



Public Health
England

Protecting and improving the nation's health

SARS-CoV-2 variant data update, England

Version 6

18 June 2021

This briefing provides an update on previous data located in technical and variant data update [briefings and updates](#) up to 11 June 2021.

Contents

Contents.....	2
Data on individual variants	5
Sources and acknowledgments	41
Data sources	41
Variant Technical Group.....	41

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 16](#).

There are 4 variants of concern and 8 variants under investigation ([Table 1](#)).

Table 1. Variant lineage and designation as of 14 June 2021 (provisionally extinct variants removed)

World Health Organization nomenclature as of 14 June 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
	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 14 June 2021	Lineage	Designation	Status
	B.1.1.1 with L452Q and F490S		Monitoring
	R.1		Monitoring
	B.1.1.28 with N501T and E484Q		Monitoring
	B.1.621		Monitoring
	B.1 with 214insQAS		Monitoring
	AT.1		Monitoring
	Lineage A with R346K, T478R and E484K		Monitoring
Lambda [^]	C.37		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 WHO, 14 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

As of 14 June 2021, 597,538 sequences of Alpha, excluding the UK, are listed from 139 countries or territories on [GISAID](#).

Epidemiology

Table 2. Number of confirmed (sequencing) and probable (genotyping) Alpha cases, by region of residence as of 14 Jun 2021

Region	Confirmed (sequencing) case number	Probable (genotyping) case number	Total case number	Proportion of all cases ¹
East Midlands	15,914	480	16,394	7.3%
East of England	19,570	186	19,756	8.8%
London	39,786	755	40,541	18.1%
North East	14,685	99	14,784	6.6%
North West	41,663	1,785	43,448	19.4%
South East	23,727	107	23,834	10.6%
South West	7,949	47	7,996	3.6%
West Midlands	18,179	1,305	19,484	8.7%
Yorkshire and Humber	35,585	905	36,490	16.3%
Unknown region	1,274	20	1,294	0.6%
Total	218,332	5,689	224,021	-

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 1. Confirmed (sequencing) and probable (genotyping) Alpha cases by specimen date and region of residence as of 14 Jun 2021

(Find accessible data used in this graph in [underlying data](#).)

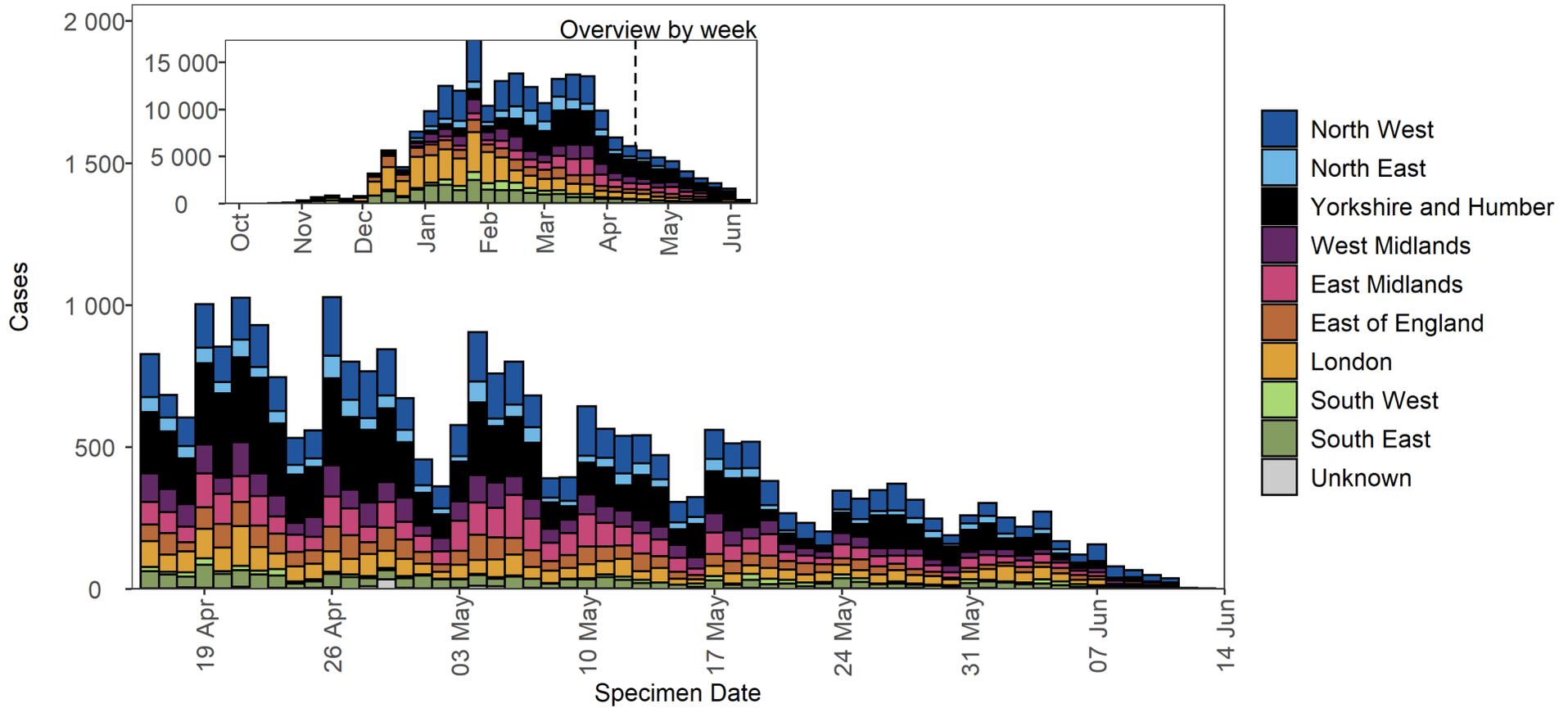


Figure 2. Confirmed (sequencing) and probable (genotyping) Alpha cases by specimen date and detection method as of 14 Jun 2021 (Find accessible data used in this graph in [underlying data.](#))

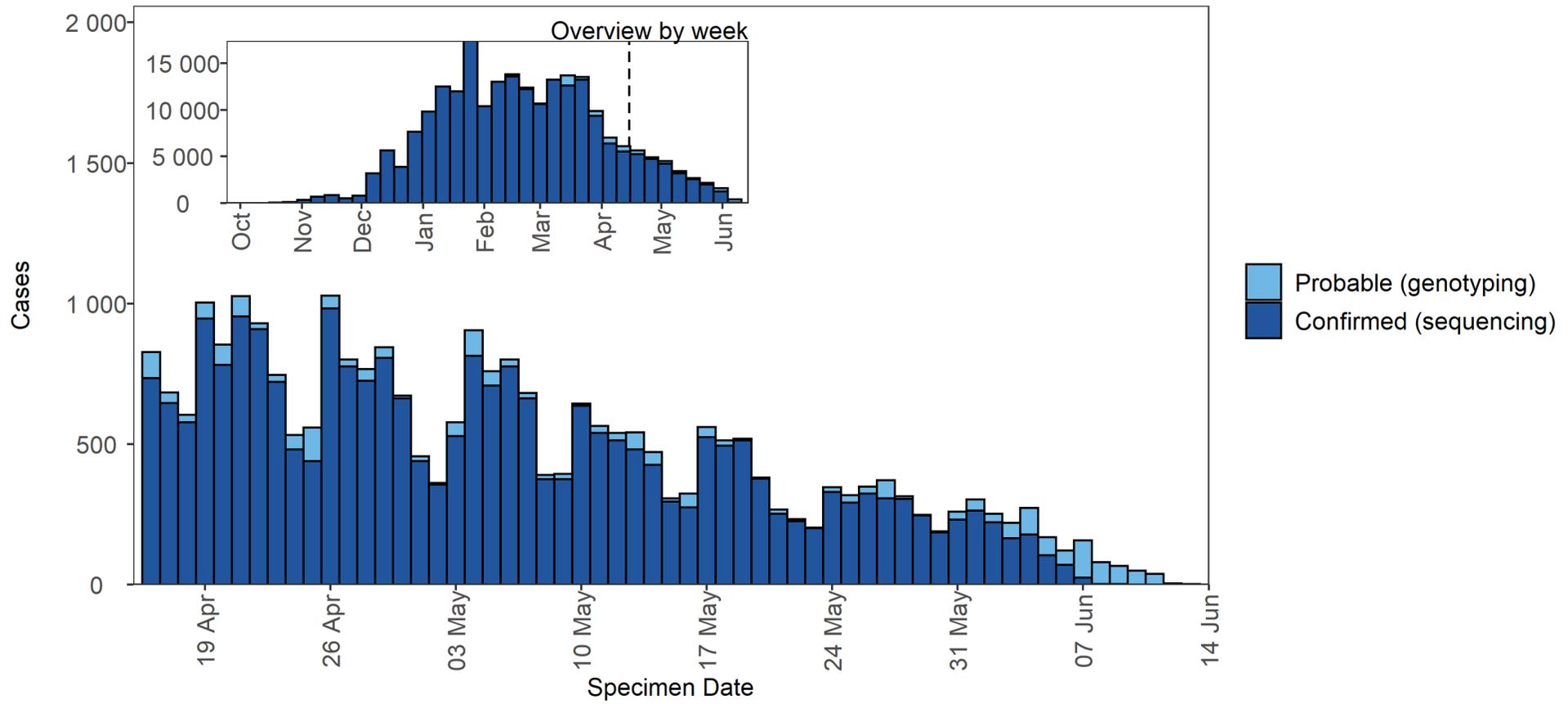
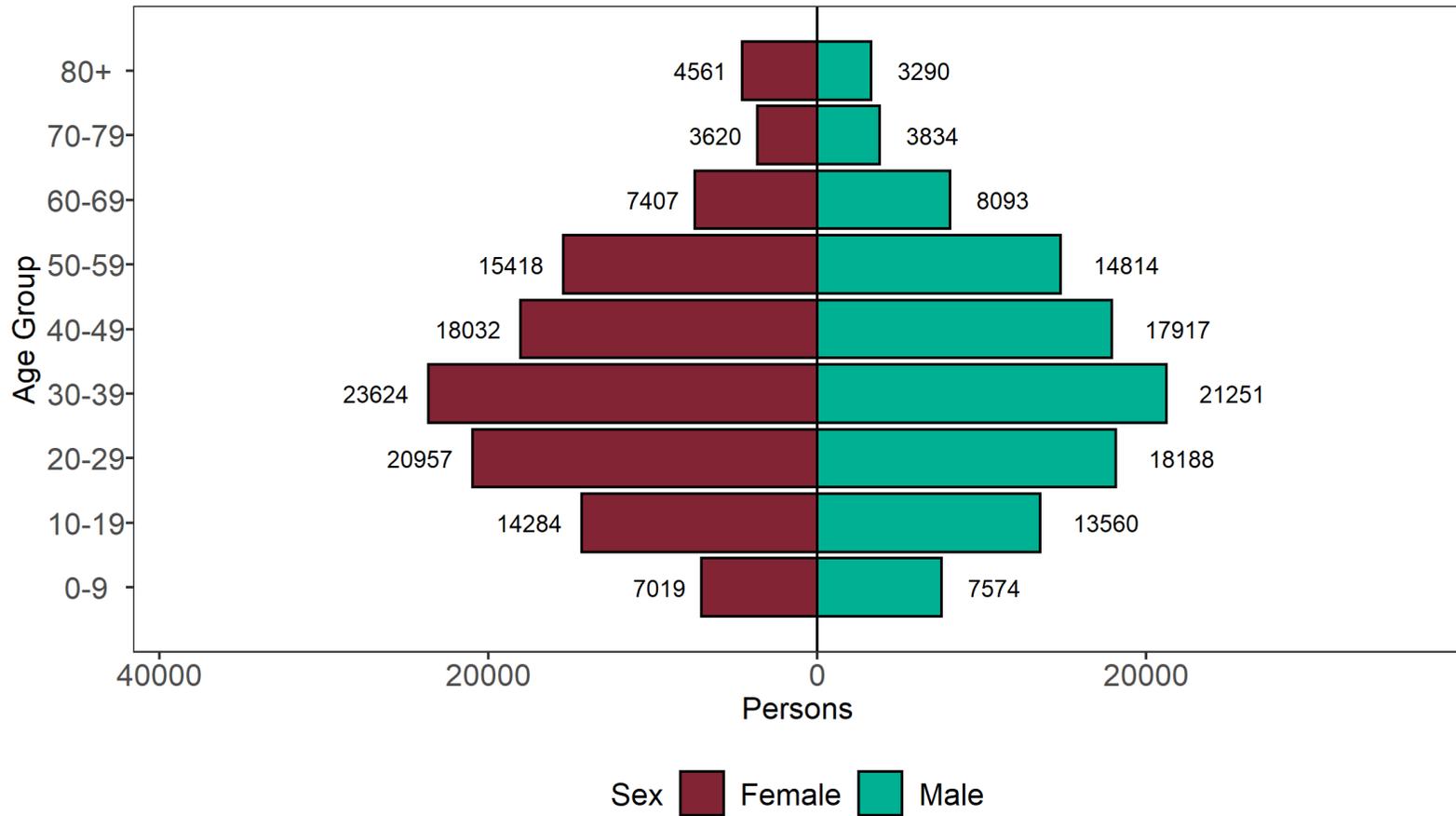


Figure 3. Age-sex pyramid of confirmed (sequencing) and probable (genotyping) Alpha cases as of June 14 2021

(Find accessible data used in this graph in [underlying data](#).)



