Public Health
England

Protecting and improving the nation's health

SARS-CoV-2 variant data update, England

Version 5

11 June 2021

This briefing provides an update on previous data located in technical and variant data update briefings and updates up to 3 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 15.

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

Table 1. Variant lineage and designation as of 7 June 2021 (provisionally extinct variants removed)

World Health Organization nomenclature as of 7 June 2021	Lineage	Designation	First detected in sequence from	Status
Alpha	B.1.1.7	VOC-20DEC-01	UK	VOC
Beta	B.1.351	VOC-20DEC-02	South Africa	VOC
Gamma	P.1	VOC-21JAN-02	Japan ex Brazil	VOC
	B.1.1.7 with E484K	VOC-21FEB-02	UK	VOC (non UK)*
Delta	B.1.617.2	VOC-21APR-02	India	VOC
Zeta	P.2	VUI-21JAN-01	Brazil	VUI
Eta	B.1.525	VUI-21FEB-03	UK	VUI
	B.1.1.318	VUI-21FEB-04	UK	VUI
Theta	P.3	VUI-21MAR-02	Philippines	VUI
Kappa	B.1.617.1	VUI-21APR-01	India	VUI
	B.1.617.3	VUI-21APR-03	India	VUI
	AV.1	VUI-21MAY-01	UK	VUI
	C.36.3	VUI-21MAY-02	Thailand ex Egypt	VUI
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

World Health Organization nomenclature as of 7 June 2021	Lineage	Designation	First detected in sequence from	Status
	B.1.214.2			Monitoring
	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

[*] VUI-21FEB-01 (A.23.1 with E484K) has not been detected in England since 23 February and internationally since 17 January 2021. It is designated provisionally extinct and has been removed from the table.

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.

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 7 June 2021, 569,495 sequences of Alpha, excluding the UK, are listed from 135 countries or territories on GISAID.

Epidemiology

Table 2. Number of confirmed (sequencing) and probable (genotyping) cases of Alpha by region of residence as of 7 June 2021

Region	Confirmed (sequencing) case number	Probable (genotyping) case number[1]	Total case number	Case proportion	Proportion of travellers among cases
East Midlands	15,739	468	16,207	7.3%	0%
East of England	19,467	164	19,631	8.9%	0%
London	38,717	751	39,468	17.9%	0%
North East	14,503	114	14,617	6.6%	0%
North West	41,459	1,645	43,104	19.5%	0%
South East	23,542	111	23,653	10.7%	0%
South West	7,863	48	7,911	3.6%	0%
West Midlands	18,056	1,269	19,325	8.7%	0%
Yorkshire and Humber	34,956	857	35,813	16.2%	0%
Unknown region	1,258	22	1,280	0.6%	0%
Total	215,560	5,449	221,009	-	0%

[1] Calculated as a proportion of all cases, including those with unknown or pending travel status. Genotyping 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 region of residence and specimen date as of 7 June 2021
(Find accessible data used in this graph in underlying data.)

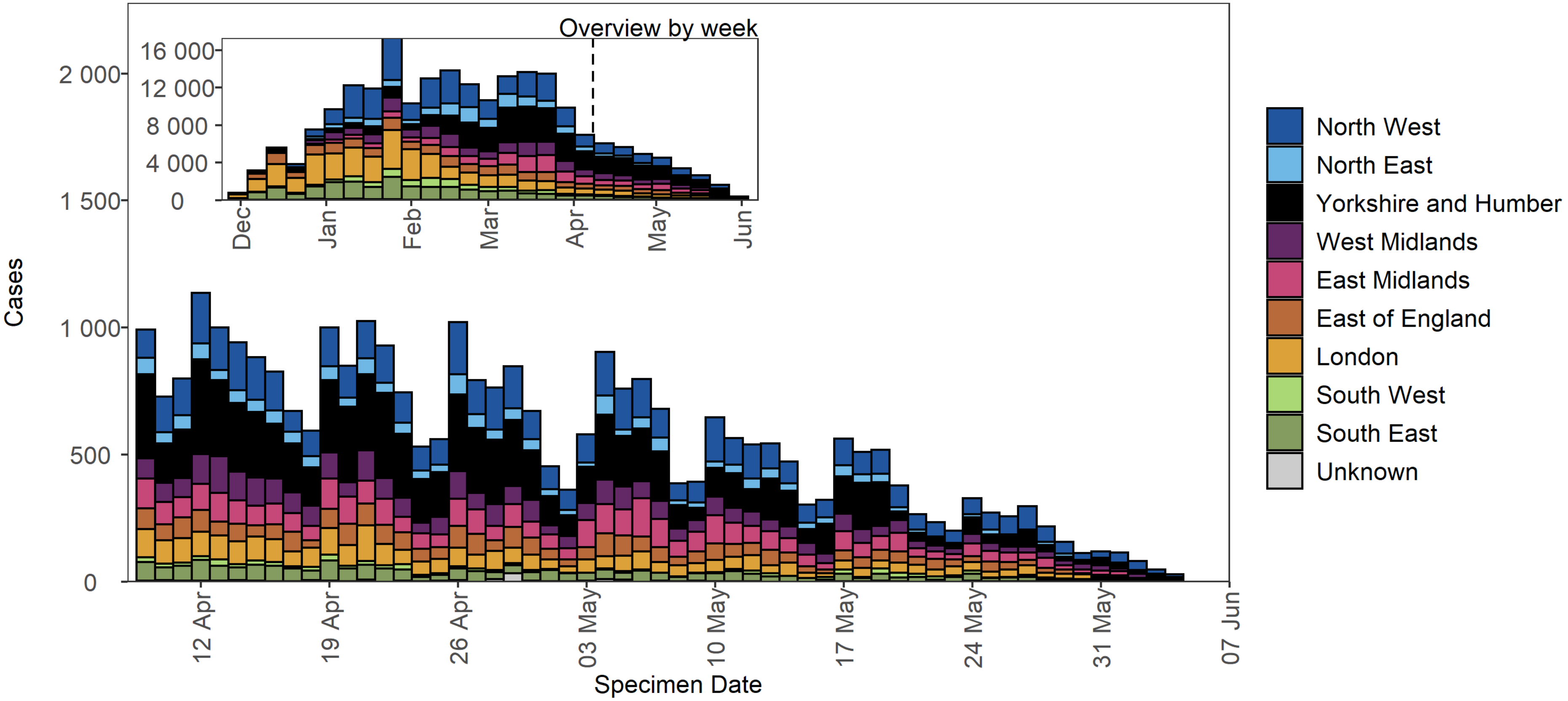


Figure 2. Confirmed (sequencing) and probable (genotyping) Alpha cases by specimen date and detection method as of 7 June 2021

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

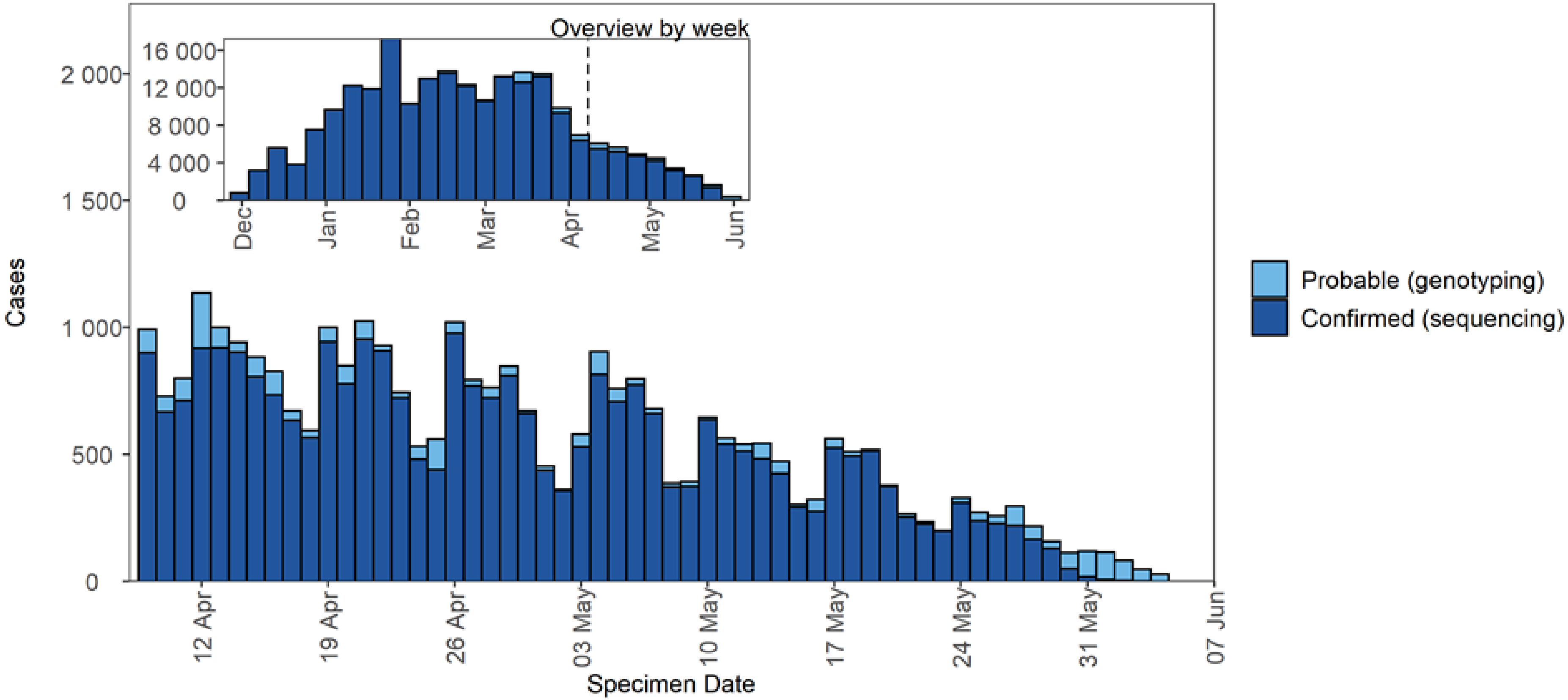
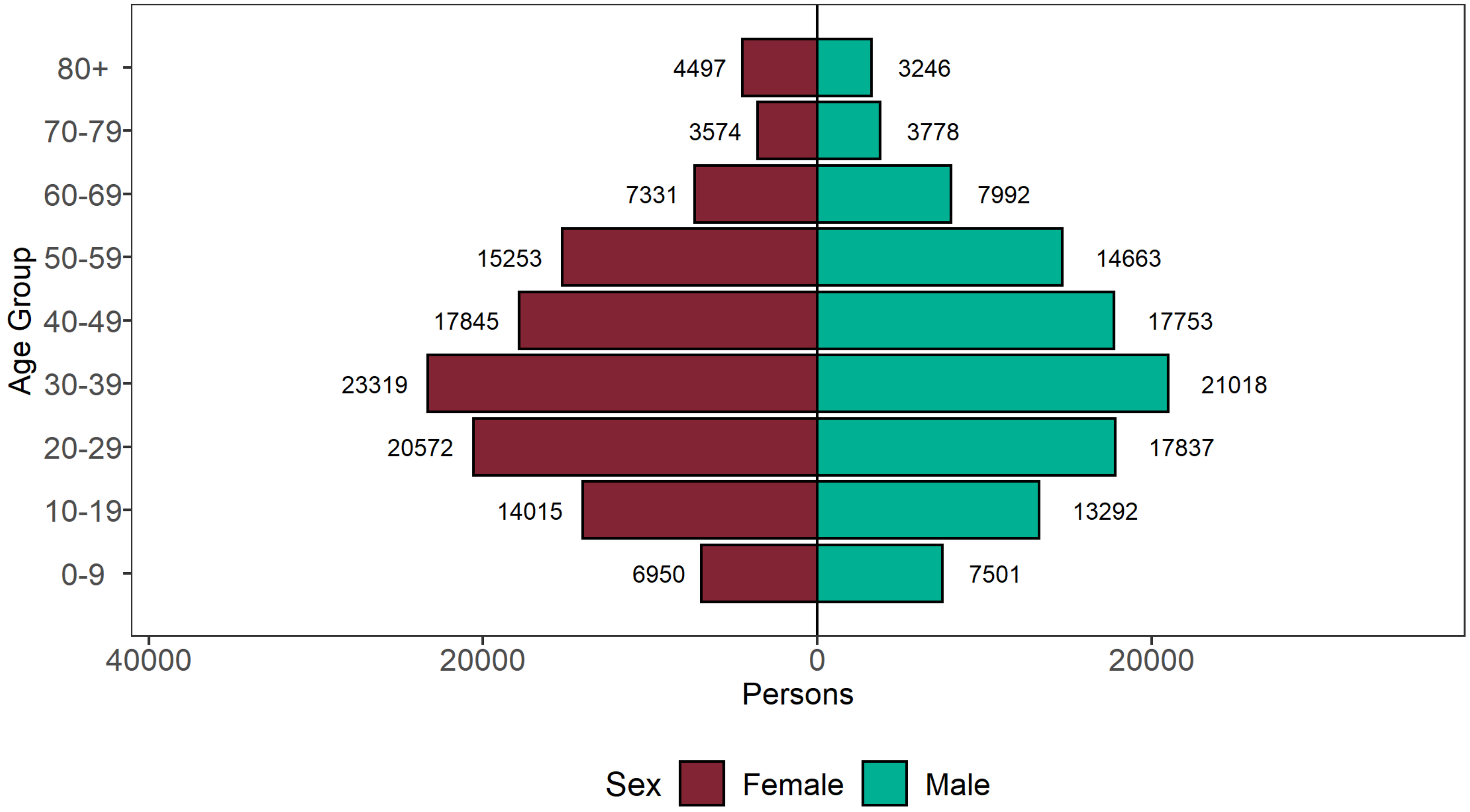


Figure 3. Age-sex pyramid of confirmed (sequencing) and probable (genotyping) Alpha cases as of June 7 2021
(Find accessible data used in this graph in underlying data.)



573 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 7 June 2021, 20,588 sequences of Beta, are listed from 95 countries or territories excluding the UK.

Epidemiology

Table 4. Confirmed (sequencing) and probable (sequencing or genotyping) Beta cases, by region of residence as of 7 June 2021

Region	Confirmed (sequencing) case number	Probable (genotyping) case number	Total case number	Case proportion[1]	Cases that have travelled	Proportion of travellers among cases
East Midlands	46	1	47	5.2%	28	59.6%
East of England	79	2	81	9.0%	45	55.6%
London	391	24	415	45.9%	177	42.7%
North East	13	7	20	2.2%	6	30%
North West	80	8	88	9.7%	32	36.3%
South East	103	2	105	11.6%	66	62.9%
South West	30	1	31	3.4%	17	54.8%
West Midlands	64	0	64	7.1%	26	40.6%
Yorkshire and Humber	31	2	33	3.6%	20	60.6%
Unknown region	21	0	21	2.3%	2	9.5%
Total	858	47	905	-	419	46.2%

[1] Calculated as a proportion of all cases, including those with unknown or pending travel status.
*Includes one probable sequencing case; all others probable genotyping.

Figure 4. Confirmed (sequencing) and probable (genotyping) Beta cases by region of residence and specimen date as of 7 June 2021

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

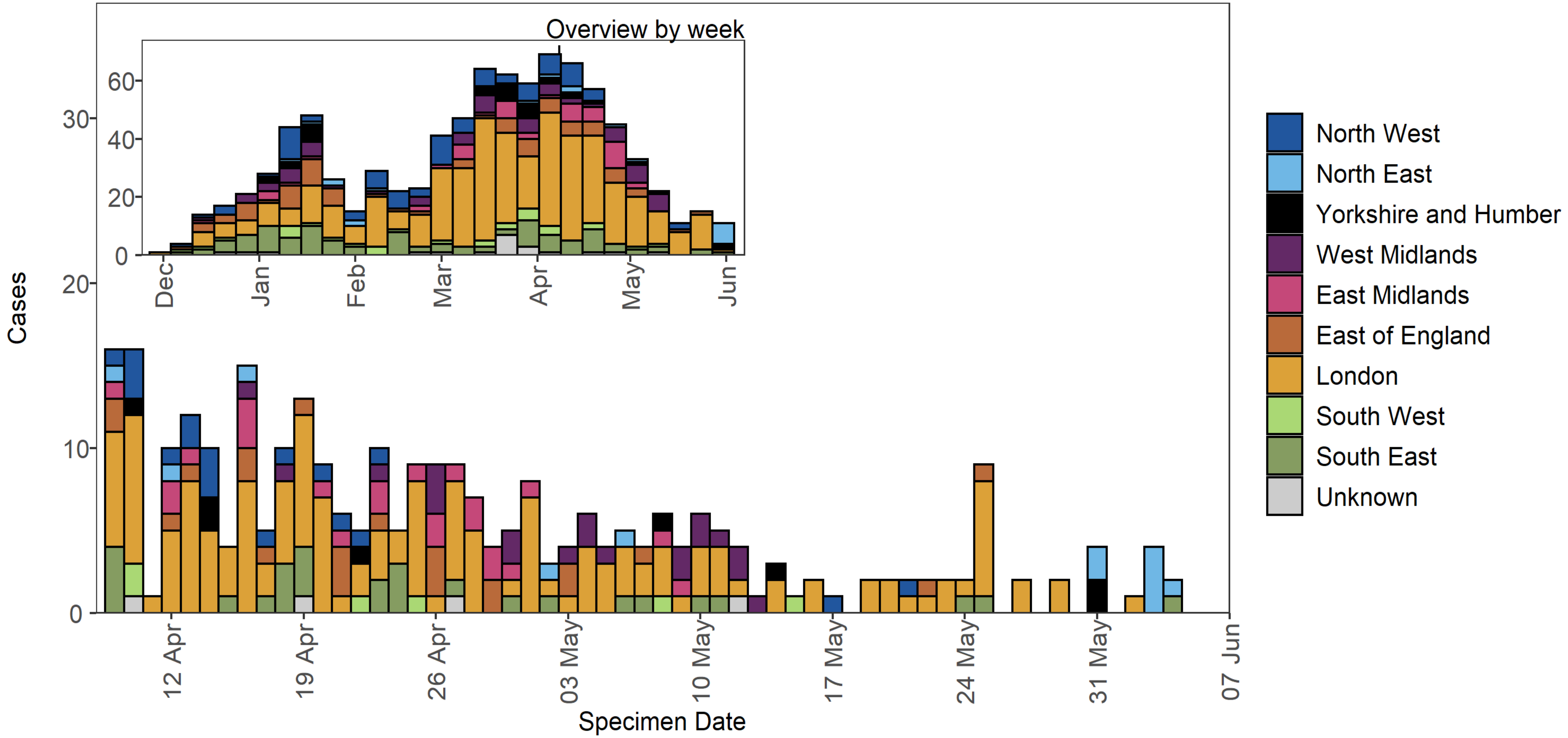


Figure 5. Confirmed (sequencing) and probable (genotyping) Beta cases by specimen date and detection method as of 7 June 2021

