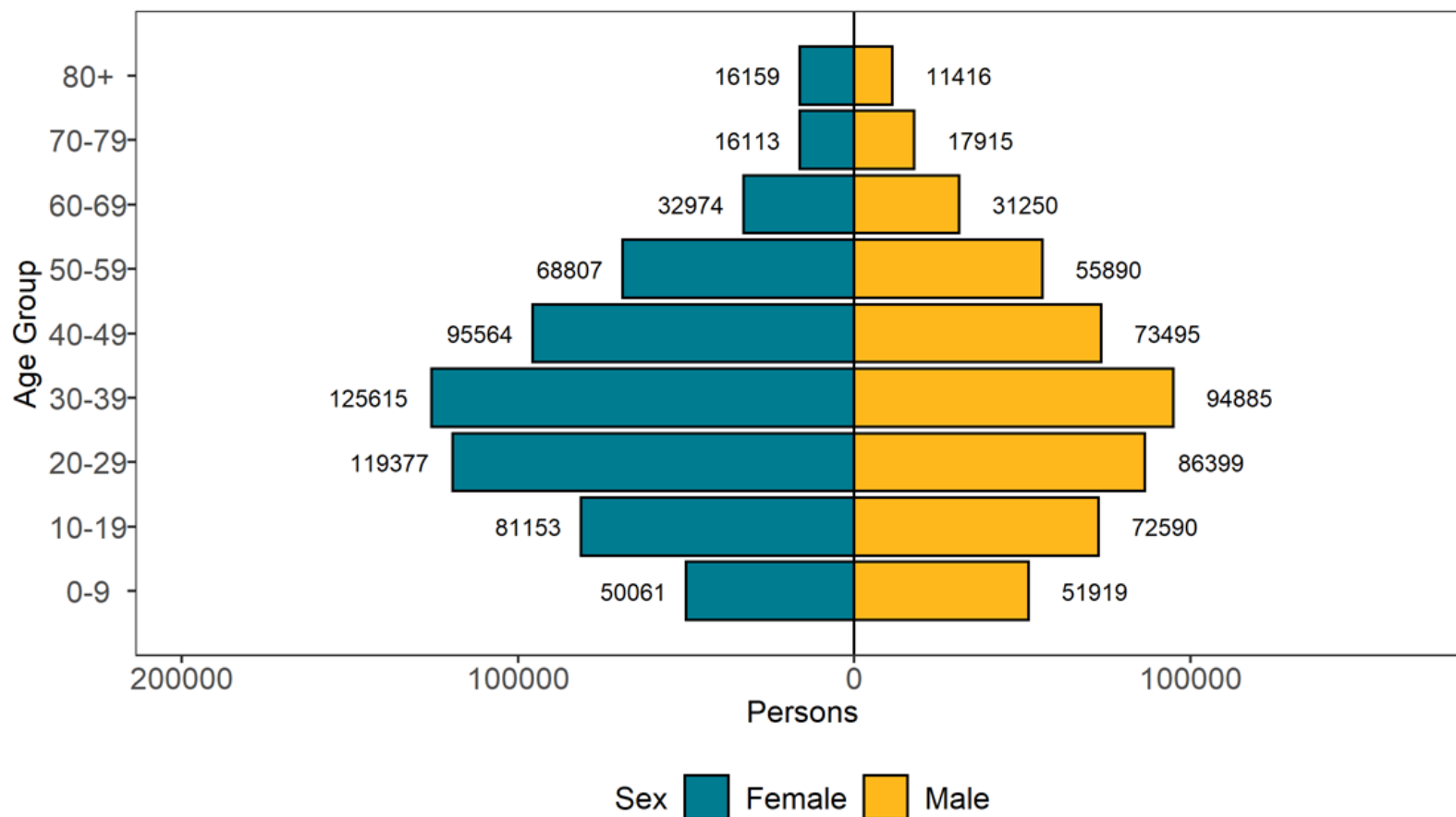
(The data used in this graph can be found in the [accompanying spreadsheet.](#))



\* Genotyped Omicron figures include BA.2.

**Figure 14. Age-sex pyramid of Omicron VOC-21NOV-01 (B.1.1.529/BA.1) cases as of 7 February 2022\***

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



3415 cases excluded where sex or age not reported

\* Genotyped Omicron figures include BA.2.

