



Public Health
England

Protecting and improving the nation's health

SARS-CoV-2 variant data update, England

Version 2

22 May 2021

This briefing provides an update on previous data located in technical and variant data update [briefings and updates](#) up to 13 May 2021.

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Surveillance data overview

This document includes routine data on variants of concern and under investigation. VUI-21APR-01, VOC-21APR-02, VUI-21APR-03 and VUI-21MAY-01 are detailed in [technical briefing 12](#).

Data on individual variants

VOC-20DEC-01 (B.1.1.7)

This variant was designated VUI 202012/01 (B.1.1.7) on detection and on review re-designated as VOC-20DEC-01 (202012/01, B.1.1.7) on 18 December 2020.

International Epidemiology

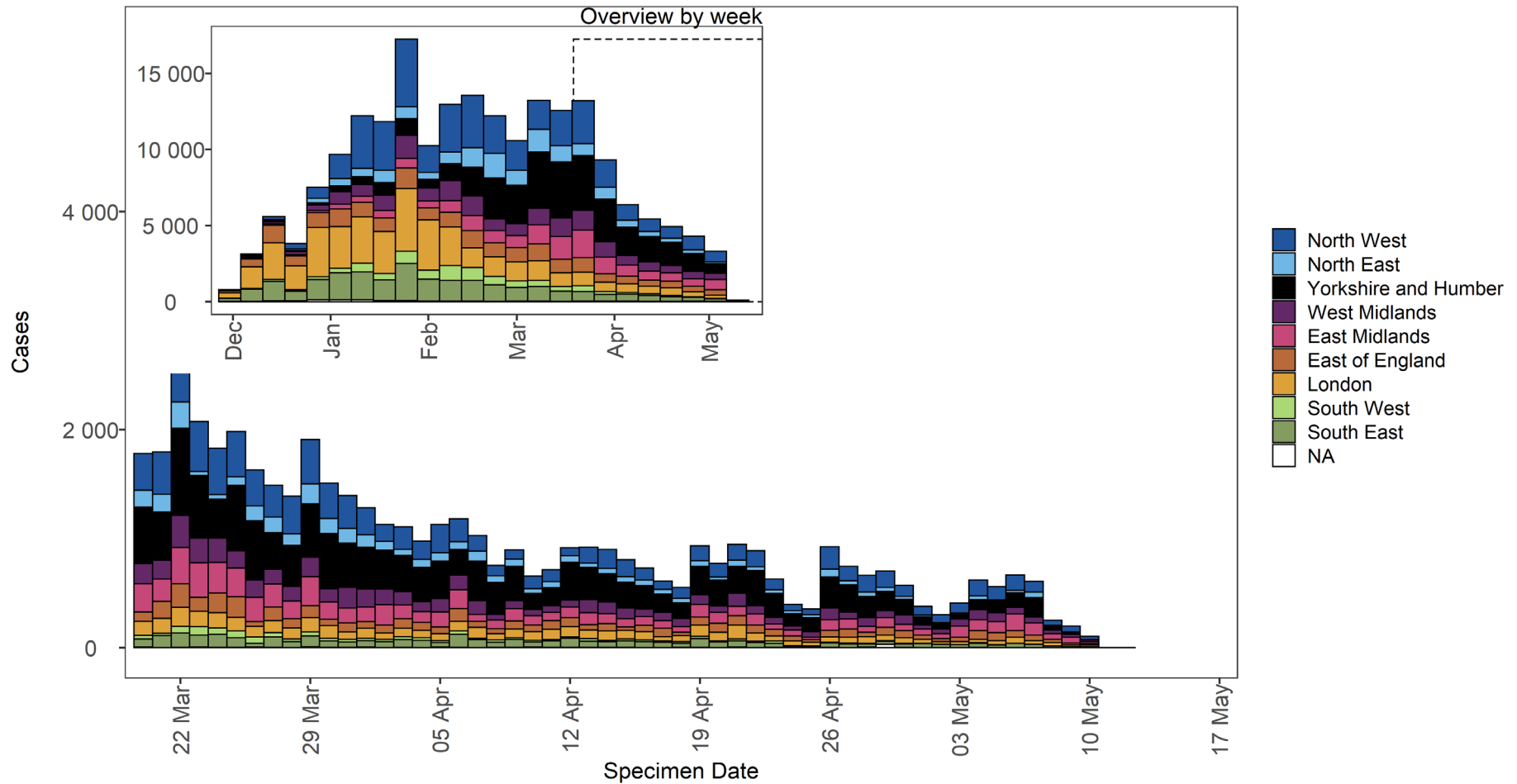
As of 19 May 2021, 410,583 sequences of VOC-20DEC-01, excluding UK, are listed from 128 countries or territories on [GISAID](#).

Epidemiology

Table 1. Number of confirmed and probable cases of VOC-20DEC-01 (B.1.1.7) by region as of 18 May 2021

Region	Case number	Case proportion
East Midlands	14,668	7.1%
East of England	18,680	9.0%
London	37,879	18.3%
North East	13,892	6.7%
North West	39,805	19.3%
South East	23,087	11.2%
South West	7,577	3.7%
West Midlands	17,260	8.4%
Yorkshire and Humber	32,535	15.7%
Unknown region	1,215	0.6%

Figure 1. Confirmed and probable VOC-20DEC-01 (B.1.1.7) cases by specimen date as of 18 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

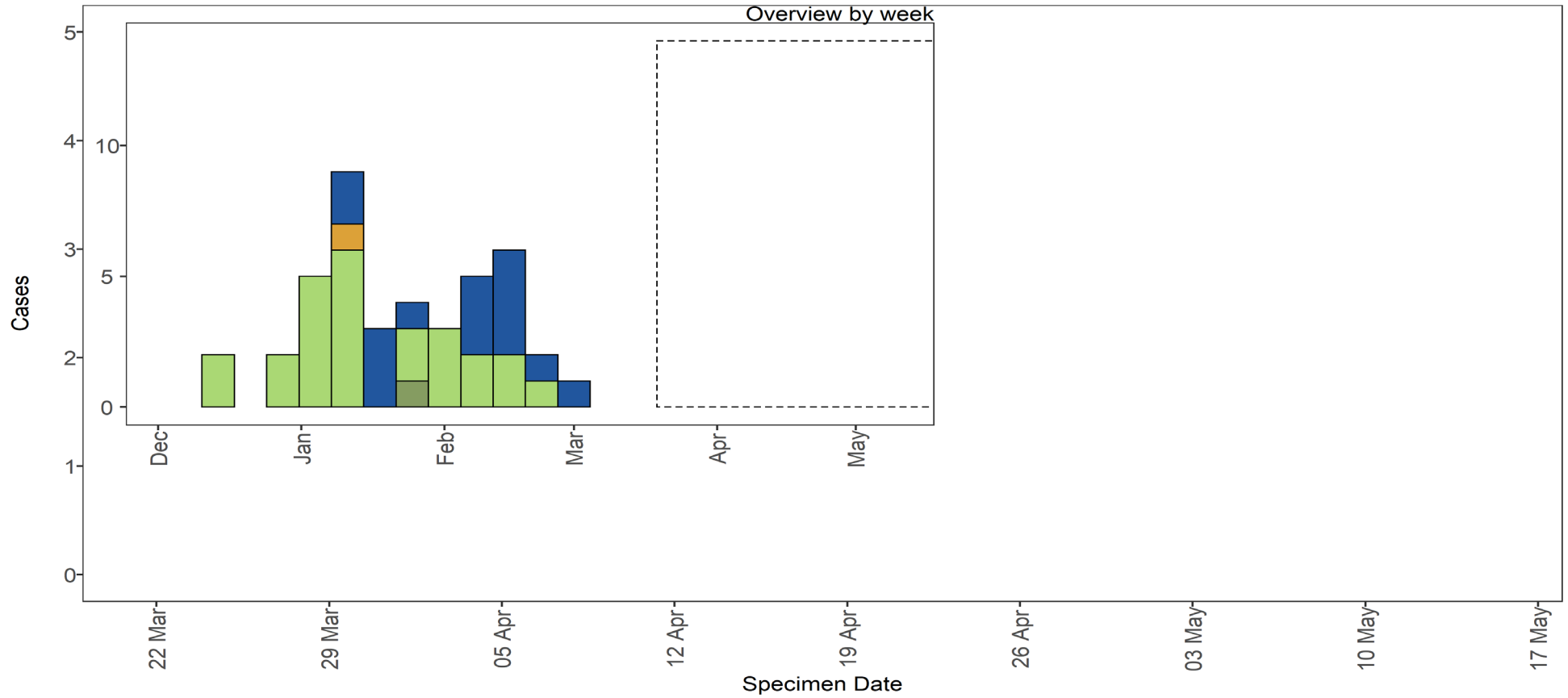
As of 19 May 2021, 8 sequences from the Netherlands and 5 sequences from Germany have been identified on [GISAID](#).

