U.S. Department of Health and Human Services Public Health Service

Centers for Disease
Control and Prevention
Atlanta, GA 30329-4027

July 26, 2021

Updated CDC Guidance for Specimen Submission for Surveillance of SARS-CoV-2

Dear Colleagues,

Thank you for your continued participation, support, and ongoing public health service in the National SARS-CoV-2 Strain Surveillance (NS3) System. NS3 is providing important national SARS-CoV-2 baseline surveillance information, increasing publicly available viral sequence data, and establishing a representative repository of virus isolates for further characterization.

This update addresses the following topics:

- NS3 submission timing has a large impact on CDC's ability to quickly detect emerging variants. Therefore, we continue to request that all jurisdictions submit specimens within 7 days of collection. If your jurisdiction does not have enough specimens to meet the requested NS3 submission number outlined in Appendix 2, we request that you still submit all available specimens collected as recently as possible, rather than wait until you have more samples to submit in larger batches. Also we will accept original specimens that are going to be, or have been sequenced, if they meet surveillance criteria and are needed to meet submission goals for your jurisdiction.
- Surveillance sequences generated by state public health labs and partners:
    - CDC wants to include baseline surveillance sequence data generated by public health labs in the estimates of lineage proportions circulating posted on the Variant Proportions website and need your help to make that possible. By adding the baseline surveillance tag to your submission it will significantly benefit your state or territory genomic surveillance data, situational awareness and improve national SARS-CoV-2 surveillance. To make this possible we have worked with NCBI and GISIAD to add a metadata tag to indicate baseline surveillance as the reason for sequencing.
    - If your state public health lab or partners are performing baseline surveillance sequencing please:
        - Submit all sequences and associated metadata to NCBI and/or GISAID as quickly as possible.
        - Review the technical assistance document and if the original specimens being sequenced meet the defining criteria, use the *baseline surveillance*

tag as described in each guidance document when submitting the sequence data to these public repositories.

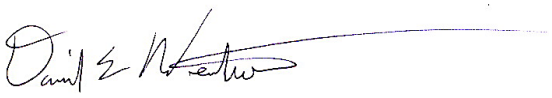
- Select 'yes' in the *Has been or will be sequenced and submitted?* field of the NS3 Supplementary Form for all specimens that have been or are planned to be sequenced by you or your partner lab(s) and for which data will be deposited in GISAID and NCBI. When this field is selected, CDC will not submit sequence data to avoid duplicate publication. Please use the same identifier for the sequence submitted to these public repositories as the specimen ID submitted to CDC.

Attached you will find the following updated documents:

- **National SARS-CoV-2 Strain Surveillance (NS3) Submissions to CDC for SARS-CoV-2 Positive Specimens [Appendix 1]**
- **CDC Recommended Number of National SARS-CoV-2 Strain Surveillance (NS3) Specimens for Weekly Submission to CDC by Jurisdiction [Appendix 2]**
- **Enhanced Surveillance for SARS-CoV-2 [Appendix 3]**
- **National SARS-CoV-2 Strain Surveillance (NS3) Frequently Asked Questions (FAQs)**

- For technical guidance, questions about forms or shipments, or sequencing-related questions, please contact the SARS-CoV-2 Sequencing Team at sarsseqshipping@cdc.gov.
- For general questions about the national sequence based surveillance strategy for SARS-CoV-2, please contact the Strain Surveillance and Emerging Variants team at eocevent506@cdc.gov.
- For technical assistance related to sequencing and bioinformatic activities at state/local labs contact Technical Outreach and Assistance for States (TOAST) at toast@cdc.gov.
- For questions about the SPHERES consortium, or for broader genomics sequencing and bioinformatics support, please contact Duncan MacCannell at fms2@cdc.gov.

