THE LANCET

Supplementary appendix

This appendix formed part of the original submission and has been peer reviewed. We post it as supplied by the authors.

Supplement to: Yen H-L, Sit THC, Brackman CJ, et al. Transmission of SARS-CoV-2 delta variant (AY.127) from pet hamsters to humans, leading to onward human-to-human transmission: a case study. *Lancet* 2022; **399:** 1070–78.

Supplementary materials

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Supplementary methods

Sample collection

All staff wore N95 masks or powered air purifying respirators, disposable coveralls, gloves and shoe covers for protection. At the time of this study investigation, animals were kept in open cages and each animal species was kept separately. For initial screening, oral and fecal swabs were randomly collected from different animal species housed in different cages in the involved pet shop and the supplying warehouse. After hamsters were identified to be infected, follow-up investigations targeted hamsters and obtained paired blood and oral swabs for laboratory investigation. Swabs samples were individually placed in virus transport medium and kept chilled with cool-packs until arrival in the laboratory. Virus transport medium comprised Medium 199 (Sigma M0393) as basal medium, 0.5% bovine serum albumin, antibiotics (penicillin g, streptomycin sulfate, polymyxin B sulfate, sulfamethoxazole, nystatin, gentamicin sulfate, ofloxacin). RT-PCR positive samples collected from the initial screening investigations were tested and independently confirmed by two laboratories (AFCD and School of Public Health, HKU). Blood samples taken from animals were kept at room temperature until arrival in the laboratory. Blood were centrifuged (3,000 rpm for 10 min at 4 °C) before harvesting serum which was stored at 4°C until testing.

RT-PCR test

RNA from swab supernatant (140 µl) was extracted by using QIAamp viral RNA minikit (Qiagen, Hilden, Germany) following the manufacturer's instructions. Eluted RNA (60 µl total) was then tested by quantitative RT-PCR assays specific for the ORF1b and N genes of SARS-CoV-2. Sequences for the primer-probe sets and RT-PCR conditions were described (Chu et al., Clin Chem 2020). Samples that were positive in both assays were classified as confirmed positives, whereas samples that were positive only in only one of these assays was classified as an inconclusive result.

Next generation sequencing

The virus genome was reverse transcribed with multiple gene-specific primers targeting different regions of the viral genome. The synthesized cDNA was then subjected to multiple overlapping 2-kb PCRs for full-genome amplification. PCR amplicons obtained from the same specimen were pooled and sequenced using ISeq sequencing platform (Illumina). The sequencing library was prepared by Nextera DNA flex. The sequencing reads generated were trimmed by fastp (Chen et al., Bioinformatics 2018) with adapter and quality filters and were mapped to a reference virus genome (Genbank accession: MN908947.3) by BWA-MEM2 (https://github.com/bwa-mem2/bwa-mem2). Potential PCR duplicates were identified and removed by samtools markdup (https://www.htslib.org/doc/samtools-markdup.html). The genome consensus sequence was generated by iVar with the PCR primer trimming protocol (minimum sequence depth >10 and minimum Q value of 30) (Grubaugh et al., Genome Biol 2019). Samples yielded poor sequencing data were excluded in the downstream analyses.

All the viral genomes deduced from this study are deposited to GISAID with the following accession numbers: EPI_ISL_9049729, EPI_ISL_9049727, EPI_ISL_9049738, EPI_ISL_9049728, EPI_ISL_9049739, EPI_ISL_9049736, EPI_ISL_9049726, EPI_ISL_9049737, EPI_ISL_9049734, EPI_ISL_9049735, EPI_ISL_9049732, EPI_ISL_9049733, EPI_ISL_9049730, EPI_ISL_9049731, EPI_ISL_9049740, EPI_ISL_9509901, EPI_ISL_9509898, EPI_ISL_9509899, EPI_ISL_9509896, EPI_ISL_9509897, EPI_ISL_9509894, EPI_ISL_9509895, EPI_ISL_9509902, EPI_ISL_9509903, EPI_ISL_9509892, EPI_ISL_9509893.