Epidemiology

Table 2. Number of confirmed and probable VOC-21FEB-02 (B.1.1.7 cluster with E484K) cases, by region of residence as of 18 May 2021

Region	Case number	Case proportion	Cases that have travelled	Proportion of travellers among cases
London	1	2.3%	0	0%
North West	15	34.9%	0	0%
South East	1	2.3%	0	0%
South West	26	60.5%	0	0%

Figure 2. Confirmed and probable VOC-21FEB-02 (B.1.1.7 cluster with E484K) cases by specimen date as of 18 May 2021
(Find accessible data used in this graph in [underlying data.](#))



VOC-20DEC-02 (B.1.351)

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.

International Epidemiology

GISAID includes data on sequences available internationally. As of the 19 May 2021, 14,993 sequences of VOC-20DEC-02, excluding UK, are listed from 86 countries or territories.

Epidemiology

Table 3. Confirmed and probable cases of VOC-20DEC-02 (B.1.351) by region as of 18 May 2021

Region	Case number	Case proportion	Cases that have travelled	Proportion of travellers among cases
East Midlands	45	5.6%	28	62.2%
East of England	82	10.2%	44	53.7%
London	366	45.8%	164	44.8%
North East	12	1.5%	5	41.7%
North West	78	9.8%	30	38.5%
South East	101	12.6%	62	61.4%
South West	27	3.4%	14	51.9%
West Midlands	58	7.2%	26	44.8%
Yorkshire and Humber	30	3.8%	19	63.3%
Unknown region	1	0.1%		N/A

Figure 3. Confirmed and probable VOC-20DEC-02 (B.1.351) cases by specimen date as of 18 May 2021
 (Find accessible data used in this graph in [underlying data.](#))

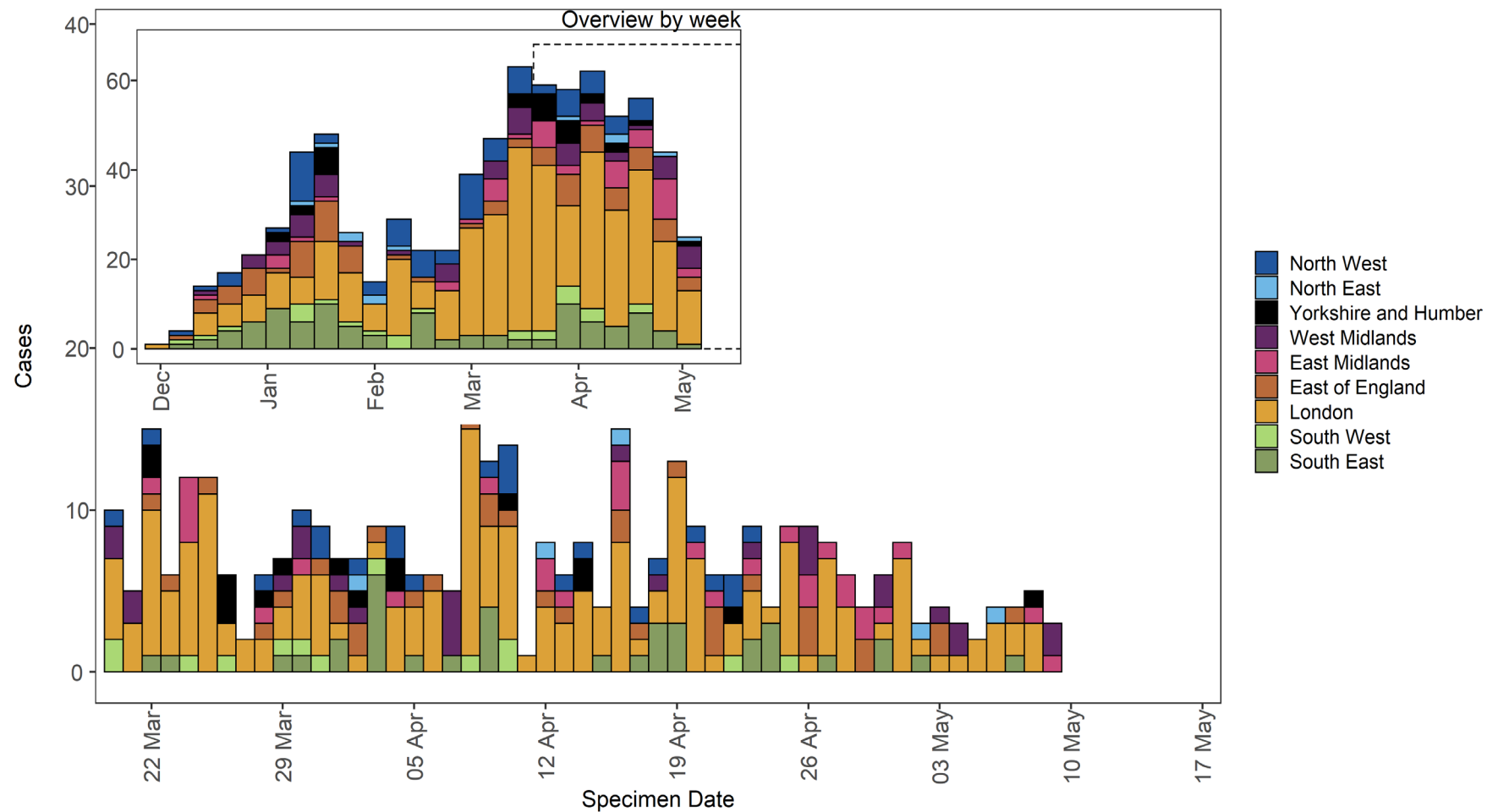
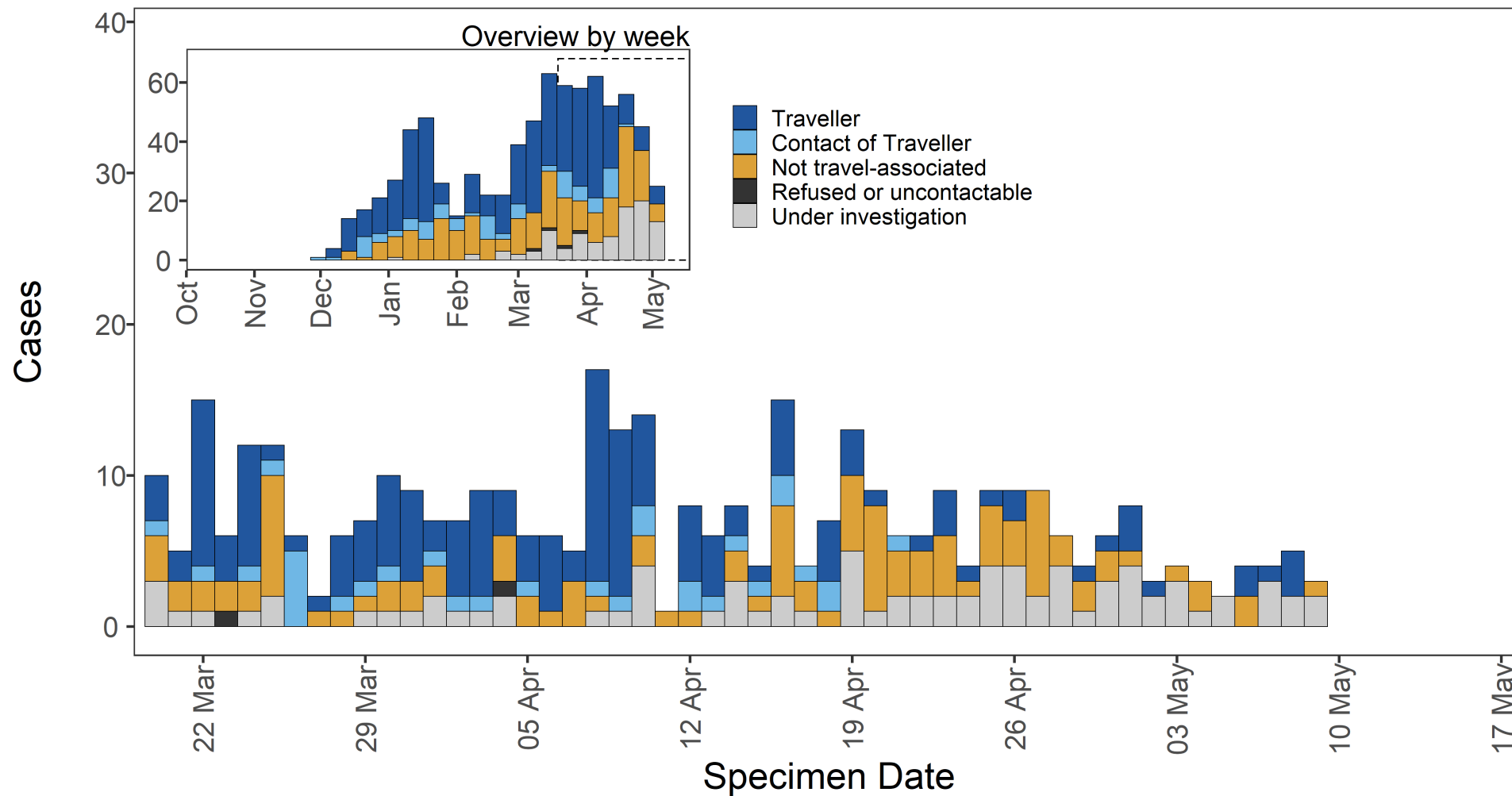


Figure 4. Travel data for confirmed and probable VOC-20DEC-02 (B.1.351) cases by specimen date as of 18 May 2021
 Larger plot includes last 60 days only. (Find accessible data used in this graph in [underlying data](#).)



