Public Health England

Protecting and improving the nation's health

SARS-CoV-2 variant data update, England

Version 1

13 May 2021

This briefing provides an update on previous data located in technical briefings up to 6 May 2021

Contents

Surveillance data overview

This document includes routine data on variants of concern and under investigation. VUI-21APR-01, VOC-21APR-02 and VUI-21APR-03 are detailed in technical briefing 11.

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

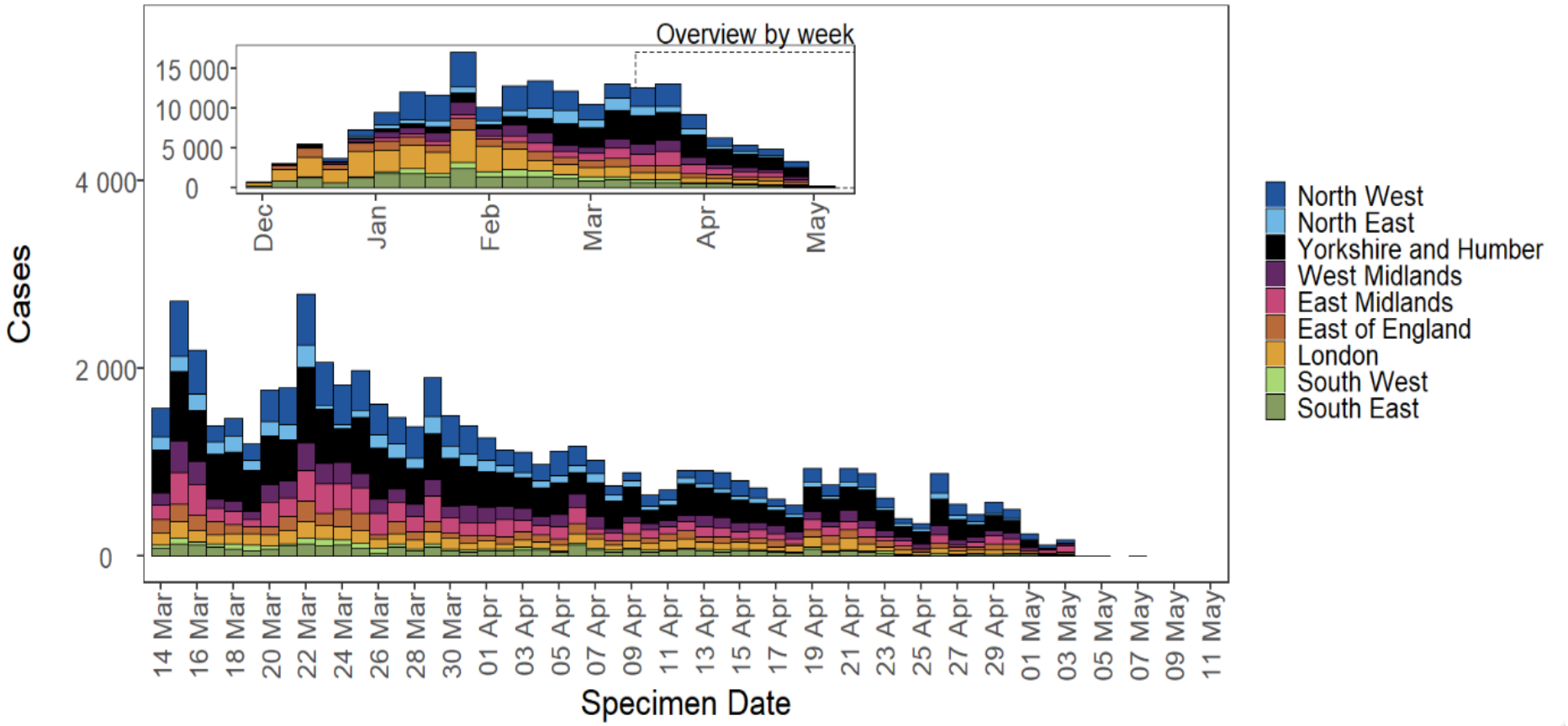
As of 12 May 2021, 334,687 sequences of VOC-20DEC-01, excluding UK, are listed from 124 countries or territories on GISAID.

Epidemiology

Table 1. Number of confirmed and probable cases of VOC-20DEC-01 (B.1.1.7) by region as of 12 May 2021

Region	Case number	Case proportion
East Midlands	13,879	6.9%
East of England	18,240	9.0%
London	37,507	18.5%
North East	13,718	6.8%
North West	38,922	19.2%
South East	22,713	11.2%
South West	7,551	3.7%
West Midlands	16,719	8.3%
Yorkshire and Humber	31,773	15.7%
Unknown region	1,207	0.6%

Figure 1. Confirmed and probable VOC-20DEC-01 (B.1.1.7) cases by specimen date as of 12 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

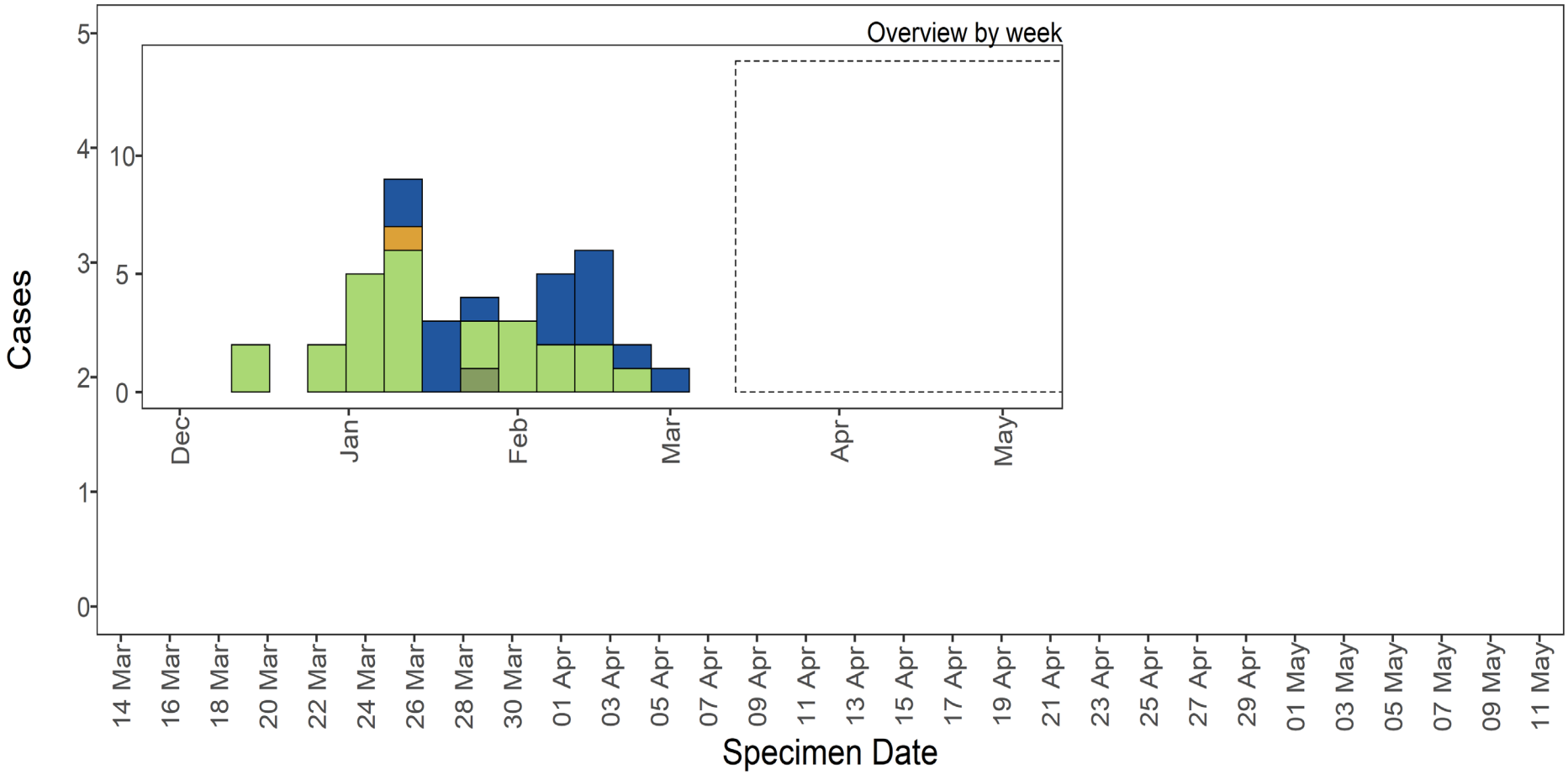
As of 12 May 2021, 7 sequences from the Netherlands and 5 sequences from Germany have been identified on GISAID.