Phylogenetic analysis

Viral genomes deduced from this study were analyzed together with a set of representative sequences available in GISAID, including (1) the top 40 most similar AY.127 sequences (number of nucleotide divergence ranged from 4 to 9, compared to the local human index case sequence);

(2) the top 5 most similar AY.127 sequences from Netherlands (number of nucleotide divergence ranged from 12 to 13, compared to the local index human case sequence); (3) all previous Hong Kong AY.127 sequences; and (4) outgroup reference sequences (from Pango lineages B, B.1.1.7, B.1.351, P.1, B.1.617.1); The public sequences of AY.127 lineage were retrieved from GISAID database on 19- January-2022. The outgroup reference sequences were retrieved from a pre-subsampled pre-aligned open database from Nextstrain (https://docs.nextstrain.org/projects/ncov/en/latest/reference/remote_inputs.html).

Surrogate virus neutralization test (svNT)

svNT kits were purchased from a commercial source (GenScript, Inc., NJ, USA) and the tests were carried out according to the manufacturer's instructions. One hundred µl of 10x diluted serum or controls samples were mixed with an equal volume of horseradish peroxidase (HRP, 6ng) conjugated to wild-type SARS-CoV-2 spike receptor binding domain (RBD) and incubated for 30 min at 37°C. Half of each mixture (100 µl) was added to each well on the microtiter plate coated with ACE-2 receptor. The plate was sealed and incubated at room temperature for 15 min at 37°C. Plates were then washed with Wash Buffer and tapped dry. One hundred µl of 3,3′,5,5′-tetramethylbenzidine (TMB) solution was added to each well and incubated in the dark at room temperature for 15 min. The reaction was stopped by addition of 50 µl of Stop Solution to each well and the absorbance read at 450 nm in an ELISA microplate reader. The assay validity was based on the optical density at 450 nm (OD450) for positive and negative control results falling within the recommended range.

Percent inhibition of each serum sample was calculated as follows: percent inhibition = (1 − sample OD value/negative-control OD value) × 100. Percent inhibition values of ≥30% are regarded as positive results, while percent inhibition values of <30% are regarded as negative results.

Plaque reduction neutralization tests (PRNT)

Duplicate serial two-fold dilutions from 1:10 to 1:320 of each hamster serum sample were incubated with 30–40 plaque-forming units of SARS-CoV-2 (Delta variant) (hCoV-19/Hong Kong/21TM280310_HKUVOC0013/2021), incubated for 1 hour and added to Vero E6 over-expressing TMRESS2 cells (Matsuyama et al., PNAS 2020) grown in 24-well tissue culture plates (TPP Techno Plastic Products AG, Trasadingen, Switzerland) in a biosafety level 3 facility. After incubation for 1 h at 37° C in 5% CO_2 incubator the cell monolayer was overlaid with 1% agarose in cell culture medium and incubated for 3 days, at which time the plates were fixed and stained. The highest serum dilution that resulted in >50% reduction in the number of virus plaques was defined as the 50% plaque reduction neutralization test ($PRNT_{50}$) antibody titre.

Virus isolation

Swabs with high viral load were inoculated onto Vero E6 cells overexpressing TMPRSS2 (Matsuyama et al., PNAS 2020) maintained in Dulbecco's Modified Eagle Medium (DMEM) medium (ThermoFisher Scientific, Waltham, MA, USA) supplemented with 10% fetal bovine serum (FBS) (ThermoFisher Scientific, Waltham, MA, USA) and 100 U/ml of penicillin–streptomycin (ThermoFisher Scientific, Waltham, MA, USA). The cells were observed daily for cytopathic effect and suspected virus isolates confirmed by RT-PCR as previously described (Chu et al., Clin Chem 2020).

