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Geneva Centre for  
Emerging Viral Diseases

Division of Infectious  
Diseases

Department of Medicine

Laboratory of virology

Division of Laboratory  
Medicine

Diagnostic Department

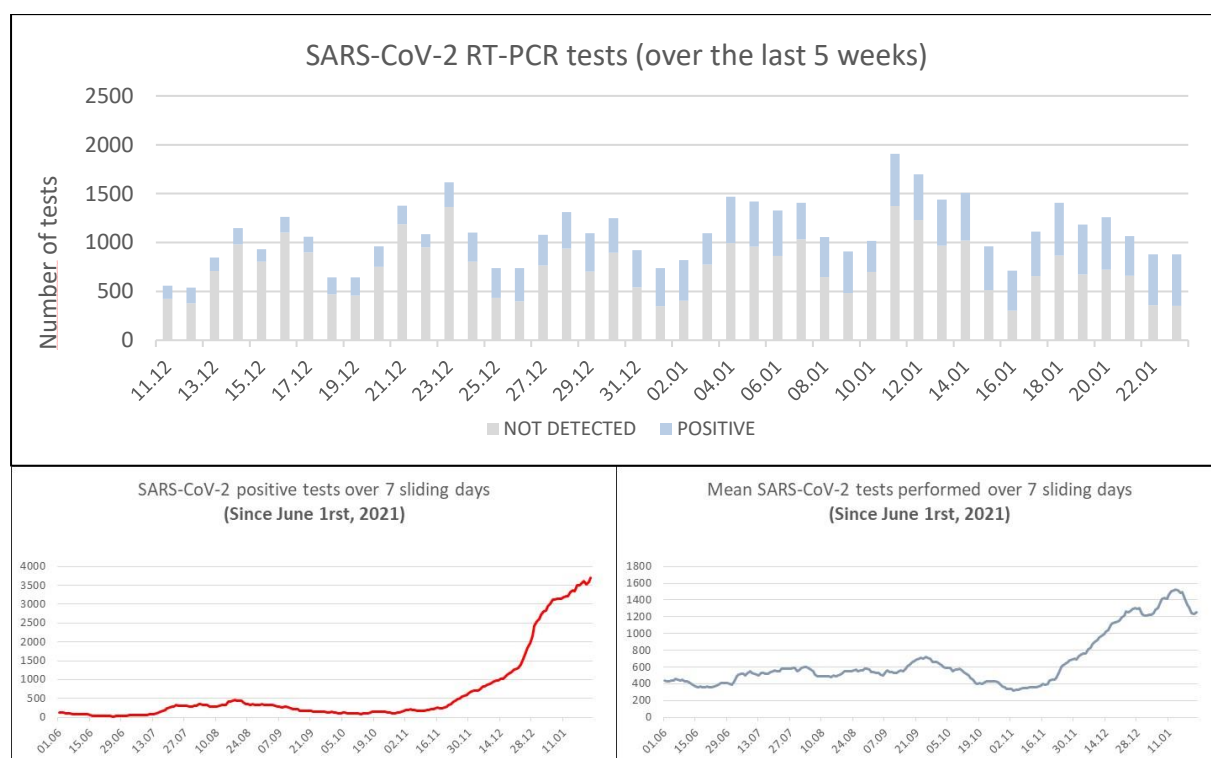
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### SARS-CoV-2 genomic surveillance in Geneva: weekly update

