DEPARTMENT OF HEALTH

MLS Laboratory Update: Updated Guidance for Submission of SARS-CoV-2 specimens for Sequencing

JANUARY04, 2022

Purpose of this Message:

MDH-PHL is changing the submission guidance for positive SARS-CoV-2 specimens. Updated guidelines are below.

Action Item:

Please review the following information and submit specimens, according to the criteria below, from patients who have **a positive SARS-CoV-2 test result** from either PCR or rapid molecular test tested at your facility.

Background:

Due to the sustained level of COVID-19 in MN, the sequencing volume has been beyond the capacity of MDH PHL. It is necessary to reduce the amount of specimens being submitted weekly for sequencing.

Additional Information:

Current Guidance: **ALL laboratories**, (regardless of size): Submit up to 5 specimens per week with a $Ct \le 30$. Please continue to send ALL positive specimens with a Ct value of ≤ 30 from the following patient categories:

- hospitalized SARS-CoV-2 positive patient
- failure of monoclonal antibody treatment

If your testing platform does not generate a Ct value, please submit any positive specimens following the current guidance above.

Note: MDH-PHL is no longer asking specifically for samples from vaccine breakthrough cases or suspected re-infection. Those samples can be submitted as part of the weekly submission for surveillance.

Please see Infectious Disease Lab COVID-19 Sample Submission Updates for specimen submission guidelines and forms.

Variant Tracking and Results Reporting: Sequencing results on submitted specimens will NOT be reported back to submitters. Results for SARS-CoV-2 variants circulating in Minnesota will be added to the publicly available NextStrain website showing the genomic epidemiology of SARS-CoV-2 strains in Minnesota.

<u>Nextstrain: Genomic epidemiology of novel coronavirus - Minnesota-focused subsampling</u> (https://nextstrain.org/groups/spheres/ncov/minnesota) Thank you for your ongoing participation and dedication to SARS-CoV-2 surveillance.

Questions please contact:

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