Sincerely,



David E. Wentworth, PhD
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COVID-19 Response Laboratory and Testing Task Force
Centers for Disease Control and Prevention
Enc: Appendix 1; Appendix 2; Appendix 3, FAQs

Appendix 1: National SARS-CoV-2 Strain Surveillance (NS3) Submissions to CDC for SARS-CoV-2 Positive Specimens

1. Beginning on Monday, August 2, 2021, CDC will accept SARS-CoV-2 positive specimens based on the revised guidance and processes below.
2. Please ship randomly selected SARS-CoV-2 positive specimens **on Monday** for overnight delivery to CDC on Tuesday. If Monday is an observed holiday, please ship on the next available business day (Tuesday). Please ship only on weekdays through Thursday.
3. Consult Appendix 2 for the recommended number of specimens to ship weekly or bi-weekly for your jurisdiction.
4. Acceptable specimen types for sequencing and potential virus characterization are the same as for the CDC SARS-CoV-2 diagnostic assays that were authorized by FDA under an EUA: upper and lower respiratory specimens, including nasopharyngeal, oropharyngeal, nasal mid-turbinate, and anterior nares (nasal swab) specimens. In addition, a nasopharyngeal wash/aspirate or nasal wash/aspirate specimen collected by a healthcare professional is acceptable, as is a naturally expectorated sputum. Acceptable specimens will be limited to those collected in media that allow for viral culture (e.g., PBS, VTM). Specimens collected in **Hologic Aptima buffer and Molecular Transport Media are excluded** from submission. For more information, see the interim specimen collection guidelines (available at https://www.cdc.gov/coronavirus/2019-nCoV/lab/guidelines-clinical-specimens.html).
5. Considerations for selecting NS3 specimens:

    a. The quality of the specimen directly affects sequencing and virus culture success. Ideally, specimens should have an RT-PCR Ct value of ≤28. If Ct values are not available, specimens that are positive/strong positive for SARS-CoV-2 may be sent (avoid weakly positive samples).

    b. The time from specimen collection to sequence characterization has a large impact on our ability to quickly detect and track proportions of emerging variants. Please send specimens that have been collected within the last 7 days whenever possible. If the number of specimens collected within the last 7 days is insufficient to meet your jurisdiction's requested number for NS3 submission (Appendix 2), please send the most recent specimens possible (i.e., up to 14 days prior to shipment).

    c. Ideally, specimens should represent geographic, demographic (e.g., age), and clinical (e.g., disease severity or outcome) diversity from across the jurisdiction. This can be achieved through random selection of specimens collected within the last 7 days.

    d. You may submit specimens that are being sequenced by you or your partners to CDC for NS3 submissions if the this will help to meet your jurisdiction's NS3 submission goal (Appendix 2). If submitting specimens being sequenced locally, please enter "yes" in the form's *Has been or will be sequenced and submitted?* field of the NS3 Supplementary Form and provide the GISAID and/or GenBank accession numbers if they are available.

        - For sequence data generated locally, that meets the baseline surveillance guidelines outlined at https://www.aphl.org/programs/preparedness/Crisis-Management/Documents/Technical-Assistance-for-Categorizing-Baseline-Surveillance.pdf add a tag to the submission as described in the guidelines. For example, a submission to GenBank would have the keyword (purposeofsampling:baselinesurveillance).

- If you or your sequencing partner(s) are already marking baseline surveillance samples using the purpose of sequencing field with the “Baseline surveillance (random sampling)” option outlined in the PHA4GE metadata specification, you do not have to change to the surveillance tagging system described above.

e. Specimens can be stored at 2–8°C for no more than 72 hours from the time of collection. The 72-hour timeframe is a strict requirement for sequencing to be completed. Specimens that require storage longer than 72 hours must be frozen at ≤ -70°C. Prior to shipping, specimens should be frozen at ≤ -70°C and shipped on dry ice.

f. Please submit original clinical specimens with at least 500 µL volume

6. Please use 1.0–2.0 mL O-ring screw cap microcentrifuge tubes labeled with the de-identified specimen ID. Please do not submit specimens in the thin, pre-barcoded tubes that were originally used in initiation of the NS3 program.

7. Please fill in the electronic Global File Accessioning Template (GFAT) form and NS3 Supplementary Form. Each specimen must be labeled with a unique identifier also included on both forms using the *SPHL Submitter Specimen ID* or the *Original Submitter Specimen ID* field (if no SPHL ID). Please fill out all GFAT fields for which you have data. Please note: **the fields highlighted in orange are required** for the processing of specimens and downstream uses of the sequence data for public health surveillance.

8. In the GFAT form, please select “NS3 - National SARS-CoV-2 Strain Surveillance" in the *Event Name* field and “1771” in the *Event ID* field. Select “NS3 - National SARS-CoV-2 Strain Surveillance” in the *Reason for Submission* field of the NS3 Supplementary Information form.

9. Specimens should be packaged and shipped as Category B infectious substances, and all requirements for proper packaging and shipping should be observed (see https://www.cdc.gov/coronavirus/2019-ncov/lab/lab-biosafety- ğuidelines.html#specimen).