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

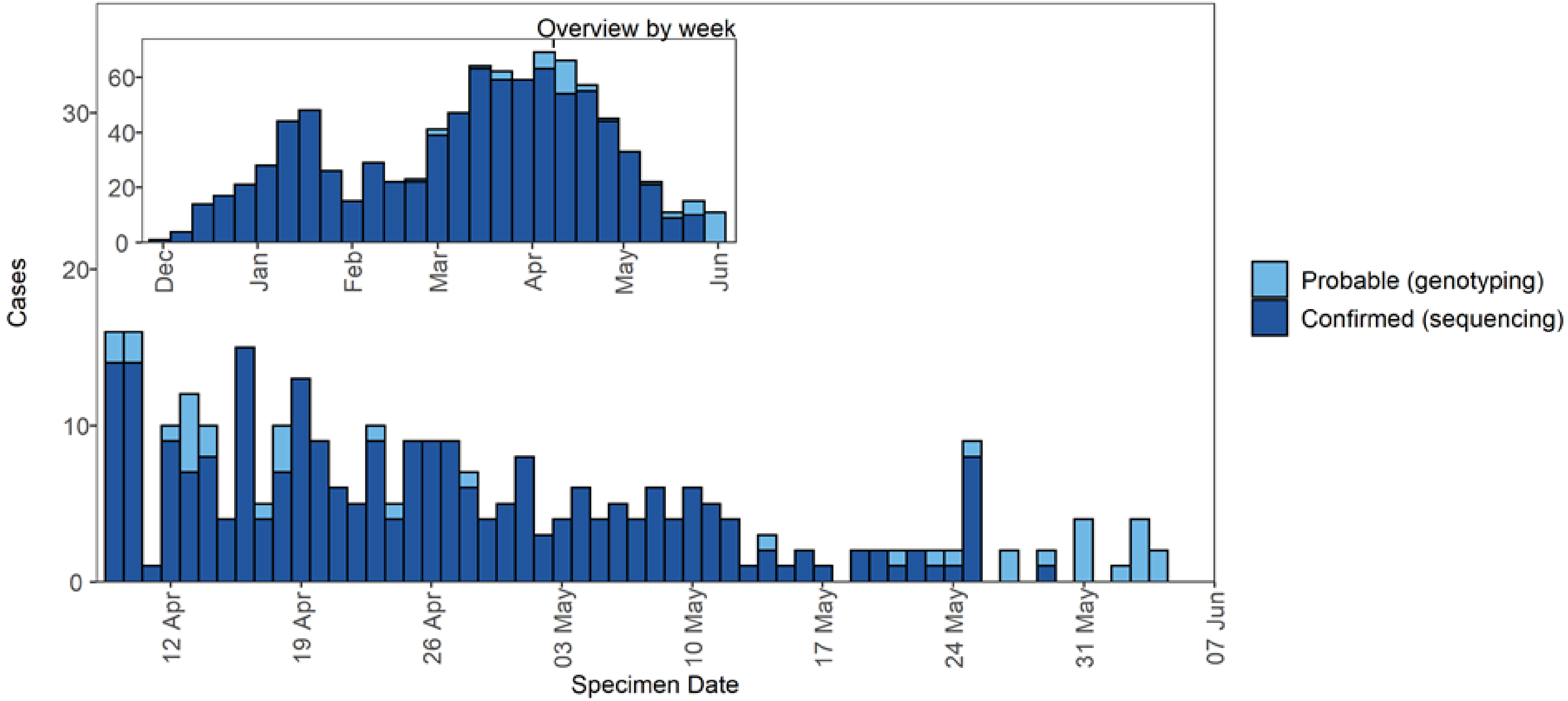


Figure 6. Travel data for confirmed (sequencing) and probable (genotyping) Beta cases by specimen date as of 7 June 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)

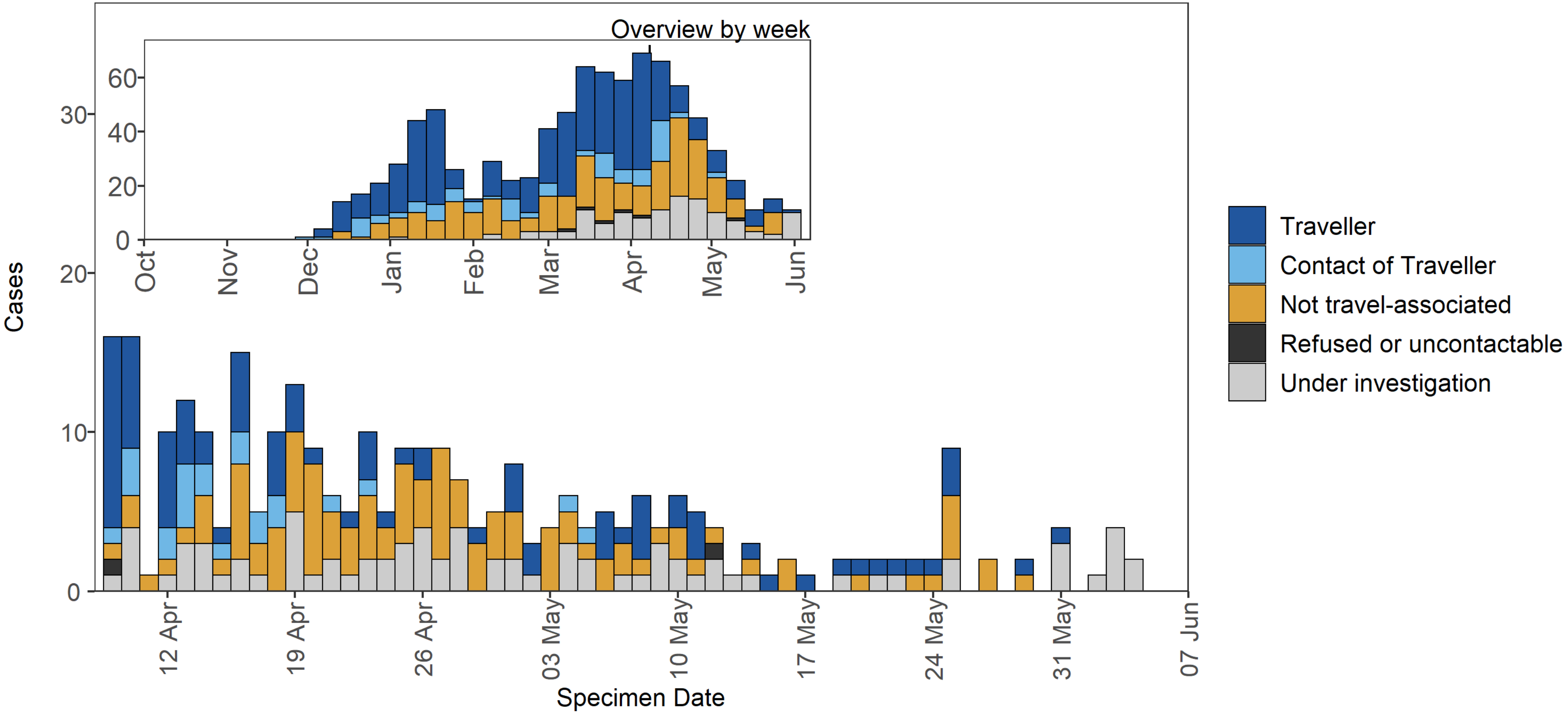
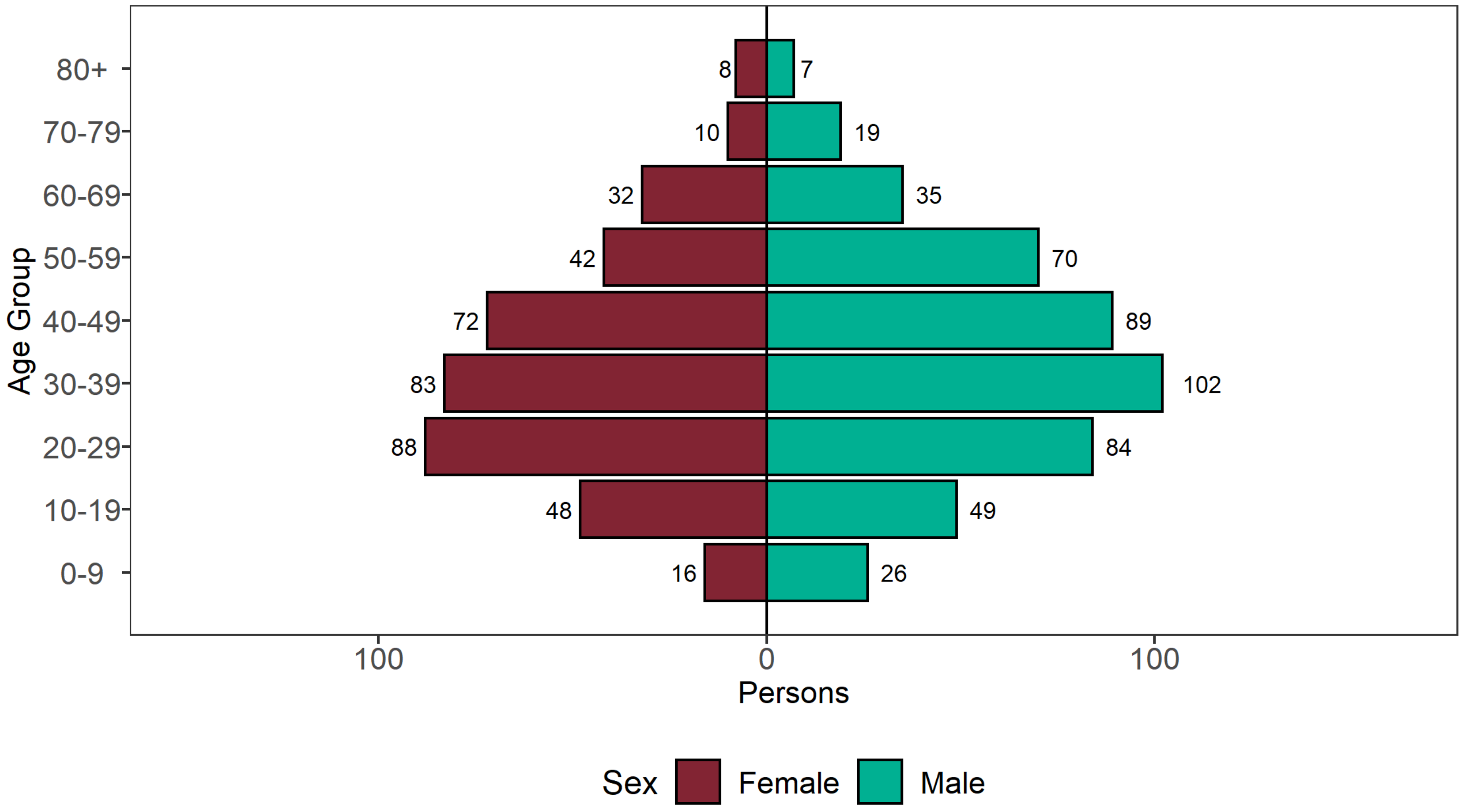


Figure 7. Age-sex pyramid of confirmed (sequencing) and probable (genotyping) Beta cases as of June 7 2021
(Find accessible data used in this graph in underlying data.)



14 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 7 June 2021, 28,217 sequences (excluding the UK) of Gamma from 53 countries.

Epidemiology

Table 5. Number of confirmed (sequencing) and probable (genotyping) cases Gamma, by region of residence as of 7 June 2021

Region	Confirmed (sequencing) case number	Probable (genotyping) case number	Total case number	Case proportion[1]	Cases that have travelled	Proportion of travellers among cases
East Midlands	3	0	3	1.5%	2	66.7%
East of England	13	0	13	6.7%	8	61.5%
London	84	32	116	59.5%	38	32.8%
North East	0	0	0	0.0%	0	0%
North West	4	3	7	3.6%	2	28.6%
South East	27	0	27	13.8%	8	29.6%
South West	9	2	11	5.6%	5	45.5%
West Midlands	6	0	6	3.1%	1	16.7%
Yorkshire and Humber	2	4	6	3.1%	1	16.7%
Unknown region	6	0	6	3.1%	3	50%
Total	154	41	195	-	68	34.9%

[1] Calculated as a proportion of all cases, including those with unknown or pending travel status.

Figure 8. Confirmed (sequencing) and probable (genotyping) Gamma cases by region of residence and specimen date as of 7 June 2021

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

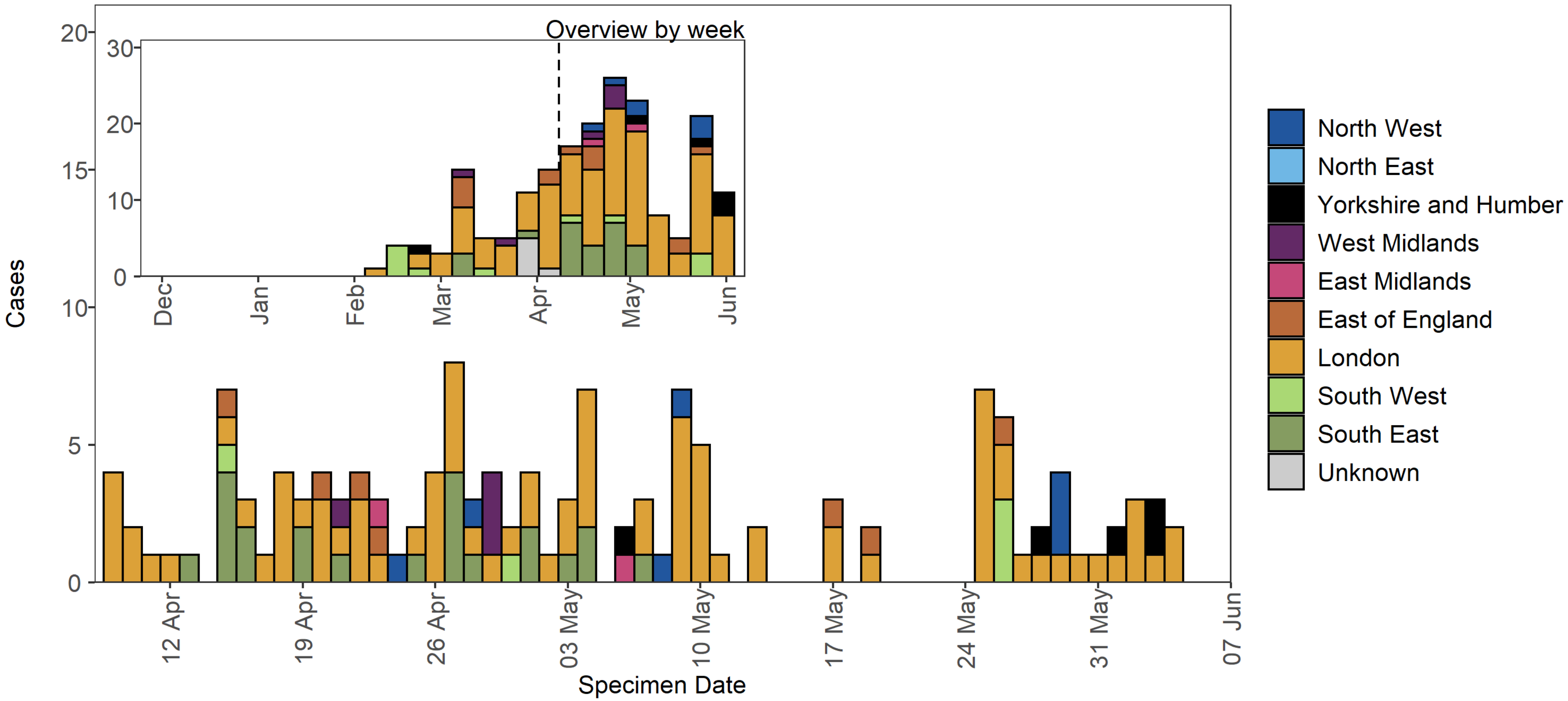


Figure 9. Confirmed (sequencing) and probable (genotyping) Gamma cases by specimen date and detection method as of 7 June 2021

