UK Health Security Agency

SARS-CoV-2 variant data update, England

Version 21

28 January 2022

This edition provides an update on previous data noted within the technical briefings and variant data updates up to 14 January 2022.

Contents

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	
Gamma (P.1) VOC-21JAN-02	VUI-21FEB-04 B.1.1.318	
Delta (B.1.617.2 and sub-lineages) VOC-21APR-02	VUI-22JAN-01 BA.2††	
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 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)	
	VUI-21FEB-03 (B.1.525)	
	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.

Enhanced analysis of Omicron VOC-21NOV-01 (B.1.1.529/BA.1) is available in Technical Briefing 34.

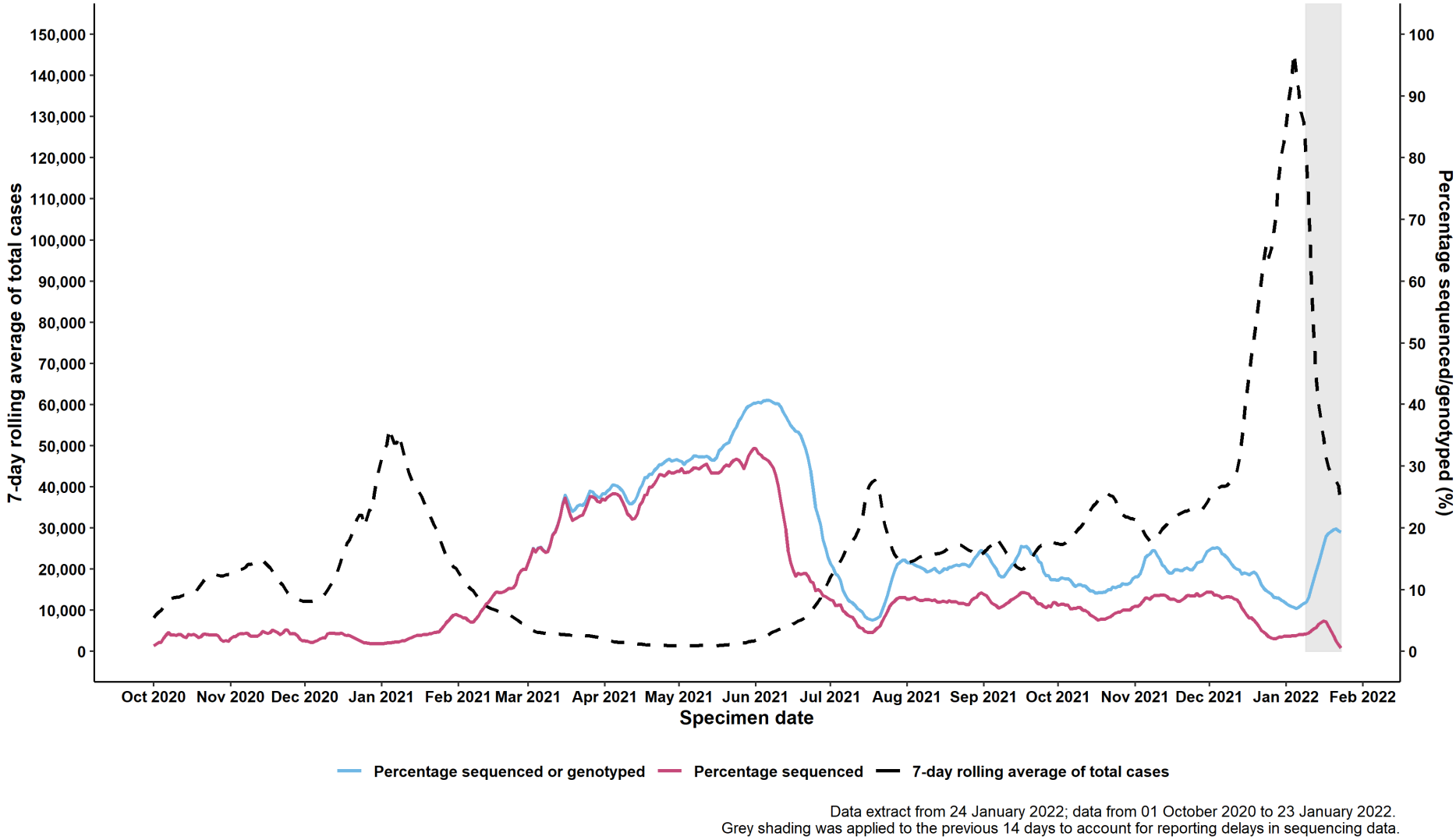
Sequencing coverage

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:

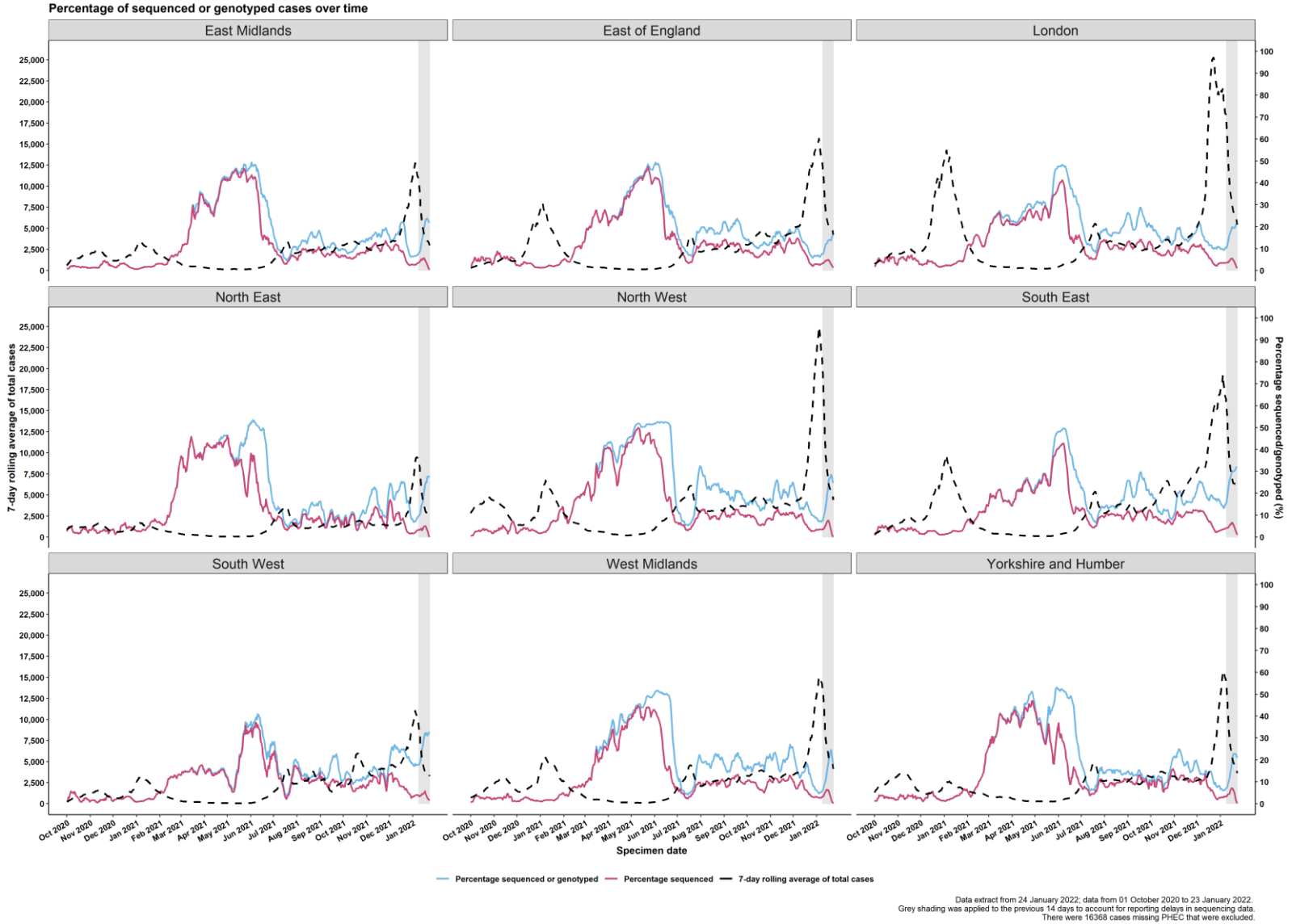
- hospitalised cases and hospital staff
- cases among international travellers
- national core priority studies
- as near random a sample as possible from each region to the maximum coverage allowed by laboratory capacity

Figure 1. Coverage of sequencing with a valid result and genotyping over time (1 October 2020 to 23 January 2022)



