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We also acknowledge the following authors from the originating labs of some of the sequences in this paper:

Virus name	**Accession numbers**	**Originating Laboratory**	**Submitting laboratory**	**Authors**
Canada/QC-L00314539/2020	EPI_ISL_745260	CHUM-Site Glen-LAB Microbiologie	Laboratoire de santé publique du Québec	Sandrine Moreira, Ioannis Ragoussis, Guillaume Bourque, Jesse Shapiro, Mark Lathrop and Michel Roger on behalf of the CoVSeQ research group (http://covseq.ca/researchgroup)
Jamaica/JAM47542/2020	EPI_ISL_756367	The Caribbean Public Health Agency	Carrington Lab, Department of PreClinical Sciences, Faculty of Medical Sciences, The University of the West Indies	Nikita S. D. Sahadeo, Gabriel Escobar, Sarah Hill, Vernie Ramkissoon, Risha Singh, SueMin Nathaniel, Jacquiline Bissor-McKenzie, Arianne Brown-Jordan, Naresh Nandram, Avery Hinds, Jerome Foster, Stanley Giddings, Karla Georges, Marsha Ivey, Rahul Naidu, , Rajini Haraksingh, Jaya Jayaraman, Chinna Chinnadurai, Adesh Ramsubhag, Nuno Faria, Oliver Pybus, Christopher Oura, Christine V. F. Carrington
Norway/7129/2020, Norway/7115/2020	EPI_ISL_738314, EPI_ISL_738313	Foerde Hospital, Department of Microbiology	Norwegian Institute of Public Health, Department of Virology	Kathrine Stene-Johansen, Kamilla Heddeland Instefjord, Hilde Elshaug, Atiya R Ali,Marie Paulsen Madsen, Rasmus Riis Kopperud, Hilde Vollan, Karoline Bragstad, Olav Hungn