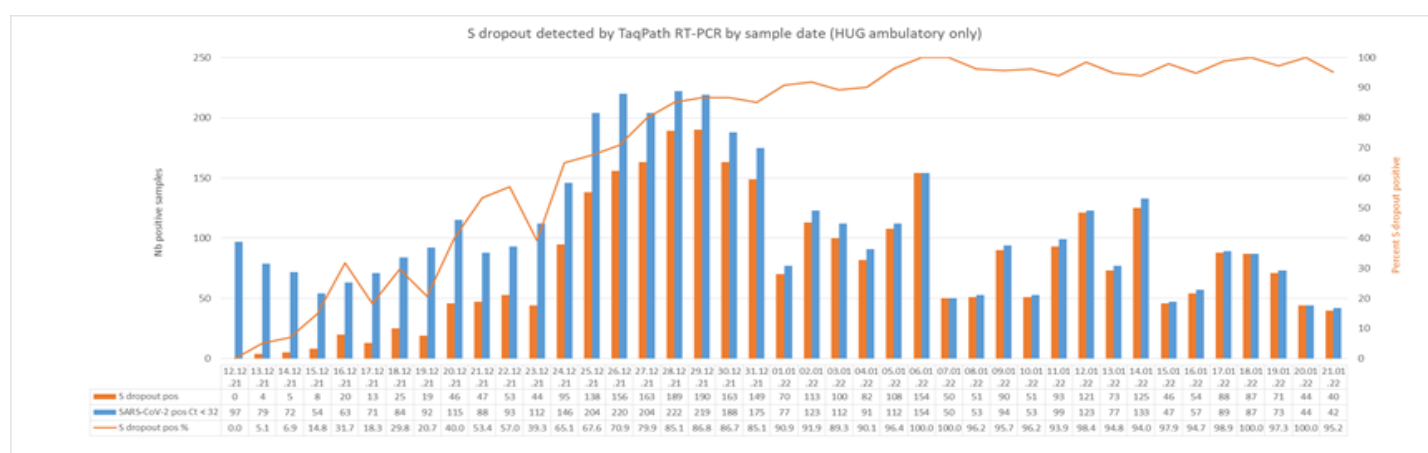
#### Highlights:

- During week 3, we continued to observe an **increase in the absolute number of positive SARS-CoV-2 tests** at the HUG laboratory of virology (Figure 1). The **mean positivity rate recorded at our outpatient symptomatic testing center continued to oscillate around 70%** since Christmas 2021. Note that as of January 25, 2022, 11 518 positive SARS-CoV-2 RT-PCR tests have already been processed by the HUG laboratory of virology since the beginning of the year.
- **The “S Drop out”** (a test used as a proxy for Omicron detection) **has been present in between 95 and 100% of the tested specimens since the first week of January in the community** (Figure 2) **and** reached similar proportion at the end of week 3 **in specimens collected from SARS-CoV-2 positive hospitalized patients** (Figure 3). This rendered the use of one available combination of monoclonal antibody treatment (casirvimab/imdevimab) no more useful in clinical practice. Not that the other mAb therapy (sotrovimab) cannot be used as an alternative therapy in hospitalized patients with severe disease as it did not showed any benefit in those patients.
- **Whole genome sequencing confirmed the predominance of Omicron and showed that all sequences retrieved from Geneva residents were BA.1 sub-lineage.** (Figure 4). The S Drop out was still a good proxy for Omicron over this period.
- As the Omicron BA.2 sub-lineage doesn't display the S Dropout, we implemented a new SNPs RT-PCR aiming to differentiate between Delta and Omicron (S371L/S373P) in S Drop out negative samples. Preliminary results of the testing of 13 random specimens collected between January 16 and 19 suggested that 3/13 of the samples were BA.2, and 10/13 Delta. This is a signal that BA.2 may be appearing in the Geneva area. This will have to be confirmed by whole genome sequencing and will be surveilled over the next weeks.