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

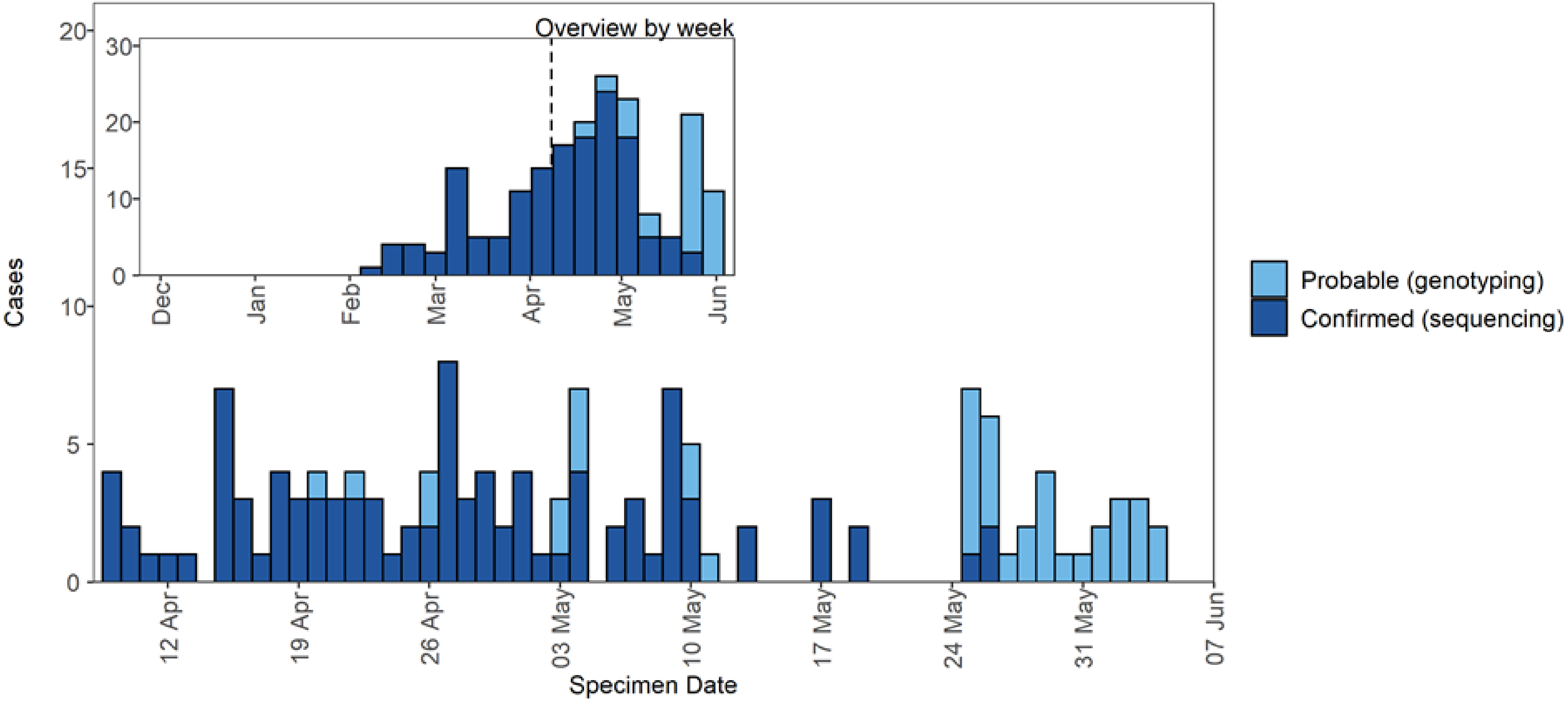


Figure 10. Travel data for confirmed (sequencing) and probable (genotyping) Gamma cases by specimen date as of 7 June 2021

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

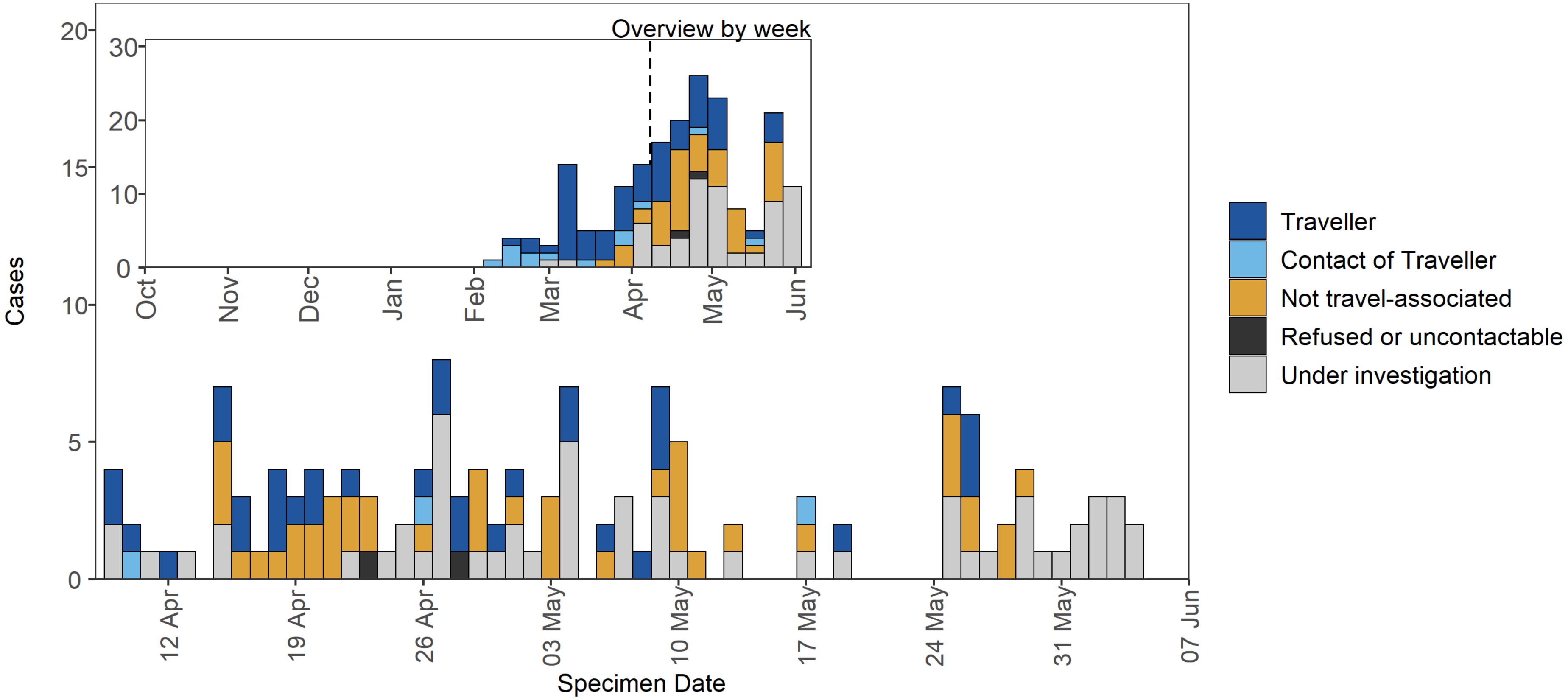
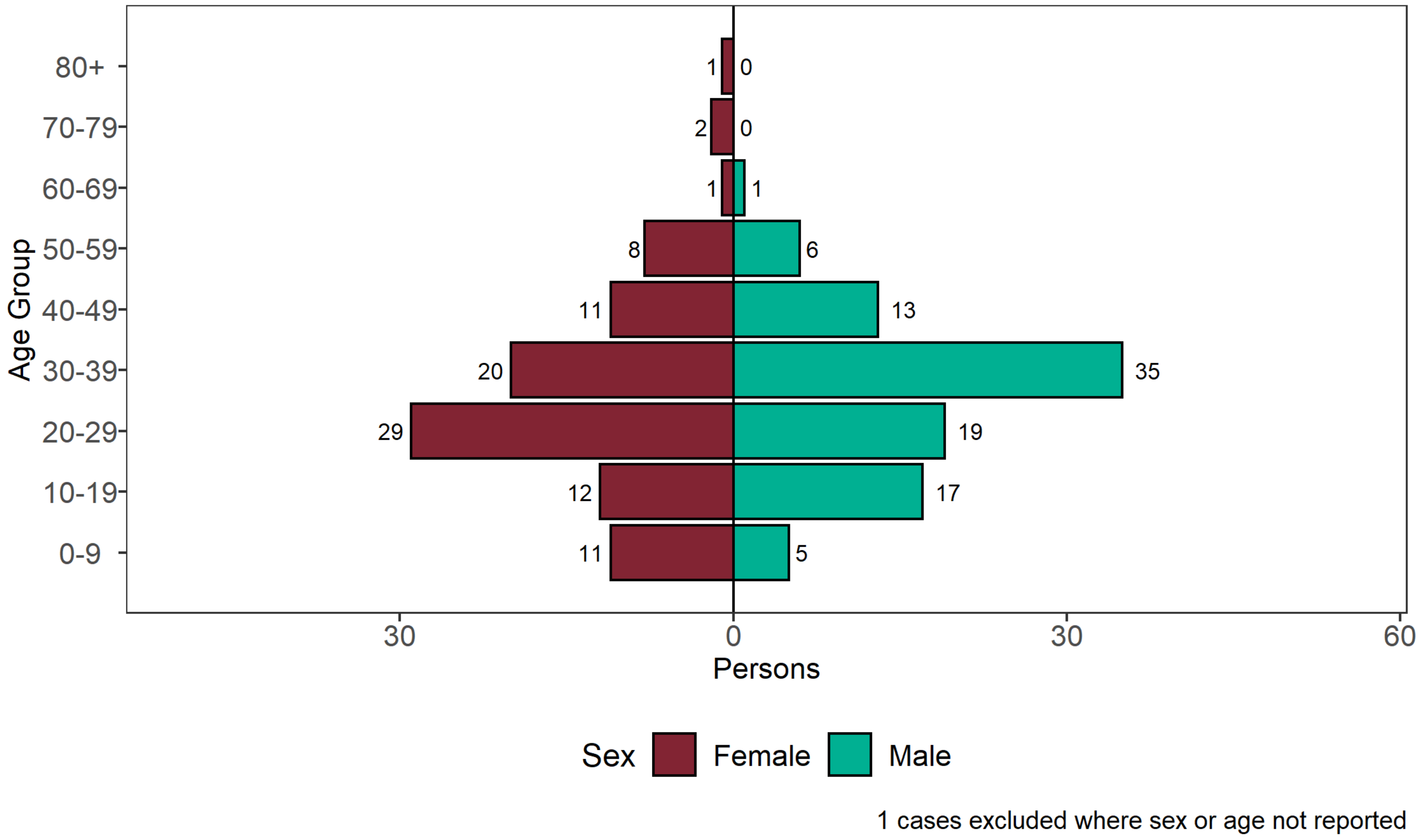


Figure 11. Age-sex pyramid of confirmed (sequencing) and probable (genotyping) Gamma cases as of June 7 2021.
(Find accessible data used in this graph in underlying data.)



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 7 June 2021, 3,253 sequences (excluding the UK) of Zeta from 37 countries.

Epidemiology

Table 6. Number of confirmed (sequencing) cases Zeta, by region of residence as of 7 June 2021

Region	Total case number	Case proportion	Cases that have travelled	Proportion of travellers among cases[1]
East Midlands	1	1.9%	0	0%
East of England	2	3.7%	1	50%
London	14	25.9%	6	42.9%
North East	0	0.0%	0	0%
North West	12	22.2%	0	0%
South East	6	11.1%	0	0%
South West	7	13.0%	0	0%
West Midlands	1	1.9%	0	0%
Yorkshire and Humber	11	20.4%	0	0%
Total	54	-	7	13%

[1] Calculated as a proportion of all cases, including those with unknown or pending travel status.

Figure 12. Confirmed (sequencing) VUI-21JAN-01 cases by specimen date and region of residence as of 7 June 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)

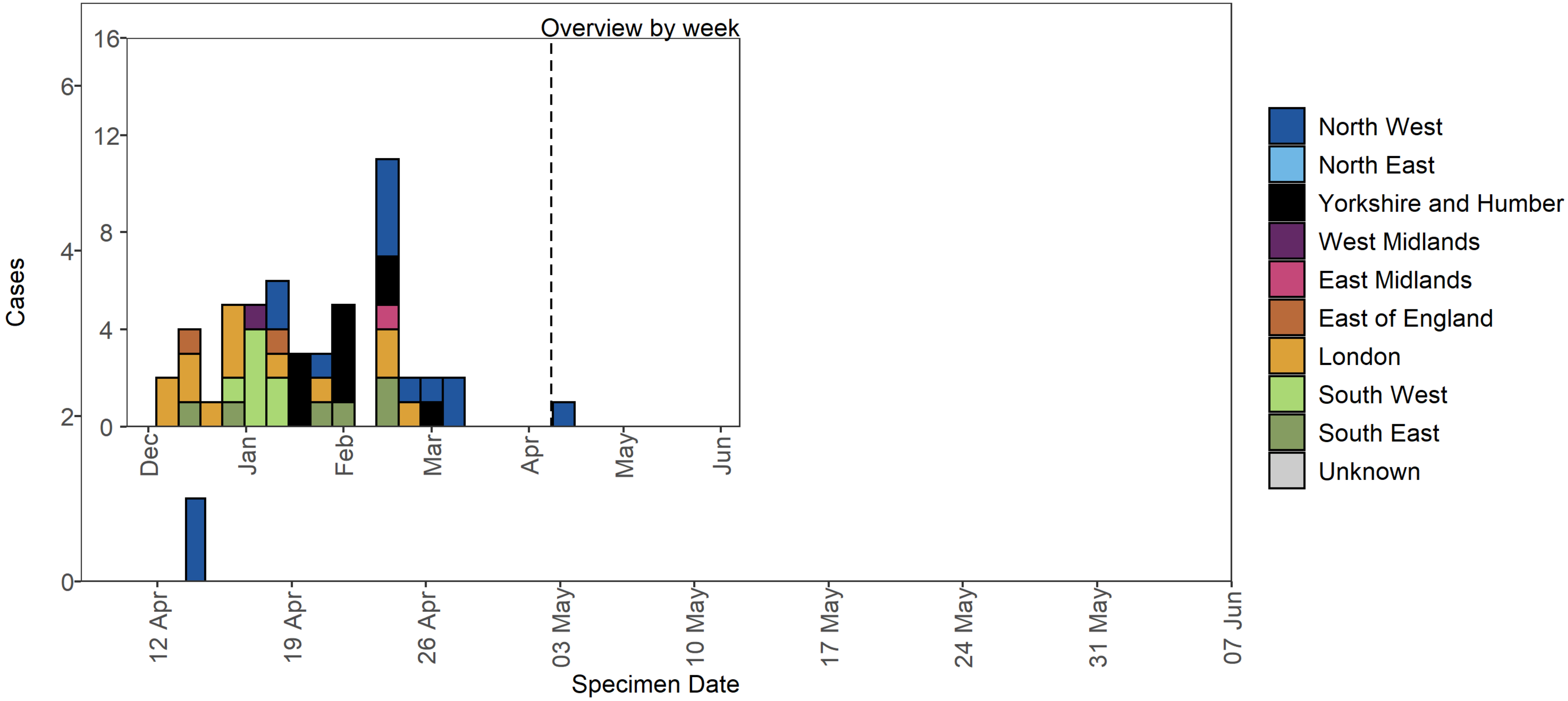


Figure 13. Travel data for confirmed (sequencing) Zeta cases by specimen date as of 7 June 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)