Oman/182621/2020	EPI_ISL_766569	Oman-National Influenza Center	Oman-National Influenza Center	Samiha Al-Kharusi, Laila Al-Balushi, Hamida Al-Barwani, Aisha Al-Busaidi, Intisar Al-Shukri, Samira Al-Mahruqi, Hanan Al-Kindi, Amina Al-Jardani
Singapore/1489/2020, Singapore/1468/2020, Singapore/1500/2020, Singapore/1502/2020, Singapore/1467/2020, Singapore/1466/2020, Singapore/1453/2020	EPI_ISL_754076 EPI_ISL_754075 EPI_ISL_754074 EPI_ISL_768618 EPI_ISL_754082 EPI_ISL_754083 EPI_ISL_728189	National Public Health Laboratory, National Centre for Infectious Diseases	National Public Health Laboratory, National Centre for Infectious Diseases	Tze Minn Mak, Sophie Octavia, Zhenyang Zhou, Lin Cui, Raymond Tzer Pin Lin
Luxembourg/LNS4604656/2020, Luxembourg/LNS7581211/2020, Luxembourg/LNS2043044/2020	EPI_ISL_770881, EPI_ISL_770880, EPI_ISL_755589	Laboratoire national de santé, Microbiology, Virology	Laboratoire national de santé, Microbiology, Microbial Genomics Platform	Anke Wienecke-Baldacchino, Catherine Ragimbeau,Jessica Tapp, Fatu Djabi, Lise Pignon, Raoul Salmon, Tamir Abdelrahman
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Italy/VEN-IZSVe-20RS2299-1_TV/2020, Italy/VEN-IZSVe-20RS2293-7_VI/2020, Italy/VEN-IZSVe-20RS2299-2_TV/2020	EPI_ISL_766580 EPI_ISL_766579 EPI_ISL_766581	ULSS 2 Treviso	Istituto Zooprofilattico Sperimentale delle Venezie	Adelaide Milani, Alessia Schivo, Annalisa Salviato, Erika Giorgia Quaranta, Ambra Pastori, Bianca Zecchin, Alice Fusaro, Calogero Terregino, Antonia Ricci
hCoV-19/France/HDF-IPP11311/2020	EPI_ISL_754842	CHU Amiens-Labo Virologie	National Reference Center for Viruses of Respiratory Infections, Institut Pasteur, Paris	Marion Barbet, Sylvie Behillil, Méline Bizard, Angela Brisebarre, Camille Capel, Etienne Simon-Lorière, Vincent Enouf, Maud Vanpeene, Sylvie van der Werf, Castelain Sandrine, François Catherine
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Italy/ABR-TE351971/2020, Italy/ABR-TE353967/2020, Italy/ABR-TE353969/2020, Italy/ABR-TE353968/2020	EPI_ISL_7308045 EPI_ISL_7308046 EPI_ISL_7308049 EPI_ISL_7308047	SIESP DIPARTIMENTO DI PREVENZIONE CHIETI	Istituto Zooprofilattico Sperimentale dell'Abruzzo e Molise "G. Caporale"	Lorusso A, Marcacci M, Di Domenico M, Ancora M, Curini V, Mangone I, Rinaldi A, Di Pasquale A, Cammà C, Puglia I, Savini G
USA/CO-CDPHE-2100156850/2020	EPI_ISL_751800	Colorado Department of Public Health and Environment	Colorado Department of Public Health and Environment	Laura Bankers, Molly C. Hetherington-Rauth, Diana Ir, Shannon Ely, Shannon R. Matzinger, Sarah Elizabeth Totten, Emily A. Travanty
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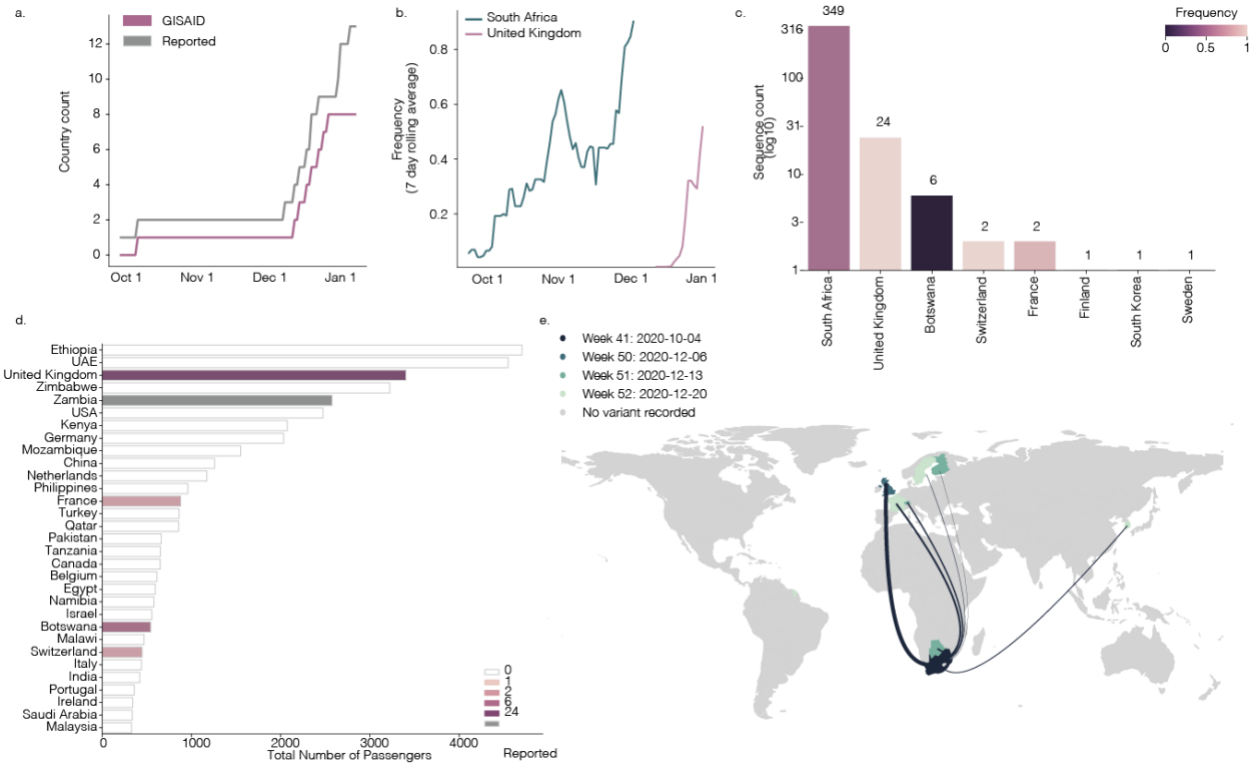
USA/FL-CDC-STM-P012/2020 USA/CA-CDC-STM-P019/2020,USA/CA-CDC-STM-P025/2020,USA/CA-CDC-STM-P017/2020	EPI_ISL_755593 EPI_ISL_755595 EPI_ISL_755596 EPI_ISL_755594	Helix/Illumina	Genomics and Discovery, Respiratory Viruses Branch, Division of Viral Diseases, Centers for Disease Control and Prevention	Peter W. Cook, Dhwani Batra, Eileen de Feo, Jan Antico, Christine Tran, Matthew Tolentino, Shannon Wickline, Kim Gietzen, Brad Sickler, Jingtao Liu, Eric Allen, Phil Febbo, Summer Galloway, Nicole L. Washington, Simon White, Geraint Levan, Kelly Schiabor Barrett, Elizabeth Cirulli, Alexandre Bolze, Ary Ascencio, Charlotte Rivera-Garcia, Ryan Cho, Jason Nguyen, Sherry Wang, Jimmy Ramirez, Tyler Cassens, Efren Sandoval, Magnus Isaksson, William Lee, David Becker, Marc Laurent, James Lu, Clinton R. Paden, Suxiang Tong, Duncan MacCannell

