Public Health
England

Protecting and improving the nation's health

SARS-CoV-2 variant data update, England

Version 8

9 July 2021

This briefing provides an update on previous data located in technical and variant data update briefings and updates up to 25 June 2021.

Contents

Surveillance data overview

This document includes routine data on variants of concern and under investigation. Delta (VOC-21APR-02, B.1.617.2) is detailed in technical briefing 18.

There are 4 variants of concern and 9 variants under investigation (Table 1).

Table 1. Variant lineage and designation as of 5 July 2021 (provisionally extinct variants removed)

World Health Organization nomenclature as of 5 July 2021	Lineage	Designation	Status
Alpha	B.1.1.7	VOC-20DEC-01	VOC
Beta	B.1.351	VOC-20DEC-02	VOC
Gamma	P.1	VOC-21JAN-02	VOC
Delta	B.1.617.2, AY.1 and AY.2	VOC-21APR-02	VOC
Zeta	P.2	VUI-21JAN-01	VUI
Eta	B.1.525	VUI-21FEB-03	VUI
	B.1.1.318	VUI-21FEB-04	VUI
Theta	P.3	VUI-21MAR-02	VUI
Kappa	B.1.617.1	VUI-21APR-01	VUI
	B.1.617.3	VUI-21APR-03	VUI
	AV.1	VUI-21MAY-01	VUI
	C.36.3	VUI-21MAY-02	VUI
Lambda^	C.37	VUI-21JUN-01	VUI
	B.1.1.7 with E484K	VOC-21FEB-02	*Monitoring
Epsilon	B.1.427/B.1.429		Monitoring
	B.1.1.7 with S494P		Monitoring
	A.27		Monitoring
Iota	B.1.526		Monitoring
	B.1.1.7 with Q677H		Monitoring
	B.1.620		Monitoring
	B.1.214.2		Monitoring

World Health Organization nomenclature as of 5 July 2021	Lineage	Designation	Status
	R.1		Monitoring
	B.1.621		Monitoring
	B.1 with 214insQAS		Monitoring
	AT.1		Monitoring
	Lineage A with R346K, T478R and E484K		Monitoring
	Delta like variant with E484A		Monitoring
	P.1 + N501T and E484Q		Monitoring
	B.1.629		Monitoring
	B.1.619		Monitoring

*VOC-21FEB-02 (B.1.1.7 with E484K). This specific clade of B.1.1.7 with E484K has not been detected in England since 1 March 2021. There is apparent transmission outside the UK based on international sequence data. It is no longer included in the data update but monitoring of international data continues.

^Designated as Variant of Interest by the World Health Organization (WHO), 14 June 2021 and as a variant under investigation by Public Health England on 23 June 2021.

Data on individual variants

Alpha

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 the World Health Organization (WHO) on 31 May 2021.

International Epidemiology

GISAID includes data on sequences available internationally. As of 5 July 2021, 698,617 sequences of Alpha, excluding the UK, are listed from 153 countries or territories on GISAID.

Epidemiology

Table 2. Number of confirmed (sequencing) and probable (genotyping) Alpha cases, by region of residence as of 5 July 2021

Region	Confirmed case number	Provisional case number	Total case number	Proportion of all cases
East Midlands	16,091	486	16,577	7.3%
East of England	19,702	176	19,878	8.8%
London	40,048	771	40,819	18.1%
North East	14,801	115	14,916	6.6%
North West	41,969	1,757	43,726	19.4%
South East	23,945	118	24,063	10.7%
South West	8,080	52	8,132	3.6%
West Midlands	18,288	1,306	19,594	8.7%
Yorkshire and Humber	35,940	890	36,830	16.3%
Unknown region	1,309	20	1,329	0.6%
Total	220,173	5,691	225,864	-

Genotyping is used to identify variants Alpha, Beta, Delta and Gamma; targets were updated in mid-May 2021 to prioritise accurate identification of Delta over Alph

Figure 1. Confirmed (sequencing) and probable (genotyping) Alpha cases by specimen date and region of residence as of 5 July 2021
(Find accessible data used in this graph in underlying data.)

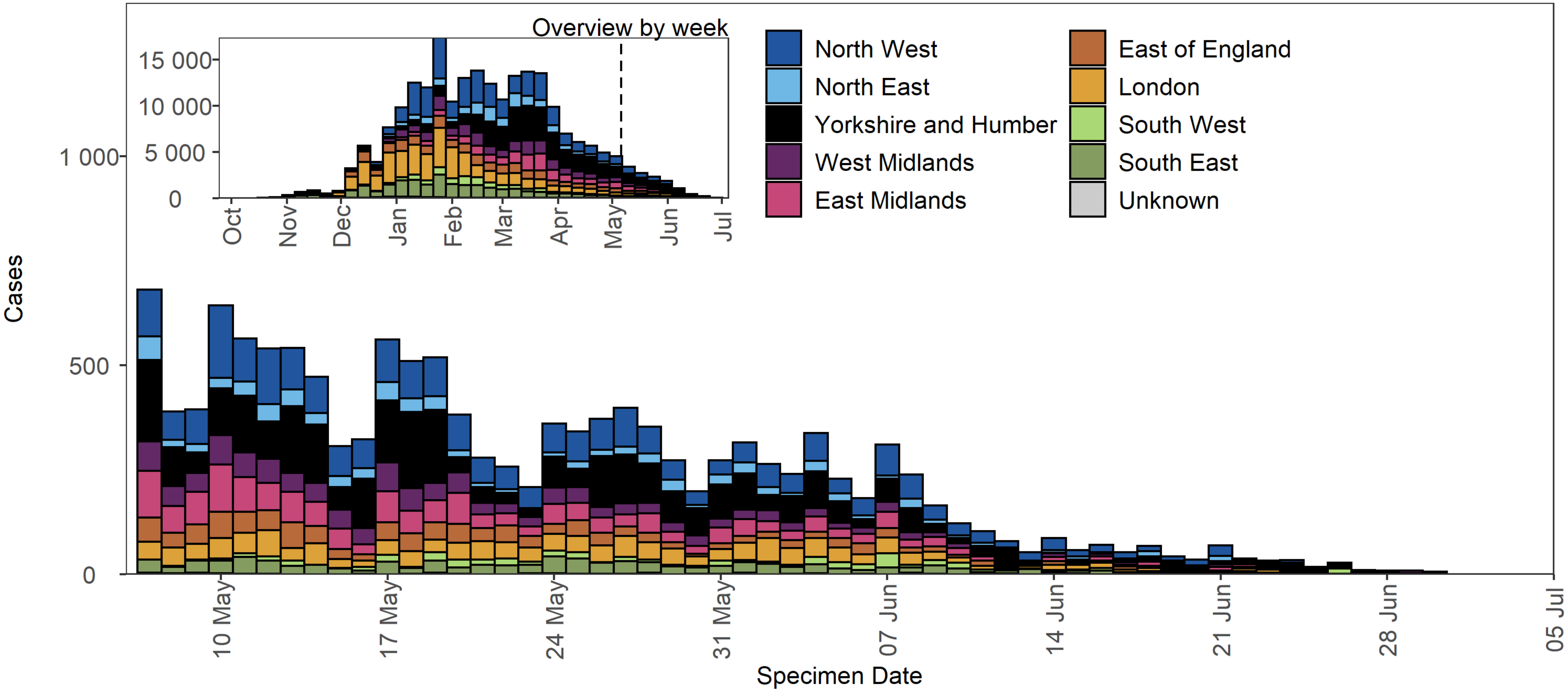


Figure 2. Confirmed (sequencing) and probable (genotyping) Alpha cases by specimen date and detection method as of 5 July 2021

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

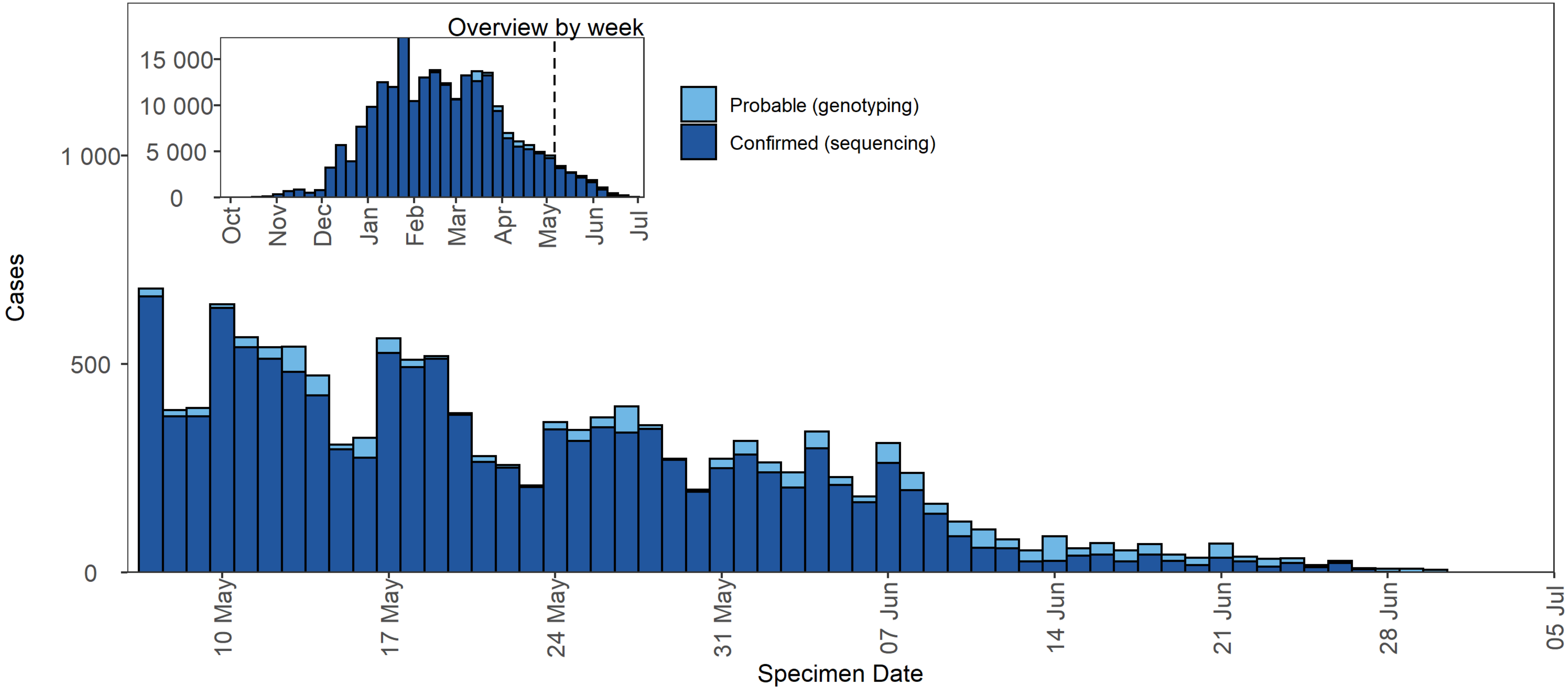
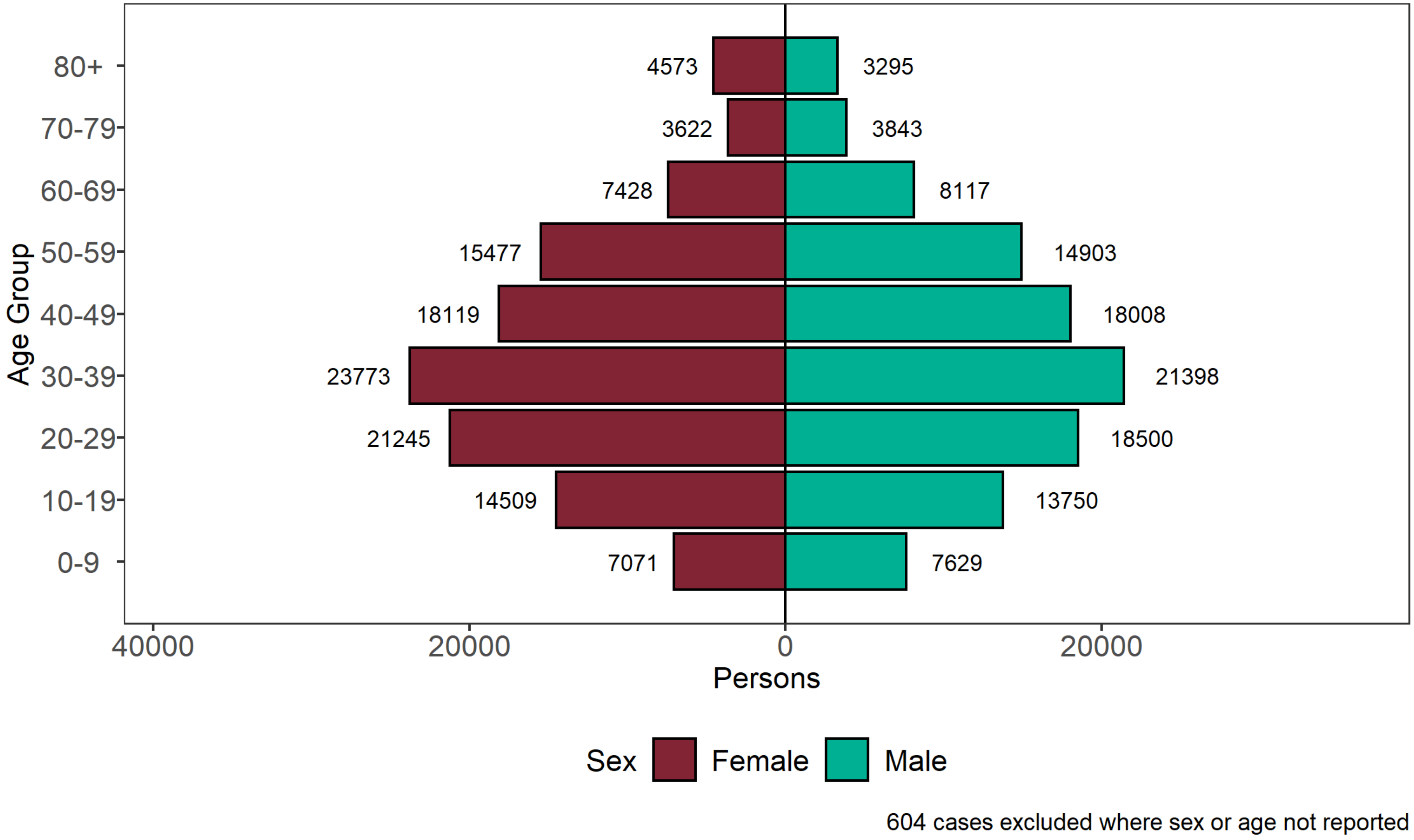


Figure 3. Age-sex pyramid of confirmed (sequencing) and probable (genotyping) Alpha cases as of 5 July 2021
(Find accessible data used in this graph in underlying data.)



Beta

B.1.351 was initially detected in South Africa. This variant was designated variant under investigation 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.

International Epidemiology

GISAID includes data on sequences available internationally. As of the 5 July 2021, 24,664 sequences of Beta, are listed from 96 countries or territories excluding the UK.

