

Report summary

There were 2 sequences uploaded to AudacityInstant and 12.8M genomes in the EpiCoV database were searched for related genomes. A total of 313 related genomes were found.

Closest related genomes

For each uploaded sequence, the table gives the sequence number within the input data, and the Accession ID (identified from the name provided in the input data). The other columns give information on the closest related genome, including the match distance, the match quality, the Accession ID, the collection date, the submission date, the lineage, and the country of origin of the matched genome. The submitting laboratories of the matched sequences are given in the footnote. See the Methods section (page 7) for more details.

Upload		Closest related genome						
No.	Upload Acc. ID	Dist.	Qual.	Accession ID	Collect. date	Subm. date	Lin.	Country / State
1		0	0.993	EPI_ISL_457800 ¹	2020-03-19	2020-06-02	A.1	USA / Maryland
2		0	0.991	EPI_ISL_457767 ¹	2020-03-29	2020-06-02	A.3	USA / Maryland

¹ Johns Hopkins Hospital Department of Pathology; ¹ Johns Hopkins Hospital Department of Pathology

Sequence 1: hCoV-19/00058/2020|StudySequence1|NA|2020-03-19|

There were 209 related genomes found (at a distance of 0 from the uploaded sequence). The minimum quality of the matches was 0.969. Amongst the related genomes, the most frequent country was USA (49.8% of genomes), the most frequent lineage was A.1 (99% of genomes), and 85.9% of the related genomes were from samples collected between 2020-03-10 and 2020-03-25.

Metadata from the EpiCoV database is shown below for the uploaded sequence (left, if it was found in the database) and for the closest related genome (right). The tables in the margin show the protein substitutions. Substitutions are shown in red and crossed out if they were not found in the other genome or were not resolved. Substitutions are shown in bold if they occurred in fewer than half of the related genomes.

Uploaded sequence

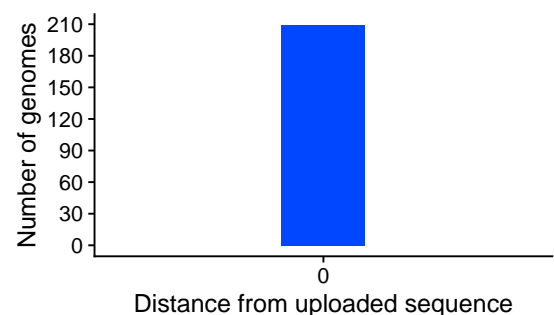
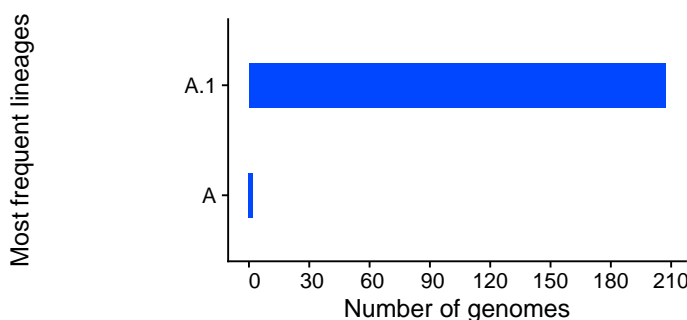
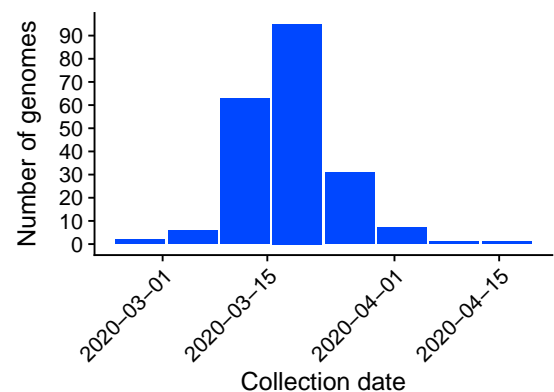
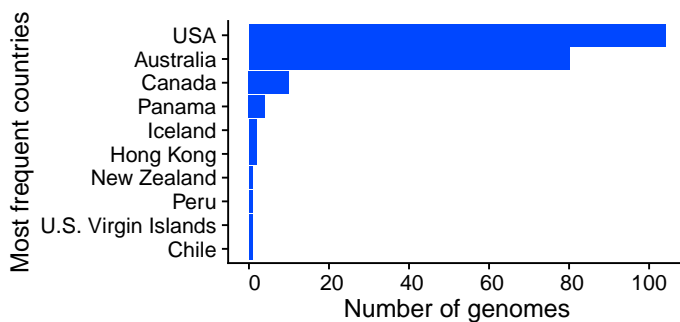
The uploaded sequence was not identified.