VOC-21JAN-02 (P.1)

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.

International Epidemiology

GISAID includes data on sequences available internationally. As of 19 May 2021, 16,155 sequences of VOC-21JAN-02 are listed from 48 countries excluding the UK.

Epidemiology

Table 4. Number of confirmed and probable cases VOC-21JAN-02 (P.1), by region of residence as of 18 May 2021

Region	Case number	Case proportion	Cases that have travelled	Proportion of travellers among cases
East Midlands	2	1.6%	1	50%
East of England	9	7.0%	5	55.6%
London	71	55.5%	32	45.1%
North East	0	0.0%	0	N/A
North West	3	2.3%	2	66.7%
South East	25	19.5%	7	28%
South West	14	10.9%	6	42.9%
West Midlands	3	2.3%	1	33.3%
Yorkshire and Humber	1	0.8%	1	100%

Figure 5. Confirmed and probable VOC-21JAN-02 (P.1) cases by specimen date as of 18 May 2021
 (Find accessible data used in this graph in [underlying data.](#))

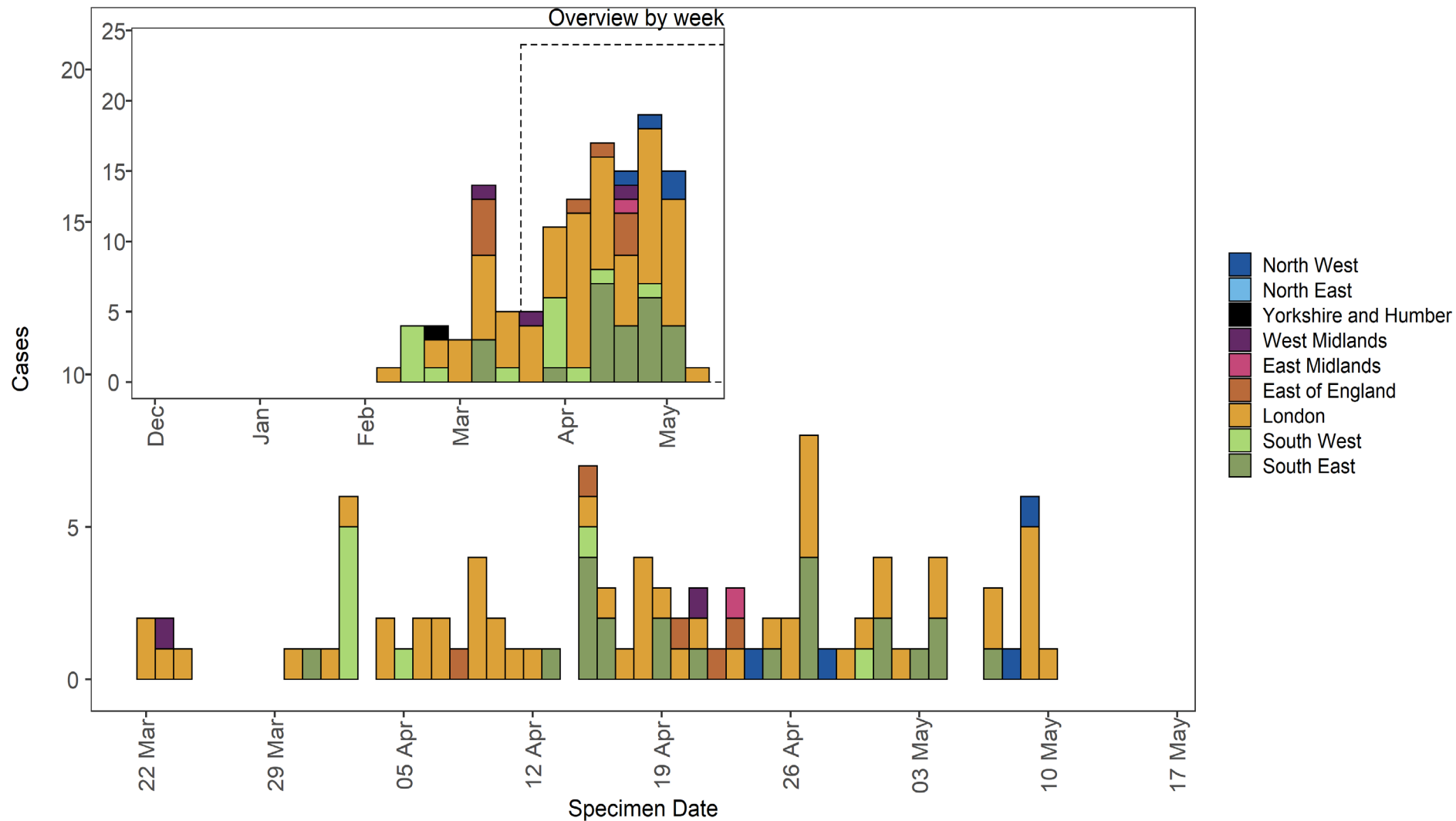
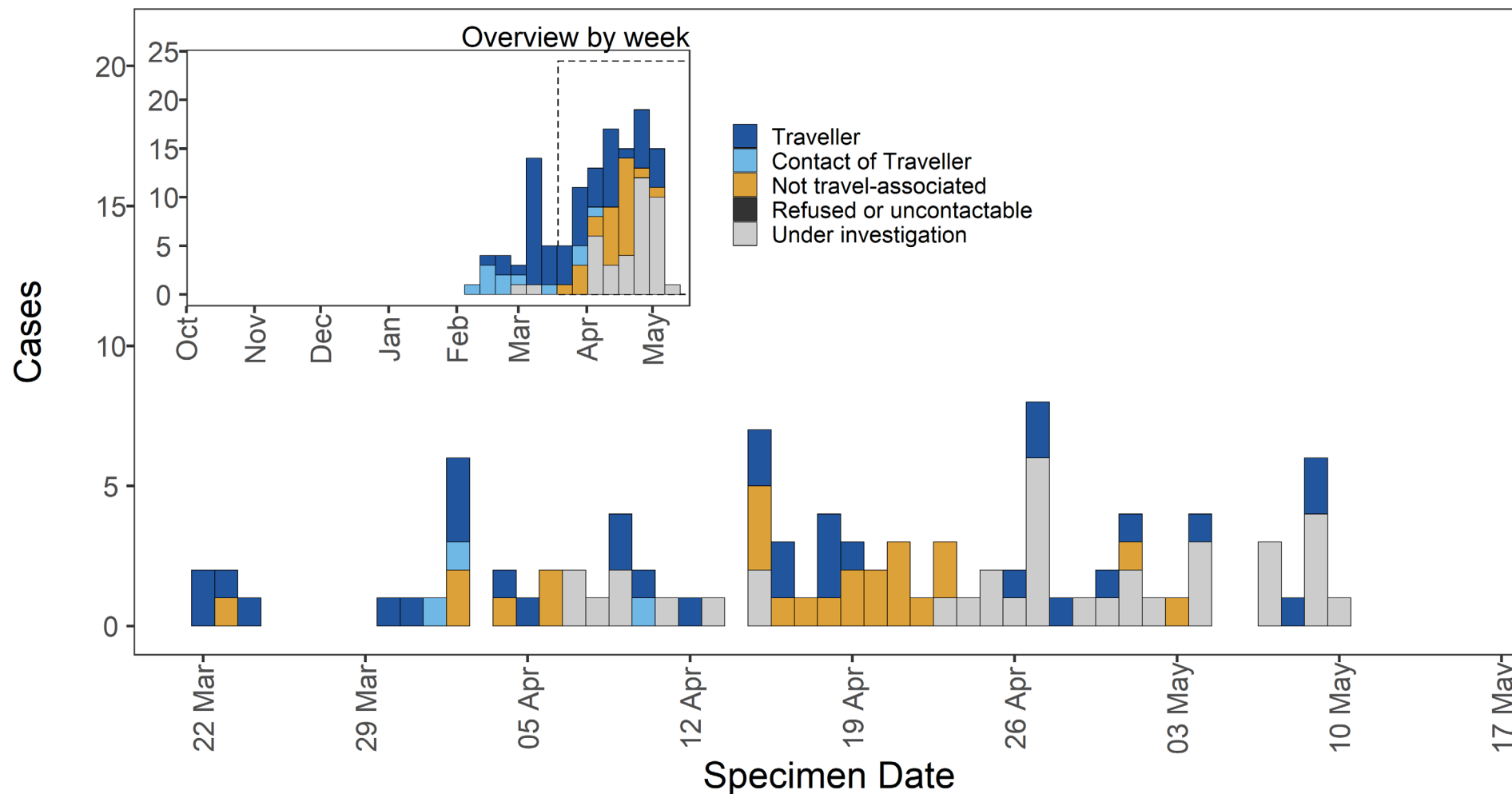


Figure 6. Travel data for confirmed and probable VOC-21JAN-02 (P.1) cases by specimen date as of 18 May 2021
 Larger plot includes last 60 days only. (Find accessible data used in this graph in [underlying data](#).)