578 cases excluded where sex or age not reported

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 14 June 2021, 21,904 sequences of Beta, are listed from 94 countries or territories excluding the UK.

Epidemiology

Table 3. Number of confirmed (sequencing) and probable (genotyping) Beta cases, by region of residence as of 14 June 2021

Region	Confirmed (sequencing) case number	Probable (genotyping) case number	Total case number	Proportion of all cases ¹
East Midlands	46	1	47	5.1%
East of England	80	2	82	8.9%
London	397	26	423	45.7%
North East	15	7	22	2.4%
North West	80	9	89	9.6%
South East	106	3	109	11.8%
South West	31	1	32	3.5%
West Midlands	64	0	64	6.9%
Yorkshire and Humber	31	6	37	4.0%
Unknown region	21	0	21	2.3%
Total	871	55	926	-

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 4. Confirmed (sequencing) and probable (genotyping) Beta cases by specimen date and region of residence as of 14 Jun 2021

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

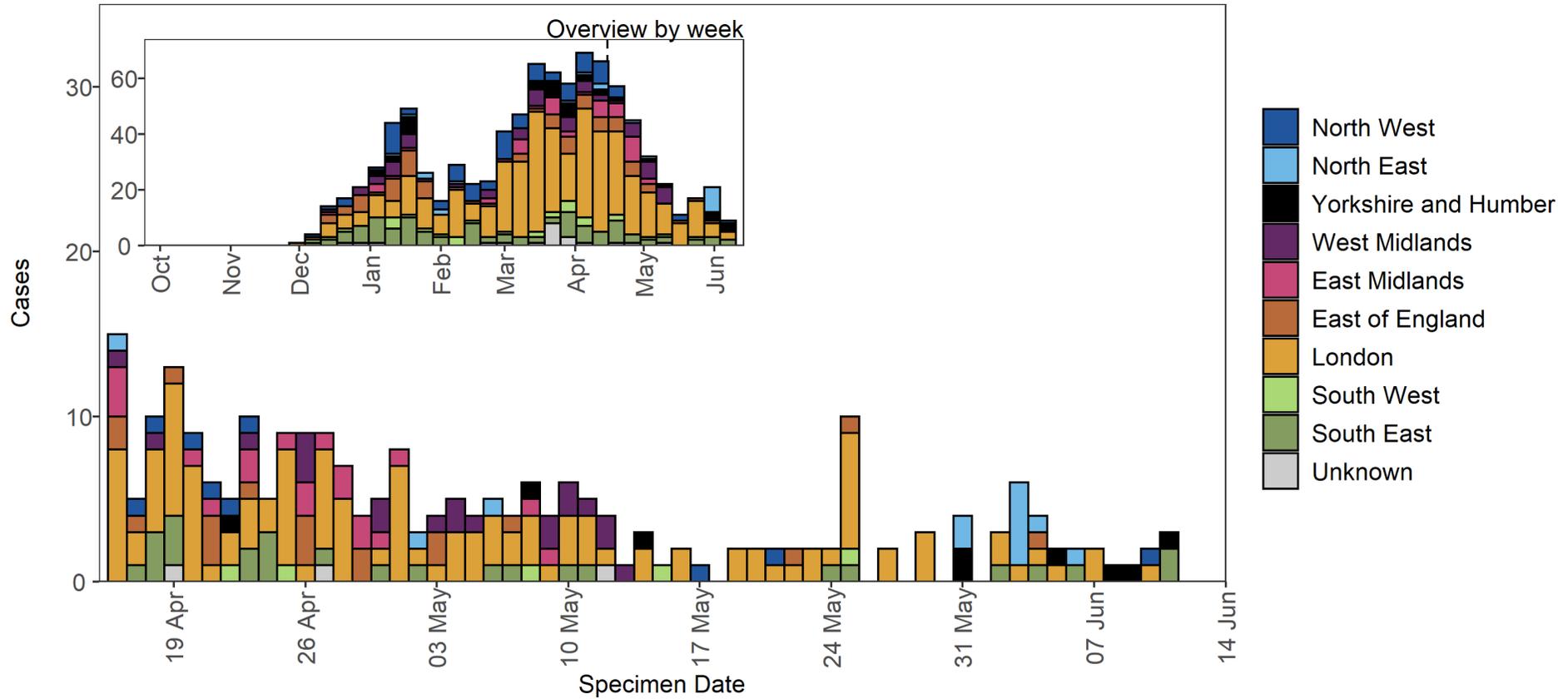


Figure 5. Confirmed (sequencing) and probable (genotyping) Beta cases by specimen date and detection method as of 14 Jun 2021 Larger plot includes last 60 days only. (Find accessible data used in this graph in [underlying data](#).)

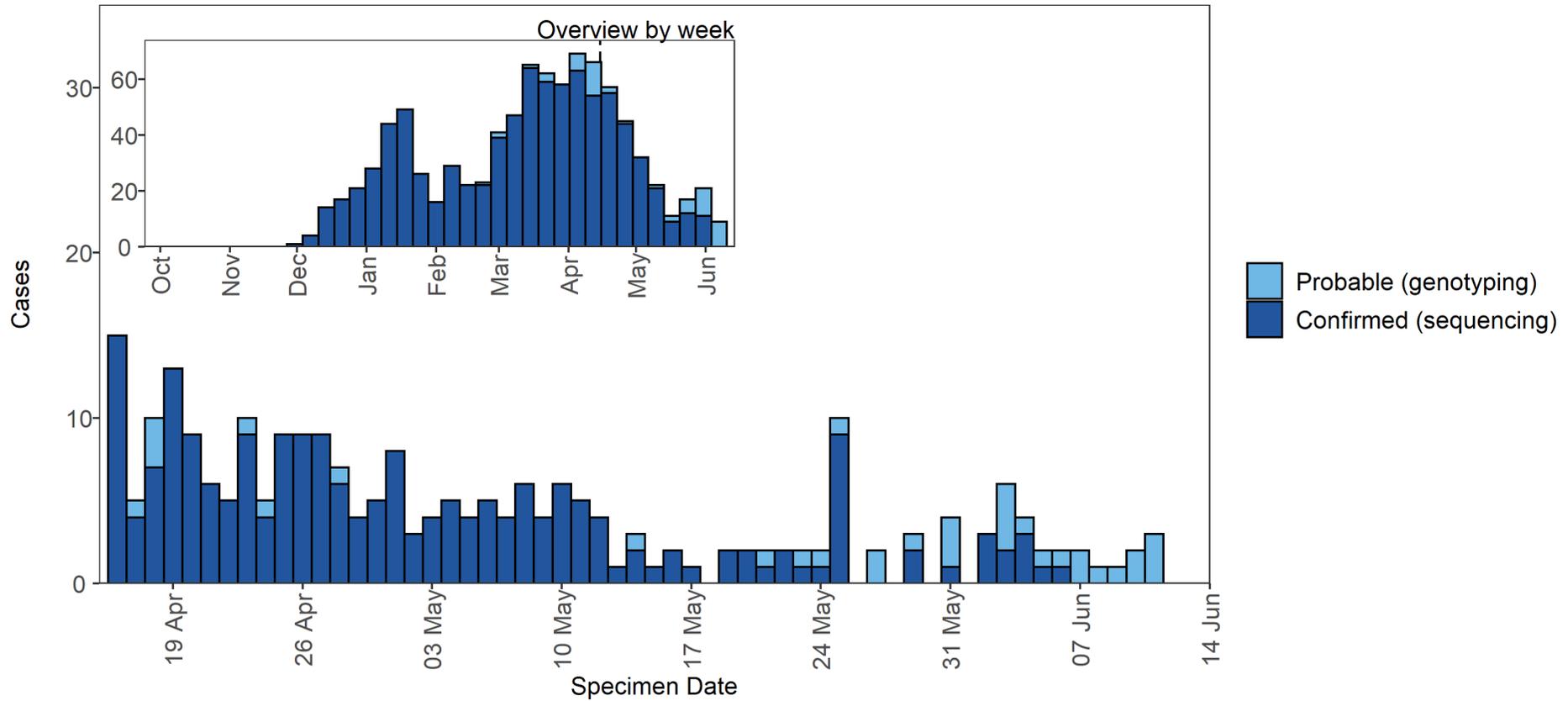
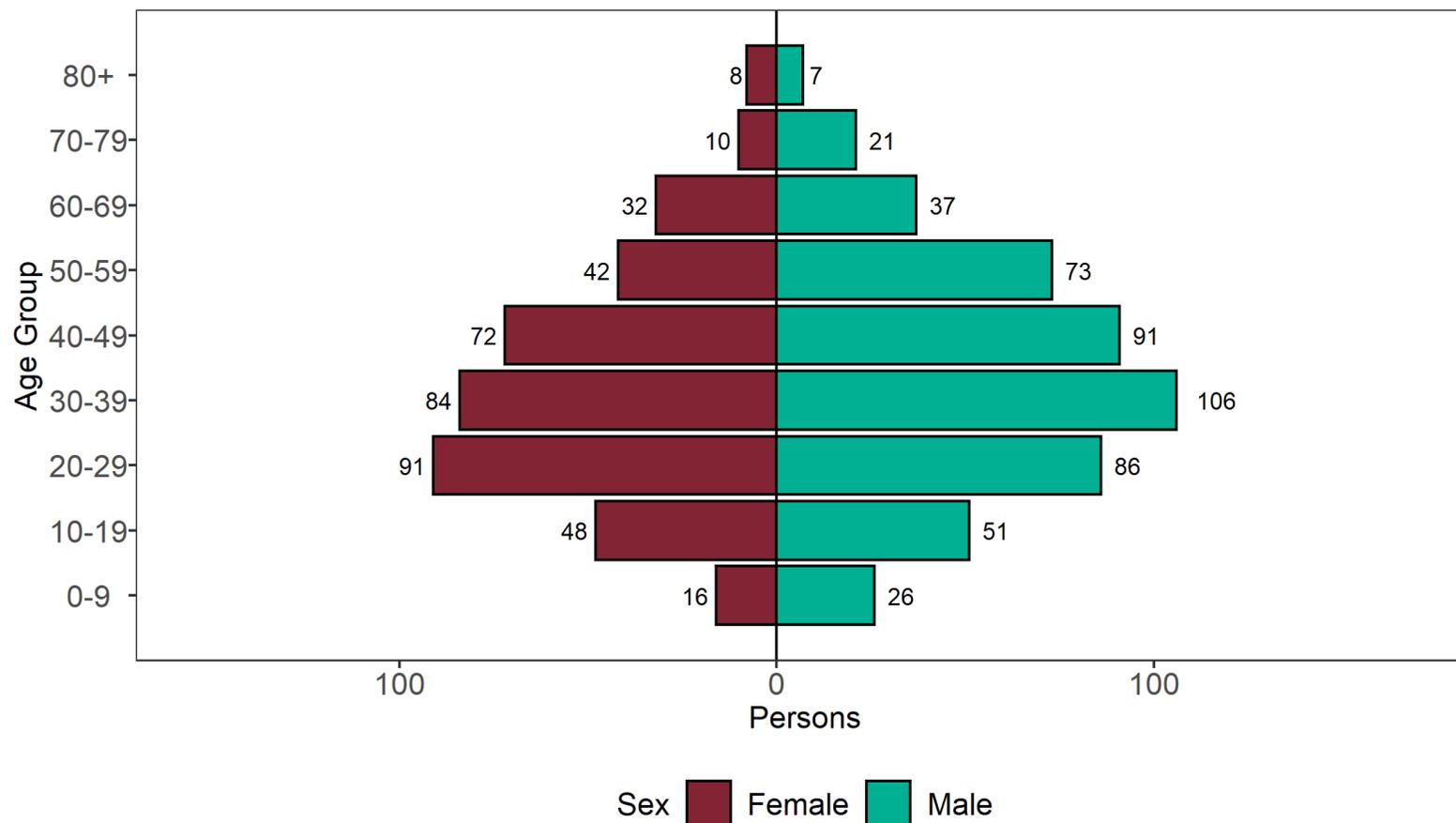


Figure 6. Age-sex pyramid of confirmed (sequencing) and probable (genotyping) Beta cases as of June 14 2021 (Find accessible data used in this graph in [underlying data](#).)



15 cases excluded where sex or age not reported

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 14 June 2021, 33,040 sequences (excluding the UK) of Gamma from 57 countries.