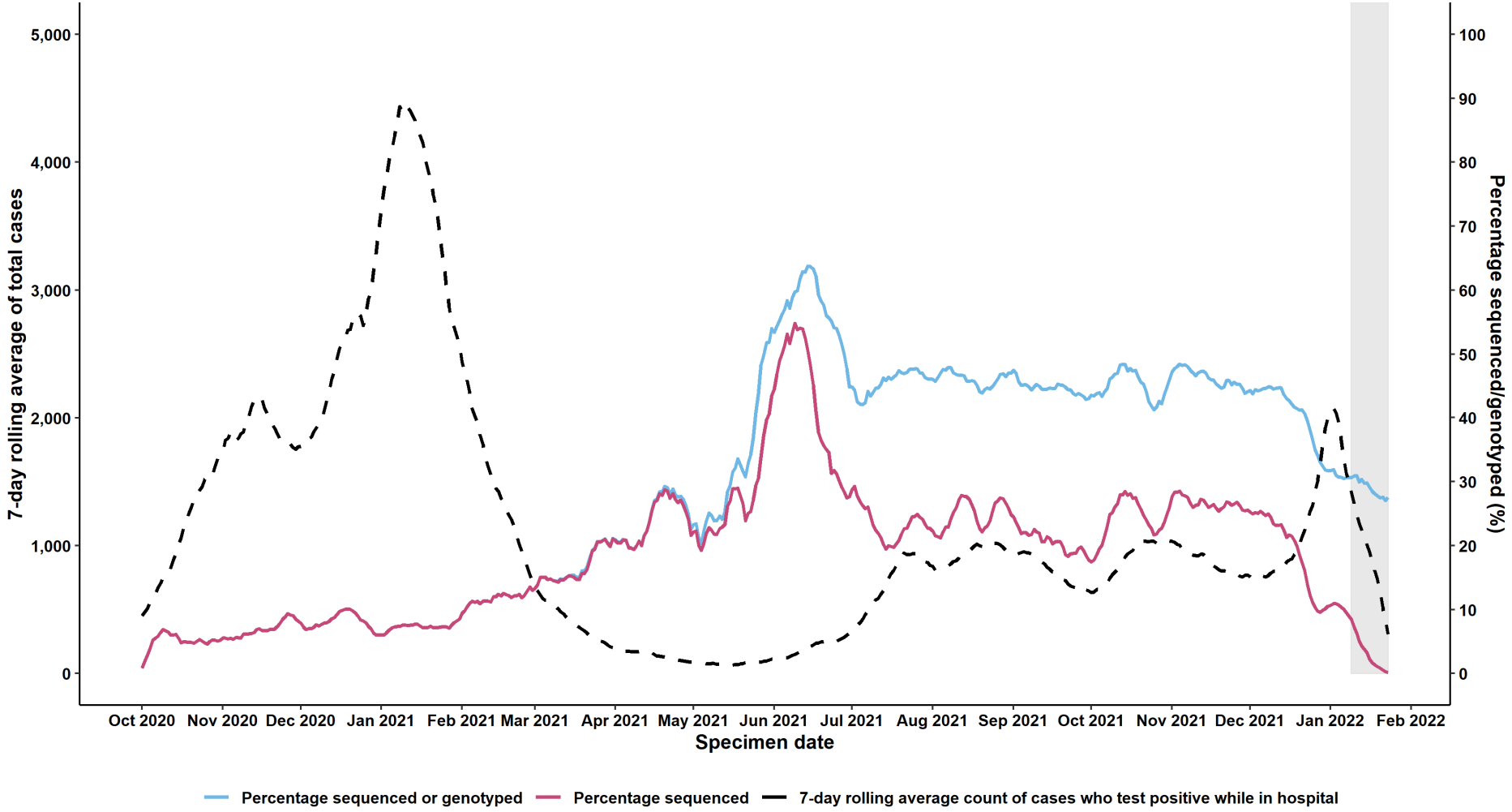
Grey shading was applied to the previous 14 days to account for reporting delays in sequencing data. (The data used in this graph can be found in the accompanying spreadsheet.)

Figure 2. Coverage of sequencing with a valid result and genotyping over time by region (1 October 2020 to 23 January 2022)



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 23 January 2022)



Data extract from 24 January 2022; data from 01 October 2020 to 23 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 and provisional Alpha - VOC-20DEC-01 (B.1.1.7) cases, by region of residence as of 24 January 2022

Region	Confirmed case number	Provisional case number	Total case number	Case proportion
East Midlands	16,165	477	16,642	7.4%
East of England	19,703	181	19,884	8.8%
London	40,326	761	41,087	18.2%
North East	14,628	110	14,738	6.5%
North West	41,891	1,713	43,604	19.3%
South East	23,927	119	24,046	10.6%
South West	8,176	50	8,226	3.6%
West Midlands	18,274	1,292	19,566	8.7%
Yorkshire and Humber	35,866	883	36,749	16.3%
Unknown region	1,225	18	1,243	0.6%
Total	220,181	5,604	225,785	-

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 24 January 2022

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

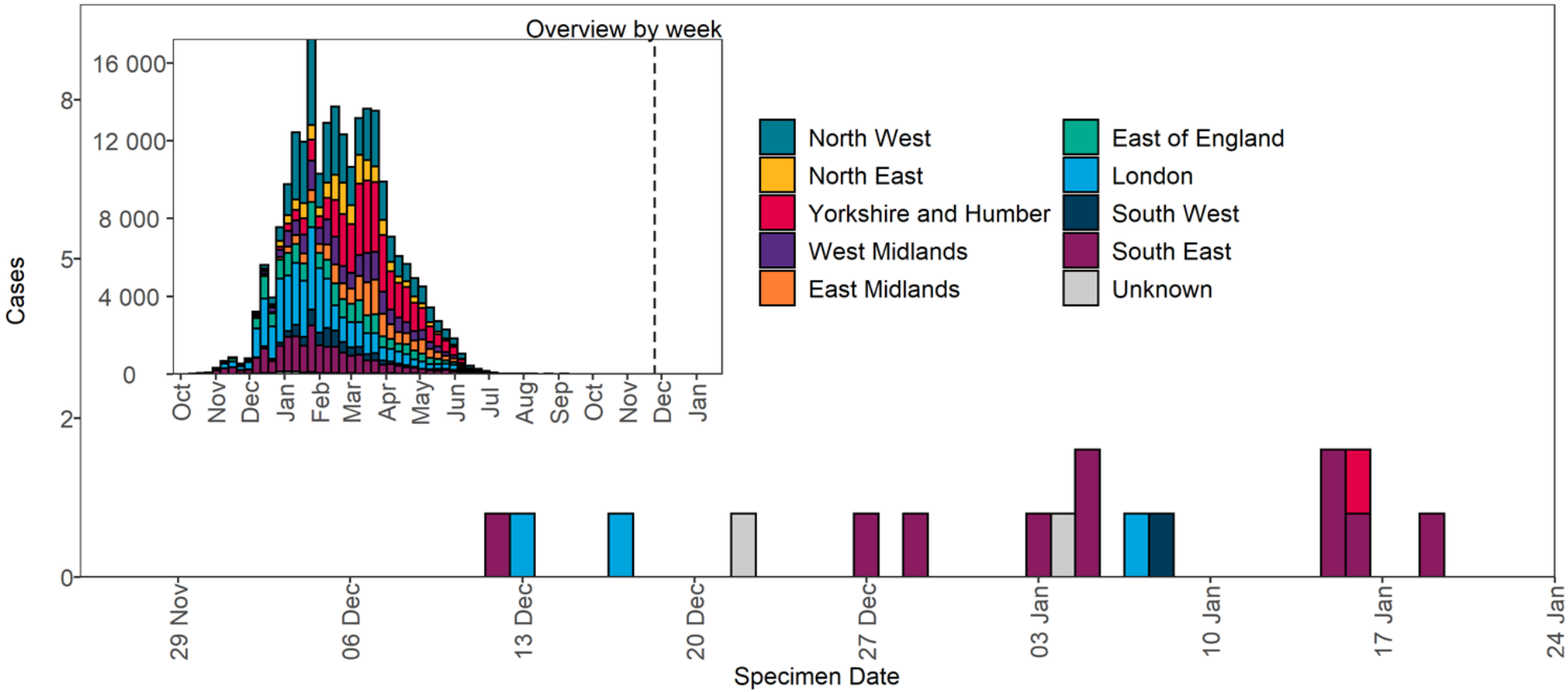


Figure 5. Confirmed (sequencing) and provisional (genotyping) Alpha - VOC-20DEC-01 (B.1.1.7) cases by specimen date and detection method as of 24 January 2022

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

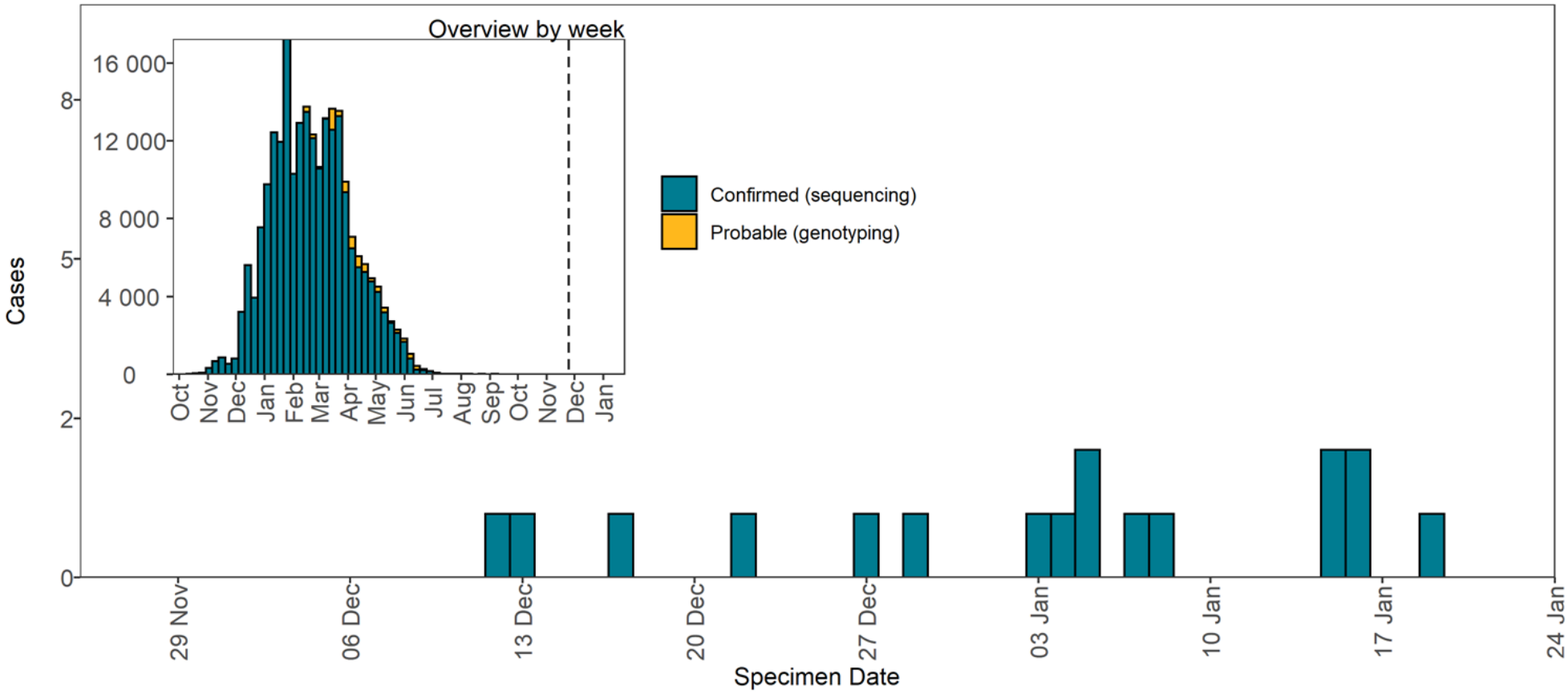
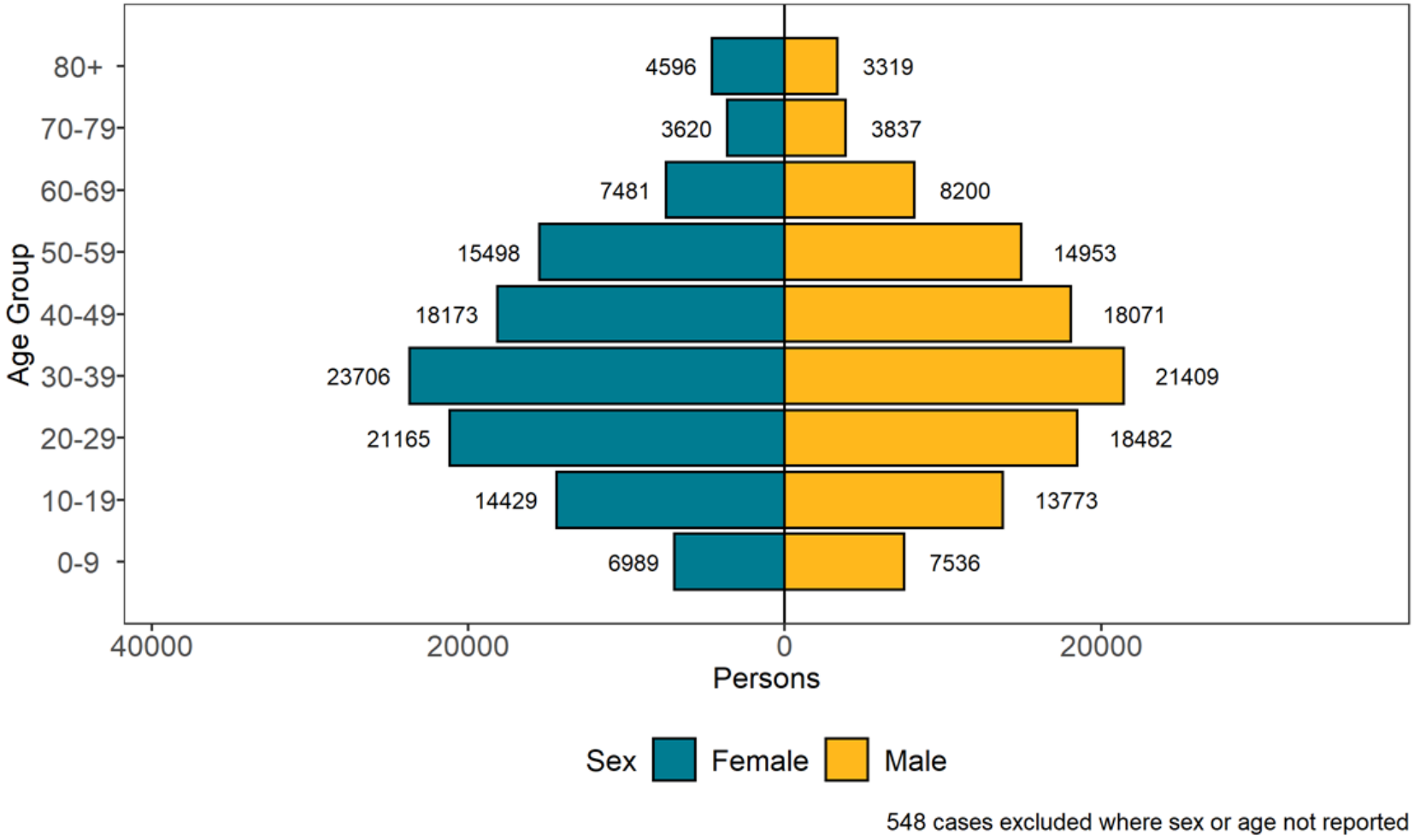


