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Geneva Centre for
Emerging Viral Diseases

Division of Infectious
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SARS-CoV-2 genomic surveillance in Geneva: bi-weekly update

Highlights:

- We observe a **tendency of increase** of the number of positive tests and of the overall positivity rate over the last two weeks (Figure 1).
- **BQ.1/BQ.1.1** sublineages increased to approximately 75% (at the expense of earlier BA.5 sublineages) to become the most prevalent in the Geneva area during weeks 46-49 (Figure 2).
- Together, BA.4 and others BA.5-like sublineages (except for BQ1 and BQ1.1) accounted for less than 20% of sequenced samples.
- **BA.2.75** sublineages were identified in almost 10% of sequenced samples.
- Prevalence of SARS-CoV2 samples with 346T mutation increased to reach 80% by the end of the week 50. (Figure 3)*

More information *:

The laboratory has introduced from week 45 the screening of the S:346T mutation (one series/week). Series from weeks 47, 48, 49 and 50 showed prevalences of 70% (66/94), 66% (61/93), and 79% (74/94), and 80% (74/93) respectively.

This mutation, among others, is found on several Omicron sub-variants, and is phenotypically associated with immune escape, notably regarding mAb treatments.

Specifically, this mutation (as well as others) is linked to abolition in neutralization *in vitro* by all currently available monoclonal antibodies available in Switzerland. In other words, there is a clear signal that these antibody-based treatments, including cilgavimab, will soon be completely ineffective.

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). **Bottom left:** SARS-CoV-2 positive tests over 7 sliding days. **Bottom right:** mean SARS-CoV-2 tests performed over 7 sliding days.