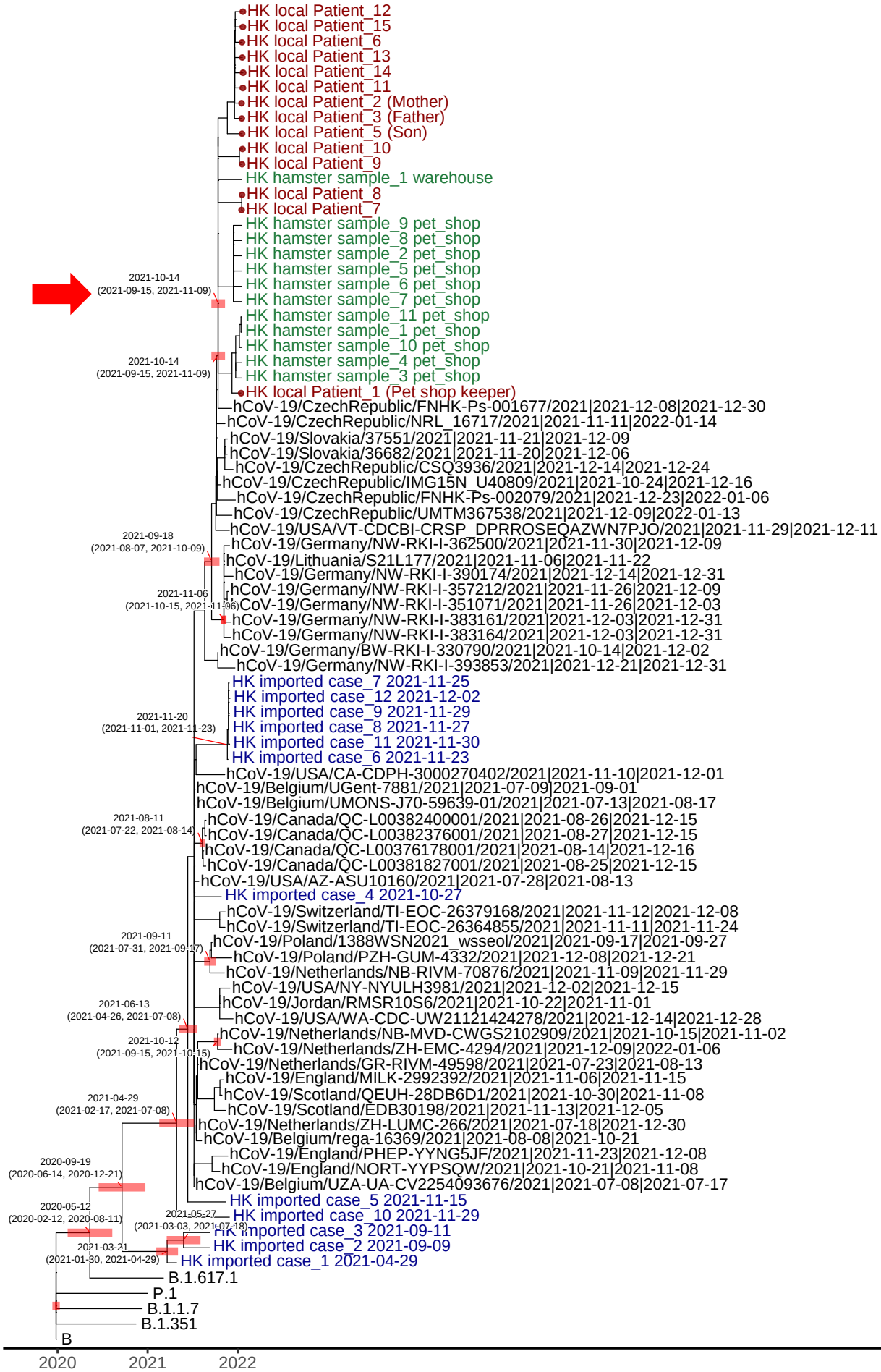
References:

Chen S, Zhou Y, Chen Y, Gu J. fastp: an ultra-fast all-in-one FASTQ preprocessor. Bioinformatics 2018; 34(17): i884-i90.

Chu DKW, Pan Y, Cheng SMS, et al. Molecular Diagnosis of a Novel Coronavirus (2019-nCoV) Causing an Outbreak of Pneumonia. Clin Chem 2020; 66(4): 549-55.

Grubaugh ND, Gangavarapu K, Quick J, et al. An amplicon-based sequencing framework for accurately measuring intrahost virus diversity using PrimalSeq and iVar. Genome Biol 2019; 20(1): 8.

Matsuyama S, Nao N, Shirato K, et al. Enhanced isolation of SARS-CoV-2 by TMPRSS2-expressing cells. Proc Natl Acad Sci U S A. 2020; 117(13):7001-7003.



Supplementary Figure. Phylogenetic Dating of most recent common ancestor of AY.127 viruses detected in hamster and human cases in this outbreak. The estimated date (95% interval range) is highlighted by an arrow.