VUI-21JAN-01 (P.2)

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.

International Epidemiology

GISAID includes data on sequences available internationally. As of 19 May 2021, 2,629 sequences (excluding UK) of VUI-21JAN-01 from 36 countries.

Epidemiology

Table 5. Number of confirmed and probable cases VUI-21JAN-01 (P.2) by region of residence as of 18 May 2021

Region	Case number	Case proportion	Cases that have travelled	Proportion of travellers among cases
East Midlands	1	1.9%	0	0%
East of England	2	3.7%	1	50%
London	14	25.9%	6	42.9%
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%

Figure 7. Confirmed and probable VUI-21JAN-01 (P.2) cases by specimen date, as of 18 May 2021
 (Find accessible data used in this graph in [underlying data.](#))

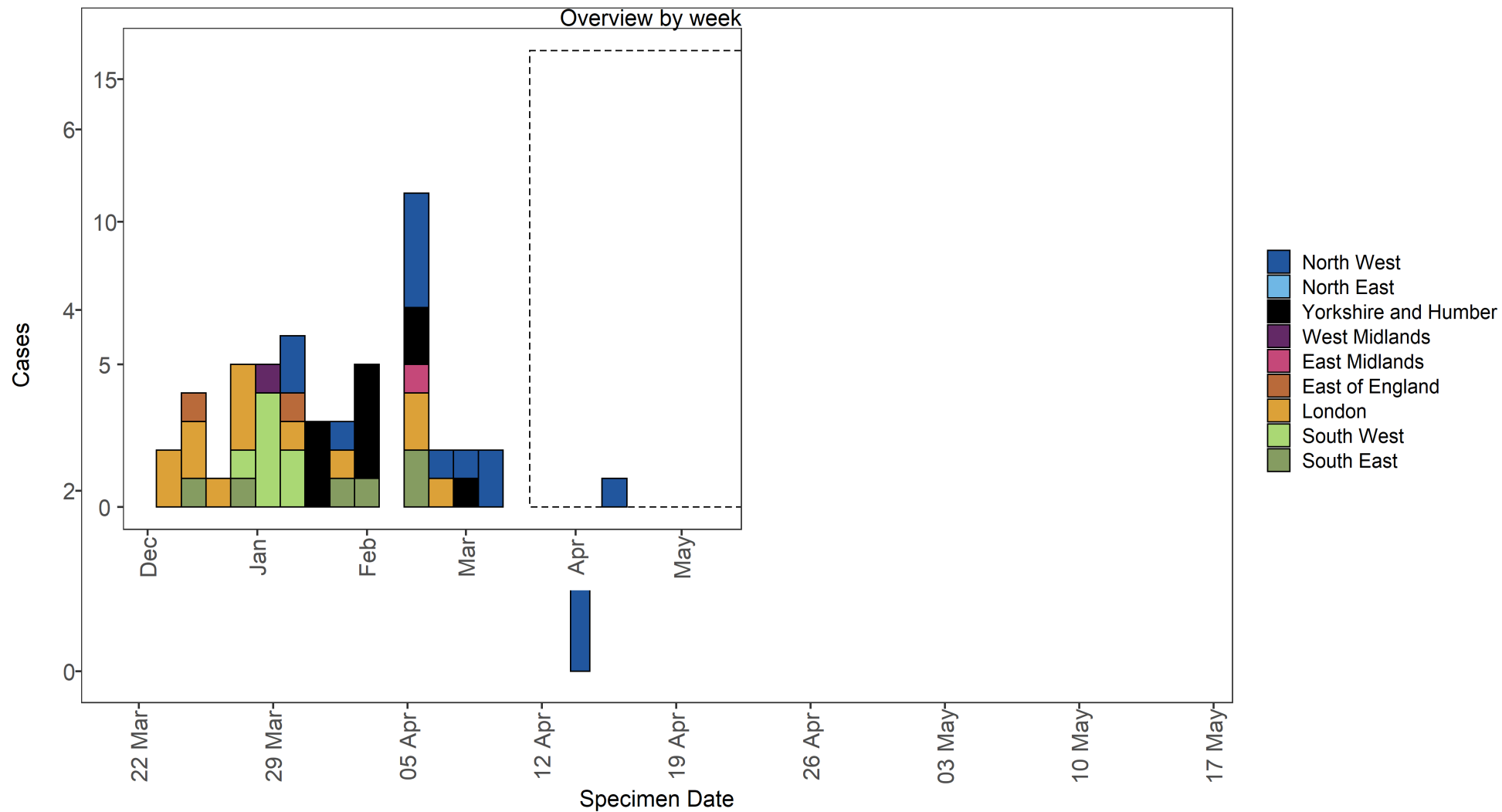
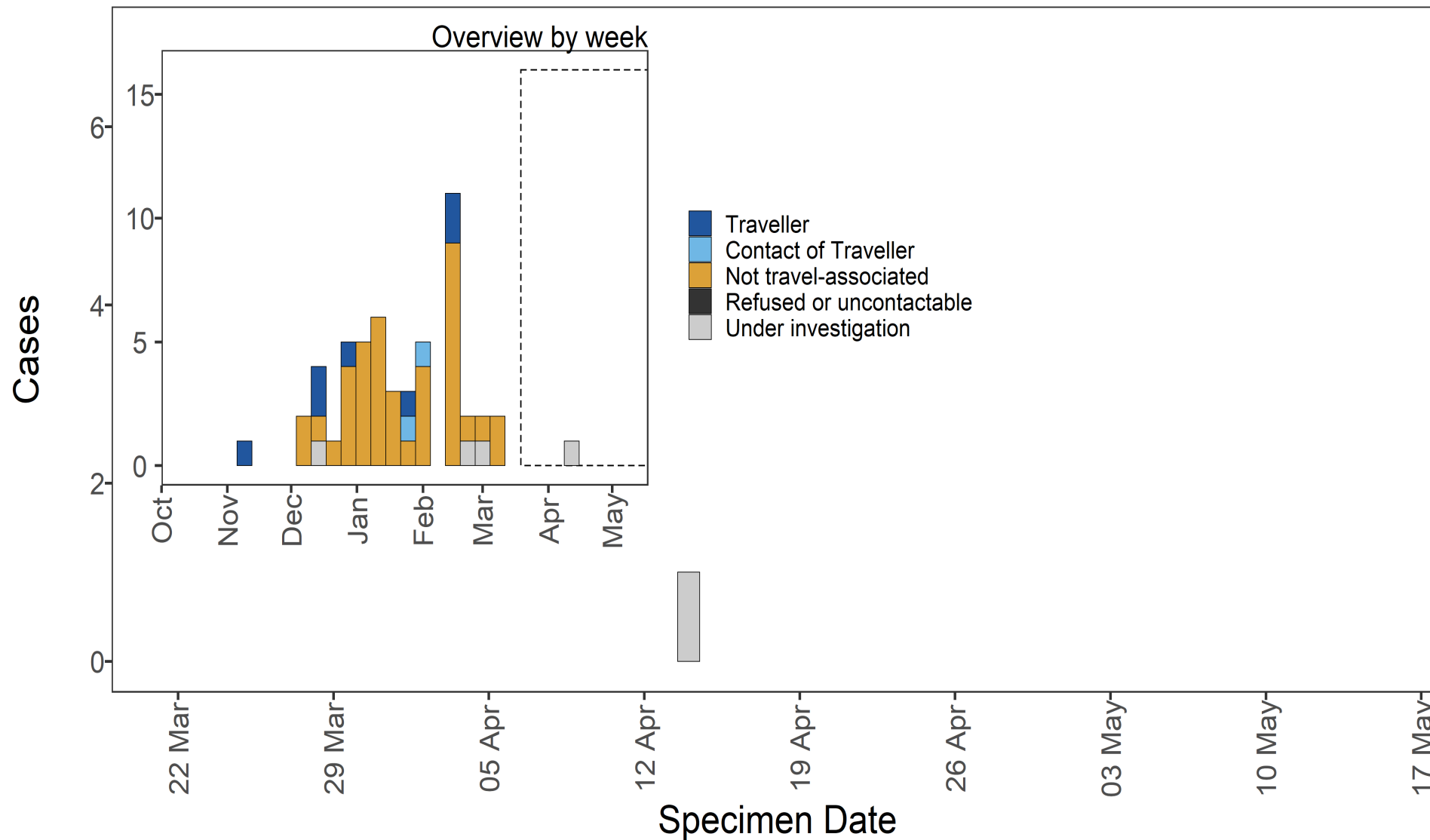


Figure 8. Travel data for confirmed and probable VUI-21JAN-01 (P.2) cases by specimen date as of 18 May 2021

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 19 May 2021, 4 sequences are listed of VUI-21FEB-01 (A.23.1 with E484K) (excluding UK) from Netherlands (1), India (2) and Israel (1).