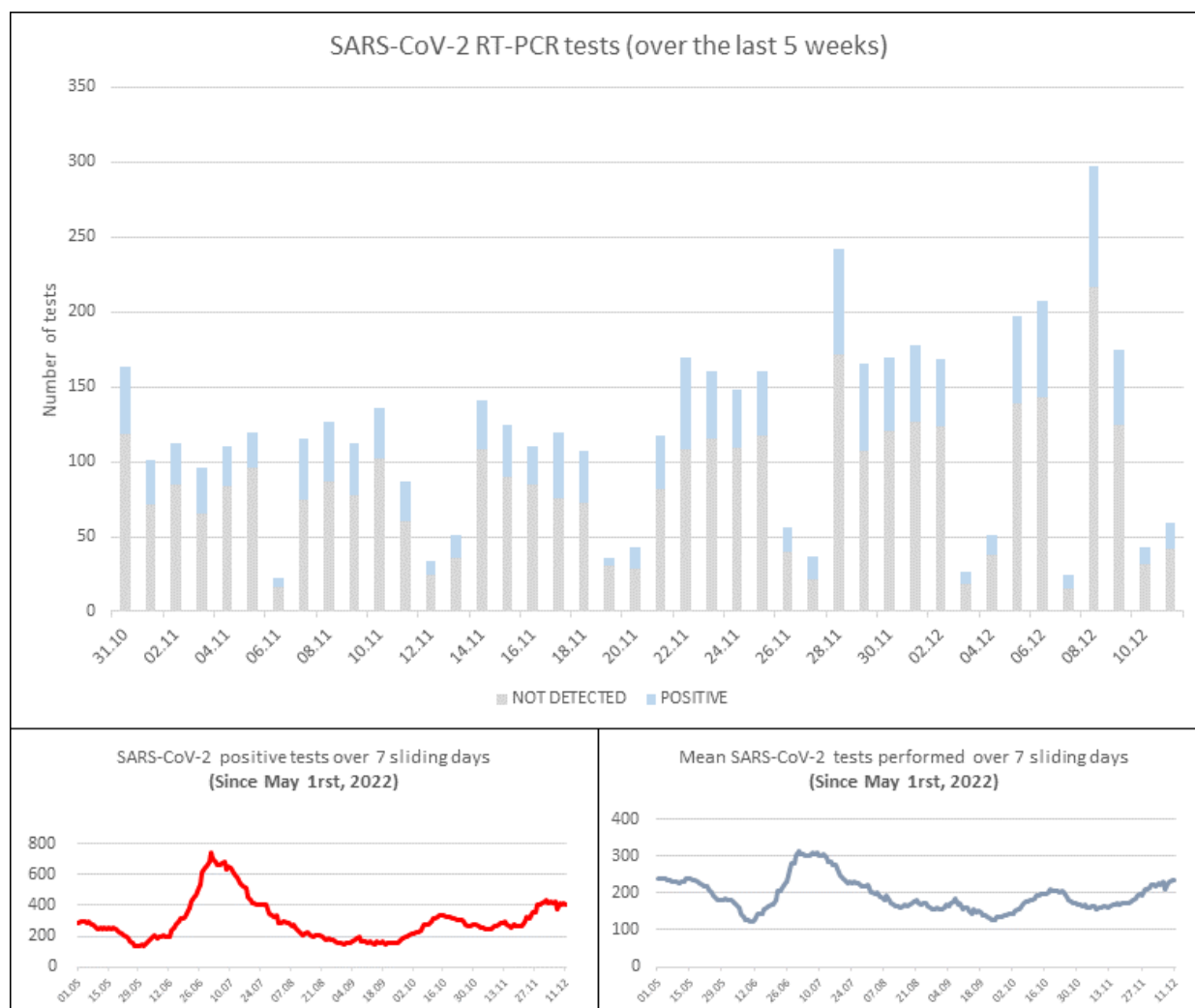


Figure 2: SARS-CoV-2 lineages identified by whole-genome sequencing at HUG from samples (Ct-value ≤ 32) collected from Geneva residents (Sentinella specimens excluded). A total of 489 sequences were included in this analysis. **Bottom Left:** Percentage of SARS-CoV-2 sequenced samples with the S:R346T/S.

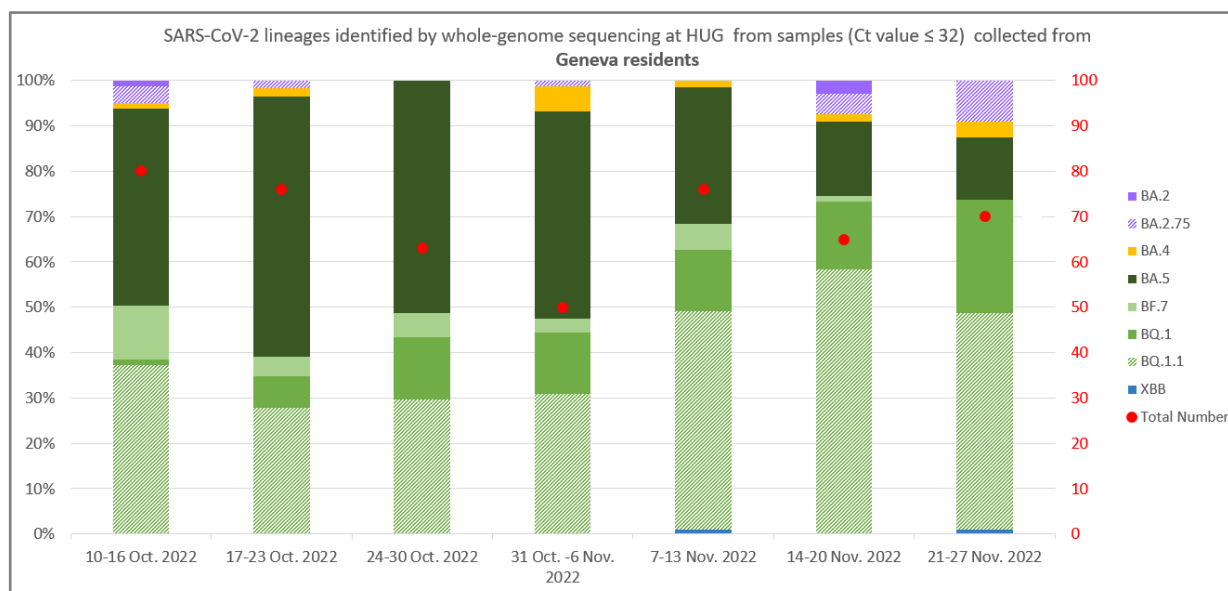
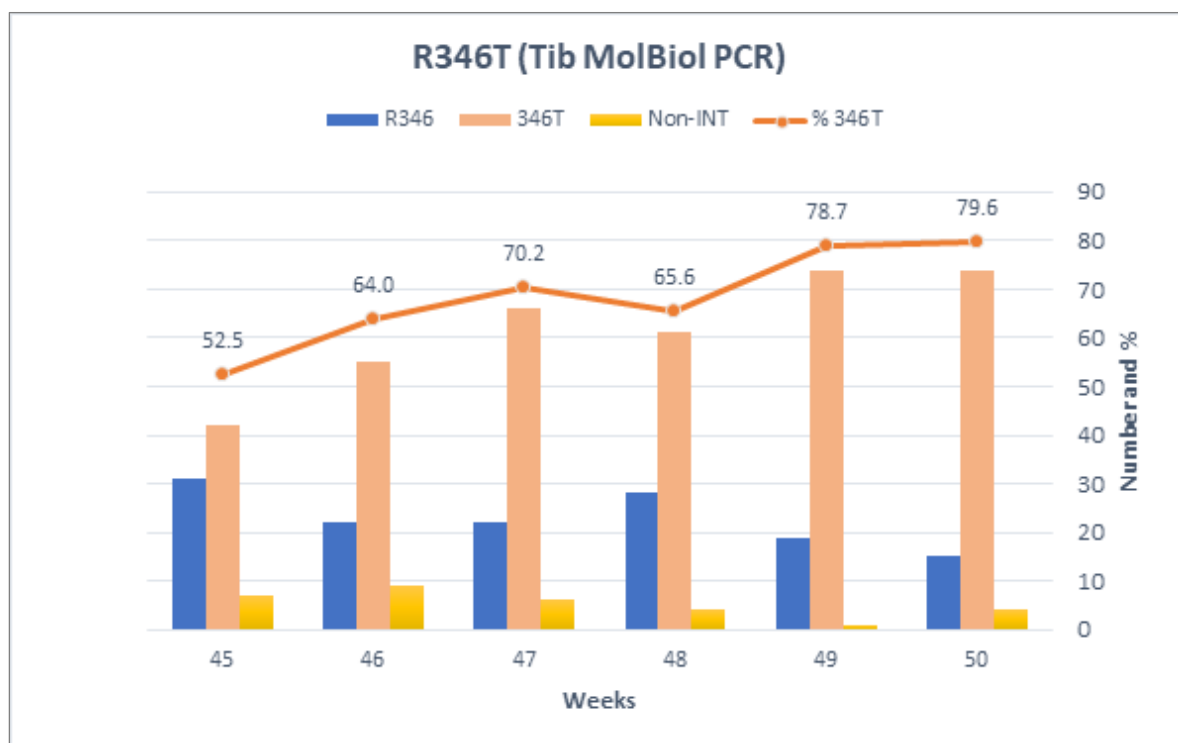


