Public Health England

Protecting and improving the nation's health

SARS-CoV-2 variant data update, England

Version 4

3 June 2021

This briefing provides an update on previous data located in technical and variant data update briefings and updates up to 27 May 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 14.

There are 5 variants of concern and 9 variants under investigation (Table 1).

Table 1. Variant lineage and designation as of 2 June 2021 (provisionally extinct variants removed)

WHO nomenclature as of 31 May 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
	B1.1.7 with E484K	VOC-21FEB-02	UK	VOC
Delta	B.1.617.2	VOC-21APR-02	India	VOC
Zeta	P.2	VUI-21JAN-01	Brazil	VUI
	A.23.1 with E484K	VUI-21FEB-01	UK	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
	B.1.214.2			Monitoring
	B.1.1.1 with L452Q and F490S			Monitoring
	R.1			Monitoring

WHO nomenclature as of 31 May 2021	Lineage	Designation	First detected in sequence from	Status
	B.1.1.28 with N501T and E484Q			Monitoring
	B.1.621			Monitoring
	B.1 with 214insQAS			Monitoring
	AT.1			Monitoring

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 WHO on 31 May 2021.

International Epidemiology

As of 1 June 2021, 529,107 sequences of Alpha, excluding the UK, are listed from 133 countries or territories on GISAID.

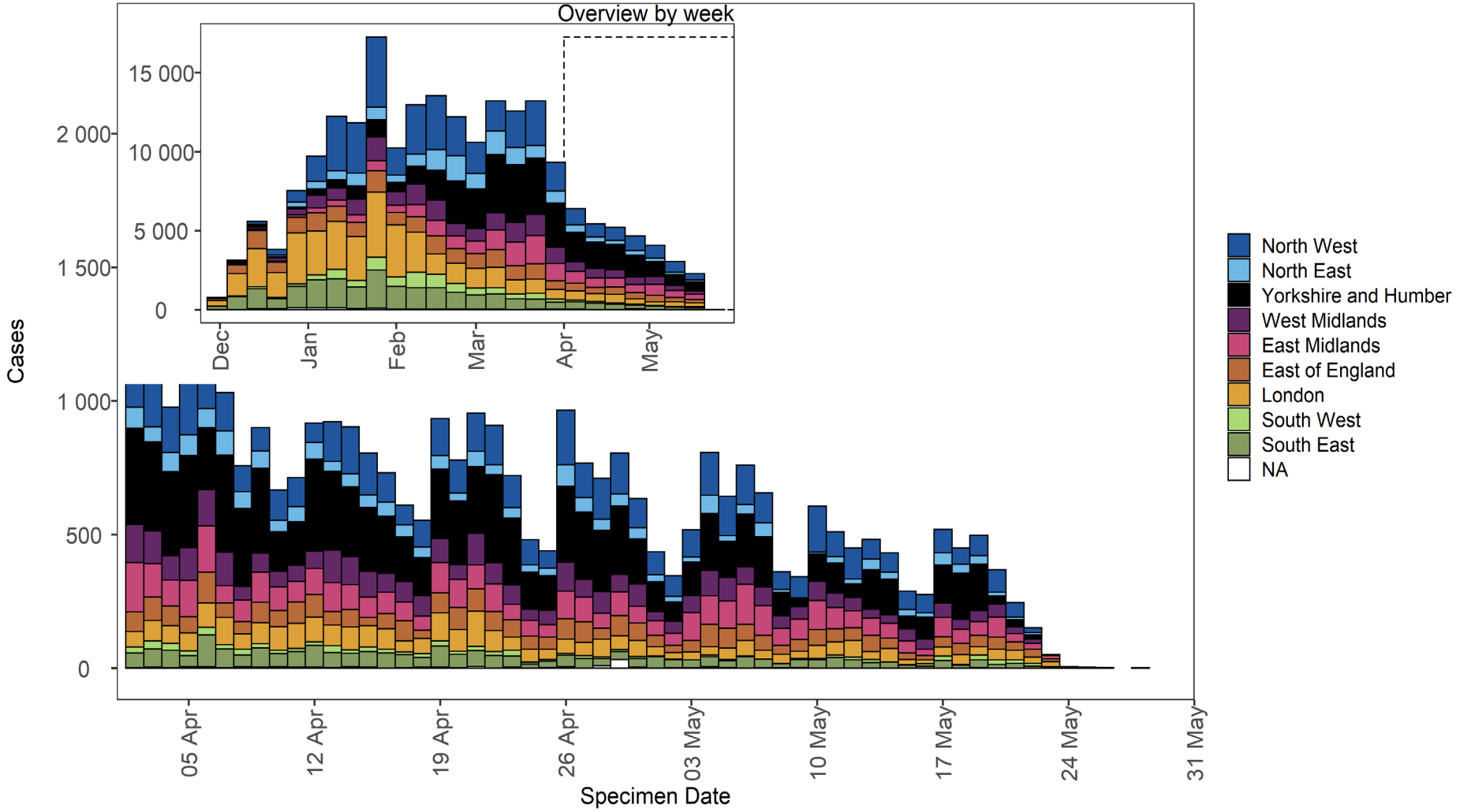
Epidemiology

Table 2. Number of confirmed and probable cases of Alpha by region of residence as of 31 May 2021

Region	Case number	Case proportion	Cases that have travelled	Proportion of travellers among cases[1]
East Midlands	15,501	7.3%	0	0%
East of England	19,305	9.0%	0	0%
London	38,547	18.1%	0	0%
North East	14,361	6.7%	0	0%
North West	41,019	19.2%	0	0%
South East	23,439	11.0%	0	0%
South West	7,721	3.6%	0	0%
West Midlands	17,887	8.4%	0	0%
Yorkshire and Humber	34,407	16.1%	0	0%
Unknown region	1,245	0.6%		N/A%
Total	213,432	-	0	0%

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

Figure 1. Confirmed and probable Alpha cases by specimen date as of 31 May 2021
(Find accessible data used in this graph in underlying data.)



VOC-21FEB-02 (B.1.1.7 cluster with E484K)

Through routine scanning of variation in VOC-20DEC-01 (B.1.1.7) a small number of B.1.1.7 sequences had acquired the spike protein mutation E484K. Information suggested more than one independent acquisition event. One cluster was predominant with evidence of community transmission and was designated variant under investigation on detection and on review re-designated as variant of concern VOC-21FEB-02 (VOC202102/02, B.1.1.7 cluster with E484K) on 5 February 2021.

International Epidemiology

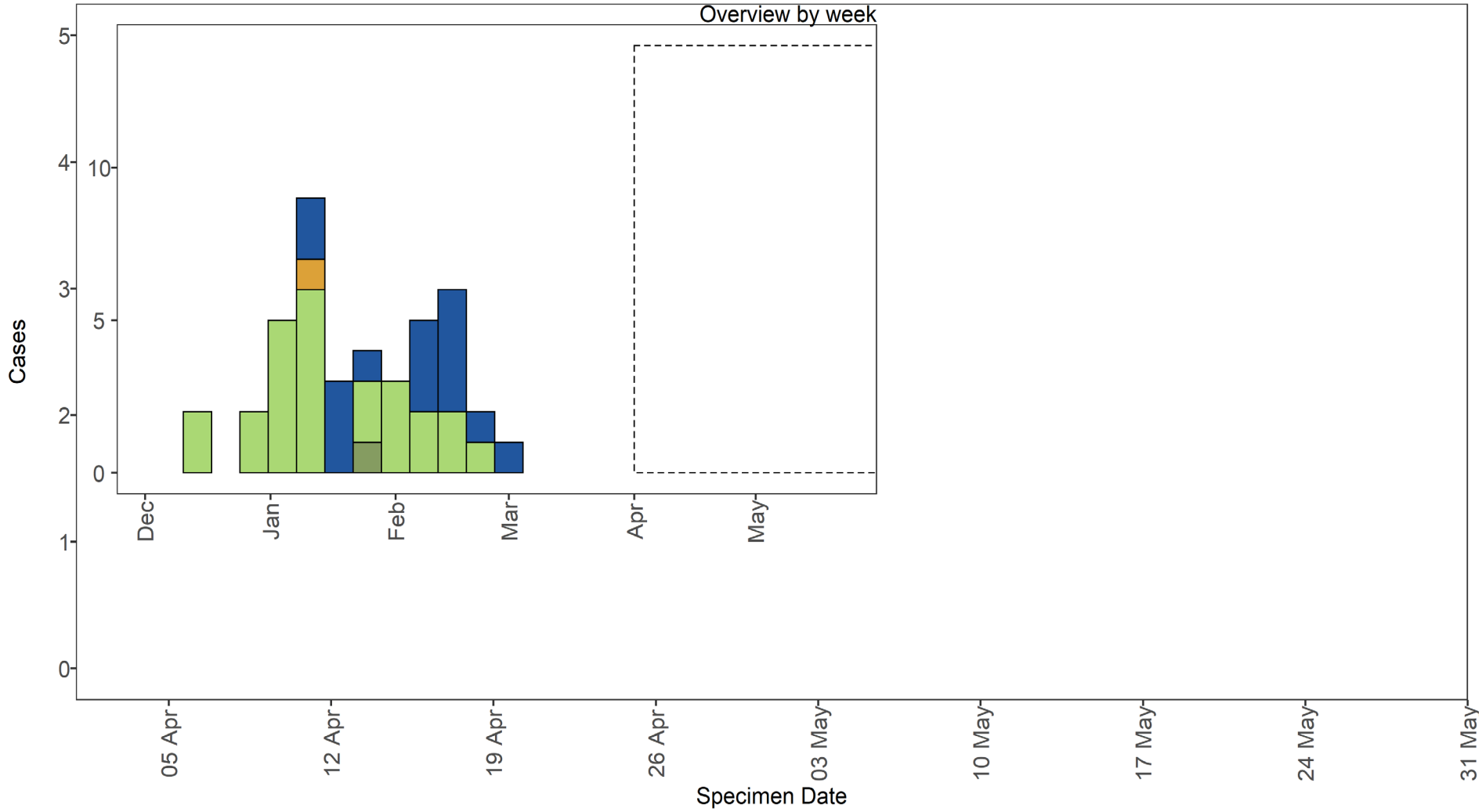
As of 1 June 2021, 9 sequences from the Netherlands and 8 sequences from Germany have been identified on GISAID.

Epidemiology

Table 3. Number of confirmed and probable VOC-21FEB-02 (B.1.1.7 cluster with E484K) cases, by region of residence as of 31 May 2021

Region	Case number	Case proportion	Cases that have travelled
East Midlands	0	0.0%	0
East of England	0	0.0%	0
London	1	2.3%	0
North East	0	0.0%	0
North West	15	34.9%	0
South East	1	2.3%	0
South West	26	60.5%	0
West Midlands	0	0.0%	0
Yorkshire and Humber	0	0.0%	0
Total	43	-	0

Figure 2. Confirmed and probable VOC-21FEB-02 (B.1.1.7 cluster with E484K) cases by specimen date as of 31 May 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. This was named Beta by WHO on 31 May 2021.

International Epidemiology

GISAID includes data on sequences available internationally. As of the 1 June 2021, 19,438 sequences of Beta, excluding the UK, are listed from 94 countries or territories.

Epidemiology

Table 4. Confirmed and probable cases of Beta, by region of residence as of 31 May 2021

Region	Case number	Case proportion	Cases that have travelled	Proportion of travellers among cases[1]
East Midlands	46	5.4%	28	60.9%
East of England	79	9.3%	44	55.7%
London	383	45.3%	172	44.9%
North East	13	1.5%	6	46.2%
North West	80	9.5%	31	38.8%
South East	102	12.1%	64	62.7%
South West	30	3.5%	17	56.7%
West Midlands	63	7.4%	26	41.3%
Yorkshire and Humber	31	3.7%	19	61.3%
Unknown region	19	2.2%	1	5.3%
Total	846	-	408	48.2%

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

Figure 3. Confirmed and probable Beta cases by specimen date as of 31 May 2021
(Find accessible data used in this graph in underlying data.)