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

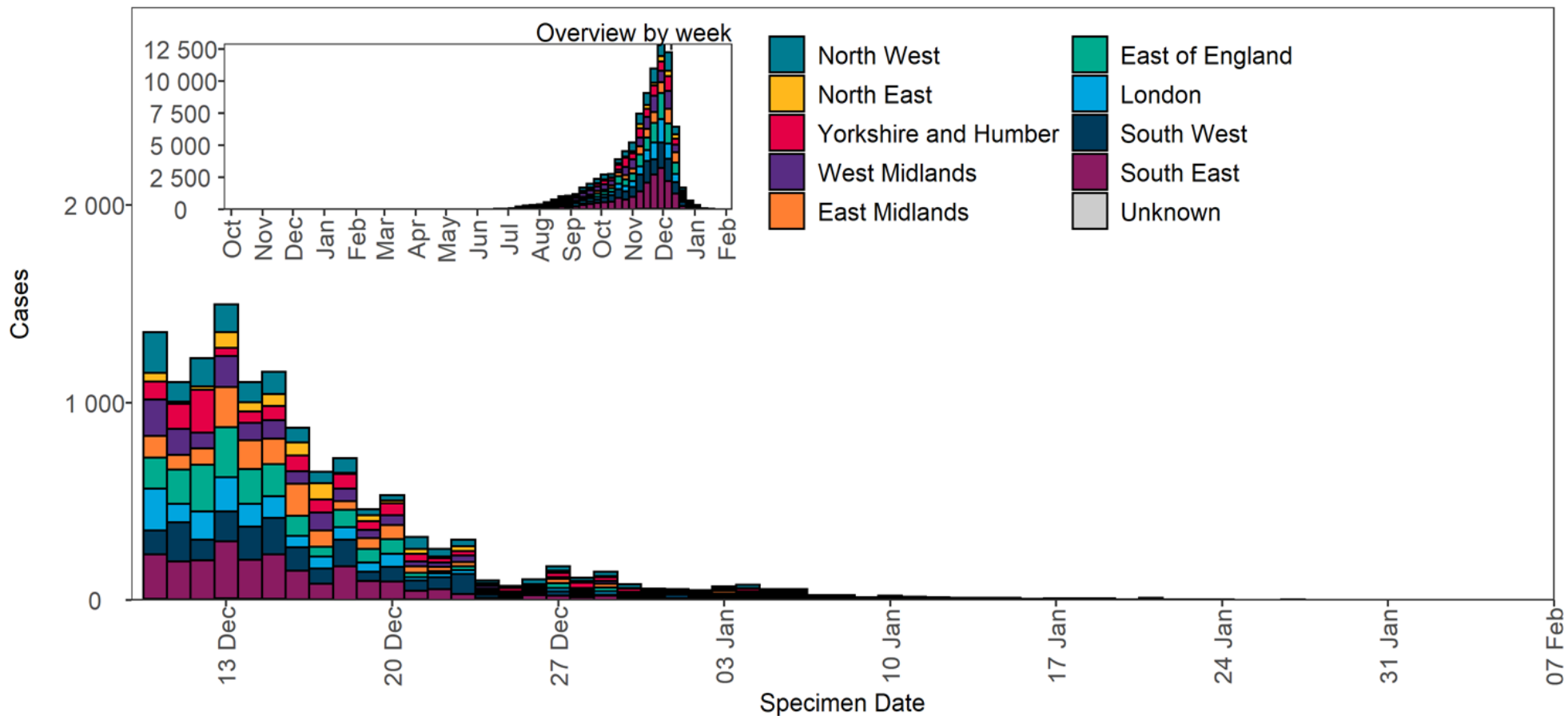
New sub-lineages of Delta are regularly identified and designated. The Delta sub-lineage AY.4.2 was designated VUI-21OCT-01 on 20 October 2021.