10. Please include a printed manifest of your specimens with your shipment.

11. Email the GFAT and NS3 Supplementary forms along with tracking information to sarsseqshipping@cdc.gov.

12. If possible, please ship specimens every Monday for overnight delivery to CDC using the following address:

ATTN: STATT Lab: Unit 66 TRL
Centers for Disease Control and Prevention
1600 Clifton Road, NE
Atlanta, Georgia, 30333
Telephone: 404-639-3931
Email: sarsseqshipping@cdc.gov

Appendix 2: Weekly Target Number of National SARS-CoV-2 Strain Surveillance (NS3) Specimens Requested for Submission to CDC by Jurisdiction

Jurisdictions are encouraged to submit specimens weekly, and to and prioritize those specimens collected in the previous 7 days. If submitting every two weeks, please submit twice the number of specimens listed for your jurisdiction (collected in the 7 days before shipment).

Abbr	Jurisdiction	No of weekly specimens*
AK	Alaska	9
AL	Alabama	11
AR	Arkansas	10
AS	American Samoa	5
AZ	Arizona	14
CA	California	35
CHI	Chicago	12
CO	Colorado	12
CT	Connecticut	11
DC	District of Columbia	10
DE	Delaware	9
FL	Florida	26
FM	Micronesia	5
GA	Georgia	17
GU	Guam	5
HI	Hawaii	9
HOU	Houston	9
IA	Iowa	10
ID	Idaho	9
IL	Illinois	17
IN	Indiana	13
KS	Kansas	10
KY	Kentucky	11
LA	Louisiana	11
LAC	Los Angeles County	19
MA	Massachusetts	14
MD	Maryland	13
ME	Maine	9
MH	Marshall Islands	5
MI	Michigan	16
MN	Minnesota	13
MO	Missouri	13
MP	Northern Marianas	5
MS	Mississippi	10
MT	Montana	9

Abbr	Jurisdiction	No of weekly specimens*
NC	North Carolina	16
ND	North Dakota	9
NE	Nebraska	9
NH	New Hampshire	9
NJ	New Jersey	16
NM	New Mexico	10
NV	Nevada	10
NY	New York	18
NYC	New York City	18
OH	Ohio	17
OK	Oklahoma	10
OR	Oregon	11
PA	Pennsylvania	18
PHL	Philadelphia	7
PR	Puerto Rico	10
PW	Palau	5
RI	Rhode Island	9
SC	South Carolina	12
SD	South Dakota	9
TN	Tennessee	13
TX	Texas	33
UT	Utah	10
VA	Virginia	16
VI	Virgin Islands	5
VT	Vermont	9
WA	Washington	14
WI	Wisconsin	13
WV	West Virginia	9
WY	Wyoming	9
	TOTAL	770

*Based on population – Minimum number of five (5) specimens per week by jurisdiction.

Appendix 3: Enhanced Surveillance for SARS-CoV-2

Since the emergence of SARS-CoV-2, national and global sequencing efforts have identified changes in the SARS-CoV-2 genetic code resulting from transmission and evolution in humans and animals. These changes can affect many aspects of our response including transmission, diagnostics, therapeutics, and vaccines. Therefore, we may ask that additional specimens be sent to CDC for a defined period of time (short-term, interim) to address variants of interest, variants of concern, or other specified viral classifications. The criteria for submitting enhanced surveillance specimens to CDC is listed in the table below and are expected to be continually updated to address gaps in our understanding. The general submission guidelines for any enhanced surveillance specimens are provided in Section 1 below, and specific details about particular variants are listed in Section 2. Information about potential vaccine breakthrough cases is listed in Section 3. We will keep you informed by updating the enhanced surveillance guidelines and communications through APHL.