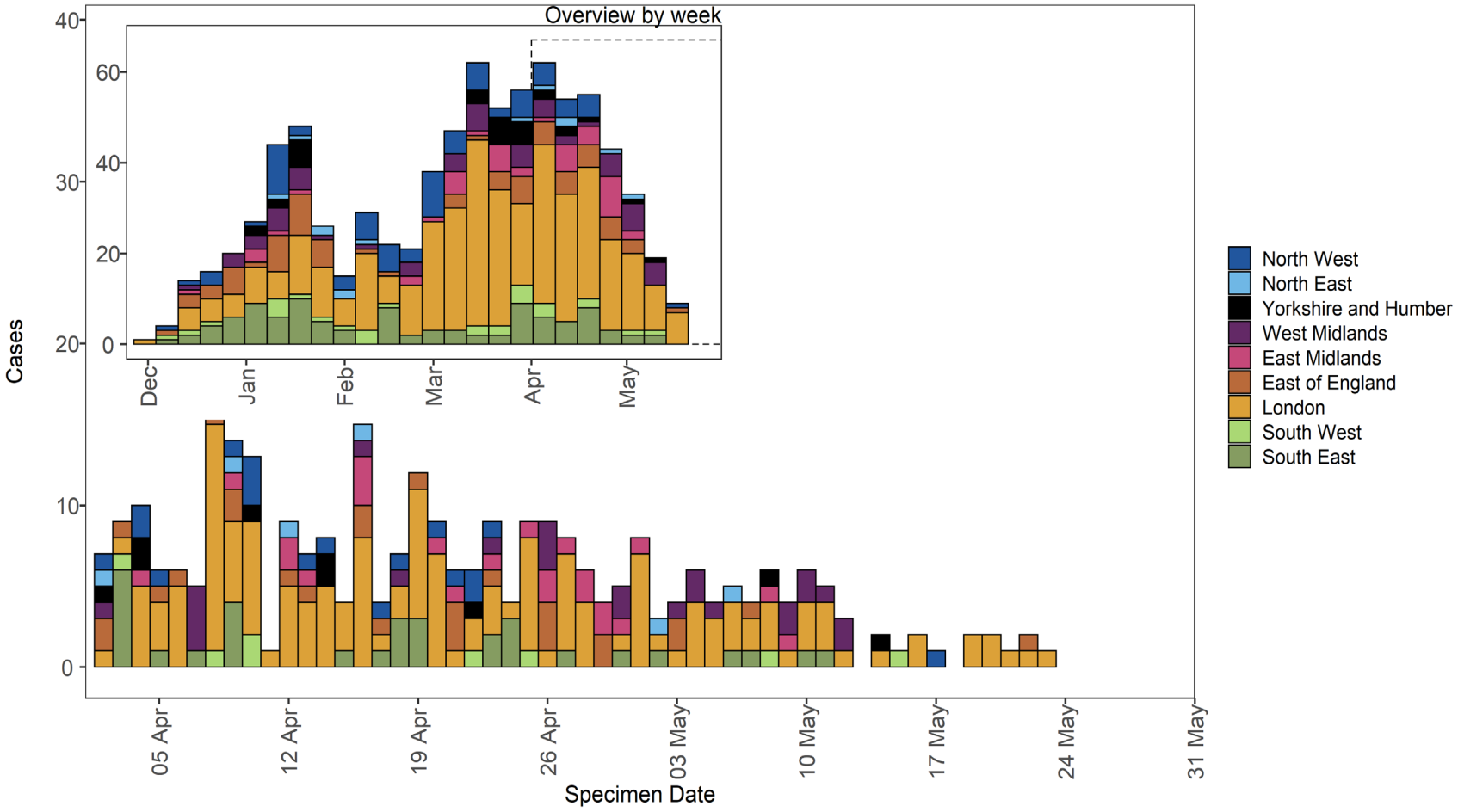
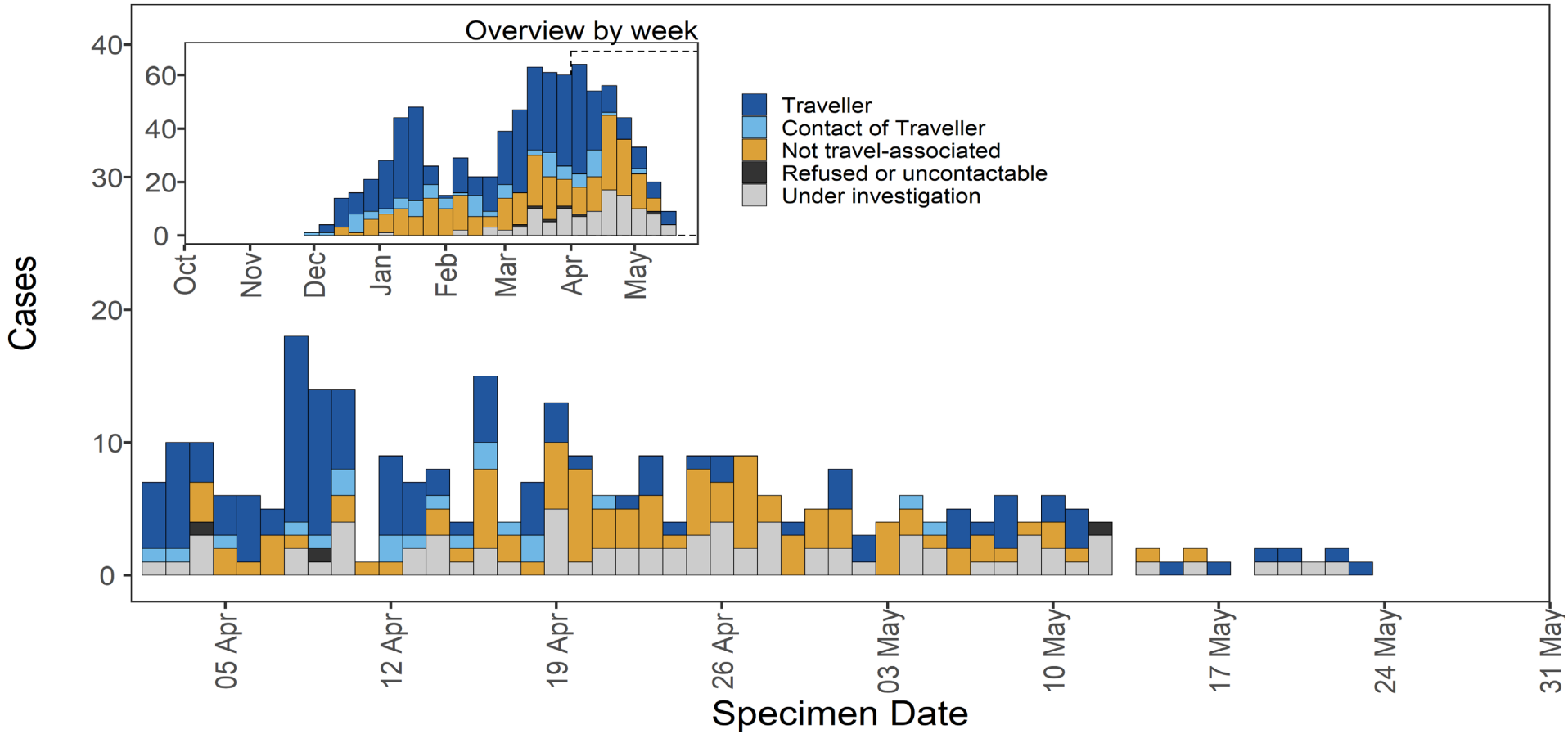


Figure 4. Travel data for confirmed and probable Beta cases by specimen date as of 31 May 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)



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 1 June 2021, 25,589 sequences (excluding the UK) of Gamma from 52 countries.

Epidemiology

Table 5. Number of confirmed and probable cases Gamma, by region of residence as of 31 May 2021

Region	Case number	Case proportion	Cases that have travelled	Proportion of travellers among cases[1]
East Midlands	3	2.0%	2	66.7%
East of England	12	7.9%	7	58.3%
London	83	55.0%	36	43.4%
North East	0	0%	0	0%
North West	4	2.6%	2	50%
South East	27	17.9%	8	29.6%
South West	8	5.3%	3	37.5%
West Midlands	6	4.0%	1	16.7%
Yorkshire and Humber	2	1.3%	1	50%
Unknown region	6	4.0%	3	50%
Total	151	-	63	41.7%

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

Figure 5. Confirmed and probable Gamma cases by specimen date as of 31 May 2021
(Find accessible data used in this graph in underlying data.)

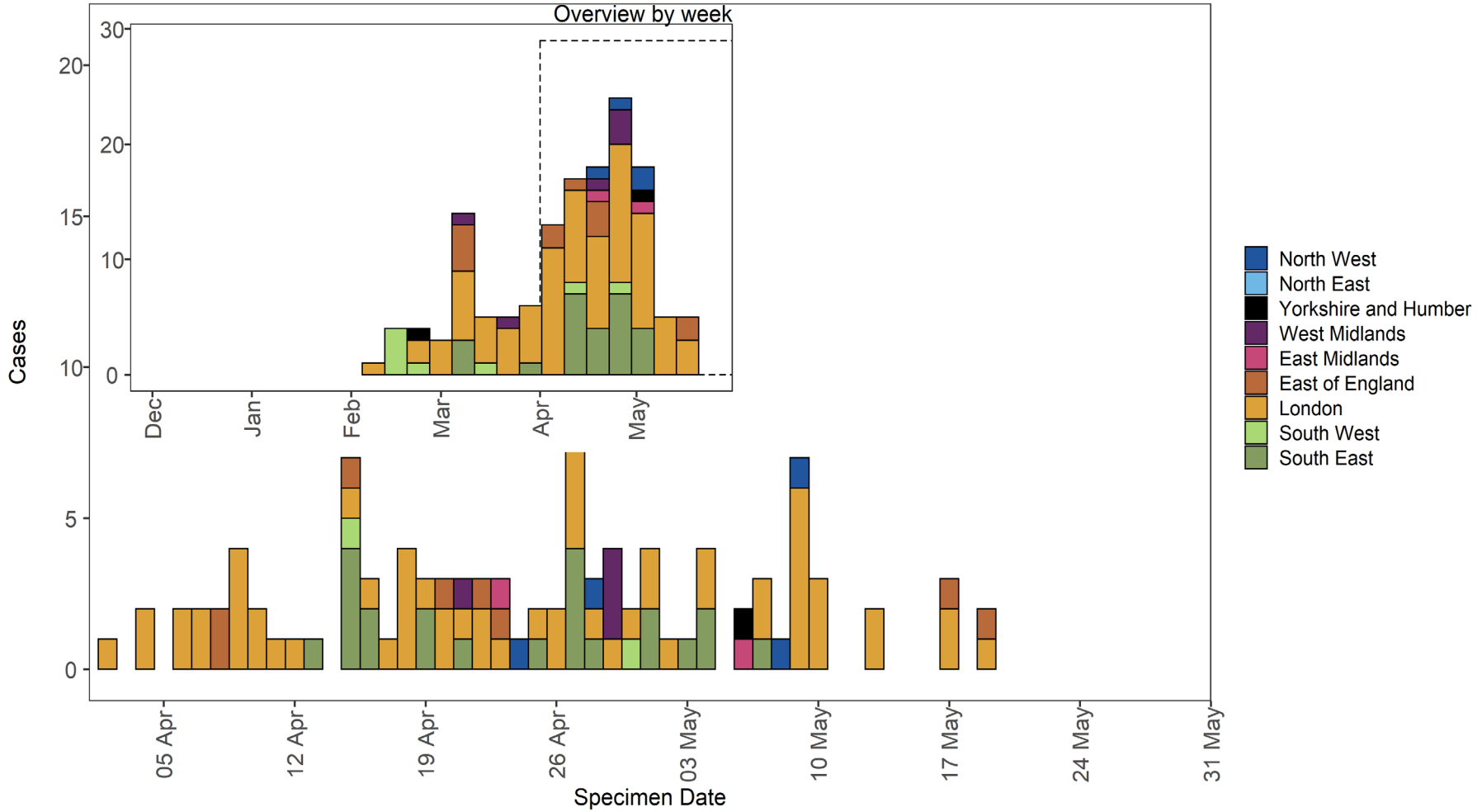
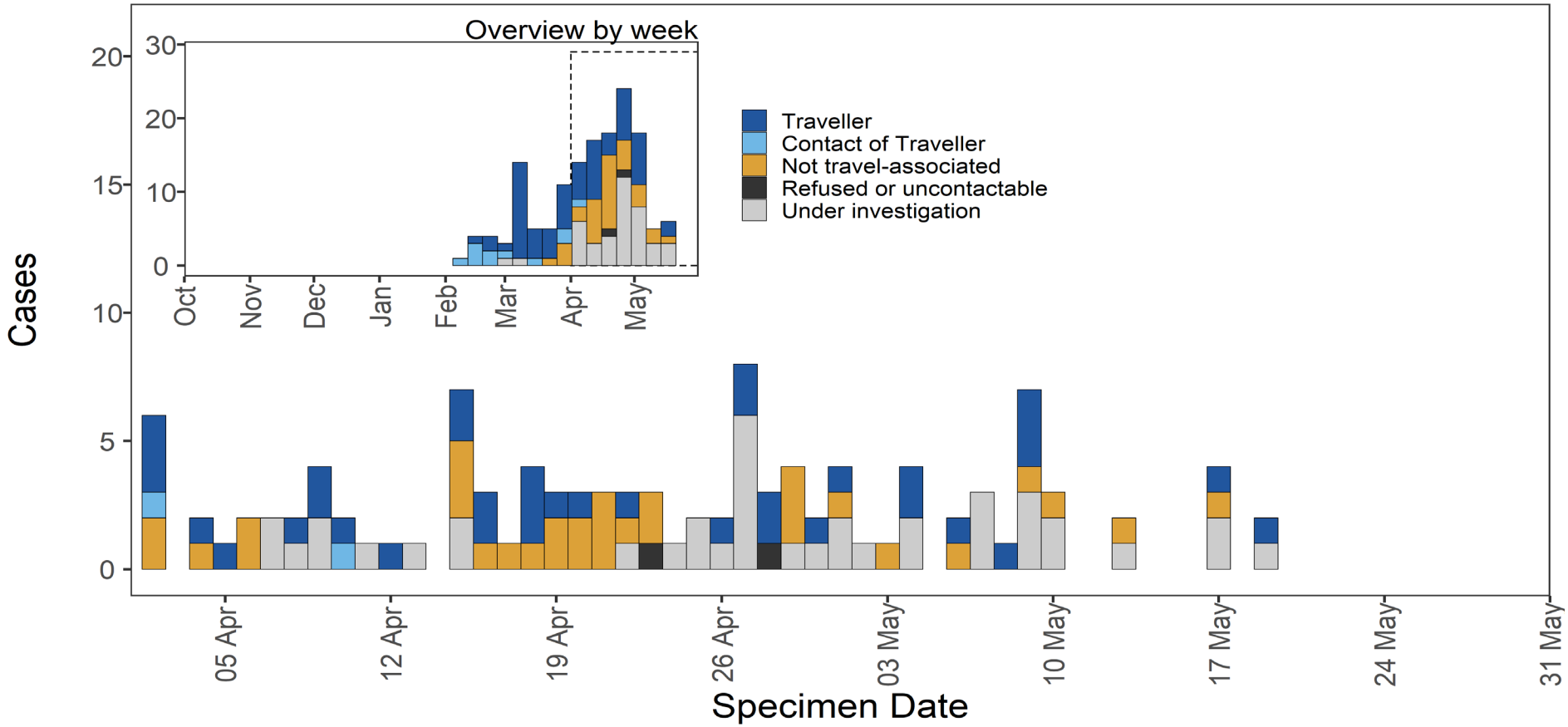


Figure 6. Travel data for confirmed and probable Gamma cases by specimen date as of 31 May 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)



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 1 June 2021, 21,914 sequences (excluding the UK) of Zeta from 50 countries.

Epidemiology

Table 6. Number of confirmed and probable cases Zeta, by region of residence as of 31 May 2021

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

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

Figure 7. Confirmed and probable Zeta cases by specimen date as of 31 May 2021
(Find accessible data used in this graph in underlying data.)