Epidemiology

Table 3. Number of confirmed (sequencing) and probable (genotyping) Beta cases, by region of residence as of 5 July 2021

[1] Genotyping is used to identify variants Alpha, Beta, Delta and Gamma; targets were updated in mid-May 2021 to prioritise accurate identification of Delta over Alpha

Region	Confirmed case number	Provisional case number	Total case number	Proportion of all cases
East Midlands	46	3	49	5.1%
East of England	81	2	83	8.6%
London	414	26	440	45.8%
North East	18	6	24	2.5%
North West	80	9	89	9.3%
South East	111	4	115	12.0%
South West	31	1	32	3.3%
West Midlands	64	1	65	6.8%
Yorkshire and Humber	32	7	39	4.1%
Unknown region	21	3	24	2.5%
Total	898	62	960	-

Figure 4. Confirmed (sequencing) and probable (genotyping) Beta cases by specimen date and region of residence as of 5 July 2021

Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)

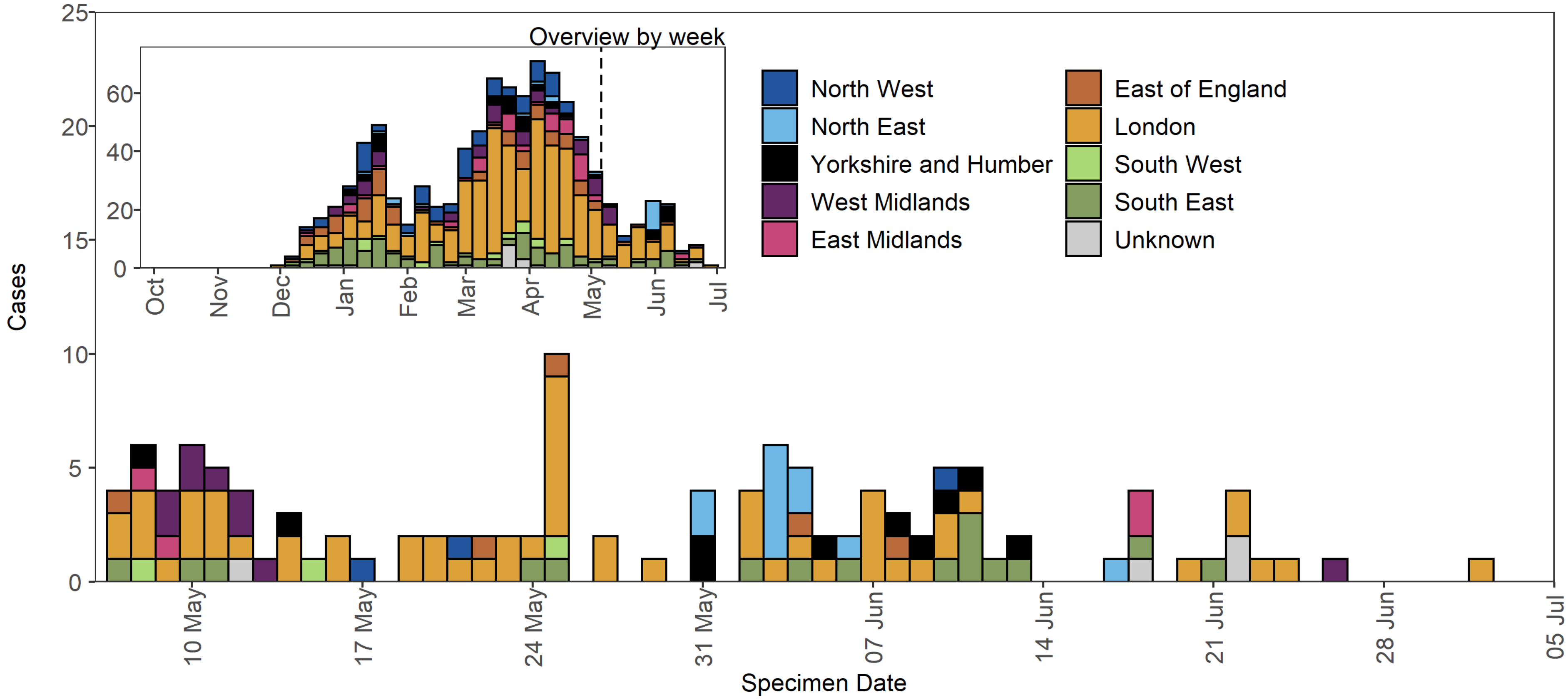


Figure 5. Confirmed (sequencing) and probable (genotyping) Beta cases by specimen date and detection method as of 5 July 2021

Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)

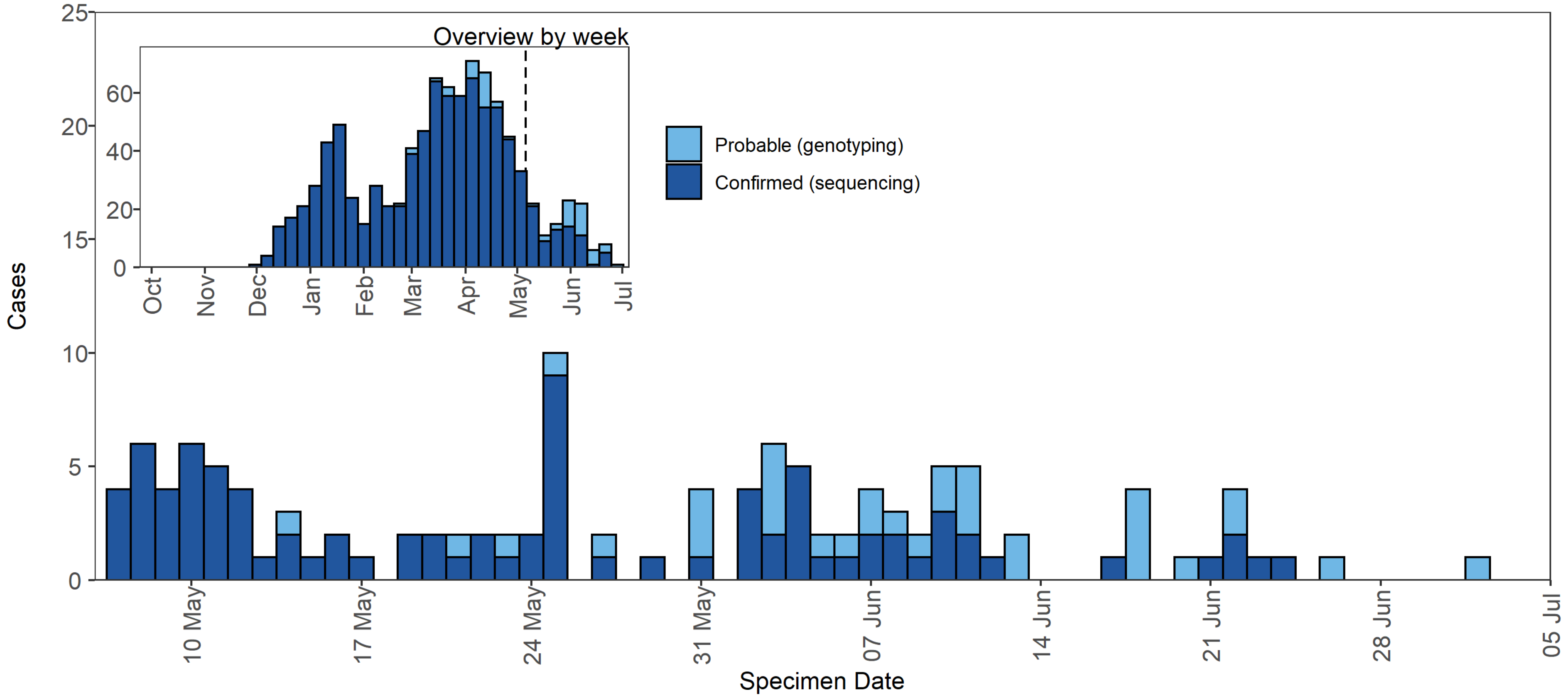
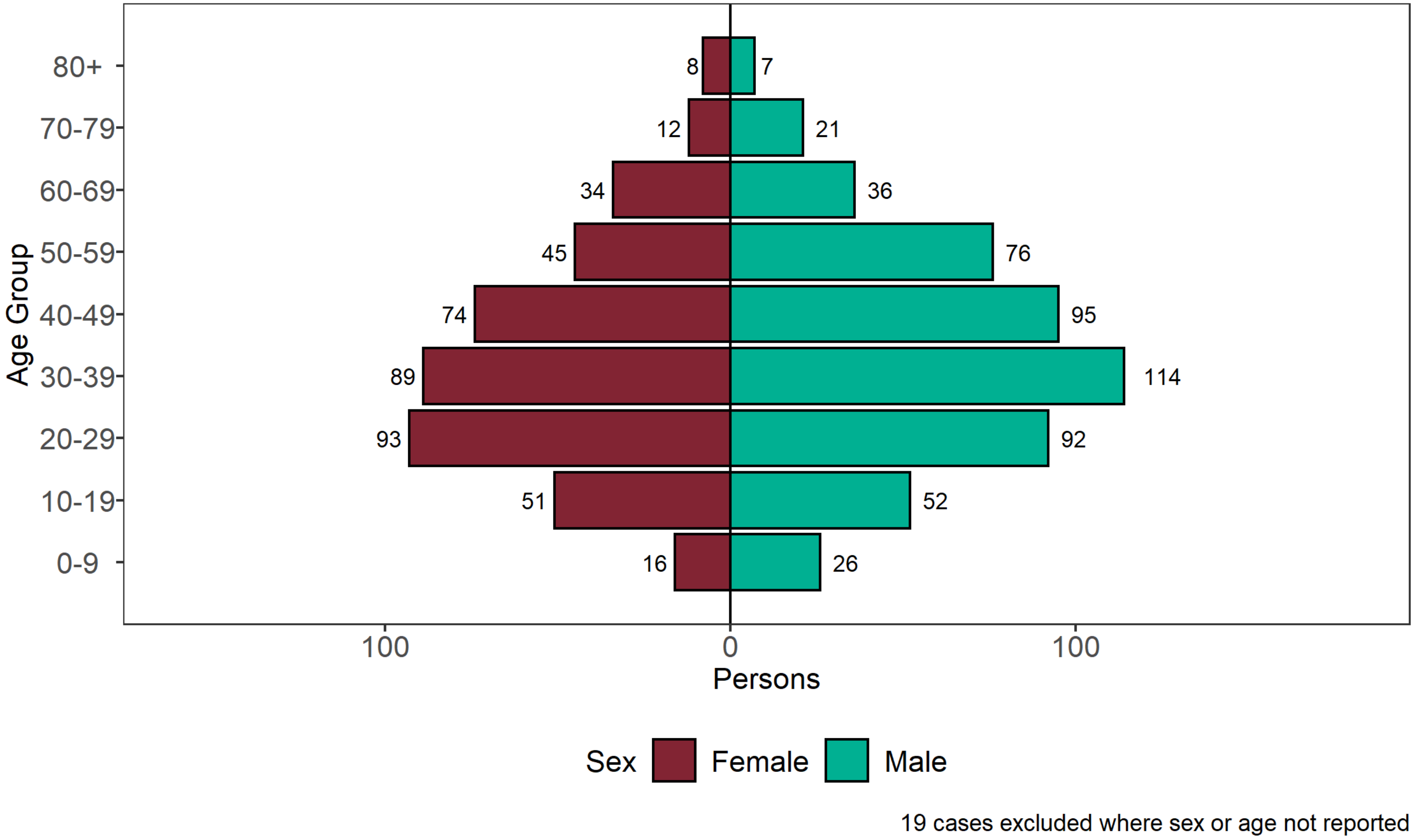


Figure 6. Age-sex pyramid of confirmed (sequencing) and probable (genotyping) Beta cases as of 5 July 2021

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



Gamma

First identified in Japan amongst travellers from Brazil, the P.1 lineage is a descendant of B.1.1.28. This variant was designated variant under investigation 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.

International Epidemiology

GISAID includes data on sequences available internationally. As of 5 July 2021, 47,511 sequences (excluding the UK) of Gamma from 63 countries.

Epidemiology

Table 4. Number of confirmed (sequencing) and probable (genotyping) Gamma cases, by region of residence as of 5 July 2021

Region	Confirmed case number	Provisional case number	Total case number	Proportion of all cases
East Midlands	3	0	3	1.3%
East of England	13	0	13	5.6%
London	109	25	134	58.0%
North East	0	4	4	1.7%
North West	9	1	10	4.3%
South East	27	4	31	13.4%
South West	10	2	12	5.2%
West Midlands	7	1	8	3.5%
Yorkshire and Humber	2	8	10	4.3%
Unknown region	6	0	6	2.6%
Total	186	45	231	-

[1] Genotyping is used to identify variants Alpha, Beta, Delta and Gamma; targets were updated in mid-May 2021 to prioritise accurate identification of Delta over Alpha

Figure 7. Confirmed (sequencing) and probable (genotyping) Gamma cases by region of residence and specimen date as of 5 July 2021

Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)

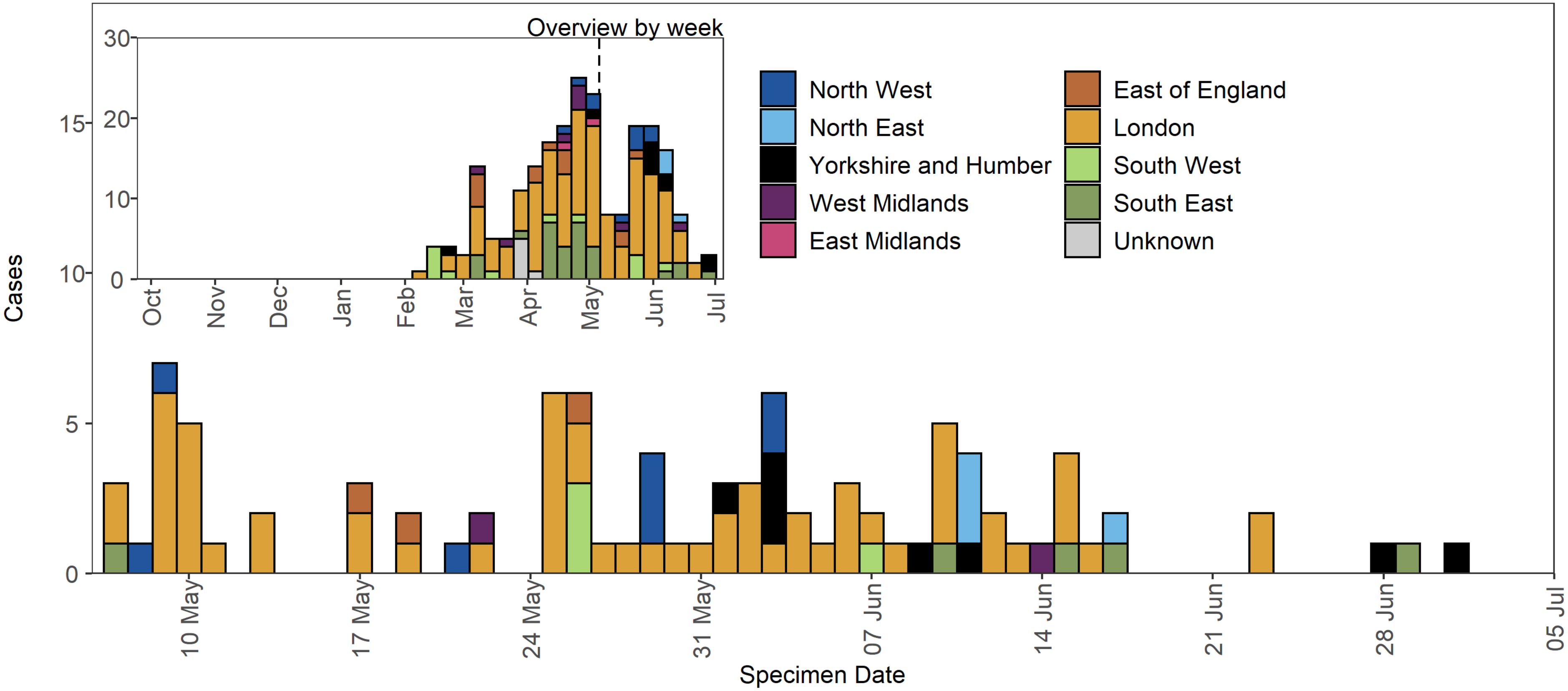


Figure 8. Confirmed (sequencing) and probable (genotyping) Gamma cases by specimen date and detection method as of 5 July 2021

Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)

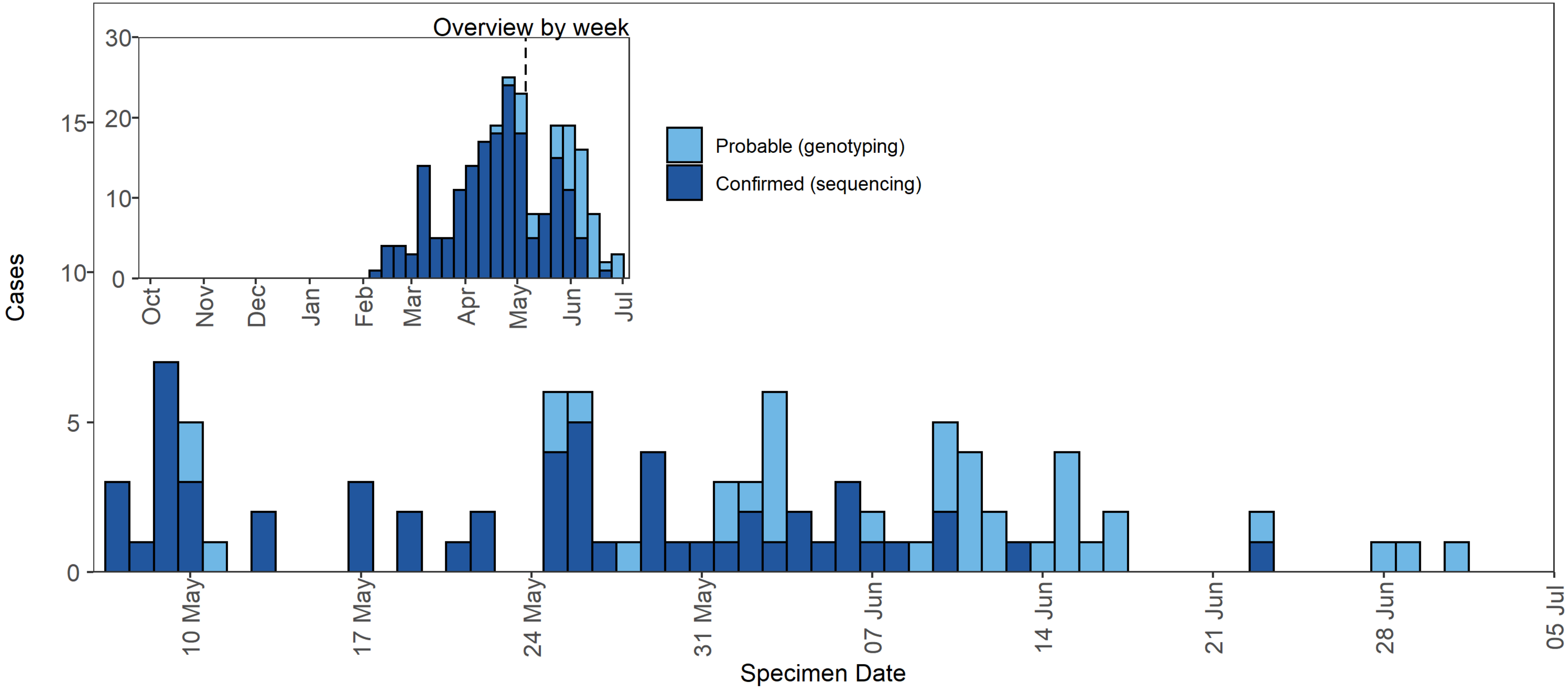
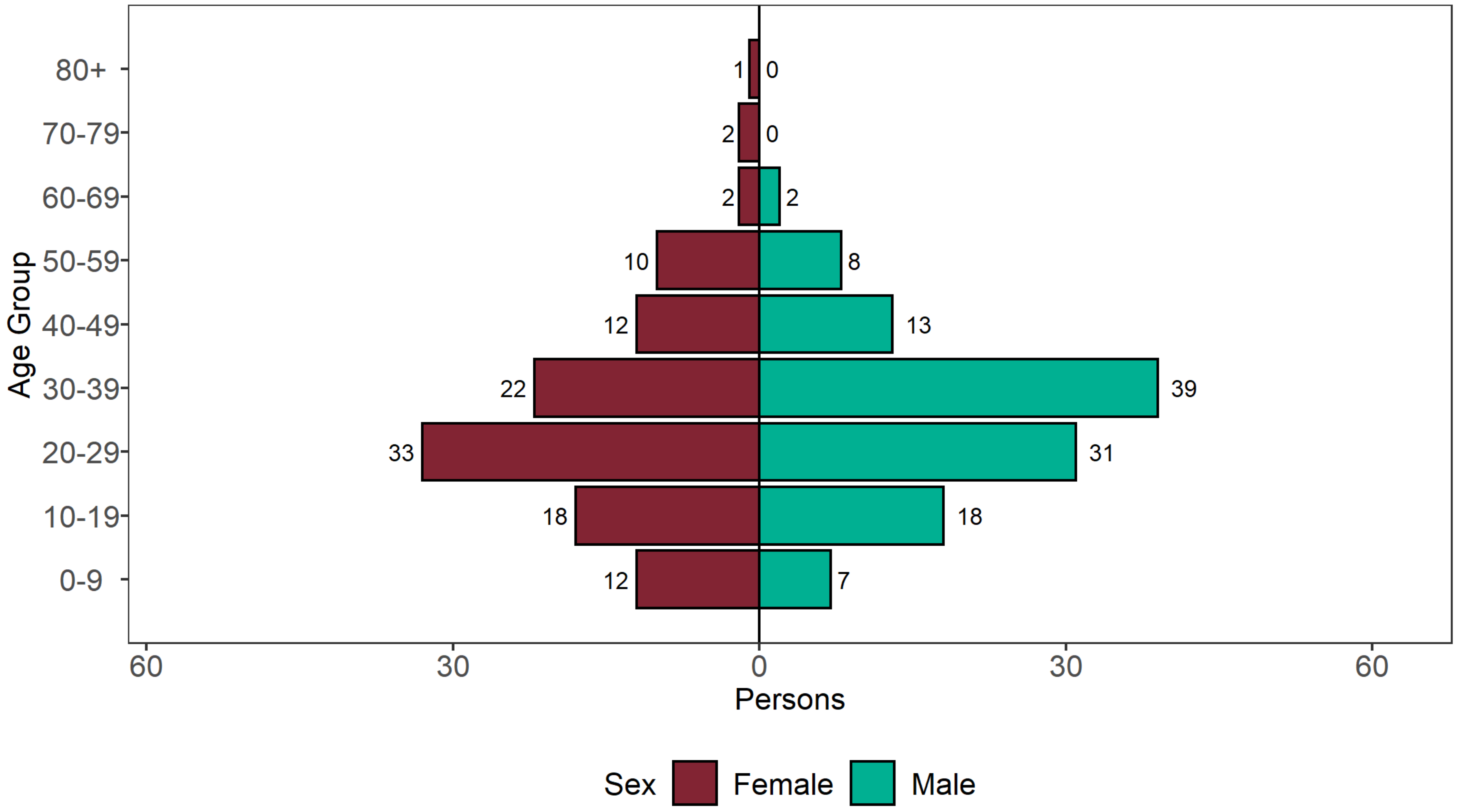


Figure 9. Age-sex pyramid of confirmed (sequencing) and probable (genotyping) Gamma cases as of 5 July 2021
(Find accessible data used in this graph in underlying data.)



1 cases excluded where sex or age not reported

Zeta

First identified in Brazil, the P.2 lineage is a descendant of B.1.1.28. This variant was designated VUI-21JAN-01 (P.2) on 13 January 2021. It was first sequenced in the UK in November 2020. This was named Zeta by WHO on 31 May 2021.

International Epidemiology

GISAID includes data on sequences available internationally. As of 5 July 2021, 4,320 sequences (excluding the UK) of Zeta from 39 countries.

Epidemiology

Table 5. Number of confirmed (sequencing) Zeta cases, by region of residence as of 5 July 2021

Region	Total case number	Proportion of all cases
East Midlands	1	1.9%
East of England	2	3.7%
London	14	25.9%
North East	0	0.0%
North West	12	22.2%
South East	6	11.1%
South West	7	13.0%
West Midlands	1	1.9%
Yorkshire and Humber	11	20.4%
Total	54	-

Figure 10. Confirmed (sequencing) Zeta cases by specimen date and region of residence as of 5 July 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)

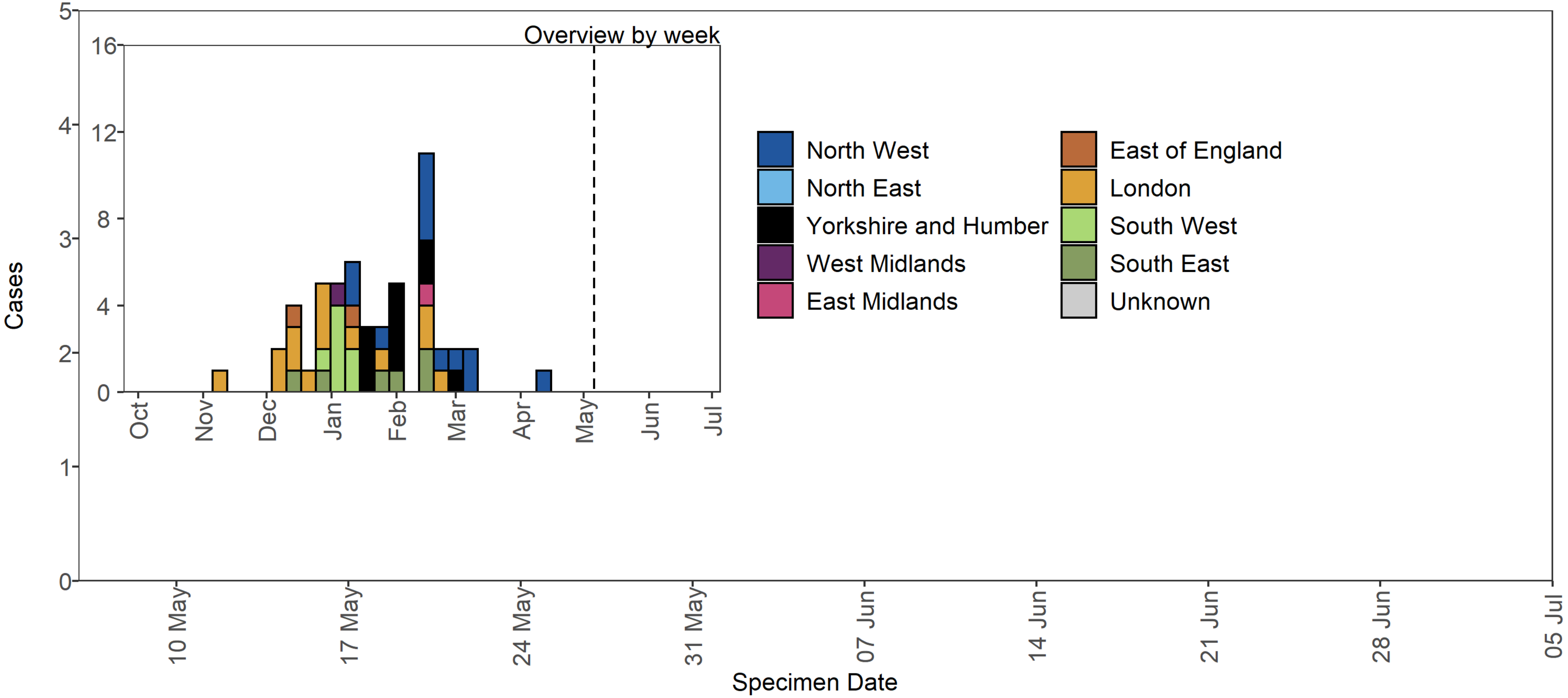
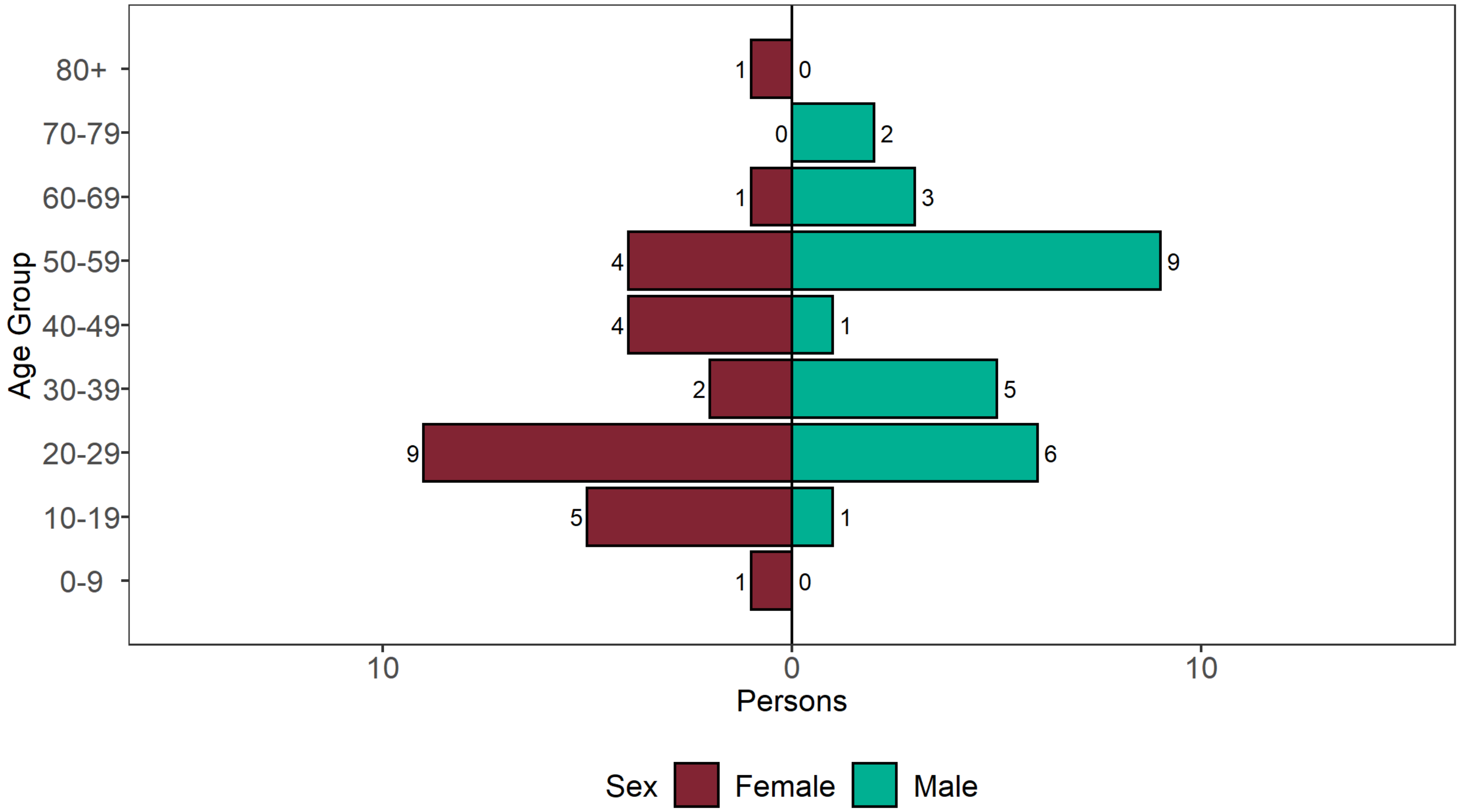


Figure 11. Age-sex pyramid of confirmed (sequencing) Zeta cases as of 5 July 2021
(Find accessible data used in this graph in underlying data.)