Epidemiology

Table 4. Number of confirmed (genotyping) and probable (genotyping) Gamma cases, by region of residence as of 14 June 2021

Region	Confirmed (sequencing) number	Probable (genotyping) number	Total case number	Proportion of all cases ¹
East Midlands	3	0	3	1.4%
East of England	13	0	13	6.1%
London	94	29	123	58.0%
North East	0	2	2	0.9%
North West	9	1	10	4.7%
South East	27	2	29	13.7%
South West	10	2	12	5.7%
West Midlands	6	0	6	2.8%
Yorkshire and Humber	2	6	8	3.8%
Unknown region	6	0	6	2.8%
Total	170	42	212	-

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 (genotyping) and probable (genotyping) Gamma cases by region of residence and specimen date as of 14 June 2021

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

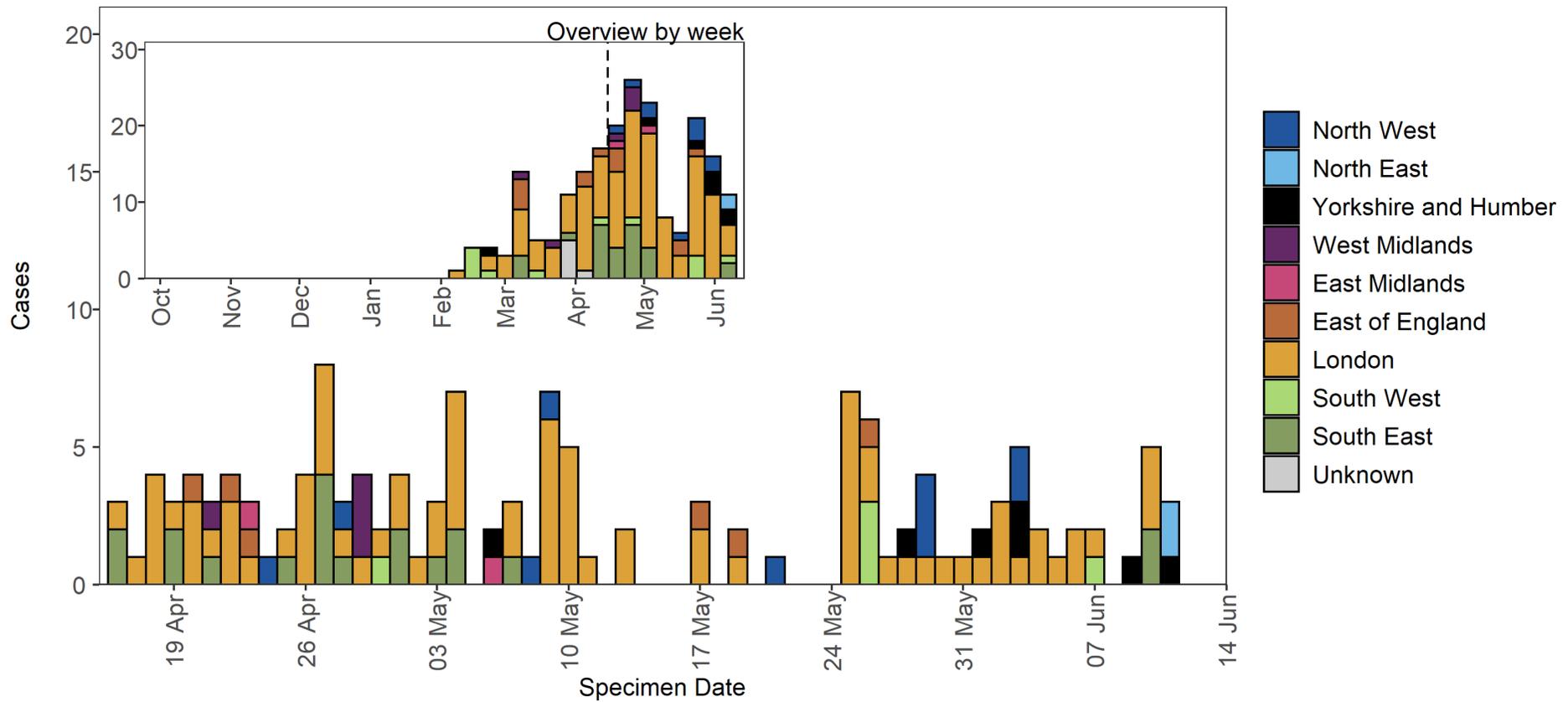


Figure 8. Confirmed (genotyping) and probable (genotyping) Gamma cases by specimen date and detection method as of 14 June 2021

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

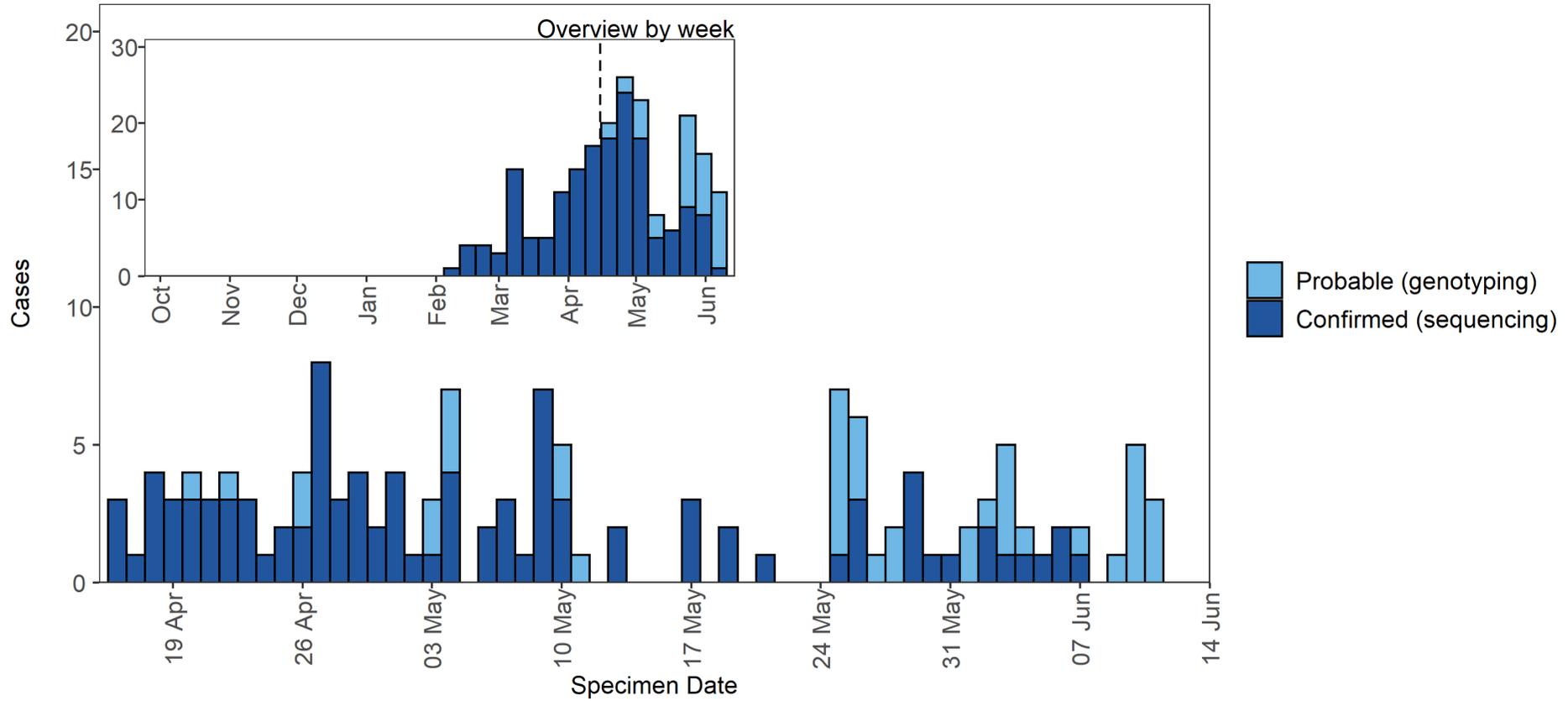
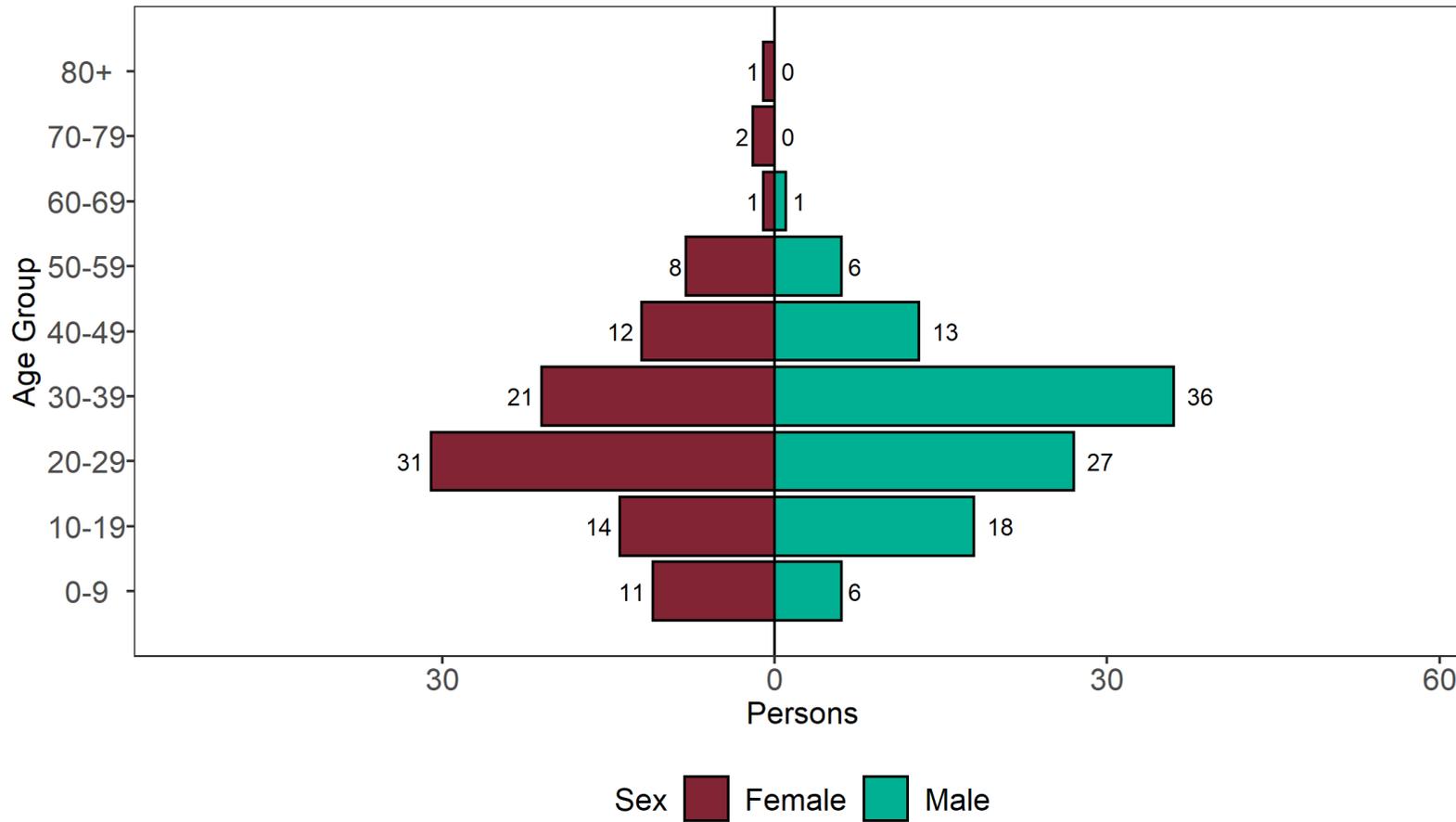


Figure 9. Age-sex pyramid of confirmed (genotyping) and probable (genotyping) Gamma cases as of 14 June 2021.
(Find accessible data used in this graph in [underlying data](#).)



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 14 June 2021, 3,428 sequences (excluding the UK) of Zeta from 37 countries.