Figure 6. Age-sex pyramid of Alpha - VOC-20DEC-01 (B.1.1.7) cases as of 24 January 2022
(The data used in this graph can be found in the accompanying spreadsheet.)



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 24 January 2022

Region	Confirmed case number	Provisional case number	Total case number	Case proportion
East Midlands	48	3	51	5.2%
East of England	85	2	87	8.8%
London	430	25	455	46.0%
North East	19	6	25	2.5%
North West	79	9	88	8.9%
South East	117	4	121	12.2%
South West	31	1	32	3.2%
West Midlands	64	1	65	6.6%
Yorkshire and Humber	32	6	38	3.8%
Unknown region	23	4	27	2.7%
Total	928	61	989	-

Figure 7. Confirmed (sequencing) and probable (genotyping) Beta - VOC-20DEC-02 (B.1.351) cases by specimen date and region of residence as of 24 January 2022

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

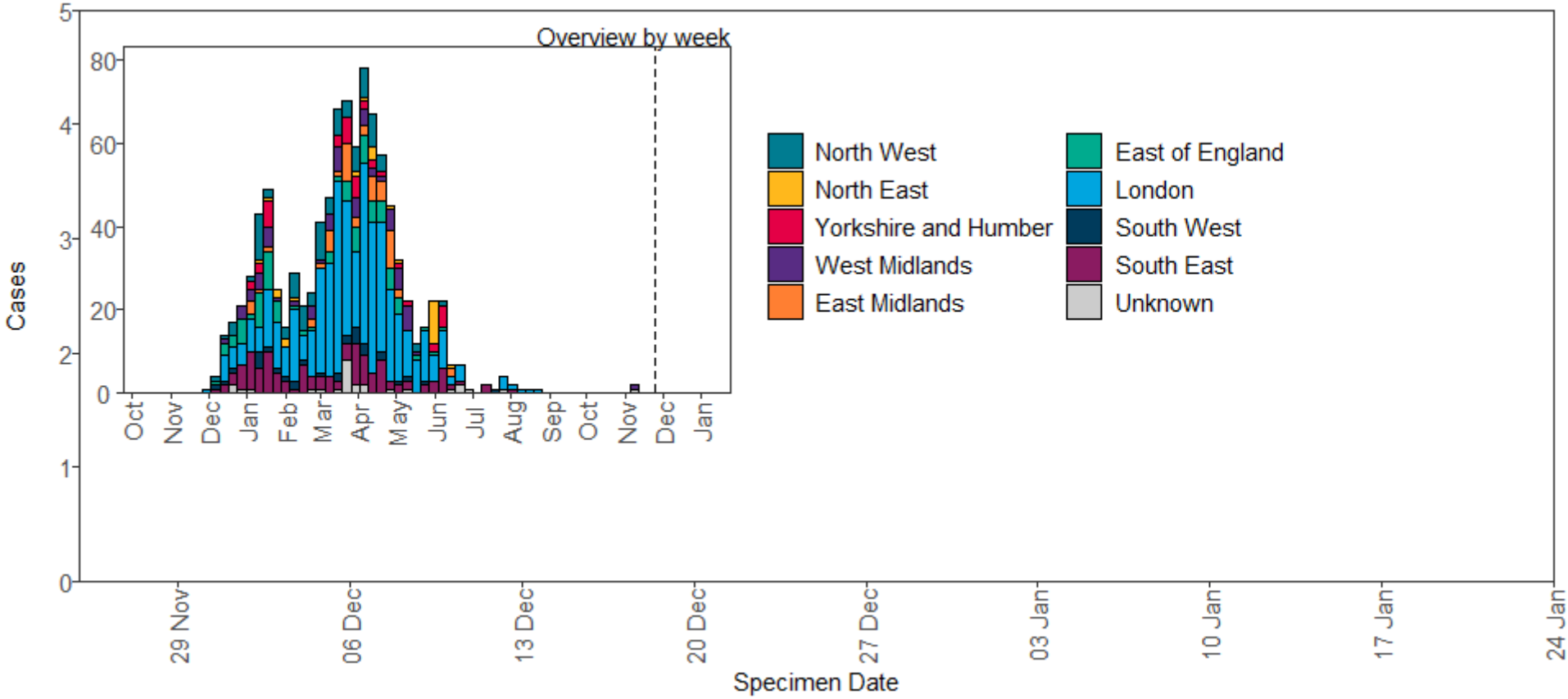


Figure 8. Confirmed (sequencing) and probable (genotyping) Beta - VOC-20DEC-02 (B.1.351) cases by specimen date and detection method as of 24 January 2022

