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Emerging Viral Diseases

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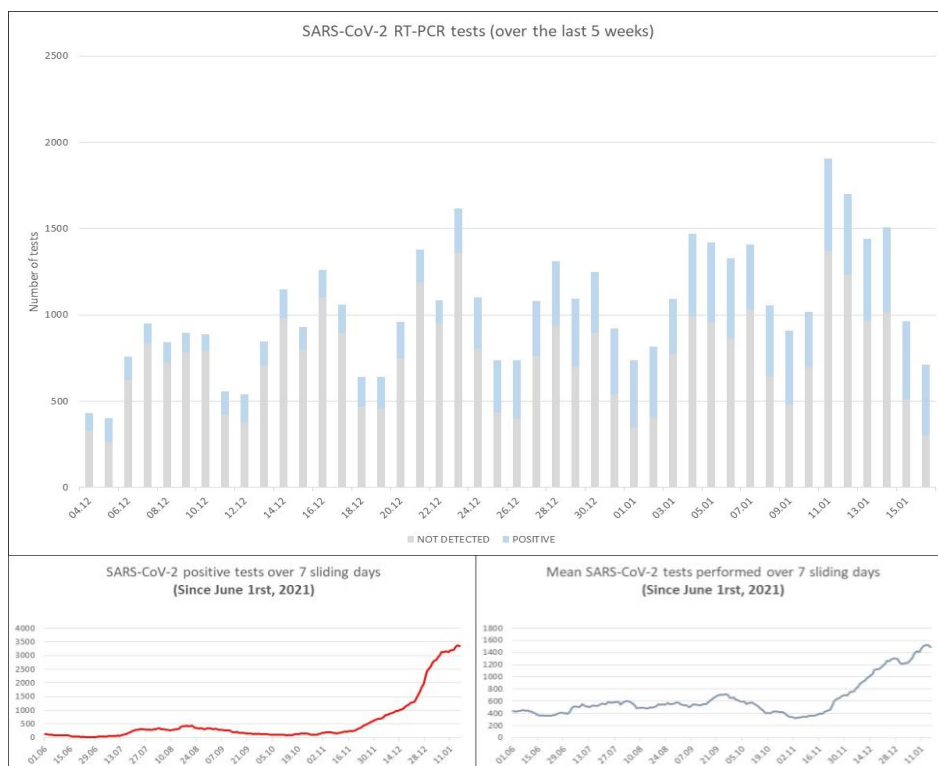
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### SARS-CoV-2 genomic surveillance in Geneva: weekly update

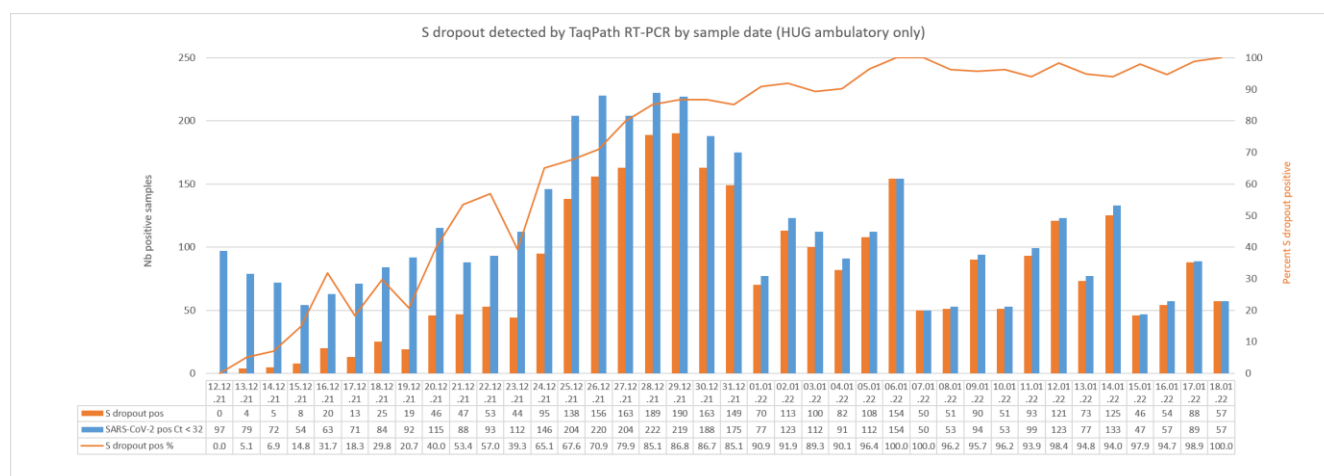
#### Highlights:

- During week 2, we continued to observe an **increase in the absolute number of positive SARS-CoV-2 tests** at the HUG laboratory of virology (Figure 1). Of note, the **mean positivity rate recorded at our outpatient symptomatic testing center continued to oscillate between 60 and 70%** on average over the last 7 days.
- **In the community, 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**. (Figure 2). The “S Drop out” is displayed by 80 to 90% of the specimens tested collected from SARS-CoV-2 positive hospitalized patients during week 2 (Figure 3).
- **The replacement of Delta (B.1.617.2) by Omicron (B.1.1.529) was confirmed by whole genome sequencing**. (Figure 4). 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.
- **All Omicron sequences but one belonged to the BA.1 sub-lineage** (Figure 4), 38% carried the R346K mutation (marker of sub-lineage differentiation/evolution). This confirmed that over week 1, the S Drop out was still a good proxy for Omicron.
- **Only one Omicron sequence belonged to the BA.2 sub-lineage** (which does not display the S Drop out). This specimen was collected in a non-Geneva resident returning from abroad, and is therefore not represented in Figure 4.
- **Remaining Delta sequences continued to display a high variability**, 4 of them analyzed in the last sequencing batch carried the E484Q mutation.