Epidemiology

Table 5. Number of confirmed (sequencing) Zeta cases, by region of residence as of 14 June 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 14 June 2021

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

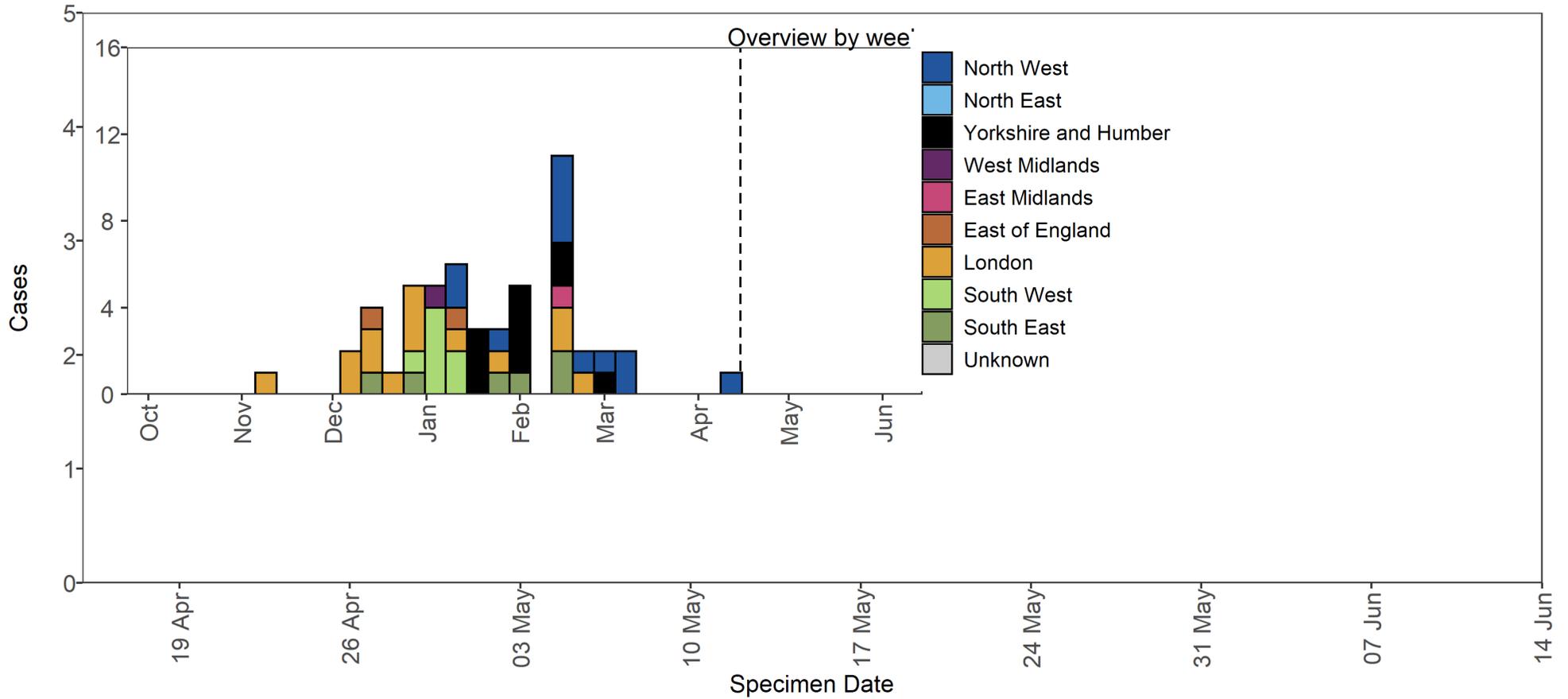
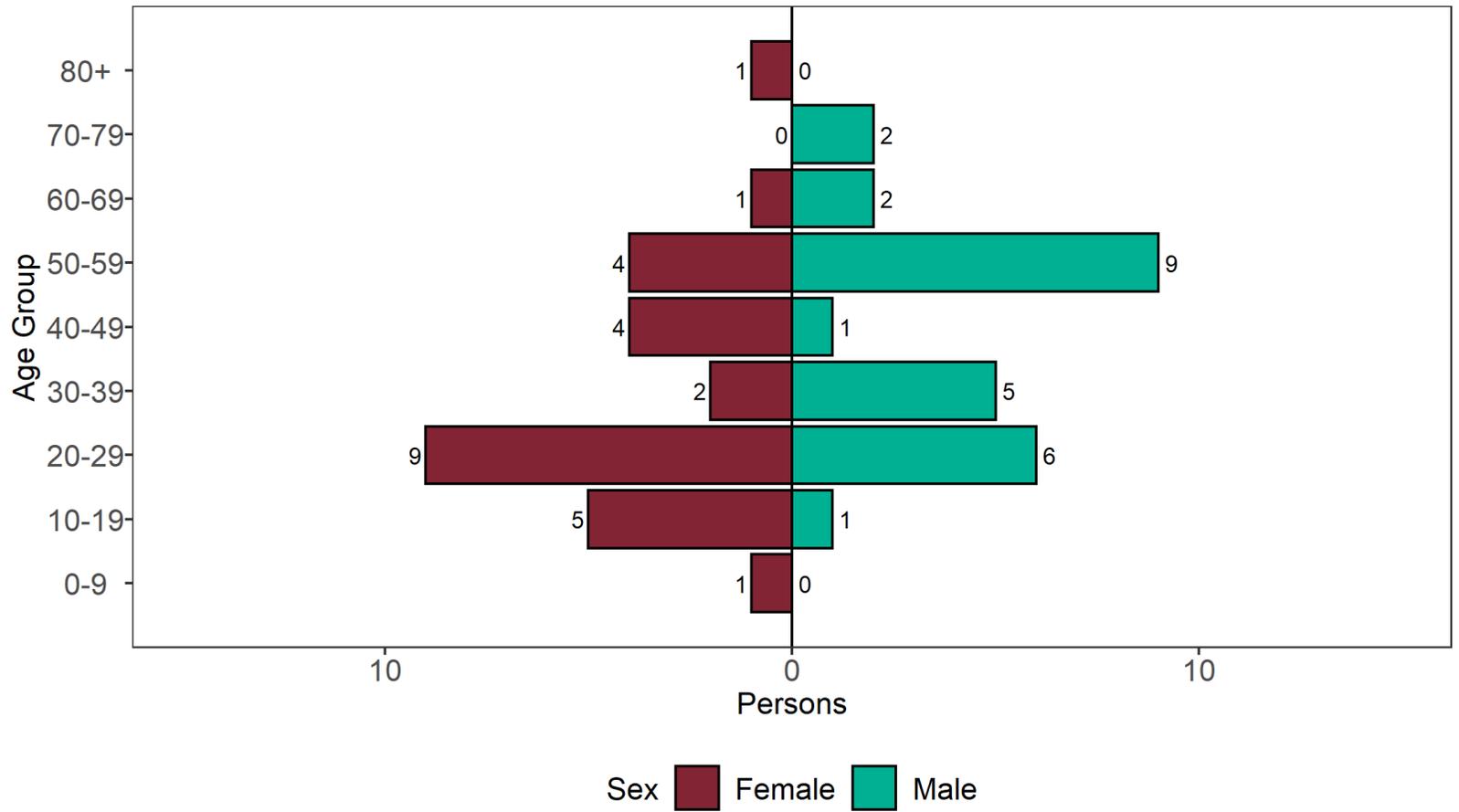


Figure 11. Age-sex pyramid of confirmed (sequencing) Zeta cases as of 14 June 2021

(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 14 June 2021, 5,581 sequences of Eta are listed, from 64 countries or territories, excluding the UK.

Epidemiology

Table 6. Number of confirmed (sequencing) Eta cases, by region of residence as of 14 June 2021

Region	Total case number	Proportion of all cases
East Midlands	10	2.3%
East of England	29	6.6%
London	156	35.4%
North East	5	1.1%
North West	77	17.5%
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	441	-

Figure 12. Confirmed (sequencing) Eta cases by specimen date and region of residence as of 14 June 2021
 Larger plot includes last 60 days only. (Find accessible data used in this graph in [underlying data](#).)

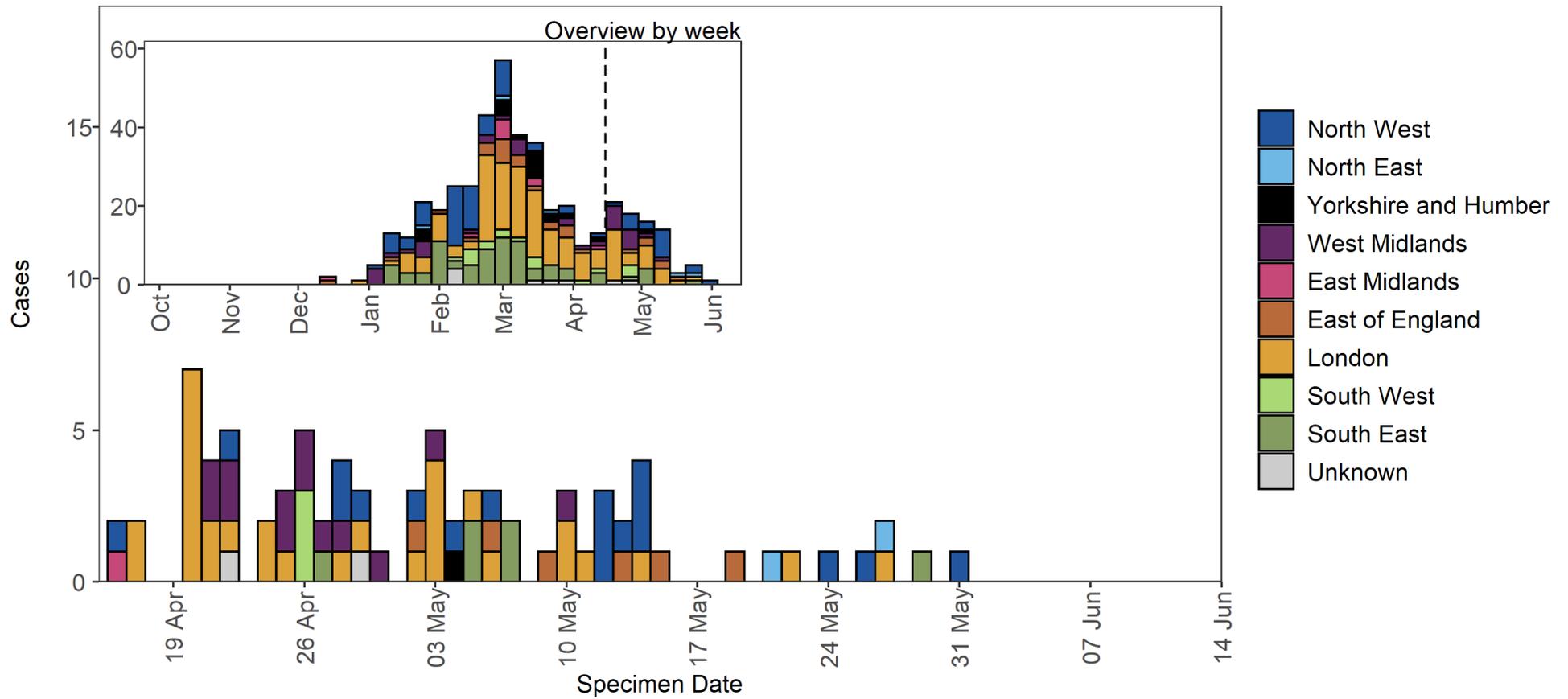
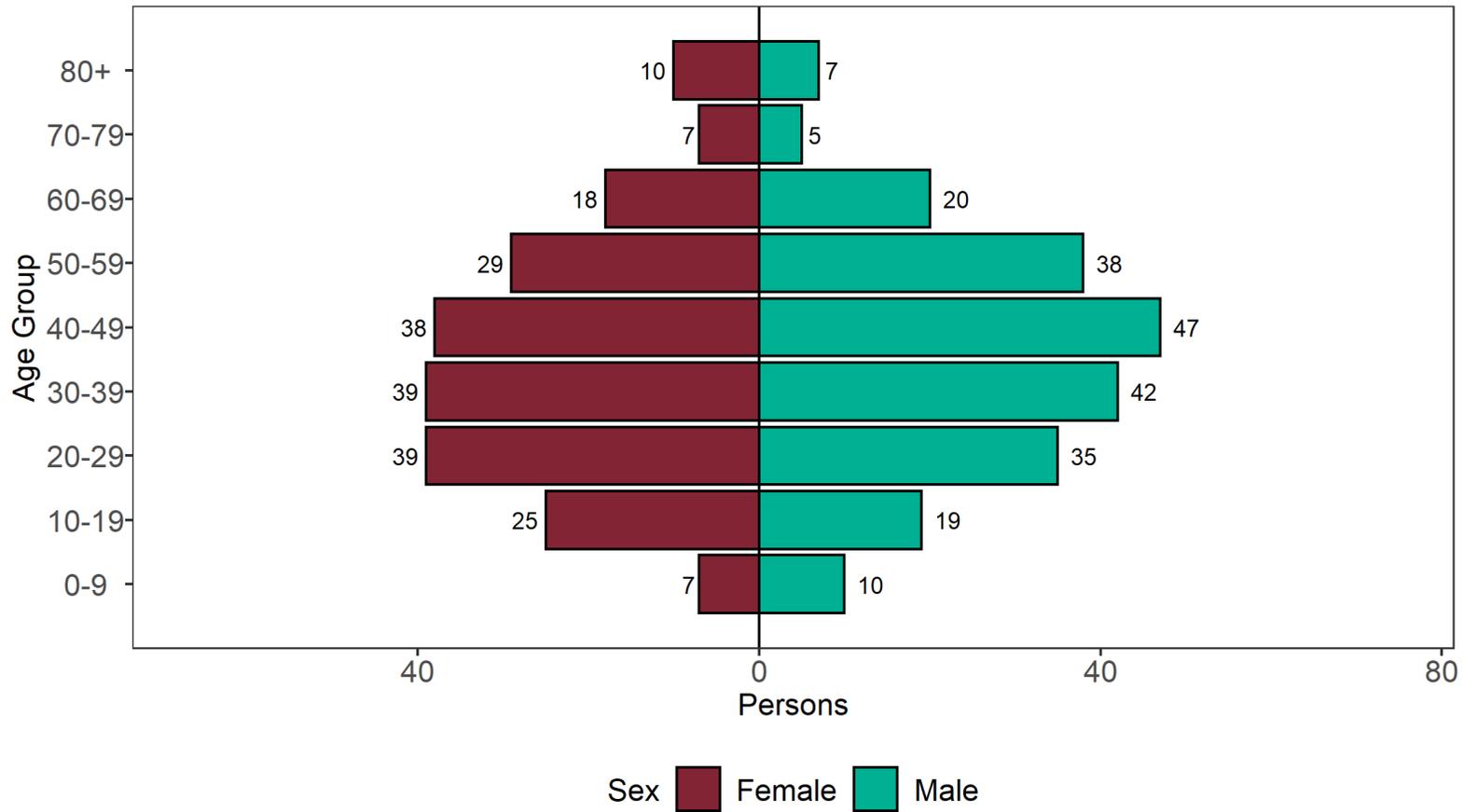


Figure 13. Age-sex pyramid of confirmed (sequencing) Eta cases as of 14 June 2021
(Find accessible data used in this graph in [underlying data](#).)