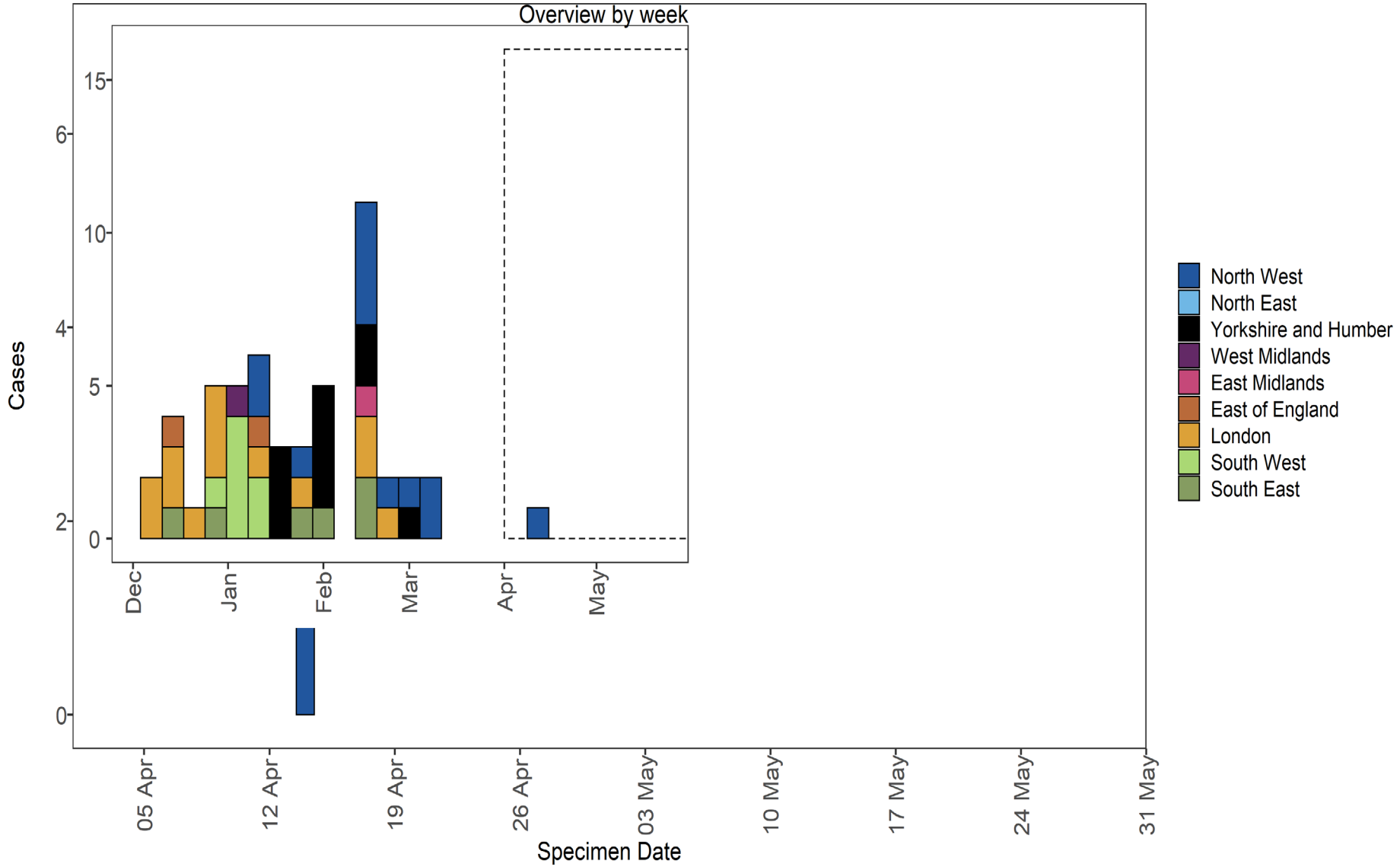
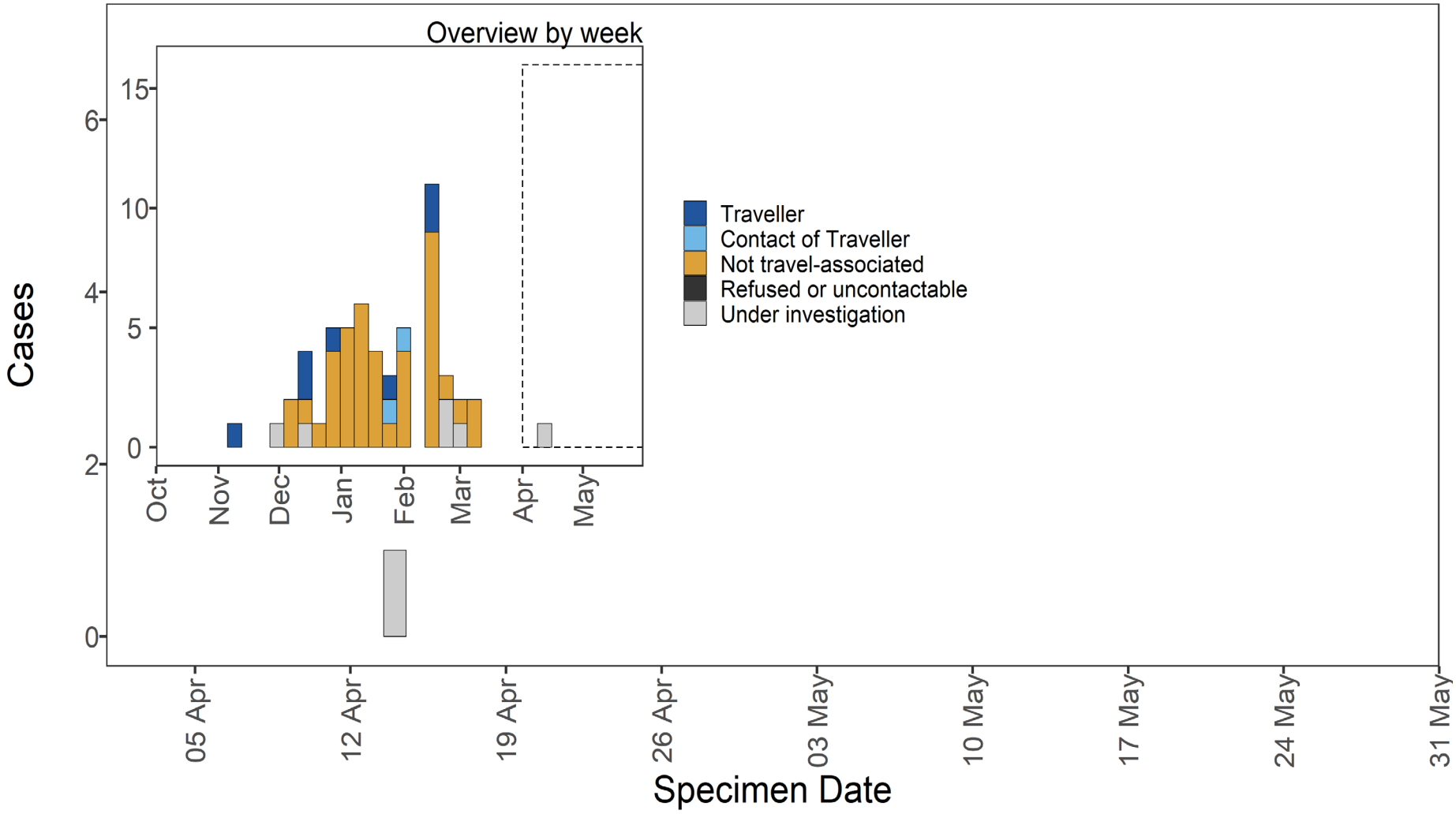


Figure 8. Travel data for confirmed and probable Zeta cases by specimen date as of 31 May 2021

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



VUI-21FEB-01 (A.23.1 with E484K)

This variant was first identified in Liverpool, UK, derived from a lineage first identified in Uganda without E484K. The variant was designated VUI-21FEB-01 (A.23.1 with E484K) on 5 February 2021. It was first detected in the UK in December 2020.

International Epidemiology

GISAID includes data on sequences available internationally. As of 1 June 2021, 4 sequences are listed of VUI-21FEB-01 (A.23.1 with E484K) (excluding the UK) from the Netherlands (1), India (2) and Israel (1).

Epidemiology

Table 7. Number of confirmed and probable VUI-21FEB-01 (A.23.1 with E484K) cases, by region of residence as of 31 May 2021

Region	Case number	Case proportion	Cases that have travelled
East Midlands	0	0.0%	0
East of England	0	0.0%	0
London	0	0.0%	0
North East	0	0.0%	0
North West	76	96.2%	0
South East	0	0.0%	0
South West	0	0.0%	0
West Midlands	1	1.3%	0
Yorkshire and Humber	0	0.0%	0
Unknown region	2	2.5%	
Total	79	-	0

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

Figure 9. Confirmed and probable VUI-21FEB-01 (A.23.1 with E484K) cases by specimen date as of 31 May 2021

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

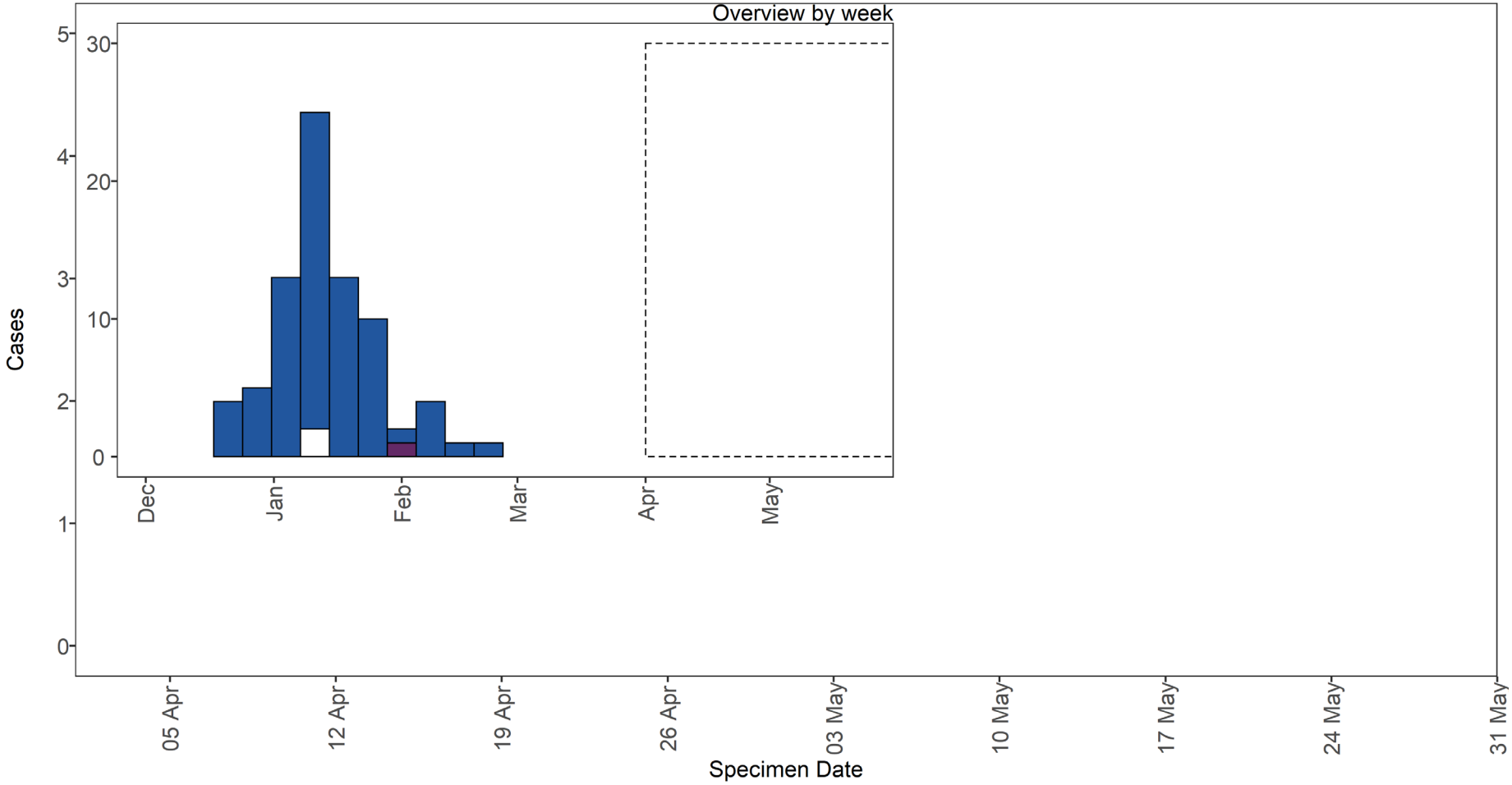
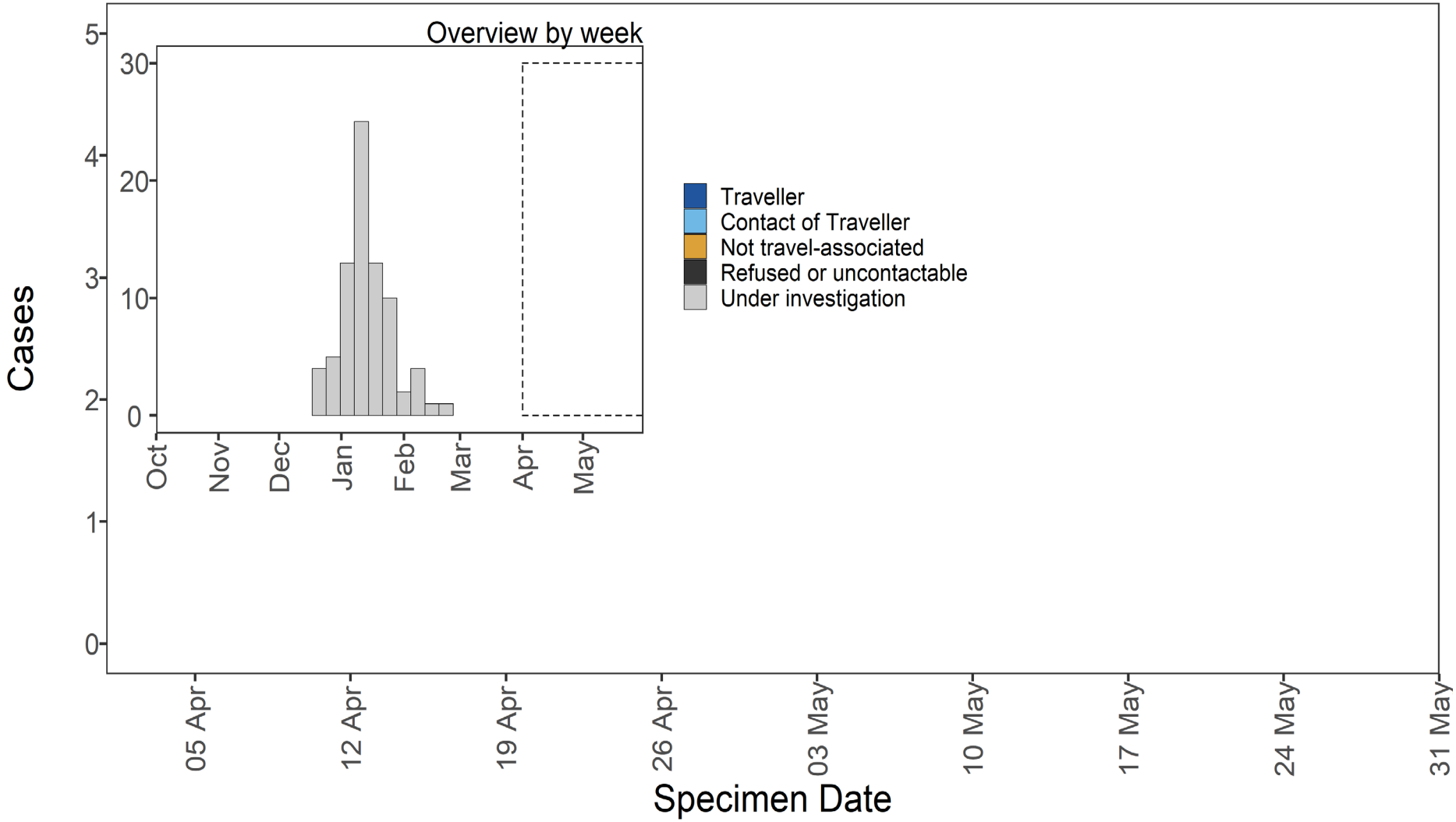


