

National SARS-CoV-2 Strain Surveillance (NS3) Frequently Asked Questions (Updated 08/30/2023)

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 bi-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 14-28 days prior to shipment. The selection of a diverse set of specimens will help ensure that a representative set of sequences is generated for national monitoring.

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-Update-Oct2021.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.

How many specimens should I send and how often?

For NS3, we are requesting that states submit specimens every other week and that you select specimens collected within 14 days of the shipment date. We are asking each state to submit a minimum of 5 specimens every two weeks, plus additional specimens based on population size (SARS-CoV-2 appendix 1, table 1).

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>).

How do I send those specimens?

Please see SARS-CoV-2 appendix 1, for detailed specimen submission information. Please ship specimens bi-weekly on Mondays, 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-xxxxxxx (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-xxxxxxx2021

GISAID hCoV-19/location/isolate/date hCoV-19/USA/XX-CDC-xxxxxxx2021

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 respviral@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-