2 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 14 June 2021, 164 international VUI-21FEB-04 (B.1.1.318) sequences, excluding the UK: Bangladesh (1), Belgium (1), Brazil (1), Cameroon (3), Canada (27), Denmark (1), France (10), Germany (16), Ghana (2), Greece (19), India (2), Italy (16), Nigeria (10), Spain (2), Sweden (4), Switzerland (15), Turkey (1), USA (33).

Epidemiology

Table 7. Number of confirmed (sequencing) VUI-21FEB-04 (B.1.1.318) cases, by region of residence as of 14 June 2021

Region	Total case number	Proportion of all cases
East Midlands	10	3.8%
East of England	33	12.4%
London	101	38.0%
North East	2	0.8%
North West	47	17.7%
South East	45	16.9%
South West	1	0.4%
West Midlands	9	3.4%
Yorkshire and Humber	11	4.1%
Unknown region	7	2.6%
Total	266	-

Figure 14. Confirmed (sequencing) VUI-21FEB-04 (B.1.1.318) cases by specimen date as of 14 June 2021
 Larger plot includes last 60 days only. (Find accessible data used in this graph in [underlying data.](#))

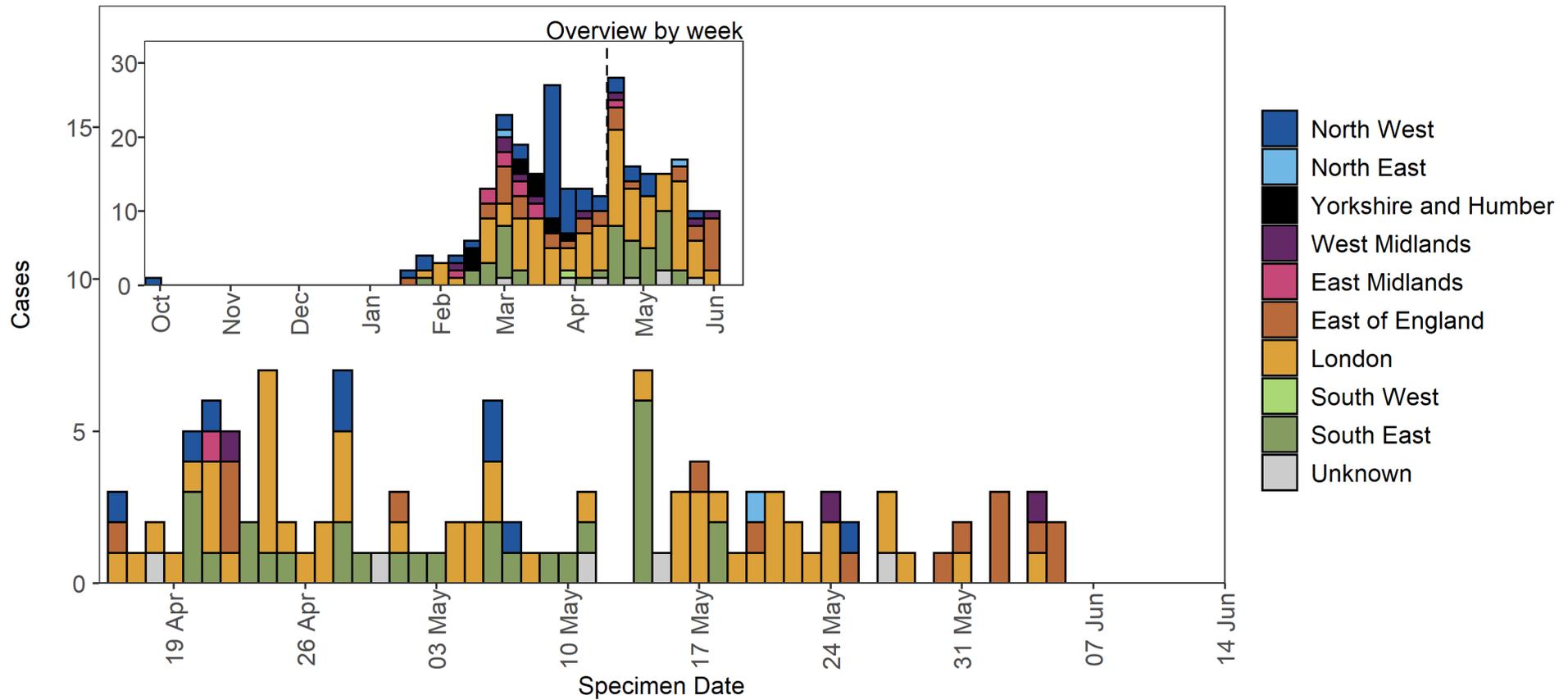
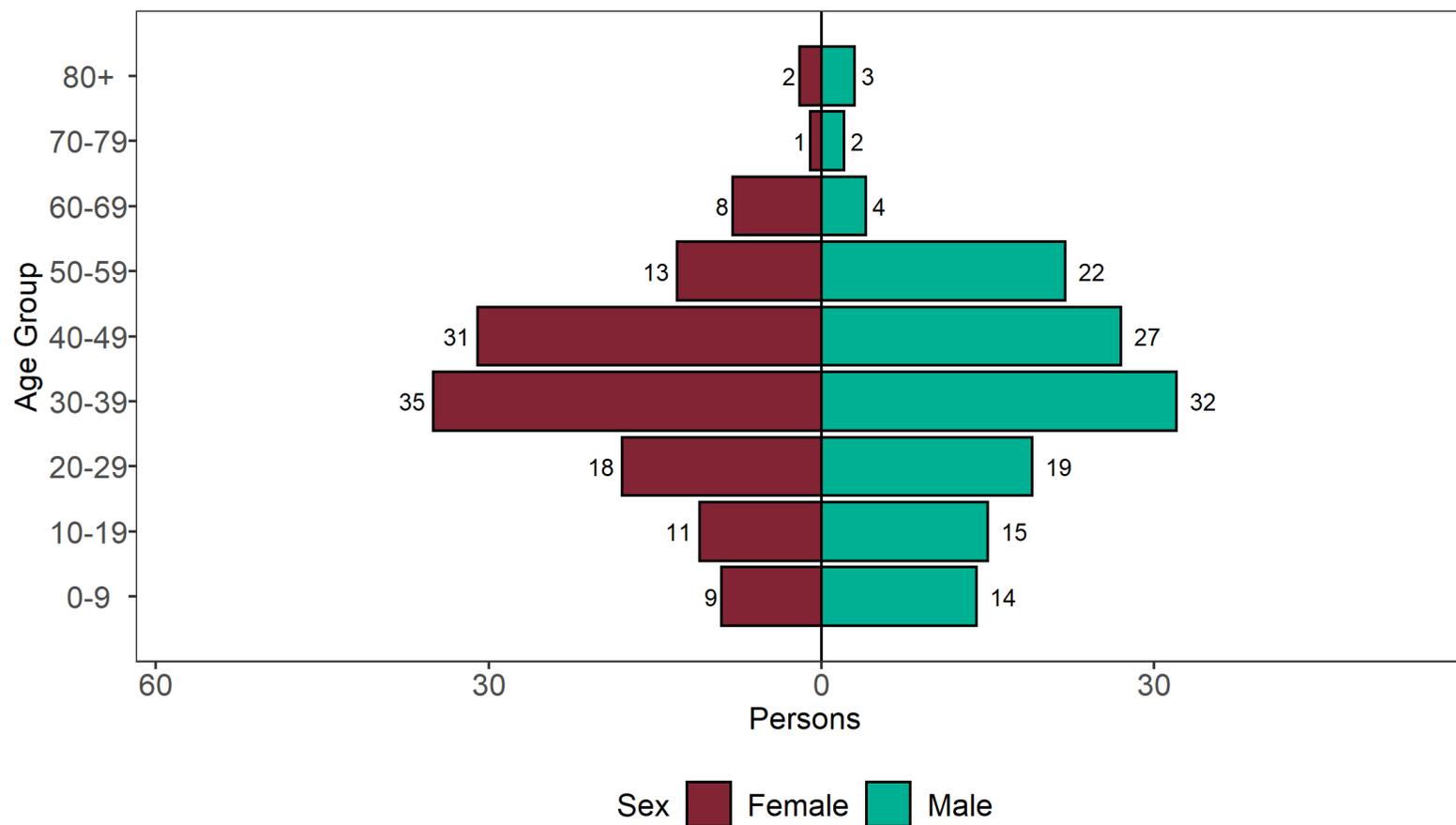


Figure 15. Age-sex pyramid of confirmed (sequencing) VUI-21FEB-04 (B.1.1.318) cases, as of 14 June 2021
(Find accessible data used in this graph in [underlying data.](#))



0 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, 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 14 June 2021, 236 sequences are listed internationally of Theta excluding the UK: Angola (1), Australia (3), China (2), Germany (8), Hong Kong (10), Japan (4), Netherlands (7), New Zealand (3), Norway (2), Philippines (179), Singapore (2), South Korea (1), USA (14).

Epidemiology

Table 8. Number of confirmed (sequencing) Theta cases, by region of residence as of 14 June 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 as of 14 June 2021