Table S1. Samples collected from Syrian hamsters at Pet Shop A and the Warehouse.

Sampling location	Cage ID	Animals in cage	Animals sampled	Positive by sVNT	Confirmed PCR positive [a]	Inconclusive PCR positive[b]	Positive by sVNT or PCR[a]	Positive rate by cage
Pet Shop A	B	20	10	2	5	1	5	50%
	C	11	5	3	2	1	3	60%
	M	1	1	0	0	0	0	0%
Warehouse	C-47	1	1	1	0	1	1	100%
	C-31	1	1	1	1	0	1	100%
	C-unknown	1	1	0	0	0	0	0%
	C-48	1	1	1	0	0	1	100%
	A-75	~ 20 [c]	4	0	0	0	0	0%
	A-1	~ 4-6 [c]	2	2	0	1	2	100%
	A-2	~ 4-6 [c]	2	2	1	0	2	100%

[a] Quantitative RT-PCR positive for SARS-CoV-2 N and Orf1a gene.

[b] Quantitative RT-PCR positive for SARS-CoV-2 N gene alone

[c] Approximate number.

Table S2. RT-PCR detection of SARS-CoV-2 infected hamsters in pet shops

Location	Animal	N	Confirmed case (+ve rate, %)[a]	Inconclusive case (+ve rate, %)[b]
Pet shop B	Chinchilla	6	0 (0.0%)	0 (0.0%)
	Guinea pig	2	0 (0.0%)	0 (0.0%)
	Hamster	34	0 (0.0%)	1 (2.9%)
	Rabbit	15	0 (0.0%)	0 (0.0%)
Pet Shop C	Guinea pig	8	0 (0.0%)	0 (0.0%)
	Hamster	49	2 (4.1%)	0 (0.0%)
	Rabbit	25	0 (0.0%)	0 (0.0%)
Pet Shop D	Chinchilla	16	0 (0.0%)	0 (0.0%)
	Hamster	14	0 (0.0%)	0 (0.0%)
Pet Shop E	Hamster	15	0 (0.0%)	0 (0.0%)
	Rabbit	14	0 (0.0%)	0 (0.0%)
Pet Shop F	Chinchilla	9	0 (0.0%)	0 (0.0%)
	Guinea pig	7	0 (0.0%)	0 (0.0%)
	Hamster	15	0 (0.0%)	0 (0.0%)

[a] Quantitative RT-PCR positive for SARS-CoV-2 N and Orf1a gene.

[b] Quantitative RT-PCR positive for SARS-CoV-2 N gene alone

Table S3: Number of nucleotide differences between viral genomes studied in this outbreak.