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 12 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 12 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 12 May 2021, 13,477 sequences of VOC-20DEC-02, excluding UK, are listed from 82 countries or territories.

Epidemiology

Table 3. Confirmed and probable cases of VOC-20DEC-02 (B.1.351) by region as of 12 May 2021

Region	Case number	Case proportion	Cases that have travelled	Proportion of travellers among cases
East Midlands	42	5.4%	28	66.7%
East of England	81	10.5%	44	54.3%
London	351	45.5%	158	45%
North East	10	1.3%	5	50%
North West	78	10.1%	30	38.5%
South East	99	12.8%	61	61.6%
South West	27	3.5%	14	51.9%
West Midlands	54	7.0%	25	46.3%
Yorkshire and Humber	29	3.8%	18	62.1%
Unknown region	1	0.1%		NA%

Figure 3. Confirmed and probable VOC-20DEC-02 (B.1.351) cases by specimen date as of 12 May 2021.
(Find accessible data used in this graph in underlying data).

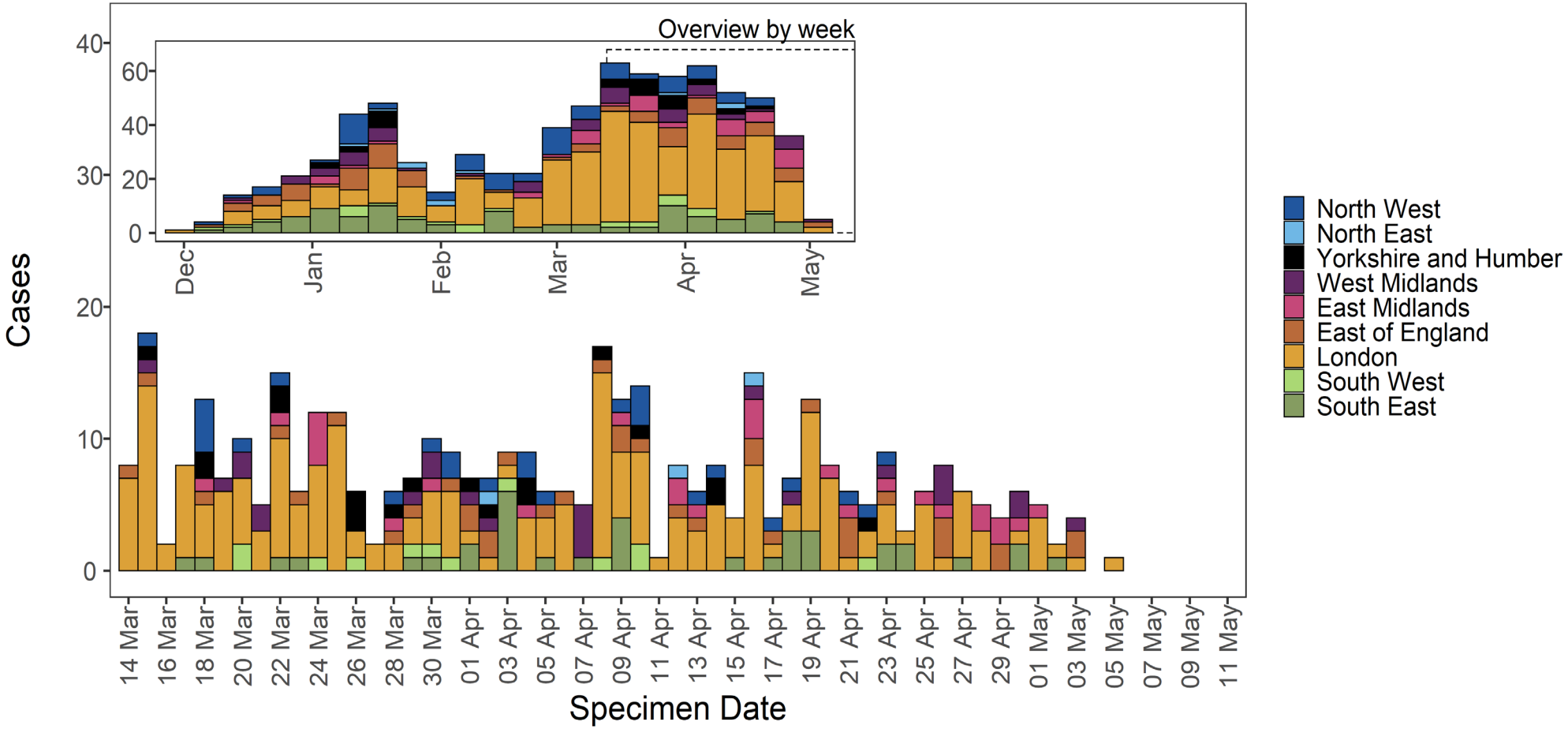
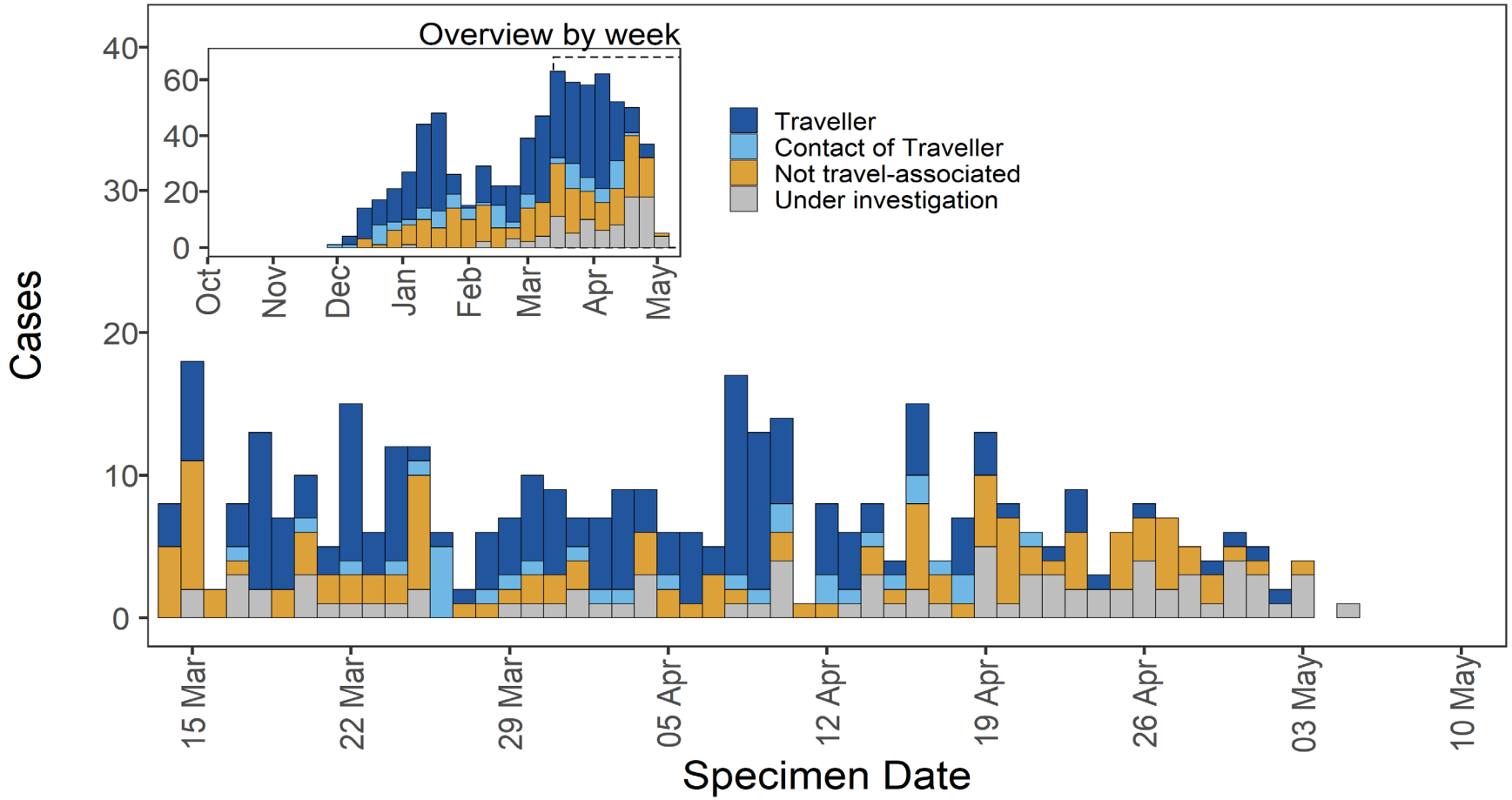


Figure 4. Travel data for confirmed and probable VOC-20DEC-02 (B.1.351) cases by specimen date as of 12 May 2021.
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data).