0 cases excluded where sex or age not reported

Eta

B.1.525 was identified as a geographically dispersed cluster in UK on the 2 February 2021. This variant was designated VUI-21FEB-03 (B.1.525) on 12 February 2021. The earliest sample date for VUI-21FEB-03 (B.1.525) in England was 15 December 2020. This was named Eta by WHO on 31 May 2021. Genotyping data is not collected for this variant.

International Epidemiology

GISAID includes data on sequences available internationally. As of 5 July 2021, 6,025 sequences of Eta are listed, from 66 countries or territories, excluding the UK.

Epidemiology

Table 6. Number of confirmed (sequencing) Eta cases, by region of residence as of 5 July 2021

Region	Total case number	Proportion of all cases
East Midlands	10	2.3%
East of England	30	6.8%
London	157	35.4%
North East	5	1.1%
North West	77	17.4%
South East	80	18.1%
South West	18	4.1%
West Midlands	35	7.9%
Yorkshire and Humber	20	4.5%
Unknown region	11	2.5%
Total	443	-

Figure 12. Confirmed (sequencing) Eta cases by specimen date and region of residence as of 5 July 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)

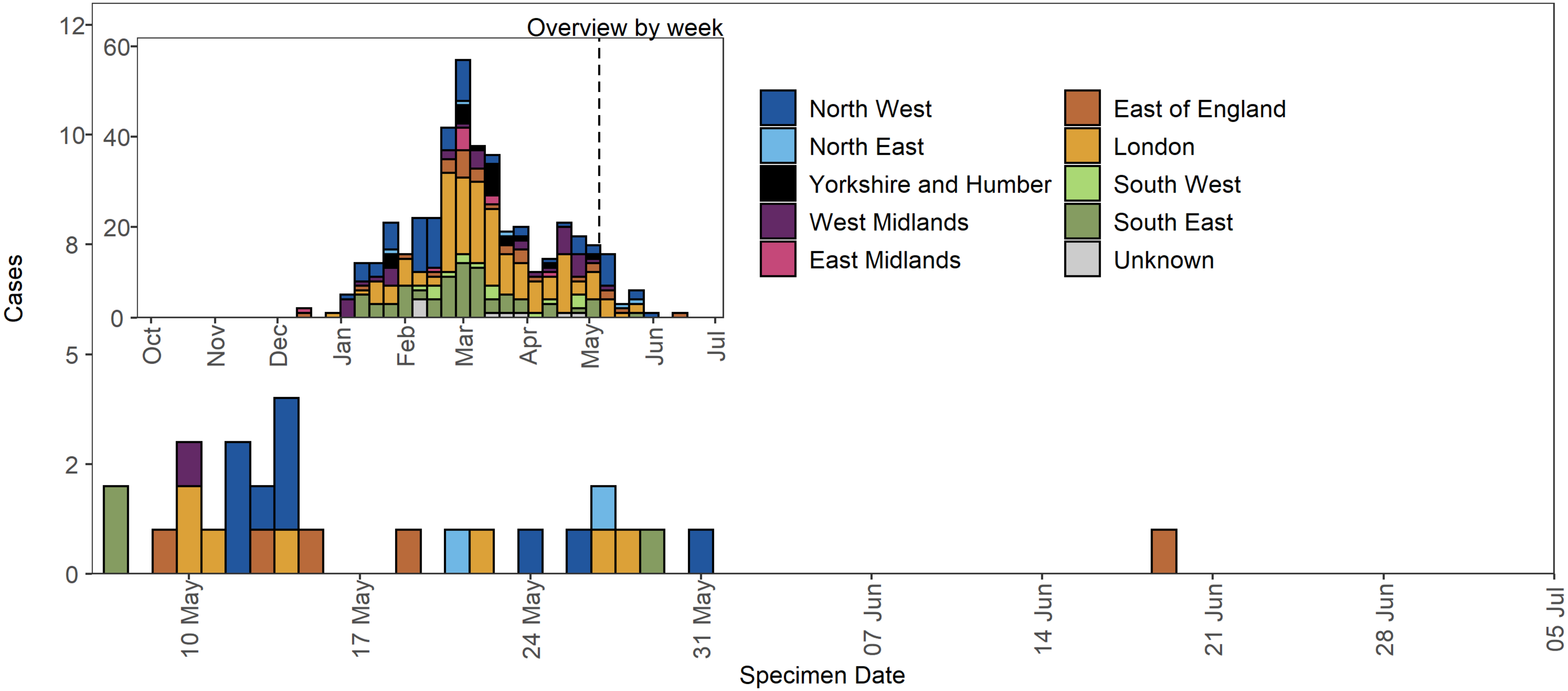
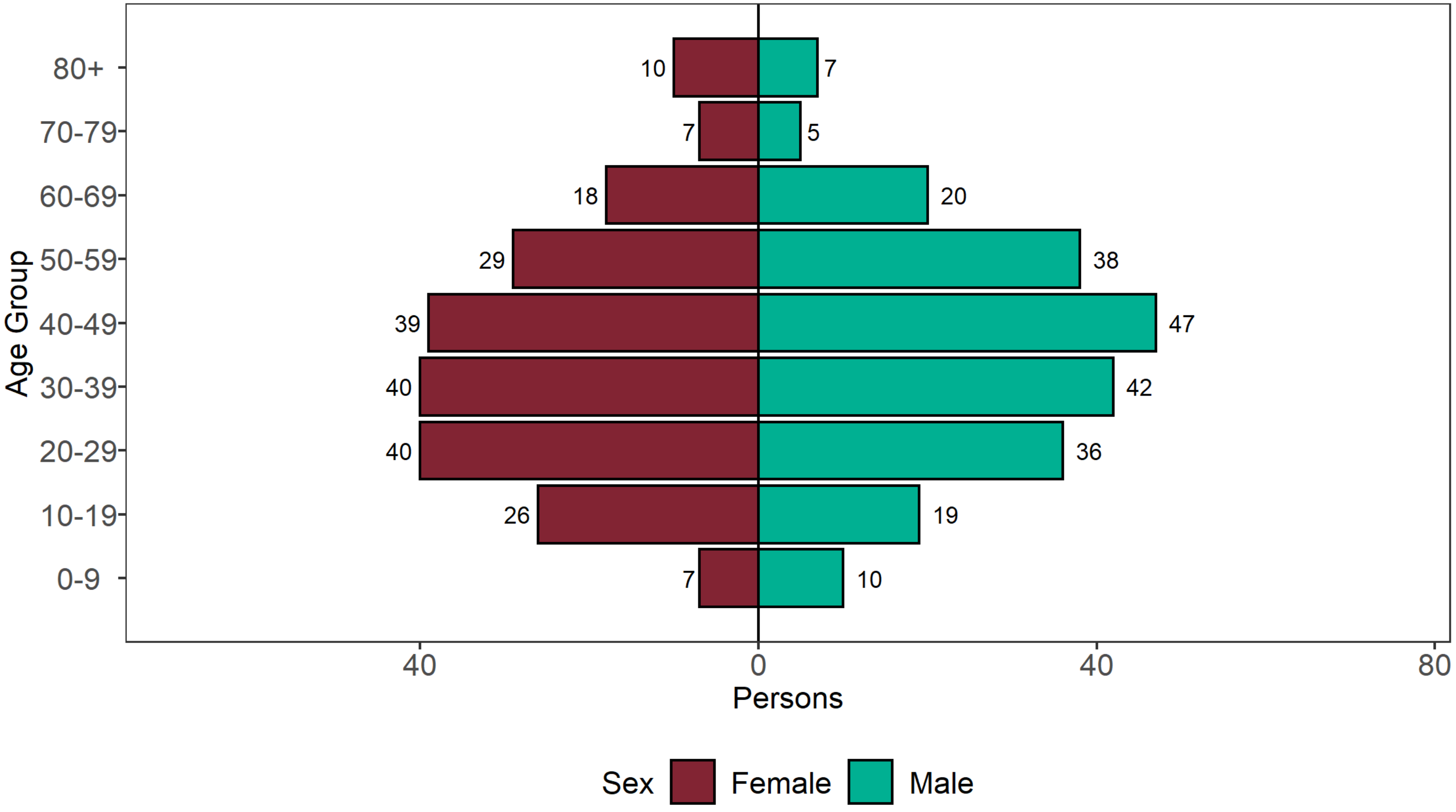


Figure 13. Age-sex pyramid of confirmed (sequencing) Eta cases as of 5 July 2021
(Find accessible data used in this graph in underlying data.)



3 cases excluded where sex or age not reported

VUI-21FEB-04 (B.1.1.318)

B.1.1.318 was identified in England in mid-February 2021 through routine horizon scanning for the development of new clusters of genomes containing E484K. This analysis identified an initial cluster of 6 cases containing E484K and other spike mutations, designated VUI-21FEB-04 (B.1.1.318) on 23 February 2021.

International Epidemiology

GISAID includes data on sequences available internationally. As of 5 July 2021, 203 international VUI-21FEB-04 (B.1.1.318) sequences from 21 countries, excluding the UK have been identified on GISAID.

Epidemiology

Table 7. Number of confirmed (sequencing) VUI-21FEB-04 (B.1.1.318) cases, by region of residence as of 5 July 2021

Region	Total case number	Proportion of all cases
East Midlands	11	3.8%
East of England	36	12.5%
London	110	38.1%
North East	2	0.7%
North West	49	17.0%
South East	48	16.6%
South West	1	0.3%
West Midlands	13	4.5%
Yorkshire and Humber	11	3.8%
Unknown region	8	2.8%
Total	289	-

Figure 14. Confirmed (sequencing) VUI-21FEB-04 (B.1.1.318) cases by specimen date and region of residence as of 5 July 2021

Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)

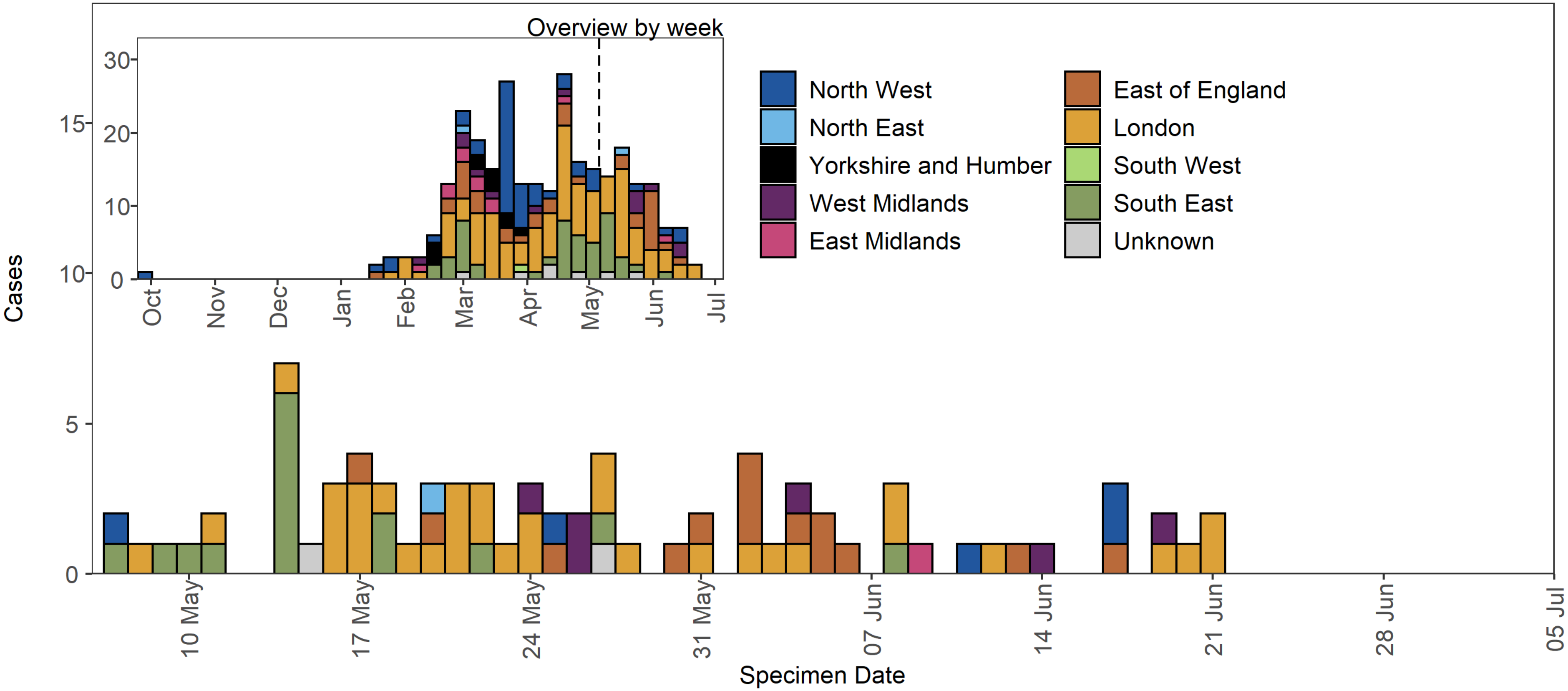
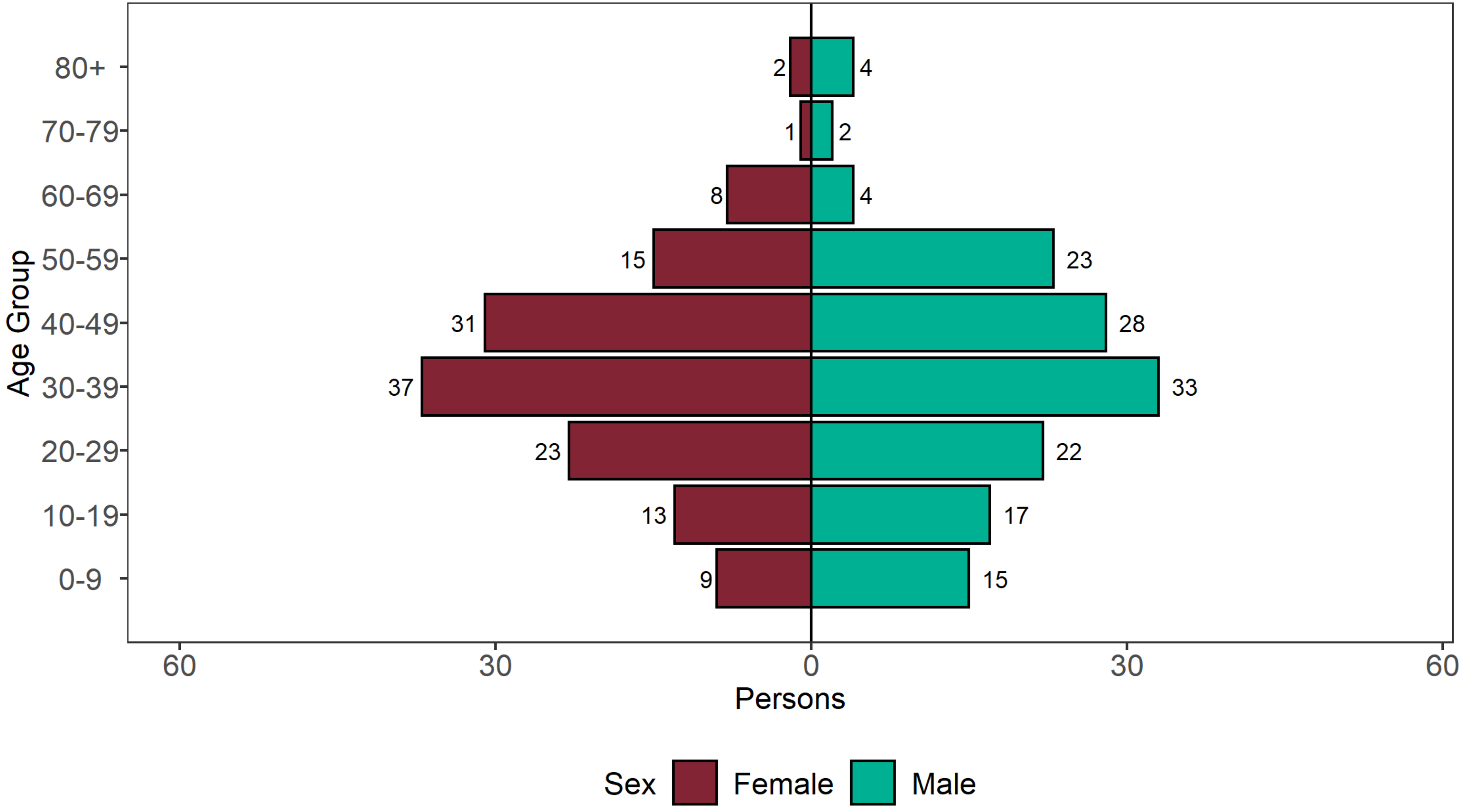