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

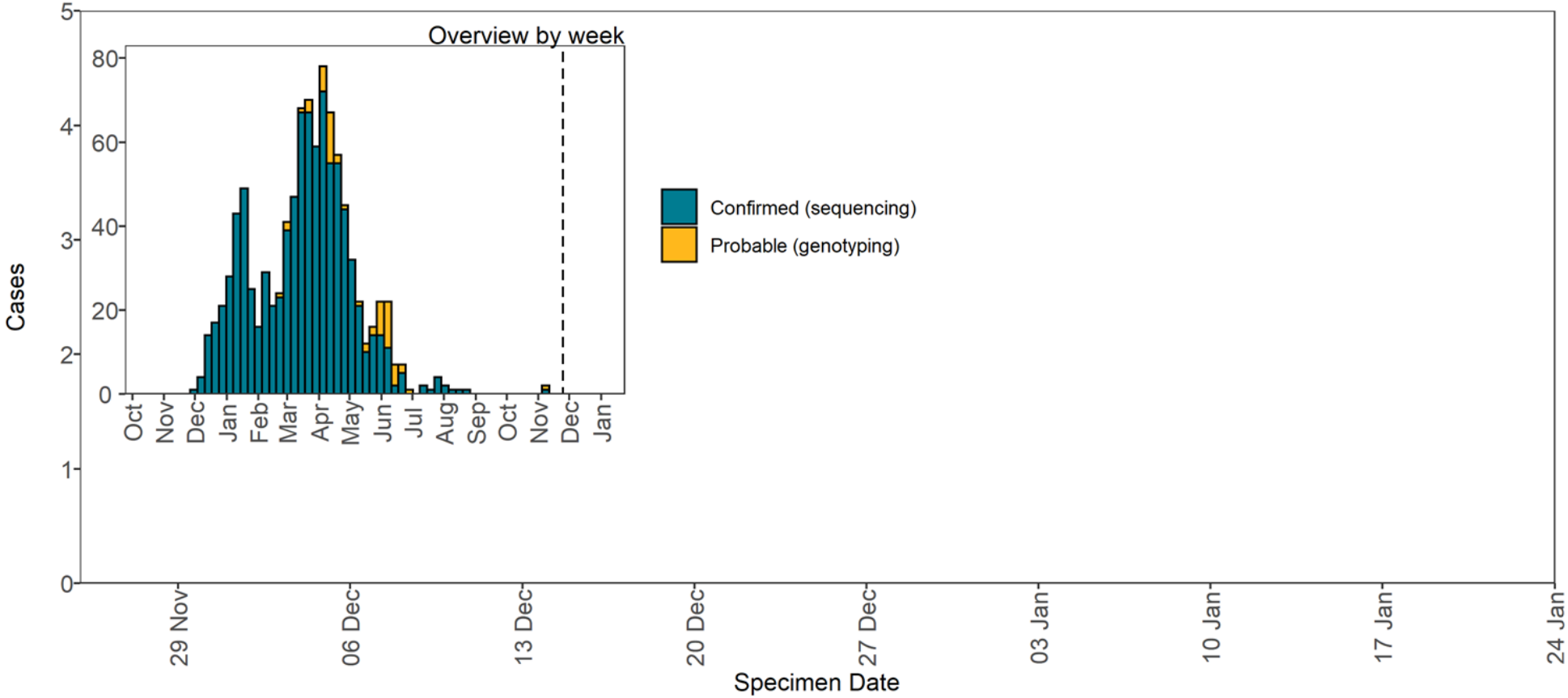
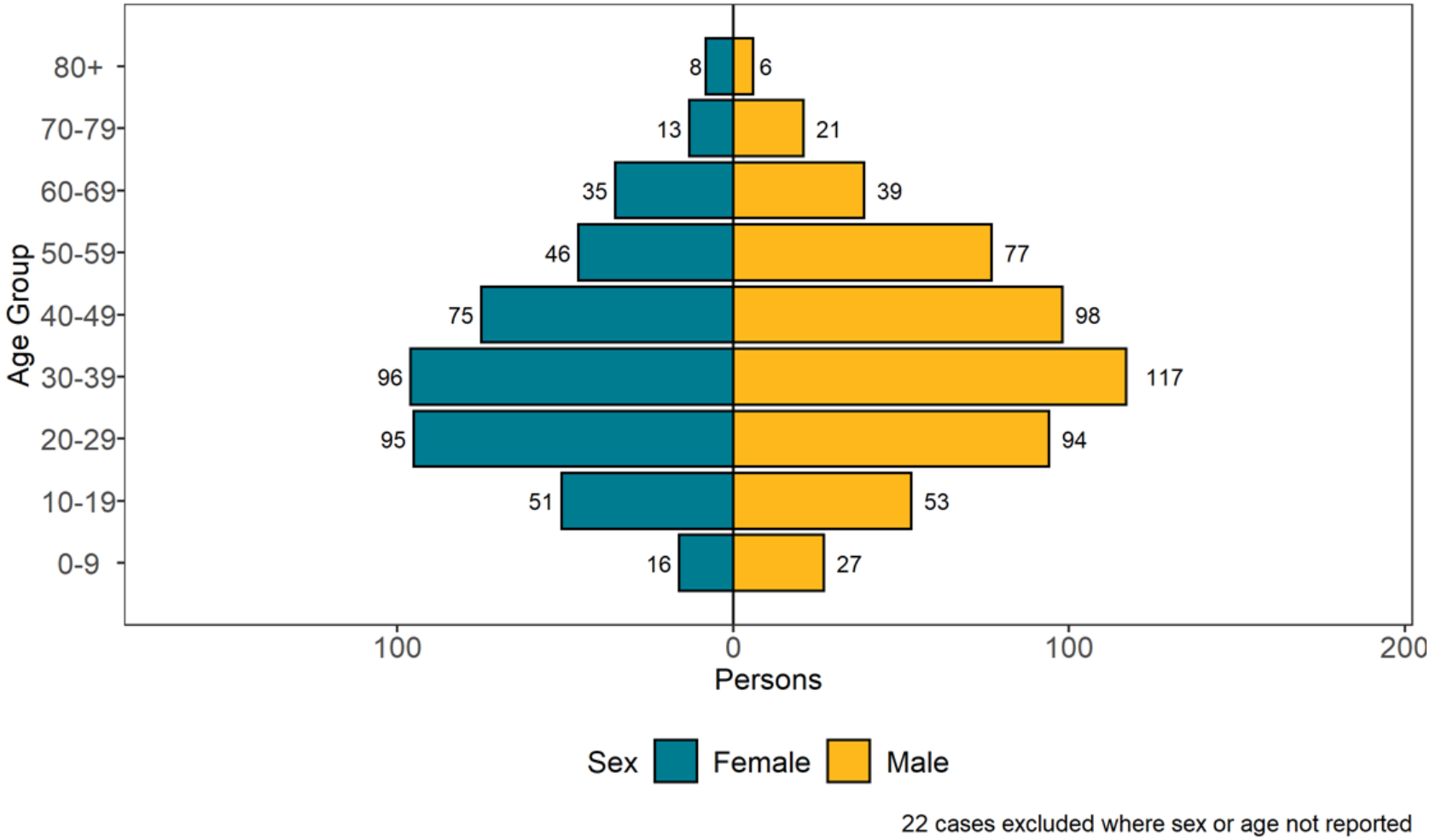


Figure 9. Age-sex pyramid of Beta - VOC-20DEC-02 (B.1.351) cases as of 24 January 2022
(The data used in this graph can be found in the accompanying spreadsheet.)



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 24 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 24 January 2022

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

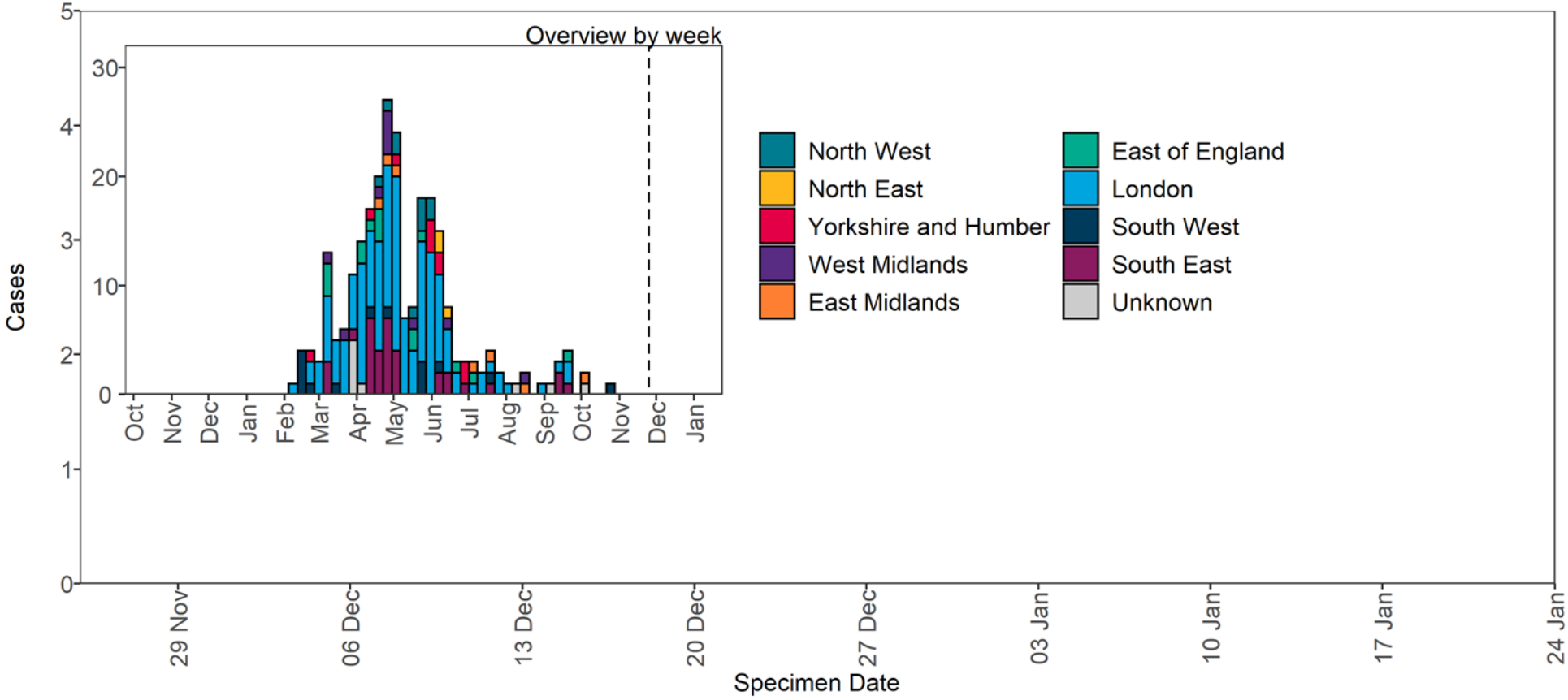


Figure 11. Confirmed (sequencing) and probable (genotyping) Gamma - VOC-21JAN-02 (P.1) cases by specimen date and detection method as of 24 January 2022