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

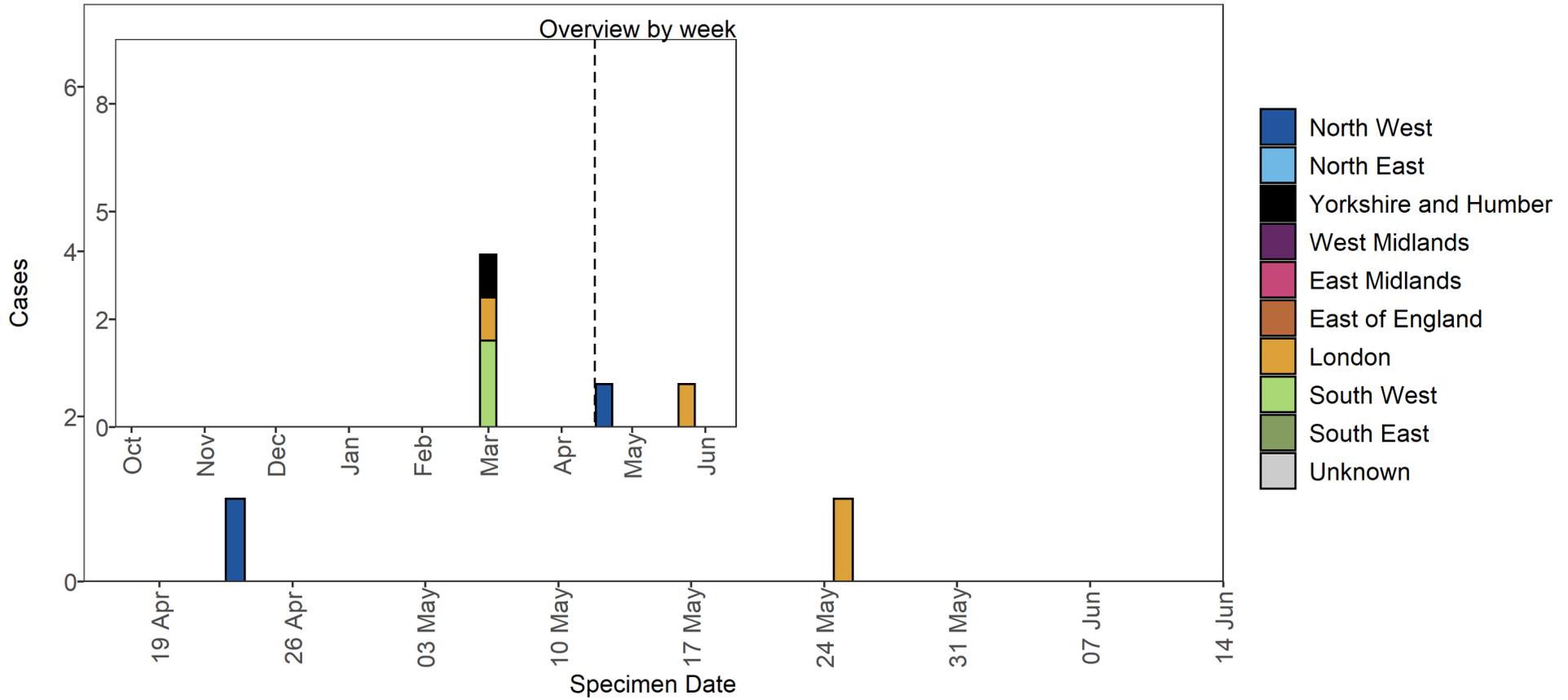
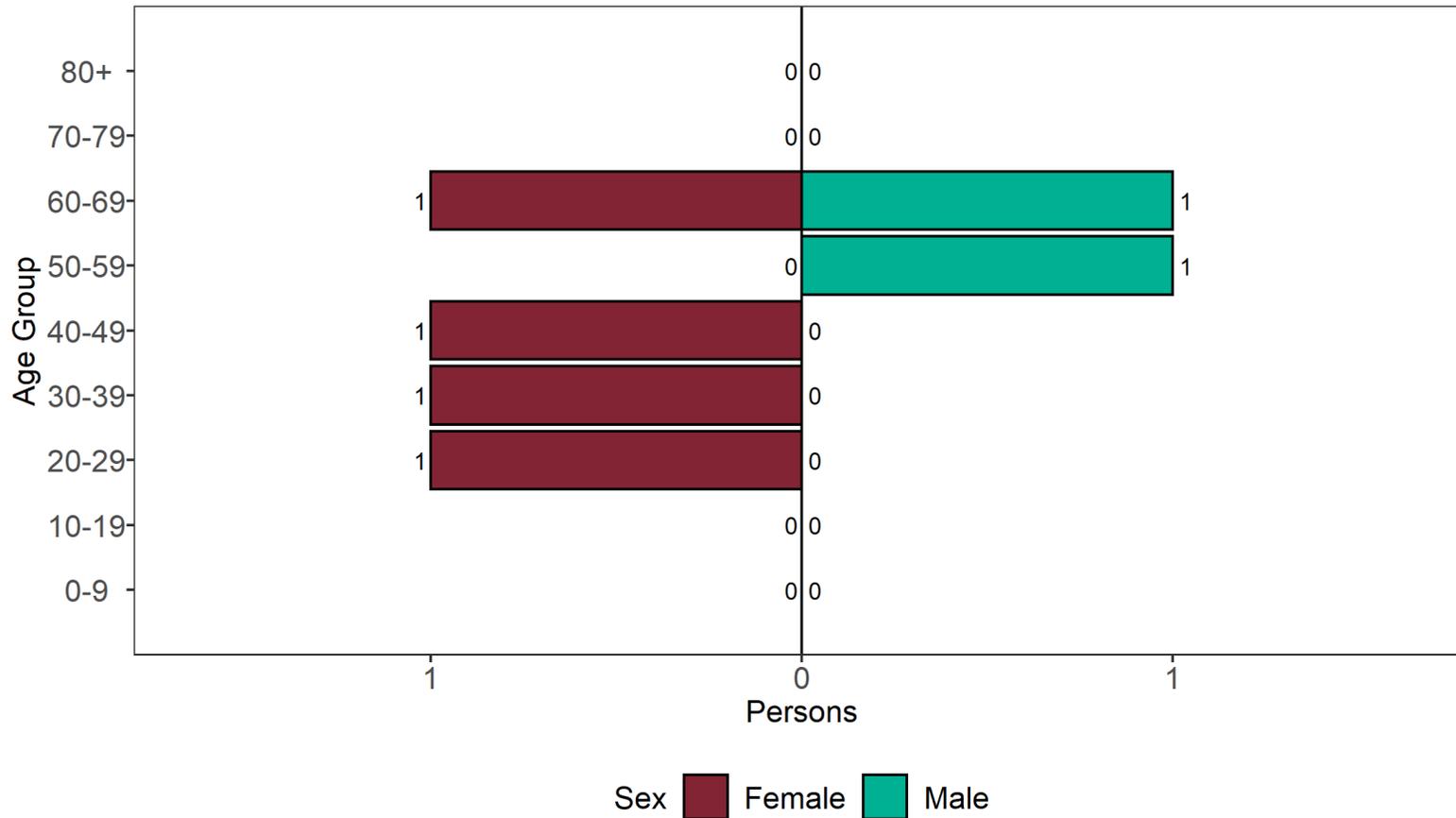


Figure 17. Age-sex pyramid of confirmed (sequencing) Theta cases as of 14 June 2021

(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 14 June 2021, 3,318 Kappa sequences from the following countries (excluding the UK) have been identified in **GISAID**: Angola (1), Australia (95), Austria (1), Bahrain (8), Belgium (10), Canada (63), China (1), Curacao (1), Czech Republic (4), Denmark (27), Finland (1), France (11), Germany (101), Ghana (5), Greece (1), Guadeloupe (2), Hong Kong (9), India (2,433), Ireland (119), Italy (6), Japan (25), Jordan (4), Luxembourg (6), Malaysia (1), Mexico (4), Nepal (3), Netherlands (10), New Zealand (4), Portugal (9), Qatar (3), Saint Martin (2), Singapore (60), Slovakia (1), Slovenia (1), South Africa (1), South Korea (12), Spain (4), Sweden (5), Switzerland (9), Thailand (1), USA (253), Uganda (1).

Epidemiology

Table 9. Number of confirmed (sequencing) Kappa cases, by region of residence as of 14 June 2021

Region	Total case number	Proportion of all cases
East Midlands	48	11.4%
East of England	31	7.3%
London	177	41.9%
North East	5	1.2%
North West	32	7.6%
South East	41	9.7%
South West	13	3.1%
West Midlands	48	11.4%
Yorkshire and Humber	18	4.3%
Unknown region	9	2.1%
Total	422	-

Figure 18. Confirmed (sequencing) Kappa cases by specimen date as of 14 June 2021
 Larger plot includes last 60 days only. (Find accessible data used in this graph in [underlying data](#).)

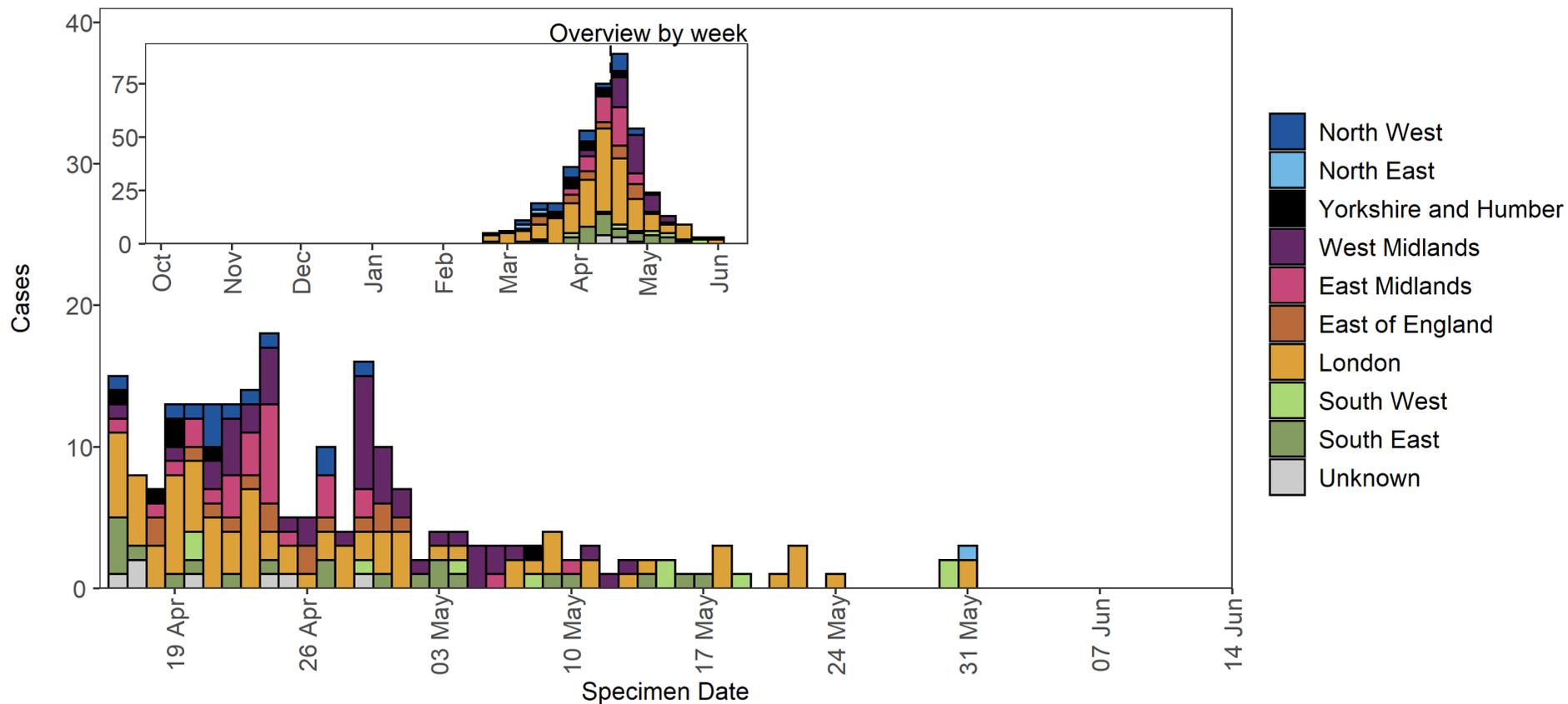
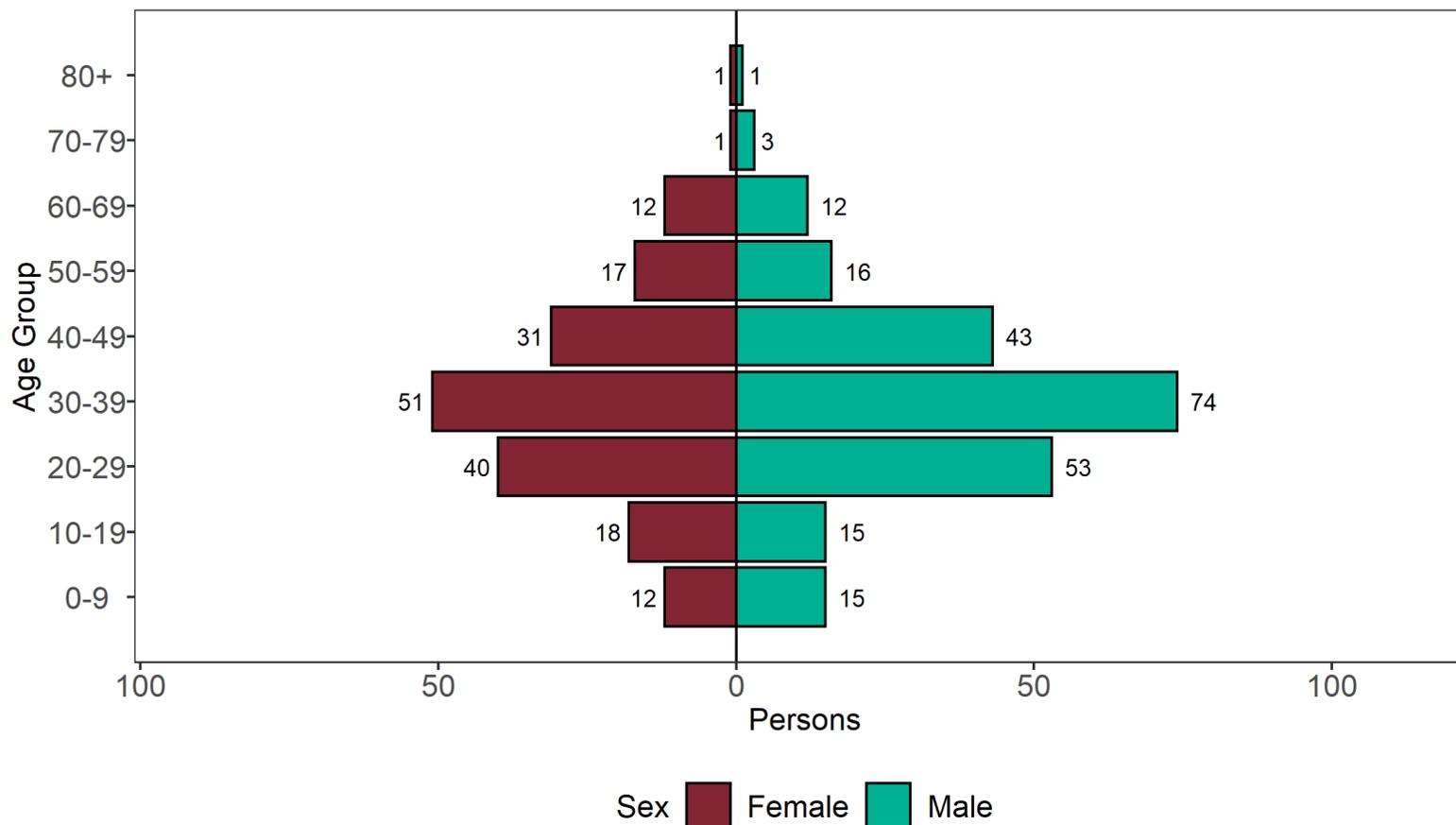


Figure 19. Age-sex pyramid of confirmed (sequencing) Kappa cases as of 14 June 2021
(Find accessible data used in this graph in [underlying data.](#))



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 14 June 2021, 99 sequences from the following countries (excluding the UK) have been identified in GISAID of VUI-21APR-03 (B.1.617.3): India (87), Japan (1), Malawi (7), Russia (2), USA (2).