Figure 15. Age-sex pyramid of confirmed (sequencing) VUI-21FEB-04 (B.1.1.318) cases, as of 5 July 2021
(Find accessible data used in this graph in underlying data.)



2 cases excluded where sex or age not reported

Theta

P.3 was identified on 9 March 2021 in a report of 33 genomes from the Philippines with 13 lineage defining mutations. This variant shares important mutations with Variants of Concern including E484K, N501Y and P681H. Based on genomic profile, Public Health England (PHE) has designated P.3 as VUI-21MAR-02 on 11 March 2021. This variant arises from B.1.1.28, the same parent lineage that gave rise to P.1 and P.2 in Brazil. Phylogenetic analysis of P.3 shows diversity indicating circulation prior to detection. This variant was named Theta by WHO on 31 May 2021.

International Epidemiology

GISAID includes data on sequences available internationally. As of 5 July 2021, 249 sequences of Theta have been identified in GISAID, excluding the UK: Angola (1), Australia (4), China (2), Germany (10), Hong Kong (10), Japan (4), Malaysia (9), Netherlands (7), New Zealand (3), Norway (2), Philippines (179), Singapore (3), South Korea (1), USA (14).

Epidemiology

Table 8. Number of confirmed (sequencing) Theta cases, by region of residence as of 5 July 2021

Region	Total case number	Proportion of all cases
East Midlands	0	0.0%
East of England	1	14.3%
London	2	28.6%
North East	0	0.0%
North West	1	14.3%
South East	0	0.0%
South West	2	28.6%
West Midlands	0	0.0%
Yorkshire and Humber	1	14.3%
Total	7	-

Figure 16. Confirmed (sequencing) Theta cases by specimen date and region of residence as of 5 July 2021

Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)

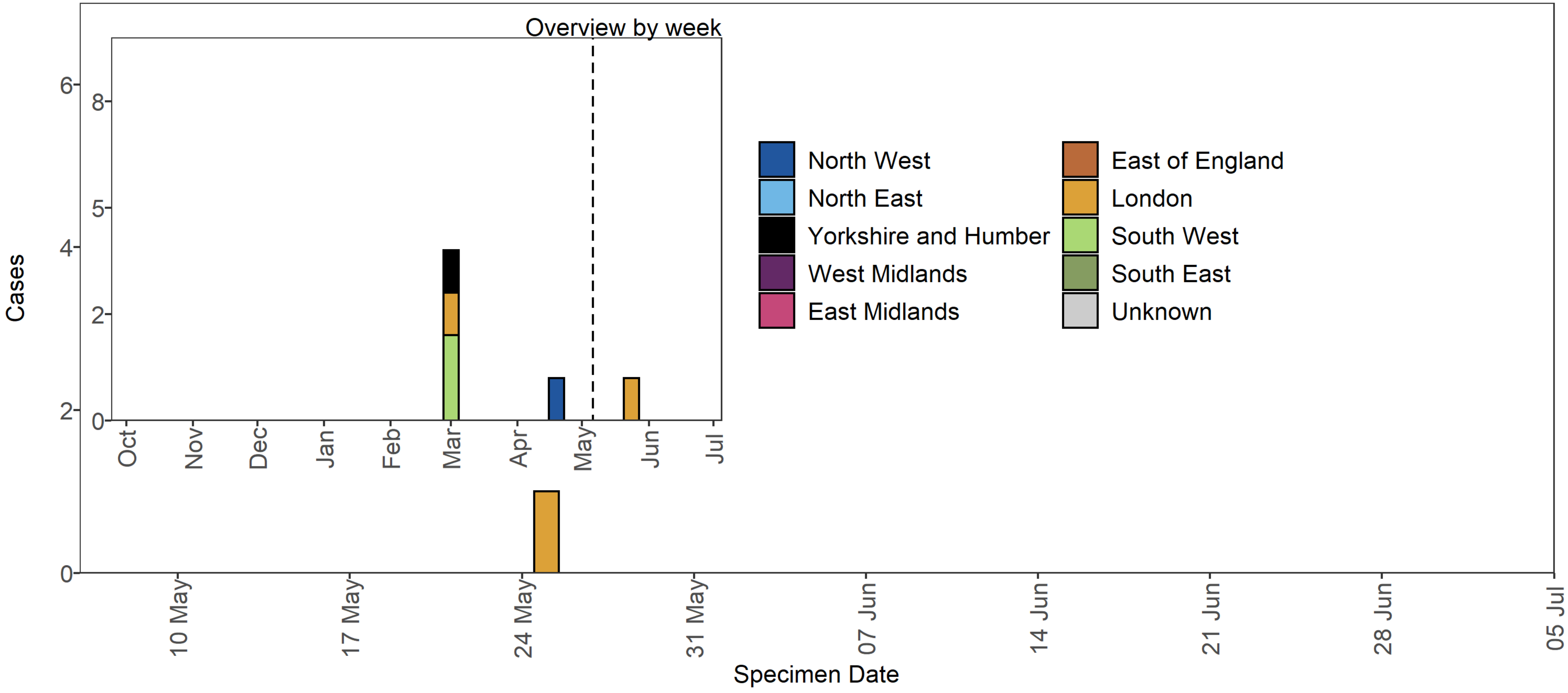
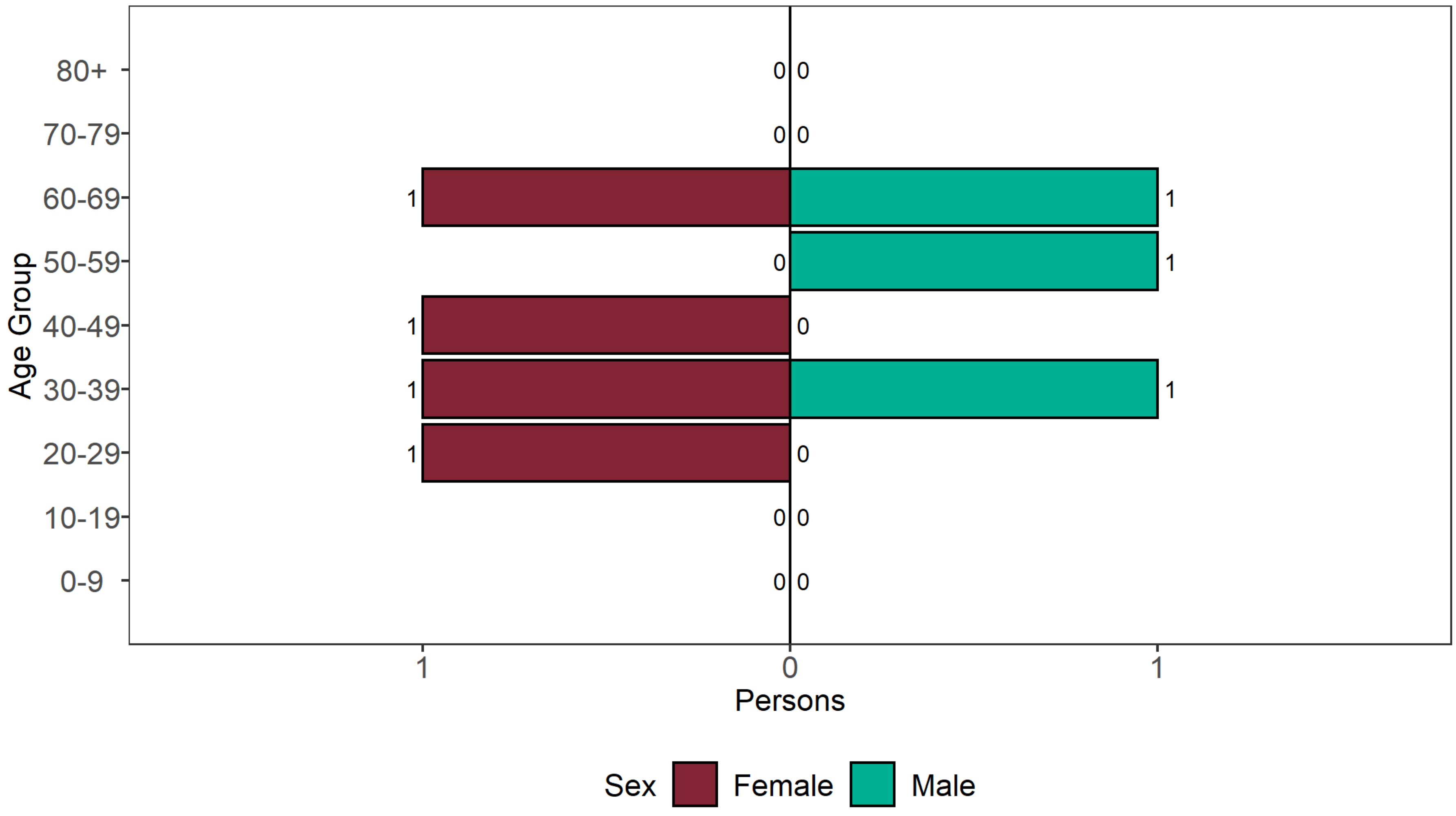


Figure 17. Age-sex pyramid of confirmed (sequencing) Theta cases as of 5 July 2021
(Find accessible data used in this graph in underlying data.)



0 cases excluded where sex or age not reported

Kappa

B.1.617 lineage was escalated to a variant under investigation on 1 April 2021 (B.1.617.1) was escalated to a separate variant under investigation on 27 April 2021 (VUI-21APR-01). This variant was named Kappa by WHO on 31 May 2021.

International Epidemiology

GISAID includes data on sequences available internationally. As of 5 July 2021, 4,412 Kappa sequences from 45 countries (excluding the UK) have been identified in GISAID.

Epidemiology

Table 9. Number of confirmed (sequencing) Kappa cases, by region of residence as of 5 July 2021

Region	Total case number	Proportion of all cases
East Midlands	50	11.2%
East of England	31	7.0%
London	197	44.2%
North East	5	1.1%
North West	32	7.2%
South East	42	9.4%
South West	14	3.1%
West Midlands	48	10.8%
Yorkshire and Humber	18	4.0%
Unknown region	9	2.0%
Total	446	-

Figure 18. Confirmed (sequencing) Kappa cases by specimen date and region of residence as of 5 July 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)