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

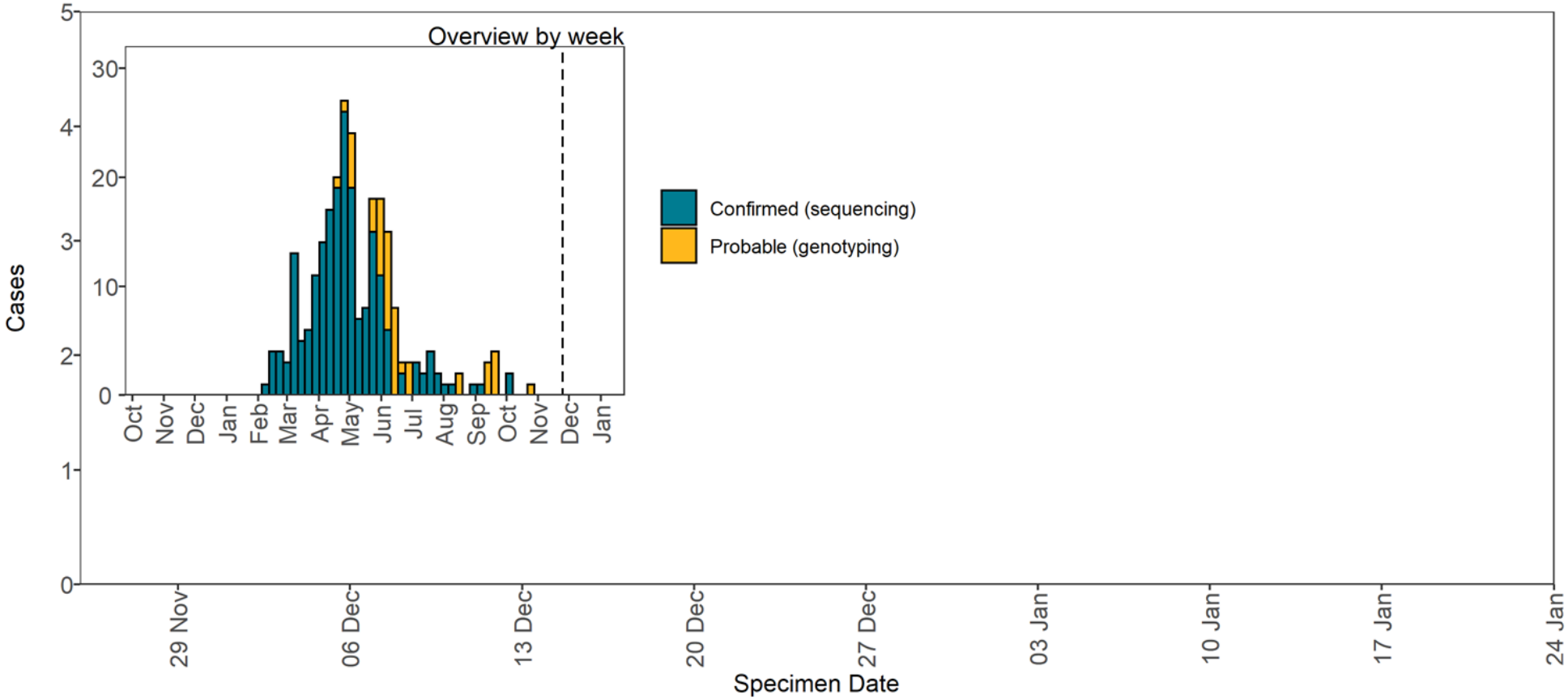
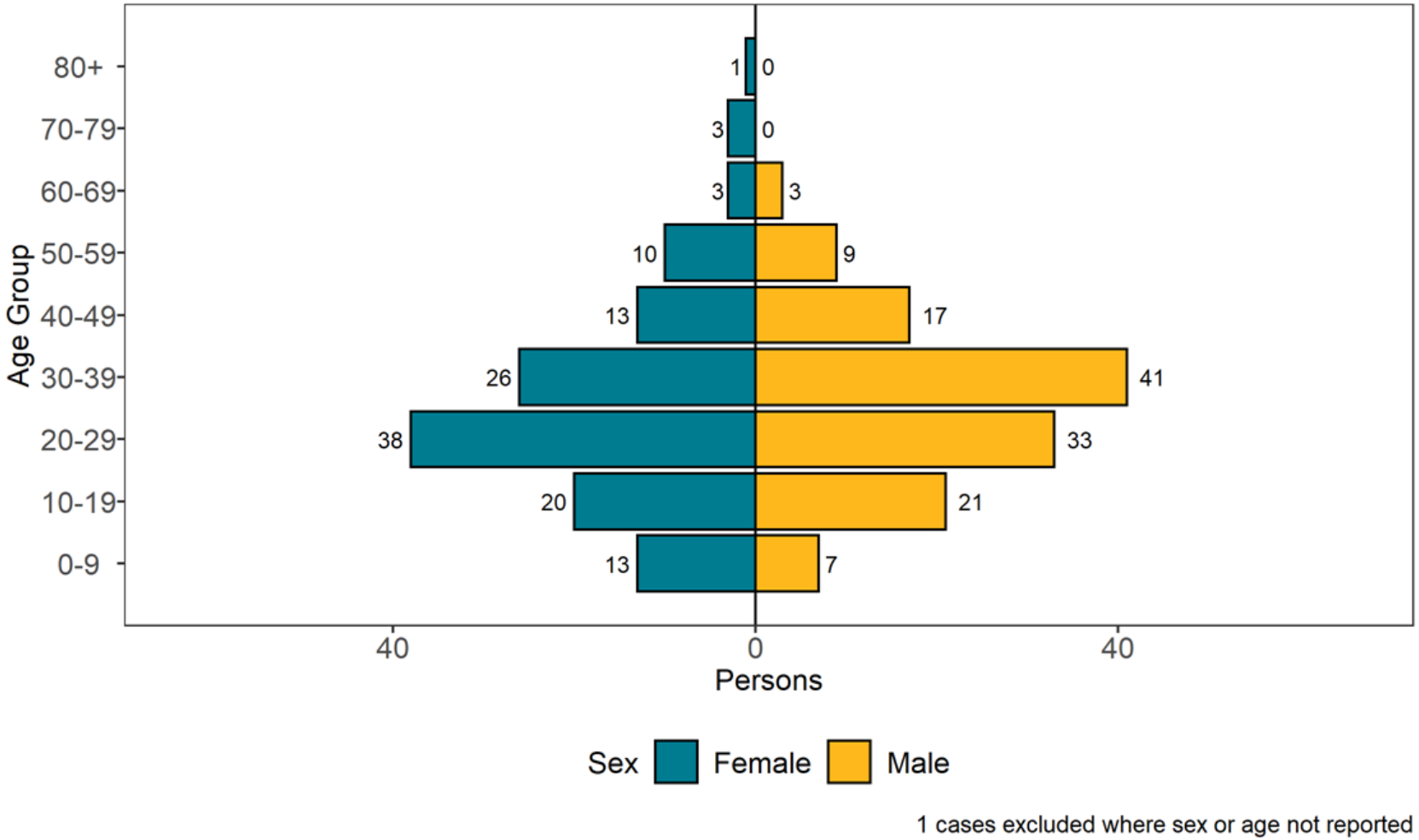


Figure 12. Age-sex pyramid of Gamma - VOC-21JAN-02 (P.1) cases as of 24 January 2022
(The data used in this graph can be found in the accompanying spreadsheet.)



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. Delta cases with changes at position S:484 were monitored separately from Delta. However, the dominant SARS-COV-2 lineage within England is now Omicron (B.1.1.529/BA.1) and all Delta lineages are shrinking. Therefore, epidemiology of Delta with additional mutations will not be included after this report.

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.

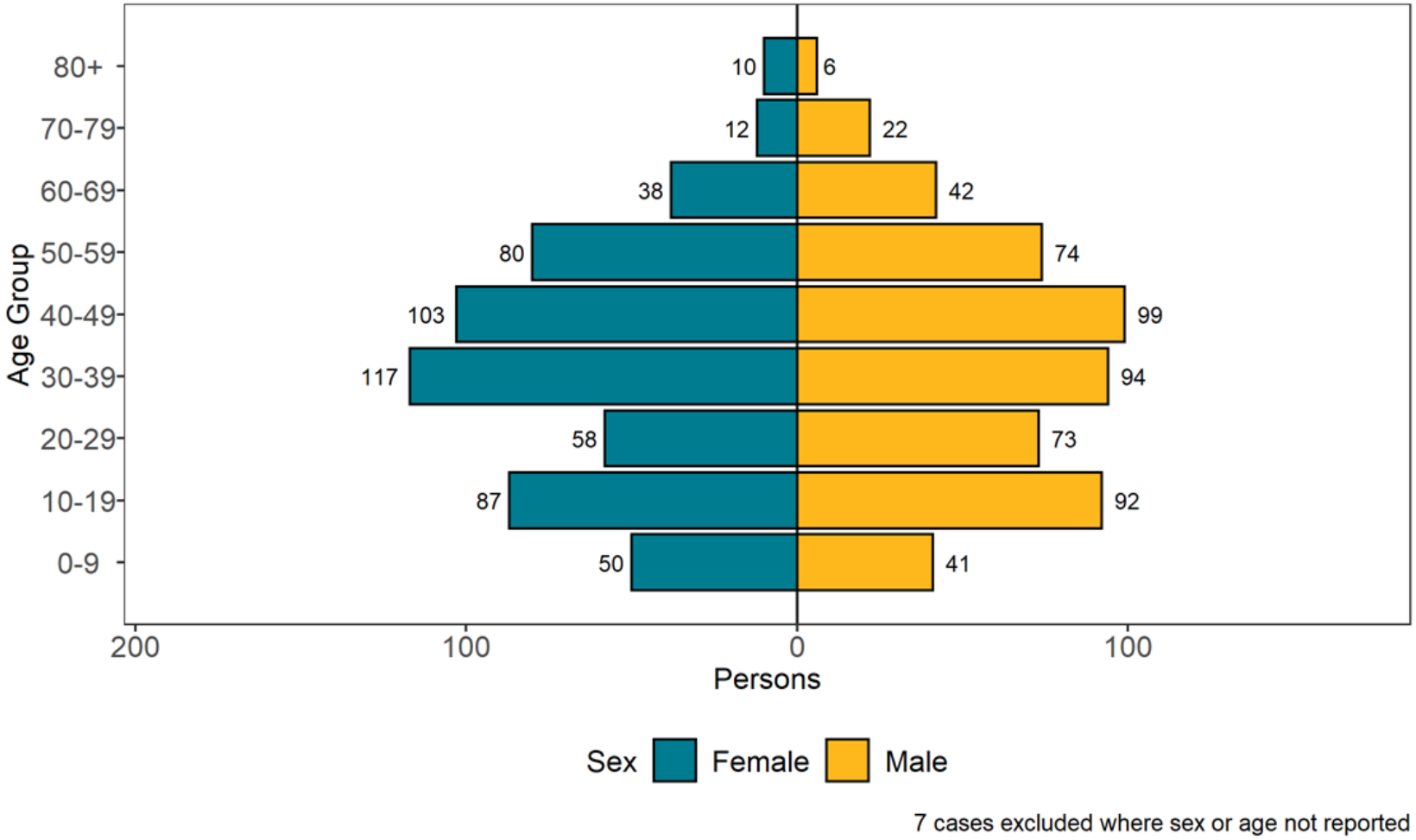
Epidemiology

Table 5. Number of confirmed (sequencing) Delta cases with E484Q mutation, by region of residence as of 24 January 2022

Region	Total case number	Case proportion
East Midlands	47	4.3%
East of England	105	9.5%
London	292	26.4%
North East	100	9.0%
North West	165	14.9%
South East	201	18.2%
South West	29	2.6%
West Midlands	69	6.2%
Yorkshire and Humber	68	6.2%
Unknown region	29	2.6%
Total	1,105	-

1,105 of the 1,314 Delta + E484Q sequences linked to a case.

Figure 13. Age-sex pyramid of confirmed (sequencing) Delta with E484Q mutation cases as of 24 January 2022
(The data used in this graph can be found in the accompanying spreadsheet.)