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 12 May 2021, 11,335 sequences of VOC-21JAN-02 are listed from 44 countries excluding the UK.

Epidemiology

Table 4. Number of confirmed and probable cases VOC-21JAN-02 (P.1), by region of residence as of 12 May 2021

Region	Case number	Case proportion	Cases that have travelled	Proportion of travellers among cases
East Midlands	2	2.0%	1	50%
East of England	9	8.8%	5	55.6%
London	55	53.9%	29	52.7%
North West	1	1.0%	1	100%
South East	18	17.6%	6	33.3%
South West	13	12.7%	5	38.5%
West Midlands	3	2.9%	1	33.3%
Yorkshire and Humber	1	1.0%	1	100%

Figure 5. Confirmed and probable VOC-21JAN-02 (P.1) cases by specimen date as of 12 May 2021.
(Find accessible data used in this graph in underlying data).

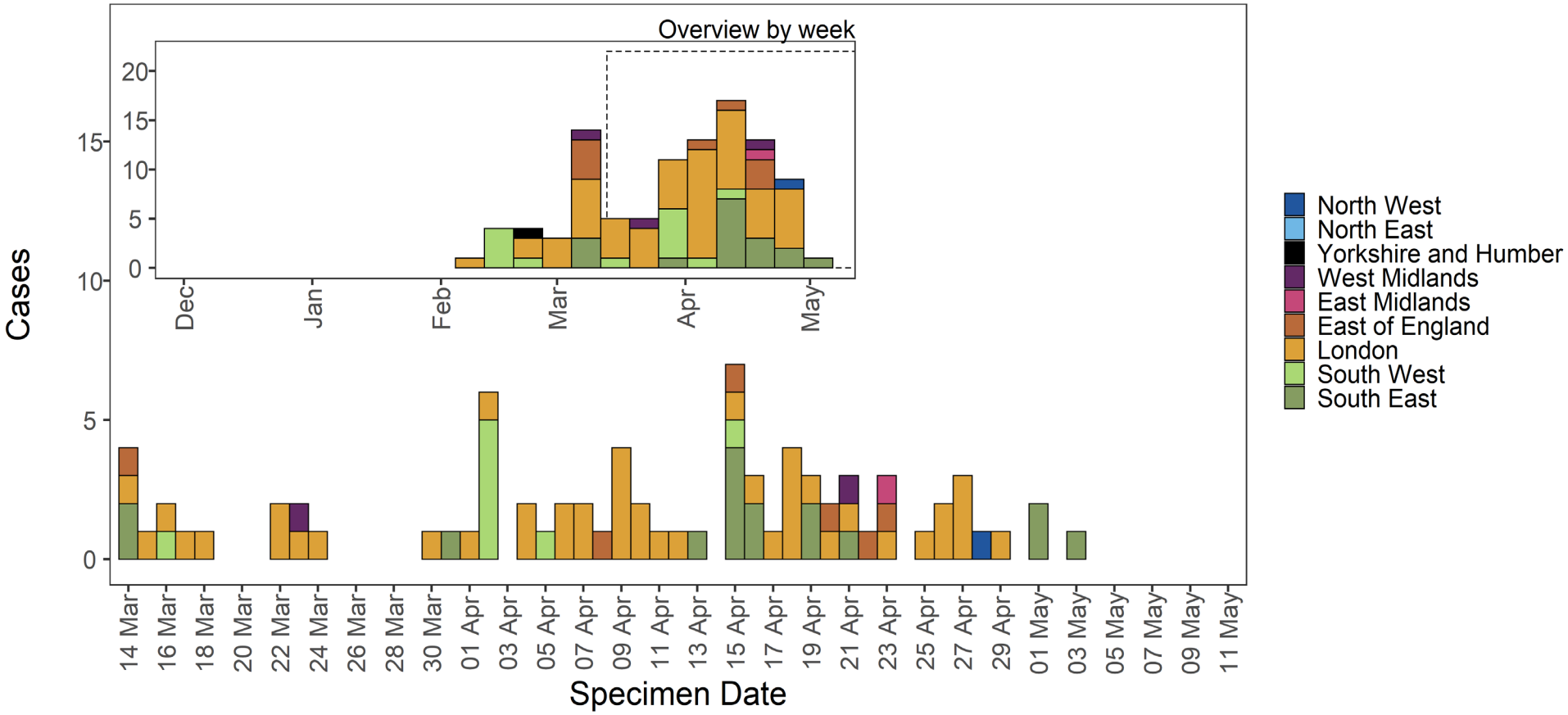
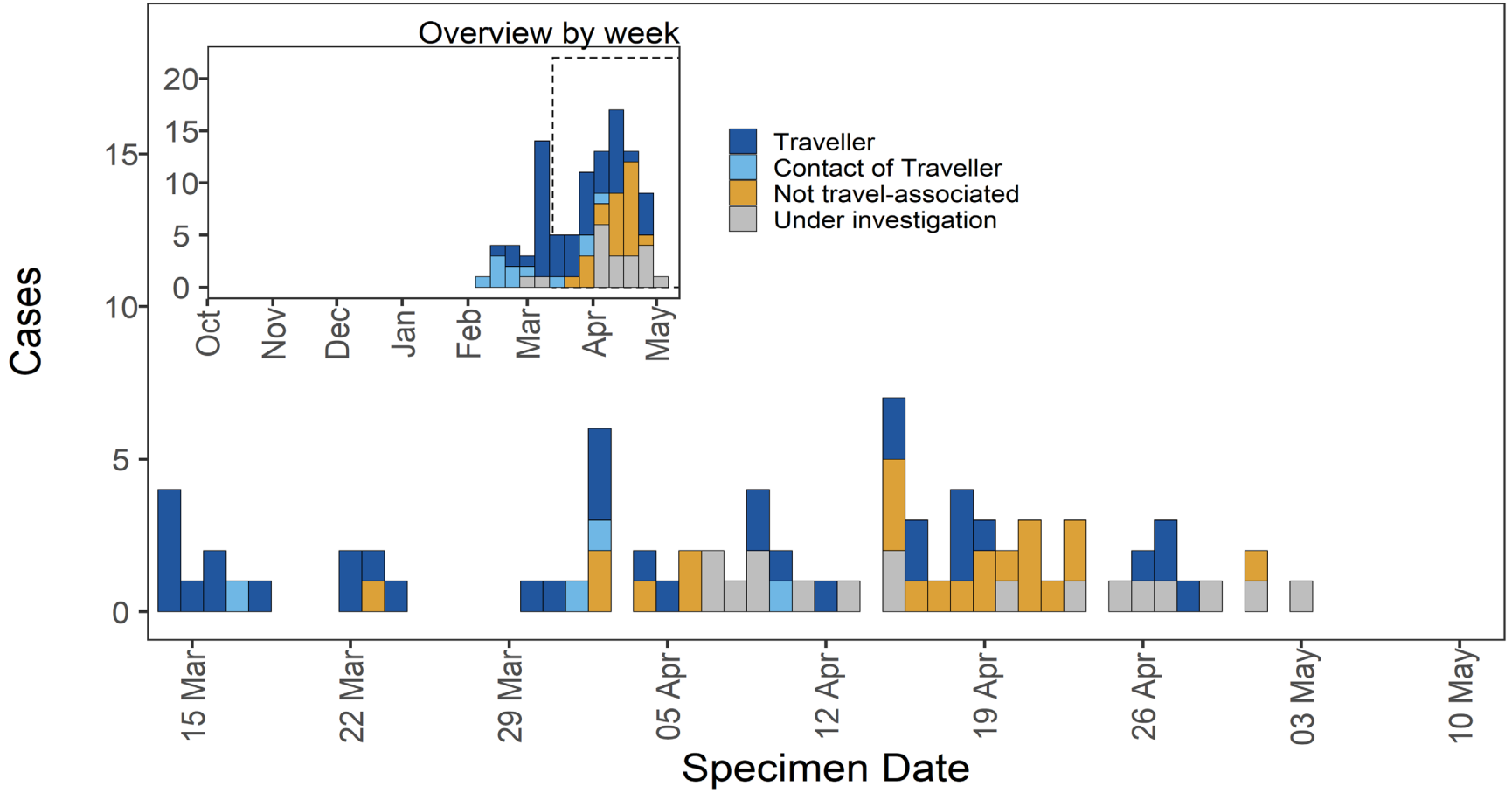


Figure 6. Travel data for confirmed and probable VOC-21JAN-02 (P.1) cases by specimen date as of 12 May 2021. Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data).