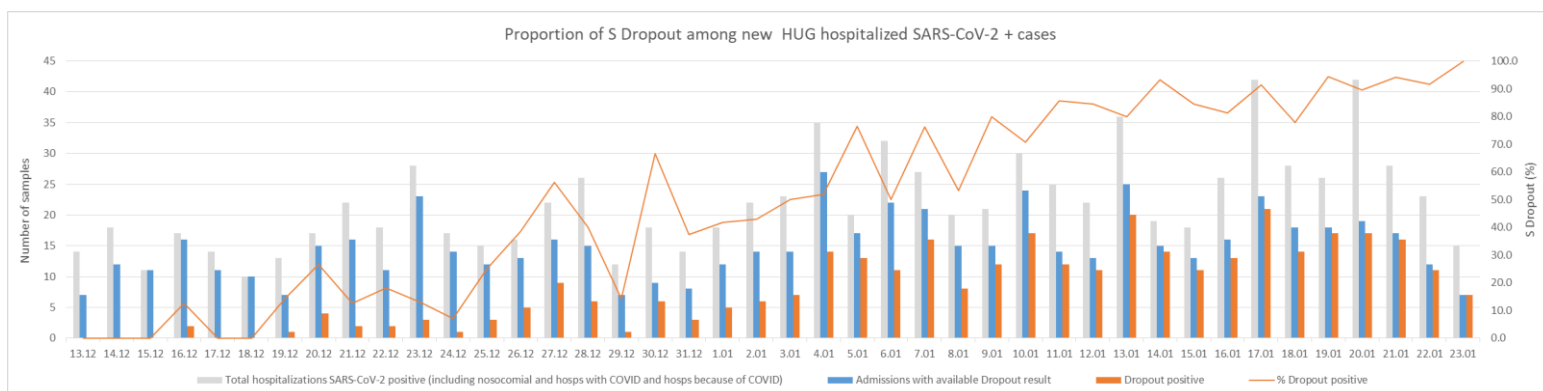
**Figure 1:** Number of SARS-CoV-2 tests performed at the HUG laboratory of virology (per day). Positive tests are displayed in light blue (top). SARS-COV-2 positive tests over 7 sliding days (bottom left) and mean SARS-COV-2 tests performed over 7 sliding days (bottom right).



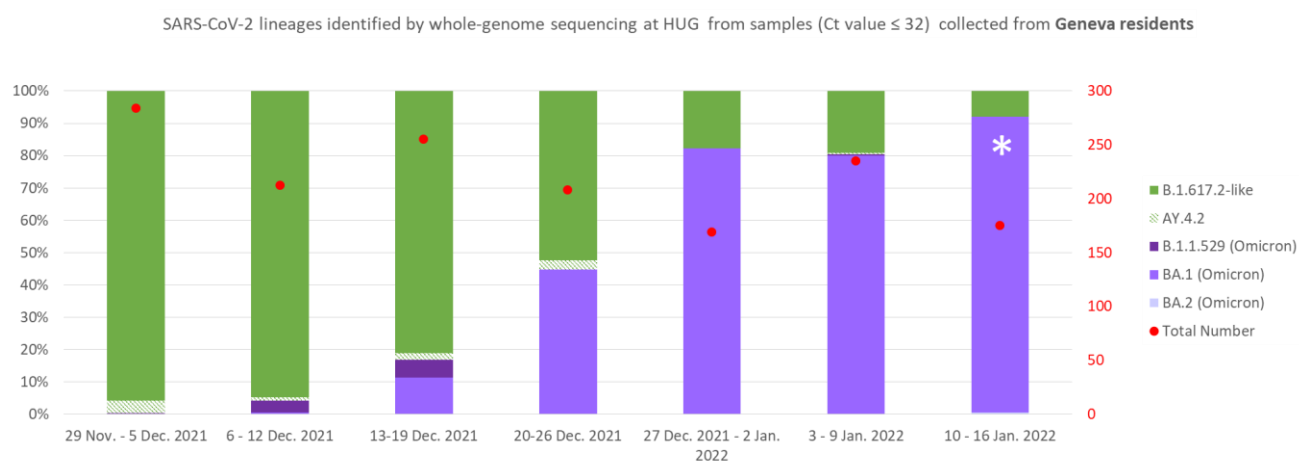
**Figure 2:** Daily evolution of the number of specimens tested for the S Drop out (used as a proxy for Omicron), number of specimens displaying the S Drop out and proportion of specimens displaying the S Drop out among specimens tested, in samples collected at our outpatient testing center (ambulatory setting). Since January 1<sup>st</sup>, 2022, included samples come exclusively from adult people screened at our outpatient testing center.



