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DOH 420-399 May 2022

Protocol for Local Health Jurisdictions (LHJs) and Tribal partners Submitting SARS-CoV-2 Specimens for Sequencing

Washington State Department of Health Public Health Laboratories

**This protocol document is intended for LHJs and Tribal partners to aid in submitting specimen for sequencing.**

The Washington State DOH is working to increase capacity for sequencing priority SARS-CoV-2 specimens. Sequencing is occurring at the Public Health Lab (PHL), as well as at partner academic laboratories. PHL sequences all of their diagnostic positives that have a Ct value < 30, you don’t need to request sequencing for PHL specimens. The following specimen types are acceptable for submission for sequencing at WA PHL:

• RNA extract (preferred)

• Nasal swab, nasopharyngeal swab, or mid-turbinate swab in VTM/UTM or transport medium

• Lower respiratory tract fluid (BAL, tracheal aspirate, or sputum) – if intubated

All specimen types should be frozen at <-70 °C and shipped on dry ice. [https://doh.wa.gov/sites/default/files/legacy/Documents/5240//SCSI-2019-nCoV.pdf](https://doh.wa.gov/sites/default/files/legacy/Documents/5240/SCSI-2019-nCoV.pdf)

**Important Note**: You will not receive reports back from specimens that have been sequenced. Sequencing data will be added to WDRS (see Appendix A, below).

Specimens that meet the following criteria may be submitted to PHL without prior approval for sequencing:

|  |  |  |
| --- | --- | --- |
| Epidemiologic criteria | Specimen criteria | How to submit |
| Outbreaks: Only submit 3-5 specimens per outbreak, because the rationale for testing specimens from suspected outbreaks is to determine whether they were caused by a concerning variant or sublineage. | |  | | --- | | All CT values  <30, OR  CT values unavailable from the test platform | | Complete: <https://redcap.link/sequencesubmission>  and ship the specimen(s) following the guidance above.  Only use the REDCap link provided above for forwarding previously positive specimens.  Newly collected specimens must be submitted through the PHL’s QRP process: <https://qrp.doh.wa.gov/> |
|  |
| Any case reporting international travel in the 14 days prior to symptom onset (or specimen collection date if asymptomatic). |
| Suspected zoonotic transmission. Approval is not required, but please notify [zd@doh.wa.gov](mailto:zd@doh.wa.gov) |
| Unusual clinical presentations that may be associated with more severe or different clinical syndromes such as critical illness or death in a previously healthy child or young adult (age <40) or any other unusual clinical presentations identified by clinicians, LHJs or Tribes. |

**If sequencing is needed from any of these labs:**

• University of Washington Virology

• Atlas Genomics

• Confluence Health / Central Washington University

• Incyte Diagnostics

• Interpath Laboratories

• Northwest Laboratories

Please send WDRS IDs to [wgs-epi@doh.wa.gov](mailto:DOH%20DCHS%20CDE%20Molecular%20Epidemiology%20%3cwgs-epi@doh.wa.gov%3e) and DOH will request sequencing. These labs are

sentinel labs that are routinely submitting specimens to PHL or do their own sequencing (UW Virology).

DOH can request specific specimens from the sentinel laboratories if needed for outbreak or other

reasons. Submitting lists from DOH helps streamline the workflow for the laboratories rather than

receiving multiple phone calls.

***Notes on Results and Data Access:***

• Specimens with high Ct values should not be sent for sequencing, due to low probability of

successful sequencing due to low amounts of virus in the specimen, and the high cost of

attempting sequencing.

• When available, sequencing results can be found in WDRS. Data is generally uploaded to WDRS

three times a week (Monday, Wednesday, Friday); see Appendix A for instructions on accessing

this data.

• Information on failed sequences will be uploaded to WDRS when available. These are not

available for all laboratories; but are available for PHL, University of Washington, Northwest Genomics, and Labcorp.

• Please note that sequencing is done for surveillance purposes and results may not be shared back with the patient or provider.

Appendix A: Accessing Sequencing Data in WDRS: <https://secureaccess.wa.gov/doh/wdrs/maven/main.do?unloadCase=true>

***External Data Question Package***

Under the Molecular Genetics section there is a repeatable block of sequence questions. Cases with sequencing information will have “Yes” in the “Was specimen selected for sequencing”.

***Wizards***

Sequencing and variant information can be found under the COVID-19 Extended Variables Wizard.

**Appendix A:**

***Reports***

Sequencing information can be found in four reports in WDRS: <https://secureaccess.wa.gov/doh/wdrs/maven/viewReport.do>

• COVID-19 Event Extract Report

• COVID-19 Outbreak linked events export

• COVID-19 Events with Variant Sequencing

• COVID-19 Vaccine Breakthrough Cases

***The following variables are associated with sequencing data (not all variables are in all reports)***

|  |  |
| --- | --- |
| S-Gene Target Failure | CDC\_N\_COV\_2019\_SEQUENCE\_SGTF |
| Was specimen selected for sequencing? (Blank, Yes, No) | CDC\_N\_COV\_2019\_SEQUENCE\_SPECIMEN |
| Reason the specimen was sequenced | CDC\_N\_COV\_2019\_SEQUENCE\_REASON |
| Lab performing the sequencing | CDC\_N\_COV\_2019\_SEQUENCE\_LAB |
| Sequence status (Complete/Low Quality/Failed) | CDC\_N\_COV\_2019\_SEQUENCE\_STATUS |
| Which database the raw sequencing data lives in? (GISAID or GenBank) | CDC\_N\_COV\_2019\_SEQUENCE\_REPOSITORY |
| The accession number of the sequence | CDC\_N\_COV\_2019\_SEQUENCE\_ACCESSION\_NUMBER |
| Lineage identified (B.1.617.2, etc.) | CDC\_N\_COV\_2019\_SEQUENCE\_VARIANT\_OPEN\_TEXT |
| Clinical accession from the original specimen that was sequenced | CDC\_N\_COV\_2019\_SEQUENCE\_CLINICAL\_ACCESSION\_NUMBER |
| Additional notes about the lineage, if any | CDC\_N\_COV\_2019\_SEQUENCE\_NOTES |

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