VUI-21JAN-01 (P2)

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 12 May 2021, 2,470 sequences (excluding UK) of VUI-21JAN-01 from 35 countries.

Epidemiology

Table 5. Number of confirmed and probable cases VUI-21JAN-01 (P.2), by region of residence as of 12 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 12 May 2021.
(Find accessible data used in this graph in underlying data.)

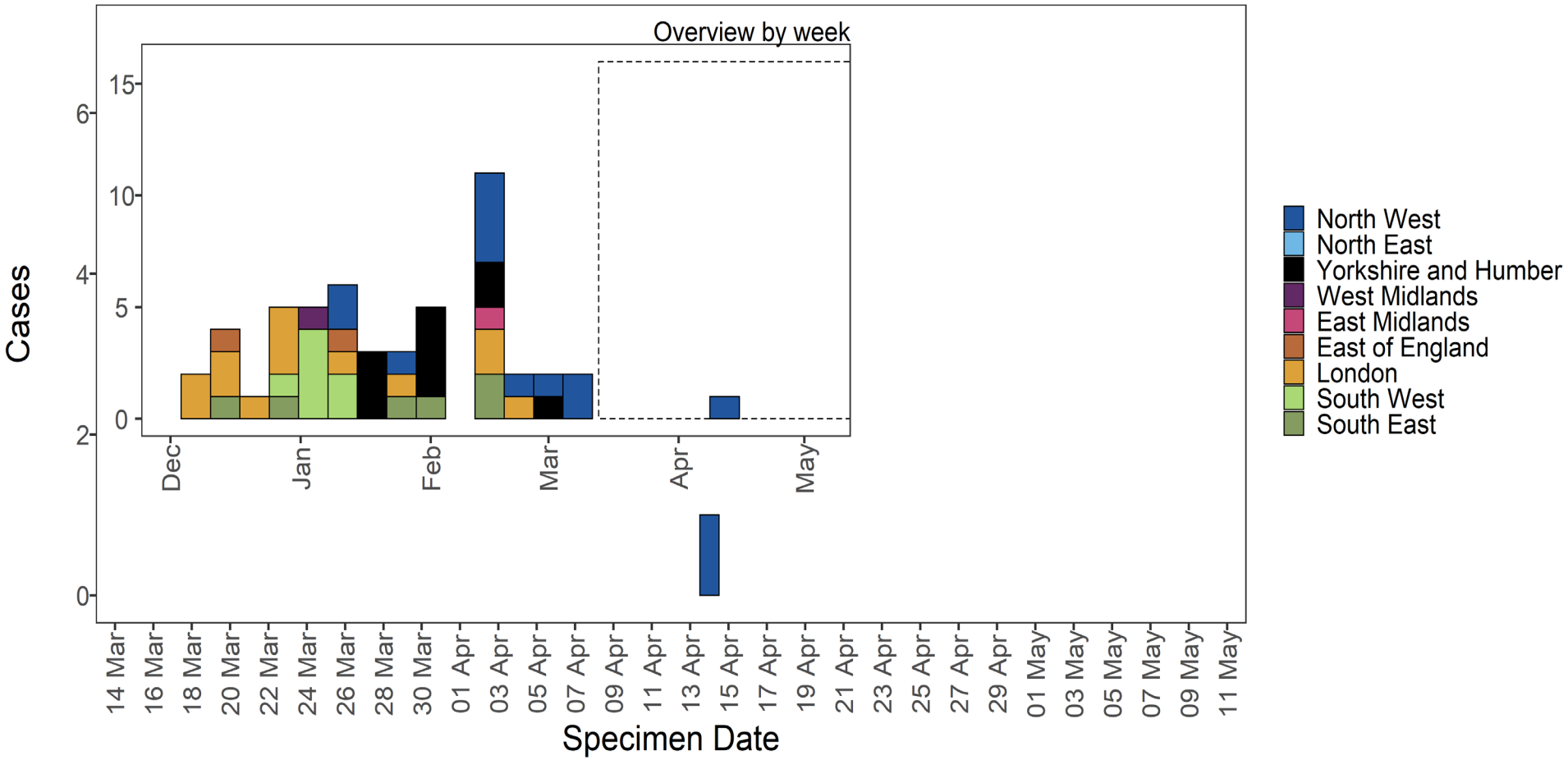
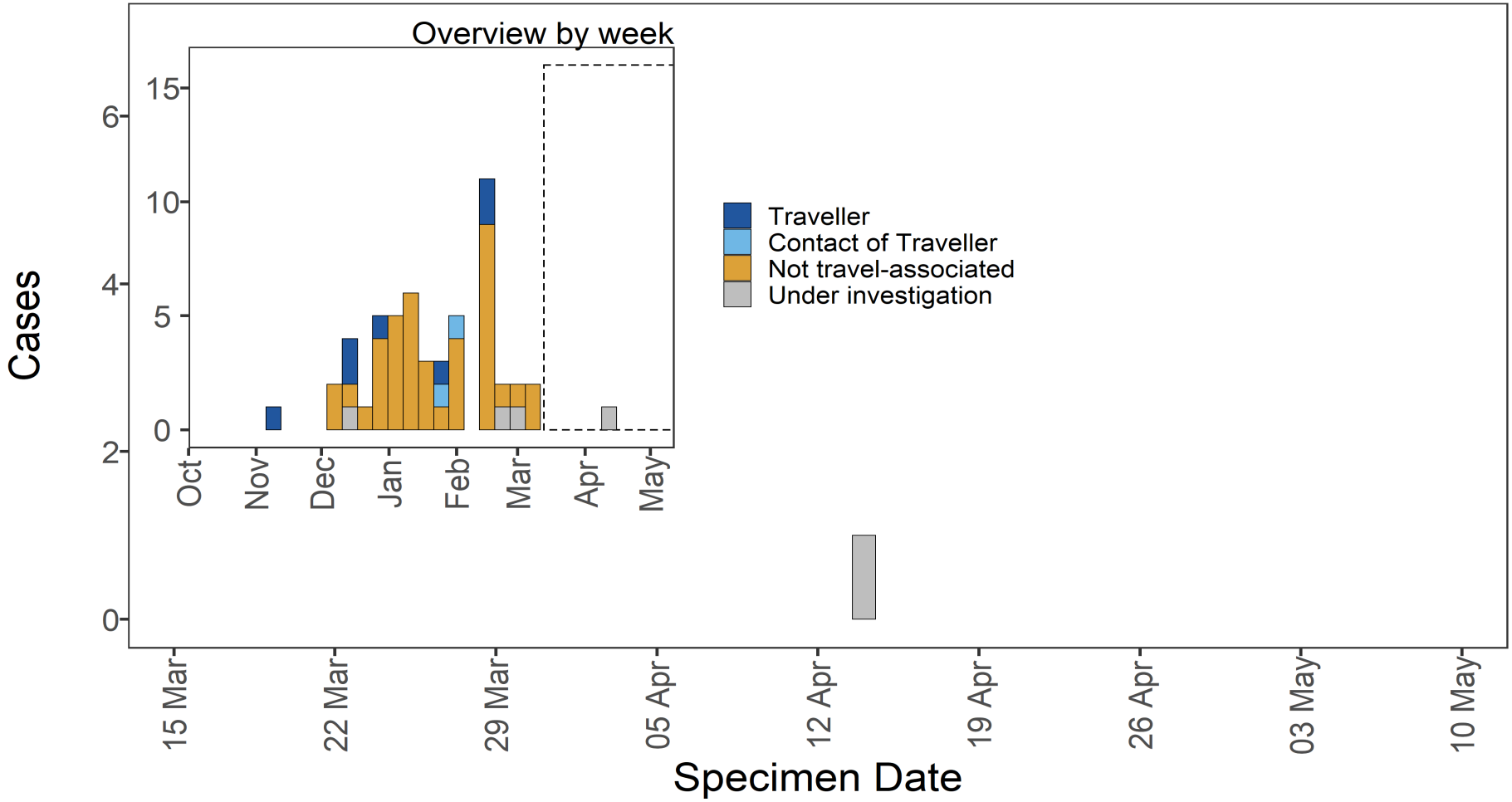


Figure 8. Travel data for confirmed and probable VUI-21JAN-01 (P.2) cases by specimen date as of 12 May 2021. Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data).