Epidemiology

Table 6. Number of confirmed and probable VUI-21FEB-01 (A.23.1 with E484K) cases, by region of residence as of 18 May 2021

Region	Case number	Case proportion	Cases that have travelled	Proportion of travellers among cases
North West	76	96.2%	0	0%
West Midlands	1	1.3%	0	0%
Unknown region	2	2.5%		N/A

Figure 9. Confirmed and probable VUI-21FEB-01 (A.23.1 with E484K) cases by specimen date as of 18 May 2021
Larger plot includes last 60 days only. (Find accessible data used in this graph in [underlying data](#).)

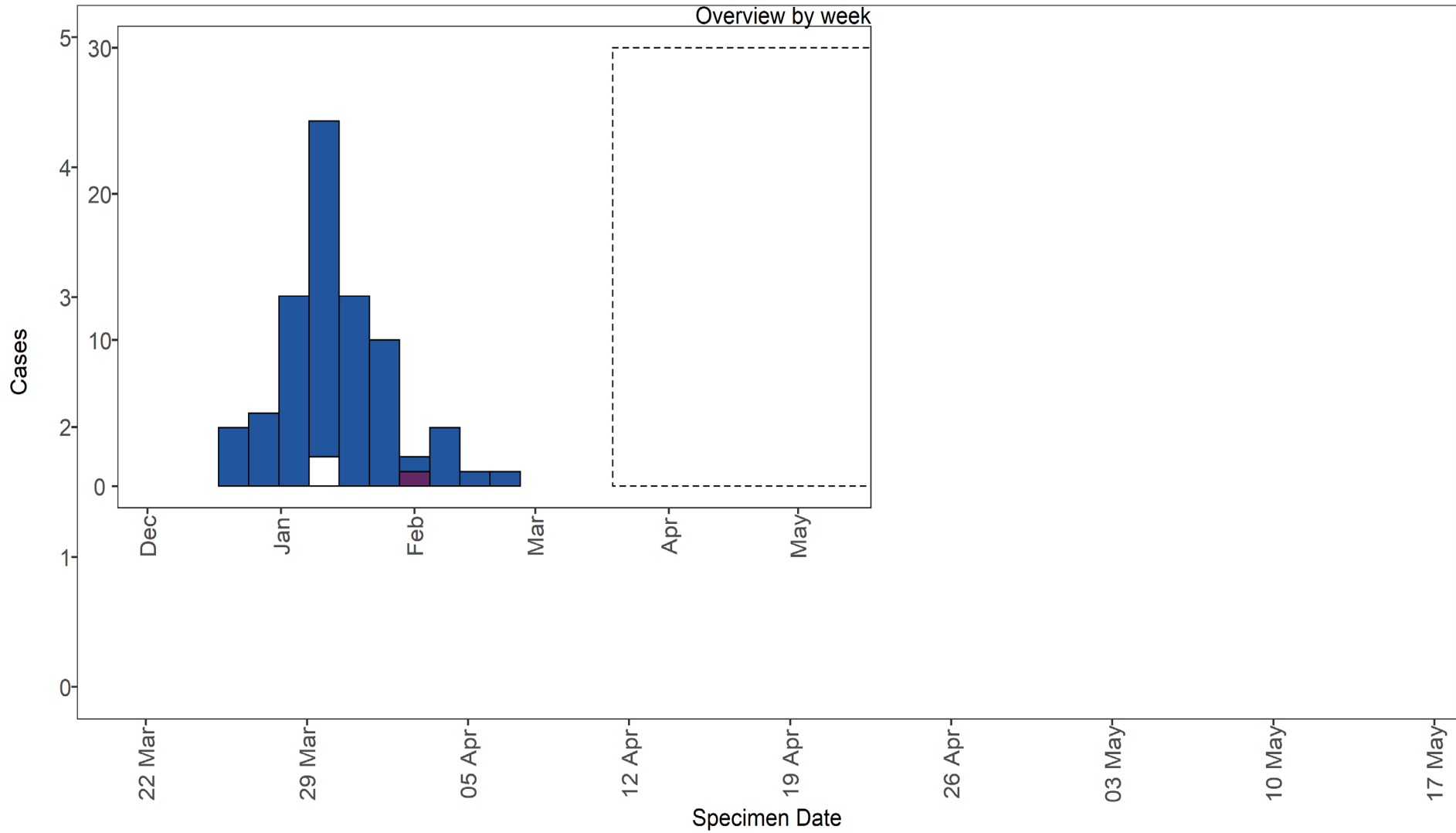
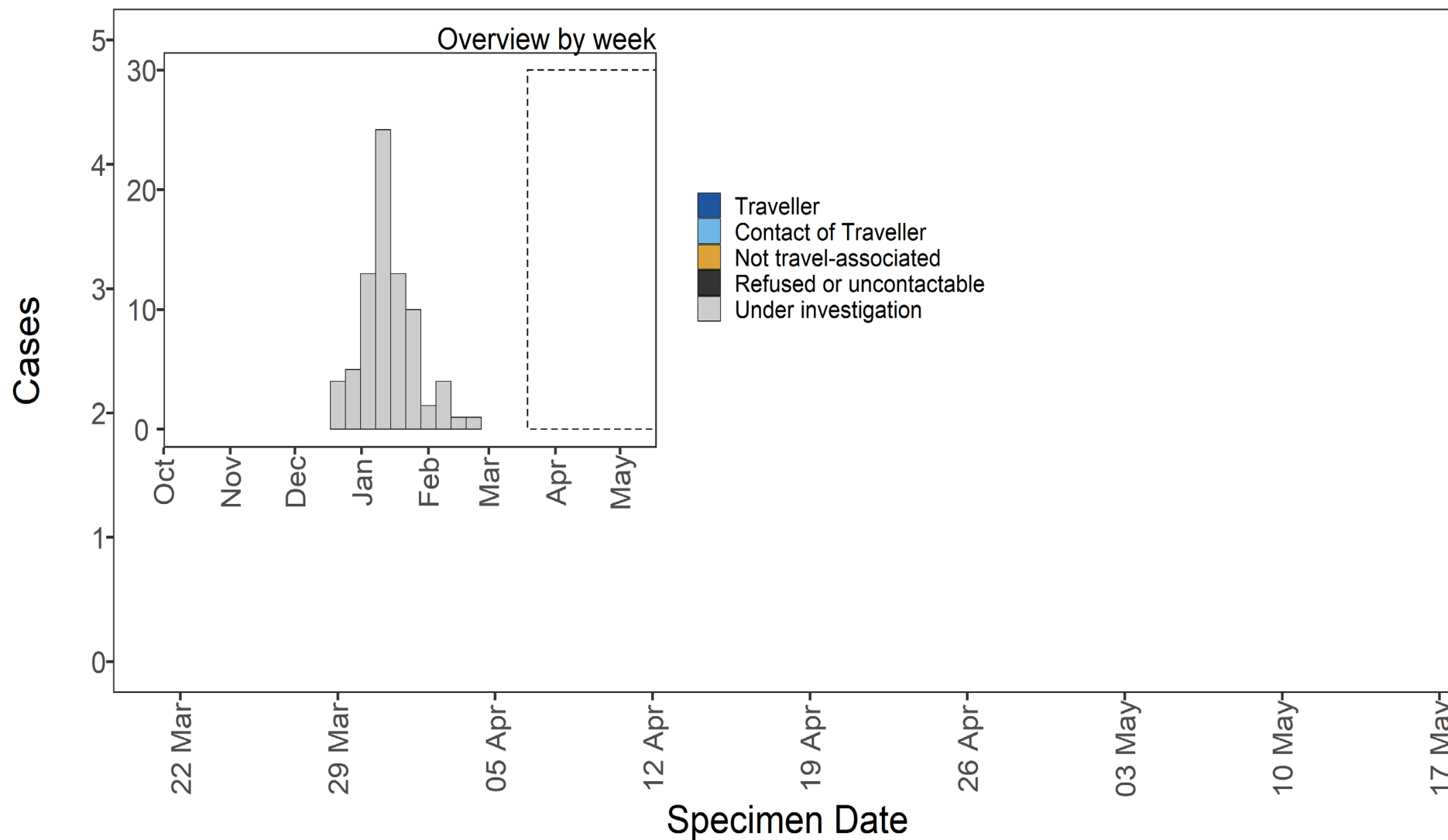


Figure 10. Travel data for confirmed and probable VUI-21FEB-01 (A.23.1 with E484K) cases by specimen date as of 18 May 2021

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



VUI-21FEB-03 (B.1.525)

First 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.