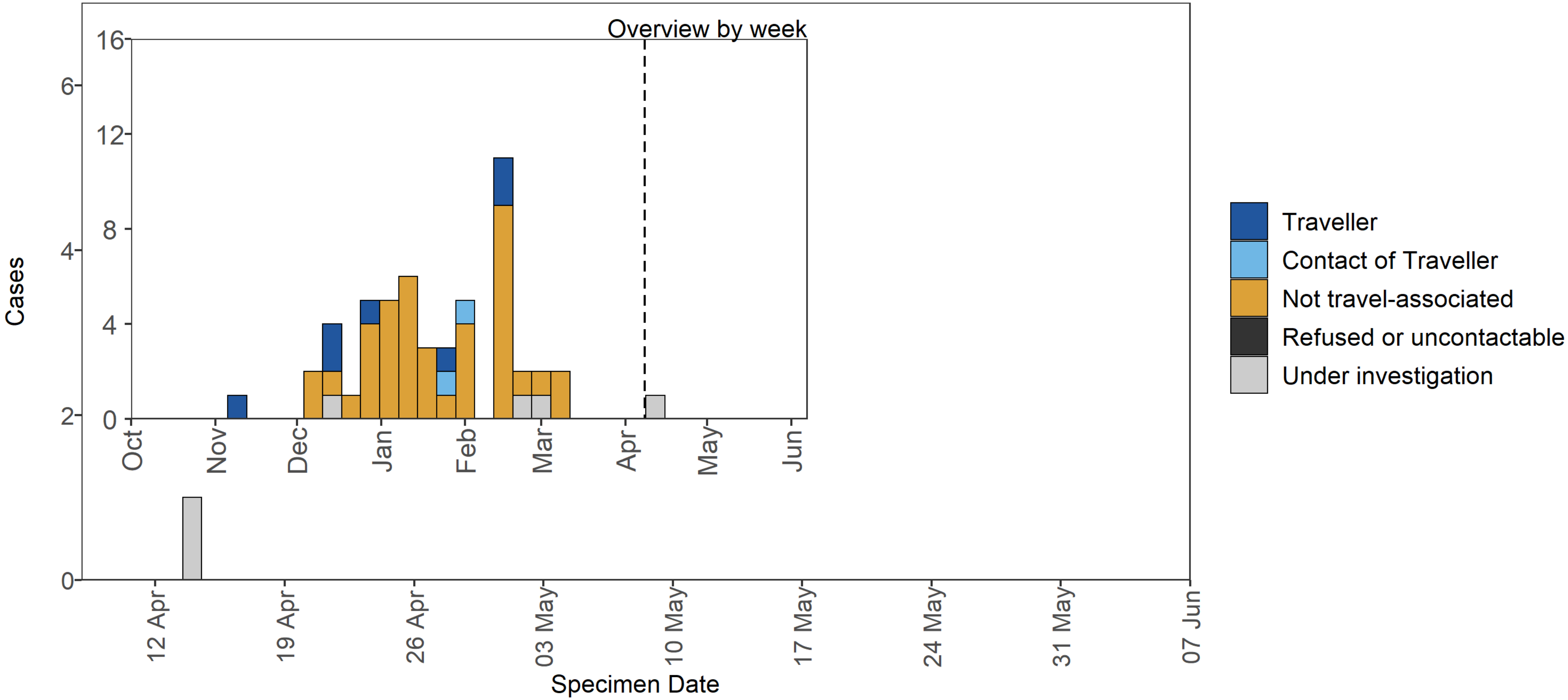
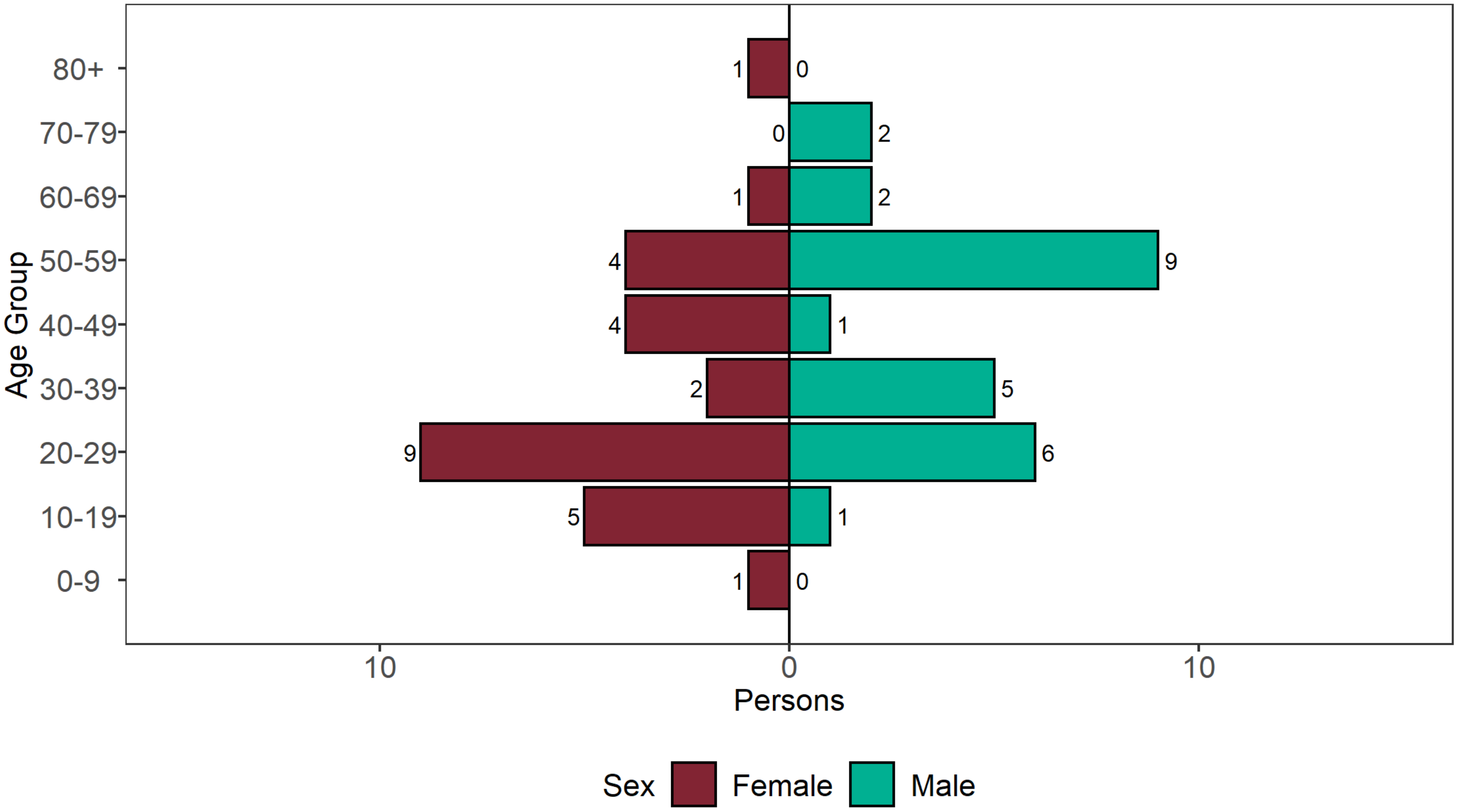


Figure 14. Age-sex pyramid of confirmed (sequencing) of Zeta cases as of 7 June 2021
(Find accessible data used in this graph in underlying data.)



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 7 June 2021, 5,191 sequences of Eta are listed, from 62 countries or territories, excluding the UK.

Epidemiology

Table 8. Number of confirmed (sequencing) Eta cases, by region of residence as of 7 June 2021

Region	Total case number	Case proportion	Cases that have travelled	Proportion of travellers among cases[1]
East Midlands	10	2.3%	5	50%
East of England	29	6.6%	22	75.9%
London	156	35.5%	94	60.3%
North East	5	1.1%	5	100%
North West	76	17.3%	19	25%
South East	80	18.2%	27	33.8%
South West	18	4.1%	6	33.3%
West Midlands	35	8.0%	13	37.1%
Yorkshire and Humber	20	4.5%	9	45%
Unknown region	11	2.5%	4	36.4%
Total	440	-	204	46.4%

[1] Calculated as a proportion of all cases, including those with unknown or pending travel status.

Figure 15. Confirmed (sequencing) Eta cases by specimen date and region of residence as of 7 June 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)

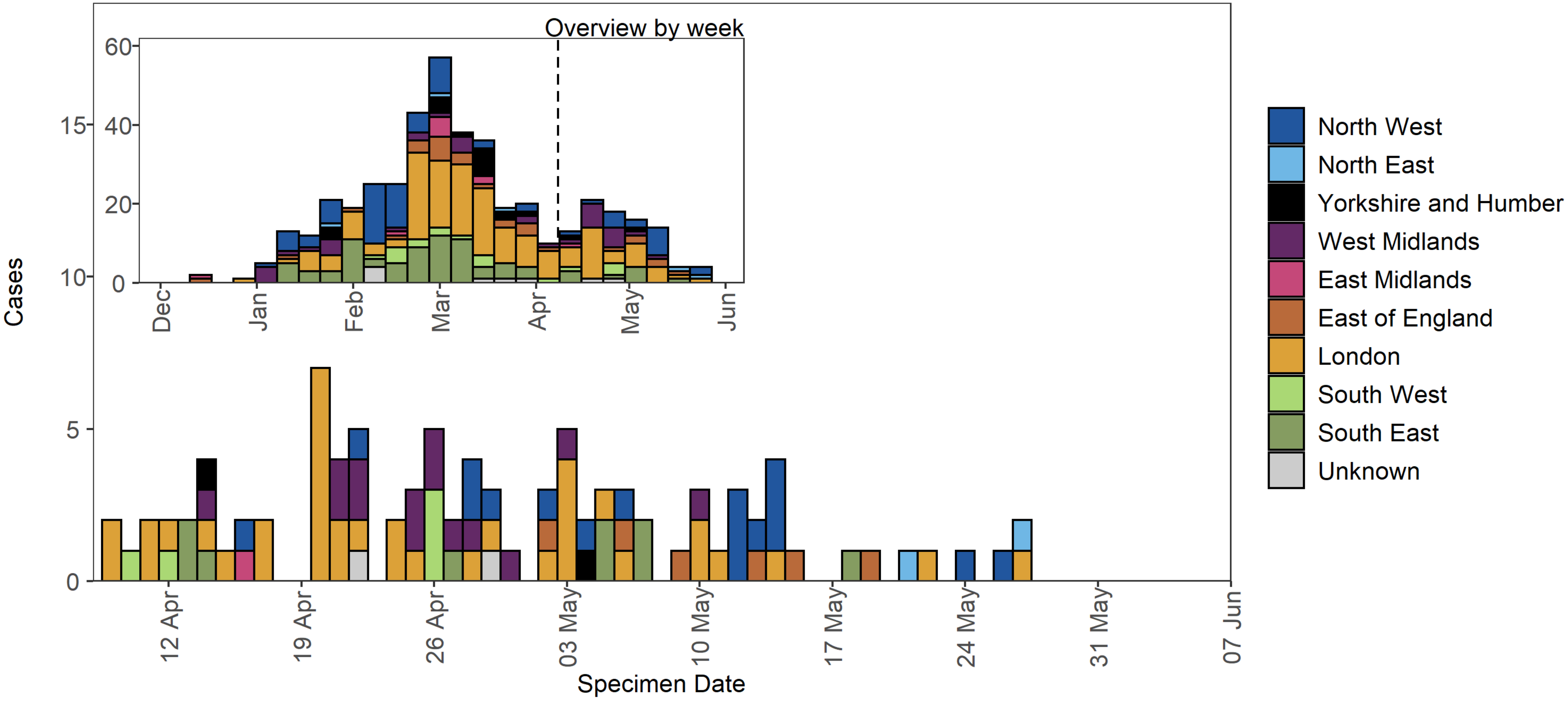


Figure 16. Travel data for confirmed (sequencing) Eta cases by specimen date as of 7 June 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)

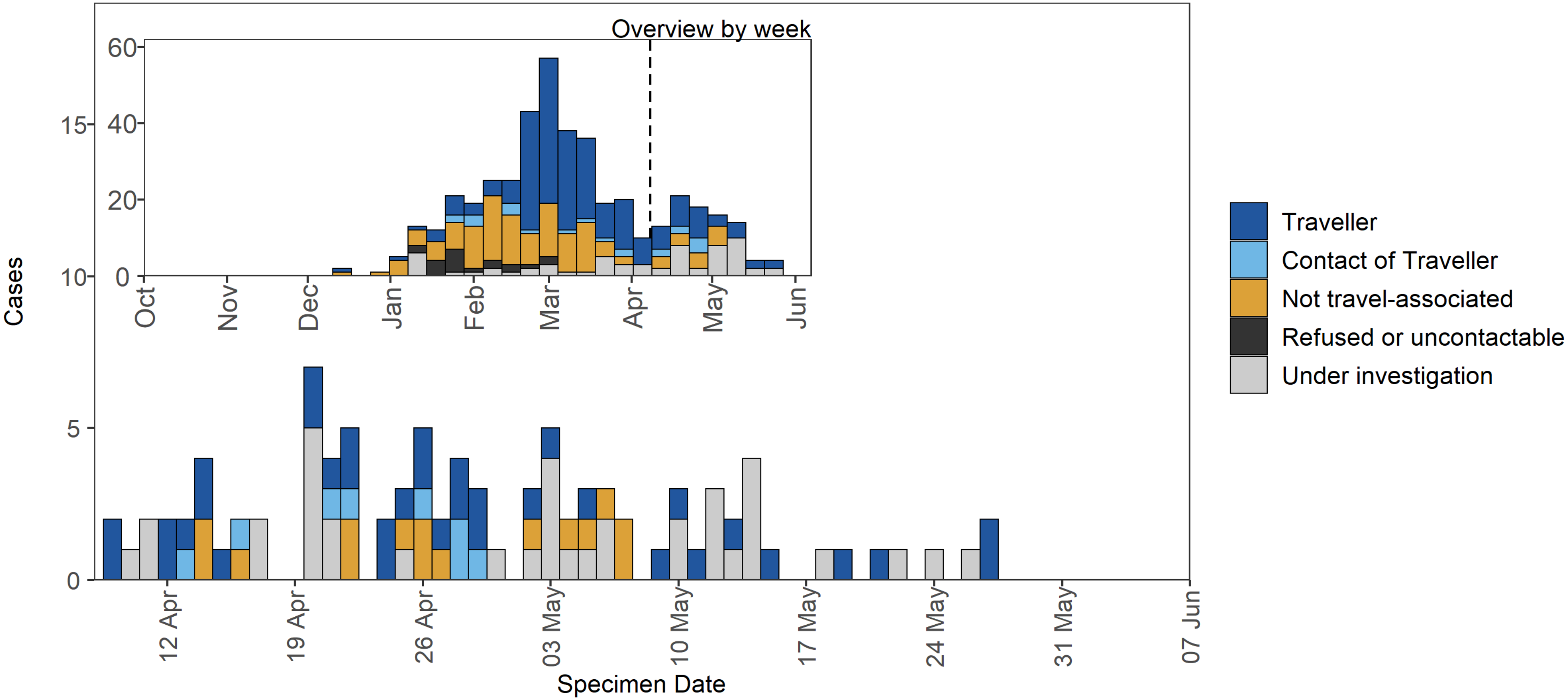
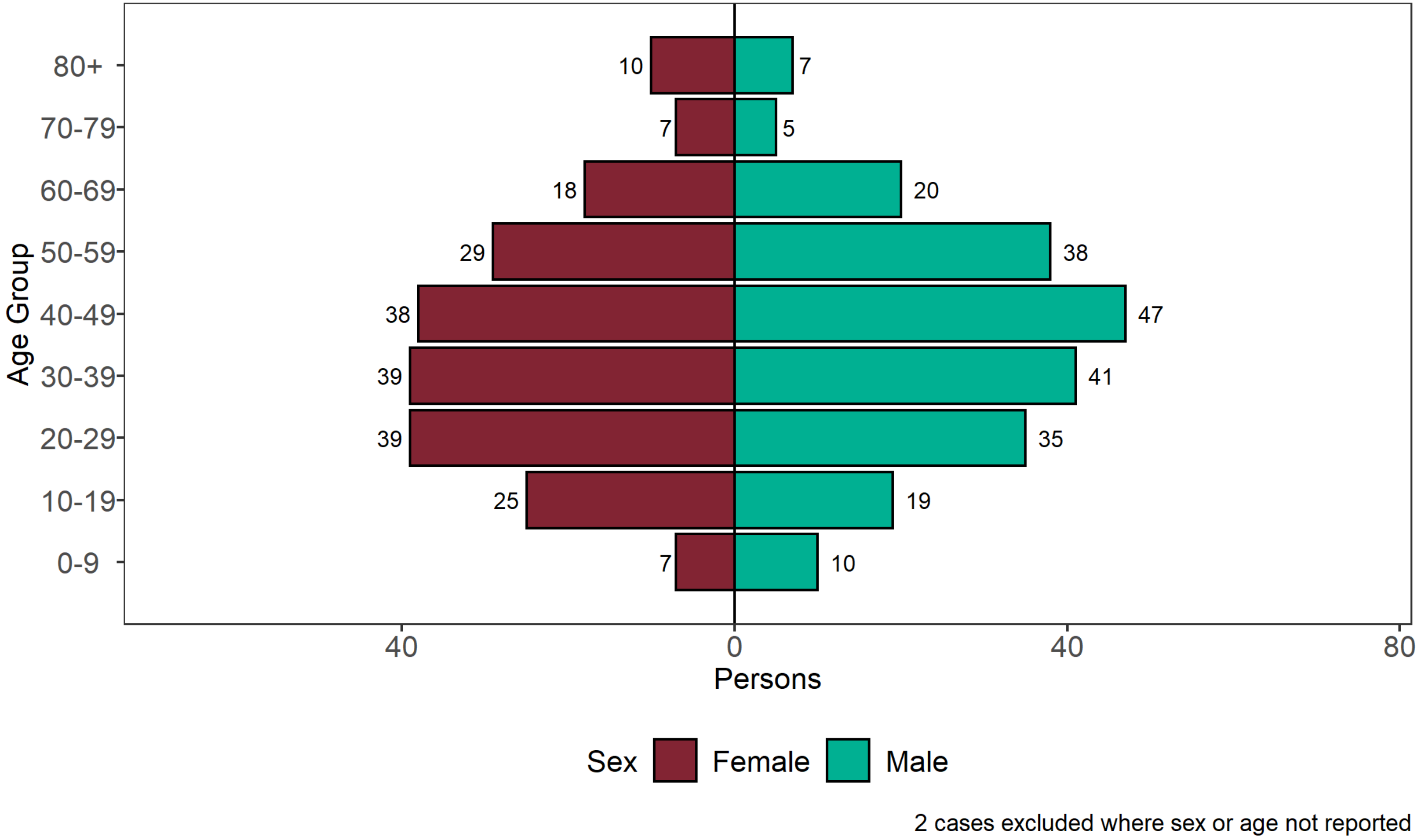


Figure 17. Age-sex pyramid of confirmed (sequencing) Eta cases as of 7 June 2021
(Find accessible data used in this graph in underlying data.)



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.

Genotyping data not collected for this variant.

International Epidemiology

GISAID includes data on sequences available internationally. As of 7 June 2021, 142 international VUI-21FEB-04 sequences, excluding the UK: Bangladesh (1), Cameroon (2), Canada (25), Denmark (1), France (8), Germany (13), Ghana (2), Greece (17), India (2), Italy (12), Nigeria (10), Sweden (4), Switzerland (15), Turkey (1), USA (29).

Table 9. Number of confirmed (sequencing) VUI-21FEB-04 (B.1.1.318) cases, by region of residence as of 7 June 2021

Region	Total case number	Case proportion	Cases that have travelled	Proportion of travellers among cases[1]
East Midlands	10	4.0%	4	40%
East of England	25	9.9%	11	44%
London	98	38.7%	41	41.8%
North East	2	0.8%	2	100%
North West	47	18.6%	11	23.4%
South East	45	17.8%	14	31.1%
South West	1	0.4%	1	100%
West Midlands	8	3.2%	4	50%
Yorkshire and Humber	11	4.3%	1	9.1%
Unknown region	6	2.4%	4	66.7%
Total	253	-	93	36.8%

[1] Calculated as a proportion of all cases, including those with unknown or pending travel status.