Epidemiology

Table 10. Number of confirmed (sequencing) VUI-21APR-03 (B.1.617.3) cases, by region of residence as of 14 June 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 14 June 2021
 Larger plot includes last 60 days only. (Find accessible data used in this graph in [underlying data](#).)

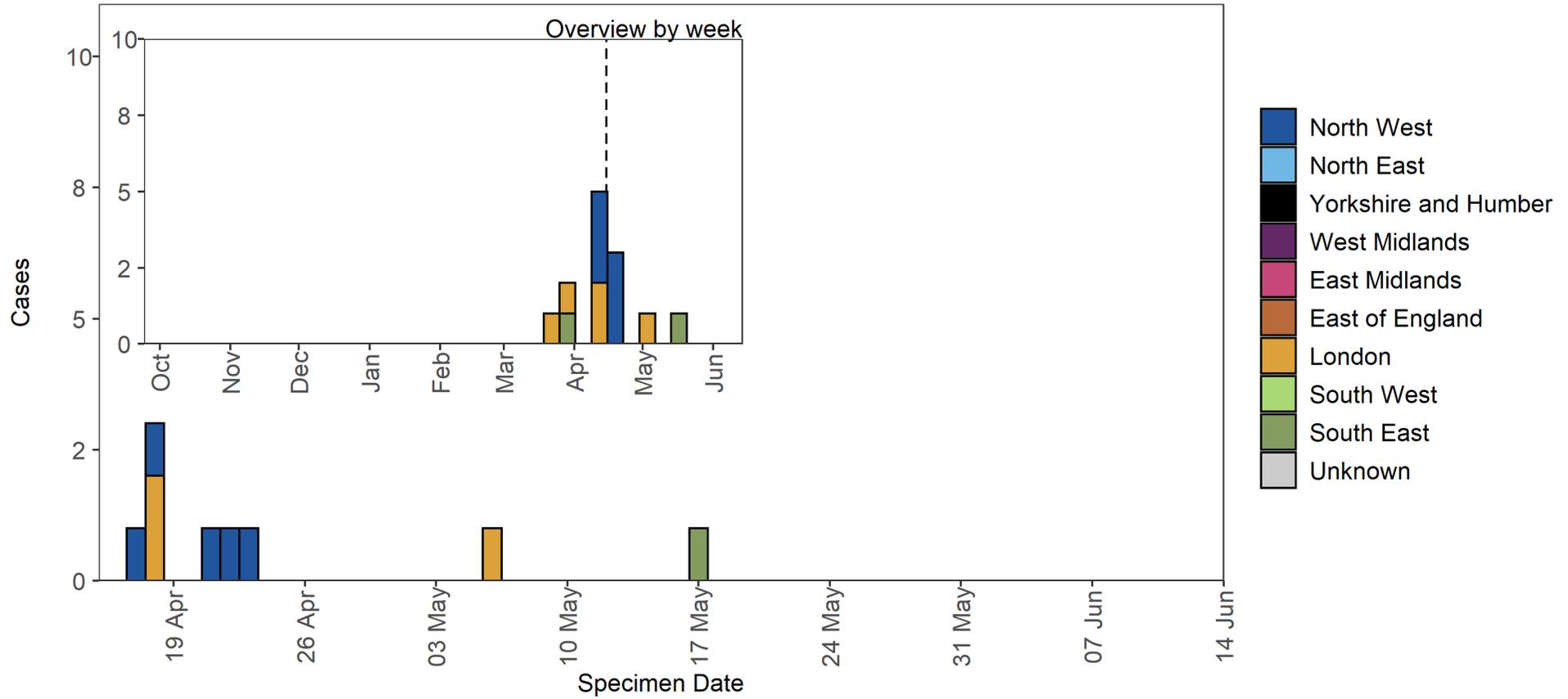
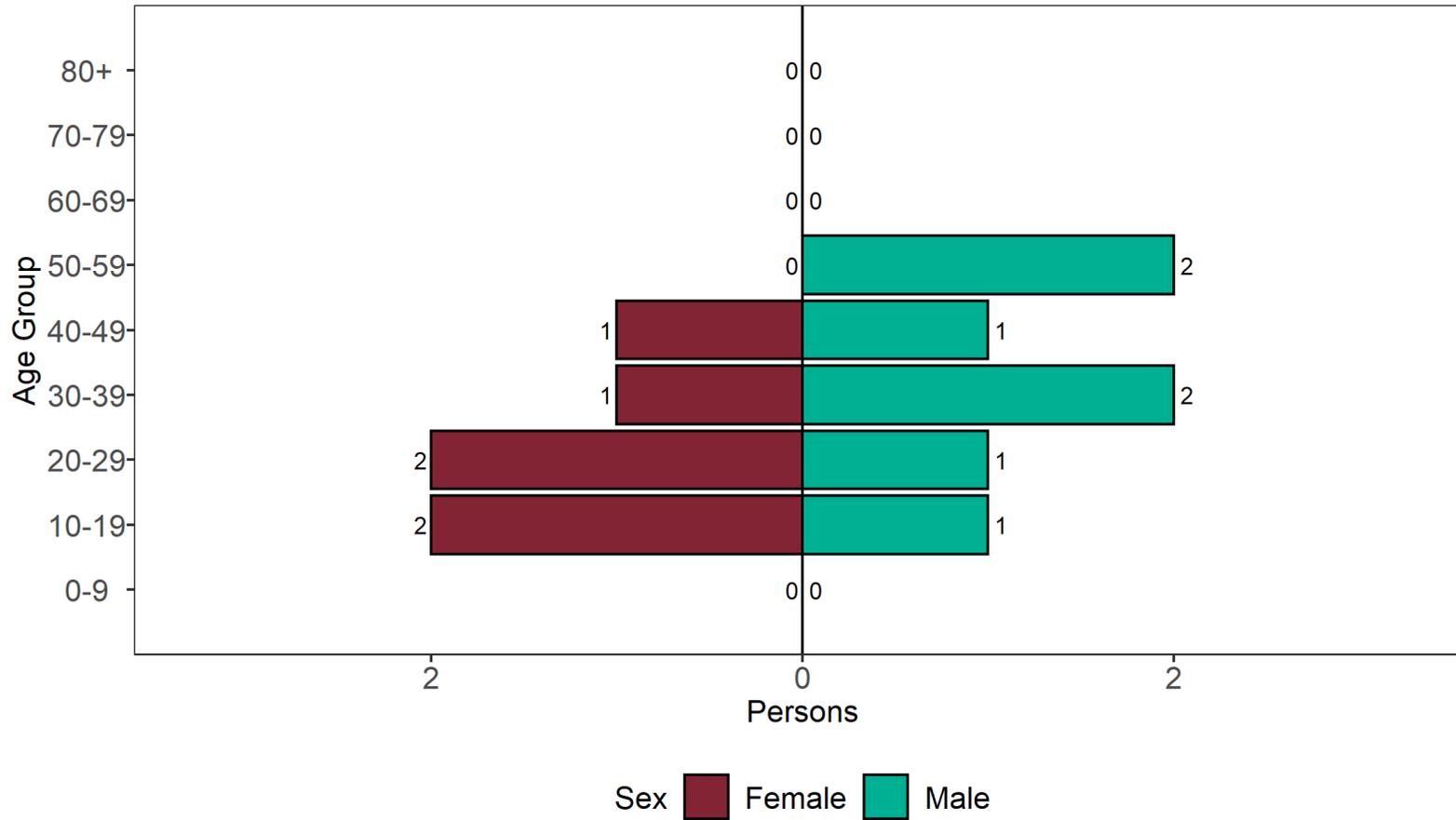


Figure 21. Age-sex pyramid of confirmed (sequencing) VUI-21APR-03 (B.1.617.3) cases as of 14 June 2021
(Find accessible data used in this graph in [underlying data.](#))



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 14 June 2021, 5 sequences of VUI-21MAY-01 (AV.1) from France have been identified on GISAID.

Epidemiology

Table 11. Number of confirmed (sequencing) VUI-21MAY-01 (AV.1) cases, by region of residence as of 14 June 2021

Region	Total case number	Proportion of all cases
East Midlands	6	3.6%
East of England	10	6.0%
London	1	0.6%
North East	1	0.6%
North West	7	4.2%
South East	0	0.0%
South West	0	0.0%
West Midlands	4	2.4%
Yorkshire and Humber	136	81.9%
Unknown region	1	0.6%
Total	166	-

Figure 22. Confirmed (sequencing) VUI-21MAY-01 (AV.1) cases by specimen date as of 14 June 2021. Larger plot includes last 60 days only. (Find accessible data used in this graph in [underlying data](#).)