	Number of nucleotide differences (Loocations in the genome)*	
Sample	Reference Sequence: Patient_1	Reference sequence: Patient_2
Patient_1 (Pet shop keeper)	-	5 (9430|9886|21707|24370|29670)
Patient_2 (Mother)	5 (9430|9886|21707|24370|29670)	-
Patient_3 (Father)	5 (9430|9886|21707|24370|29670)	0
Patient_5 (Son)	9 (9430|9886|21707|24370|26422|26830|27382|28277|29670)	4 (26422|26830|27382|28277)
Patient_6	6 (9430|9886|21707|22339|24370|29670)	1 (22339)
Patient_7	17(6968|6997|7002|7119|7162|7200|7262|9430|9615|12073|14772|20115|21691|21707|29635|29659|29670)	16(6968|6997|7002|7119|7162|7200|7262|9615|9886|12073|14772|20115|21691|24370|29635|29659)
Patient_8	17(6968|6997|7002|7119|7162|7200|7262|9430|9615|12073|14772|20115|21691|21707|29635|29659|29670)	16(6968|6997|7002|7119|7162|7200|7262|9615|9886|12073|14772|20115|21691|24370|29635|29659)
Patient_9	11(259|7081|7113|7194|9430|9886|12003|17510|19011|21157|21707)	10 (259|7081|7113|7194|12003|17510|19011|21157|24370|29670)
Patient_10	10(7081|7113|7194|9430|9886|12003|19011|21157|21707|28254)	10 (12|7081|7113|7194|12003|19011|21157|24370|28254|29670)
Patient_11	6 (9430|9886|21707|22339|24370|29670)	1 (22339)
Patient_12	7 (9430|9886|19329|21707|22339|24370|29670)	2 (19329|22339)
Patient_13	8 (9430|9886|20351|22339|22821|23276|24370|29670)	4 (20351|22339|22821|23276)
Patient_14	9 (9430|9886|21707|22339|24370|28254|28269|28270|29670)	4 (22339|28254|28269|28270)
Patient_15	9 (5239|9430|9886|14408|16604|21707|22339|24370|29670)	5 (2882|5239|14408|16604|22339)
HK hamster sample_1 pet_shop	1 (27549)	6 (9430|9886|21707|24370|27549|29670)
HK hamster sample_2 pet_shop	4 (5467|21707|21839|29670)	5 (5467|9430|9886|21839|24370)
HK hamster sample_3 pet_shop	1 (27549)	5 (9430|9886|24370|27549|29670)
HK hamster sample_4 pet_shop	5 (21427|21629|21663|25999|27549)	10 (9430|9886|21427|21629|21663|21707|24370|25999|27549|29670)
HK hamster sample_5 pet_shop	5 (5467|21707|21839|29696|29742)	8 (5467|9430|9886|21839|24370|29670|29696|29742)
HK hamster sample_6 pet_shop	3 (5467|21707|29670)	4 (5467|9430|9886|24370)
HK hamster sample_7 pet_shop	2 (21707|29670)	3 (9430|9886|24370)
HK hamster sample_8 pet_shop	9 (5467|6810|8204|21707|21819|21839|22063|25937|29670)	10 (5467|6810|8204|9430|9886|21819|21839|22063|24370|25937)
HK hamster sample_9 pet_shop	5 (5467|21707|21839|29670|29679)	7 (5467|9430|9886|21839|24370|29679|29808)
HK hamster sample_10 pet_shop	1 (27549)	6 (9430|9886|21707|24370|27549|29670)
HK hamster sample_11 pet_shop	1 (27549)	6 (9430|9886|21707|24370|27549|29670)
HK hamster sample_1 warehouse	13(7851|9430|9886|17358|18151|19245|21459|21549|21707|27131|29642|29670|29679)	10 (7851|17358|18151|19245|21459|21549|24370|27131|29642|29679)

*Viral genome ofPatient 1 or 2 is used as the reference sequence. Sequencing gaps are ignored in this analysis.

Table S4. Non-silent mutations found in AY.127 from infected humans and hamsters.

Position	Nt mutation	Gene	AA mutation*	hCoV-19/Czech 1**	hCoV-19/Czech 2**	hCoV-19/Czech 3**	hCoV-19/Czech 4**	Patient 1 (Pet shop keeper)	Patient 2 (Mother)	Patient 3 (Father)	Patient 5 (Son)	Patient 6	Patient 7	Patient 8	Patient 9	Patient 10	Patient 11	Patient 12	Patient 13	Patient 14	Patient 15	Patient 16	Patient 17	Patient 18	Patient 19	Patient 20	Hamster sample 1 pet shop	Hamster sample 1 warehouse	Hamster sample 2 pet shop	Hamster sample 3 pet shop	Hamster sample 4 pet shop	Hamster sample 5 pet shop	Hamster sample 6 pet shop	Hamster sample 7 pet shop	Hamster sample 8 pet shop	Hamster sample 9 pet shop	Hamster sample 10 pet shop	Hamster sample 11 pet shop
21614	C/T	S	L18F	N	N	N	N	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	-	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	-	Y	Y	Y	Y	Y	Y	Y	Y
21707	C/T	S	H49Y	N	N	N	N	Y	N	N	N	N	N	N	N	N	N	N	-	N	N	N	N	N	N	N	Y	N	N	-	Y	N	N	N	N	N	Y	Y
22842	A/G	S	D427G	N	N	N	N	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y
29670	C/T	ORF10	T38I	N	N	N	N	N	Y	Y	Y	Y	Y	Y	N	N	Y	Y	Y	Y	Y	N	N	N	N	N	N	Y	Y	N	N	N	Y	Y	Y	Y	N	N

* Unique amino acid mutations reproducibility found in both studied human and hamster cases;

**Studied European AY.127 sequences:

1) hCoV-19/Czech Republic/FNHK-Ps-002079/2021|2021-12-23|2022-01-06
2) hCoV-19/Czech Republic/UMTM367538/2021|2021-12-09|2022-01-13
3) hCoV-19/Czech Republic/NRL_16717/2021|2021-11-11|2022-01-14
4) hCoV-19/Czech Republic/FNHK-Ps-001677/2021|2021-12-08|2021-12-30

- Sequence gap

Table S5: SARS-CoV-2 sequences downloaded from GISAID (https://www.gisaid.org/) for the current study.