National and state level variant proportions are available on CDC's website:
CDC COVID Data Tracker

Brief description of enhanced surveillance efforts (details below in Section 2)*

Reason for Submission in Supplementary Form	Selection criteria**	Specimen submission - GFAT Event ID	Variant Case Notification by Jurisdiction to CDC
ES21-01 – SARS-CoV-2 S gene target failure	• As of April 12, 2021, CDC is no longer requesting case notifications or submission of specimens of B.1.1.7 variants confirmed by jurisdictions.	Closed	Closed
ES21-02 – B.1.351 Lineage (20H/501Y.V2 or B.1.351)	• As of April 12, 2021, CDC is no longer requesting case notifications or submission of specimens of B.1.351 variants confirmed by jurisdictions.	Closed	Closed
ES21-03 - Additional variants	• Special circumstances with prior approval from CDC	1850	Open
ES21-04 - Vaccine Breakthroughs	• Positive EUA diagnostic test result ≥ 14 days after completion of FDA authorized vaccination series • See Section 3 below for inclusion and exclusion criteria	1890	Open
ES21-05 - P1 lineage	• As of April 12, 2021, CDC is no longer requesting case notifications or submission of specimens of P.1 variants confirmed by jurisdictions.	Closed	Closed
*No special reporting or submission of specimens are needed at this time for newly classified variants of interest or variants of concern. If this guidance changes, including when new variants of interest are classified, CDC will notify partners of changes to reporting and specimen submission guidelines.			
**Please submit original clinical specimens with at least 300 µL volume and ideally Ct value ≤ 28 by RT-PCR.			

Section 1. Submission of specimens for Enhanced Surveillance

1. If a variant is identified based on criteria in Appendix 3 and detailed descriptions below, please notify CDC by emailing eocevent506@cdc.gov. Please include the number of variant specimens and information about the specimens including relevant sequence, clinical, and epidemiology data.

2. Acceptable specimen types for sequencing and potential virus characterization are the same as for regular NS3 surveillance described in Appendix 1.

3. Specimens can be stored at 2–8°C for no more than 72 hours from the time of collection. The 72-hour timeframe is a strict requirement for sequencing to be completed. Specimens that require storage longer than 72 hours must be frozen at ≤ -70°C. Prior to shipping, specimens should be frozen at ≤ -70°C and shipped on dry ice.

4. Please submit original clinical specimens with at least 300 µL volume.

5. Acceptable specimens will be limited to those collected in media that allows for viral culture (e.g., PBS, VTM). Specimens collected in Hologic Aptima buffer and Molecular Transport Media are excluded from submission.

6. Sequencing and virus culture success are directly impacted by the quantity and quality of the specimen. Acceptable specimens will be limited to those with Ct values ≤28. If Ct values are not available, specimens that are positive for SARS-CoV-2 can be sent.

7. Please use 1.0–2.0 mL O-ring screw cap microcentrifuge tubes labeled with the de-identified specimen ID. Please **do not** submit specimens in the thin pre-barcoded tubes that were used in the early period of this program.

8. Please fill in the electronic Global File Accessioning Template (GFAT) form and NS3 Supplementary Form. Each specimen must be labeled with a unique identifier on both forms using the *SPHL Specimen ID* or *Original Submitter Specimen ID* (if no SPHL ID).

9. Please indicate “Emerging Variants” for the *Event Name* and “1850” for the *Event ID* in the GFAT form (see Table above).

10. Use the “Reason for Submission” field in the NS3 Supplementary Form to indicate *Enhanced Surveillance* by selecting “ES21-XX” (where “XX” is the number in the table above for the appropriate reason for submission).

11. Specimens should be packaged and shipped as Category B, and all requirements for proper packaging and shipping should be observed (see https://www.cdc.gov/coronavirus/2019-ncov/lab/lab-biosafety-guidelines.).

12. Please include a printed manifest of your specimens with your shipment.

13. Email the GFAT and NS3 Supplementary Form along with tracking information to sarsseqshipping@cdc.gov.

14. Please ship specimens weekly (preferred) or bi-weekly, Monday through Thursday, for overnight delivery to CDC using the following address:

ATTN: STATT Lab: Unit 66 TRL
Centers for Disease Control and Prevention
1600 Clifton Road, NE
Atlanta, Georgia, 30333
Telephone: 404-639-3931
Email: sarsseqshipping@cdc.gov

Section 2. Enhanced Surveillance – Emerging Variants (Updated 4/7/2021)

I. ES21-01: SARS-CoV-2 positive Spike Gene Target Failure (SGTF) - CLOSED

II. ES21-02: B.1.351 Lineage (20H/501Y.V2 or B.1.351) - CLOSED

III. ES21-03 Additional Variants

This category is reserved for special circumstances and should only be used with prior approval from the CDC (eocevent506@cdc.gov). If you have identified viruses with some unique characteristics matching other emerging variants of interest (e.g., E484K, or deletions in the S protein) through sequencing or other lab developed tests, please contact CDC to discuss options for submission and characterization.