Closest related genome

Accession ID: EPI_ISL_457800
 Distance: 0
 Match quality: 0.993
 Location: USA / Maryland
 Collection date: 2020-03-19
 Submission date: 2020-06-02
 Lineage: A.1
 Clade: S

Prot. subs.:
 NS8 L84S
 NSP13 P504L
 Y541C

Related genomes



Distance from uploaded sequence

Distance	Color
0	Blue
1	Light Blue
2	Cyan
3	Green
4	Yellow
5	Orange
6+	Red

Identical genomes

Accession ID	Tip	Collect. date	Subm. date	Lin.	Cla.	Dist.	Qual.	Country / State
EPI_ISL_457800 ¹		2020-03-19	2020-06-02	A.1	S	0	0.993	USA / Maryland

Other related genomes (60 of 208)

Accession ID	Tip	Collect. date	Subm. date	Lin.	Cla.	Dist.	Qual.	Country / State
EPI_ISL_604785 ²		2020-03-14	2020-10-30	A.1	S	0	0.993	USA / Missouri
EPI_ISL_604225 ²		2020-03-14	2020-10-30	A.1	S	0	0.993	USA / Michigan
EPI_ISL_604159 ²		2020-03-15	2020-10-30	A.1	S	0	0.993	USA / Utah
EPI_ISL_603913 ²		2020-03-19	2020-10-30	A.1	S	0	0.993	USA / California
EPI_ISL_2549580 ³		2020-03-09	2021-06-16	A.1	S	0	0.993	USA / Colorado
EPI_ISL_10553013 ⁴		2020-03-18	2022-03-01	A.1	S	0	0.993	Canada / Ontario
EPI_ISL_8767125 ⁵		2020-03-20	2022-01-17	A.1	S	0	0.993	Australia / New South Wales / Sydney
EPI_ISL_509494 ⁶		2020-03-22	2020-08-05	A.1	S	0	0.993	Australia / New South Wales
EPI_ISL_605021 ²		2020-03-16	2020-10-30	A.1	S	0	0.993	USA / California
EPI_ISL_418816 ⁷		2020-03-11	2020-03-31	A.1	S	0	0.993	Canada / British Columbia
EPI_ISL_509517 ⁶		2020-03-22	2020-08-05	A.1	S	0	0.993	Australia / New South Wales
EPI_ISL_603818 ²		2020-03-16	2020-10-30	A.1	S	0	0.993	USA / Massachusetts
EPI_ISL_571019 ²		2020-03-19	2020-10-05	A.1	S	0	0.993	USA / Arizona
EPI_ISL_604902 ²		2020-03-15	2020-10-30	A.1	S	0	0.993	USA / California
EPI_ISL_571504 ²		2020-03-23	2020-10-05	A.1	S	0	0.993	USA / California
EPI_ISL_604904 ²		2020-03-16	2020-10-30	A.1	S	0	0.993	USA / California
EPI_ISL_3568405 ⁵		2020-03-24	2021-08-23	A.1	S	0	0.993	Australia / New South Wales / Sydney
EPI_ISL_604607 ²		2020-03-12	2020-10-30	A.1	S	0	0.993	USA / Utah
EPI_ISL_2364207 ⁴		2020-03	2021-06-01	A.1	S	0	0.993	Canada / Ontario
EPI_ISL_2549608 ³		2020-03-10	2021-06-16	A.1	S	0	0.993	USA / Colorado
EPI_ISL_2549609 ³		2020-03-10	2021-06-16	A.1	S	0	0.993	USA / Colorado
EPI_ISL_2549612 ³		2020-03-10	2021-06-16	A.1	S	0	0.993	USA / Colorado
EPI_ISL_2549613 ³		2020-03-10	2021-06-16	A.1	S	0	0.993	USA / Colorado
EPI_ISL_509515 ⁶		2020-03-22	2020-08-05	A.1	S	0	0.993	Australia / New South Wales
EPI_ISL_3568319 ⁵		2020-03-12	2021-08-23	A.1	S	0	0.993	Australia / New South Wales / Sydney