Accession ID	Originating lab	Submitting lab	Authors
EPI_ISL_2931358	Home Quarantine Taskforce	Hong Kong Department of Health	Alan K.L. Tsang, Peter C.W. Yip, Ken H.L. Ng, Edman T.K. Lam, Rickjason C.W. Chan
EPI_ISL_2988236	Platform BIS UZA/UAntwerpen	Labo Klinische Biologie, UZA	Marie Le Mercier, Jasmine Coppens, Kathleen Holemans, Ines Verbesselt, Basil Britto Xavier, Christine Lammens, Veerle Matheeussen, Herman Goossens
EPI_ISL_3385638	Arizona State University	Arizona State University	Ajeet Bains, LaRinda A. Holland, Matthew F. Smith, Peter T. Skidmore, Rabia Maqsood, Nicholas J. Mellor, Nathaniel Johnson, Joshua LaBaer, Vel Murugan, Efrem S. Lim
EPI_ISL_3390190	Dutch COVID-19 response team	National Institute for Public Health and the Environment (RIVM)	Adam Meijer, Harry Vennema, Dirk Eggink, Jeroen Cremer, Sharon van den Brink, Bas van der Veer, AnneMarie van den Brandt, Lisa Wijsman, Kim Freriks, Ryanne Jaarsma, Euníce Then, Lynn Aarts, Sanne Bos, Stijn van Rossum, Florian Zwagemaker, Dennis Schmitz, Annelies Kroneman, Karim Hajji, Chantal Reusken, on behalf of the national COVID-19 response team
EPI_ISL_3453216	National Platform bis UMONS/Jolimont	National Platform bis UMONS/Jolimont	François Dufrasne, Guillaume Bayon-Vicente, Florian Juszczak, Laetitia Gheysen, Eric Tarantino, Gautier Detry, Ruddy Wattiez
EPI_ISL_3868482	Lab voor klinische biologie	Lab voor klinische biologie	Marija Janevska, Hannelore Hamerlinck, Bruno Verhasselt
EPI_ISL_4342661	North Lantau Hospital	Hong Kong Department of Health	Alan K.L. Tsang, Peter C.W. Yip, Ken H.L. Ng, Edman T.K. Lam, Rickjason C.W. Chan
EPI_ISL_4342666	Home Quarantine Taskforce	Hong Kong Department of Health	Alan K.L. Tsang, Peter C.W. Yip, Ken H.L. Ng,