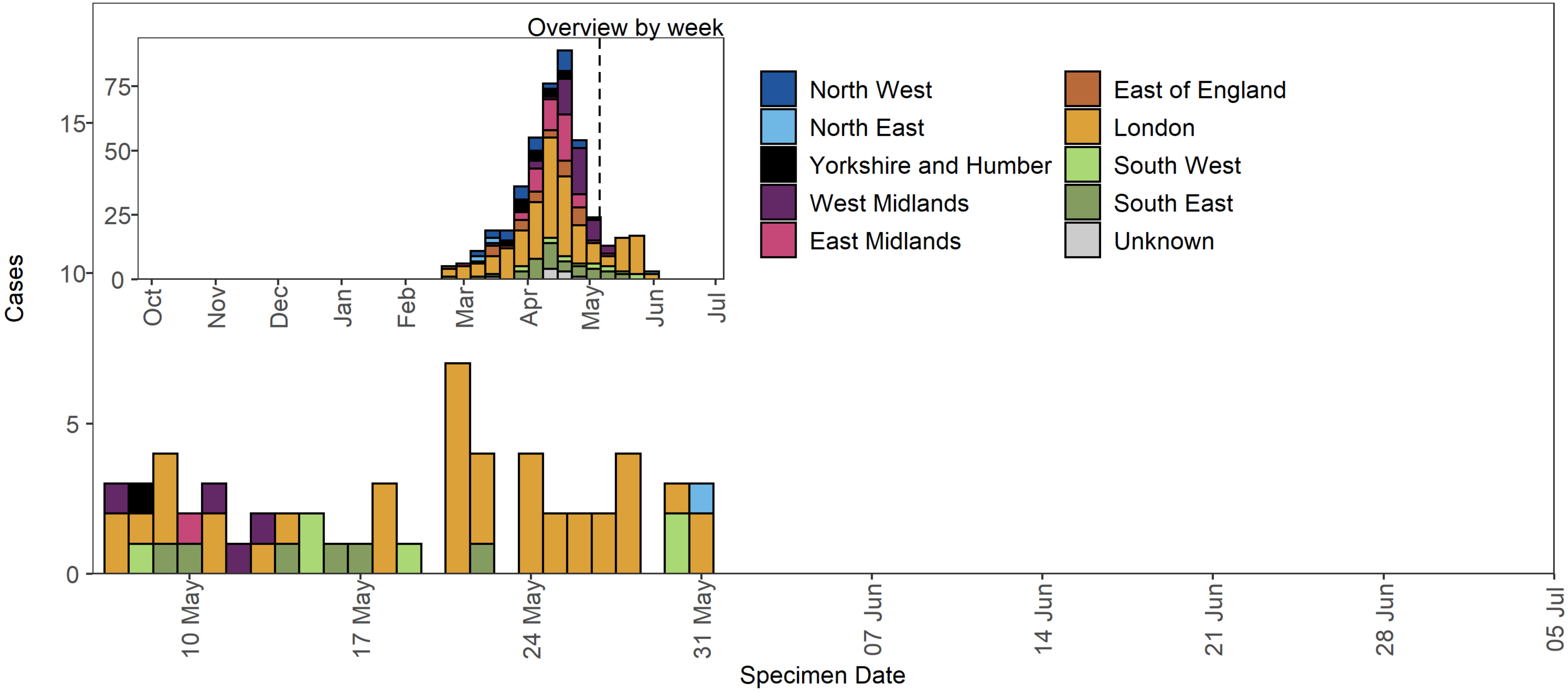
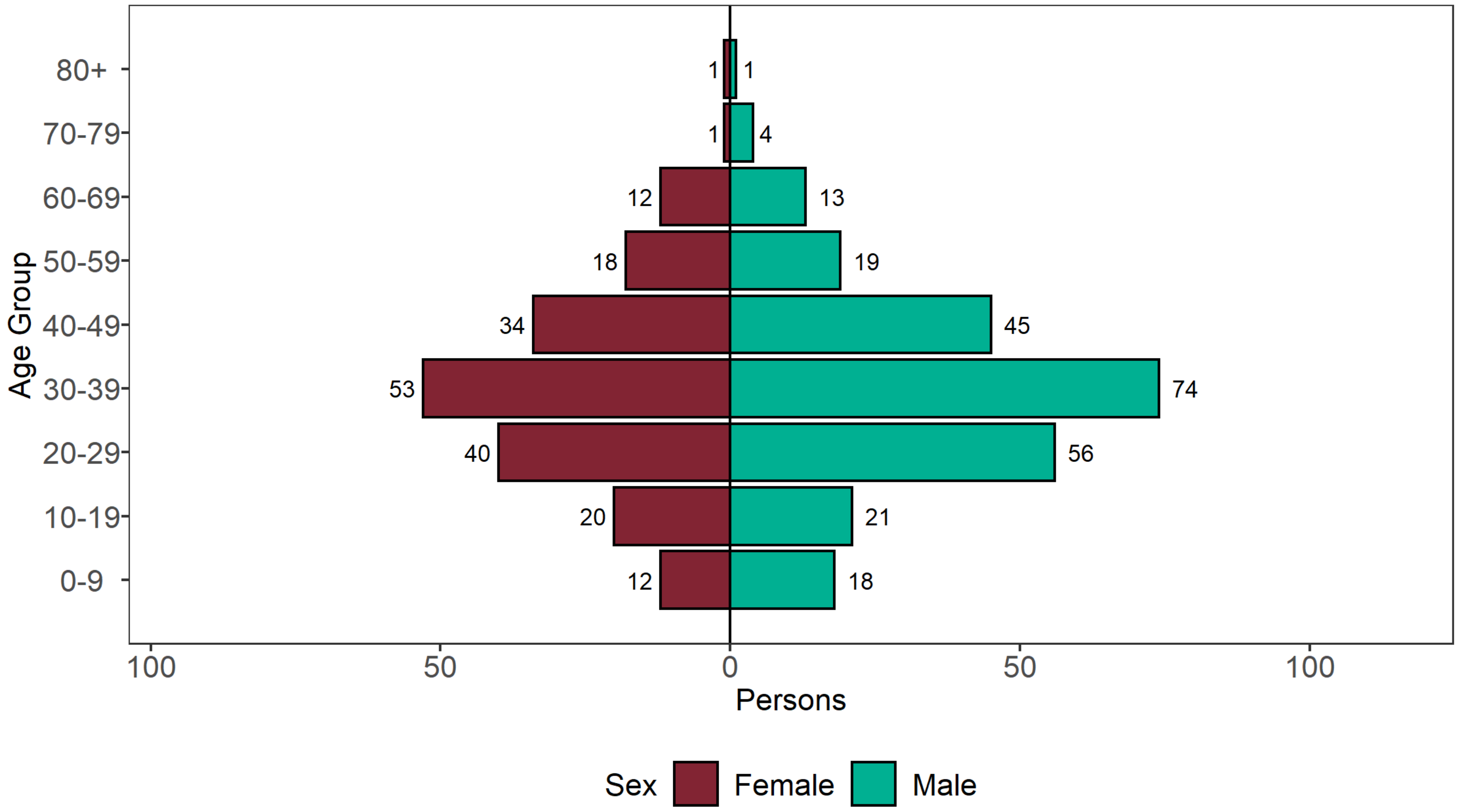


Figure 19. Age-sex pyramid of confirmed (sequencing) Kappa cases as of 5 July 2021
(Find accessible data used in this graph in underlying data.)



4 cases excluded where sex or age not reported

VUI-21APR-03 (B.1.617.3)

B.1.617 lineage was escalated to a variant under investigation on 1 April 2021. VUI-21APR-03 (B.1.617.3) was escalated to a variant under investigation on 28 April 2021.

International Epidemiology

GISAID includes data on sequences available internationally. As of 5 July 2021, 165 sequences of VUI-21APR-03 (B.1.617.3) from the following countries (excluding the UK) have been identified in GISAID: India (152), Japan (1), Malawi (7), Russia (2), Singapore (1), USA (2).

Epidemiology

Table 10. Number of confirmed (sequencing) VUI-21APR-03 (B.1.617.3) cases, by region of residence as of 5 July 2021

Region	Total case number	Proportion of all cases
East Midlands	0	0.0%
East of England	0	0.0%
London	5	38.5%
North East	0	0.0%
North West	6	46.2%
South East	2	15.4%
South West	0	0.0%
West Midlands	0	0.0%
Yorkshire and Humber	0	0.0%
Total	13	-

Figure 20. Confirmed (sequencing) VUI-21APR-03 (B.1.617.3) cases by region of residence and specimen date as of 5 July 2021

Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)

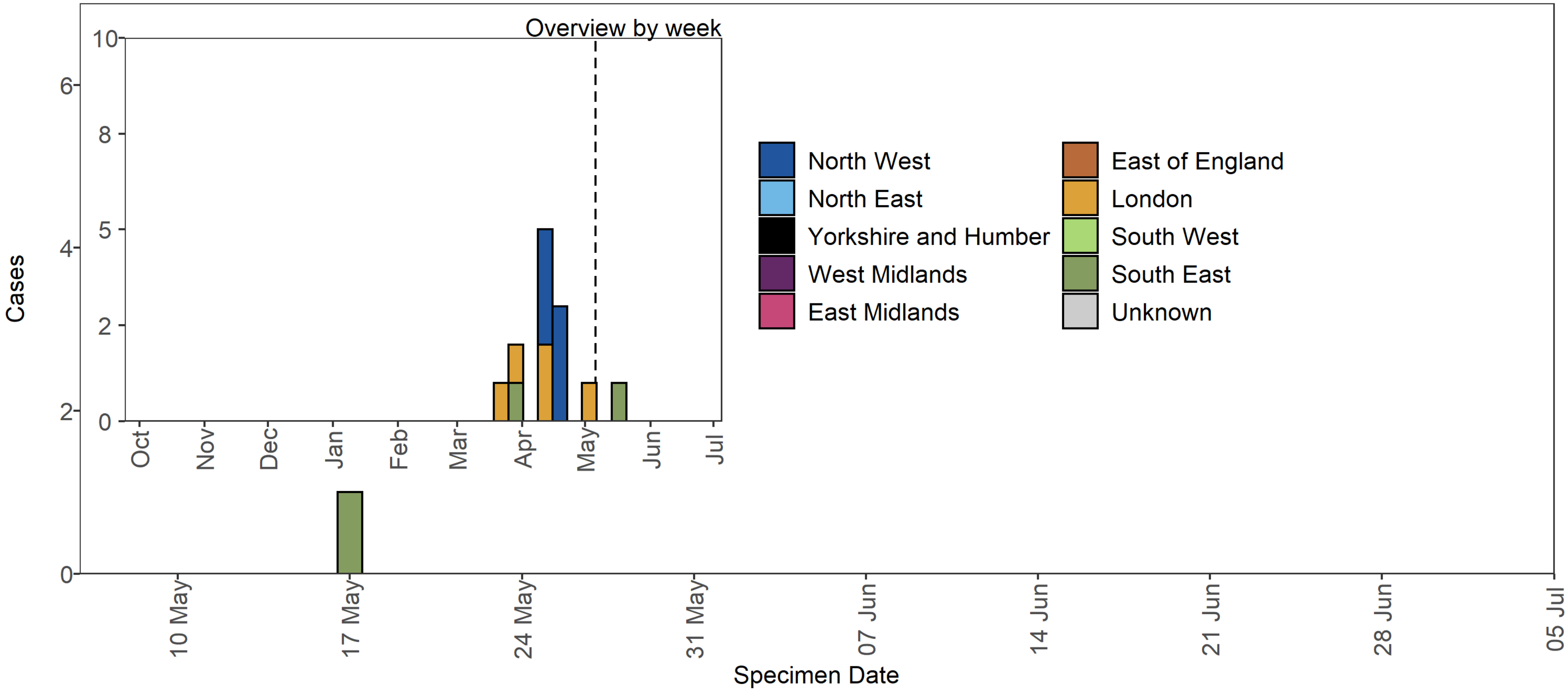
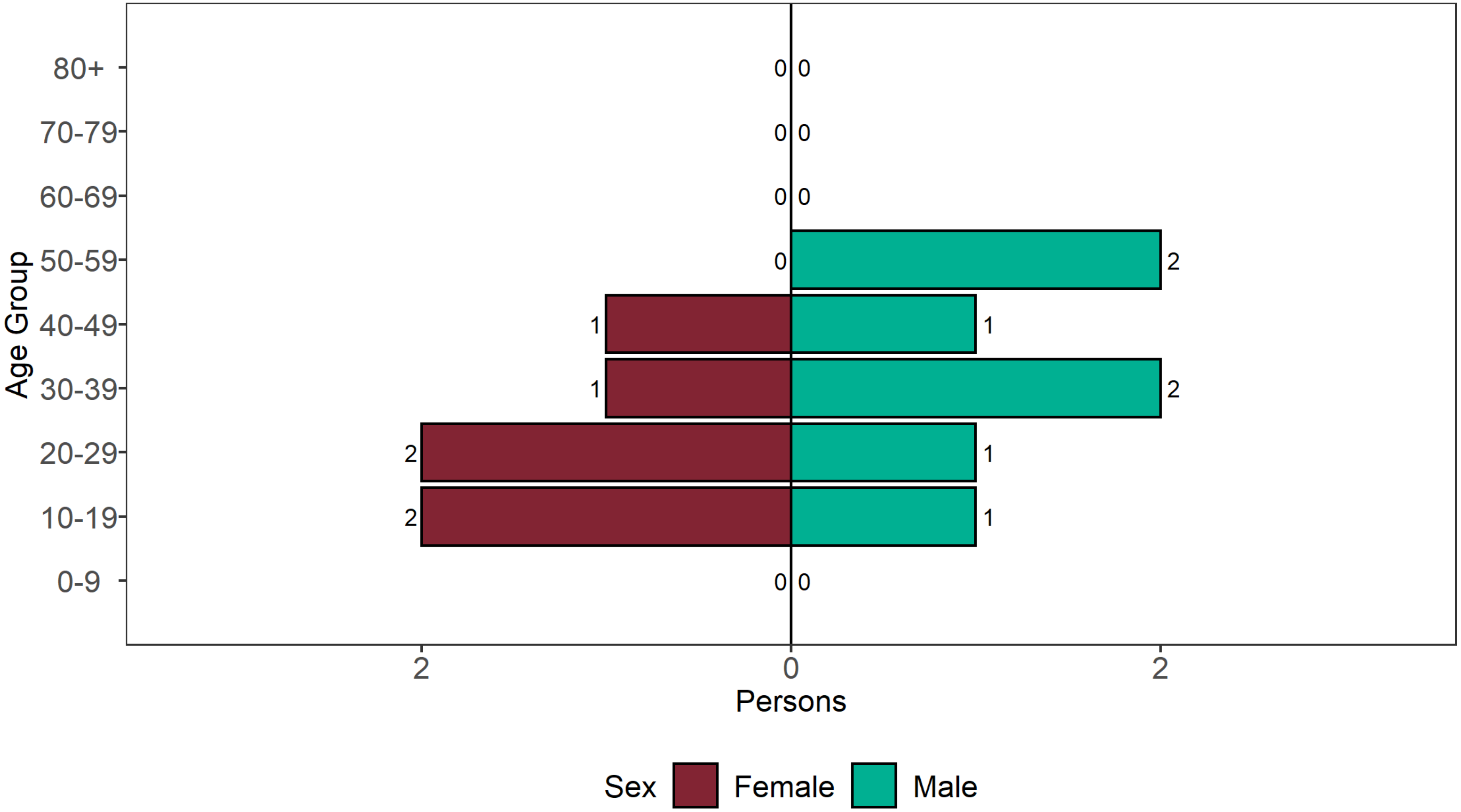


Figure 21. Age-sex pyramid of confirmed (sequencing) VUI-21APR-03 (B.1.617.3) cases as of 5 July 2021
(Find accessible data used in this graph in underlying data.)



0 cases excluded where sex or age not reported

VUI-21MAY-01 (AV.1)

AV.1 was first detected in UK sequences and was designated under investigation on 14 May 2021 as VUI-21MAY-01 on the basis of the mutation profile and apparent localised cluster in Yorkshire and Humber region.

International Epidemiology

GISAID includes data on sequences available internationally. Excluding the UK, as of 5 July 2021, 5 sequences of VUI-21MAY-01 (AV.1) from France have been identified in GISAID.