Figure 18. Confirmed (sequencing) VUI-21FEB-04 (B.1.1.318) cases by specimen date as of 7 June 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)

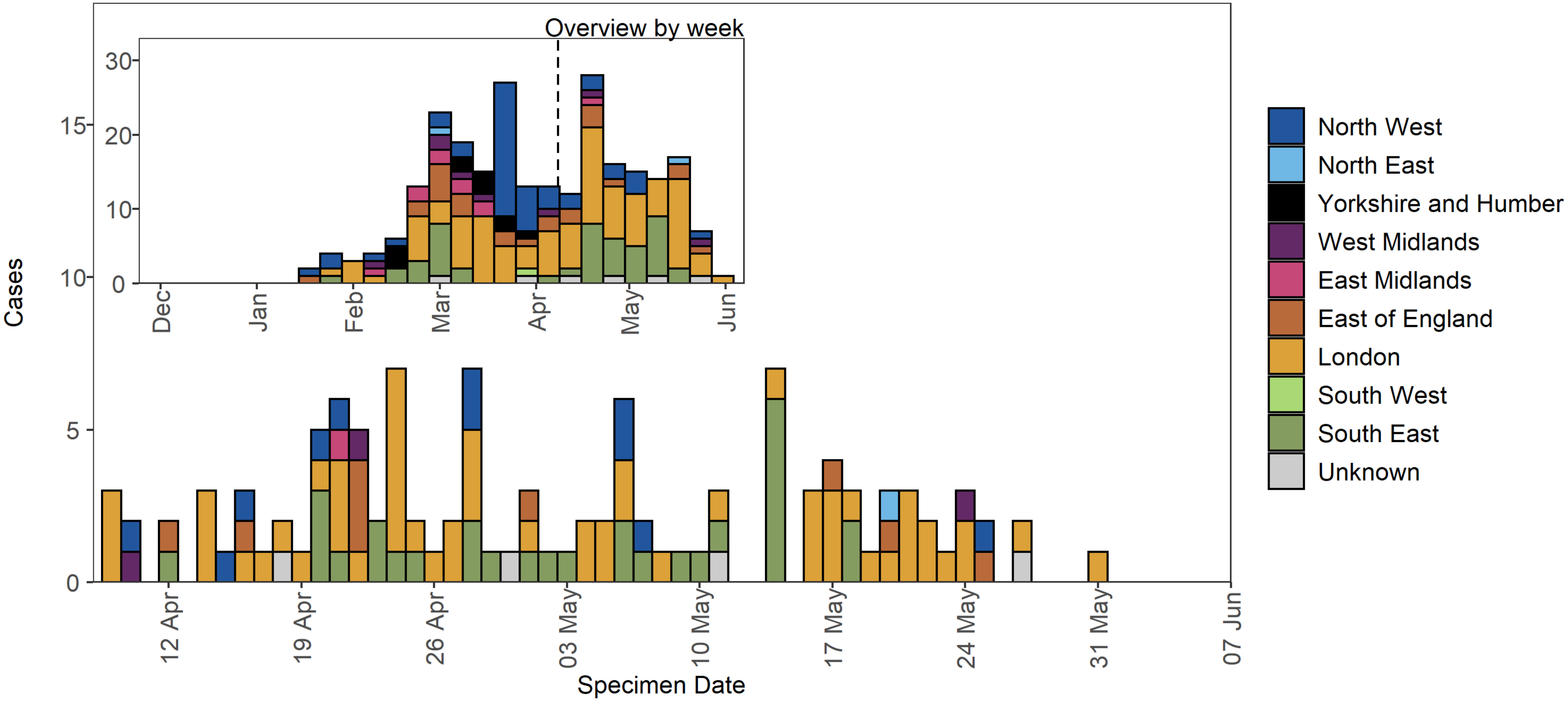


Figure 19. Travel data for confirmed (sequencing) VUI-21FEB-04 (B.1.1.318) cases by specimen date as of 7 June 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)

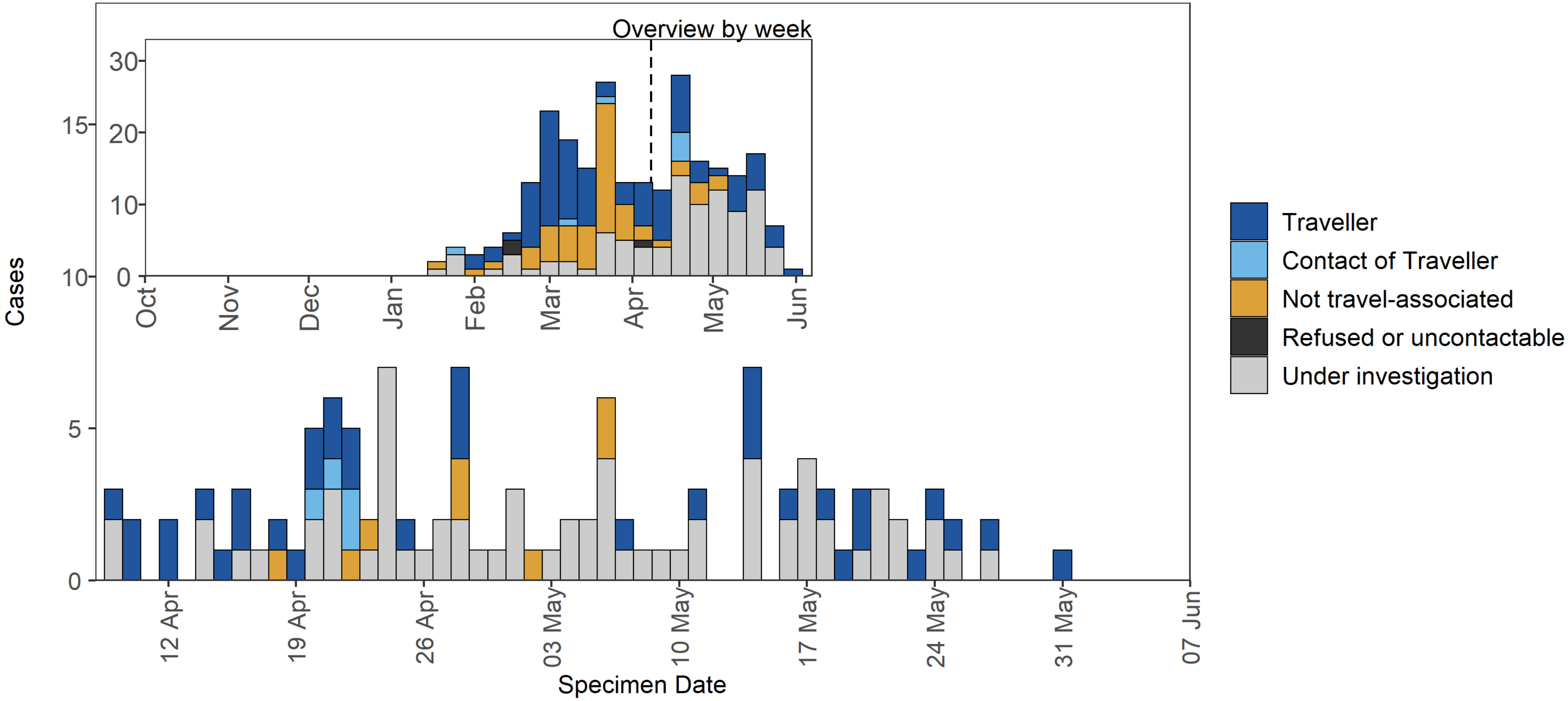
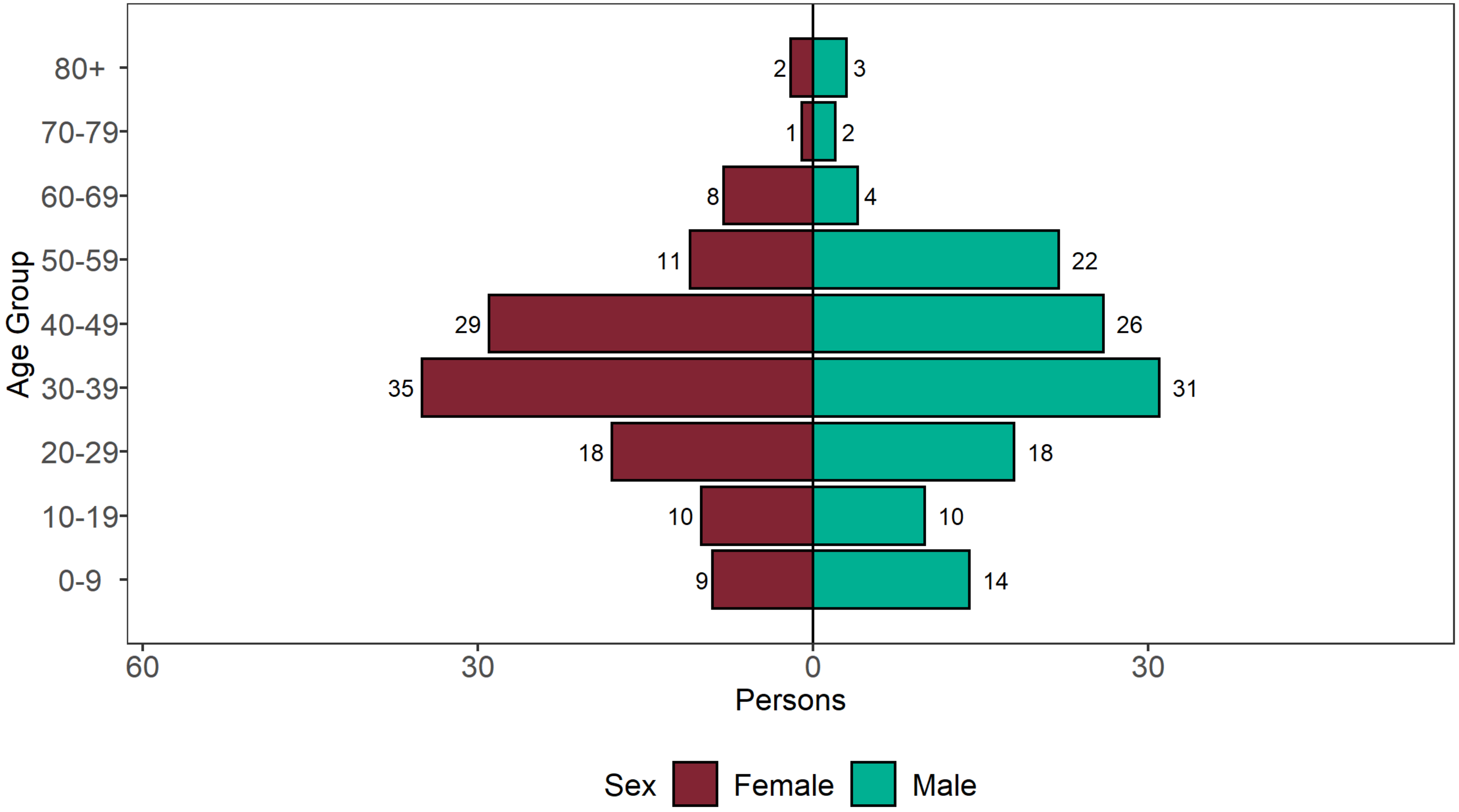


Figure 20. Age-sex pyramid of confirmed (sequencing) VUI-21FEB-04 (B.1.1.318) cases, as of 7 June 2021
(Find accessible data used in this graph in underlying data.)



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 7 June 2021, 229 sequences are listed internationally of Theta excluding the UK: Australia (3), China (2), Germany (8), Hong Kong (10), Japan (4), Netherlands (6), New Zealand (3), Norway (2), Philippines (179), Singapore (2), South Korea (1), USA (9).

Table 10. Number of confirmed (sequencing) Theta cases, by region of residence as of 7 June 2021

Region	Total case number	Case proportion	Cases that have travelled	Proportion of travellers among cases[1]
East Midlands	0	0.0%	0	0%
East of England	1	14.3%	1	100%
London	2	28.6%	1	50%
North East	0	0.0%	0	0%
North West	1	14.3%	1	100%
South East	0	0.0%	0	0%
South West	2	28.6%	2	100%
West Midlands	0	0.0%	0	0%
Yorkshire and Humber	1	14.3%	1	100%
Total	7	-	6	85.7%

[1] Calculated as a proportion of all cases, including those with unknown or pending travel status.

Figure 21. Confirmed (sequencing) Theta cases by specimen date as of 7 June 2021

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

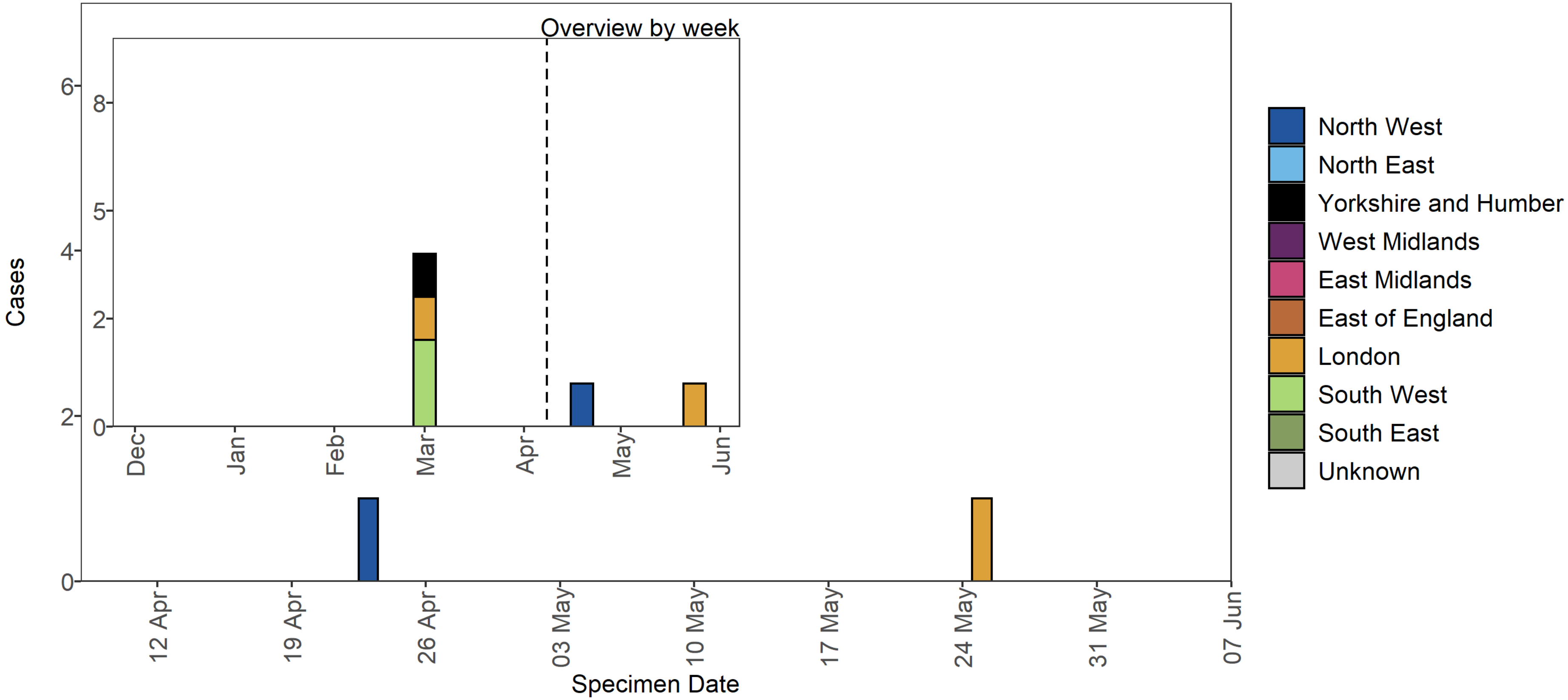


Figure 22. Travel data for confirmed (sequencing) Theta cases by specimen date as of 7 June 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)

