



NC DEPARTMENT OF  
**HEALTH AND  
HUMAN SERVICES**

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Division of Public Health

June 16, 2021 (replaces version dated February 12, 2021)

To: All North Carolina Clinicians and Laboratories  
From: Scott Shone, PhD, HCLD (ABB), Public Health Laboratory Director  
Zack Moore, MD, MPH, State Epidemiologist  
Re: Genetic Sequencing of SARS-CoV-2 Respiratory Samples (2 pages)

This memo provides updated information about SARS-CoV-2 genomic sequencing and guidance to laboratories and clinicians for requesting sequencing and reporting vaccine breakthrough cases and variants of interest to the North Carolina Division of Public Health (NC DPH)

### **Background**

Multiple SARS-CoV-2 variants are circulating globally and within the United States and new variants continue to emerge as the virus mutates. The CDC classifies as Variants of Concern (VOC) those variants for which there is evidence of increased transmissibility, decreased efficacy of therapeutics, increased morbidity or mortality, or decreased immunity from previous infection or vaccination. Variants of Interest (VOI) have specific genetic markers that have been associated with changes to receptor binding, reduced neutralization by antibodies generated against previous infection or vaccination, reduced efficacy of treatments, potential diagnostic impact, or predicted increase in transmissibility or disease severity. A full list of VOCs/VOIs and data on [variant proportions](#) and the national and state level is available on the [CDC website](#).

The FDA has a [web page](#) to share the latest information on impacts of viral mutations on diagnostic test performance. At this point, the impact of currently circulating variants on diagnostic test sensitivity is believed to be low; additional information will be shared as it becomes available.

The North Carolina State Laboratory of Public Health (NC SLPH) is participating in the National SARS-CoV-2 Strain Surveillance (NS3) program, which requires regular submission of select positive SARS-CoV-2 samples to CDC for sequencing and viral characterization. NC SLPH has also developed internal capacity for sequencing and plans for strain surveillance.

### **Guidance for NC Laboratories**

In order to better identify emerging variants of concern in North Carolina, NC DPH is requesting that clinical laboratories performing genomic sequencing report all sequencing results via existing ELR or CLDA reporting. Please review existing [NC DPH](#) and [CDC guidance](#) and contact [ELR.SupportServices@dhhs.nc.gov](mailto:ELR.SupportServices@dhhs.nc.gov) or [CLDA.SupportServices@dhhs.nc.gov](mailto:CLDA.SupportServices@dhhs.nc.gov) for guidance on how to include sequencing results in ELR or CLDA results.

Laboratories may be contacted by public health officials or clinicians to request submission of samples of interest (e.g. vaccine breakthrough cases or cases related to an outbreak or cluster) to SLPH for sequencing for surveillance purposes. Samples for submission must meet the Residual Clinical Specimen Submission Criteria and laboratories are requested to coordinate with public health officials to facilitate sequencing of these samples.

**NC DEPARTMENT OF HEALTH AND HUMAN SERVICES • DIVISION OF PUBLIC HEALTH**

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### **Guidance for NC Clinicians**

Clinicians may submit samples for sequencing for cases meeting one or more of the criteria below. Cases meeting criteria marked with \*\* below may be submitted without prior approval, all other cases require prior approval by the Communicable Disease Branch Epidemiologist On-Call at 919-733-3419.

- \*\*Persons who have a positive diagnostic test at least 14 days after completing vaccination with an FDA authorized vaccine (meaning after two doses for Pfizer and Moderna vaccines or one dose of Janssen vaccine) and with no previous positive test in the preceding 45 days.
- \*\*Persons with suspected re-infection, if:
  - Both the initial and subsequent positive sample are available for submission, OR
  - The positive test was collected at least 90 days after their initial positive and the person had new onset of COVID-19 symptoms requiring hospitalization
- Persons with severe immune compromise with prolonged infection
- Persons with international travel within 14 days before symptom onset/positive test
- \*\*Pediatric deaths
- \*\*Cases of multisystem inflammatory syndrome in children (MIS-C)
- Cases of multisystem inflammatory syndrome in adults (MIS-A)
- Outbreak or cluster

Requests for sequencing should be submitted via the [secure online submission form](#) and the [SLPH COVID-19 Testing Requisition Form](#) must be included with all specimens shipped. Because SARS-CoV-2 variant analysis is currently not a CLIA approved assay, sequencing is for surveillance purposes only. Results will be reported to the NC DPH Communicable Disease Branch and not communicated back to the provider.

### **Residual Clinical Specimen Submission Criteria**

- Positive clinical specimens tested with PCR must have cycle threshold (Ct) values  $\leq 30$
- If no Ct value is available or if the initial positive test was an antigen test, PCR testing will be run on the specimen and the specimen will be sequenced if appropriate based on PCR results
- Specimens in molecular transport media are not acceptable
- Specimens must have at least 500 $\mu$ L of volume
- Specimens must be frozen at -70°C within 72 hours of collection or be refrigerated at 2°C to 8°C and arrive at SLPH no more than 72 hours after collection
- Frozen specimens must be shipped overnight frozen on dry ice

For questions about the secure online submission form or for approval to submit specimens for sequencing, please contact the epidemiologist on call at 919-733-3419. For technical questions about clinical specimen submission, please contact NC SLPH at [slph.covid19@dhhs.nc.gov](mailto:slph.covid19@dhhs.nc.gov).