

**SARS-CoV-2 genomic surveillance in Geneva: monthly update
Weeks 10 - 24 2024**

Caveat: Data published by our laboratory might reveal some trends regarding local epidemiology. In terms of representiveness, this data should be interpreted cautiously due to possible cluster effects.

Highlights:

- The weekly **number of positive tests** performed by our laboratory **has been low since March, 2024** (Figure 1), with a positivity rate over 7 sliding days below 5%. Over the last 2 weeks, this rate progressively increased again and reached 12% at the end of week 24, with an absolute number of positive tests increasing but remaining low (23 and 39 for weeks 23 and 24 respectively).
- Since January, **all identified sequences were JN.1** and descendants (Figure 2). The proportion of the sequences carrying the FLiRT mutations progressively increased in Geneva, as well as in Switzerland, over time to reach 60% and 40% respectively, the majority of it being KP.2.

More information can be found in the monthly national surveillance report available at <https://www.hug.ch/centre-maladies-virales-emergentes/programme-sequencage-national-du-sars-cov-2>

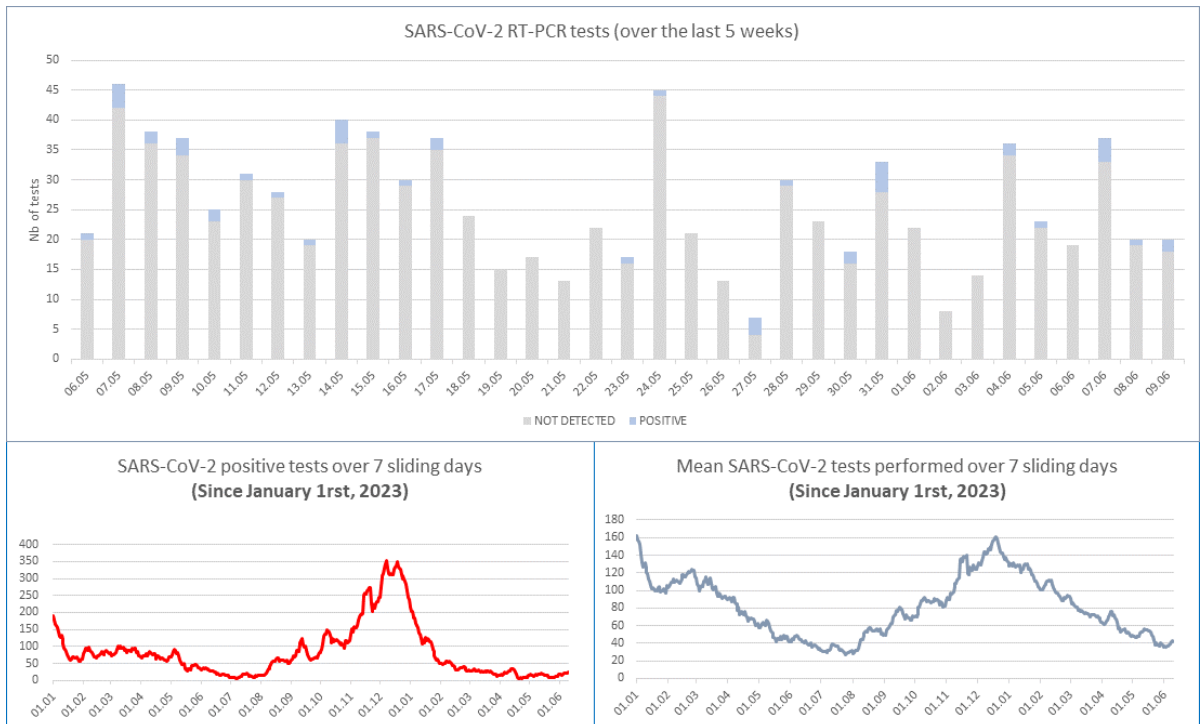


Figure 1: Number of SARS-CoV-2 tests performed at the HUG laboratory of virology (per day). Positive tests are displayed in light blue (top). Bottom left: SARS-CoV-2 positive tests over 7 sliding days. Bottom right: mean SARS-CoV-2 tests performed over 7 sliding days.