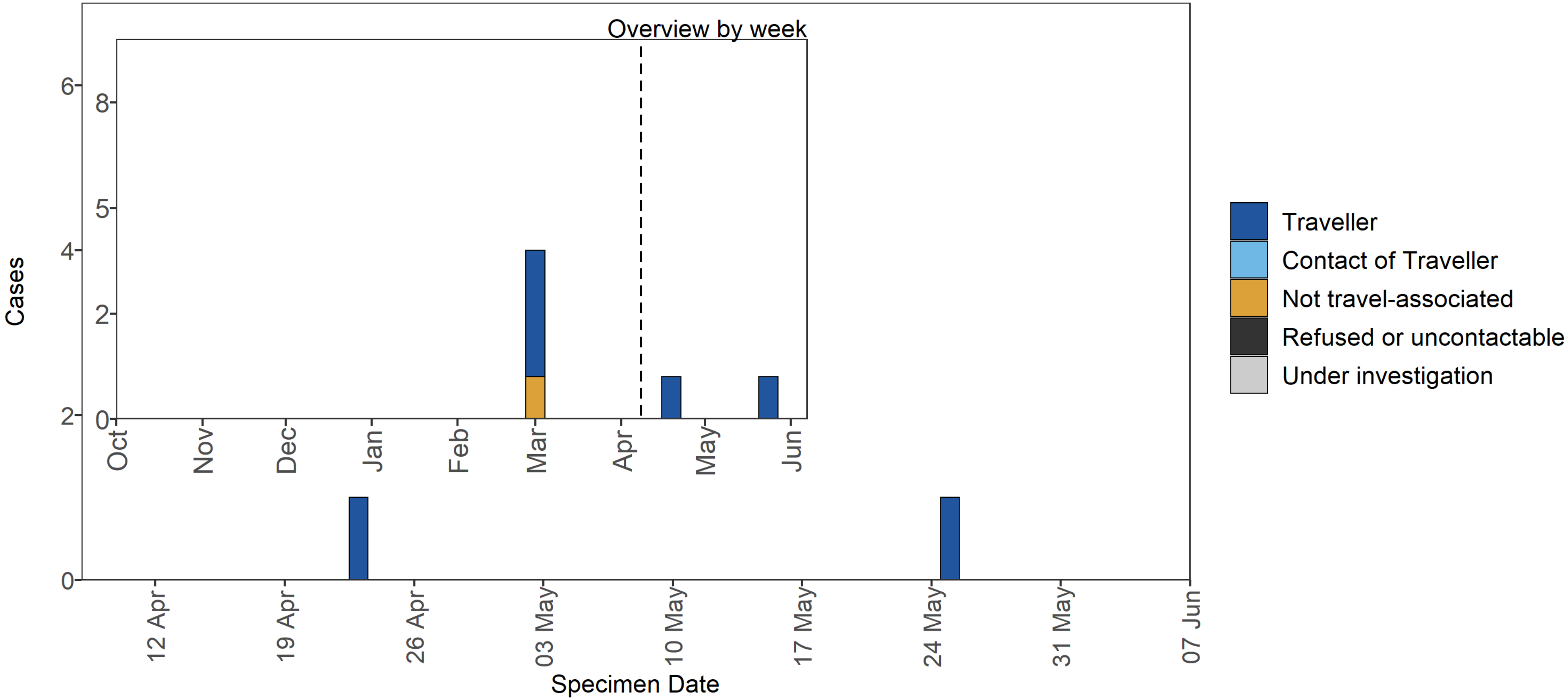
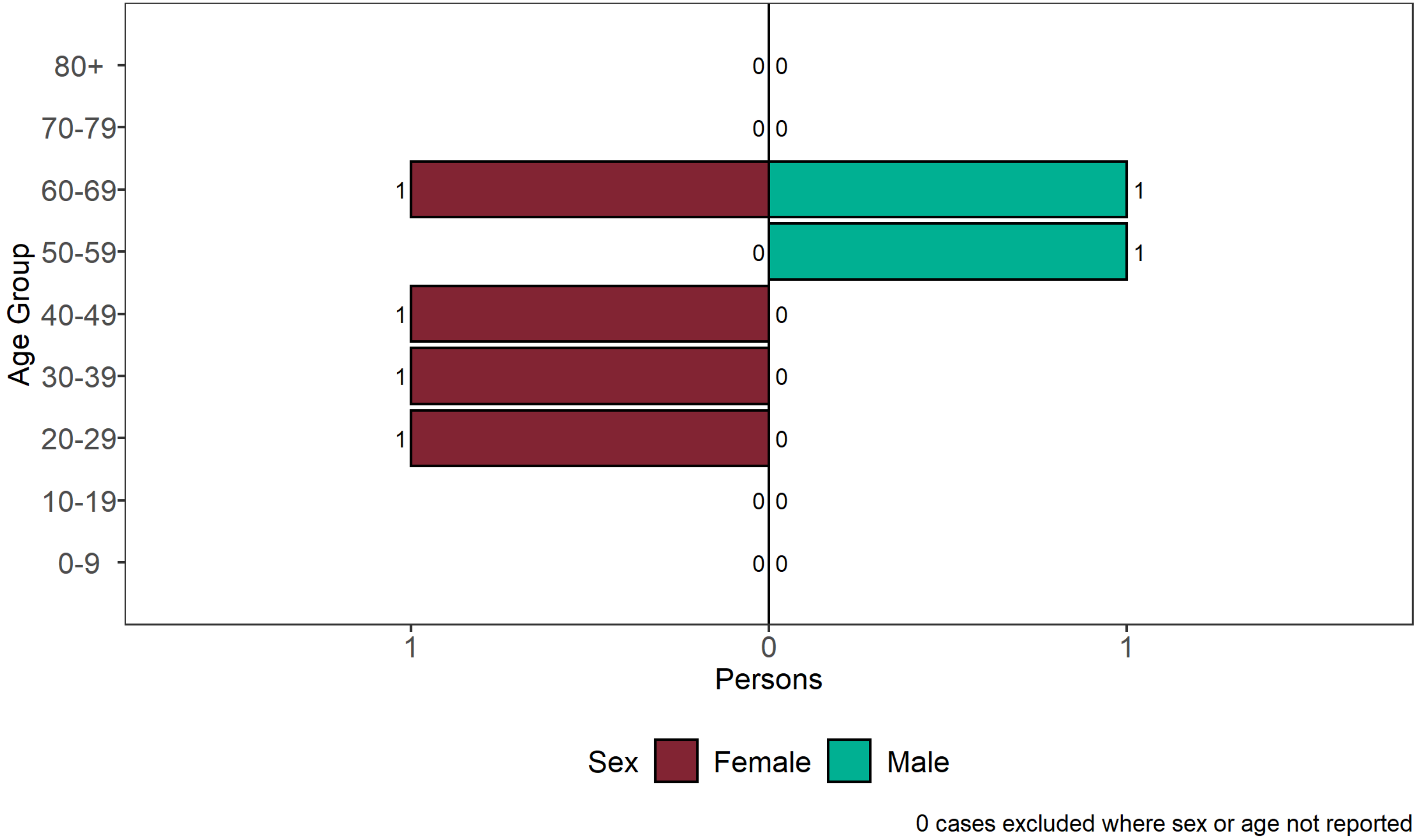


Figure 23. Age-sex pyramid of confirmed (sequencing) Theta cases as of 7 June 2021
(Find accessible data used in this graph in underlying data.)



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 was named Kappa by WHO on 31 May 2021.

International surveillance

GISAID includes data on sequences available internationally. As of 7 June 2021, 2,556 Kappa sequences from the following countries (excluding the UK) have been identified in GISAID: Australia (73), Austria (1), Bahrain (8), Belgium (10), Canada (39), China (1), Curacao (1), Czech Republic (4), Denmark (27), Finland (1), France (9), Germany (95), Ghana (5), Greece (1), Guadeloupe (2), Hong Kong (9), India (1,777), Ireland (88), Italy (6), Japan (25), Jordan (4), Luxembourg (6), Malaysia (1), Mexico (4), Nepal (2), Netherlands (9), New Zealand (4), Portugal (9), Qatar (3), Saint Martin (2), Singapore (60), Slovakia (1), South Africa (1), South Korea (5), Spain (4), Sweden (5), Switzerland (9), Thailand (1), USA (243), Uganda (1).

Table 11. Number of confirmed (sequencing) Kappa cases, by region of residence as of 7 June 2021

Region	Total case number	Case proportion	Cases that have travelled	Proportion of travellers among cases[1]
East Midlands	48	11.5%	24	50%
East of England	31	7.4%	20	64.5%
London	175	41.8%	101	57.7%
North East	4	1.0%	2	50%
North West	32	7.6%	22	68.8%
South East	41	9.8%	24	58.5%
South West	13	3.1%	9	69.2%
West Midlands	48	11.5%	19	39.6%
Yorkshire and Humber	18	4.3%	12	66.7%
Unknown region	9	2.1%	5	55.6%
Total	419	-	238	56.8%

[1] Calculated as a proportion of all cases, including those with unknown or pending travel status.

Figure 24. Confirmed (sequencing) Kappa cases by specimen date as of 7 June 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)

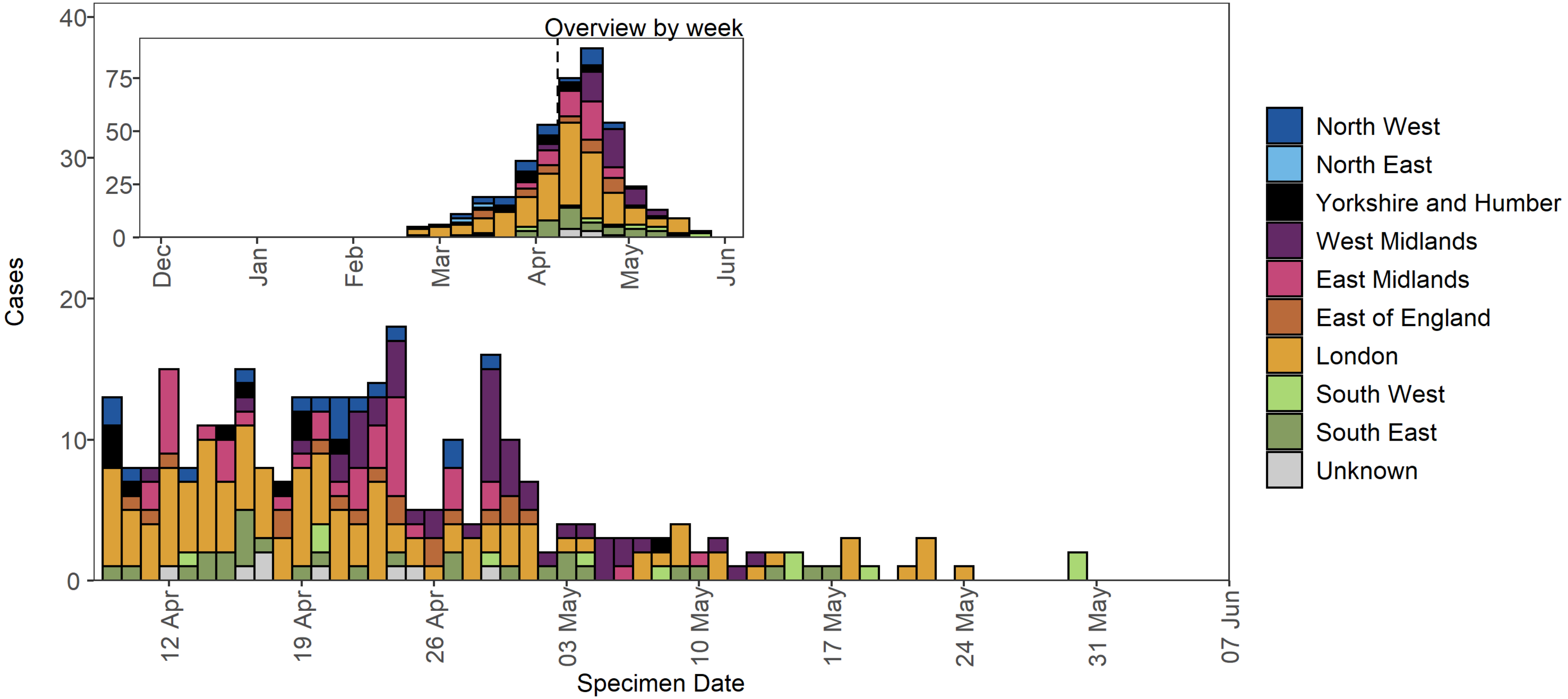


Figure 25. Travel data for confirmed (sequencing) Kappa cases by specimen date as of 7 June 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)

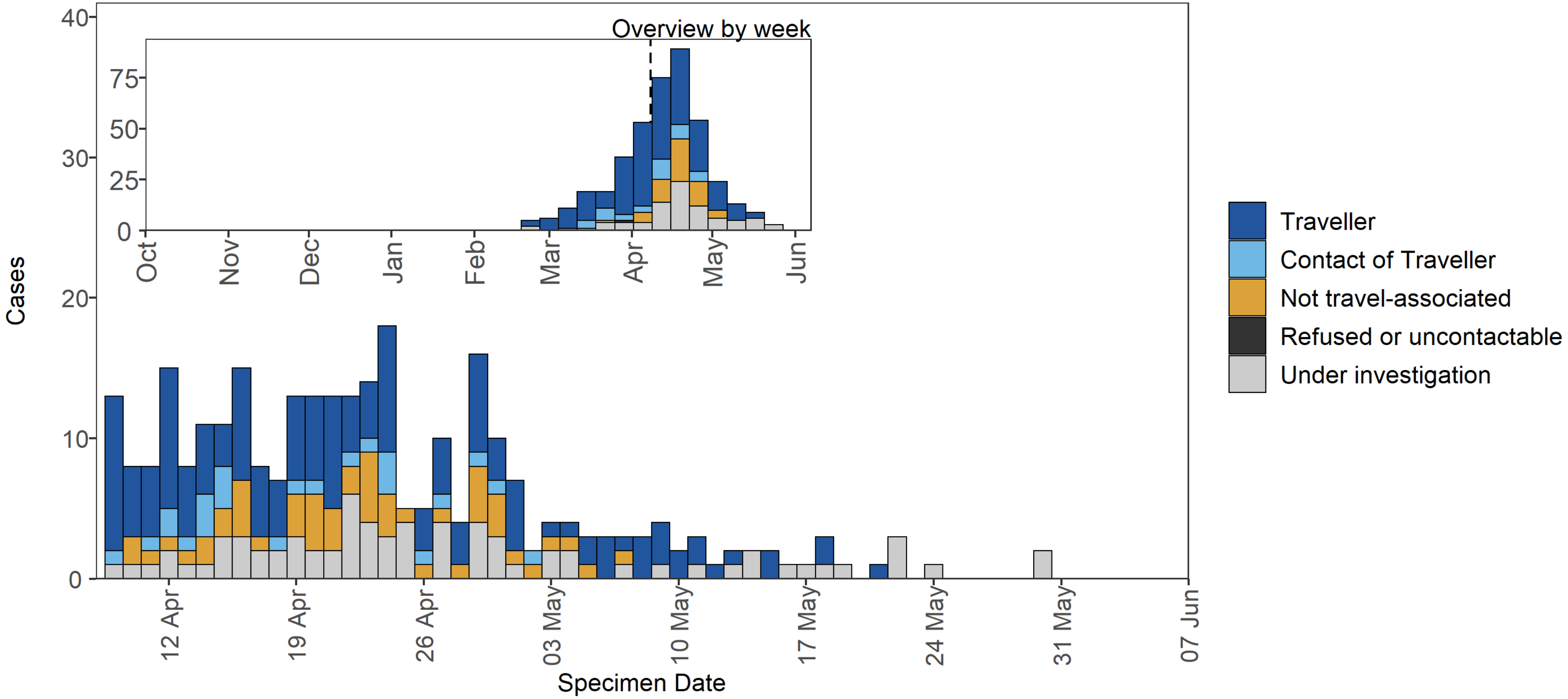
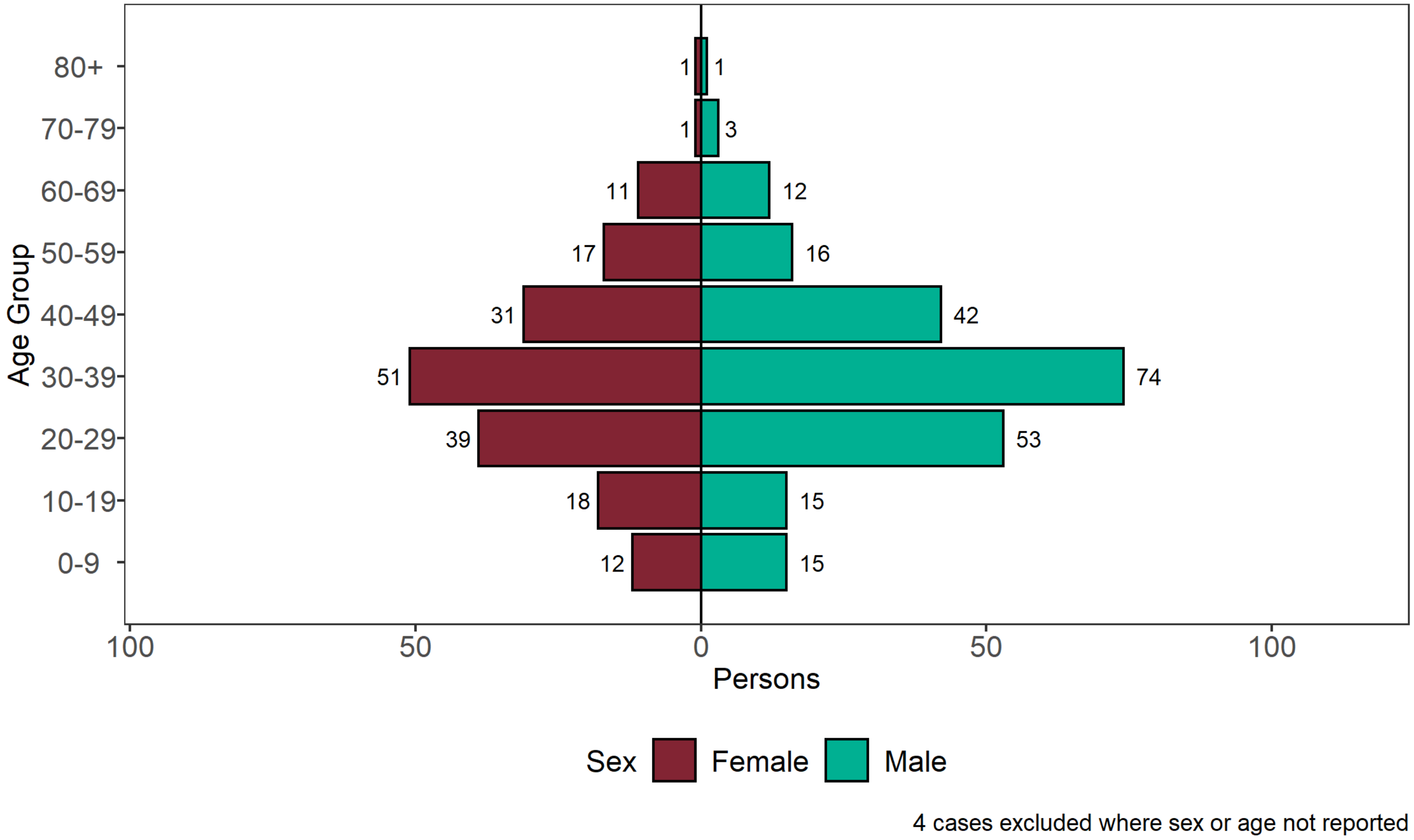


Figure 26. Age-sex pyramid of confirmed (sequencing) Kappa cases as of 7 June 2021
(Find accessible data used in this graph in underlying data.)



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 surveillance

GISAID includes data on sequences available internationally. As of 7 June 2021, 75 sequences from the following countries (excluding the UK) have been identified in GISAID of VUI-21APR-03 (B.1.617.3): India (72), Russia (2), USA (1).

Table 12. Number of confirmed (sequencing) VUI-21APR-03 (B.1.617.3) cases, by region of residence as of 7 June 2021

Region	Total case number	Case proportion	Cases that have travelled	Proportion of travellers among cases[1]
East Midlands	0	0.0%	0	0%
East of England	0	0.0%	0	0%
London	5	38.5%	3	60%
North East	0	0.0%	0	0%
North West	6	46.2%	2	33.3%
South East	2	15.4%	1	50%
South West	0	0.0%	0	0%
West Midlands	0	0.0%	0	0%
Yorkshire and Humber	0	0.0%	0	0%
Total	13	-	6	46.2%

[1] Calculated as a proportion of all cases, including those with unknown or pending travel status.