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 12 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 12 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 12 May 2021. Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data)

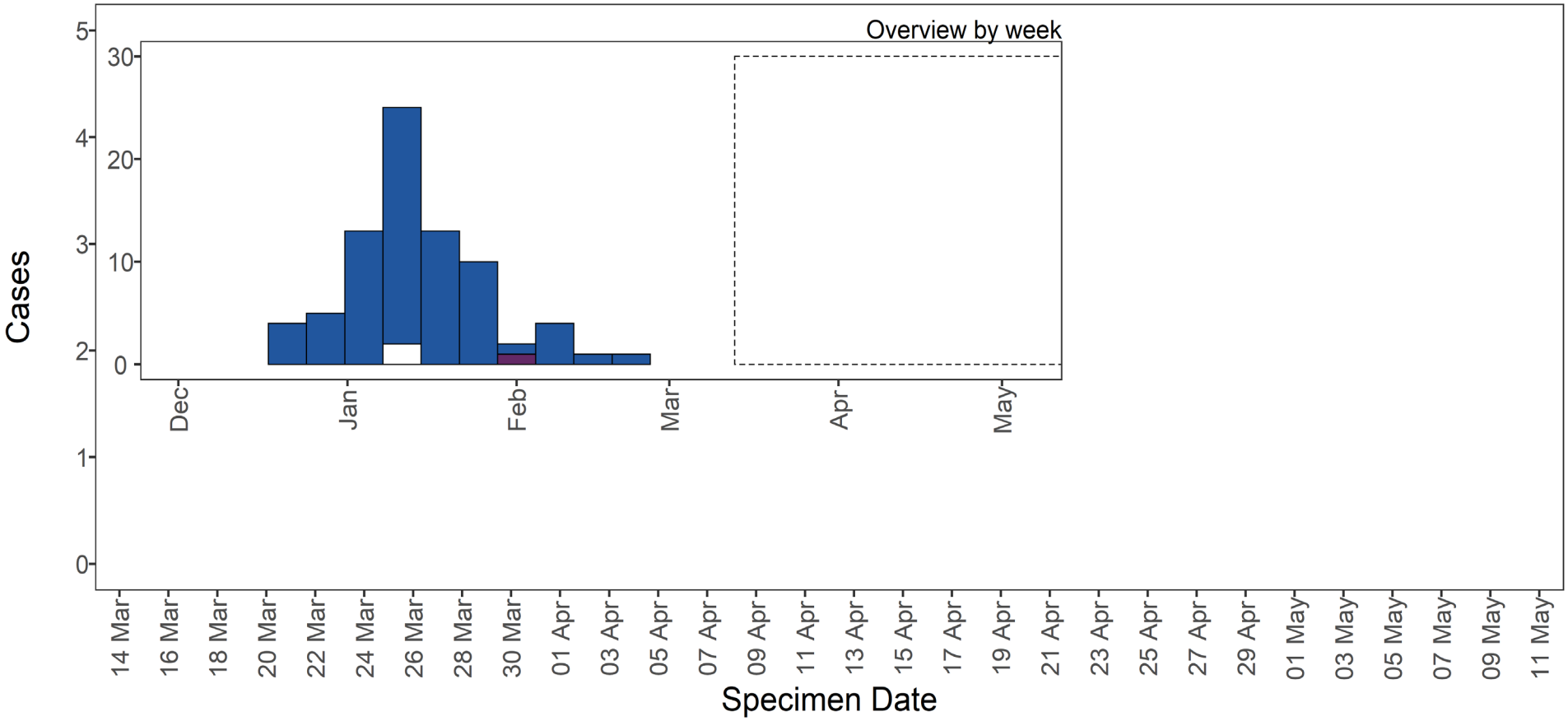
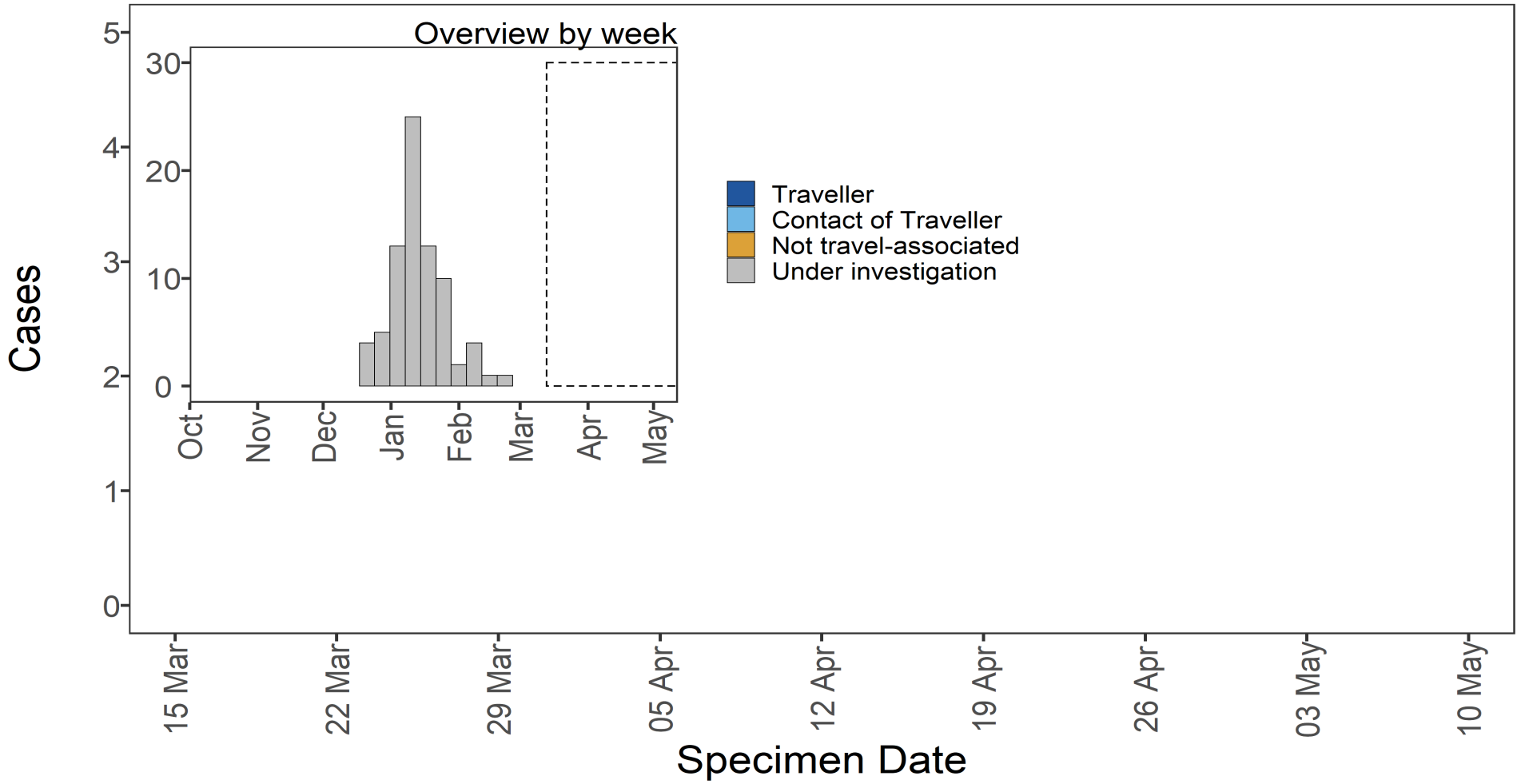


Figure 10. Travel data for confirmed and probable VUI-21FEB-01 (A.23.1 with E484K) cases by specimen date as of 12 May 2021. Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data).



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 12 May 2021, 2,936 sequences of VUI-21FEB-03 are listed, from 49 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 12 May 2021

Region	Case number	Case proportion	Cases that have travelled	Proportion of travellers among cases
East Midlands	10	2.5%	5	50%
East of England	26	6.6%	19	73.1%
London	141	35.9%	89	63.1%
North East	3	0.8%	3	100%
North West	69	17.6%	19	27.5%
South East	74	18.8%	25	33.8%
South West	18	4.6%	6	33.3%
West Midlands	31	7.9%	11	35.5%
Yorkshire and Humber	19	4.8%	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 12 May 2021. Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data).