			Edman T.K. Lam, Rickjason C.W. Chan
EPI_ISL_4542252	WSSE w Olsztynie	Wojewodzka Stacja Sanitarno-Epidemiologiczna w Olsztynie, Laboratorium Badan Epidemiologiczno-Klinicznych	Sylwia Krzetowska, Monika Czerminska, Ewa Liszewska, Tomasz Jakubczak, Marta Lukian, Patryk Bielecki, Aleksandra Kobiatko, Emilia Tarabasz, Paulina Rozycka, Barbara Dolinska
EPI_ISL_5403355	KU Leuven, Rega Institute, Clinical and Epidemiological Virology	KU Leuven, Rega Institute, Clinical and Epidemiological Virology	Tony Wawina-Bokalanga, Bert Vanmechelen, Joan Marti-Carerras, Piet Maes
EPI_ISL_5804658	Jordan Royal Medical Services Mobile Biological Lab	Jordan Royal Medical Services Genomics Core Lab	Dr. Rame Hamdi khasawneh, Ali Alhuniti, Osama Alshdaifat, Mohammad Barmawi , Abdullah Almuhasen , Alanood Alhabashnah
EPI_ISL_5852875	Microvida	Microvida	Suzan D. Pas, Jaco J. Verweij, Joep J. J. M. Stohr
EPI_ISL_6018539	Northumbria University / South Tees Hospitals NHS Foundation Trust / North Cumbria Integrated Care NHS Foundation Trust / North Tees and Hartlepool NHS Foundation Trust / Newcastle Hospitals NHS Foundation Trust	COVID-19 Genomics UK (COG-UK) Consortium	Darren L Smith,Andrew Nelson,Matthew Bashton,Greg R Young,Joshua Loh,John Allan,Mohammad A Tariq,Giles S Holt,Gary Black,Wen C Yew,Lynn Dover,Paul Baker,Steve Liggett,Sarah Essex,Jane Greenaway,Debra Padgett,Clive Graham,Garren Scott,Edward Barton,Emma Swindells,Brendan Payne,Jennifer Collins,Yusri Taha,Gary Eltringham
EPI_ISL_6047550	Lighthouse Lab in Glasgow	Wellcome Sanger Institute for the COVID-19 Genomics UK (COG-UK) Consortium	Harper VanSteenhouse, Yumi Kasai, David Gray, Carol Clugston, Anna Dominiczak and Alex Alderton, Roberto Amato, Jeffrey Barrett, Sonia Goncalves, Ewan Harrison, David K. Jackson, Ian Johnston, Dominic Kwiatkowski, Cordelia Langford, John Sillitoe on behalf of the Wellcome Sanger Institute

			COVID-19 Surveillance Team
EPI_ISL_6299307	Lighthouse Lab in Milton Keynes	Wellcome Sanger Institute for the COVID-19 Genomics UK (COG-UK) Consortium	The Lighthouse Lab in Milton Keynes and Alex Alderton, Roberto Amato, Jeffrey Barrett, Sonia Goncalves, Ewan Harrison, David K. Jackson, Ian Johnston, Dominic Kwiatkowski, Cordelia Langford, John Sillitoe on behalf of the Wellcome Sanger Institute COVID-19 Surveillance Team
EPI_ISL_6602081	Viesoji istaiga Vilniaus universiteto ligonine Santaros klinikos	Vilnius University Hospital Santaros Klinikos, Center of Laboratory Medicine	Daniel Naumovas, Ligita Raugaite, Monika Katenaite, Rimvydas Norvilas, Dovile Juozapaite, Ingrida Olendraite, Gytis Dudas
EPI_ISL_6685928	Labor team w AG	Laboratorio di Microbiologia, Istituto di Medicina di Laboratorio EOLAB, Ente Ospedaliero Cantonale	Martinetti Lucchini Gladys, Valeria Spina
EPI_ISL_6853878	Dutch COVID-19 response team	National Institute for Public Health and the Environment (RIVM)	Adam Meijer, Harry Vennema, Dirk Eggink, Jeroen Cremer, Sharon van den Brink, Bas van der Veer, AnneMarie van den Brandt, Lisa Wijsman, Kim Freriks, Ryanne Jaarsma, Lynn Aarts, Sanne Bos, Stijn van Rossum, Linda van Someren, Florian Zwagemaker, Dennis Schmitz, Annelies Kroneman, Karim Hajji, Ivo van Walle, Chantal Reusken, on behalf of the national COVID-19 response team
EPI_ISL_6947967	CDPH VBL	California Department of Public Health	Emily Smith on behalf of CDPH-COVIDNet
EPI_ISL_6953936	Labor Blackholm MVZ	Robert Koch Institute	unknown