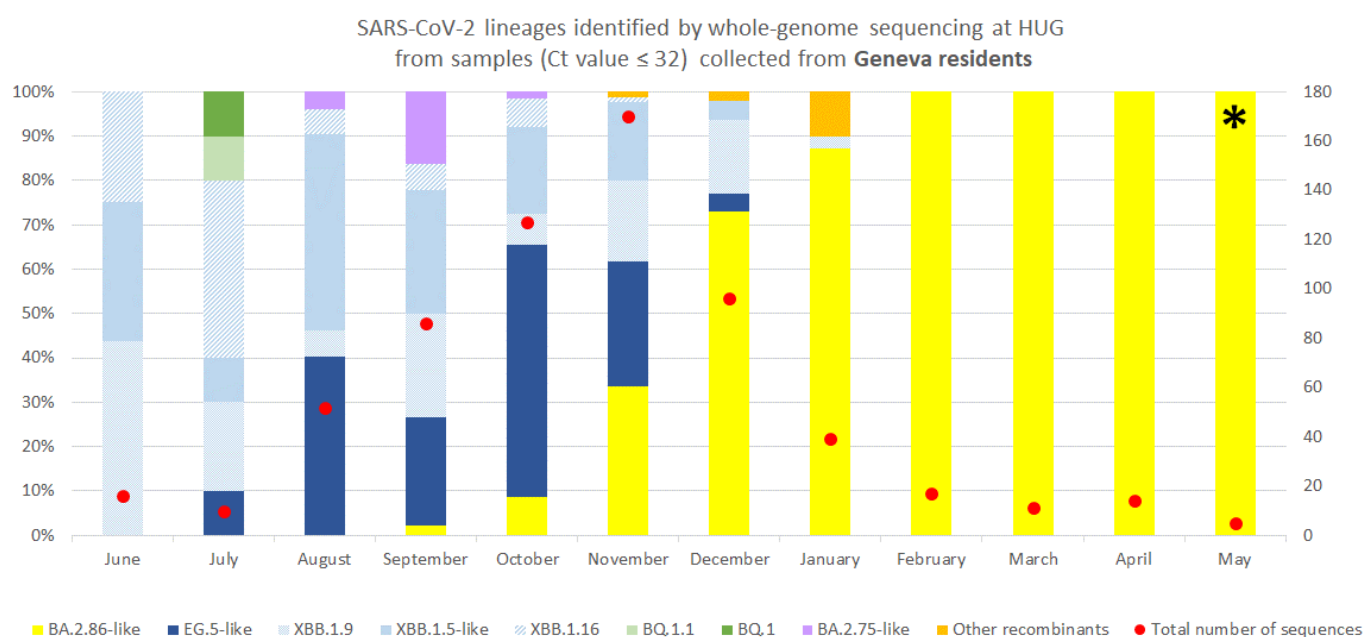


Figure 2: SARS-CoV-2 lineages identified by whole-genome sequencing at HUG from samples (Ct-value ≤ 32) collected from Geneva residents (Sentinella specimens excluded). *Sequencing is still ongoing for the month of May. BQ.1 and BQ.1.1 (here depicted in green) are BA.5 derivatives. EG.5-like variants are descendent lineages of XBB.1.9.2, which has the same spike amino acid profile as XBB.1.5. BA.2.86 is a highly divergent variant first identified in July 2023, carrying more than 30 different mutations in the Spike protein compared to the previous XBB lineages. JN.1, the most common BA.2.86 sublineage, displays an additional spike mutation (L455S).

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

The number of SARS-CoV-2 RT-PCR tests performed at the Geneva University Hospitals (HUG) represented around 81% (1372/1690) of the total number of tests performed in the canton of Geneva during the month of May, 2024. Roughly 65% (62/96) of the positive specimens collected in the Geneva area were processed at HUG during the month of May, 2024. An additional 65 positive specimens were tested at HUG from June 1 to June 16, 2024. Specimens analyzed at the HUG originate mainly from hospitalized patients.

The number of positive tests in the canton and the total number of tests done during the surveilled weeks are available on the [website of the Federal Office of Public Health](#).

Methods and collaborations

WGS is conducted in close collaboration with the Health 2030 Genome Center in Geneva. The national genomic surveillance program has been ongoing in Switzerland since March 1, 2021, and includes specimens collected at the HUG with a Ct-value ≤ 32 . Phylogenetic analysis data are produced by Nextstrain in collaboration with Richard Neher's group at the University of Basel. Geographic distribution, transmission advantage estimates and exact numbers of available sequences over time in the canton of Geneva are available on the CoVpectrum 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. Please refer to the EpiScope report (EpiScope | ge.ch) for epidemiological data.

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Geraldine Duc for the Geneva Cantonal Physician team.