EPI_ISL_509520 ⁶		2020-03-20	2020-08-05	A.1	S	0	0.993	Australia / New South Wales
EPI_ISL_500620 ⁶		2020-03-22	2020-07-29	A.1	S	0	0.993	Australia / New South Wales
EPI_ISL_603832 ²		2020-03-16	2020-10-30	A.1	S	0	0.993	USA / Massachusetts
EPI_ISL_467840 ²		2020-03-16	2020-06-15	A.1	S	0	0.993	USA / California
EPI_ISL_603848 ²		2020-03-13	2020-10-30	A.1	S	0	0.993	USA / Utah
EPI_ISL_604849 ²		2020-03-13	2020-10-30	A.1	S	0	0.993	USA / Utah
EPI_ISL_604653 ²		2020-03-16	2020-10-30	A.1	S	0	0.993	USA / California
EPI_ISL_604860 ²		2020-03-13	2020-10-30	A.1	S	0	0.993	USA / Utah
EPI_ISL_571426 ²		2020-03-18	2020-10-05	A.1	S	0	0.993	USA / Colorado
EPI_ISL_604202 ²		2020-03-16	2020-10-30	A.1	S	0	0.993	USA / California
EPI_ISL_571715 ²		2020-03-17	2020-10-05	A.1	S	0	0.993	USA / California
EPI_ISL_500685 ⁶		2020-03-21	2020-07-29	A.1	S	0	0.993	Australia / New South Wales
EPI_ISL_2549577 ³		2020-03-05	2021-06-16	A.1	S	0	0.993	USA / Colorado
EPI_ISL_604143 ²		2020-03-16	2020-10-30	A.1	S	0	0.993	USA / Utah
EPI_ISL_536274 ⁸		2020-03-27	2020-09-15	A.1	S	0	0.993	Canada / Quebec
EPI_ISL_604780 ²		2020-03-13	2020-10-30	A.1	S	0	0.993	USA / Georgia
EPI_ISL_604146 ²		2020-03-15	2020-10-30	A.1	S	0	0.993	USA / Utah
EPI_ISL_2549648 ³		2020-03-10	2021-06-16	A.1	S	0	0.993	USA / Colorado
EPI_ISL_890487 ⁸		2020-03-25	2021-01-29	A.1	S	0	0.993	Canada / Quebec
EPI_ISL_3568541 ⁵		2020-04-18	2021-08-23	A.1	S	0	0.993	Australia / New South Wales / Sydney
EPI_ISL_429819 ⁹		2020-03-18	2020-04-24	A.1	S	0	0.993	Canada / Manitoba
EPI_ISL_604852 ²		2020-03-12	2020-10-30	A.1	S	0	0.993	USA / Utah
EPI_ISL_604890 ²		2020-03-16	2020-10-30	A.1	S	0	0.993	USA / California
EPI_ISL_419391 ¹⁰		2020-03-14	2020-04-02	A.1	S	0	0.993	USA / Minnesota
EPI_ISL_604691 ²		2020-03-16	2020-10-30	A.1	S	0	0.993	USA / Colorado
EPI_ISL_3568093 ⁵		2020-03-23	2021-08-23	A.1	S	0	0.993	Australia / New South Wales / Sydney
EPI_ISL_2549615 ³		2020-03-10	2021-06-16	A.1	S	0	0.993	USA / Colorado
EPI_ISL_2549581 ³		2020-03-09	2021-06-16	A.1	S	0	0.993	USA / Colorado
EPI_ISL_579458 ¹¹		2020-03-24	2020-10-14	A.1	S	0	0.993	New Zealand / Canterbury
EPI_ISL_467917 ²		2020-03-12	2020-06-15	A.1	S	0	0.993	USA / Utah
EPI_ISL_2549619 ³		2020-03-10	2021-06-16	A.1	S	0	0.993	USA / Colorado
EPI_ISL_509504 ⁶		2020-03-15	2020-08-05	A.1	S	0	0.993	Australia / New South Wales
EPI_ISL_571162 ²		2020-03-21	2020-10-05	A.1	S	0	0.993	USA / California
EPI_ISL_604118 ²		2020-03-16	2020-10-30	A.1	S	0	0.993	USA / Utah
EPI_ISL_8767097 ⁵		2020-03-22	2022-01-17	A.1	S	0	0.993	Australia / New South Wales / Sydney