Epidemiology

Table 11. Number of confirmed (sequencing) VUI-21MAY-01 (AV.1) cases, by region of residence as of 5 July 2021

Region	Total case number	Proportion of all cases
East Midlands	7	3.8%
East of England	11	5.9%
London	1	0.5%
North East	1	0.5%
North West	7	3.8%
South East	0	0.0%
South West	0	0.0%
West Midlands	4	2.2%
Yorkshire and Humber	153	82.7%
Unknown region	1	0.5%
Total	185	-

Figure 22. Confirmed (sequencing) VUI-21MAY-01 (AV.1) cases by specimen date and region or residence as of 5 July 2021. Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)

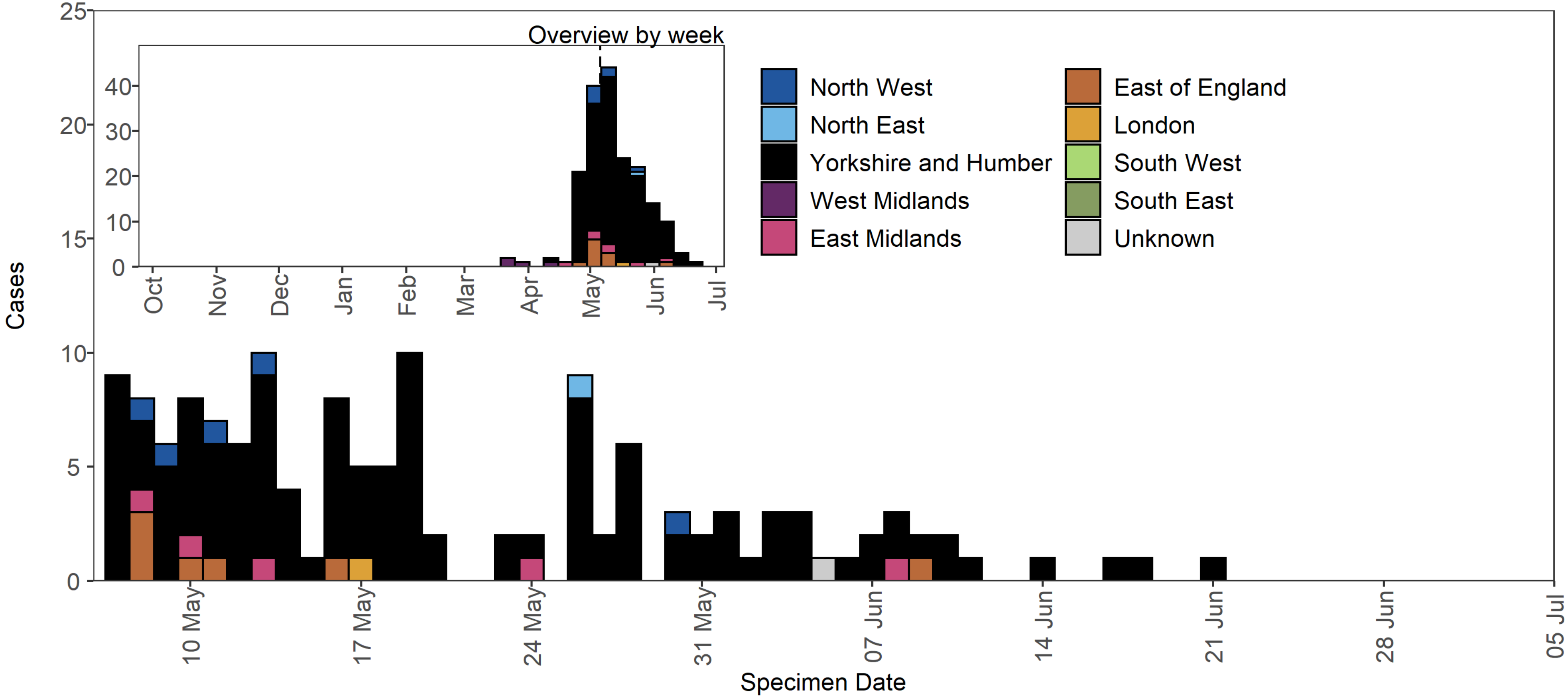
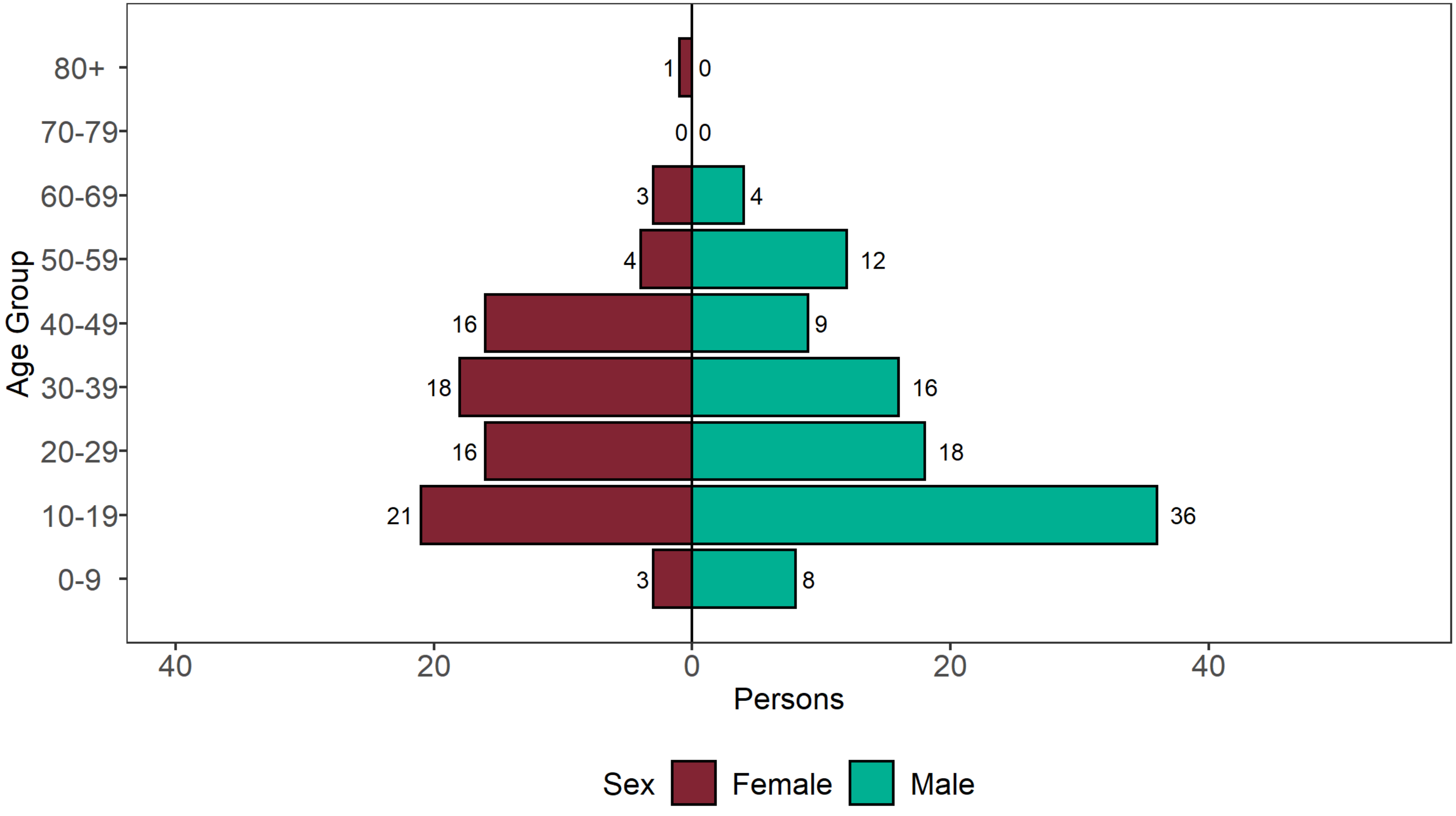


Figure 23. Age-sex pyramid of confirmed (sequencing) VUI-21MAY-01 (AV.1) cases as of 5 July 2021
(Find accessible data used in this graph in underlying data.)



0 cases excluded where sex or age not reported

VUI-21MAY-02 (C.36.3)

C.36.3 was designated a Variant Under Investigation on 24 May 2021 (VUI-21MAY-02) on the basis of the mutation profile and increased importation from a widening international area.

International Epidemiology

GISAID includes data on sequences available internationally. Excluding the UK, as of 5 July 2021, 1380 sequences of VUI-21MAY-02 (C.36.3) from 46 countries have been identified in GISAID

Epidemiology

Table 12. Number of confirmed (sequencing) VUI-21MAY-02 (C.36.3) cases, by region of residence as of 5 July 2021

Region	Total case number	Proportion of all cases
East Midlands	8	5.7%
East of England	21	15.0%
London	41	29.3%
North East	1	0.7%
North West	14	10.0%
South East	13	9.3%
South West	4	2.9%
West Midlands	10	7.1%
Yorkshire and Humber	26	18.6%
Unknown region	2	1.4%
Total	140	-

Figure 24. Confirmed (sequencing) VUI-21MAY-02 (C.36.3) cases by specimen date and region of residence as of 5 July 2021

Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)

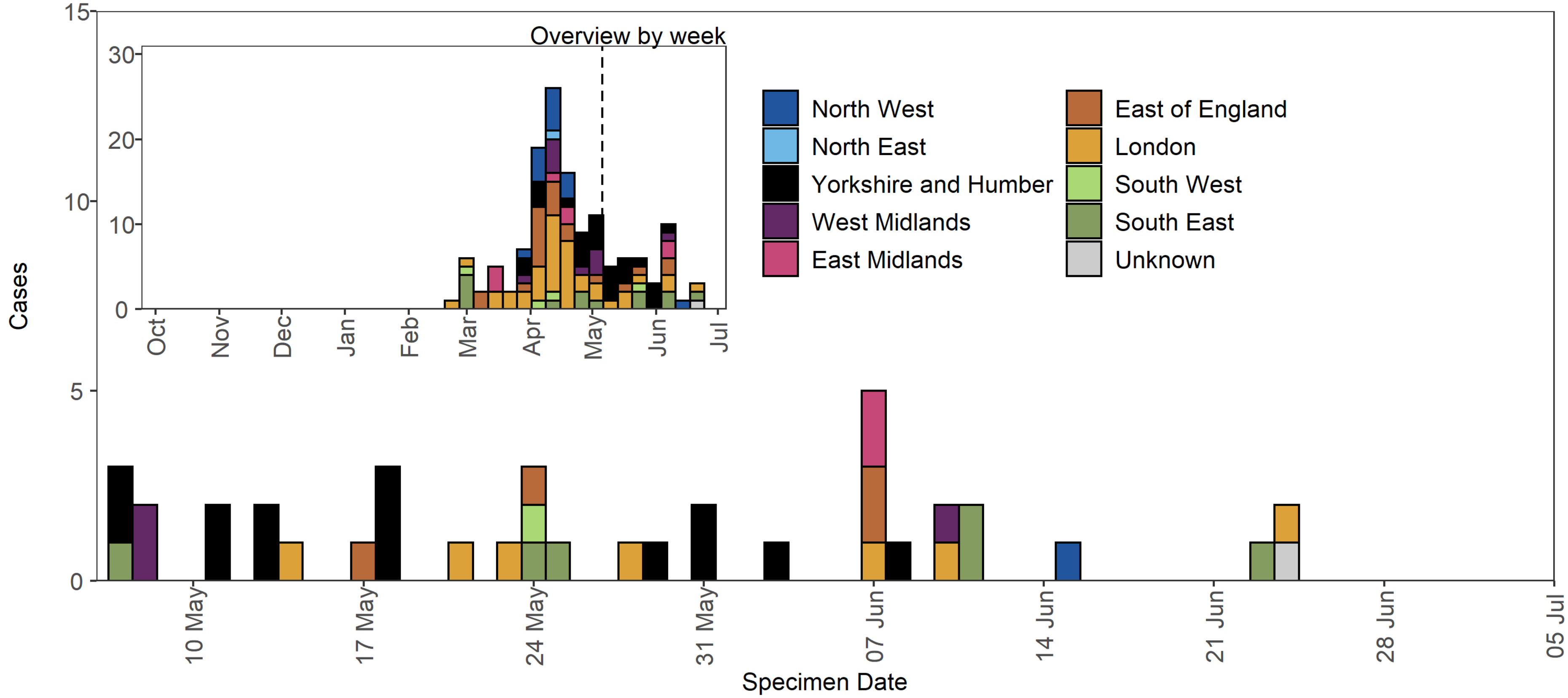
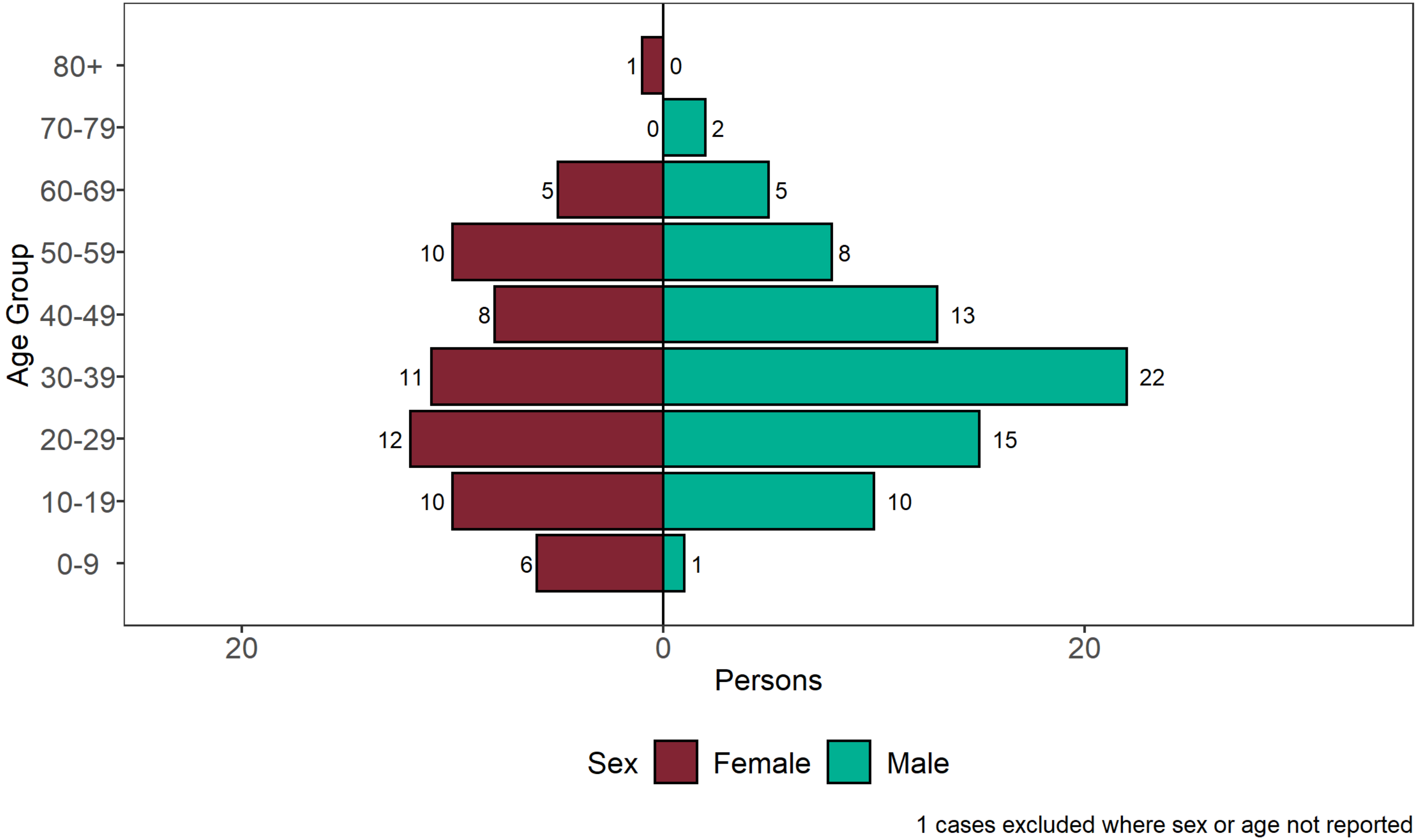


Figure 25. Age-sex pyramid of confirmed (sequencing) VUI-21MAY-02 (C.36.3) cases as of 5 July 2021
(Find accessible data used in this graph in underlying data.)



Lambda (C.37, VUI-21JUN-01)

Lambda was identified through international variant horizon scanning and was made a signal in monitoring by PHE on 14 April 2021 (lineage B.1.1.1 at the time). On 14 June 2021, WHO designated lineage C.37 as a new variant of interest, Lambda based on evidence of continued emergence and suspected phenotypic implications. Lambda was designated a variant under investigation (VUI-21JUN-01) by PHE on the 23 June 2021.