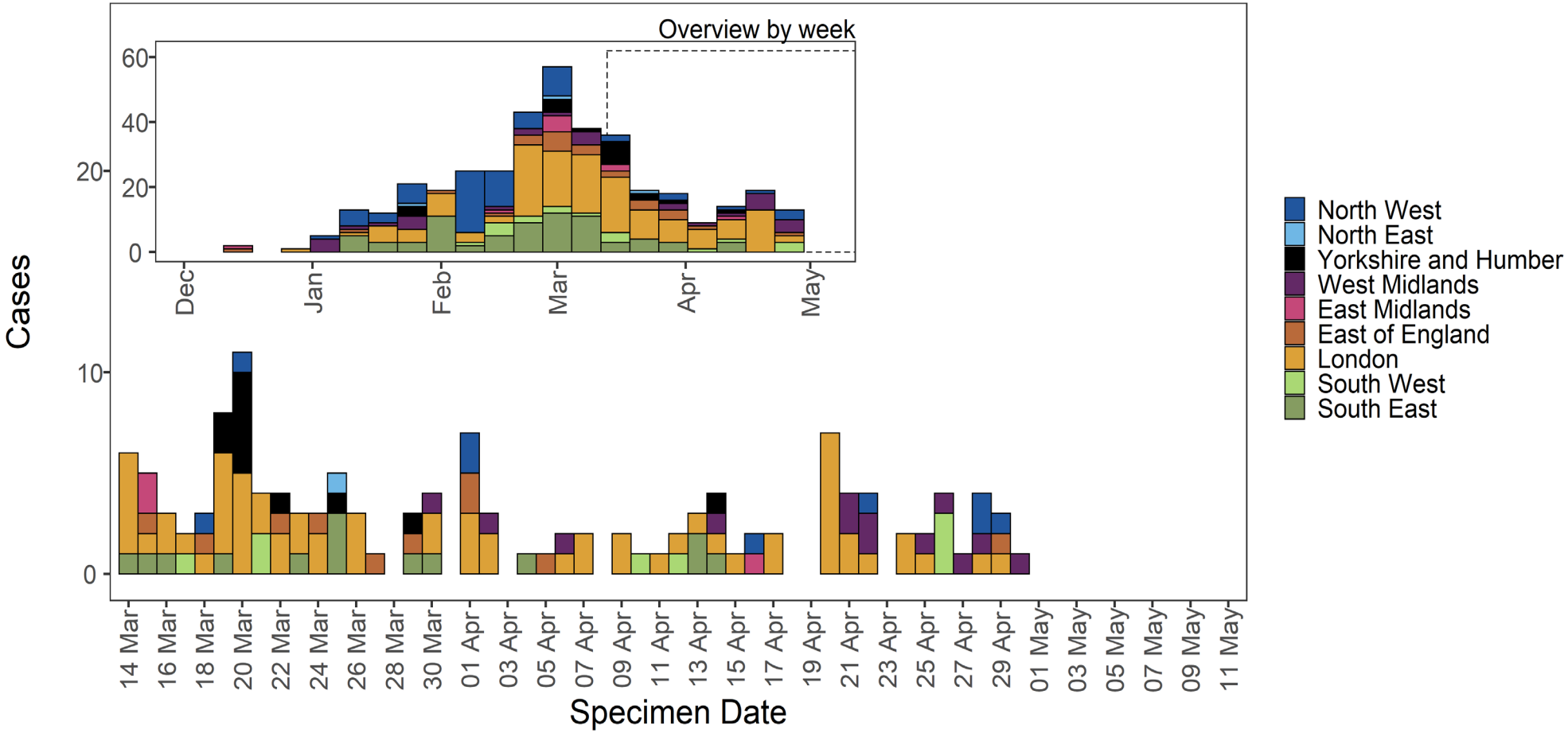
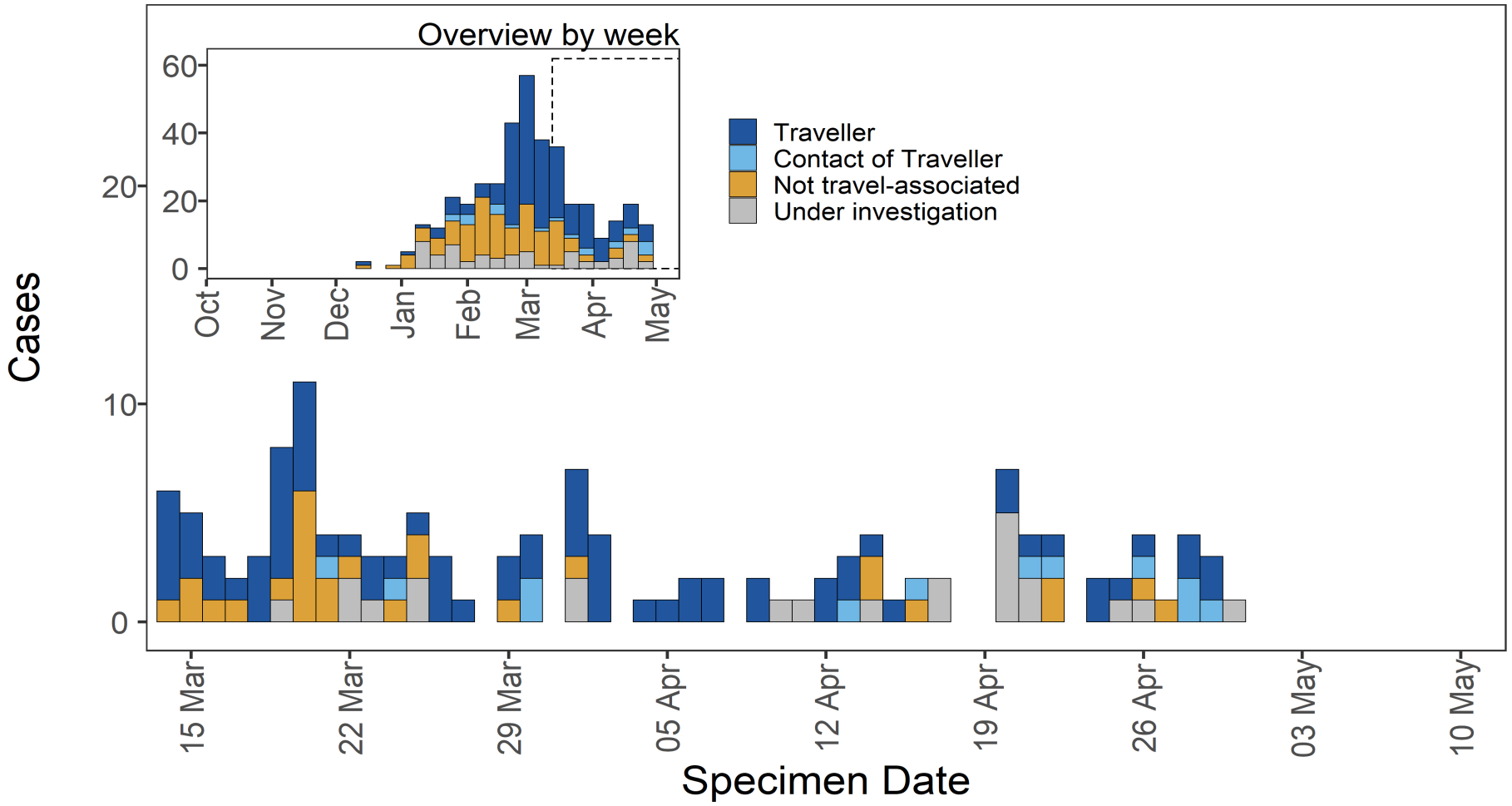


Figure 12. Travel data for confirmed and probable VUI-21FEB-03 (B.1.525) cases by specimen date as of 12 May 2021. Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data).



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 12 May 2021, 57 international VUI-21FEB-04 sequences, excluding UK. (USA 20, Switzerland 10, Nigeria 6, Germany 7, Italy 6, India 1, Sweden 4, Bangladesh 1, France 1, Denmark 1).

Table 8. Number of confirmed and probable VUI-21FEB-04 (B.1.1.318) cases, by region of residence as of 12 May 2021

Region	Case number	Case proportion	Cases that have travelled	Proportion of travellers among cases
East Midlands	10	5.3%	4	40%
East of England	23	12.1%	13	56.5%
London	67	35.3%	32	47.8%
North East	1	0.5%	1	100%
North West	41	21.6%	8	19.5%
South East	29	15.3%	10	34.5%
South West	1	0.5%	1	100%
West Midlands	7	3.7%	4	57.1%
Yorkshire and Humber	11	5.8%	1	9.1%

Figure 13. Confirmed and probable VUI-21FEB-04 (B.1.1.318) cases by specimen date as of 12 May 2021. Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data).