International Epidemiology

GISAID includes data on sequences available internationally. As of 19 May 2021, 3,391 sequences of VUI-21FEB-03 are listed, from 54 countries or territories excluding UK.

Epidemiology

Table 7. Number of confirmed and probable cases VUI-21FEB-03 (B.1.525) by region of residence as of 18 May 2021

Region	Case number	Case proportion	Cases that have travelled	Proportion of travellers among cases
East Midlands	10	2.4%	5	50%
East of England	28	6.8%	21	75%
London	147	35.9%	89	60.5%
North East	3	0.7%	3	100%
North West	71	17.4%	19	26.8%
South East	79	19.3%	26	32.9%
South West	18	4.4%	6	33.3%
West Midlands	32	7.8%	12	37.5%
Yorkshire and Humber	19	4.6%	9	47.4%
Unknown region	2	0.5%	1	50%

Figure 11. Confirmed and probable cases VUI-21FEB-03 (B.1.525) by specimen date as of 18 May 2021
 Larger plot includes last 60 days only. (Find accessible data used in this graph in [underlying data](#).)

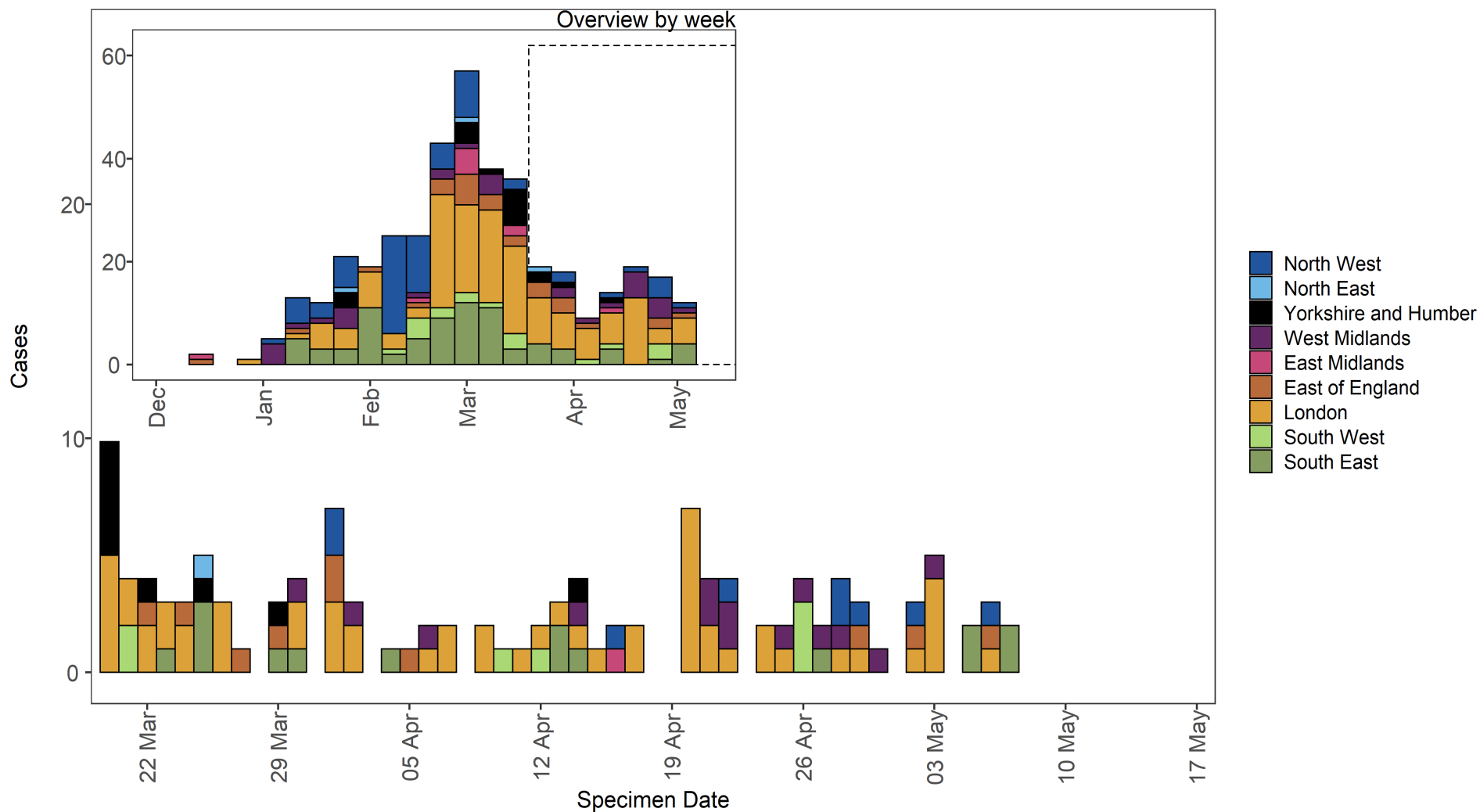
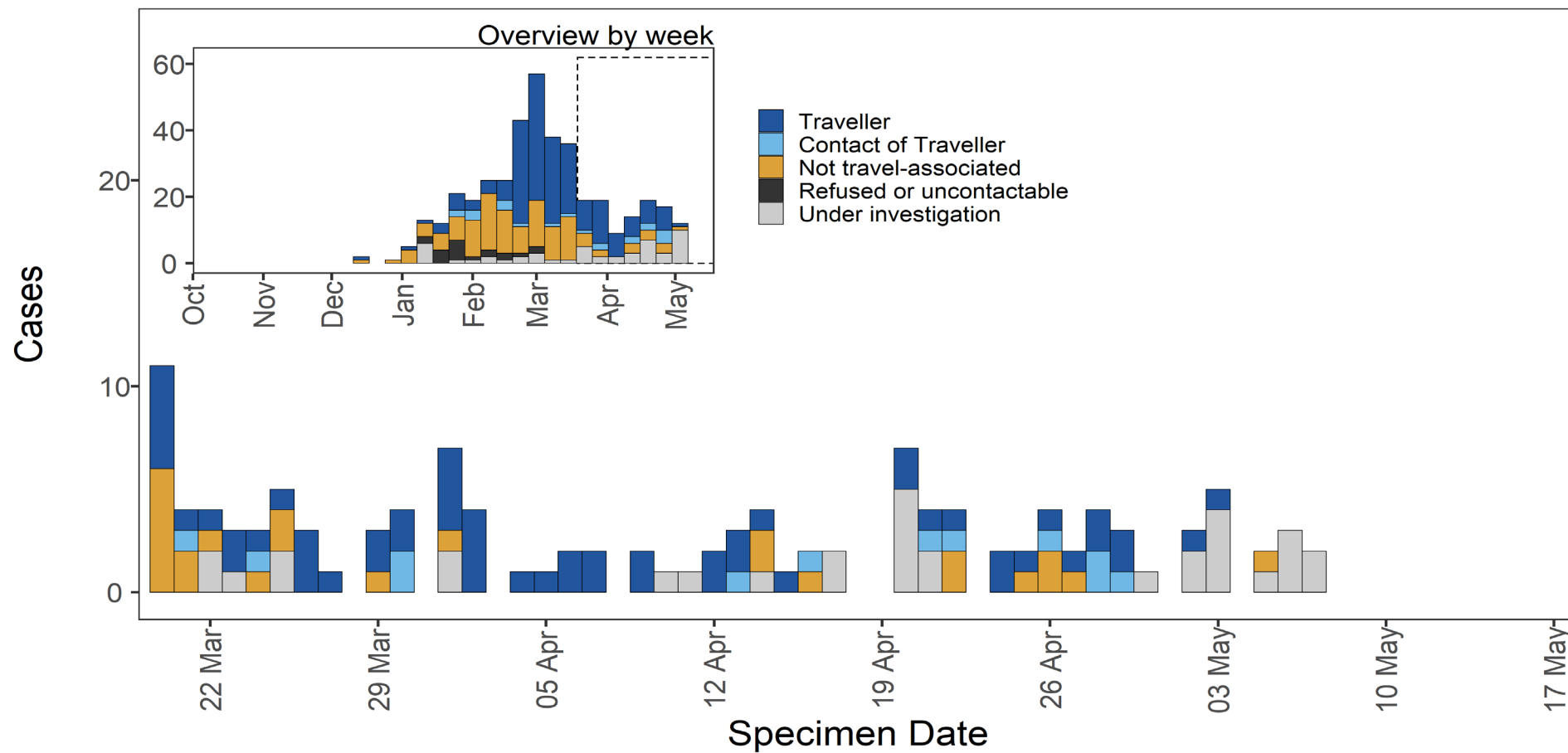


Figure 12. Travel data for confirmed and probable VUI-21FEB-03 (B.1.525) cases by specimen date as of 18 May 2021

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



VUI-21FEB-04 (B.1.1.318)

The VUI-21FEB-04 is lineage B.1.1.318 and 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 19 May 2021, 74 international VUI-21FEB-04 sequences, excluding UK. (Bangladesh 1, Canada 2, Denmark 1, France 2, Germany 11, Ghana 1, India 2, Italy 7, Nigeria 8, Sweden 4, Switzerland 12, USA 23).