¹Johns Hopkins Hospital Department of Pathology; ²Quest Diagnostics; ³Colorado Department of Public Health and Environment; ⁴Public Health Ontario Laboratory; ⁵Virology Research Laboratory; Area of Virology, Serology and Virology Division (SAViD), New South Wales Health Pathology Randwick; ⁶Area of Virology, Serology and Virology Division (SAViD), New South Wales Health Pathology Randwick; ⁷BCCDC Public Health Laboratory; ⁸Laboratoire de santé publique du Québec; ⁹National Microbiology Laboratory; ¹⁰Minnesota Department of Health, Public Health Laboratory; ¹¹Institute of Environmental Science and Research (ESR)

Sequence 2: hCoV-19/00112/2020|StudySequence2|NA|2020-03-29|

There were 104 related genomes found (at a distance of 1 or less from the uploaded sequence). The minimum quality of the matches was 0.918. Amongst the related genomes, the most frequent country was USA (93.3% of genomes), the most frequent lineage was A.3 (100% of genomes), and 85.4% of the related genomes were from samples collected between 2020-03-13 and 2020-04-13.

Metadata from the EpiCoV database is shown below for the uploaded sequence (left, if it was found in the database) and for the closest related genome (right). The tables in the margin show the protein substitutions. Substitutions are shown in red and crossed out if they were not found in the other genome or were not resolved. Substitutions are shown in bold if they occurred in fewer than half of the related genomes.

Uploaded sequence

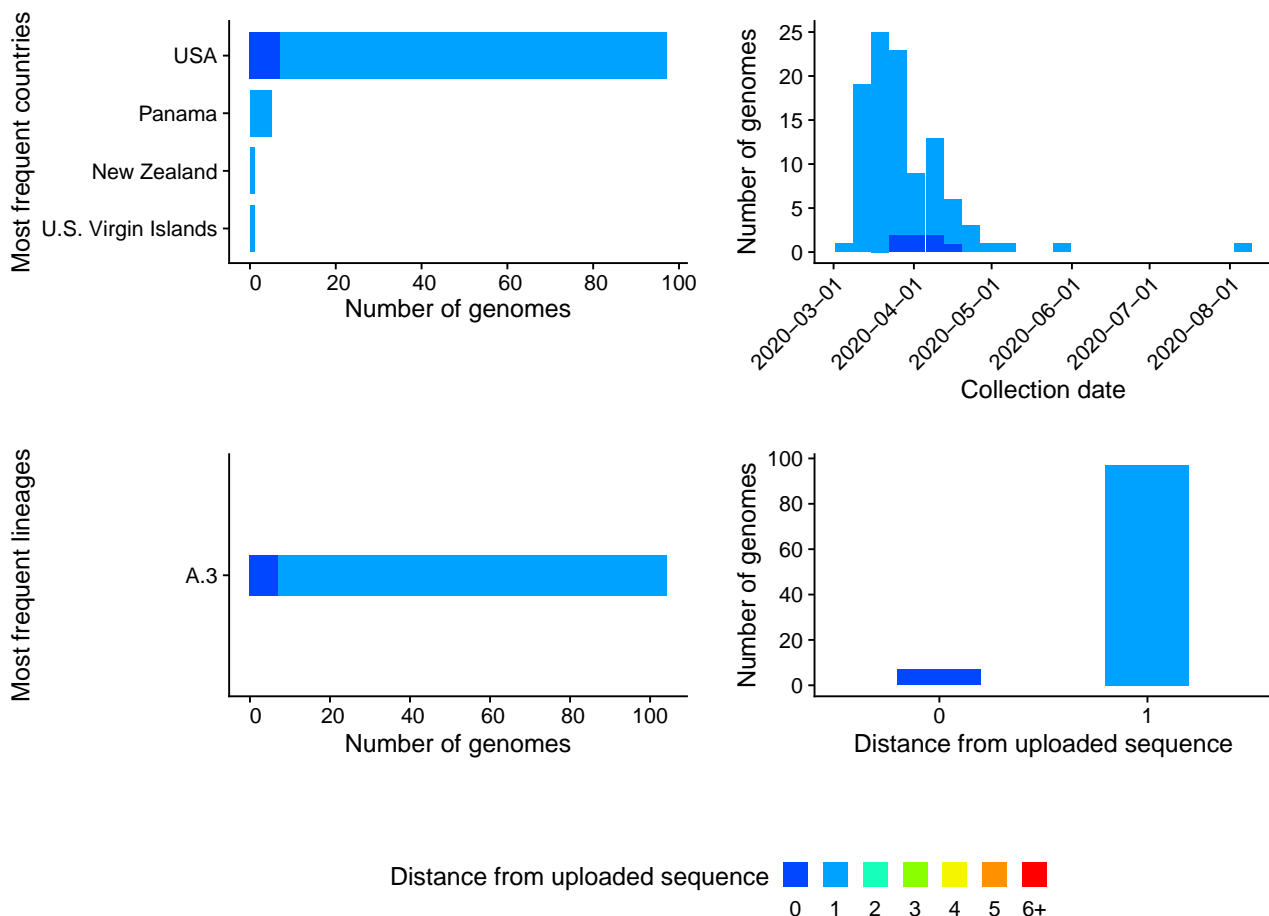
The uploaded sequence was not identified.