Figure 10. Travel data for confirmed and probable VUI-21FEB-01 (A.23.1 with E484K) cases by specimen date as of 31 May 2021. Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)



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.

International Epidemiology

GISAID includes data on sequences available internationally.
As of 1 June 2021, 4,997 sequences of Eta are listed, from 62 countries or territories, excluding the UK.

Epidemiology

Table 8. Number of confirmed and probable cases Eta, by region of residence as of 31 May 2021

Region	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	6.7%	22	75.9%
London	155	35.6%	93	60%
North East	4	0.9%	4	100%
North West	74	17.0%	19	25.7%
South East	80	18.3%	27	33.8%
South West	18	4.1%	6	33.3%
West Midlands	35	8.0%	13	37.1%
Yorkshire and Humber	20	4.6%	9	45%
Unknown region	11	2.5%	4	36.4%
Total	436	-	202	46.3%

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

Figure 11. Confirmed and probable cases Eta by specimen date as of 31 May 2021

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

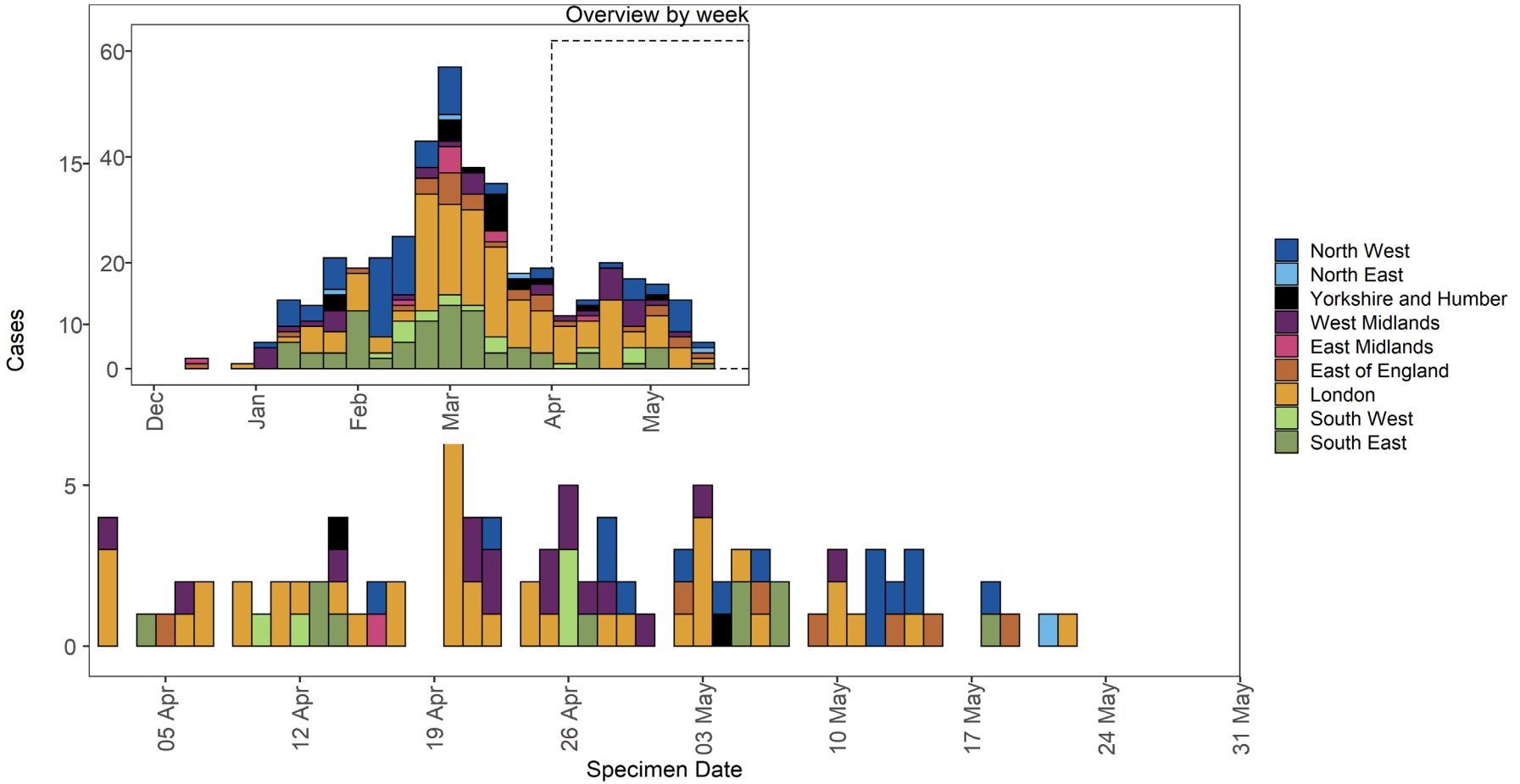
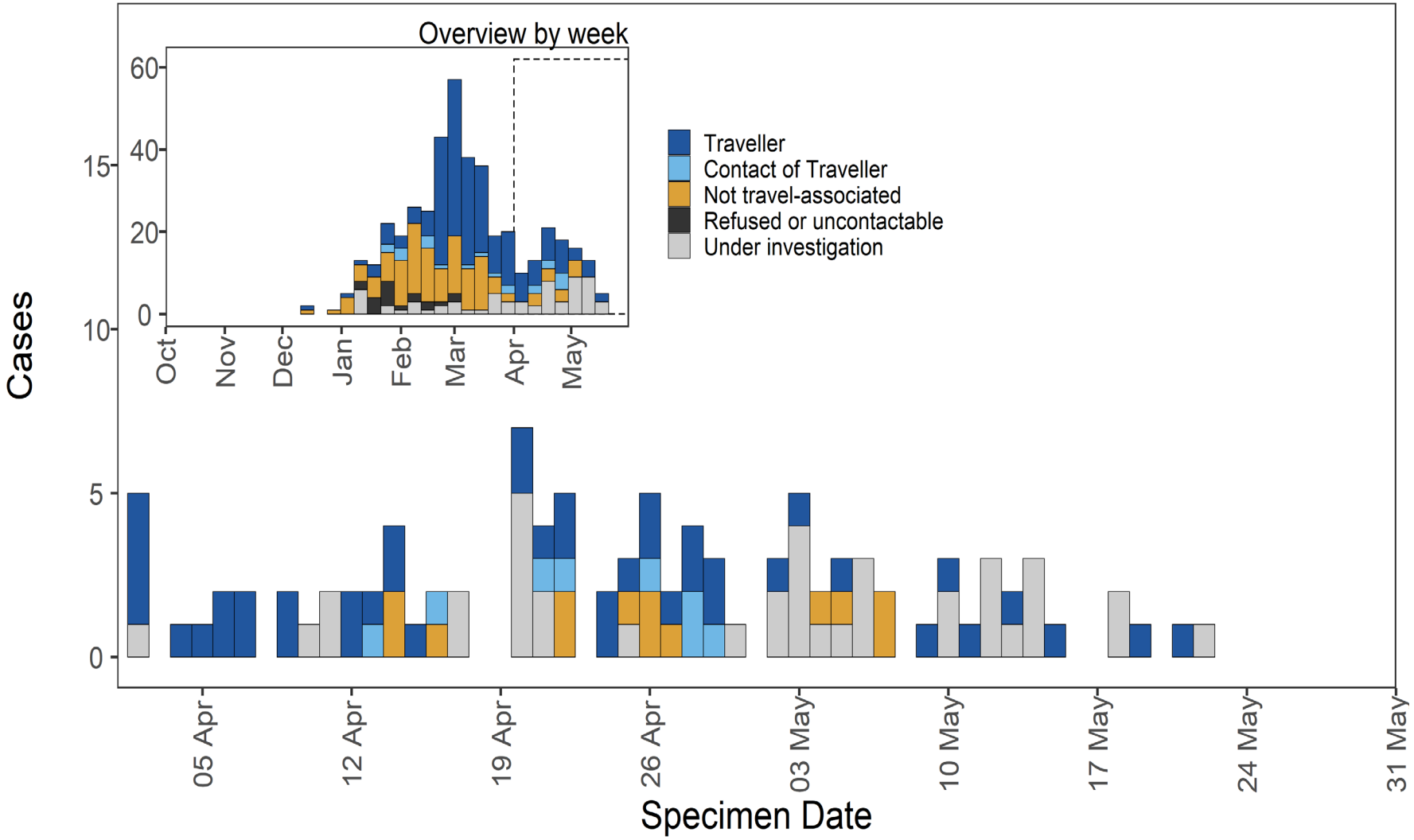


Figure 12. Travel data for confirmed and probable Eta cases by specimen date as of 31 May 2021

Larger plot includes last 60 days only. (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.

International Epidemiology

GISAID includes data on sequences available internationally. As of 1 June 2021, 121 international VUI-21FEB-04 sequences, excluding the UK: Bangladesh (1), Cameroon (2), Canada (25), Denmark (1), France (7), Germany (12), Ghana (1), Greece (2), India (2), Italy (12), Nigeria (10), Sweden (4), Switzerland (15), USA (27).

Table 9. Number of confirmed and probable VUI-21FEB-04 (B.1.1.318) cases, by region of residence as of 31 May 2021

Region	Case number	Case proportion	Cases that have travelled	Proportion of travellers among cases[1]
East Midlands	10	4.1%	4	40%
East of England	23	9.5%	11	47.8%
London	93	38.3%	39	41.9%
North East	2	0.8%	2	100%
North West	45	18.5%	10	22.2%
South East	45	18.5%	14	31.1%
South West	1	0.4%	1	100%
West Midlands	7	2.9%	4	57.1%
Yorkshire and Humber	11	4.5%	1	9.1%
Unknown region	6	2.5%	3	50%
Total	243	-	89	36.6%

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

Figure 13. Confirmed and probable VUI-21FEB-04 (B.1.1.318) cases by specimen date as of 31 May 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)