EPI_ISL_7111466	Labor Dr. Wisplinghoff - Köln	Robert Koch Institute	unknown
EPI_ISL_7161014	Virology Department, Royal Infirmary of Edinburgh, NHS Lothian / School of Biological Sciences, University of Edinburgh	COVID-19 Genomics UK (COG-UK) Consortium	McHugh M, Dewar R, Cotton S, Gallagher A, Maloney D, Fernandez G, O'Toole Á, Scher E, Hill V, McCrone JT, Colquhoun R, Yu X, Jackson B, Rambaut A, Templeton K
EPI_ISL_7211829	Public Health Authority of the Slovak Republic	Biomedical Centre Martin, Jessenius Faculty of Medicine in Martin, Comenius University	Dusan Loderer, Katarina Janikova, Ivana Kasubova, Maria Skerenova, Marian Grendar
EPI_ISL_7346967	Respiratory Virus Unit, Microbiology Services Colindale, Public Health England	COVID-19 Genomics UK (COG-UK) Consortium	PHE Covid Sequencing Team
EPI_ISL_7372961	Synlab	Laboratorio di Microbiologia	Martinetti Lucchini Gladys, Valeria Spina
EPI_ISL_7380587	Public Health Authority of the Slovak Republic	Public Health Authority of the Slovak Republic	Barbora Kotvasová, Lucia Ševčíková, Terézia Vrabľová, Anna Gičová, Elena Tichá, Miroslav Böhmer, Tomáš Szemes, Pavol Mišenko
EPI_ISL_7406523	Quarantine Camp	Hong Kong Department of Health	Alan K.L. Tsang, Peter C.W. Yip, Patricia K. L. Leung, Ken H.L. Ng, Edman T.K. Lam, Rickjason C.W. Chan
EPI_ISL_7406607	North Lantau Hospital	Hong Kong Department of Health	Alan K.L. Tsang, Peter C.W. Yip, Patricia K. L. Leung, Ken H.L. Ng, Edman T.K. Lam, Rickjason C.W. Chan
EPI_ISL_7420956	Labor Dr. Wisplinghoff - Köln	Robert Koch Institute	unknown
EPI_ISL_7436963	Labor Dr. Wisplinghoff - Köln	Robert Koch Institute	unknown
EPI_ISL_7544609	Broad Institute Clinical Research Sequencing Platform	Infectious Disease Program, Broad Institute of Harvard and MIT	Siddle,K.J., Adams,G., Pearlman,L., Gladden-Young,A., Vicente,G., Blumenstiel,B., DeFelice,M., Lee,M., McGovern,S., Lagerborg,K., Rudy,M., DeRuff,K., Carter,A., Normandin,E., Bauer,M., Reilly,S., Tomkins-Tinch,C., Loreth,C., Chaluvadi,S., Meldrim,J., Granger,B., Lemieux,J.E., Birren,B.W., Sabeti,P.C., Larkin,K., Dodge,S.,

			Lennon,N., Madoff,L., Brown,C., Gallagher,G., Smole,S., Park,D.J., Gabriel,S., and MacInnis,B.L.
EPI_ISL_7699856	NYU Langone Health	Departments of Pathology and Medicine, New York University School of Medicine	Adriana Heguy, Dacia Dimartino, Emily Guzman, Christian Marier, Peter Meyn, Sitharam Ramaswami, Gael Westby, Paul Zappile, Yutong Zhang, Guiqing Wang
EPI_ISL_7704832	Laboratoire de santé publique du Québec	Laboratoire de santé publique du Québec	Sandrine Moreira, Ioannis Ragoussis, Guillaume Bourque, Jesse Shapiro, Mark Lathrop and Judith Fafard on behalf of the CoVSeQ research group
EPI_ISL_7705124	Laboratoire de santé publique du Québec	Laboratoire de santé publique du Québec	Sandrine Moreira, Ioannis Ragoussis, Guillaume Bourque, Jesse Shapiro, Mark Lathrop and Judith Fafard on behalf of the CoVSeQ research group
EPI_ISL_7705142	Laboratoire de santé publique du Québec	Laboratoire de santé publique du Québec	Sandrine Moreira, Ioannis Ragoussis, Guillaume Bourque, Jesse Shapiro, Mark Lathrop and Judith Fafard on behalf of the CoVSeQ research group
EPI_ISL_7714100	Laboratoire de santé publique du Québec	Laboratoire de santé publique du Québec	Sandrine Moreira, Ioannis Ragoussis, Guillaume Bourque, Jesse Shapiro, Mark Lathrop and Judith Fafard on behalf of the CoVSeQ research group
EPI_ISL_7727994	Fakultní nemocnice Bulovka	Institute of Molecular Genetics CAS	Jan Pačes, Miluše Hradilová, Jana Šáchová, Martin Zmuda, Ondřej Moravčík, Lucie Pfeiferová, Michal Kolář

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EPI_ISL_8061988	Nemocnice Hodonin	University Hospital Brno, CMBG	Bezdicek Matej, Svaton Jan, Kristyna Dufkova, Lengerova Martina, Dolejska Monika
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