Figure 27. Confirmed (sequencing) VUI-21APR-03 (B.1.617.3) cases by region of residence and specimen date as of 7 June 2021

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

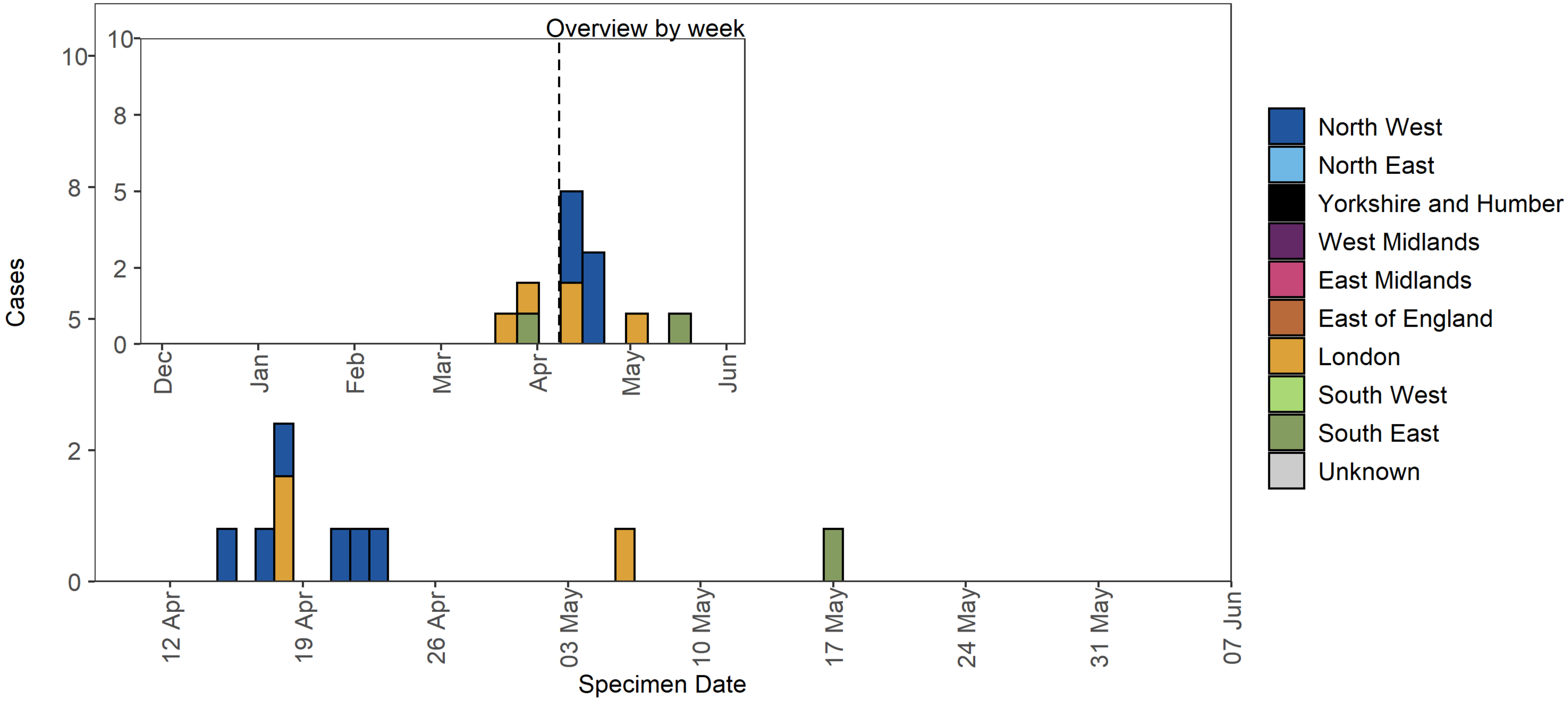


Figure 28. Travel data for confirmed (sequencing) VUI-21APR-03 (B.1.617.3) cases by specimen date as of 7 June 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)

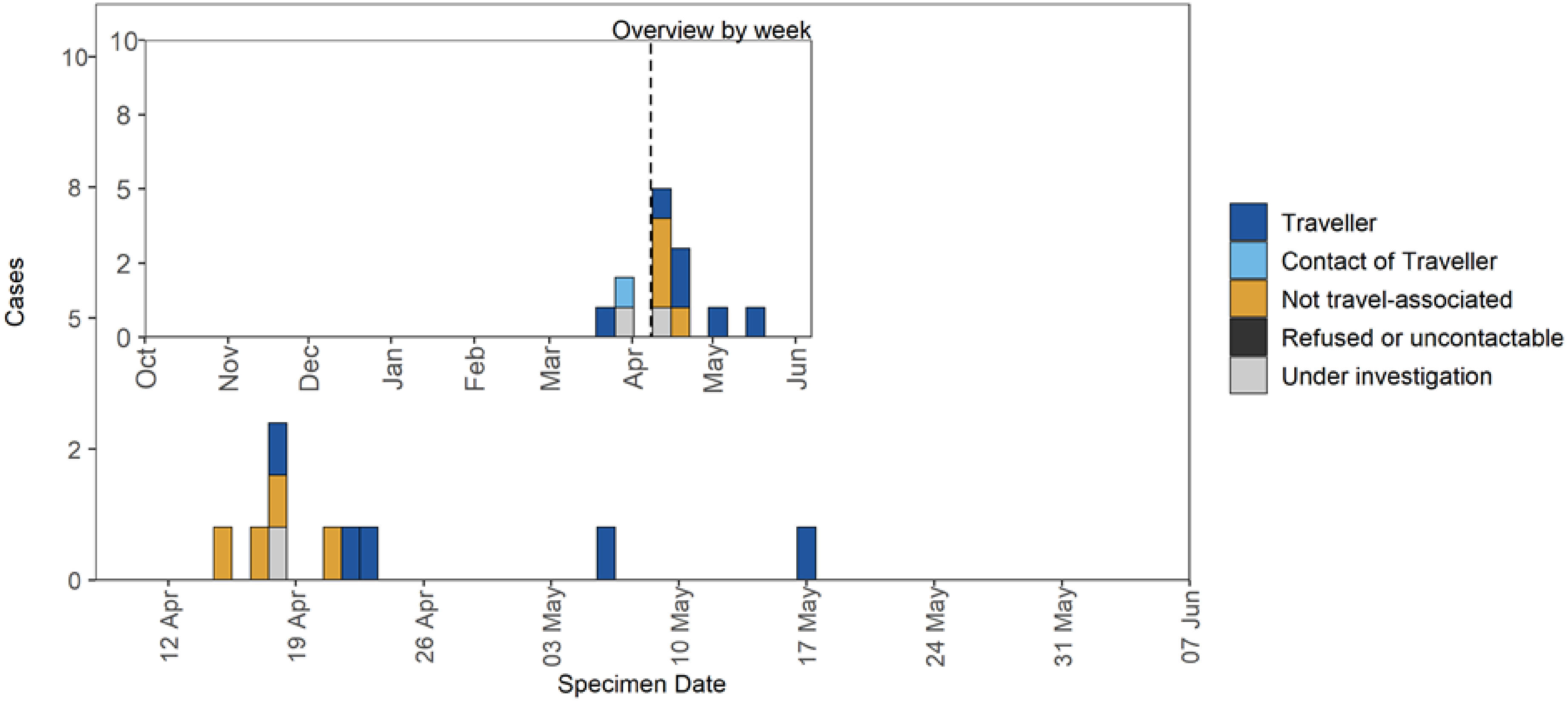
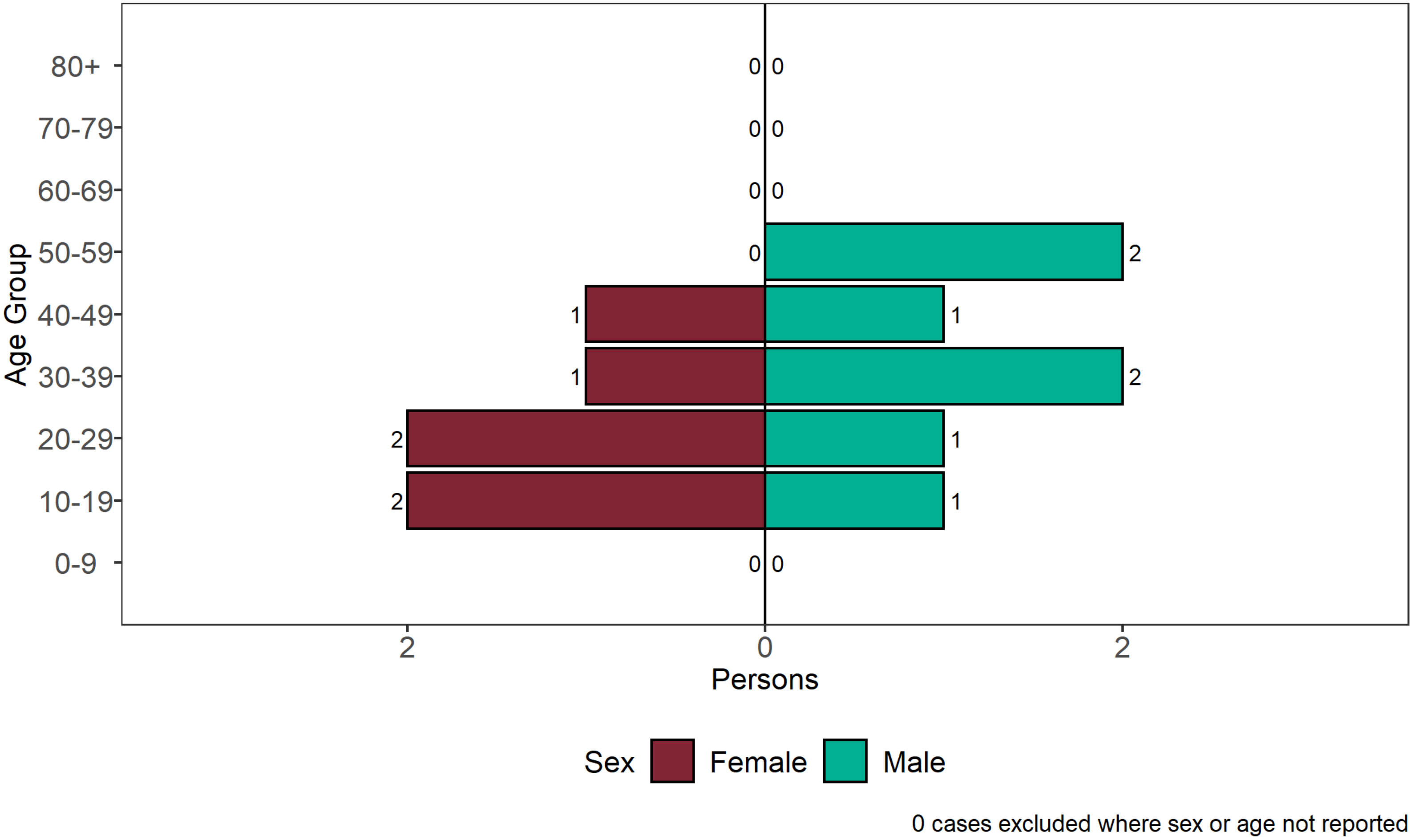


Figure 29. Age-sex pyramid of confirmed (sequencing) VUI-21APR-03 (B.1.617.3) cases as of 7 June 2021
(Find accessible data used in this graph in underlying data.)



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 surveillance

GISAID includes data on sequences available internationally excluding the UK. As of 7 June 2021, 5 sequences of VUI-21MAY-01 (AV.1) from France have been identified on GISAID.

Table 13. Number of confirmed (sequencing) VUI-21MAY-01 (AV.1) cases, by region of residence as of 7 June 2021

Region	Total case number	Case proportion	Cases that have travelled	Proportion of travellers among cases[1]
East Midlands	6	4.2%	0	0%
East of England	10	7.0%	0	0%
London	1	0.7%	0	0%
North East	0	0.0%	0	0%
North West	6	4.2%	0	0%
South East	0	0.0%	0	0%
South West	0	0.0%	0	0%
West Midlands	4	2.8%	0	0%
Yorkshire and Humber	116	81.1%	1	0.9%
Total	143	-	1	0.7%

[1] Calculated as a proportion of all cases, including those with unknown or pending travel status.

Figure 30. Confirmed (sequencing) and probable (genotyping) VUI-21MAY-01 (AV.1) cases by specimen date as of 7 June 2021

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

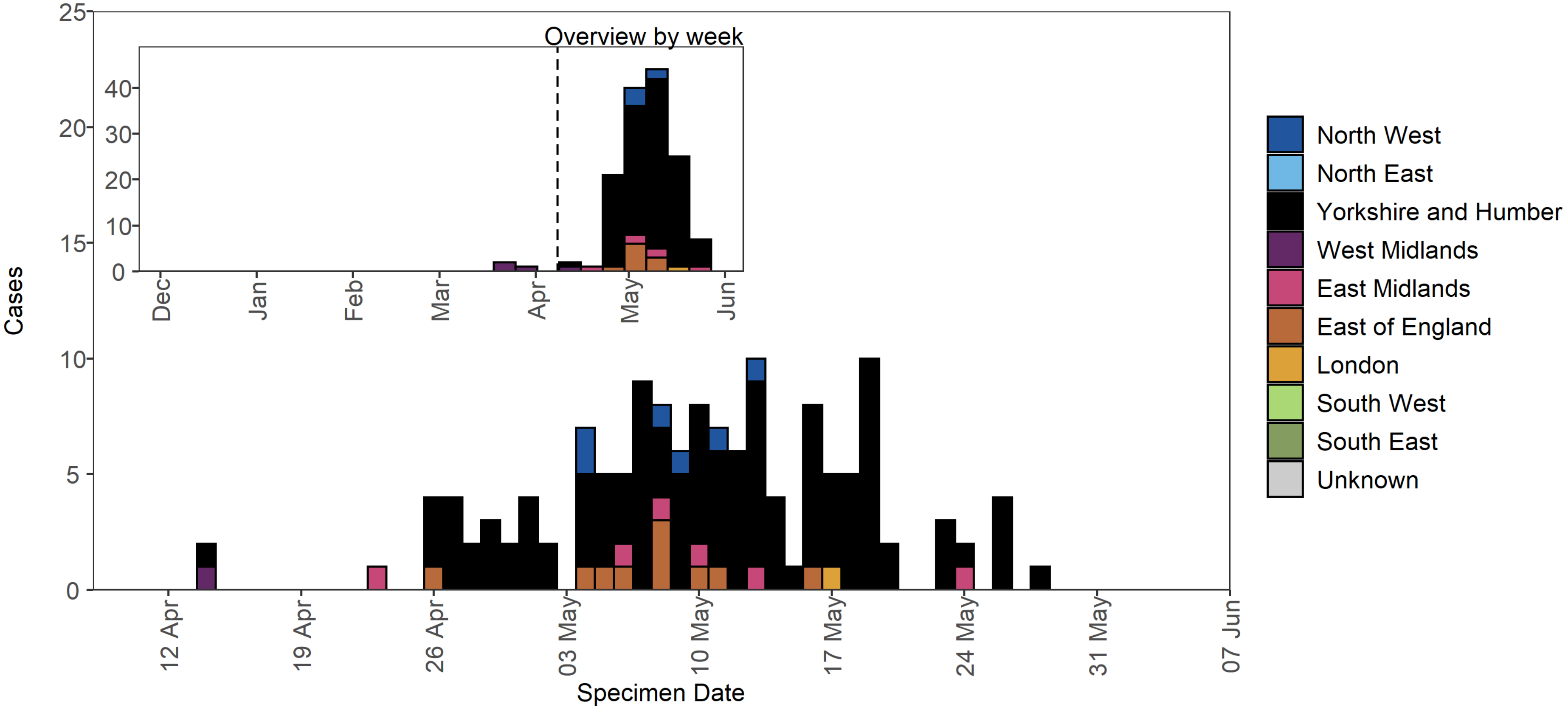


Figure 31. Travel data for confirmed (sequencing) and probable (genotyping) VUI-21MAY-01 (AV.1) cases by specimen date as of 7 June 2021