IV. ES21-05 P.1 lineage - CLOSED

Section 3. Enhanced Surveillance - Potential Vaccine Breakthroughs (Updated 4/7/2021)

ES21-04 Vaccine Breakthroughs

CDC is currently defining suspect vaccine breakthrough cases as a U.S. resident who has SARS-CoV-2 RNA or antigen detected on a respiratory specimen collected ≥ 14 days after completing the full series of an FDA-authorized SARS-CoV-2 vaccine (e.g., two doses of the Moderna or Pfizer vaccine, one dose of Johnson and Johnson vaccine). Acceptable specimens are the same as those listed above in Appendix 1.

A case will be excluded from further investigation if: 1) the patient received a COVID-19 vaccine that is not authorized by FDA; 2) the respiratory specimen that was positive for SARS-CoV-2 RNA or antigen was collected < 14 days after completing vaccination; or 3) the patient had a previous positive test for SARS-CoV-2 RNA or antigen on a specimen collected < 45 days prior to the most recent positive test and prior to vaccination or < 14 days after completing the full vaccination series.

1. On Monday, January 25, 2021, CDC began accepting potential vaccine breakthrough specimens based on the guidance below.

2. Please send up to twenty (20) potential vaccine breakthrough specimens weekly as previously described in Section 1. If convenient, these can be included with NS3 specimen shipment to CDC but please indicate which specimens are being submitted for this purpose:
    a. Please indicate “ES21-04 - Vaccine Breakthrough” in the *Reason for Submission* field of the NS3 Supplementary Form.
    b. On the GFAT, indicate “Vaccine Breakthroughs” for *Event Name* and “1890” for *CDC EVENT ID*.
    c. Please enter your REDCap database case ID in the GFAT Comments filed [Column GM].

National SARS-CoV-2 Strain Surveillance (NS3) Frequently Asked Questions

Why is CDC organizing this?
There are multiple goals for routinely sequencing and characterizing clinical specimens that are positive for SARS-CoV-2 as part of the public health response to the COVID-19 pandemic. These can broadly be grouped into two primary objectives:

1. **Population-level molecular epidemiology/virus monitoring**: By routinely acquiring sequences and associated metadata from a subset of COVID-19 cases, CDC aims to monitor the spread of viral lineages across time and within populations.
2. **Virus characterization**: By routinely collecting standardized epidemiologic and clinical data, and linking these with associated virus sequences, sequencing can be a valuable tool to identify viral variants that might have vaccine and/or therapeutic resistance, different transmissibility, pathogenicity, or clinical outcomes.

What are we asking from state public health labs?
For NS3, we request all laboratories provide on a weekly basis: laboratory confirmed, deidentified, diagnostic specimens (with Ct values ≤28) and standardized metadata on a representative selection of COVID-19 cases. We are seeking specimens **collected within the 7 days prior to shipment** representing a variety of demographic and clinical characteristics and geographic locations. The selection of a diverse set of specimens will help ensure that a representative set of sequences is generated for national monitoring.

For enhanced surveillance activities, which started in January 2021, we request all state laboratories provide additional specimens, for a defined, specified period of time (short-term, interim), to specifically address contemporary SARS-CoV-2 variants of interest. Variants of interest are identified through genomic analysis of circulating viruses. Criteria for selecting variants of interest for submission are outlined in Appendix 3, Section 2, which will be continually updated with changes communicated through updates to the guidance and through APHL.

What is sequence "tagging" and why are we asking labs to do it?

State and jurisdictional laboratories sequence for many reasons. The sequences generated as part of "targeted" efforts can bias baseline surveillance estimates. However, if sequences are being generated locally the submitters can "tag" their samples with a keyword marking them as baseline surveillance samples as described in detail at:
https://www.aphl.org/programs/preparedness/Crisis-Management/Documents/Technical-Assistance-for-Categorizing-Baseline-Surveillance.pdf

> For example; for NCBI: purposeofsampling:baselinesurveillance and for GISAID: in Sampling Strategy/covv_sampling_strategy include keyword Baseline surveillance

This allows you and the CDC to quickly identify unbiased samples sequenced as part of a baseline surveillance effort. CDC will include these sequences in our variant proportion analysis and report it on the COVID Data tracker page.