### Epidemiology

**Table 6. Number of confirmed (sequencing) VUI-21OCT-01 cases, by region of residence as of 7 February 2022**

Region	Total case number	Confirmed (sequenced) case number	Case proportion
East Midlands	7,400	7,400	7.9%
East of England	11,708	11,708	12.5%
London	10,478	10,478	11.2%
North East	2,967	2,967	3.2%
North West	9,618	9,618	10.3%
South East	19,068	19,068	20.4%
South West	13,509	13,509	14.5%
West Midlands	10,274	10,274	11.0%
Yorkshire and Humber	7,923	7,923	8.5%
Unknown region	402	402	0.4%
Total	93,347	93,347	-

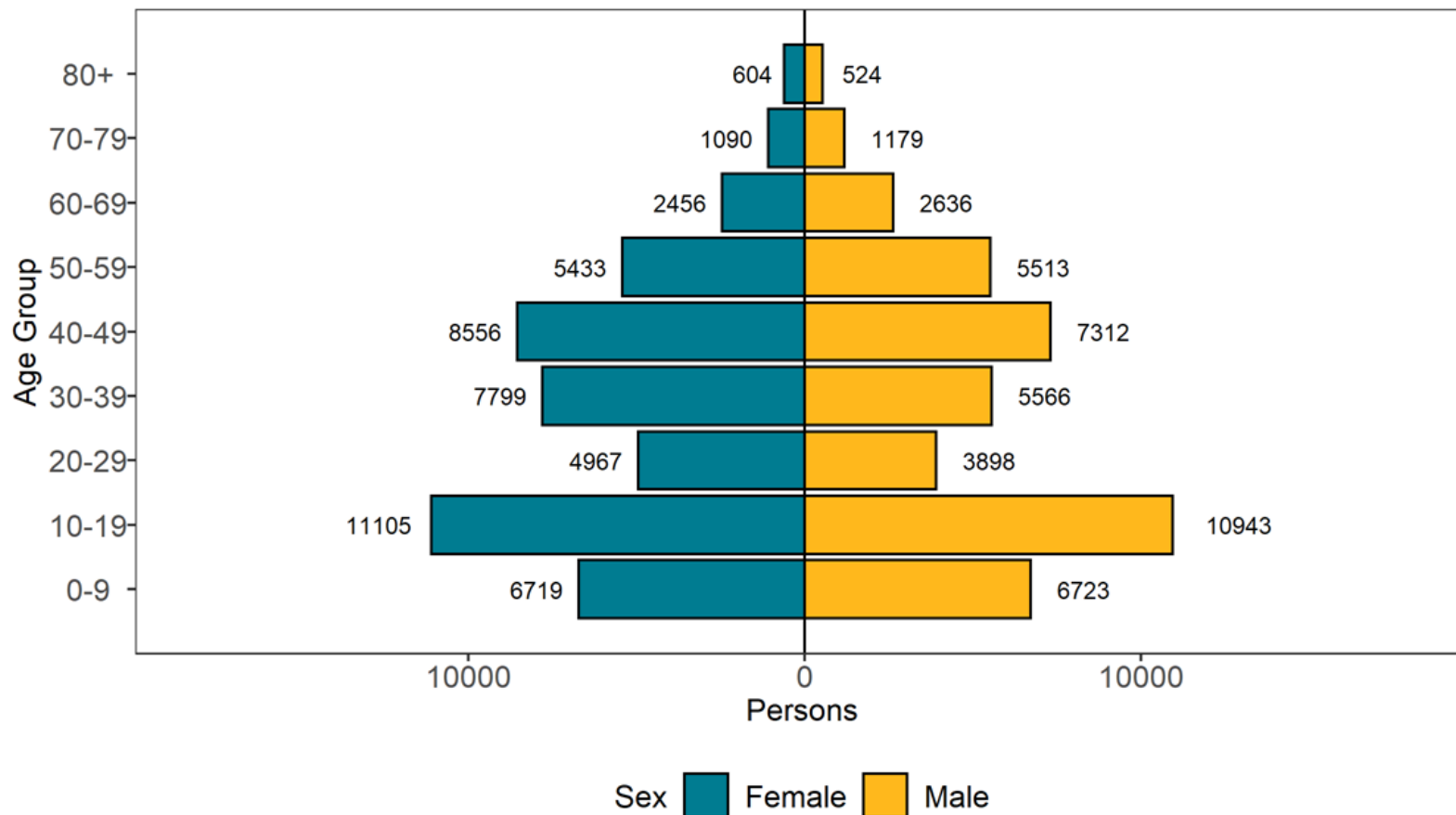
**Figure 15. Confirmed (sequencing) VUI-21OCT-01 (AY 4.2) cases by specimen date and region of residence as of 7 February 2022**  
 (The data used in this graph can be found in the [accompanying spreadsheet.](#))