Closest related genome

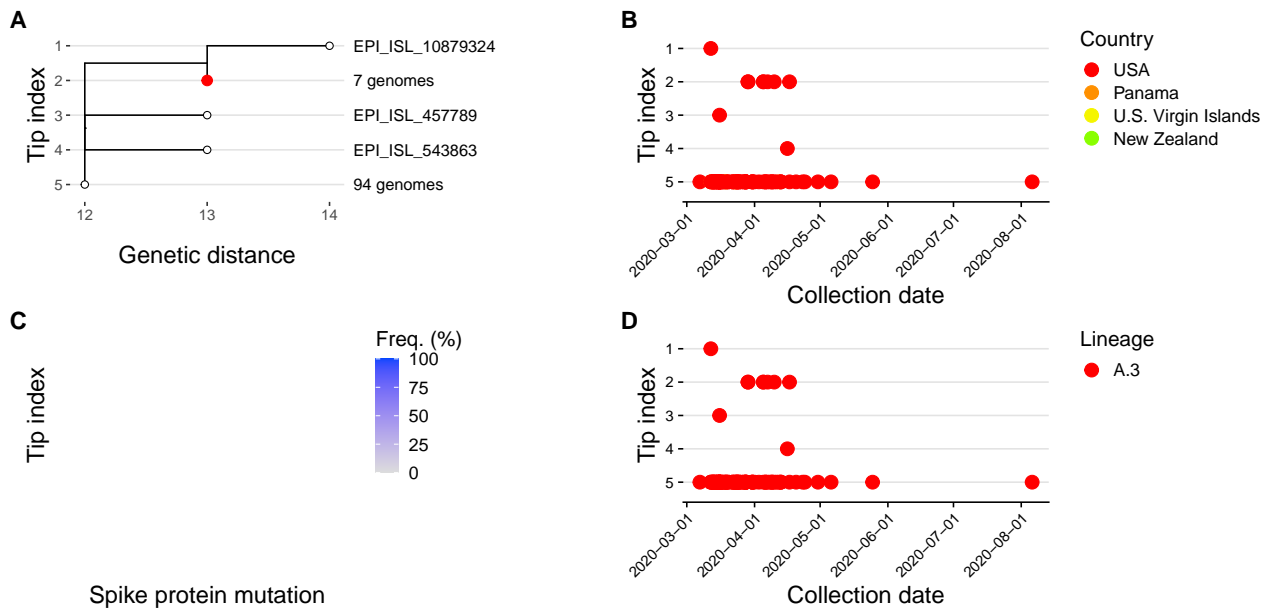
Accession ID: EPI_ISL_457767
 Distance: 0
 Match quality: 0.991
 Location: USA / Maryland
 Collection date: 2020-03-29
 Submission date: 2020-06-02
 Lineage: A.3
 Clade: S

Prot. subs.:
 NSP1 D75E
 NSP3 P153L
 NS8 L84S
 V62L
 NSP8 M129I
 NSP14 F233L
 N A208G

Related genomes



A maximum-likelihood tree of the uploaded sequence, related genomes, and an outgroup (the WIV04 reference sequence from Wuhan). The figure shows (A) the tree, with branch lengths given by the genetic distance (the estimated number of mutations). The uploaded sequence is indicated by a red dot. Tips are labelled by the Accession ID, or the number of genomes in the group. (B) the collection date of the sequences within each tip group, coloured by location. (C) the frequency of occurrence of spike mutations within each tip group. (D) The collection date of the sequences within each tip group, coloured by lineage.