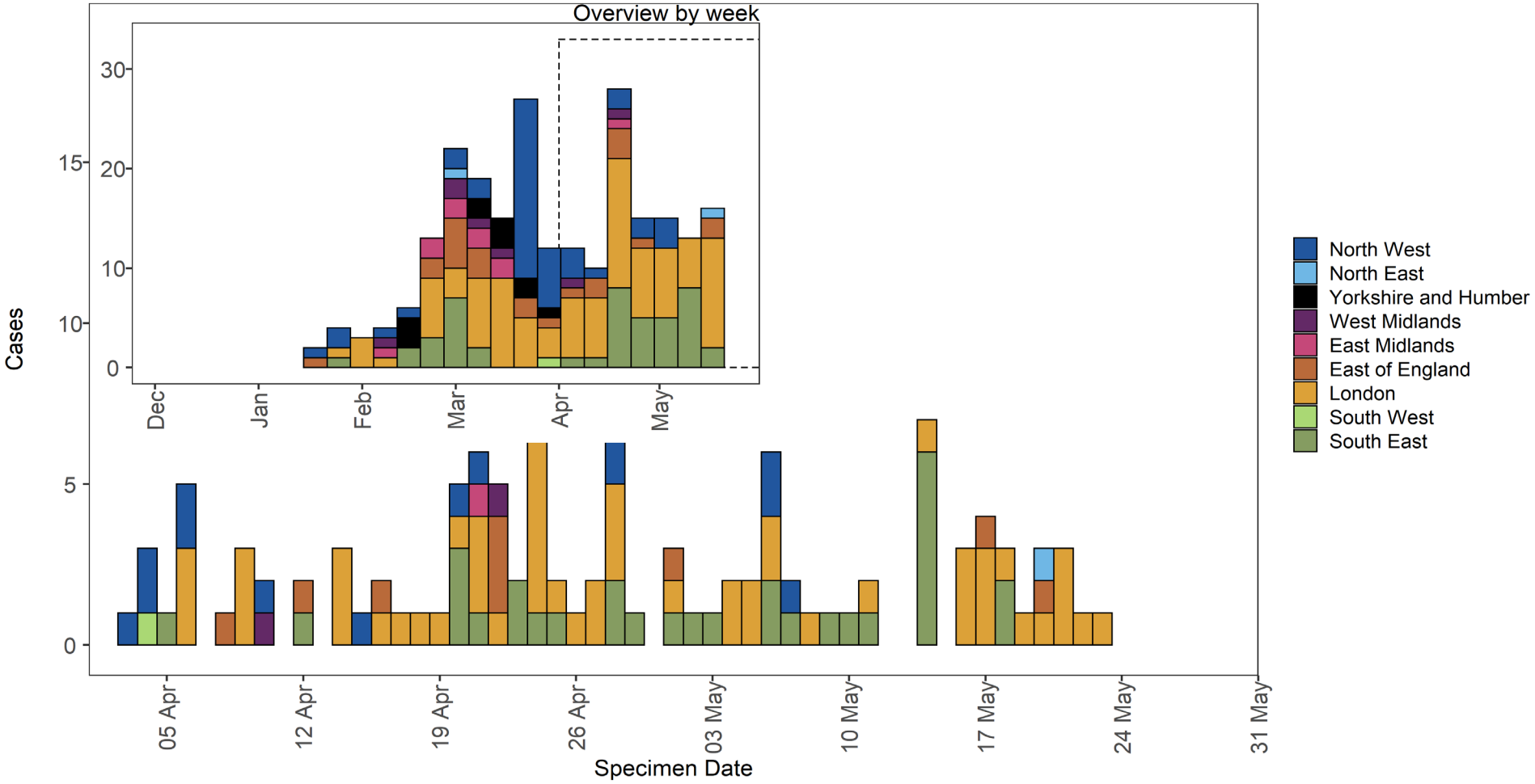
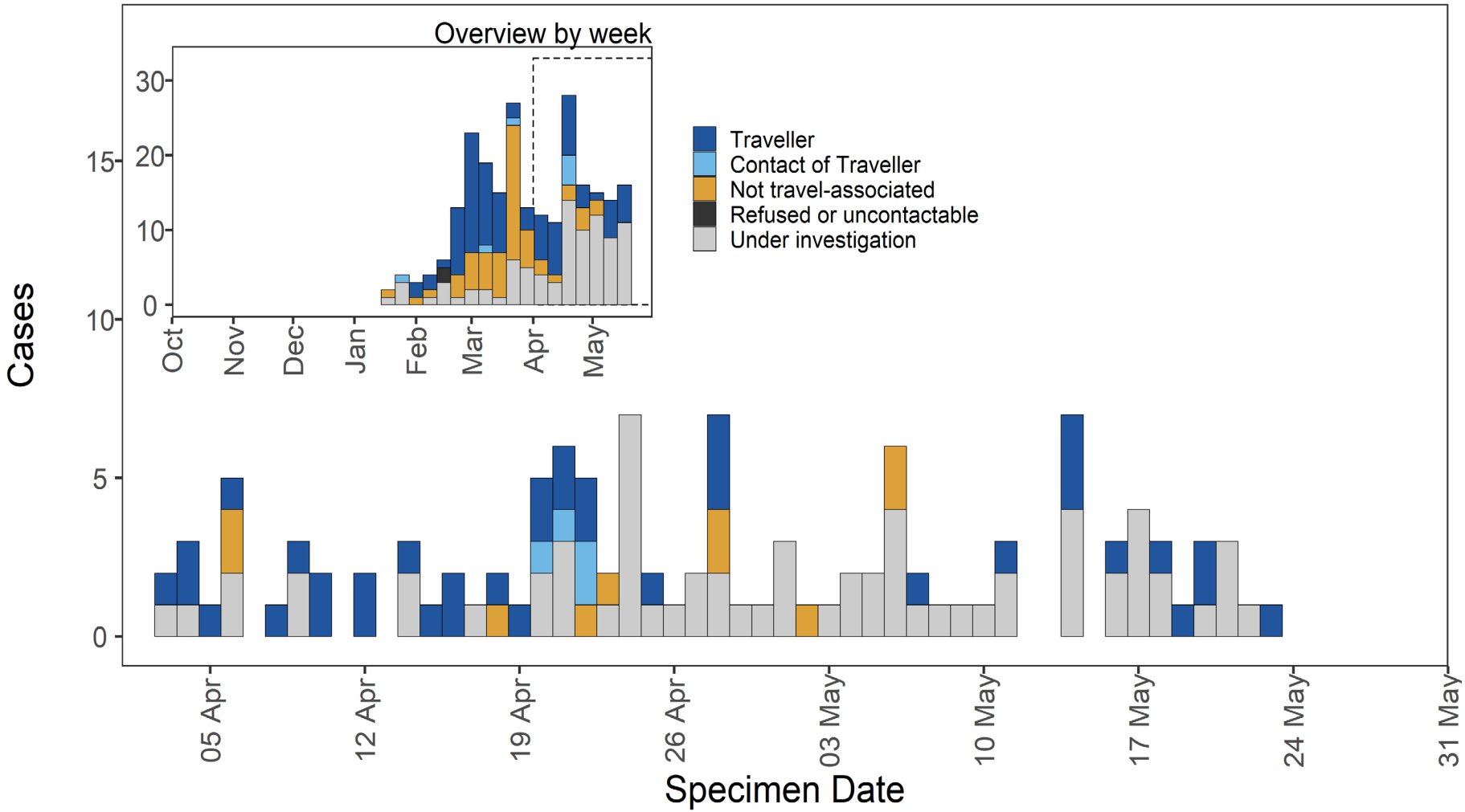


Figure 14. Travel data for confirmed and probable VUI-21FEB-04 (B.1.1.318) cases by specimen date as of 31 May 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)



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 1 June 2021, 227 sequences are listed internationally of Theta excluding the UK: Australia (3), China (1), Germany (8), Hong Kong (10), Japan (4), Netherlands (6), New Zealand (3), Norway (2), Philippines (179), Singapore (2), South Korea (1), USA (8).

Table 10. Number of confirmed and probable Theta cases, by region of residence as of 31 May 2021

Region	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	16.7%	1	100%
London	1	16.7%	0	0%
North East	0	0.0%	0	0%
North West	1	16.7%	1	100%
South East	0	0.0%	0	0%
South West	2	33.3%	2	100%
West Midlands	0	0.0%	0	0%
Yorkshire and Humber	1	16.7%	1	100%
Total	6	-	5	83.3%

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

Figure 15. Confirmed and probable Theta cases by specimen date as of 31 May 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)

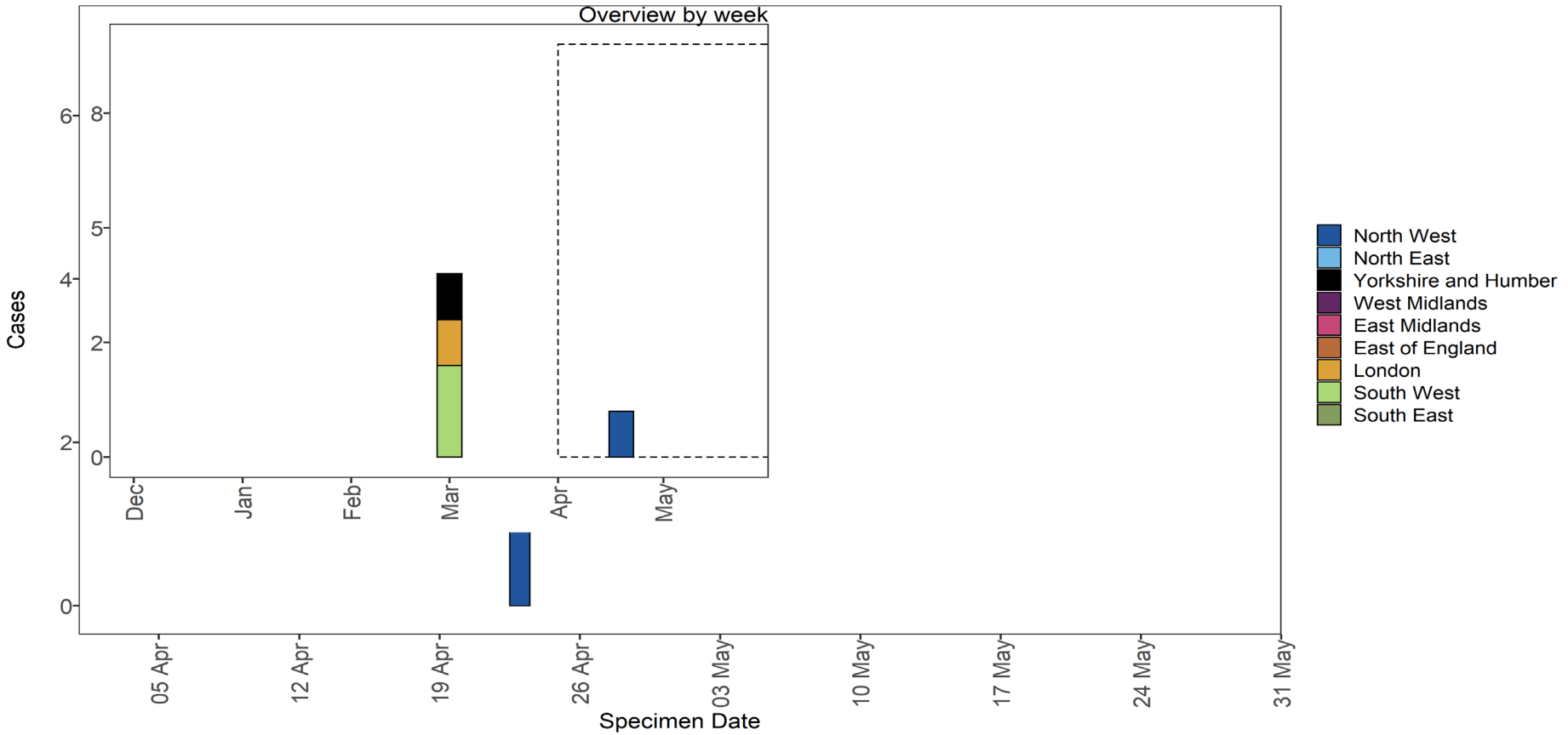
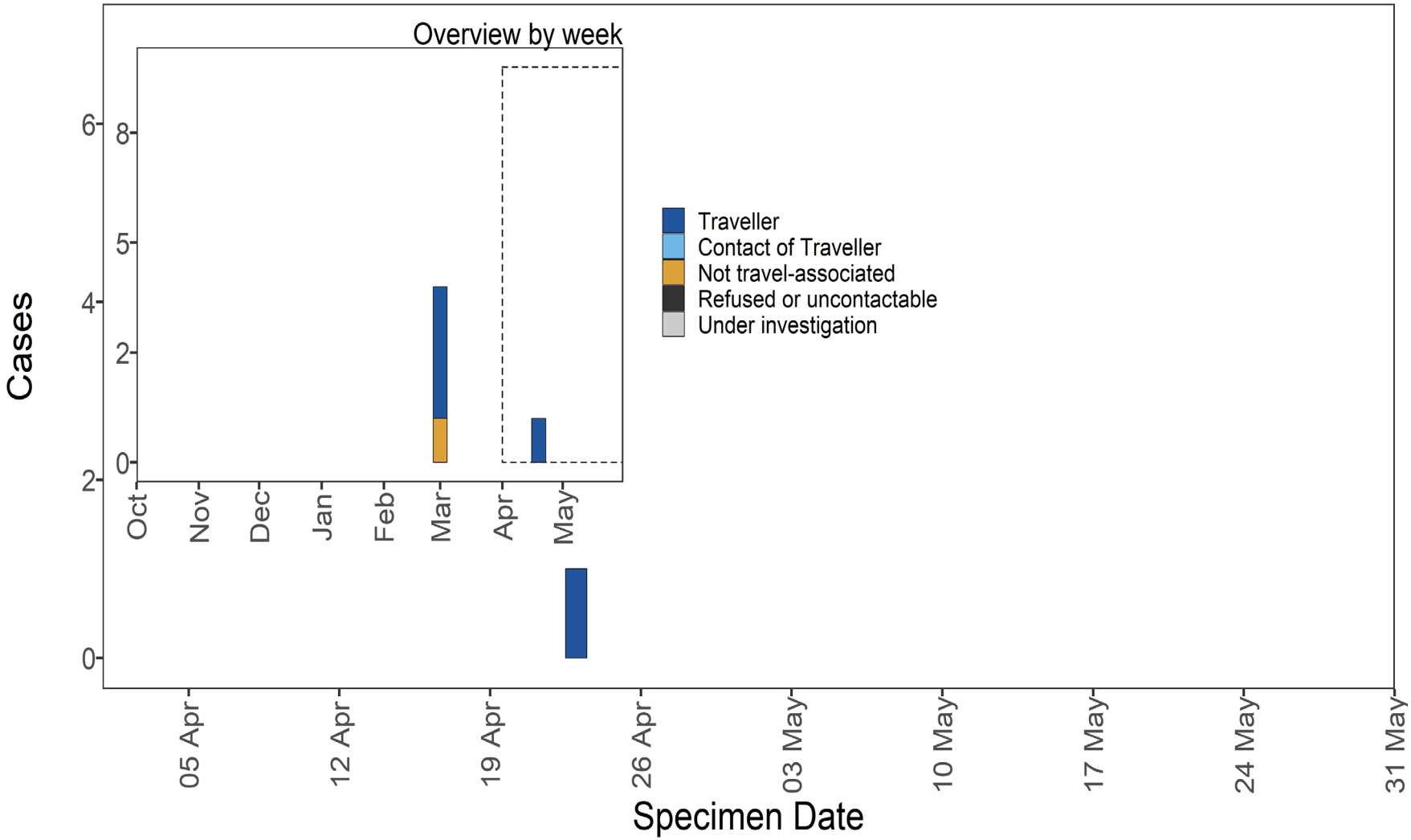


Figure 16. Travel data for confirmed and probable Theta cases by specimen date as of 31 May 2021

Larger plot includes last 60 days only. (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 1 June 2021, 2,353 Kappa sequences from the following countries (excluding the UK) have been identified in GISAID: Australia (37), Austria (1), Bahrain (8), Belgium (8), Canada (38), Curacao (1), Czech Republic (4), Denmark (27), Finland (1), France (7), Germany (85), Ghana (4), Greece (1), Guadeloupe (2), Hong Kong (9), India (1,667), Ireland (58), Italy (5), Japan (24), Jordan (4), Luxembourg (5), Malaysia (1), Mexico (3), Nepal (2), Netherlands (9), New Zealand (4), Portugal (9), Qatar (3), Saint Martin (2), Singapore (60), South Korea (5), Spain (4), Sweden (5), Switzerland (9), Thailand (1), USA (239), Uganda (1).