**Figure 16. Age-sex pyramid of VUI-21OCT-01 (AY 4.2) cases as of 7 February 2022**

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



287 cases excluded where sex or age not reported

## 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.

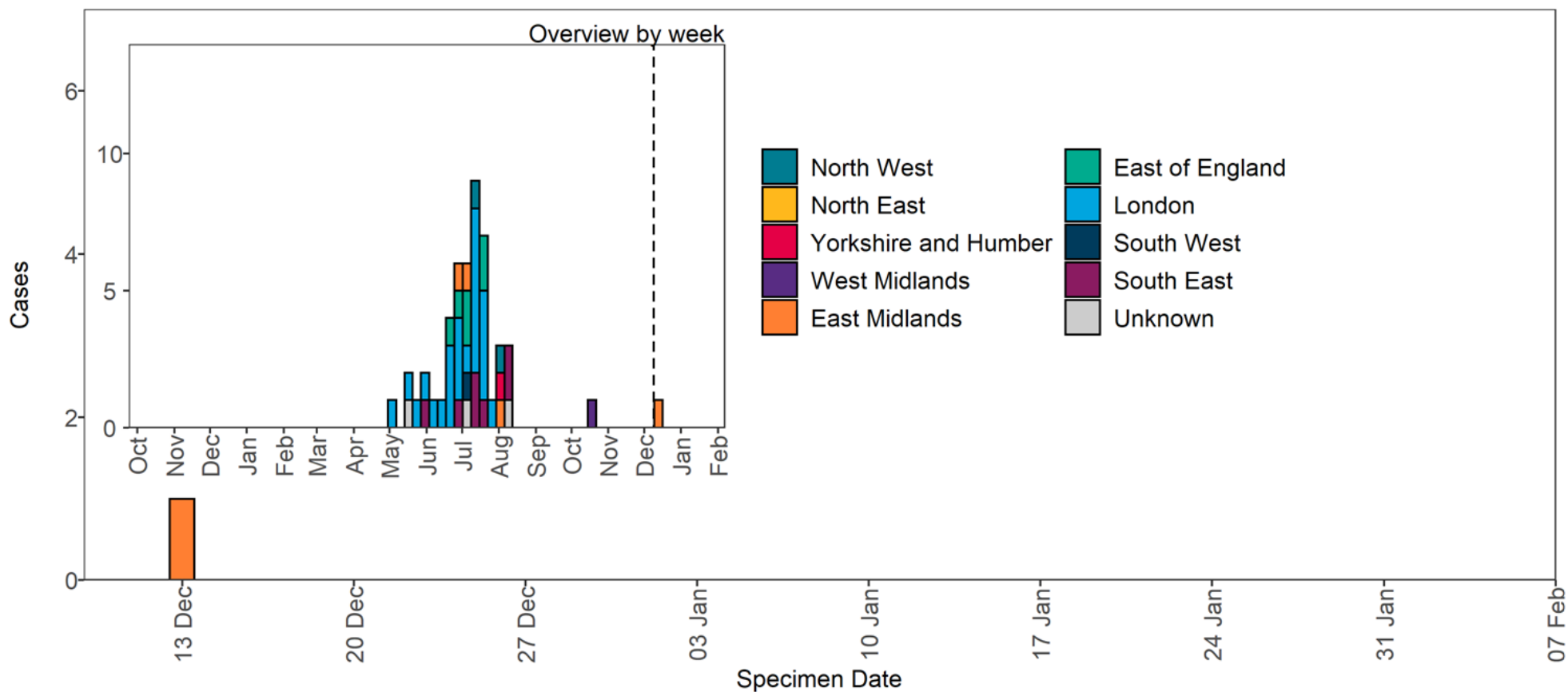
### Epidemiology

**Table 7. Number of confirmed (sequencing) Mu - VUI-21JUL-01 (B.1.621) cases, by region of residence as of 7 February 2022**

Region	Total case number	Confirmed (sequenced) case number	Case proportion
East Midlands	4	4	8.2%
East of England	6	6	12.2%
London	24	24	49.0%
North East	0	0	0.0%
North West	2	2	4.1%
South East	7	7	14.3%
South West	1	1	2.0%
West Midlands	1	1	2.0%
Yorkshire and Humber	1	1	2.0%
Unknown region	3	3	6.1%
Total	49	49	-