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

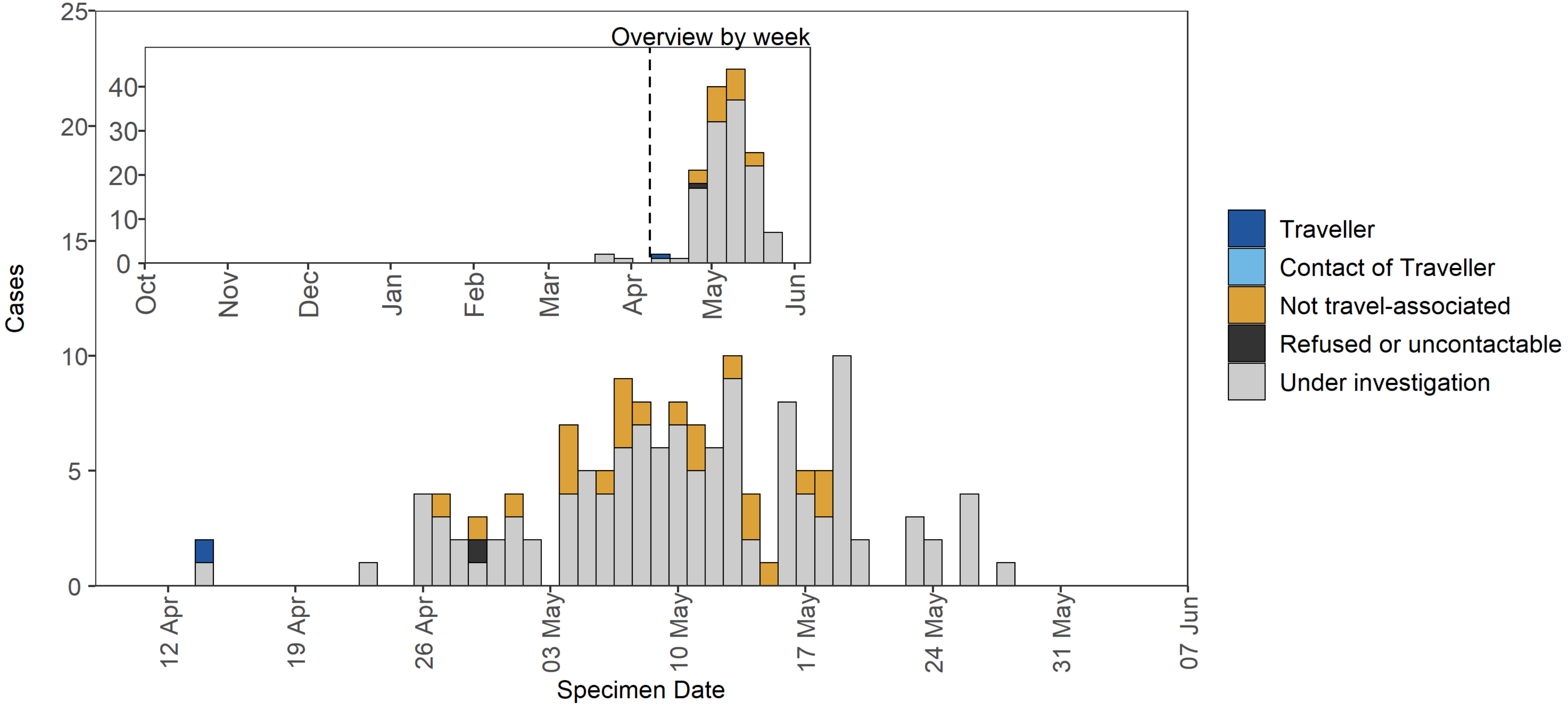
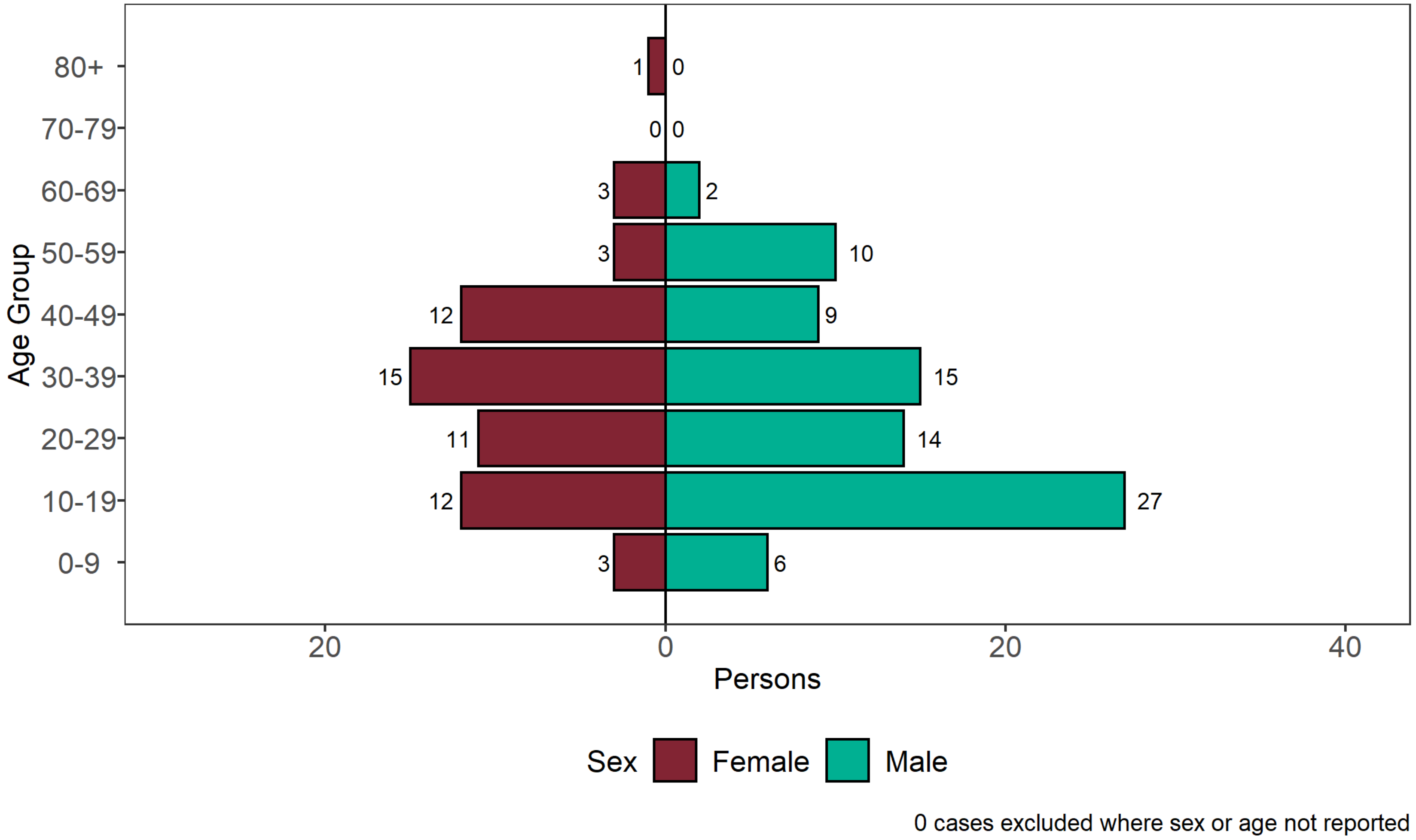


Figure 32. Age-sex pyramid of confirmed (sequencing) VUI-21MAY-01 (AV.1) cases as of 7 June 2021
(Find accessible data used in this graph in underlying data.)



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 surveillance

GISAID includes data on sequences available internationally excluding the UK. As of 7 June 2021, 786 sequences of VUI-21MAY-02 (C.36.3) from 39 countries have been identified on GISAID

Table 14. Number of confirmed (sequencing) VUI-21MAY-02 (C.36.3) cases, by region of residence as of 7 June 2021

Region	Total case number	Case proportion	Cases that have travelled	Proportion of travellers among cases[1]
East Midlands	6	4.9%	3	50%
East of England	19	15.6%	5	26.3%
London	37	30.3%	15	40.5%
North East	1	0.8%	1	100%
North West	13	10.7%	6	46.2%
South East	10	8.2%	4	40%
South West	4	3.3%	2	50%
West Midlands	9	7.4%	4	44.4%
Yorkshire and Humber	23	18.9%	6	26.1%
Total	122	-	46	37.7%

[1] Calculated as a proportion of all cases, including those with unknown or pending travel status.

Figure 33. Confirmed and provision genotyping VUI-21MAY-02 (C.36.3) cases by specimen date and region of residence as of 7 June 2021

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

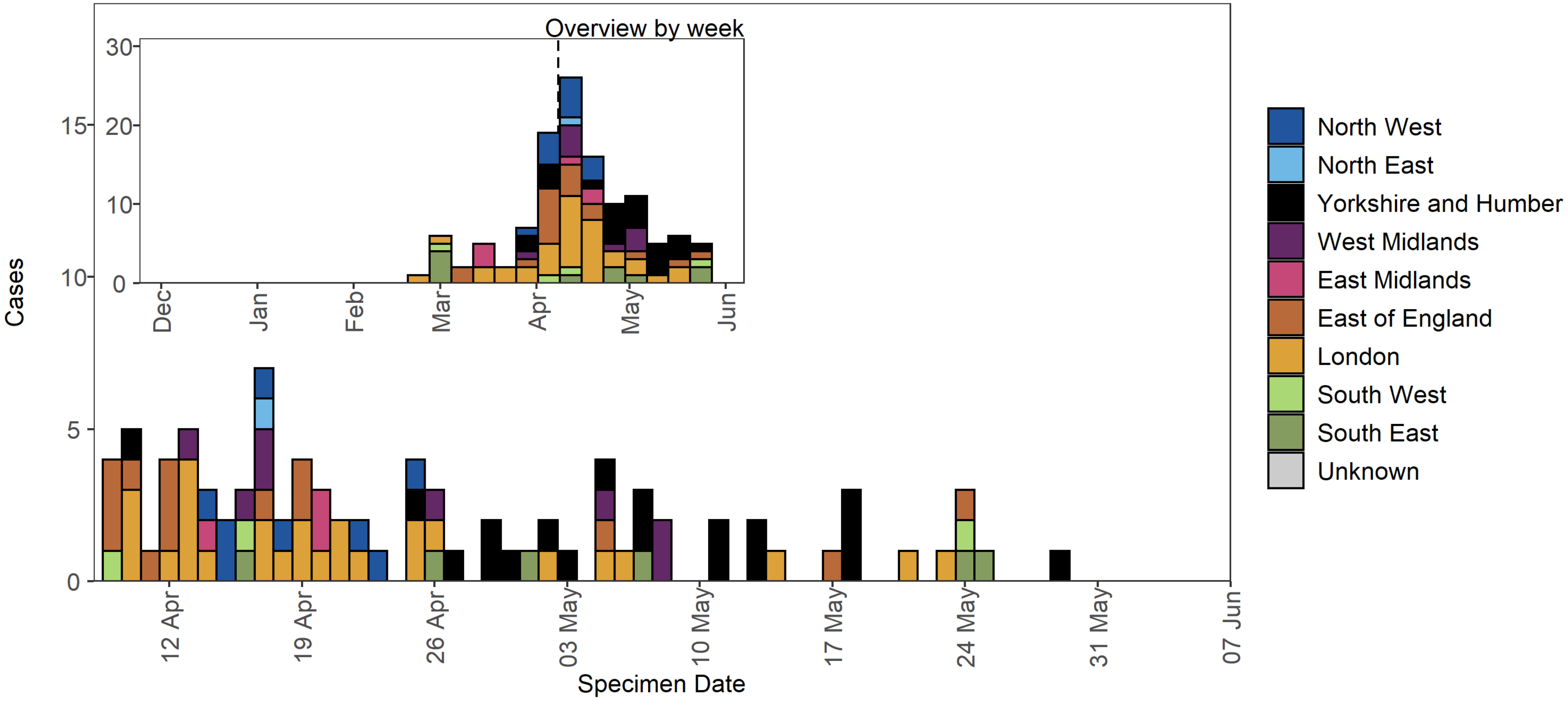


Figure 34. Travel data for confirmed (sequencing) VUI-21MAY-02 (C.36.3) cases by specimen date as of 7 June 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)

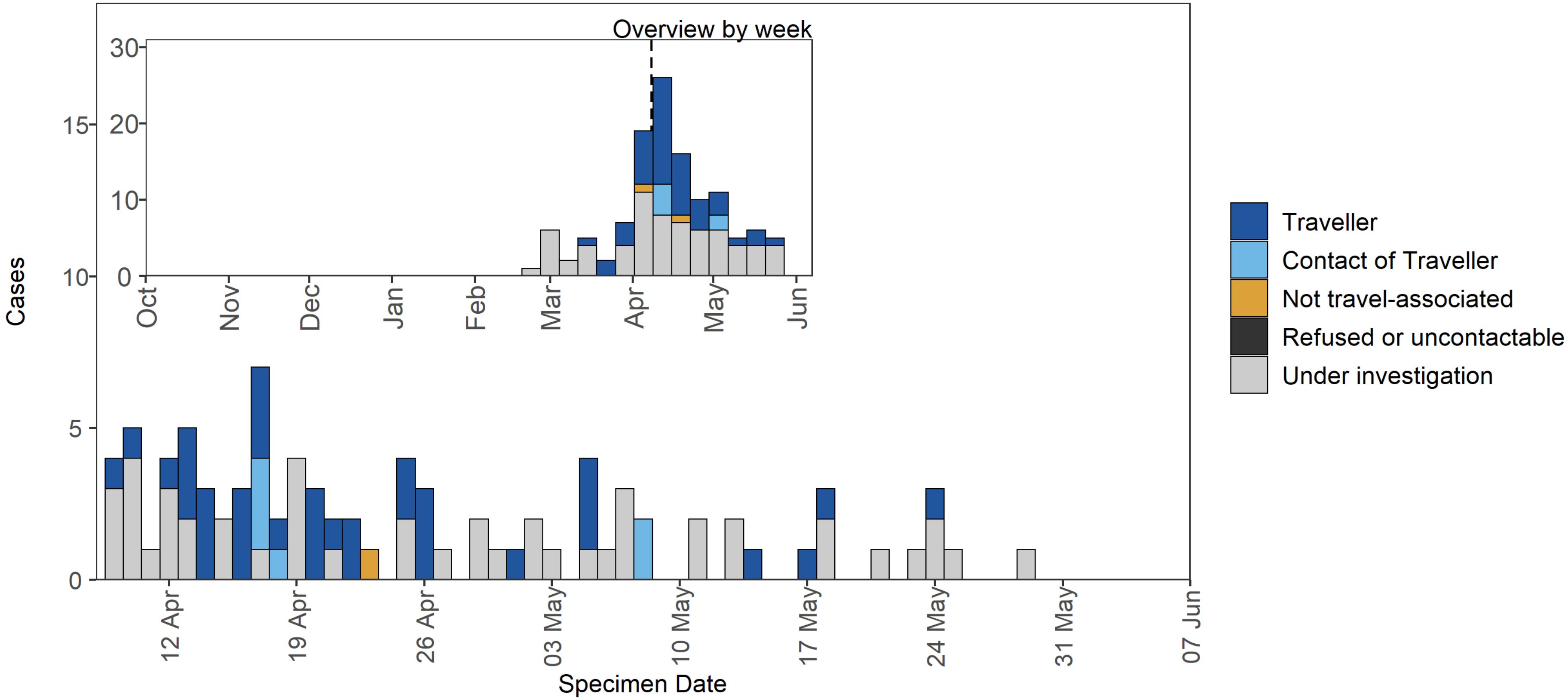
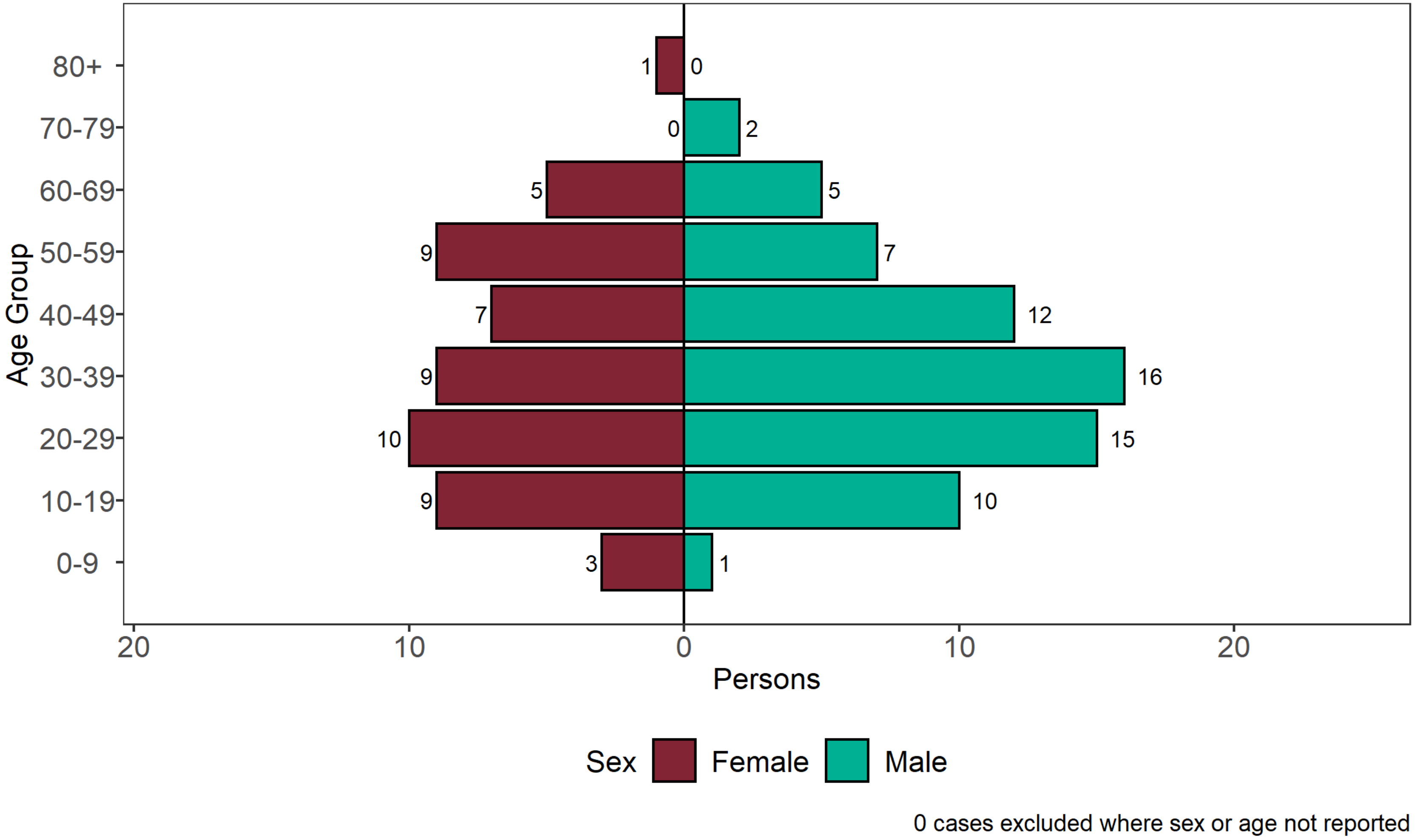


Figure 35. Age-sex pyramid of confirmed (sequencing) VUI-21MAY-02 (C.36.3) cases as of 7 June 2021
(Find accessible data used in this graph in underlying data.)



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

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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