Identical genomes

Accession ID	Tip	Collect. date	Subm. date	Lin.	Cla.	Dist.	Qual.	Country / State
EPI_ISL_457767 ¹	2	2020-03-29	2020-06-02	A.3	S	0	0.991	USA / Maryland

Other related genomes (60 of 103)

Accession ID	Tip	Collect. date	Subm. date	Lin.	Cla.	Dist.	Qual.	Country / State
EPI_ISL_2885043 ¹	2	2020-04-05	2021-07-09	A.3	S	0	0.980	USA / Maryland
EPI_ISL_457783 ¹	2	2020-03-29	2020-06-02	A.3	S	0	0.976	USA / Maryland
EPI_ISL_2885083 ¹	2	2020-04-10	2021-07-09	A.3	S	0	0.973	USA / Maryland
EPI_ISL_11963253 ¹	2	2020-04-07	2022-04-11	A.3	S	0	0.965	USA / Maryland
EPI_ISL_11168632 ¹	2	2020-04-05	2022-03-18	A.3	S	0	0.965	USA / Maryland
EPI_ISL_10952558 ¹	2	2020-04-17	2022-03-11	A.3	S	0	0.965	USA / Maryland
EPI_ISL_10879324 ¹	1	2020-03-12	2022-03-10	A.3	S	1	0.965	USA / Maryland
EPI_ISL_457789 ¹	3	2020-03-16	2020-06-02	A.3	S	1	0.976	USA / Maryland
EPI_ISL_543863 ²	4	2020-04-16	2020-09-24	A.3	S	1	0.950	USA / Texas / Houston
EPI_ISL_2884998 ¹	5	2020-03-31	2021-07-09	A.3	S	1	0.982	USA / Maryland
EPI_ISL_578459 ³	5	2020-04-13	2020-10-13	A.3	S	1	0.982	USA / Wisconsin / Racine County
EPI_ISL_543910 ²	5	2020-04-17	2020-09-24	A.3	S	1	0.982	USA / Texas / Houston
EPI_ISL_471226 ³	5	2020-04-13	2020-06-19	A.3	S	1	0.982	USA / Wisconsin
EPI_ISL_561346 ⁴	5	2020-03-24	2020-09-30	A.3	S	1	0.981	USA / Delaware / New Castle County
EPI_ISL_4026004 ⁵	5	2020-04-09	2021-09-08	A.3	S	1	0.980	USA / Illinois / Chicago
EPI_ISL_516656 ⁶	5	2020-04-30	2020-08-21	A.3	S	1	0.979	USA / Virginia
EPI_ISL_457782 ¹	5	2020-03-24	2020-06-02	A.3	S	1	0.977	USA / Maryland
EPI_ISL_626464 ⁷	5	2020-03-28	2020-11-09	A.3	S	1	0.976	USA / Illinois / Chicago
EPI_ISL_4026001 ⁵	5	2020-03-31	2021-09-08	A.3	S	1	0.976	USA / Illinois / Chicago
EPI_ISL_435126 ¹	5	2020-03-20	2020-04-30	A.3	S	1	0.976	USA / Maryland
EPI_ISL_434686 ¹	5	2020-03-20	2020-05-01	A.3	S	1	0.976	USA / Maryland
EPI_ISL_604326 ⁸	5	2020-03-16	2020-10-30	A.3	S	1	0.975	USA / Florida
EPI_ISL_2885143 ¹	5	2020-05-06	2021-07-09	A.3	S	1	0.975	USA / Maryland
EPI_ISL_936513 ⁷	5	2020-05-25	2021-02-05	A.3	S	1	0.975	USA / Illinois / Lake County
EPI_ISL_434923 ²	5	2020-03-28	2020-05-01	A.3	S	1	0.975	USA / Texas
EPI_ISL_2691736 ¹	5	2020-08-06	2021-06-26	A.3	S	1	0.975	USA / Maryland
EPI_ISL_579237 ⁹	5	2020	2020-10-14	A.3	S	1	0.975	New Zealand / Auckland
EPI_ISL_604151 ⁸	5	2020-03-14	2020-10-30	A.3	S	1	0.975	USA / Utah