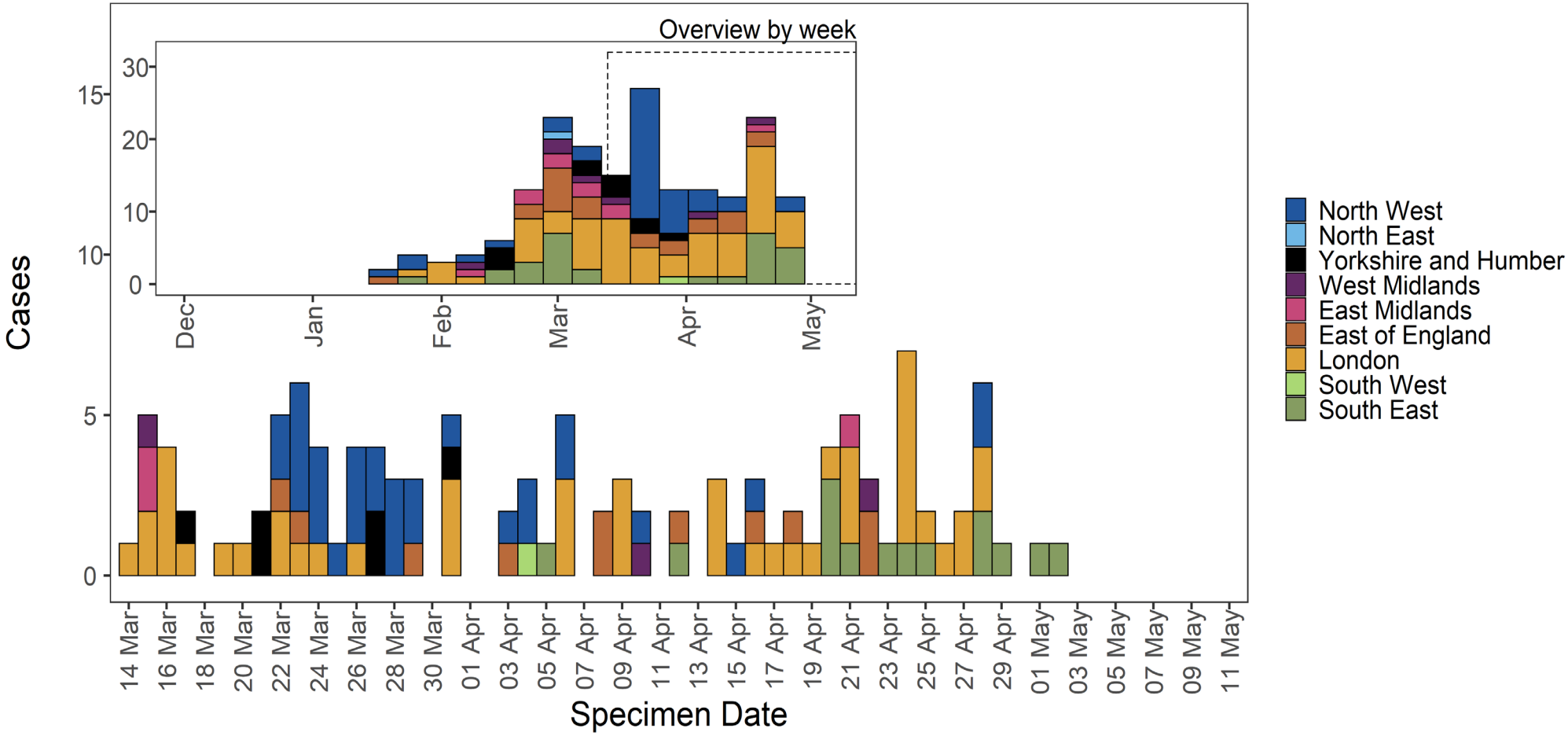
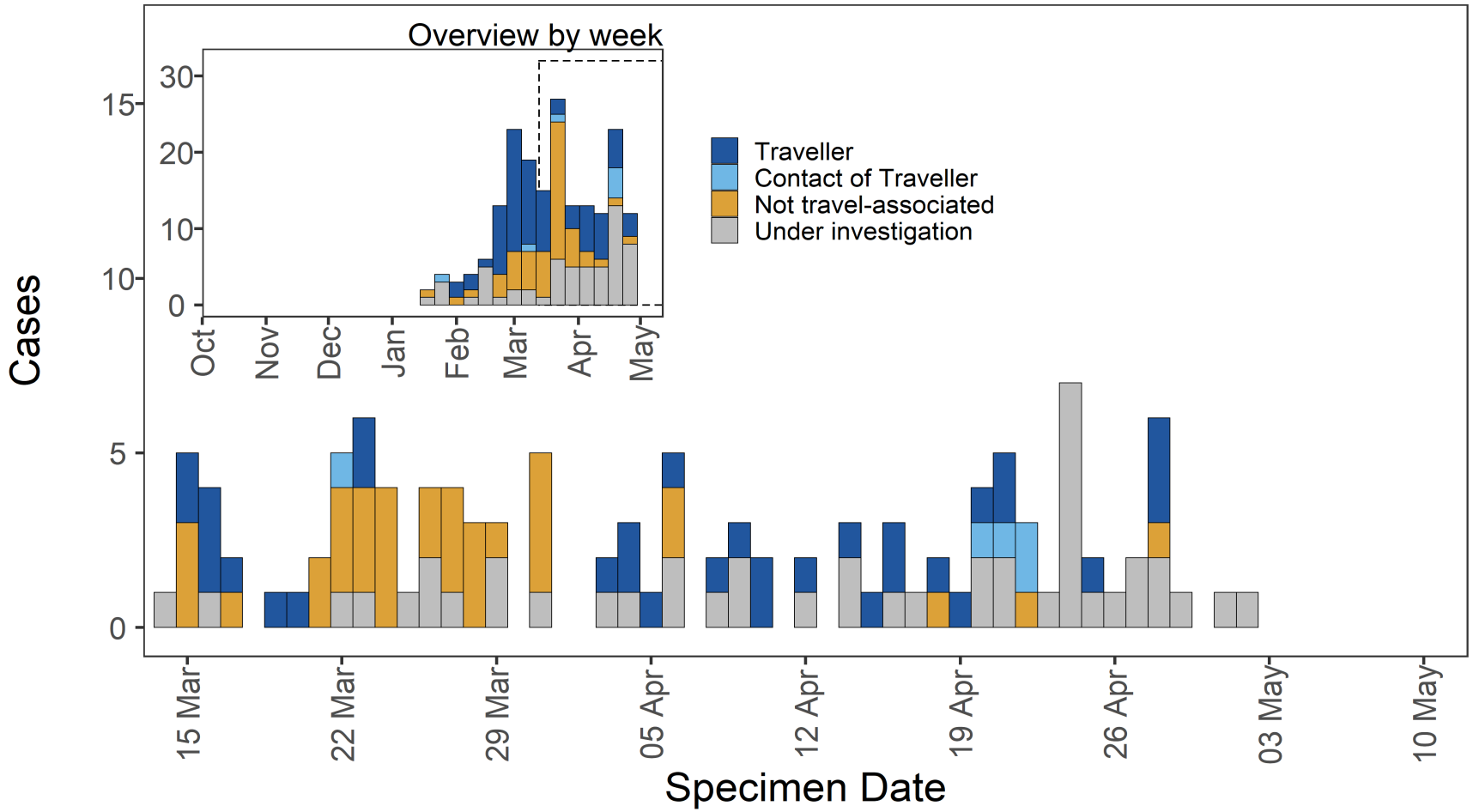


Figure 14. Travel data for confirmed and probable VUI-21FEB-04 (B.1.1.318) cases by specimen date as of 12 May 2021.
Larger plot includes last 60 days only. (Find accessible data used in this graph in underlying data).



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 12 May 2021,120 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 81, Singapore 1, South Korea 1, USA 3).

Table 9. Number of confirmed and probable VUI-21MAR-02 (P.3) cases, by region of residence as of 12 May 2021

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

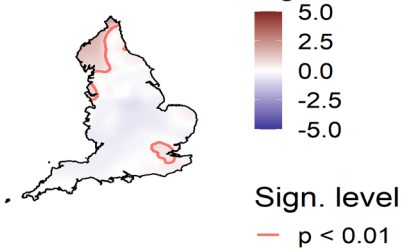
Spatial variation in risk for variants

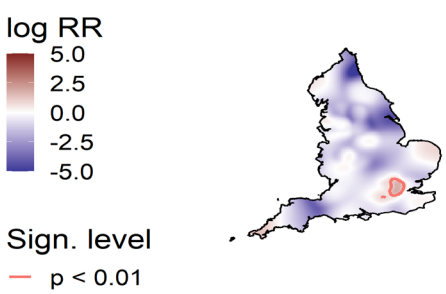
Spatial variation in risk

The spatial risk surface is estimated by comparing the smoothed intensity of cases (variants of concern) and controls (PCR +ve, non-variants of concern) across a defined geographical area to produce an intensity (or risk) ratio. If the ratio is ~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 >1 indicate an increased risk and values <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.