Why is data from our state/jurisdiction not included in the table indicating the "Proportions of Variants of Concern and Other Lineages by State or Jurisdiction" on the COVID Data Tracker website?
CDC is not able to determine if sequences deposited by individual states is baseline surveillance data or if it is from large scale studies or outbreaks under investigation. This can be addressed by tagging your data as baseline surveillance data as described above. The additional state level data is very helpful for your own situational awareness and to understand if variants that evade therapeutics are circulating at

proportions that may impact clinical guidance or recommendations by the FDA.

What is our commitment to you?
For NS3, CDC will deposit sequence results into public repositories in a timely manner and provide routine national level analyses to monitor trends in transmission of the virus in the United States.

For enhanced surveillance activities, which started in January 2021, CDC will provide results more rapidly and follow up directly with the state or territorial epidemiologist in the event of unexpected or unusual observations (e.g., sequence confirmation of a variant of concern). Such sequence data will not be made available publicly until communication with the relevant jurisdictional partners have occurred. CDC will serve as an available resource for questions or further technical guidance on use of SARS-CoV-2 genomic data.

How many specimens should I send and how often?
For NS3, we are requesting that states submit specimens every week and that you select specimens collected within 7 days of the shipment date. We are asking each state to submit a minimum of 5 specimens every week, plus additional specimens based on population size (see Appendix 2).

For enhanced surveillance activities, which started in January 2021, we are requesting additional specimens that are suspect variants of concern. Each state can submit up to twenty specimens from cases representing potential emerging variants or vaccine breakthrough cases as outlined in the criteria described in Appendix 3. Given the need to rapidly characterize new viral lineages as they emerge, these requests will often be short-term, and will be opened and closed through updated versions of the NS3 guidance documents and disseminated via communications with APHL.

How should I select specimens to send?

For NS3, we are asking states to select a diverse set of specimens that represent multiple geographic locations not associated with a single outbreak event and, if possible, varying demographic characteristics and clinical outcomes. It is important that all specimens have a relatively low Ct value (≤28) and have been stored properly (for more information, see https://www.cdc.gov/coronavirus/2019-ncov/lab/guidelines-clinical-specimens.html).

For enhanced surveillance activities, please see Appendix 3.

How do I send those specimens?
Please see Appendix 1, for detailed specimen submission information. Please ship specimens on **every Monday** (or bi-weekly), in 1.0–2.0 mL O-ring screw cap centrifuge tubes. If this date is an observed holiday, please ship on the next available business day (Tuesday through Thursday). Include a printed specimen manifest. Ship overnight on dry ice using your usual courier, such as FedEx or UPS, to the following address:

ATTN: STATT Lab: Unit 66 TRL
Centers for Disease Control and Prevention
1600 Clifton Road, NE
Atlanta, Georgia, 30333
Telephone: 404-639-3931
Email: sarsseqshipping@cdc.gov

Where will the sequence data be deposited?
Once genomic sequences are obtained and assessed for quality, the consensus sequence data will be uploaded and released into GenBank and GISAID with a minimum set of metadata. Raw sequence reads will be deposited into the Sequence Read Archive (SRA) at a later date, once quality assurances have been met and any human reads have been removed. The following metadata information will be

included in all sequence data submissions: specimen type, collection date, gender, age, and geolocation information including state. Race will not be reported to these public databases. Sequences will be named according to their geographical location, as per established conventions (e.g., SARS-CoV-2/human/USA/XX (state acronym)-CDC-xxxxxxxx (unique identifier)/2021). CDC is included in the name to reference that it was sequenced at CDC and not by the state public health laboratory or other entity. Note that NCBI and GISAID require slightly different naming conventions:

ICTV (NCBI) SARS-CoV-2/host/location/isolate/date
SARS-CoV-2/human/USA/XX-CDC-xxxxxxxx2021

GISAID hCoV-19/location/isolate/date
hCoV-19/USA/XX-CDC-xxxxxxxx2021

Where will NS3 results be reported?
Summarized results will be available through the NS3 Reporting Dashboard in the CDC Secure Access Management System located at: https://amdportal-sams.cdc.gov/. Users can login with the "SAMS Credentials" option. For access to the SAMS system and OAMD Portal please contact eocevent506@cdc.gov. A guidance document for the reporting system can be found here. Proportions of lineage results will be reported on COVID-data tracker (https://covid.cdc.gov/covid-data-tracker/?utm_source=newsletter&utm_medium=email&utm_campaign=newsletter_axiosam&stream=top#variant-proportions).