EPI_ISL_578361 ³	5	2020-04-23	2020-10-13	A.3	S	1	0.975	USA / Wisconsin / Racine County
EPI_ISL_604310 ⁸	5	2020-03-19	2020-10-30	A.3	S	1	0.975	USA / California
EPI_ISL_604865 ⁸	5	2020-03-13	2020-10-30	A.3	S	1	0.975	USA / Utah
EPI_ISL_604025 ⁸	5	2020-03-16	2020-10-30	A.3	S	1	0.975	USA / Georgia
EPI_ISL_604551 ⁸	5	2020-03-14	2020-10-30	A.3	S	1	0.975	USA / Minnesota
EPI_ISL_571293 ⁸	5	2020-03-17	2020-10-05	A.3	S	1	0.975	USA / Georgia
EPI_ISL_604695 ⁸	5	2020-03-16	2020-10-30	A.3	S	1	0.975	USA / Georgia
EPI_ISL_604697 ⁸	5	2020-03-16	2020-10-30	A.3	S	1	0.975	USA / Georgia
EPI_ISL_571939 ⁸	5	2020-03-16	2020-10-05	A.3	S	1	0.975	USA / Louisiana
EPI_ISL_604144 ⁸	5	2020-03-14	2020-10-30	A.3	S	1	0.975	USA / Utah
EPI_ISL_467921 ⁸	5	2020-03-13	2020-06-15	A.3	S	1	0.975	USA / Utah
EPI_ISL_429970 ⁶	5	2020-03-28	2020-04-24	A.3	S	1	0.975	USA / Virginia
EPI_ISL_426119 ¹⁰	5	2020-03-23	2020-04-14	A.3	S	1	0.975	USA / Washington
EPI_ISL_454384 ¹¹	5	2020-03-31	2020-05-28	A.3	S	1	0.975	USA / Pennsylvania / Allegheny County
EPI_ISL_434590 ⁶	5	2020-04-09	2020-04-30	A.3	S	1	0.975	USA / Virginia
EPI_ISL_434592 ⁶	5	2020-04-10	2020-04-30	A.3	S	1	0.975	USA / Virginia
EPI_ISL_884541 ¹²	5	2020-03-24	2021-01-25	A.3	S	1	0.975	USA
EPI_ISL_454851 ¹³	5	2020-03-31	2020-05-28	A.3	S	1	0.975	USA / Pennsylvania / Pittsburgh
EPI_ISL_884552 ¹²	5	2020-03-28	2021-01-25	A.3	S	1	0.975	USA
EPI_ISL_1278057 ¹⁴	5	2020-04-07	2021-03-18	A.3	S	1	0.975	USA / Georgia
EPI_ISL_1278058 ¹⁴	5	2020-04-05	2021-03-18	A.3	S	1	0.975	USA / Georgia
EPI_ISL_468563 ⁸	5	2020-03-13	2020-06-16	A.3	S	1	0.975	USA / California
EPI_ISL_648026 ¹⁵	5	2020-03-15	2020-11-20	A.3	S	1	0.975	USA / Mississippi
EPI_ISL_911470 ¹⁶	5	2020-03-24	2021-02-01	A.3	S	1	0.975	USA / Indiana / Indianapolis
EPI_ISL_427583 ¹⁷	5	2020-03-16	2020-04-19	A.3	S	1	0.975	USA / New York / Manhattan
EPI_ISL_464167 ¹⁵	5	2020-03-19	2020-06-11	A.3	S	1	0.975	U.S. Virgin Islands
EPI_ISL_855282 ¹⁸	5	2020-03-15	2021-01-19	A.3	S	1	0.975	USA / New York
EPI_ISL_460186 ¹⁹	5	2020-03-22	2020-05-26	A.3	S	1	0.975	USA / Massachusetts
EPI_ISL_526811 ⁶	5	2020-03-28	2020-09-02	A.3	S	1	0.975	USA / Virginia
EPI_ISL_455355 ¹⁴	5	2020-03-13	2020-05-29	A.3	S	1	0.975	USA / Georgia
EPI_ISL_13896670 ⁵	5	2020-03-28	2022-07-18	A.3	S	1	0.975	USA / Illinois / Chicago
EPI_ISL_14379882 ²⁰	5	2020-04-09	2022-08-10	A.3	S	1	0.975	USA / Illinois / Cook County