Lambda carries a number of mutations with suspected phenotypic implications, such as a potential increased transmissibility or possible increased resistance to neutralizing antibodies[1]. It is characterised by mutations in the spike protein, including G75V, T76I, del247/253, L452Q, F490S, D614G and T859N; however, there is currently limited evidence on the full extent of the impact associated with these genomic changes, and further robust studies into the phenotypic impacts are needed to better understand the impact on countermeasures and to control the spread. Further studies are also required to validate the continued effectiveness of vaccines.[2] The risk assessment for Lambda is published separately for the first time.

International Epidemiology

As of 5 July 2021, 2077 sequences on GISAID have been assigned to the C.37 lineage. C.37 sequences have been uploaded from Argentina (87), Aruba (2), Australia (1), Belgium (1), Bolivia (1), Brazil (2), Canada (3), Chile (815), Colombia (18), Denmark (1), Ecuador (45), France (14), Germany (93), Israel (25), Italy (4), Mexico (61), Netherlands (1), Peru (236), Portugal (2), Saint Kitts and Nevis (10), Spain (48), Switzerland (7), USA (599), Uruguay (1).

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[1] Romero PE and others (2021). Novel sublineage within B.1.1.1 currently expanding in Peru and Chile, with a convergent deletion in the ORF1a gene.
(Δ3675-3677) and a novel deletion in the Spike gene (Δ246-252, G75V, T76I, L452Q, F490S, T859N). Virologica.org, 24 Apr 2021.

[2] Weekly epidemiological update on COVID-19 to 15 June 2021

Lambda: international genomic surveillance data

- Lambda is highly prevalent in several South American countries, particularly in Peru and Chile. Lower prevalence of this variant has been reported in North America and Europe (Figure 26).
- Although sequencing in many countries is limited, C.37 represents a low proportion of the available global genomic dataset at present (Figure 27).

Figure 26. Prevalence of Lambda mapped, based on uploads to GISAID in the last 90 days.

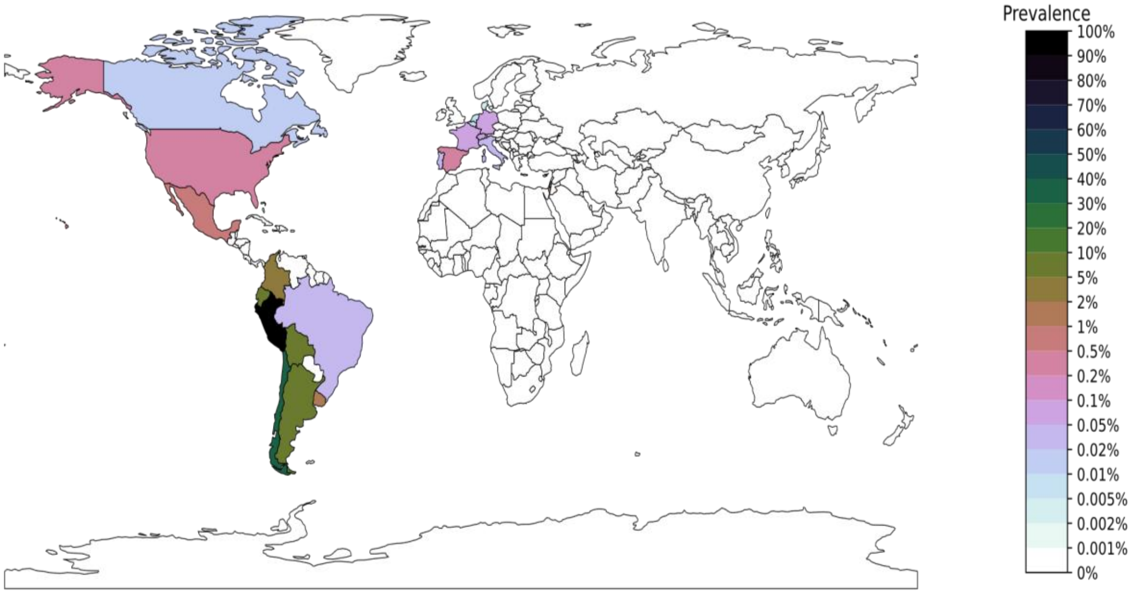
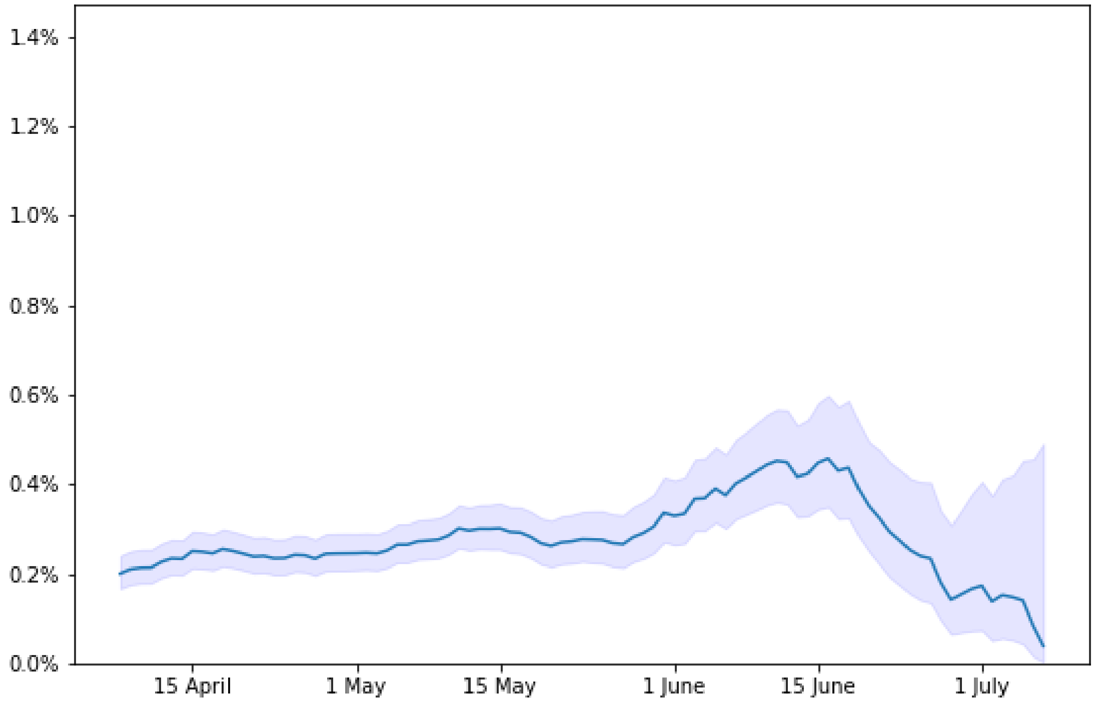


Figure 27. Prevalence of Lambda, amongst all sequences on GISAID, obtained using a 2-week rolling window



Epidemiology

There have been a small number of cases, primarily imports, of Lambda (C.37) in the United Kingdom (UK). As of the 5 July 2021, there have been 8 cases of Lambda in the UK between 23 February and 18 June 2021. Six cases were in London, one in the South West, and one in the West Midlands. Six cases have a history of travel overseas; 2 cases have not provided information.

No deaths have been reported within 28 days.

Cases are managed in line with the approach for emerging variants with review of contact tracing, additional data collection, testing of identified contacts, and consideration of targeted case finding as required where there is evidence of community transmission.

Table 13. Number of confirmed (sequencing) Lambda (C.37) cases, by region of residence as of 5 July 2021

Region	Total case number	Proportion of all cases
East Midlands	0	0.0%
East of England	0	0.0%
London	6	75.0%
North East	0	0.0%
North West	0	0.0%
South East	0	0.0%
South West	1	12.5%
West Midlands	1	12.5%
Yorkshire and Humber	0	0.0%
Total	8	-

Figure 28. Confirmed (sequencing) Lambda cases by specimen date and region of residence as of 5 July 2021. Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)

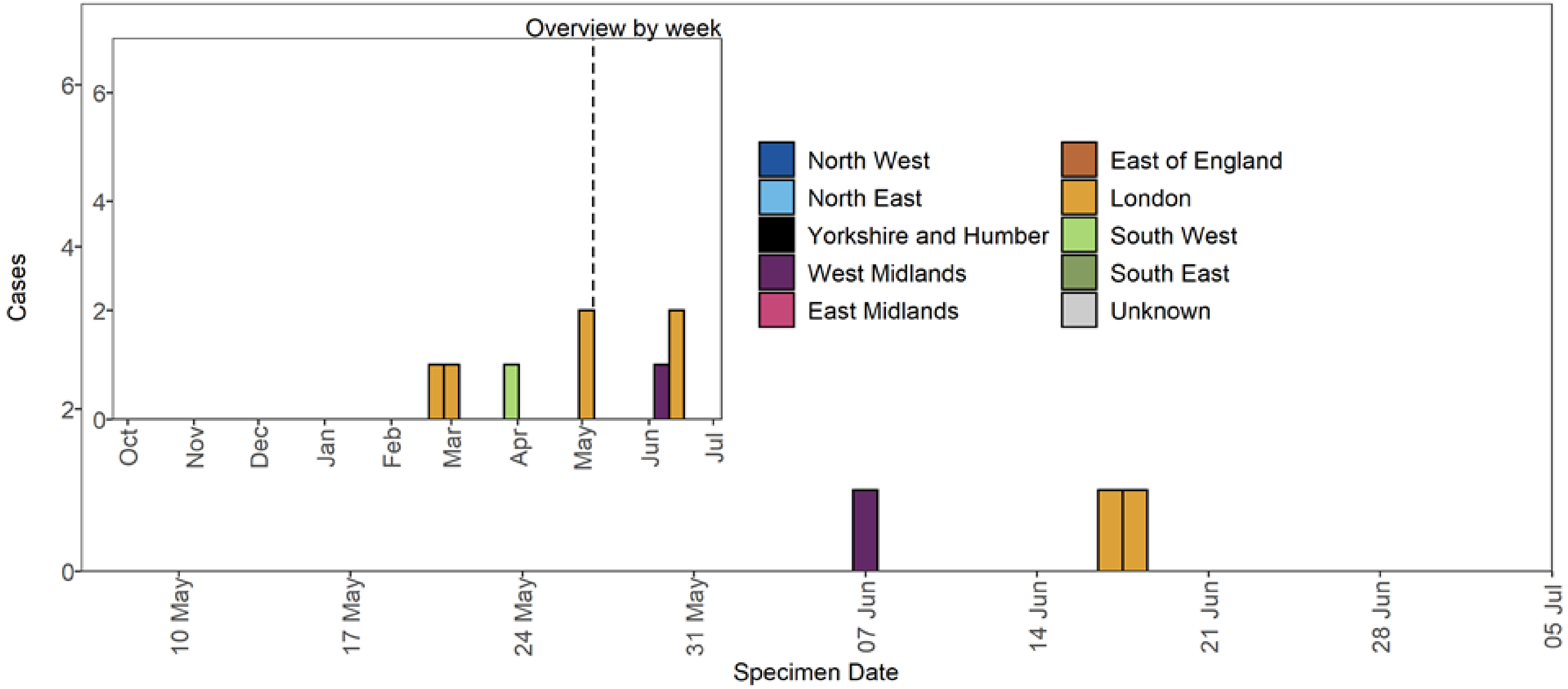
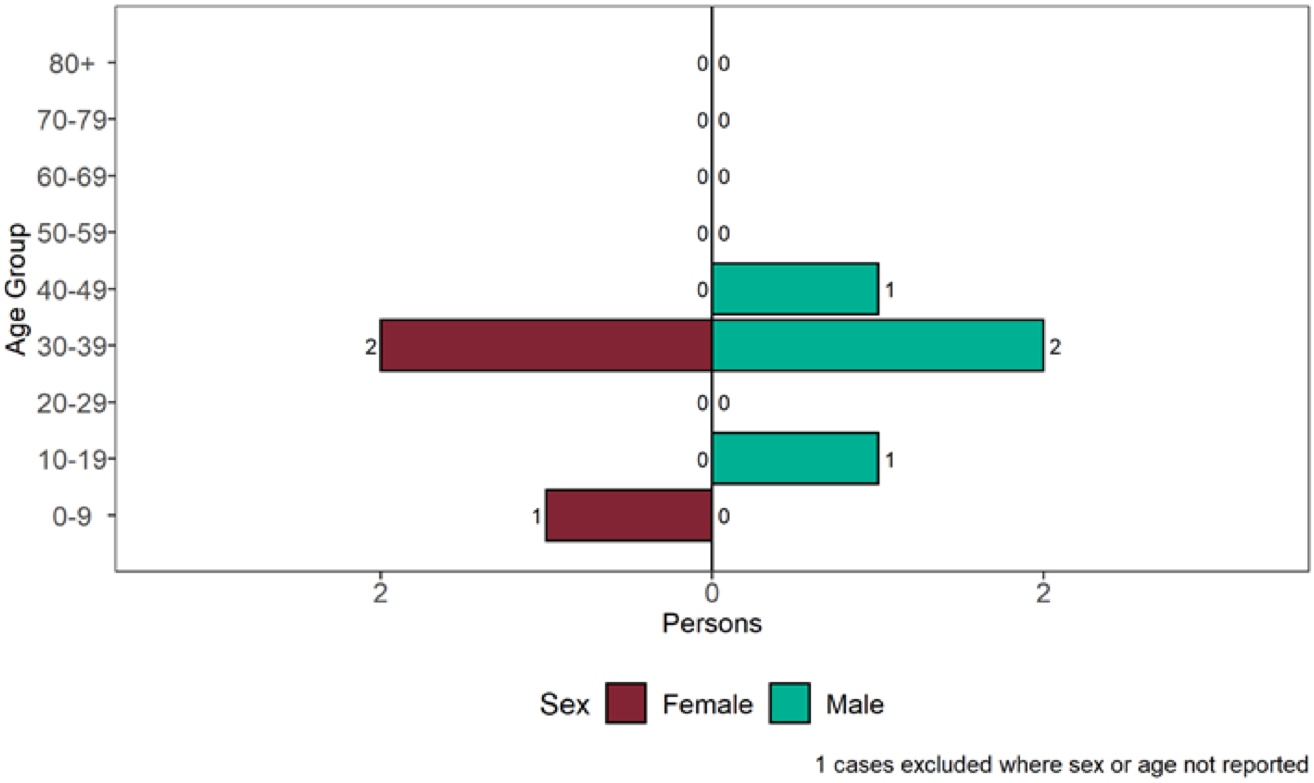


Figure 29. Age-sex pyramid of confirmed (sequencing) Lambda cases as of 5 July 2021 (Find accessible data used in this graph in underlying data.)



Sources and acknowledgments

Data sources

Data used in this investigation is derived from the COG-UK dataset, the PHE Second Generation Surveillance System (SGSS), NHS Test and Trace, the Secondary Uses Service (SUS) dataset and Emergency Care Data Set (ECDS). Data on international cases are derived from reports in GISAID, the media and information received via the International Health Regulations National Focal Point (IHRNFP) and Early Warning and Response System (EWRS).

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 5 March 2021. The repository can be accessed on GitHub. They 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 Public Health England. 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

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PHE Outbreak Surveillance Team
PHE Epidemiology Cell
PHE Contact Tracing Cell Data Team
PHE International Cell

Variant Technical Group Membership

The PHE Variant Technical Group includes representation from the following organisations: PHE, DHSC, BEIS, 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 Public Health England

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