Table 11. Number of confirmed and probable Kappa cases, by region of residence as of 31 May 2021

Region	Case number	Case proportion	Cases that have travelled	Proportion of travellers among cases[1]
East Midlands	48	11.6%	24	50%
East of England	31	7.5%	20	64.5%
London	173	41.9%	101	58.4%
North East	4	1.0%	2	50%
North West	32	7.7%	22	68.8%
South East	41	9.9%	24	58.5%
South West	11	2.7%	9	81.8%
West Midlands	48	11.6%	19	39.6%
Yorkshire and Humber	16	3.9%	12	75%
Unknown region	9	2.2%	5	55.6%
Total	413	-	238	57.6%

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

Figure 17. Confirmed and probable Kappa cases by specimen date as of 31 May 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)

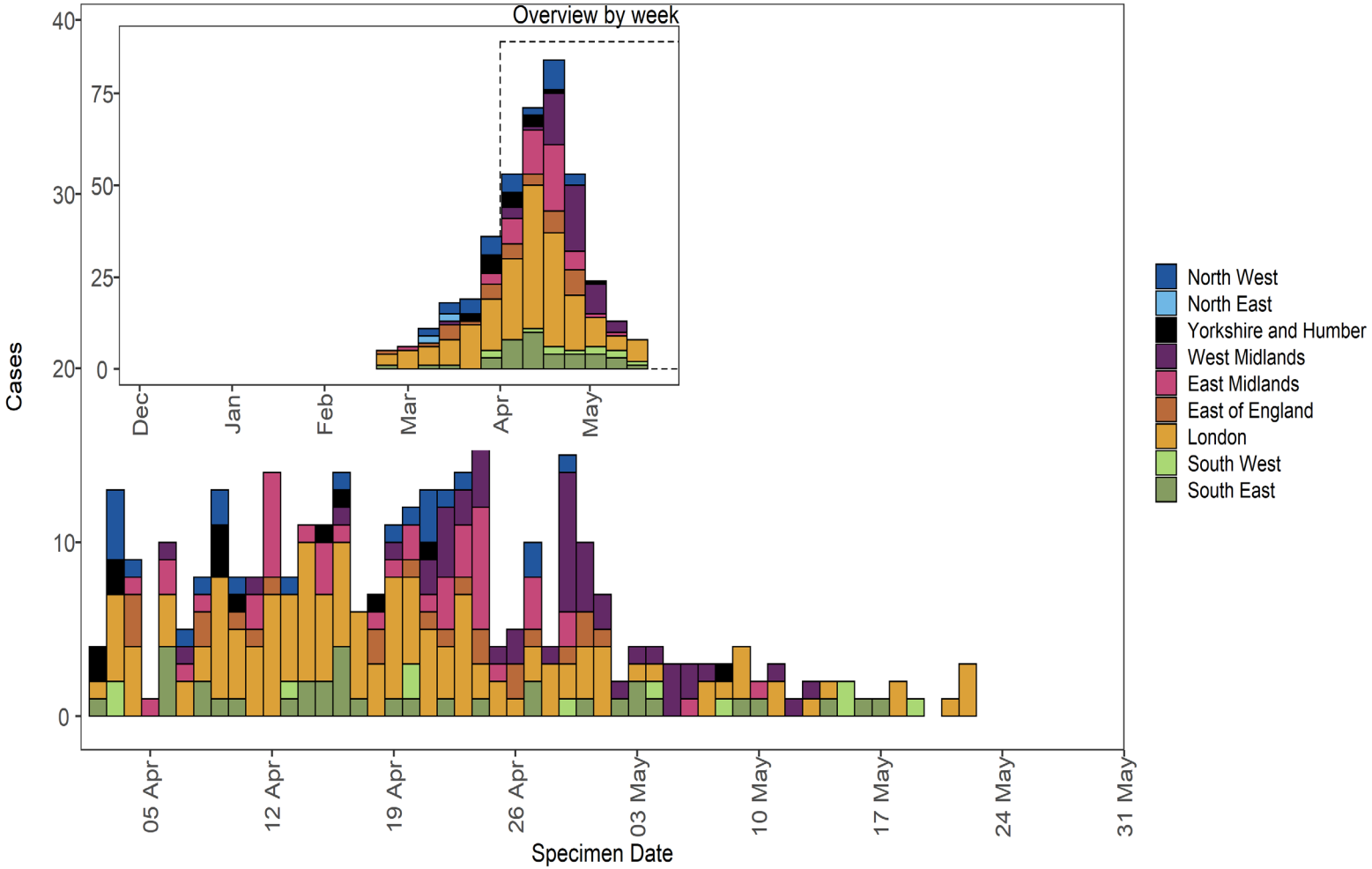
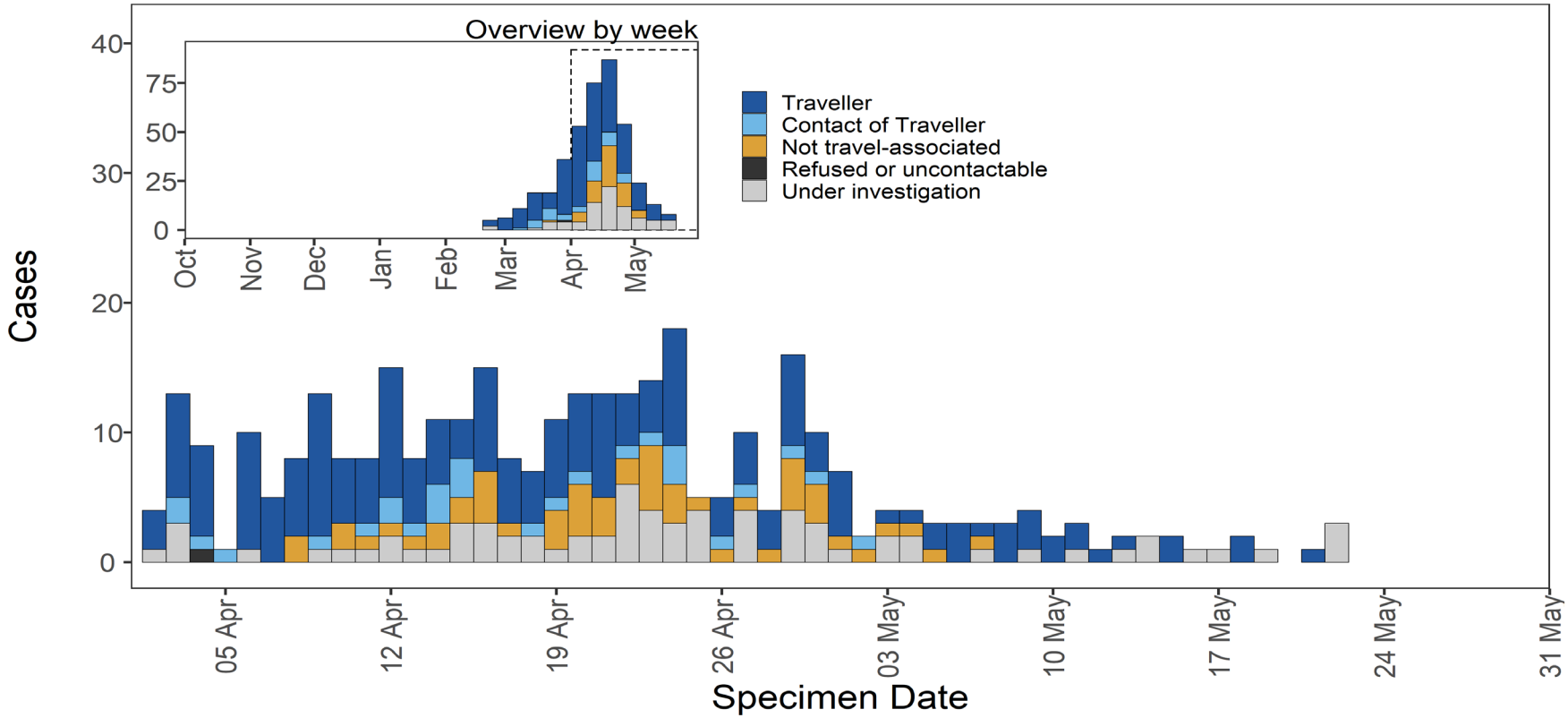


Figure 18. Travel data for confirmed and probable Kappa cases by specimen date as of 31 May 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.) N/A indicates information is pending or not available.



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 1 June 2021, 71 sequences from the following countries (excluding the UK) have been identified in GISAID of VUI-21APR-03 (B.1.617.3): India (68), Russia (2), USA (1).

Table 12. Number of confirmed and probable VUI-21APR-03 (B.1.617.3) cases, by region of residence as of 31 May 2021

Region	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	35.7%	3	60%
North East	0	0.0%	0	0%
North West	7	50.0%	3	42.9%
South East	2	14.3%	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	14	-	7	50%

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

* Denominator is all cases, including those with unknown or pending travel status.

Figure 19. Confirmed and probable VUI-21APR-03 (B.1.617.3) cases by specimen date as of 31 May 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)

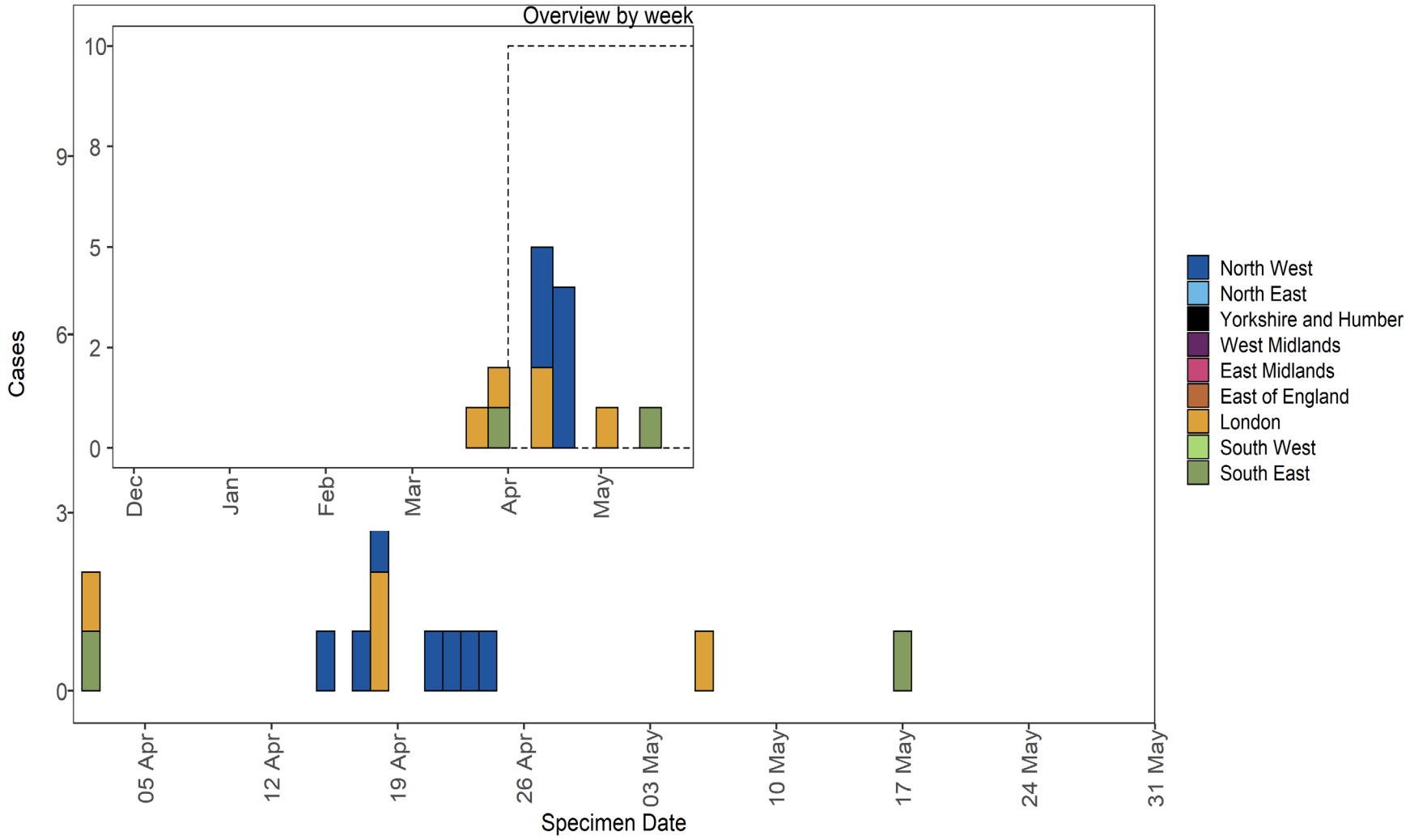
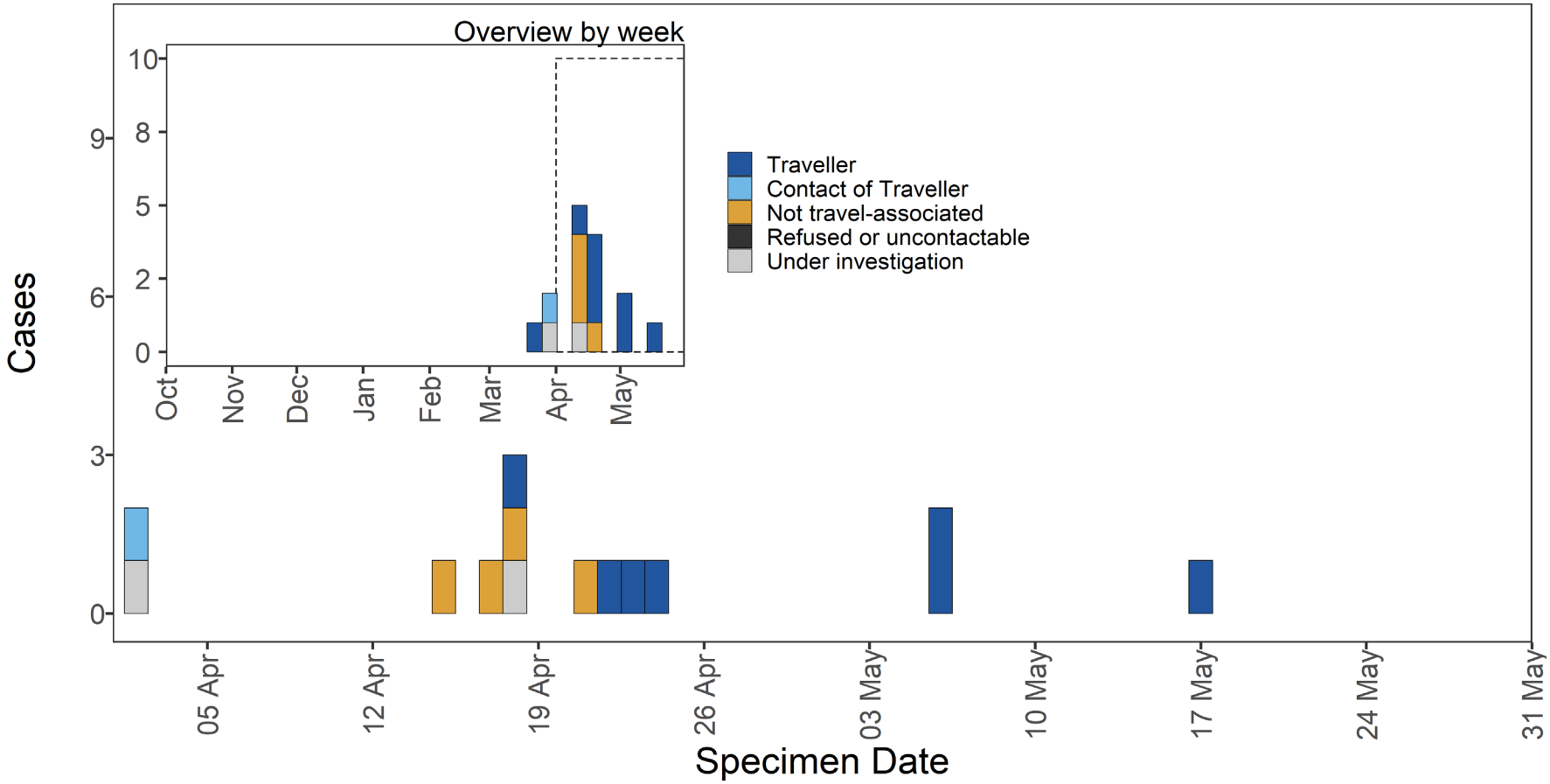