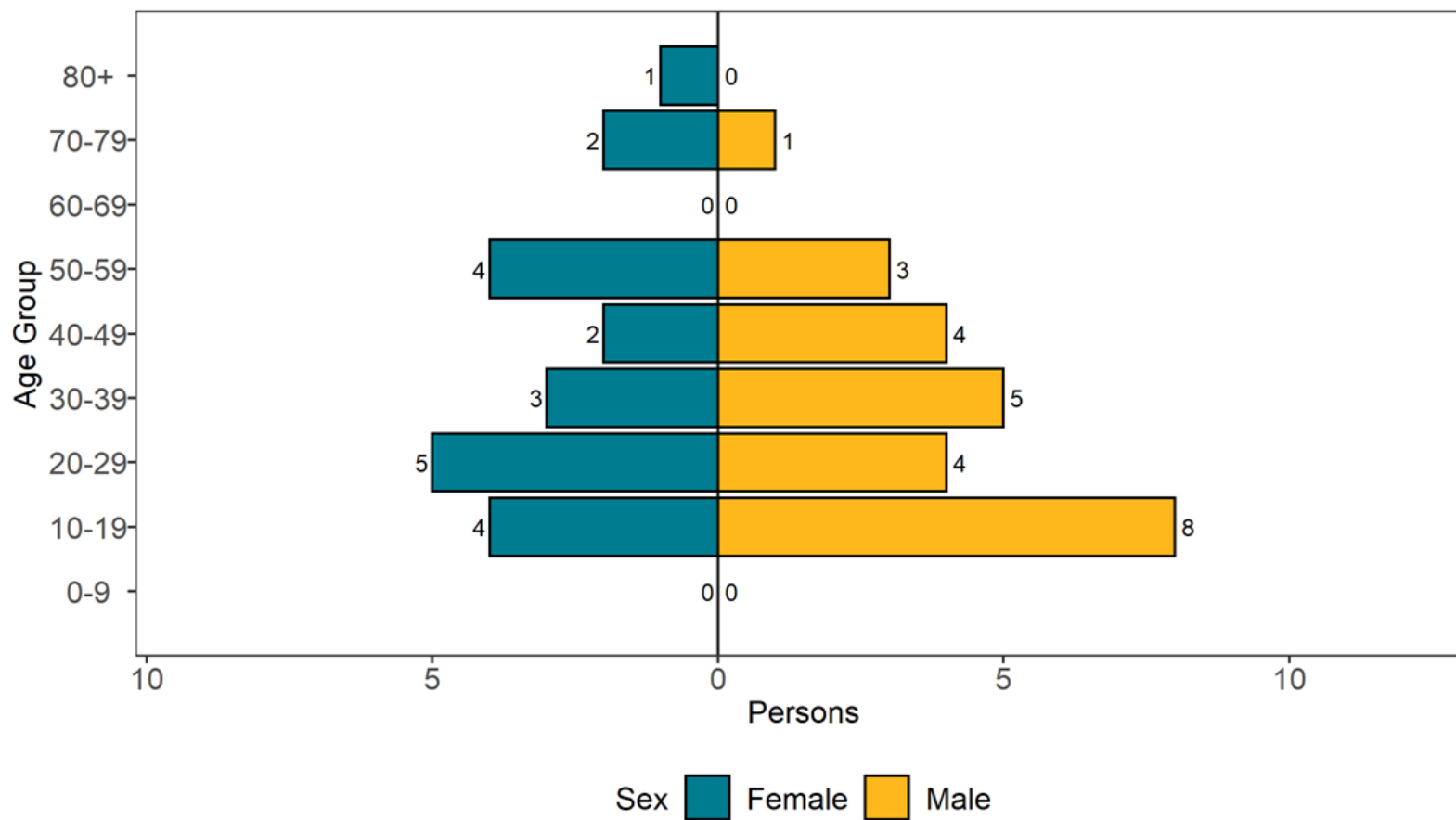
**Figure 17. Confirmed (sequencing) Mu - VUI-21JUL-01 (B.1.621) cases by specimen date and region of residence as of 7 February 2022**

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



**Figure 18. Age-sex pyramid of Mu - VUI-21JUL-01 (B.1.621) cases as of 7 February 2022**

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



3 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 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 is 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.

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# About the UK Health Security Agency

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