Supplementary materials



Supplementary Figure 1: a) Shows the cumulative number of countries with reports of lineage B.1.351 (black line) and cumulative number of genomes of B.1.351 deposited in GISAID. **b)** Rolling seven day average of the proportion of B.1.1.7 genomes in countries with more than ten sequences of the variant, and with more than ten days between the first B.1.1.7 sequence and the most recent one compared to all sampled genomes in that country. **c)** Number of sequences (log10) per country. Colour indicates the proportion of sequences that are classified as lineage B.1.351 **d)** Number of air travellers from South Africa during October 2020. Colour indicates the number of sampled genomes of lineage B.1.351. **e)** Map of international flights to countries with B.1.351 sequences. Colours indicate the date of earliest detection of B.1.351 in each country. The width of the lines indicates the number of flights. International Air Transport Association data used here account for ~90% of passenger travel itineraries on commercial flights, excluding transportation via unscheduled charter flights (the remainder is modelled using market intelligence). Data shown represents origin-destination journeys during October 2020. Routes to countries that have not yet detected B.1.351 and deposited data on GISAID are not included.

Supplementary table 1: Defining mutations for lineages of interest (see main text).

Lineage	Defining mutations
B.1.1.7	orf1ab:T1001I; orf1ab:A1708D; orf1ab:I2230T; del:11288:9; del:21765:6; del:21991:3; S:N501Y; S:A570D; S:P681H; S:T716I; S:S982A; S:D1118H; Orf8:Q27*; Orf8:R52I; Orf8:Y73C; N:D3L; N:S235F
B.1.351/501Y-V2	E:P71L; N:T205I; orf1a:K1655N; S:D80A; S:D215G; S:K417N; S:E484K; S:N501Y; S:E484K

Supplementary File 1:

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