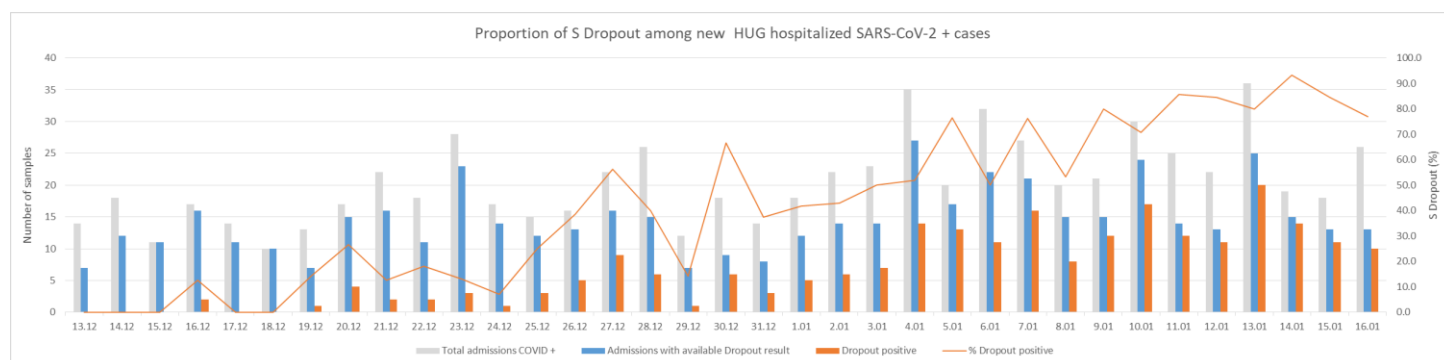
**Figure 1:** Number of SARS-CoV-2 tests performed at the HUG laboratory of virology (per day). Positive tests are displayed in light blue (top). SARS-CoV-2 positive tests over 7 sliding days (bottom left) and mean SARS-CoV-2 tests performed over 7 sliding days (bottom right).



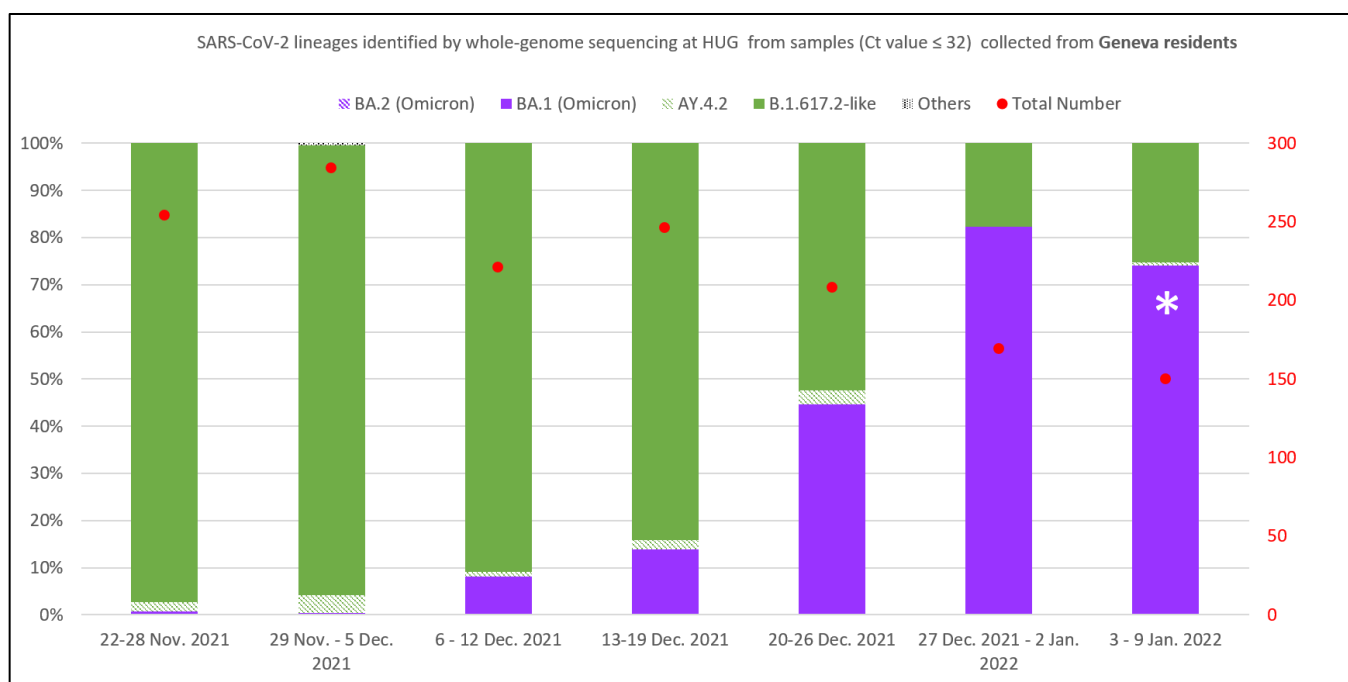
**Figure 2:** Daily evolution of the number of specimens tested for the S Drop out (used as a proxy for Omicron), number of specimens displaying the S Drop out and proportion of specimens displaying the S Drop out among specimens tested, in samples collected at our outpatient testing center (ambulatory 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 Dropout (used as a proxy for Omicron), number of specimens displaying the S Dropout and proportion of specimens displaying the S Dropout 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). Note that sequencing is still ongoing for week 1 (January 3 to January 9, 2022). A total of 1532 sequences are counted in this analysis.



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## 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. Whole genome sequencing performed on SARS-CoV-2 positive samples allows for definitive confirmation.

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”.

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.