Figure 20. Travel data for confirmed and probable VUI-21APR-03 (B.1.617.3) cases by specimen date as of 31 May 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)



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

Table 13. Number of confirmed and probable VUI-21MAY-01 (AV.1) cases, by region of residence as of 31 May 2021

Region	Case number	Case proportion	Cases that have travelled	Proportion of travellers among cases[1]
East Midlands	5	4.1%	0	0%
East of England	10	8.2%	0	0%
London	1	0.8%	0	0%
North East	0	0.0%	0	0%
North West	6	4.9%	0	0%
South East	0	0.0%	0	0%
South West	0	0.0%	0	0%
West Midlands	4	3.3%	0	0%
Yorkshire and Humber	96	78.7%	1	1%
Total	122	-	1	0.8%

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

Figure 21. Confirmed and probable VUI-21MAY-01 (AV.1) cases by specimen date as of 31 May 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)

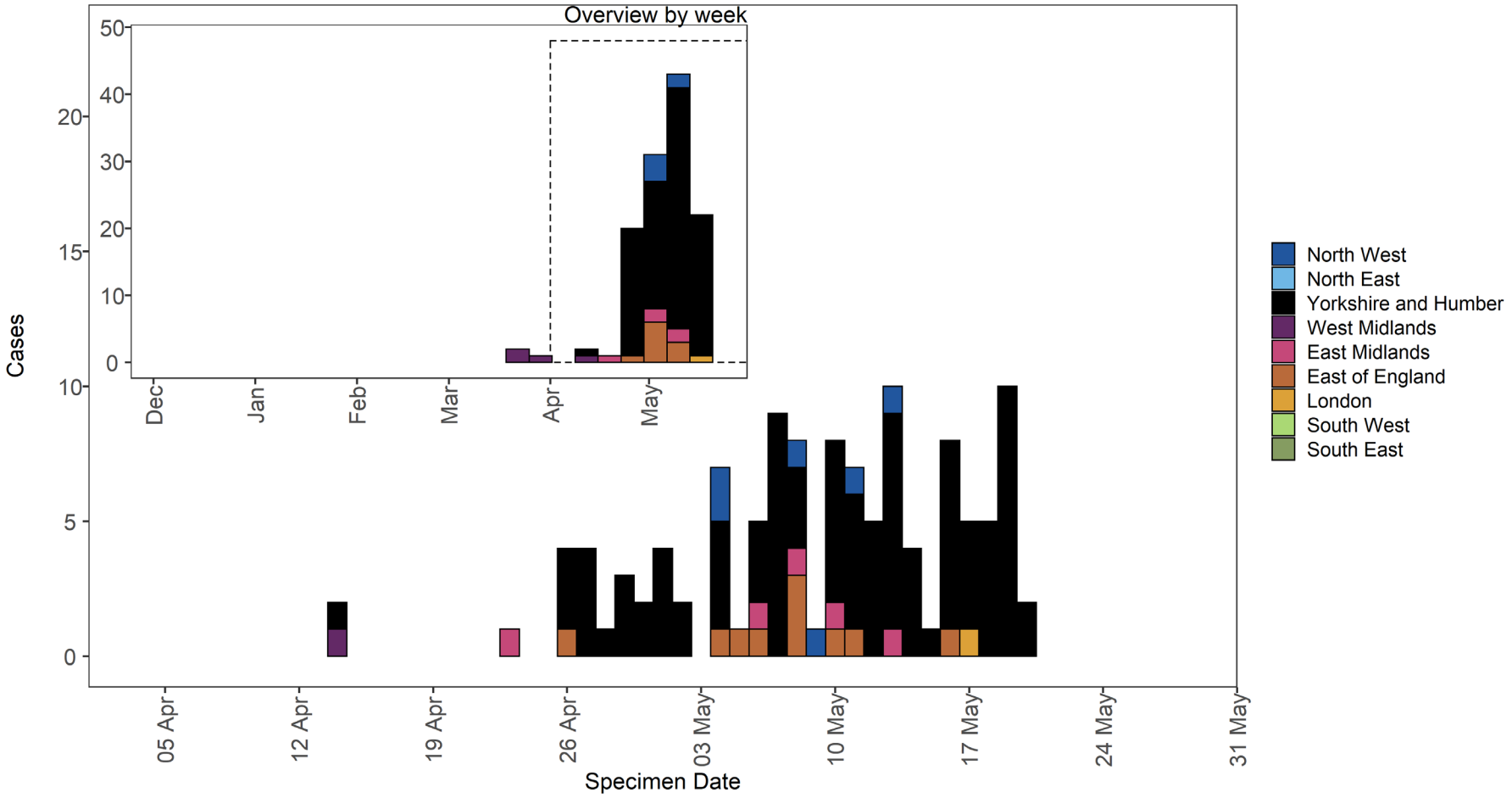
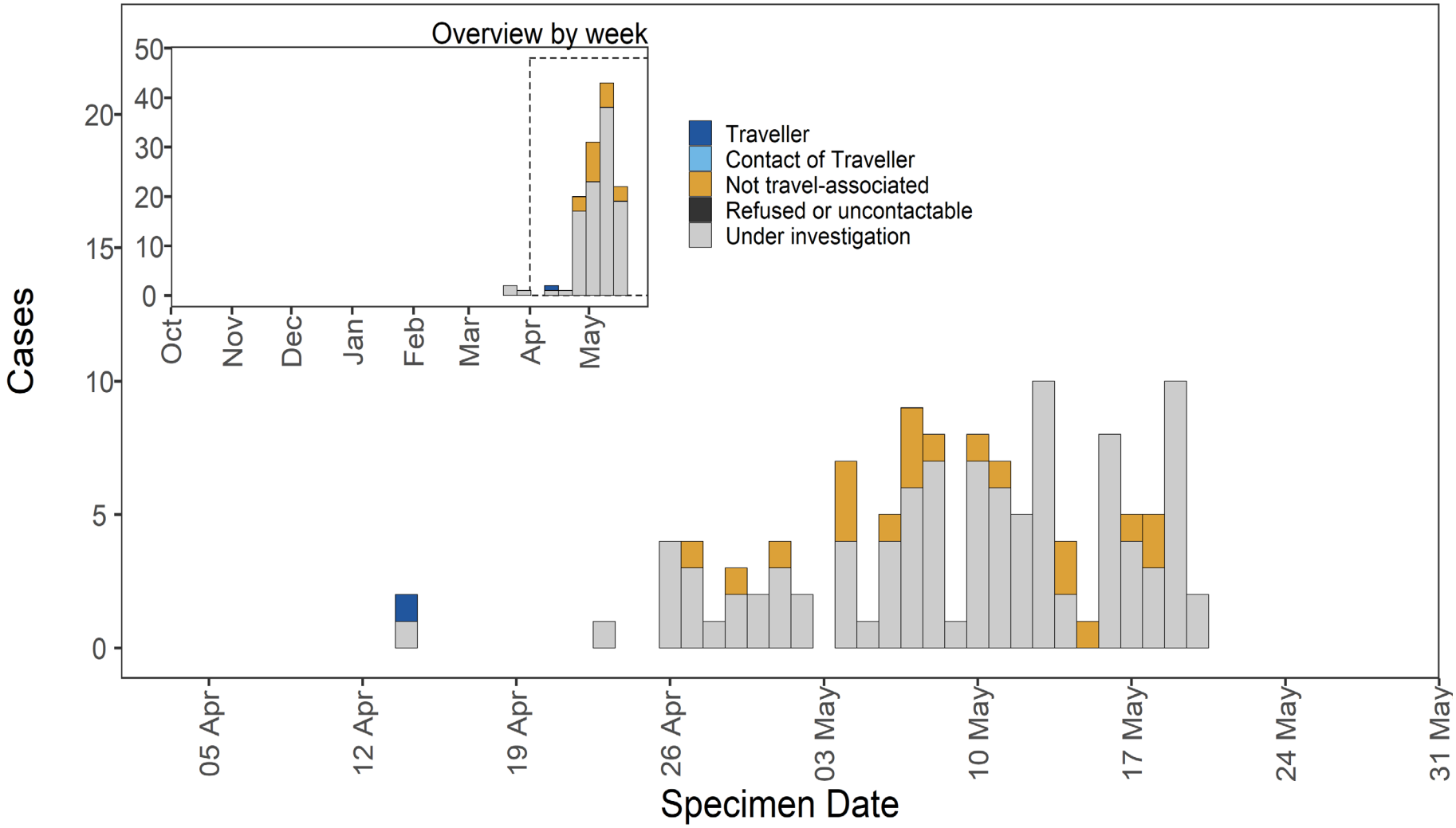


Figure 22. Travel data for confirmed and probable VUI-21MAY-01 (AV.1) cases by specimen date as of 31 May 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)



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 1 June 2021, 643 sequences of VUI-21MAY-02 (C.36.3) from 35 countries have been identified on GISAID

Table 14. Number of confirmed and probable VUI-21MAY-02 (C.36.3) cases, by region of residence as of 31 May 2021

Region	Case number	Case proportion	Cases that have travelled	Proportion of travellers among cases[1]
East Midlands	6	5.1%	3	50%
East of England	18	15.4%	5	27.8%
London	37	31.6%	15	40.5%
North East	1	0.9%	1	100%
North West	13	11.1%	5	38.5%
South East	8	6.8%	3	37.5%
South West	3	2.6%	2	66.7%
West Midlands	9	7.7%	4	44.4%
Yorkshire and Humber	22	18.8%	6	27.3%
Total	117	-	44	37.6%

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

Figure 23. Confirmed and probable VUI-21MAY-02 (C.36.3) cases by specimen date as of 31 May 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)