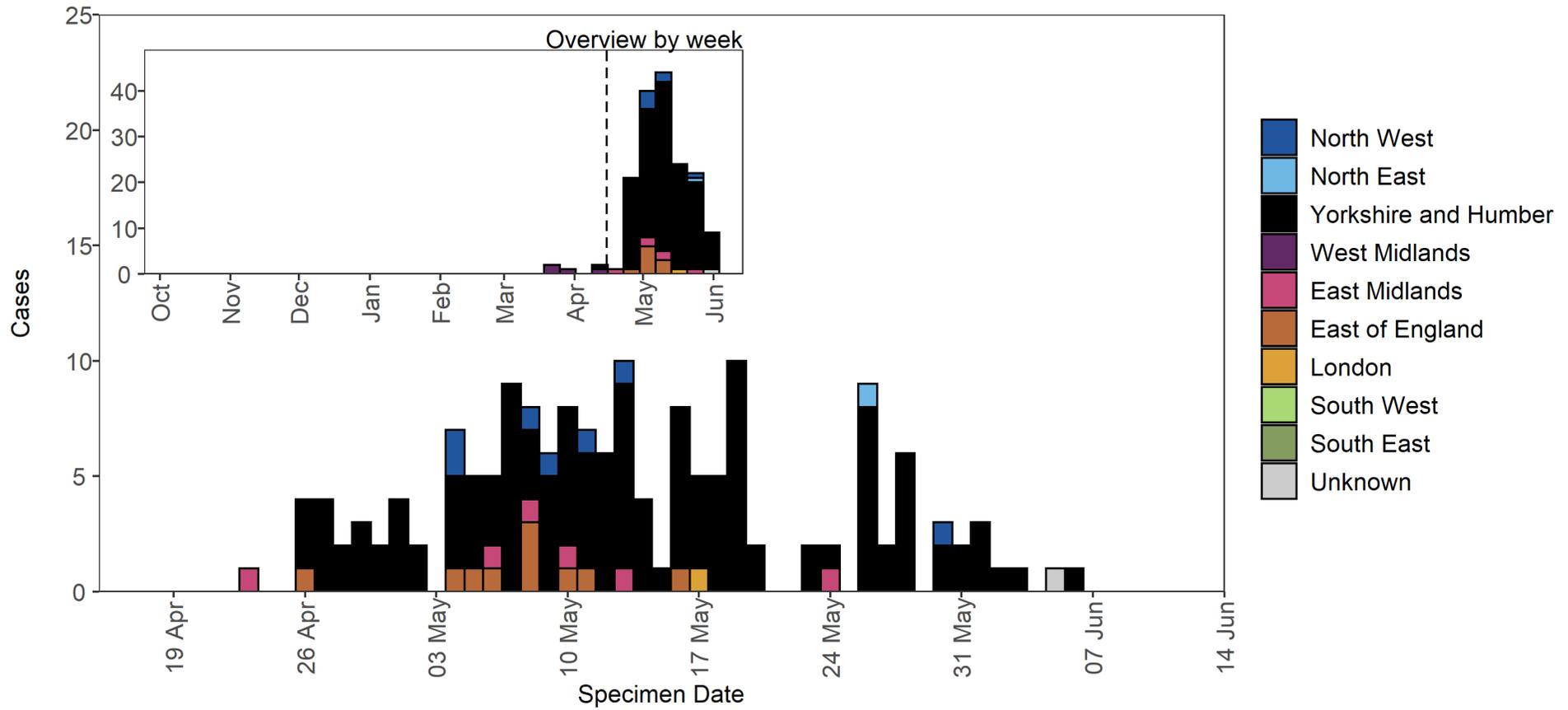
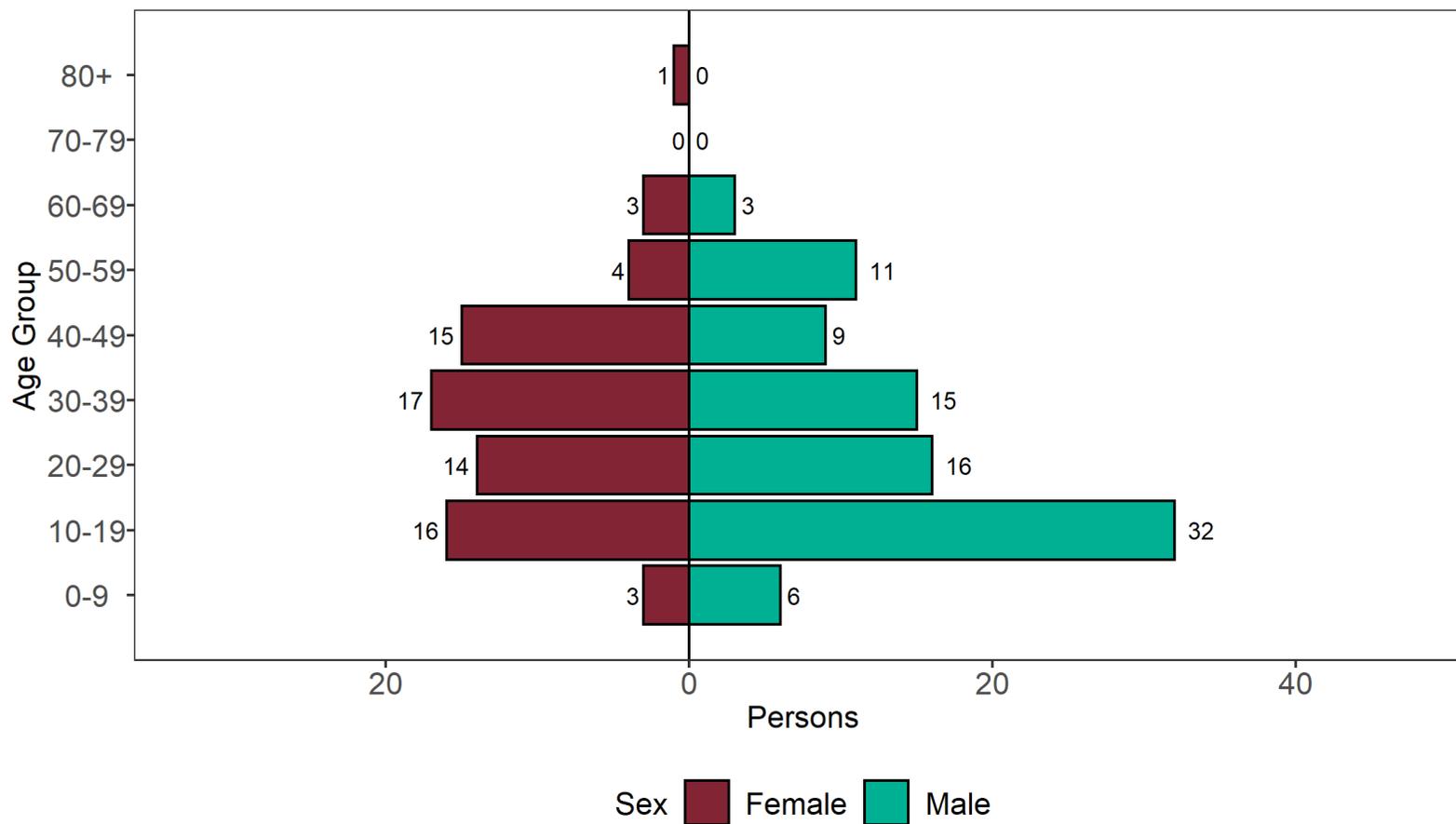


Figure 23. Age-sex pyramid of confirmed (sequencing) VUI-21MAY-01 (AV.1) cases as of 14 June 2021
 (Find accessible data used in this graph in [underlying data.](#))



1 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 14 June 2021, 924 sequences of VUI-21MAY-02 (C.36.3) from 41 countries have been identified on GISAID

Epidemiology

Table 12. Number of confirmed (sequencing) VUI-21MAY-02 (C.36.3) cases, by region of residence as of 14 June 2021

Region	Total case number	Proportion of all cases
East Midlands	6	4.8%
East of England	19	15.1%
London	37	29.4%
North East	1	0.8%
North West	13	10.3%
South East	10	7.9%
South West	4	3.2%
West Midlands	9	7.1%
Yorkshire and Humber	26	20.6%
Unknown region	1	0.8%
Total	126	-

Figure 24. Confirmed and provision genotyping VUI-21MAY-02 (C.36.3) cases by specimen date and region of residence as of 14 June 2021

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

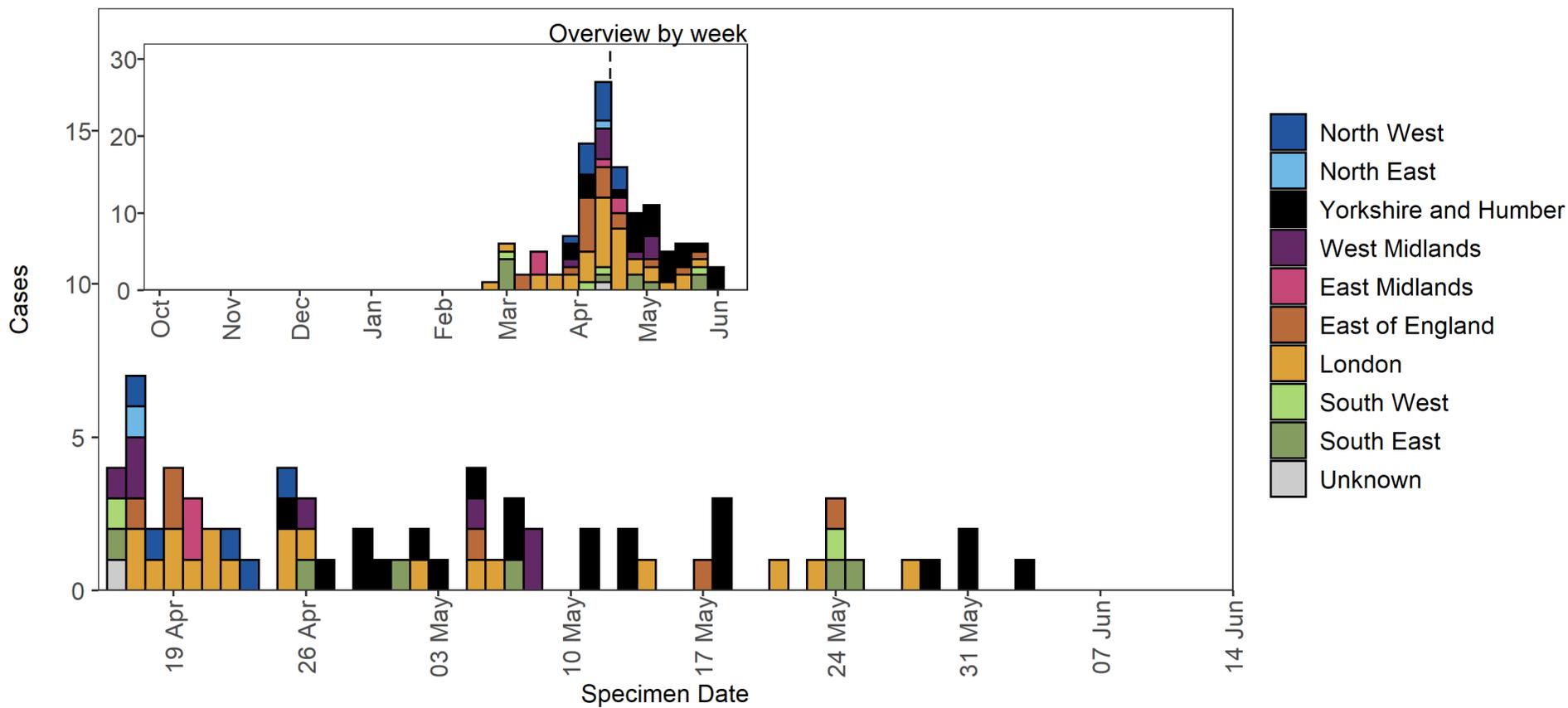
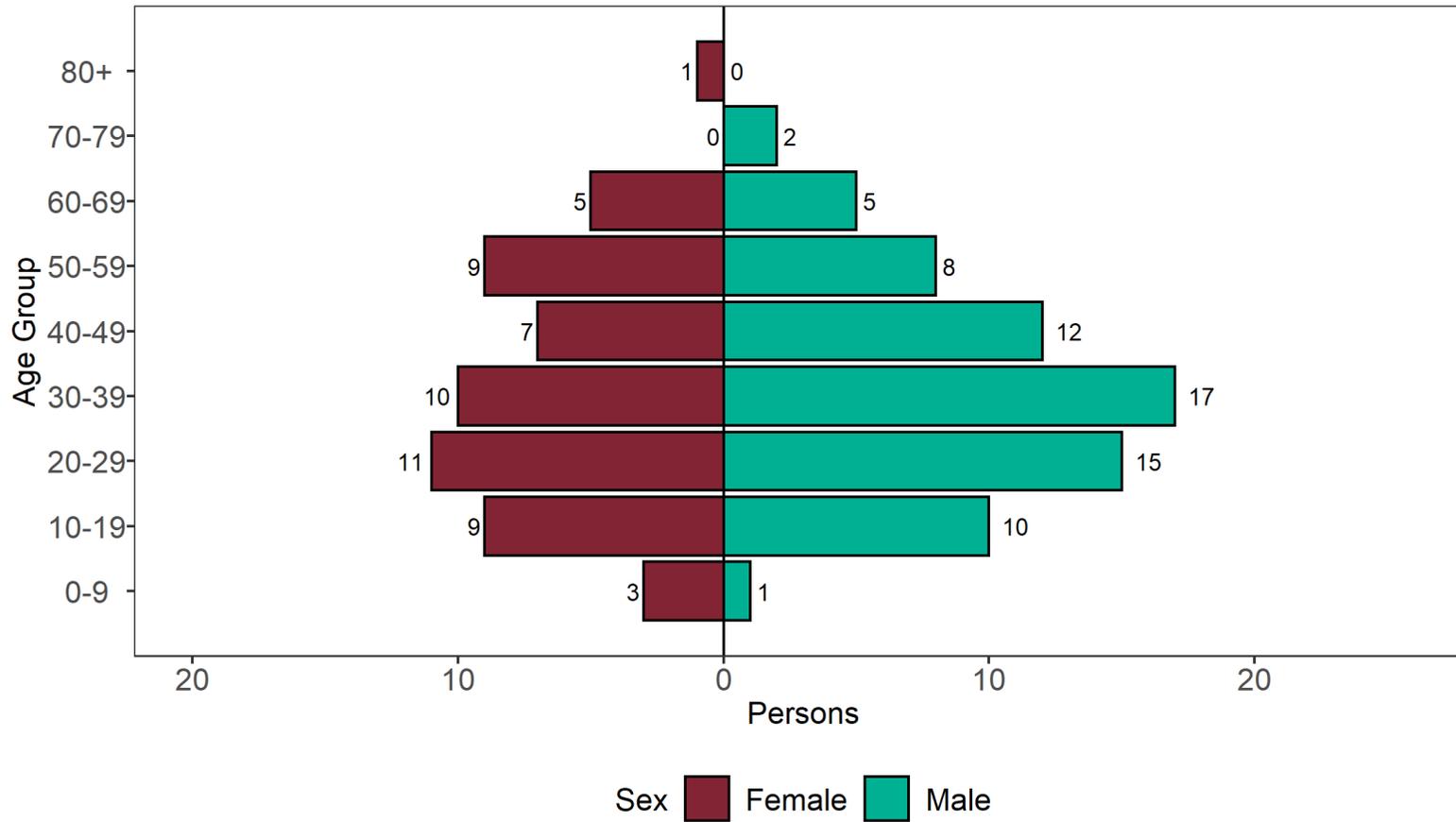


Figure 25. Age-sex pyramid of confirmed (sequencing) VUI-21MAY-02 (C.36.3) cases as of 14 June 2021
(Find accessible data used in this graph in [underlying data.](#))



1 cases excluded where sex or age not reported

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

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

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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