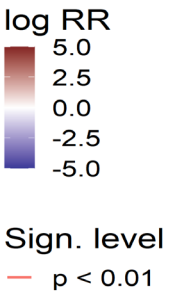
Figure 15. Spatial variation in risk for VOC data from 1 October 2020, as of 5 May 2021, excluding cases that have travelled.
(Supplementary data is not available for this figure).

VOC-20DEC-01

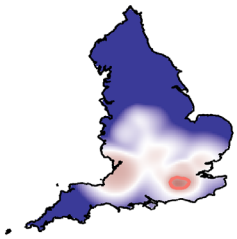


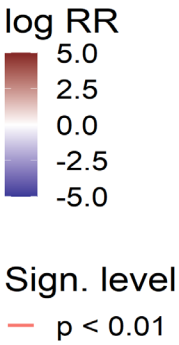


VOC-20DEC-02

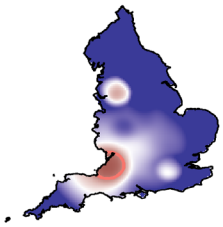


VOC-21JAN-02





VOC-21FEB-02



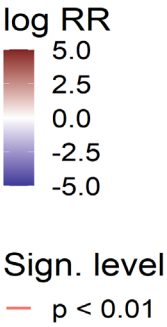
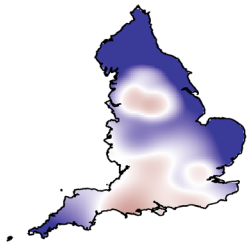
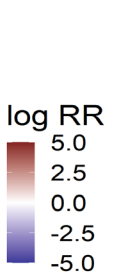


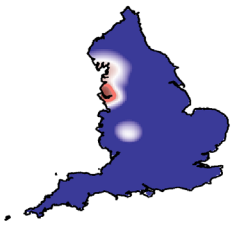
Figure 16. Spatial variation in risk for VUI data from 1 October 2020, as of 5 May 2021, excluding cases that have travelled.
(Supplementary data is not available for this figure).

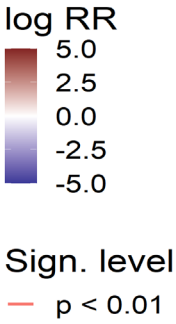
VUI-21JAN-01



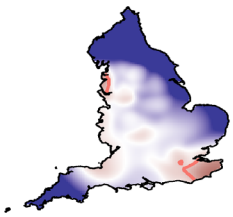


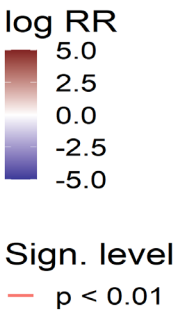
VUI-21FEB-01



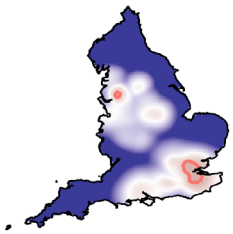


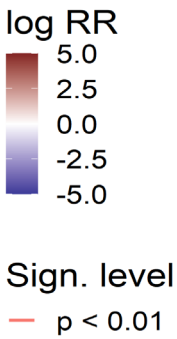
VUI-21FEB-03





VUI-21FEB-04





Secondary attack rates

Secondary attack rates are shown in Table 10. These are based on positive tests amongst contacts named to NHS Test and Trace by an original case identified with a confirmed or probable variant of concern or variant under investigation.

Secondary attack rates are shown for cases with and without travel history. In non-travel settings, only close contacts (household members, face to face contact, people within 1 metre of the case for 1 minute or longer, or people within 2 metres for 15 minutes) named by the original case are included. In travel settings the contacts reported are not restricted to only close contacts named by the case (for example, they may include contacts on a plane linked by additional contact tracing efforts), leading to likely deflation of secondary attack rates amongst travellers compared to non-travellers. In addition, people recently returning from overseas are subject to stricter quarantine measures and may moderate their behaviour towards contacts. Travel history indicates, but does not confirm, where infection of the original case occurred.

Secondary attack rates for contacts of non-travel cases with variants of concern or under investigation except VOC-21FEB-02 are not significantly different from that for contacts of non-travel cases with VOC-20DEC-01. No transmission events were identified to contacts of cases with VOC-21FEB-02. Estimates of secondary attack rates for contacts of those that have travelled with variants of concern or variants under investigation were all considerably lower than those that have not travelled, due to the difference in contact definition.

Table 10. Case numbers and travel status including proportion and secondary attack rate for 5 January 2021 to 21 April 2021, data as at 12 May 2021

Variant	Cases in those that have travelled (with contacts)	Cases in those that have not travelled or unknown (with contacts)	Case proportion that have travelled	Secondary Attack Rate among contacts of those that have travelled (95% CI) [secondary cases/contacts]	Secondary Attack Rate among contacts of cases that have not travelled or unknown (95% CI) [secondary cases/contacts]
VOC-20DEC-01	3,663 (78.5% with contacts)	158,692 (74.0% with contacts)	2.30%	1.7% (1.6% - 1.8%) [1,128/65,383]	10.0% (9.9% - 10.1%) [32,591/326,364]
VOC-20DEC-02	279 (73.1% with contacts)	275 (62.5% with contacts)	50.40%	2.6% (2.1% - 3.1%) [106/4,144]	9.1% (6.9% - 12.0%) [46/504]
VUI-21JAN-01	3 (66.7% with contacts)	32 (75.0% with contacts)	8.60%	Unavailable [0/137]	8.1% (3.5% - 17.5%) [5/62]
VOC-21JAN-02	47 (59.6% with contacts)	41 (61.0% with contacts)	53.40%	1.7% (0.7% - 3.9%) [5/295]	14.6% (8.7% - 23.4%) [13/89]
VUI-21FEB-01	0 (0 with contacts)	63 (60.3% with contacts)	0.00%	Unavailable [0/0]	8.6% (4.4% - 16.1%) [8/93]
VOC-21FEB-02	1 (100.0% with contacts)	33 (81.8% with contacts)	2.90%	Unavailable [0/96]	0.0% (0.0% - 3.3%) [0/111]
VUI-21FEB-03	178 (70.8% with contacts)	158 (71.5% with contacts)	53.00%	1.1% (0.8% - 1.5%) [44/3872]	9.2% (6.4% - 13.1%) [27/293]
VUI-21FEB-04	74 (66.2% with contacts)	87 (78.2% with contacts)	46.00%	0.6% (0.4% - 1.1%) [13/2050]	9.8% (6.3% - 15.0%) [18/183]

Variant	Cases in those that have travelled (with contacts)	Cases in those that have not travelled or unknown (with contacts)	Case proportion that have travelled	Secondary Attack Rate among contacts of those that have travelled (95% CI) [secondary cases/contacts]	Secondary Attack Rate among contacts of cases that have not travelled or unknown (95% CI) [secondary cases/contacts]
VUI-21MAR-01	1 (100.0% with contacts)	0 (0 with contacts)	100.00%	Unavailable [0/7]	Unavailable [0/0]
VUI-21MAR-02	3 (33.3% with contacts)	1 (100.0% with contacts)	75.00%	Unavailable [0/4]	Unavailable [0/3]

Secondary attack rates are marked as ‘Unavailable’ when count of contacts is less than 50 or count of exposing cases is less than 20. Travel-linked cases for secondary attack rates are identified positively in NHS Test and Trace data using multiple PHE sources. A case is considered as being travel-linked if: EpiCell or Health Protection Teams have found evidence of international travel, their NHS Test and Trace record mentions an event associated with international travel, their NHS Test and Trace record was created after notification via IHR NFP, they have been marked for priority contact tracing in NHS Test and Trace for reasons of travel.
Some travel-linked cases may be missed by these methods and would be marked as non-travel-linked or unknown. Secondary attack rates from NHS Test and Trace should generally be considered lower bounds due to the nature of contact tracing and testing. Data provided is for period 5 January 2021 to 21 April 2021 in order to allow time for contacts to become cases, hence case counts are lower than other sources. Provisional results are excluded.

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

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PHE Genomics Cell
PHE Outbreak Surveillance Team
PHE Epidemiology Cell
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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: May 2021
PHE gateway number: GW-8310

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