Figure 3: Number and proportion of SARS-CoV-2 screened samples with and without the S:R346T mutation. Non-interpretable samples are displayed as "Non-INT".



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 Emma Hodcroft for the Geneva Center for Emerging Viral Diseases.
 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 **33%** (1572/4750) and **35%** (1631/4720) of the total number of tests performed in the canton of Geneva during weeks **48 and 49** of 2022, respectively. Roughly **26%** and **29%** of the positive specimens collected in the Geneva area were processed at HUG during weeks 48 and 49 (423/1629 and (400/1399), respectively. Samples collected from symptomatic individuals at our outpatient testing center are tested by RT-PCR. 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 weeks are available on the website from Federal Office of Public Health ([COVID- 19 Suisse | Coronavirus | Dashboard \(admin.ch\)](https://www.bfs.admin.ch/bfs/fr/topics/santite/themes/covid-19/suisse/coronavirus)).

During weeks 48 and 49 in the canton of Geneva, the number of RT-PCR tests and the number of confirmed cases **increased** compared to the two previous weeks and the proportion of positive tests also **increased**.

Methods and collaborations

Of note, the laboratory has introduced from week 45 the screening of the S:346T mutation using the SARS Spike R346T kit (TIB Molbiol).

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. The national genomic surveillance program is ongoing in Switzerland since March 1, 2021 and includes specimens collected at HUG with a Ct-value ≤ 32 . 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 and analyzed by Emma Hodcroft, from the Geneva Center of Emerging Viral Diseases and University of Geneva. In addition, partial Sanger sequencing may be done by our laboratory.

Geographic distribution, transmission advantage estimates and detailed numbers of available sequences over time in the canton of Geneva are 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 report of the cantonal physician team.