Table 8. Number of confirmed and probable VUI-21FEB-04 (B.1.1.318) cases, by region of residence as of 18 May 2021

Region	Case Number	Case Proportion	Cases that have travelled	Proportion of travellers among cases
East Midlands	10	4.9%	4	40%
East of England	23	11.2%	13	56.5%
London	76	37.1%	32	42.1%
North East	1	0.5%	1	100%
North West	43	21.0%	9	20.9%
South East	32	15.6%	11	34.4%
South West	1	0.5%	1	100%
West Midlands	7	3.4%	4	57.1%
Yorkshire and Humber	11	5.4%	1	9.1%
Unknown region	1	0.5%		N/A

Figure 13. Confirmed and probable VUI-21FEB-04 (B.1.1.318) cases by specimen date as of 18 May 2021
 Larger plot includes last 60 days only. (Find accessible data used in this graph in [underlying data](#).)

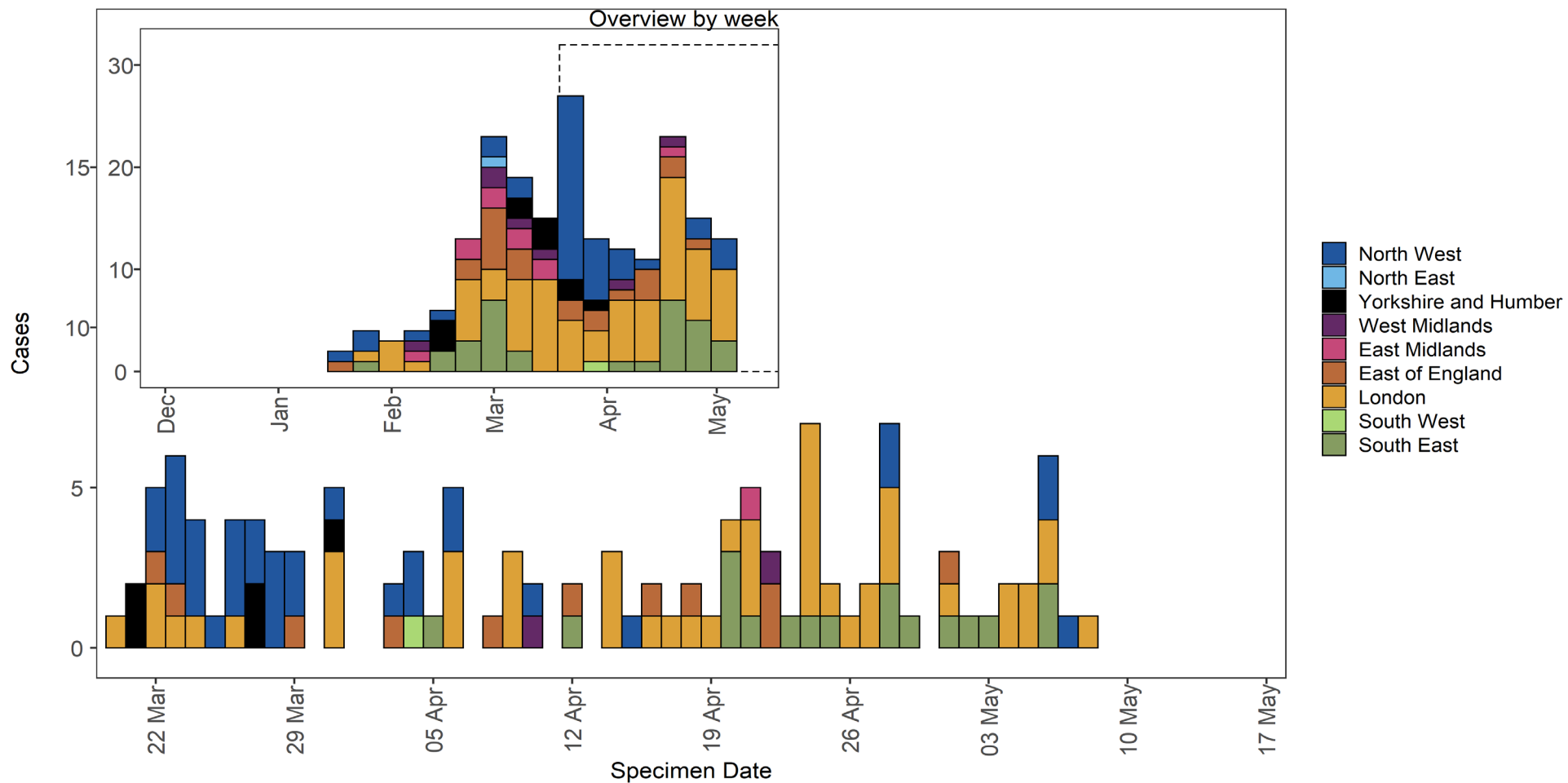
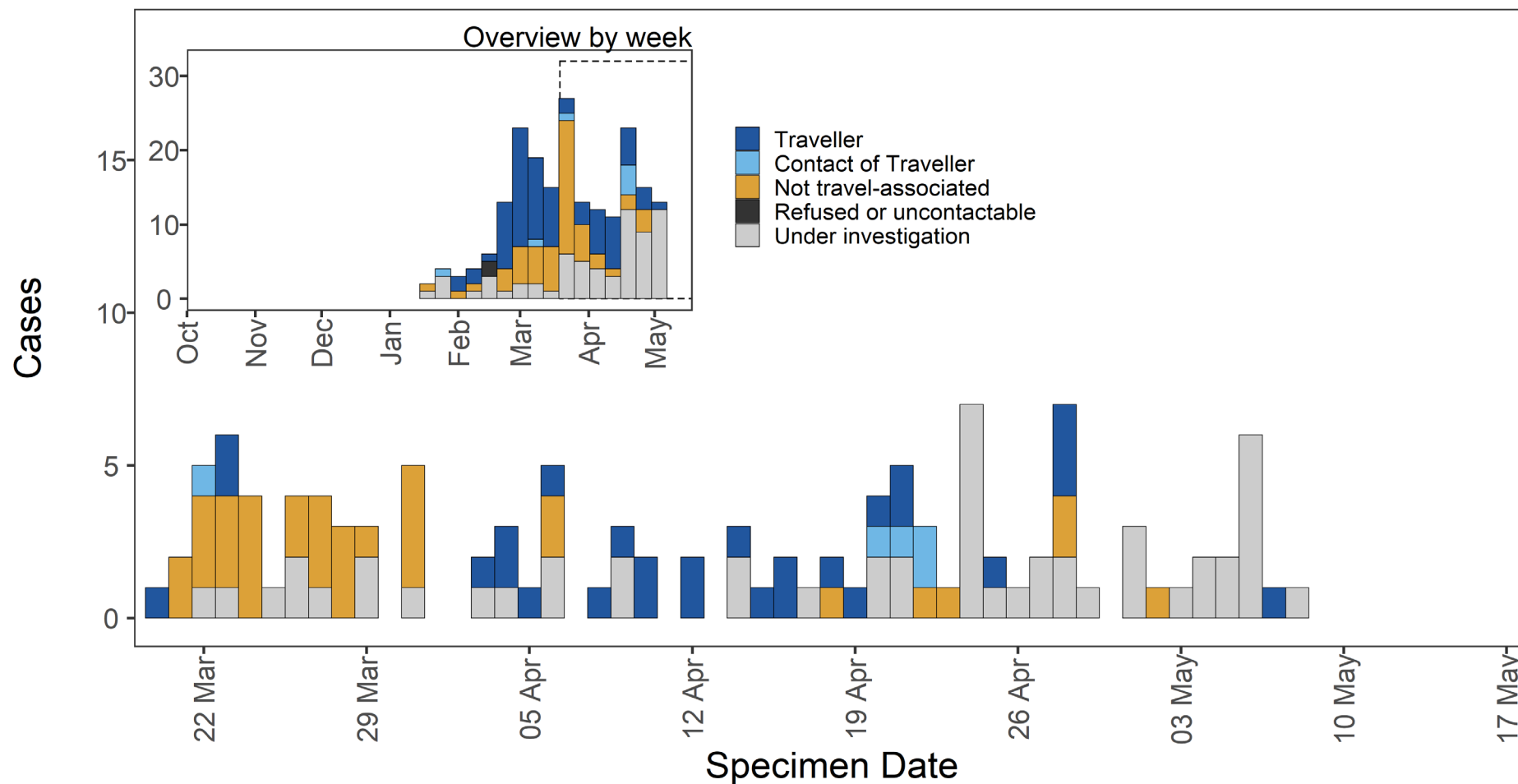


Figure 14. Travel data for confirmed and probable VUI-21FEB-04 (B.1.1.318) cases by specimen date as of 18 May 2021
 Larger plot includes last 60 days only. (Find accessible data used in this graph in [underlying data](#).)