¹ Johns Hopkins Hospital Department of Pathology; ² Houston Methodist Hospital; ³ Wisconsin State Laboratory of Hygiene Communicable Disease Division; ⁴ Delaware Public Health Lab; ⁵ Northwestern University - Center for Pathogen Genomics and Microbial Evolution; ⁶ Virginia DCLS; ⁷ Ozer Lab; ⁸ Quest Diagnostics; ⁹ Institute of Environmental Science and Research (ESR); ¹⁰ UW Virology Lab; ¹¹ Microbial Genome Sequencing Center, Microbial Genomic Epidemiological Laboratory; ¹² Molecular Microbiology & Immunology, University of Missouri; ¹³ Microbial Genomic Epidemiology Laboratory, University of Pittsburgh; ¹⁴ Piantadosi Lab, Emory Department of Pathology; ¹⁵ Pathogen Discovery, Respiratory Viruses Branch, Division of Viral Diseases, Centers for Disease Control and Prevention; ¹⁶ Clinical Diagnostics Laboratory, Diagnostic & Experimental Pathology, Lilly Research Laboratories; ¹⁷ Mason Lab; ¹⁸ Institute for Computational Biomedicine, Weill Cornell Medicine; ¹⁹ Infectious Disease Program, Broad Institute of Harvard and MIT; ²⁰ Rush University Medical Center

Methods

The distance between two sequences

AudacityInstant calculates the distance between two sequences as the number of differences between them. For example, if one sequence has an 'A' at site 1,000, and another sequence has a 'T' at the same site, then the sequences are different at this site. If the sites contain ambiguities (such as 'N', 'M', 'W', etc.) then the sequences are different if there are no bases that are consistent with both sequences. For example, if one sequence had an 'N' at site 1,000, and the other sequence had a 'T' then this would not be counted as a difference, as all bases (including 'T') are consistent with an 'N'.

The quality of a distance score

Because a site marked as 'N' or '-' (gap) is consistent with any base, low quality sequences that contain many 'N's may closely match many other sequences. To avoid low-quality matches, a probabilistic difference is calculated for each site:

- If the sites are not ambiguous and are identical, the probabilistic difference is 0.0
- If the sites are different, the probabilistic difference is 1.0.
- Otherwise, we calculate the probability they are different by randomly drawing possible bases, using the frequency of each base ('A', 'C', 'G', or 'T') at that site as calculated across the entire database.

A match quality, between zero and one, is calculated by as one minus the average probabilistic difference. A low quality match (less than 0.95) indicates a high occurrence of ambiguous bases in either or both sequences, and these ambiguities are typically 'N's or gaps.

Identifying uploaded sequences

EpiCoV genomes are identical to the uploaded sequence if the masked and aligned sequences match at every site, including the ambiguities. Identical sequences always have a distance of 0 between them, but, because of ambiguities, not all distance 0 sequences are identical. The Accession ID of the uploaded sequence is taken from the name supplied with the data, and the EpiCoV genome with that Accession ID is assumed to be the same as the uploaded sequence, if they are identical.

Matching uploaded sequences

Here is a brief description of the steps that produce the results, for each uploaded sequence:

1. The uploaded sequence is aligned to the reference genome (WIV04) using MAFFT, and insertions are removed;
2. The sequence is masked, removing sites that are prone to errors;
3. The masked sequence is matched against every aligned and masked genome in the EpiCoV database, and the distance and quality of the match is calculated;
4. All genomes are selected that have a match quality of 0.95 or higher, and that are at a threshold distance or closer. The threshold distance is chosen to include relevant matches, while restricting the number of selected genomes.
5. The selected genomes are annotated with metadata from EpiCoV.

The closest related genome

The closest related genome is the highest quality match within the set of genomes that are closest to the uploaded sequence (where identical sequences are treated as closer than other zero-distance sequences, and where the uploaded sequence is not included). If the uploaded sequence is low quality, with many ambiguous sites, or if it is far from any of the genomes in EpiCoV, then it is possible for no related sequences to be found.

Data download

This report is prepared from the information that is available in the ZIP file download from AudacityInstant. The full set of related genomes is available in the spreadsheet file 'neighbours.csv'.

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