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 24 January 2022

Region	Total case number	Case proportion
East Midlands	14	5.3%
East of England	13	4.9%
London	11	4.2%
North East	47	17.7%
North West	114	43.0%
South East	14	5.3%
South West	17	6.4%
West Midlands	3	1.1%
Yorkshire and Humber	28	10.6%
Unknown region	4	1.5%
Total	265	-

265 of the 355 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 24 January 2022

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

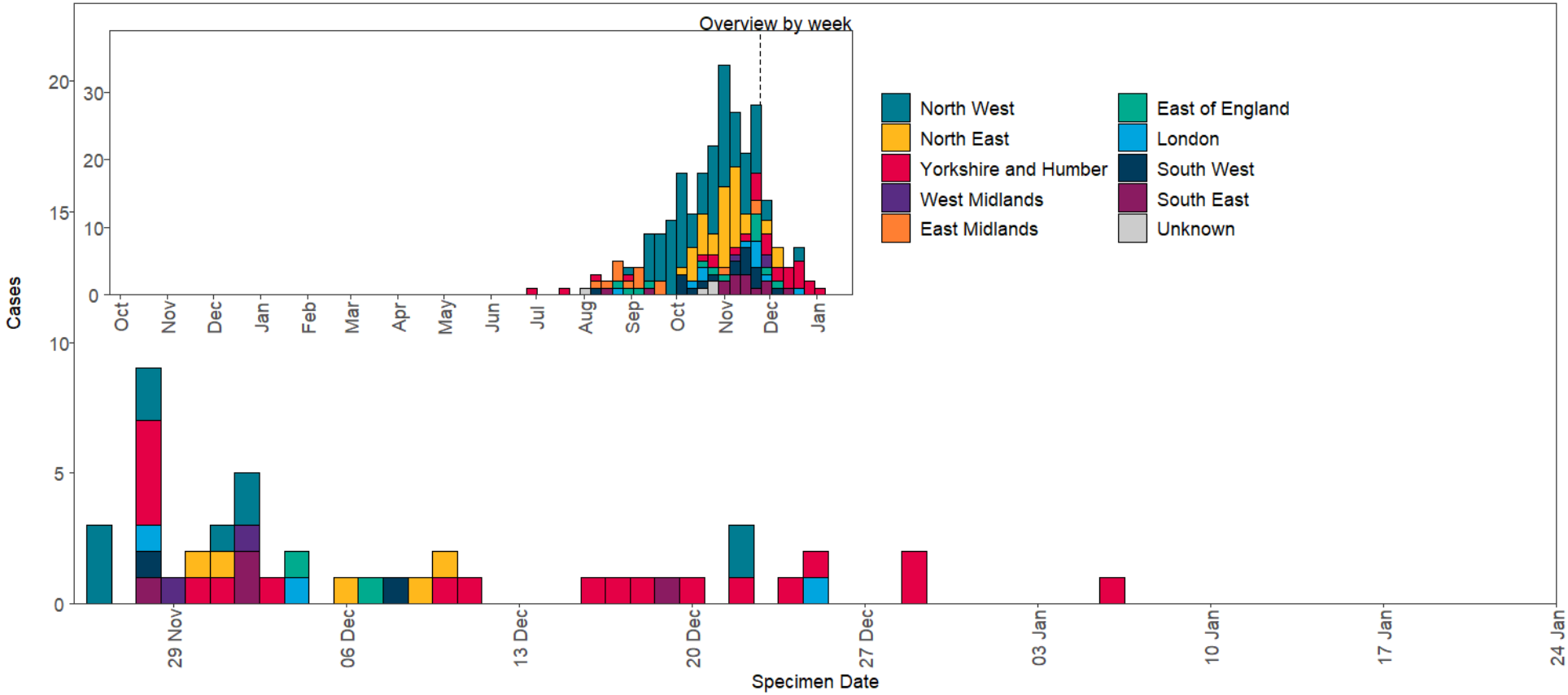
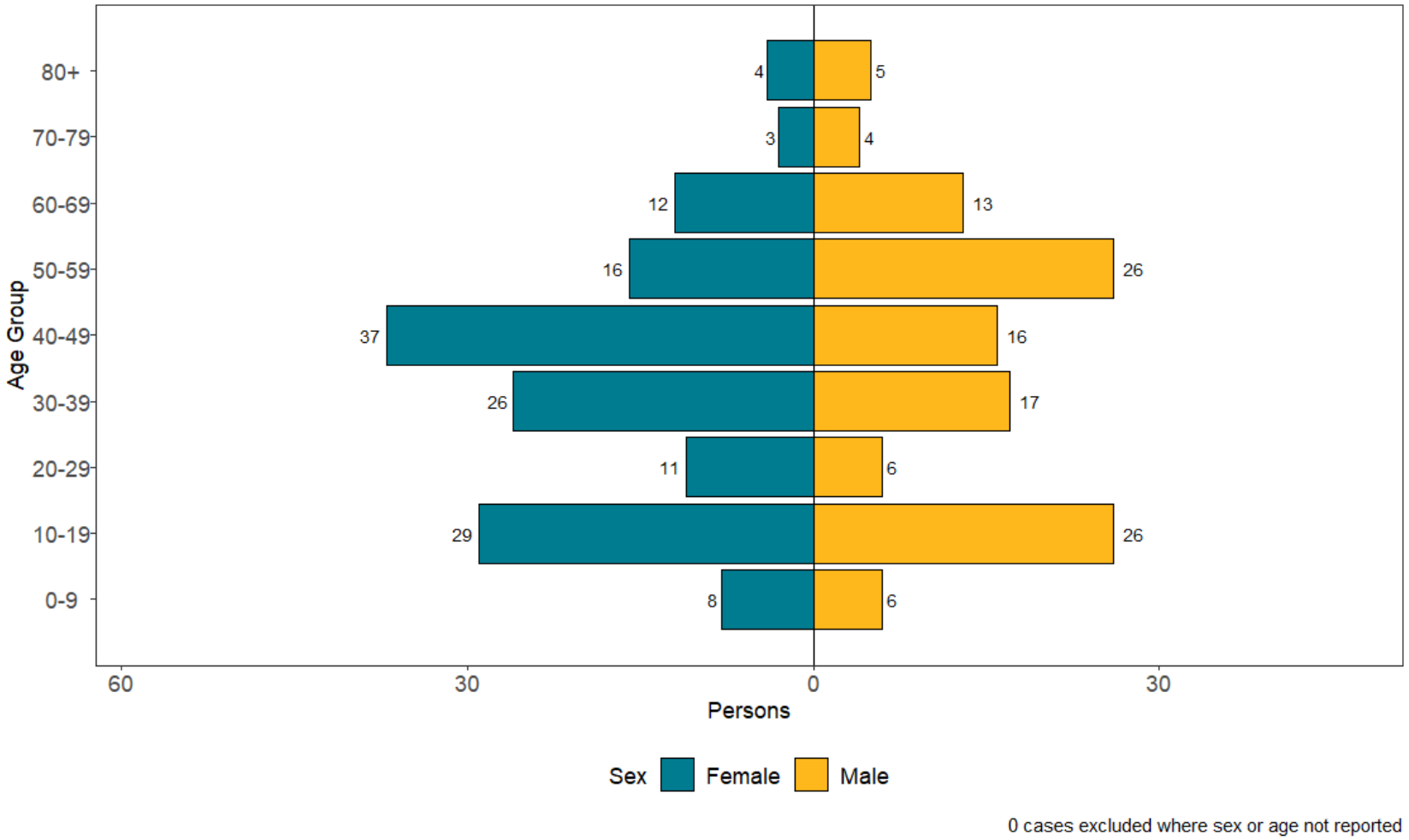


Figure 15. Age-sex pyramid of confirmed (sequencing) Delta with E484K mutation cases as of 24 January 2022
(The data used in this graph can be found in the accompanying spreadsheet.)



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 UKHSA Variant Technical Group and on review re-designated as VOC-21NOV-01 on 27 November 2021.

Epidemiology

Table 7. Number of confirmed (sequenced) and provisional (genotyped) Omicron VOC-21NOV-01 (B.1.1.529/BA.1) cases, by region of residence as of 24 January 2022

Region	Total case number	Confirmed (sequenced) case number	Provisional (genotyped) case number	Percentage of sequences from England that are in this region
East Midlands	57,604	17,675	39,929	7.2%
East of England	61,943	24,484	37,459	7.8%
London	146,438	47,867	98,571	18.3%
North East	42,305	8,715	33,590	5.3%
North West	108,927	36,118	72,809	13.6%
South East	162,965	34,925	128,040	20.4%
South West	92,206	18,010	74,196	11.5%
West Midlands	62,200	22,021	40,179	7.8%
Yorkshire and Humber	61,740	21,803	39,937	7.7%
Unknown region	2,835	1,425	1,410	0.4%
Total	799,163	233,043	566,120	-

Figure 16. Confirmed and provisional Omicron VOC-21NOV-01 (B.1.1.529/BA.1) cases by specimen date and region of residence as of 24 January 2022