VUI-21MAR-02 (P.3)

The VUI-21MAR-02 (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 VUI-21MAR-02 (P.3) 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.

International Epidemiology

GISAID includes data on sequences available internationally. As of 19 May 2021, 145 sequences are listed internationally of VUI-21MAR-02 excluding UK. (Australia 3, China 1, Germany 8, Hong Kong 8, Japan 3, Netherlands 6, New Zealand 3, Norway 2, Philippines 105, Singapore 1, South Korea 1, USA 4).

Table 9. Number of confirmed and probable VUI-21MAR-02 (P.3) cases, by region of residence as of 18 May 2021

Region	Case number	Case proportion	Cases that have travelled	Proportion of travellers among cases
East Midlands	0	0.0%	0	N/A
East of England	1	16.7%	1	100%
London	1	16.7%	0	0%
North East	0	0.0%	0	N/A
North West	1	16.7%	1	100%
South East	0	0.0%	0	N/A
South West	2	33.3%	2	100%
West Midlands	0	0.0%	0	N/A
Yorkshire and Humber	1	16.7%	1	100%

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 15** 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 16** 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 15. Spatial variation in risk for VOC data from 1 October 2020, as of 18 May 2021, excluding cases that have travelled
(Supplementary data is not available for this figure.)

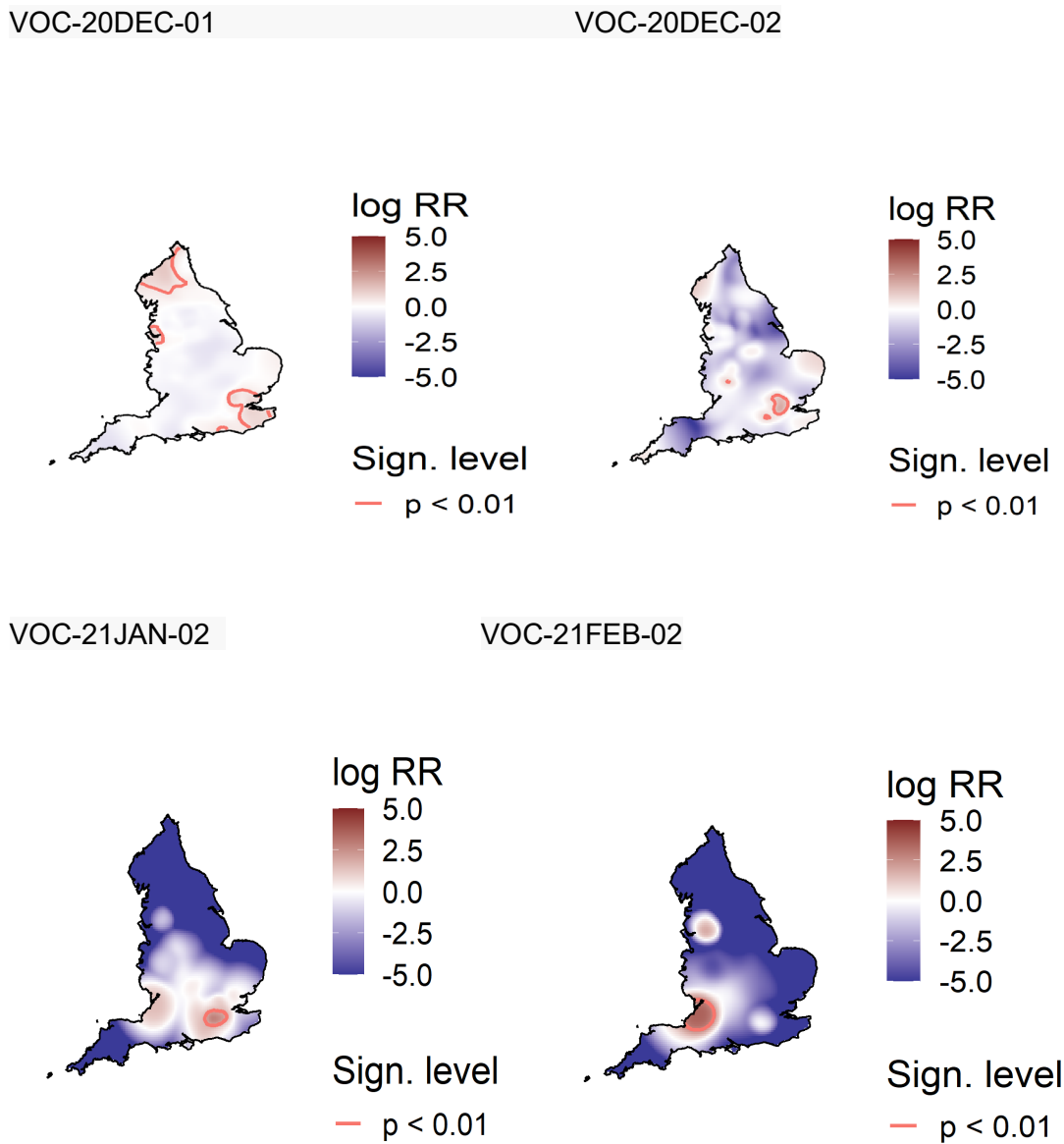
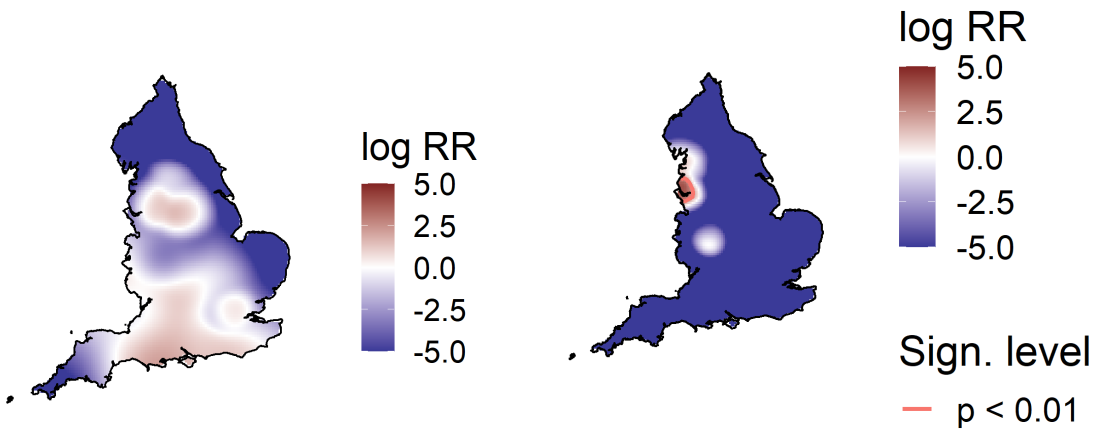


Figure 16. Spatial variation in risk for VUI data from 1 October 2020, as of 18 May 2021, excluding cases that have travelled
(Supplementary data is not available for this figure.)

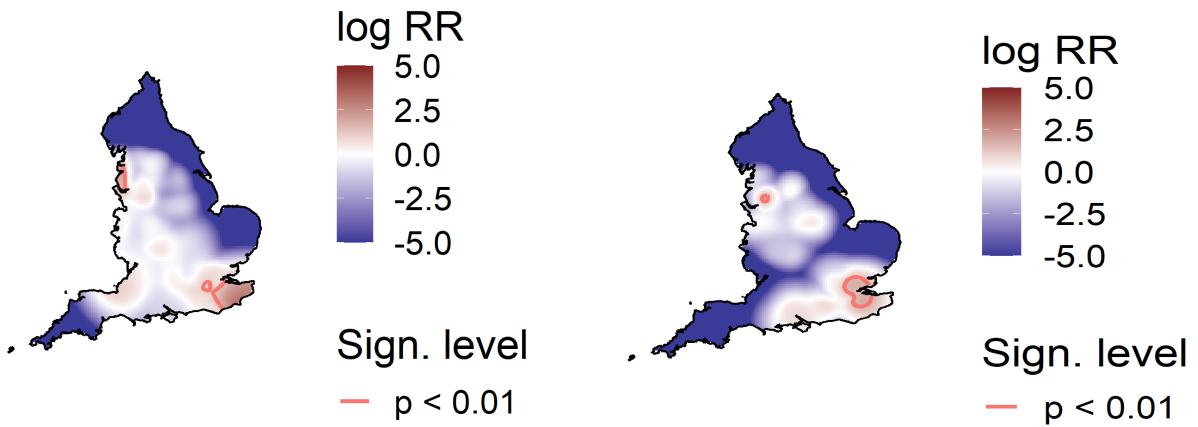
VUI-21JAN-01

VUI-21FEB-01



VUI-21FEB-03

VUI-21FEB-04



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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