**Figure 3:** Number of specimens tested for the S Drop out (used as a proxy for Omicron), number of specimens displaying the S Drop out and proportion of specimens displaying the S Drop out among specimens tested, in samples collected in new SARS-CoV-2 positive hospitalized patients.



**Figure 4:** SARS-CoV-2 lineages identified by whole-genome sequencing at HUG from samples (Ct-value  $\leq 32$ ) collected from Geneva residents (Sentinella specimens excluded). Sequencing is still ongoing for week 2 (January 10 to January 17, 2022). A total of 1538 sequences are counted in this analysis. Note that specimen collection for WGS shifted towards hospitalized patients during week 1, explaining the rebound in the number of Delta cases over this week, due to the delay between what is observed in the community and hospitalizations.



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Pauline Brindel for the Geneva Cantonal Physician team.

### The laboratory of virology of the Geneva University Hospitals as a sentinel site for the Geneva area

The number of tests (PCR and antigen tests) performed at the Geneva University Hospitals represented around 20% of the total number of tests performed in the canton of Geneva during the whole 2021 year. Roughly 25% of the positive specimens collected in the Geneva area were processed at HUG during this period. Samples collected at our outpatient testing center are RT-PCR-based for symptomatic individuals. Specimens analyzed in our laboratory originate from ambulatory and hospitalized patients as well as symptomatic and/or asymptomatic health care workers.

The number of positive tests in the canton and the total number of tests done during the surveilled week are available on the website from Federal Office of Public Health ([COVID-19 Suisse | Coronavirus | Dashboard \(admin.ch\)](https://www.admin.ch/gov/de/infomedia/covid19)). During week 3, in the canton of Geneva, over 6000 RT-PCR tests were performed per day for several days in a row among which around 50% were positive. For further epidemiological data, please refer to the weekly report of the cantonal physician team. Over the same time period, 8803 RT-PCR tests were processed by the HUG laboratory of virology, among which 3708 (42%) were positive.

## Methods and collaborations

Screening for the “S drop out” was implemented at HUG on SARS-CoV-2 positive specimens with a Ct-value  $\leq 32$  that were tested for primary diagnosis in our laboratory on November 28 (Taqpath RT-PCR assay). The “S drop out” corresponds to the S-gene PCR target being not amplified (“dropping out”), while the two other PCR targets are still detected, and serves as a proxy for Omicron.

All positive specimen were tested for the S drop out between December 1 and 31, 2021. Since January 2022, all specimens originating from hospitalized patients and a selection of specimens collected from ambulatory patients are tested for the “S Drop out”.

The SNPs RT-PCR S371L/S373P allows for differentiation between Delta, BA.1 and BA.2 Omicron sublineage, and was tested at HUG on a random selection (n=13) of SARS-CoV-2 “S Drop out” negative samples collected since week 3. It will be used to screen for BA.2 Omicron sublineage circulation.

Whole genome sequencing performed on SARS-CoV-2 positive samples allows for definitive sublineage/variant identification.

WGS is carried out in close collaboration with the Health 2030 Genome Center in Geneva and Philippe Le Mercier from the Swiss Institute of Bioinformatics. Since March 1, 2021, the sequencing has been done within the Swiss national SARS-CoV-2 genomic and variants surveillance program. Specimens collected at HUG with a Ct-value  $\leq 32$  are sequenced. In some instances, sequencing can be done on specimens sent by other laboratories in Switzerland within the surveillance program or by request of the cantonal physician team. Phylogenetic analysis data are produced by Nextstrain, in collaboration with Richard Neher's group at the University of Basel. In addition, partial Sanger sequencing may be done by our laboratory.

Geographic distribution, transmission advantage estimates and detailed number of available sequences over time in the canton of Geneva is available on the covSPECTRUM platform, run by Tanja Stadler's group at ETH Zurich.

These reports are produced in collaboration with the Geneva Cantonal Physician team, which provides information on epidemiological links. For epidemiological data, please refer to the weekly report of the cantonal physician team.