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

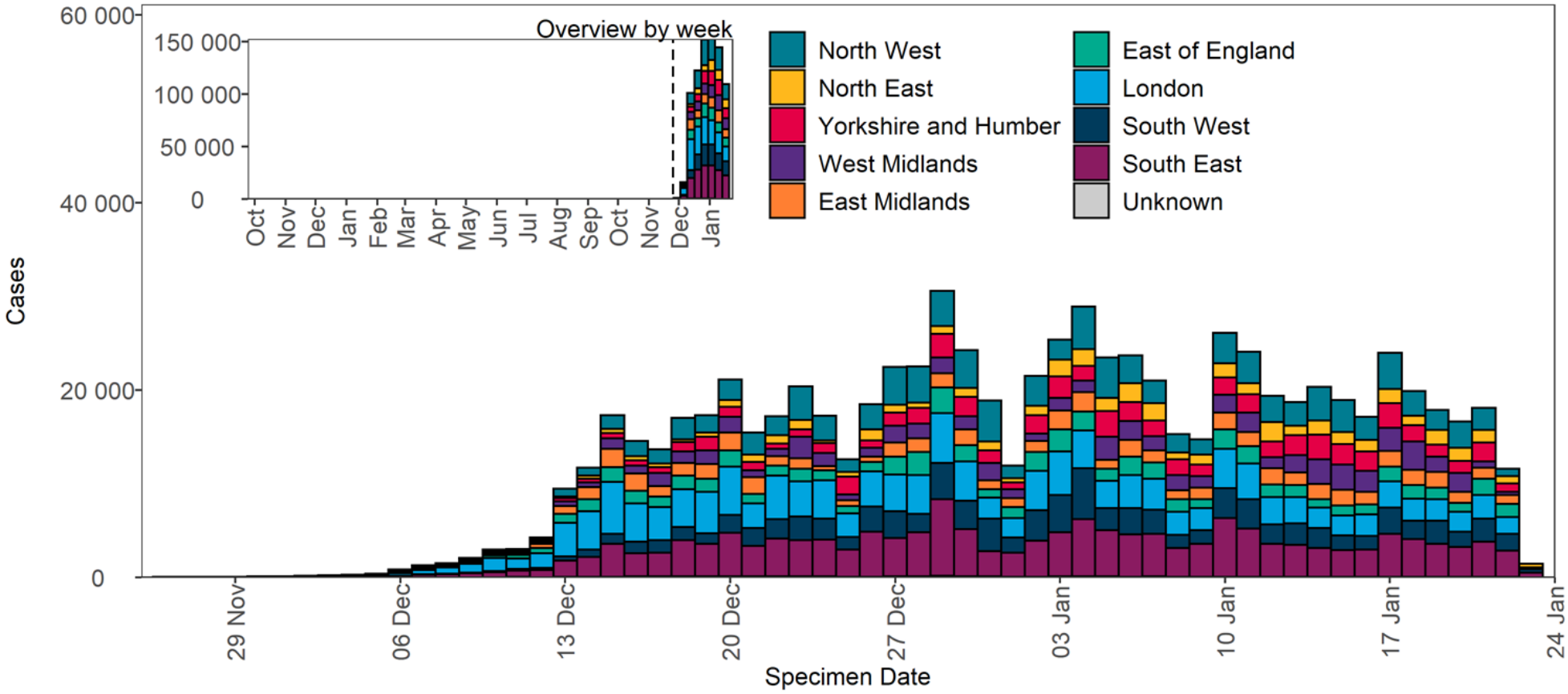
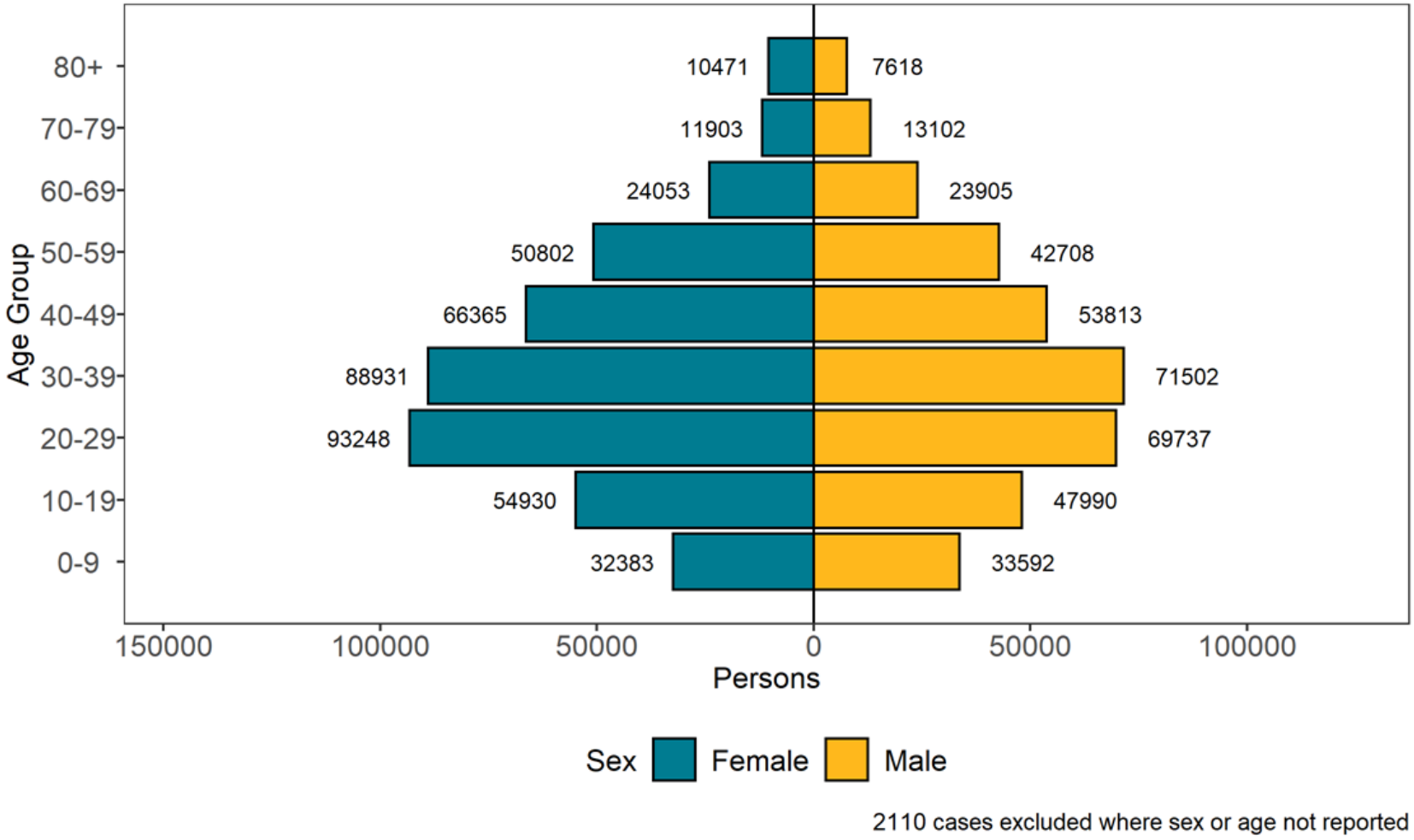


Figure 17. Age-sex pyramid of Omicron VOC-21NOV-01 (B.1.1.529/BA.1) cases as of 24 January 2022
(The data used in this graph can be found in the accompanying spreadsheet.)



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 8. Number of confirmed (sequencing) VUI-21OCT-01 cases, by region of residence as of 24 January 2022

Region	Confirmed case number	Provisional case number	Total case number	Case proportion
East Midlands	7,179	0	7,179	7.8%
East of England	11,679	0	11,679	12.7%
London	10,434	0	10,434	11.3%
North East	2,902	0	2,902	3.2%
North West	9,438	0	9,438	10.2%
South East	18,778	0	18,778	20.4%
South West	13,424	0	13,424	14.6%
West Midlands	10,141	0	10,141	11.0%
Yorkshire and Humber	7,849	0	7,849	8.5%
Unknown region	296	0	296	0.3%
Total	92,120	0	92,120	-

Figure 18. Confirmed (sequencing) VUI-21OCT-01 (AY 4.2) cases by specimen date and region of residence as of 24 January 2022

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

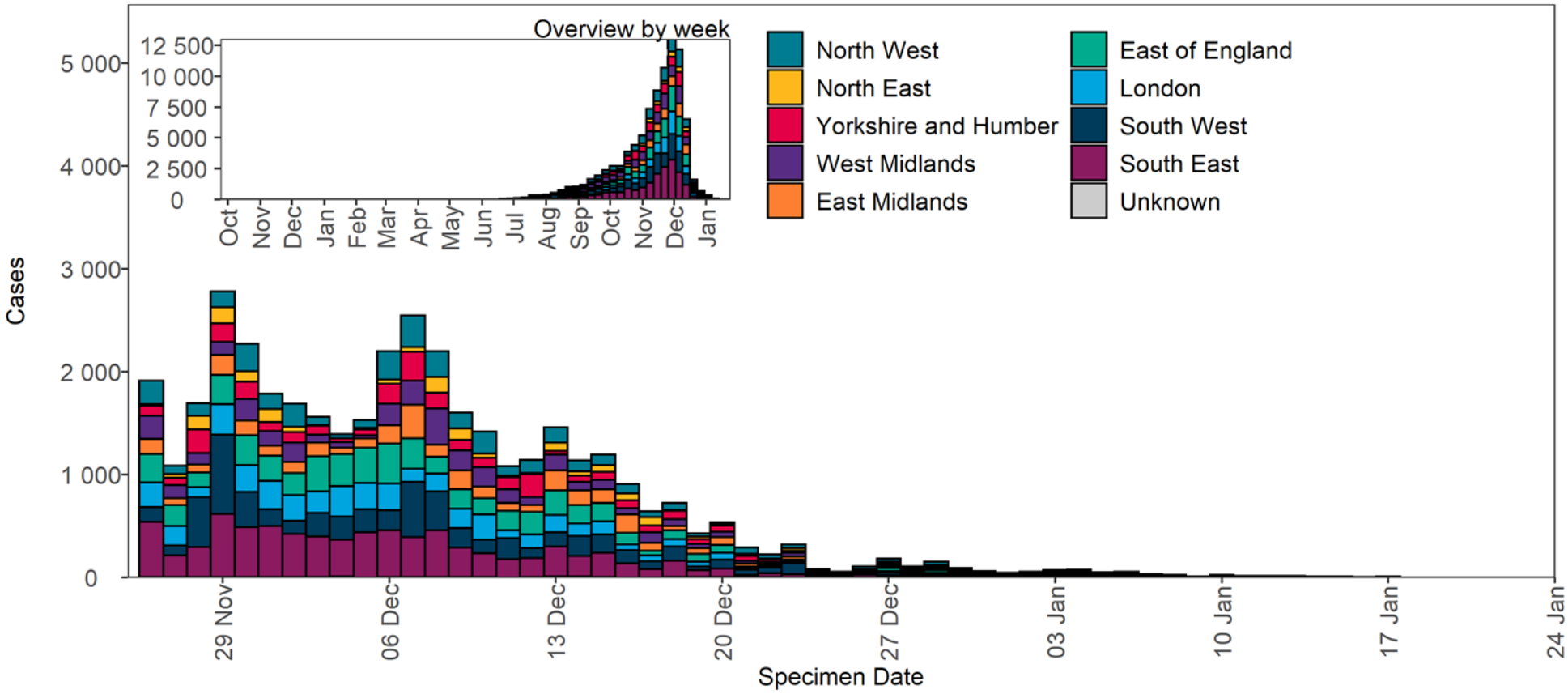
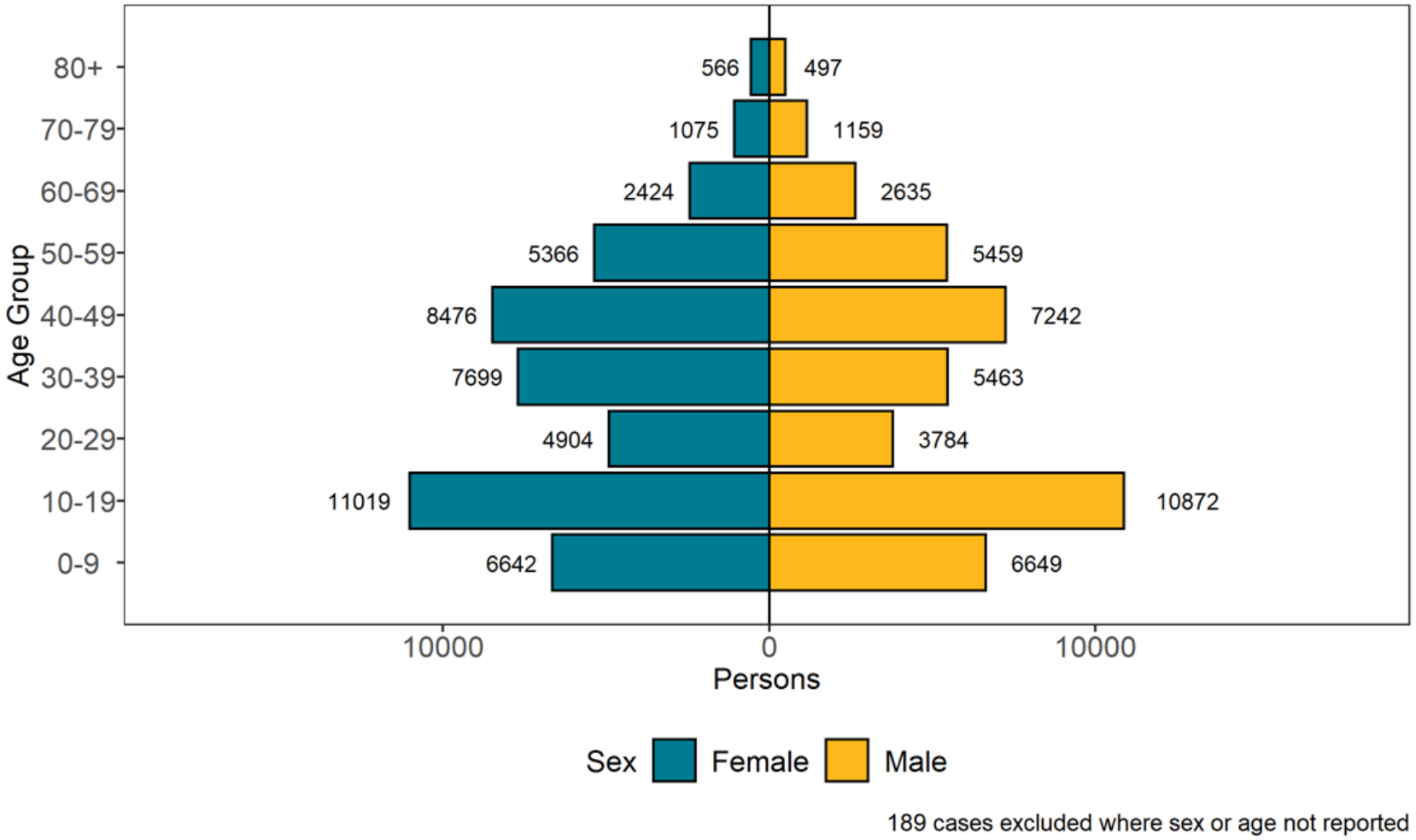


