Recommendation and requirements for diagnostic sequencing of SARS-CoV-2
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Purpose:
This document provides a short overview for diagnostic laboratories and cantonal physicians regarding the indication, requirements of material, sample storage, protocol, data sharing, and quality of diagnostic sequencing of SARS-CoV-2 within diagnostic microbiology laboratories in Switzerland. This document was written and approved by all laboratories mentioned below. This document will be updated regularly on the Swiss Society of Microbiology website (www.swissmicrobiology.ch).

Due to the current epidemiological situation, with a potential threat of two new SARS-CoV-2 variants from the United Kingdom (N501Y V1; B1.1.7) and South Africa (N501Y V2), the Federal Office of Public Health recommends that in certain PCR-confirmed patient, the viral variant should be determined. Of note, currently at various centers (including the reference laboratory) N501Y-specific PCRs are in validation. Once these new PCRs will be validated with sufficient sensitivity and specificity, this may allow a more targeted approach to identify samples for sequencing confirmation. New emerging strains may also be included with specific PCR screens or with broad sequencing approaches.

Indication for sequencing for confirmation of N501Y V1/V2 variants:
- Travelling (directly or indirectly) from the United Kingdom or South Africa.
- PCR-confirmed patient with a previous confirmed contact to a symptomatic person (acute respiratory tract infection) from United Kingdom or South Africa.
- S Gene Drop out in the Thermo Fisher PCR assay (molecular evidence) and Link to UK.

Please check with the sequencing laboratory if a sequencing is required and what the technical and workflow requirements are (see below more details.)

Material:
- Respiratory material from upper or lower airways of a PCR confirmed case
- This material could be one of the following materials: nasopharyngeal swabs in viral transport media, fluid from a bronchoalveolar lavage, tracheal secretion, saliva/sputum in viral transport media, etc.
- Extracted RNA from different material
- Ideally there is a high viral load present (with Ct Values <30, corresponding to about 100,000 copies/ml or more). This increases the success rate of sequencing. Lower viral loads should be discussed with the laboratory.

Sample storage:
Please store the sample or the extracted RNA as fast as possible at least at –20°C (ideally -70°C) until the sample is shipped for sequencing. Avoid repeated freezing and thawing of the samples prior to shipment.

Sample transport:
Shipment of viral transport media and/or extracted RNA should be done under frozen conditions with sufficient dry ice. Samples should be properly labeled. Standard patient metadata should be sent electronically, if possible, including Name, date of birth, address and telephone number of the patient, sample identifier, date of isolation, and Ct-value of initial PCR, type of material (native or RNA) to the sequencing laboratory. A contact person with cell phone number should be added in case of questions to the submitting laboratory.

Established sequencing and analytical protocols:
Protocols for whole genome sequencing of SARS-CoV-2 are based on the Artic v3 protocol. Sequencing can be done via short reads (Illumina based sequencing) or via long reads (Oxford Nanopore Technology). Alternatively, relevant gene segments covering the mutations of concern can be amplified and sequenced by Sanger Sequencing. The sequencing protocol has to follow a detailed quality management system following the guidelines of the Swiss Accreditation (SAS; ISO 17025) with tracking of reagent lot numbers, detailed SOPs, infrastructure maintenance documentation, reference strains regularly used, determined validated acceptance criteria for a successful sequencing run, etc.

All laboratories listed below fulfill these criteria and also have an established bioinformatic analytical pipeline.

Data sharing:
The sequencing data is rapidly shared and discussed between sequencing laboratories in order to identify potential transmission chains and provide a detailed report to the Federal Office of Public Health and the cantonal physician. Due to the general importance for public health, the anonymized sequencing data is also immediately shared via GISAID (gisaid.org) and experts of the science COVID19 Task Force, which could be used for modelling and international context analysis. Clinical sensitive information is only shared between diagnostic laboratories, involved clinicians, Federal Office of Public Health, and cantonal physicians.

Qualification of laboratories:
- Microbiological diagnostic laboratories with SAS accreditation in sequencing (Sanger and/or long read sequencing; https://www.sas.admin.ch/).
- Laboratories with dedicated reference function for the Federal Office of Public Health (e.g. CRIVE).

These diagnostic recommendations have been written/approved by the following laboratories:

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