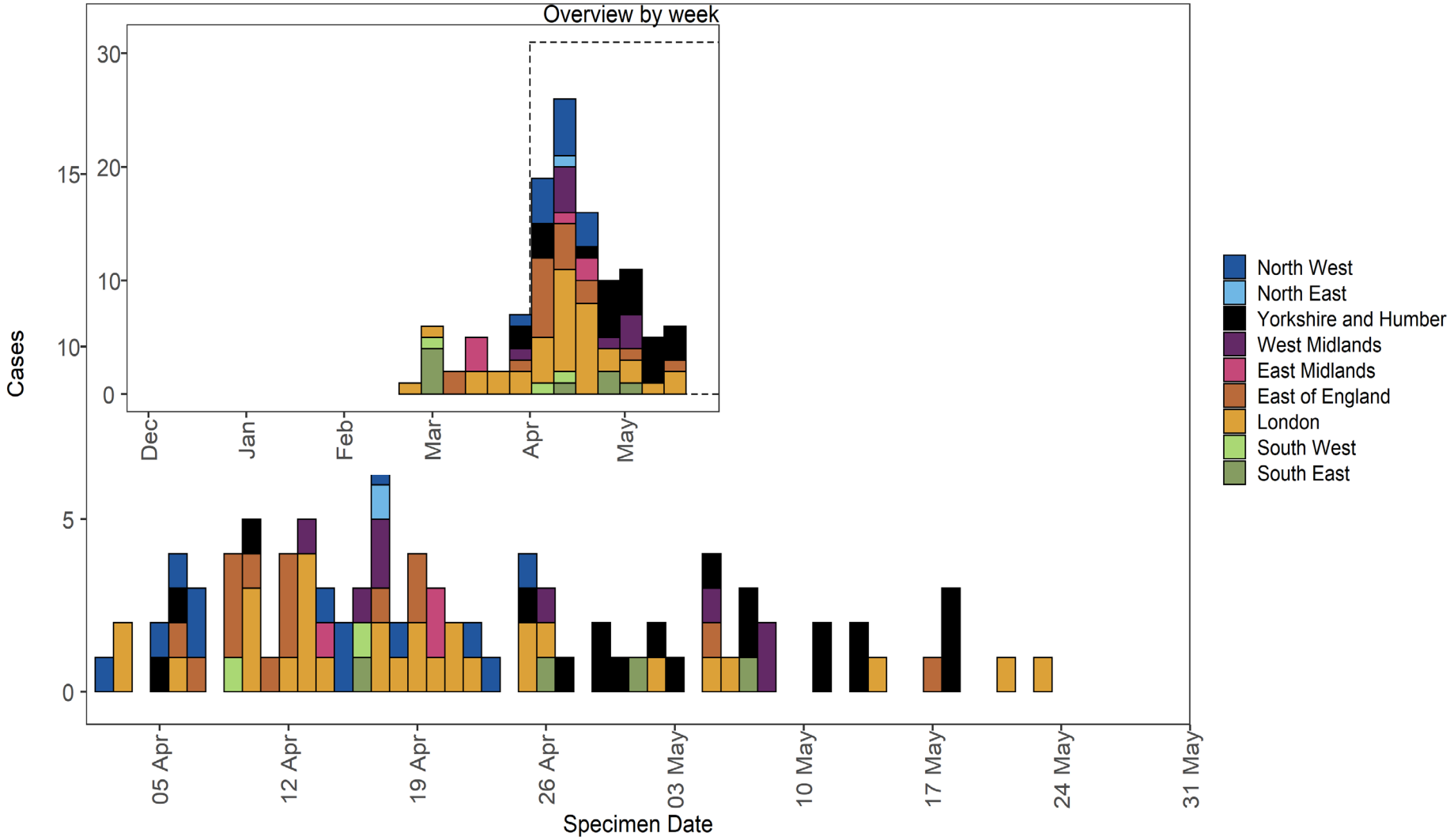
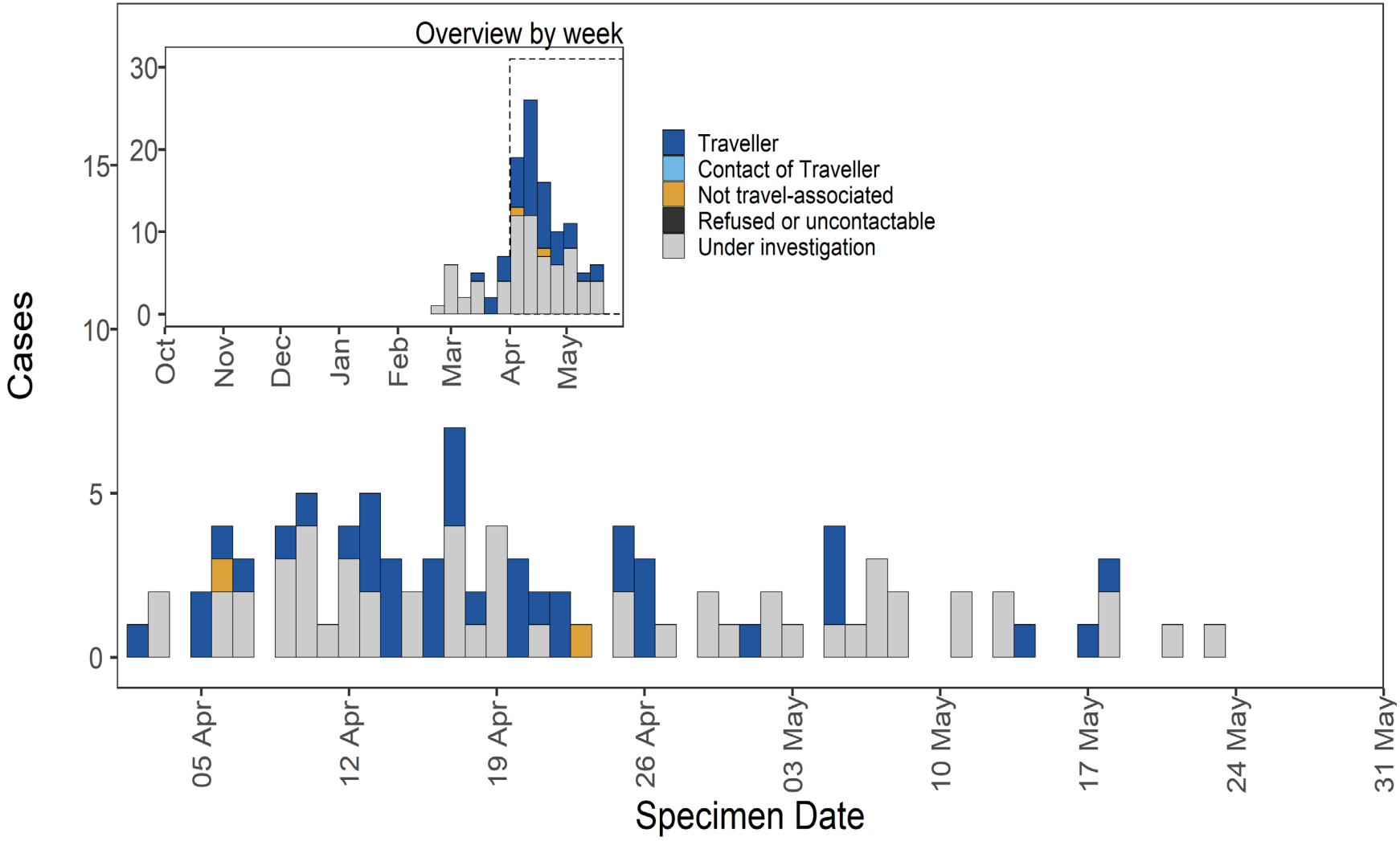


Figure 24. Travel data for confirmed and probable VUI-21MAY-02 (C.36.3) cases by specimen date as of 31 May 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data.)



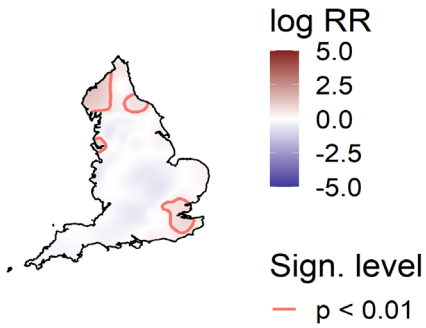
Spatial variation in risk for variants

Spatial variation in risk

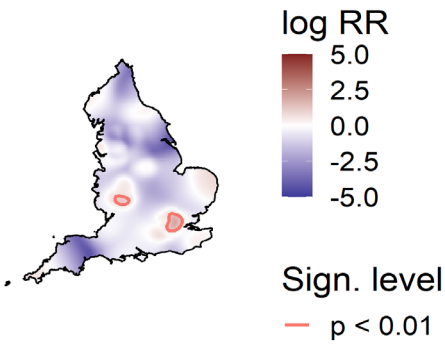
The spatial risk surface is estimated by comparing the smoothed intensity of cases (variants of concern) and controls (PCR positive, non-variants of concern) across a defined geographical area to produce an intensity (or risk) ratio. If the ratio is approximately 1, this suggests that the risk of infection is unrelated to spatial location. Evidence of spatial variation in risk occurs where the intensities differ. Ratio values greater than 1 indicate an increased risk and values less than 1 indicate lower risk. Figure 25 highlights areas of significantly increased risks for variants of concern, areas of significantly increased risk were identified for all variants of concern. Supplementary data is not available for this figure. Figure 26 highlights areas of significantly increased risks for variants under investigation, areas of significantly increased risk were identified for multiple variants under investigation. Supplementary data is not available for this figure.

Figure 25. Spatial variation in risk for VOC data from 1 October 2020, as of 25 May 2021, excluding cases that have travelled
(Supplementary data is not available for this figure).

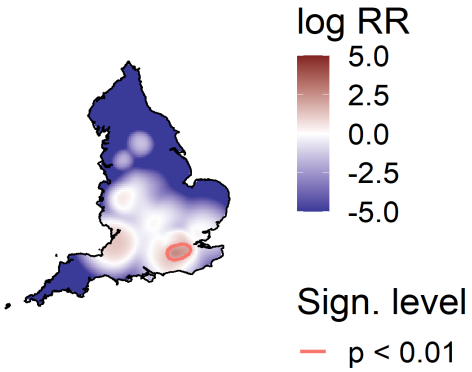
Alpha



Beta



Gamma



VOC-21FEB-02

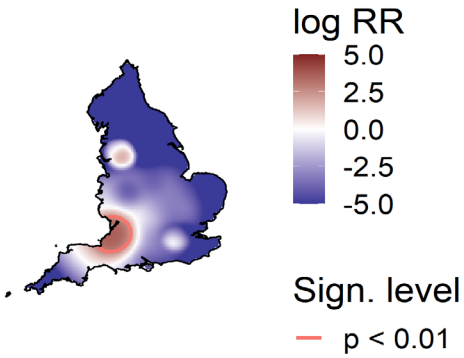
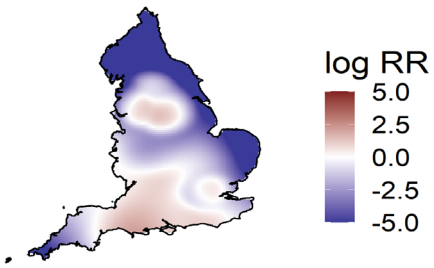
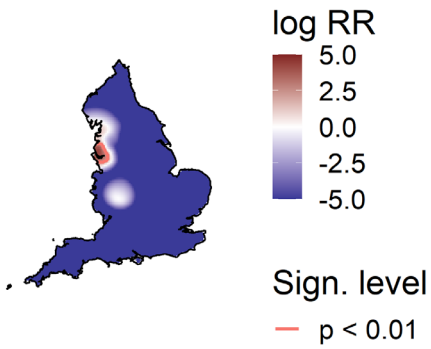


Figure 26. Spatial variation in risk for VUI data from 1 October 2020, as of 25 May 2021, excluding cases that have travelled
(Supplementary data is not available for this figure.)

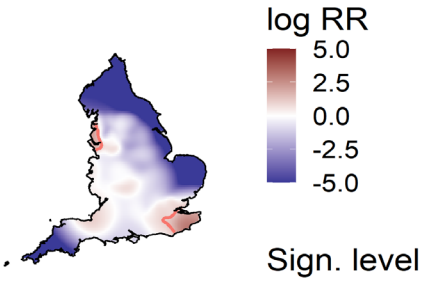
Zeta



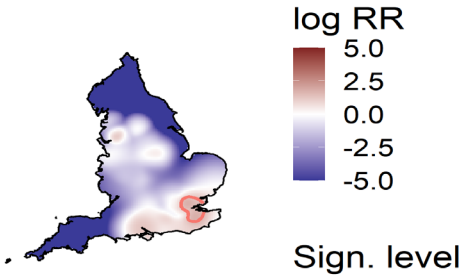
VUI-21FEB-01



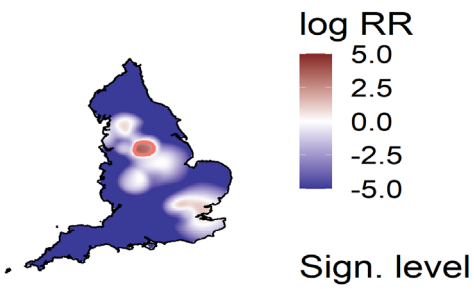
Eta



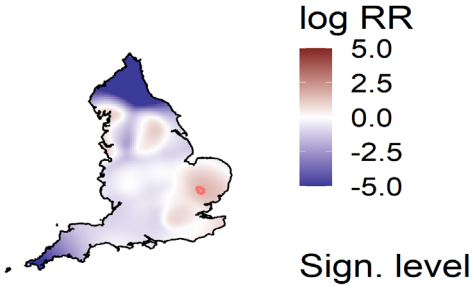
VUI-21FEB-04



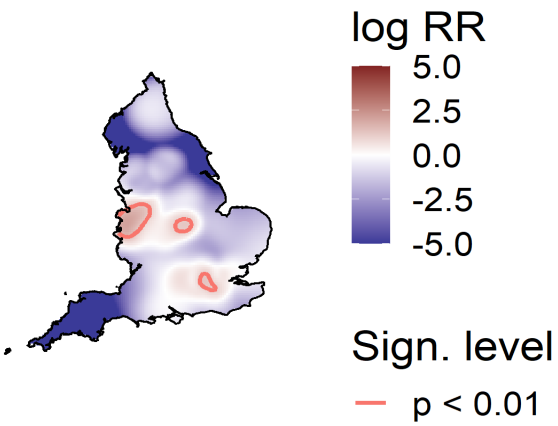
VUI-21MAY-01



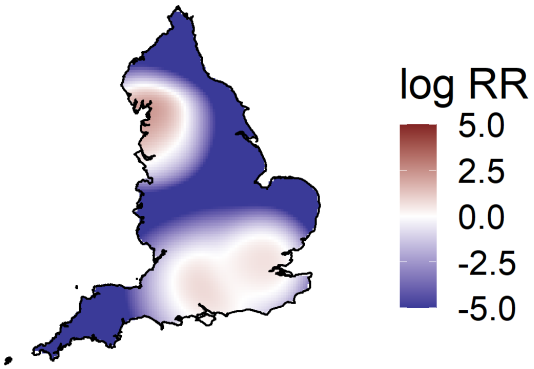
VUI-21MAY-02



Kappa



VUI-21APR-03



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.

Acknowledgements

The authors are grateful to those teams and groups providing data for this analysis including: the Lighthouse Laboratories, COG-UK, the Wellcome Sanger Institute, the PHE Epidemiology Cell, Contact Tracing, Genomics and Outbreak Surveillance Teams.

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Published: June 2021
PHE gateway number: GOV-8529

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