Figure 19. Age-sex pyramid of VUI-21OCT-01 (AY 4.2) cases as of 24 January 2022
(The data used in this graph can be found in the accompanying spreadsheet.)



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 9. Number of confirmed (sequencing) Mu - VUI-21JUL-01 (B.1.621) cases, by region of residence as of 24 January 2022

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

Figure 20. Confirmed (sequencing) Mu - VUI-21JUL-01 (B.1.621) cases by specimen date and region of residence as of 24 January 2022

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

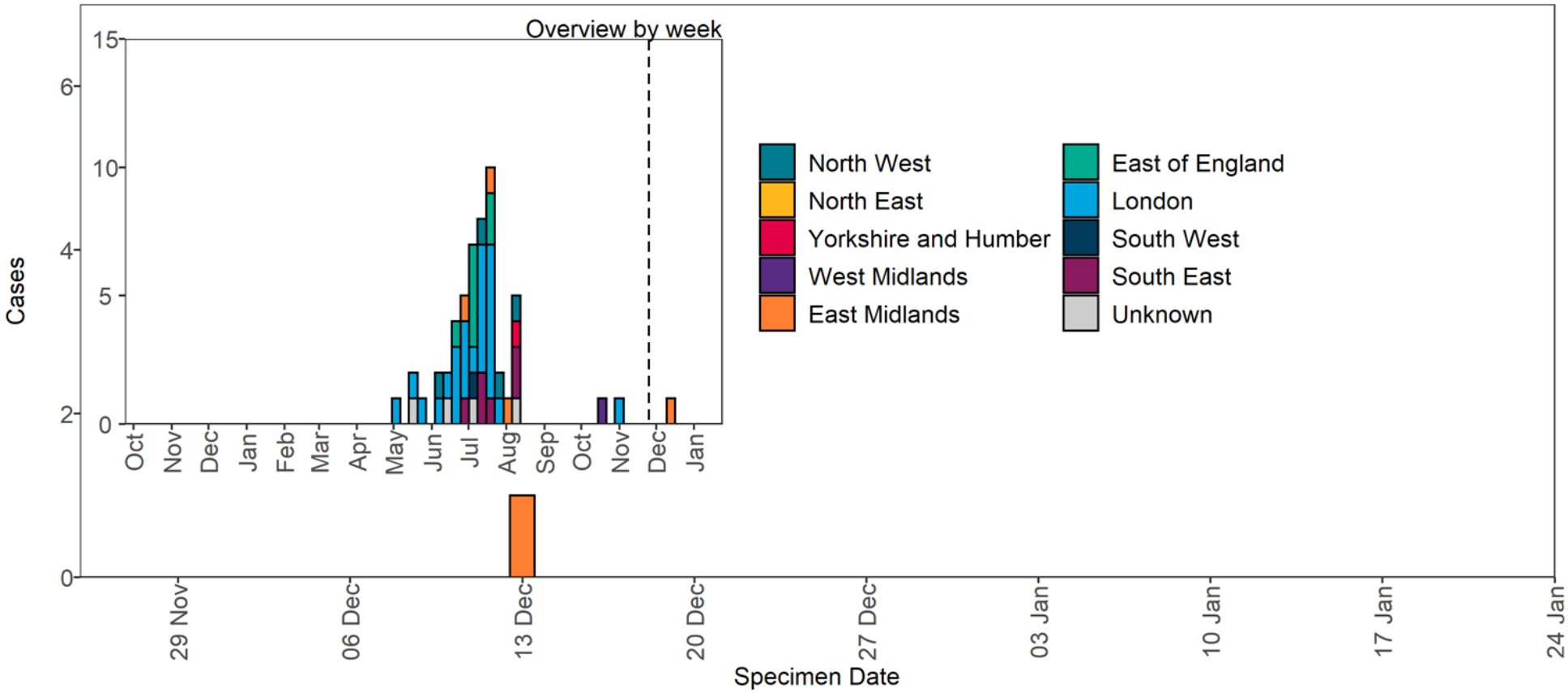
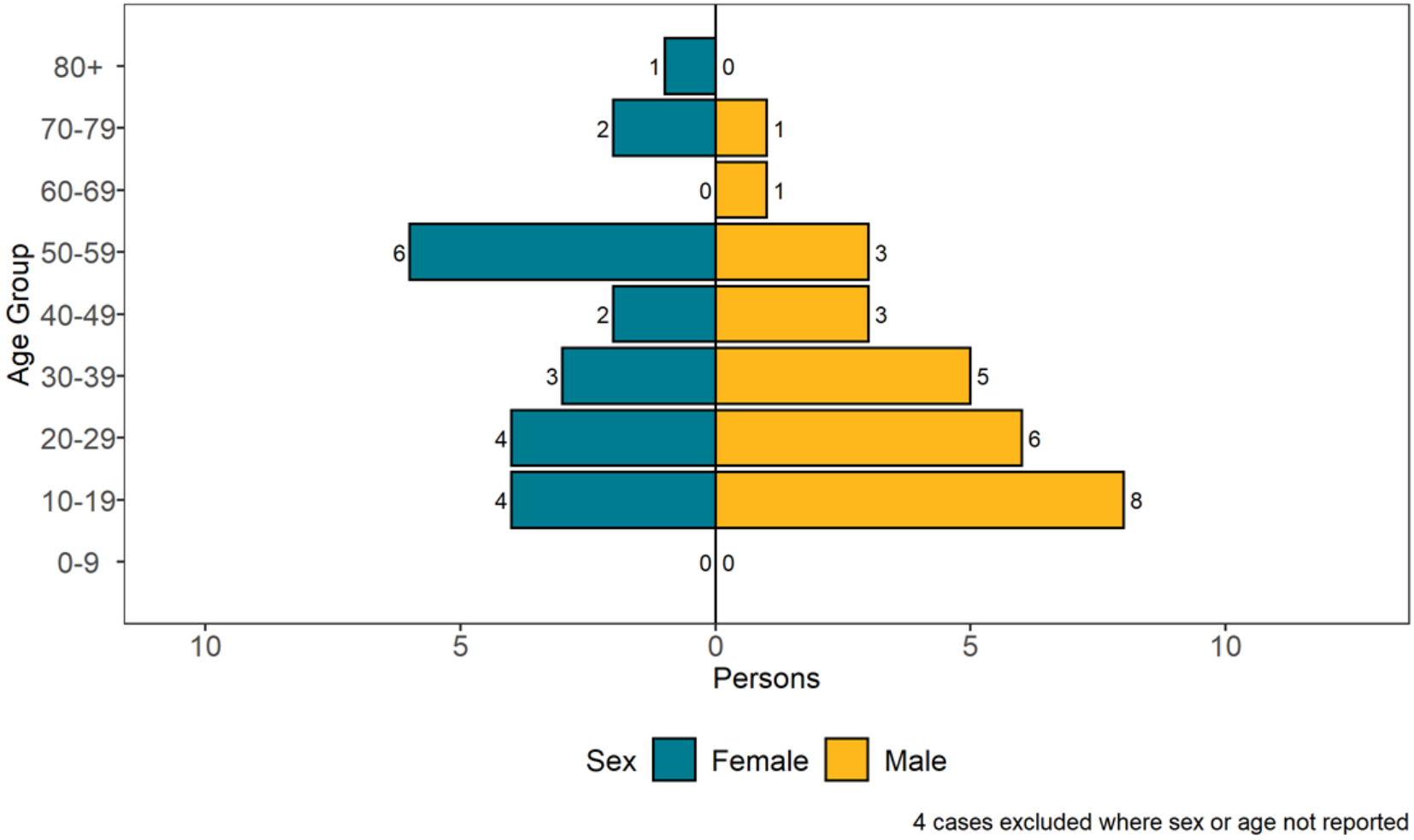


Figure 21. Age-sex pyramid of Mu - VUI-21JUL-01 (B.1.621) cases as of 24 January 2022
(The data used in this graph can be found in the accompanying spreadsheet.)



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

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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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