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N/réf : LK/MS/PV

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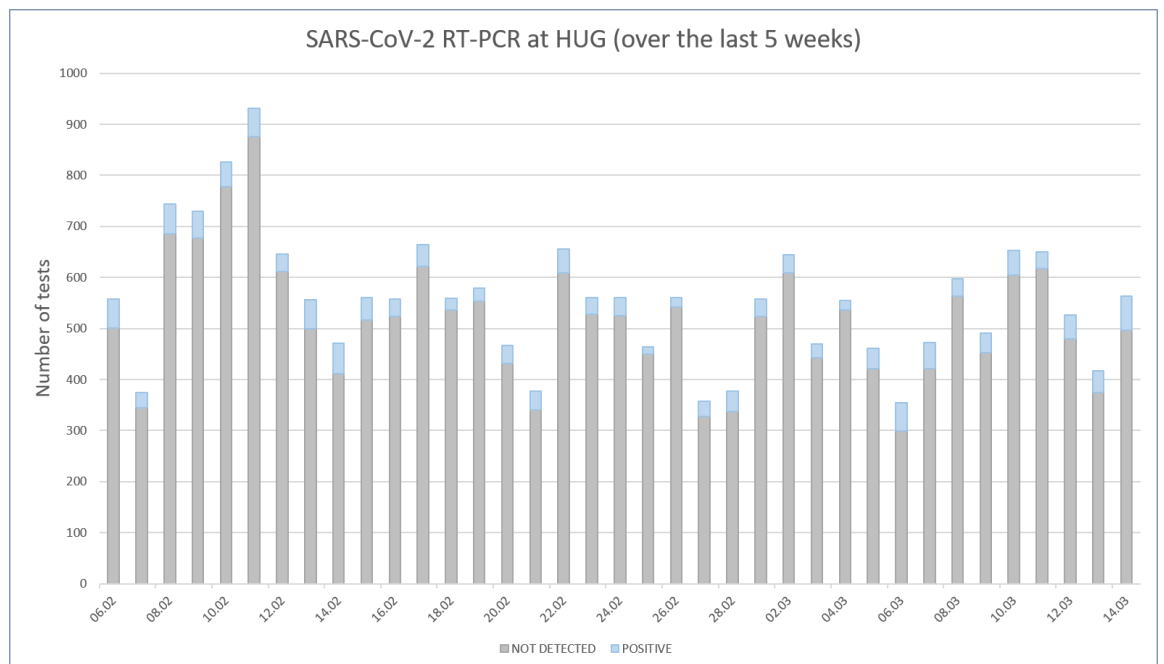
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## SARS-CoV-2 variants: follow-up of previous updates in Geneva

### SARS-CoV-2 testing at HUG



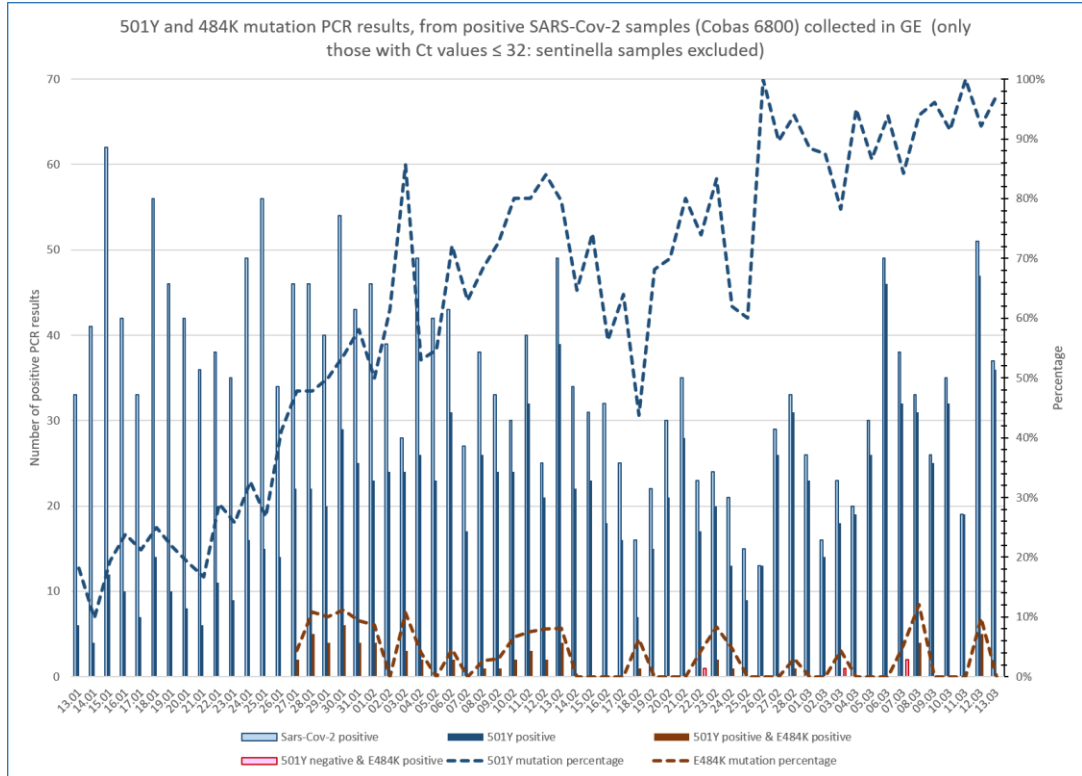
Among all SARS-CoV-2 RT-PCR-positive samples identified in our laboratory, all those with a Ct value  $\leq 32$  are subsequently screened for the 501Y and 484K mutation by specific RT-PCR assays.

Starting date of N501Y mutation screening: January, 5, 2021.

Starting date of E484K mutation screening: January, 27, 2021.

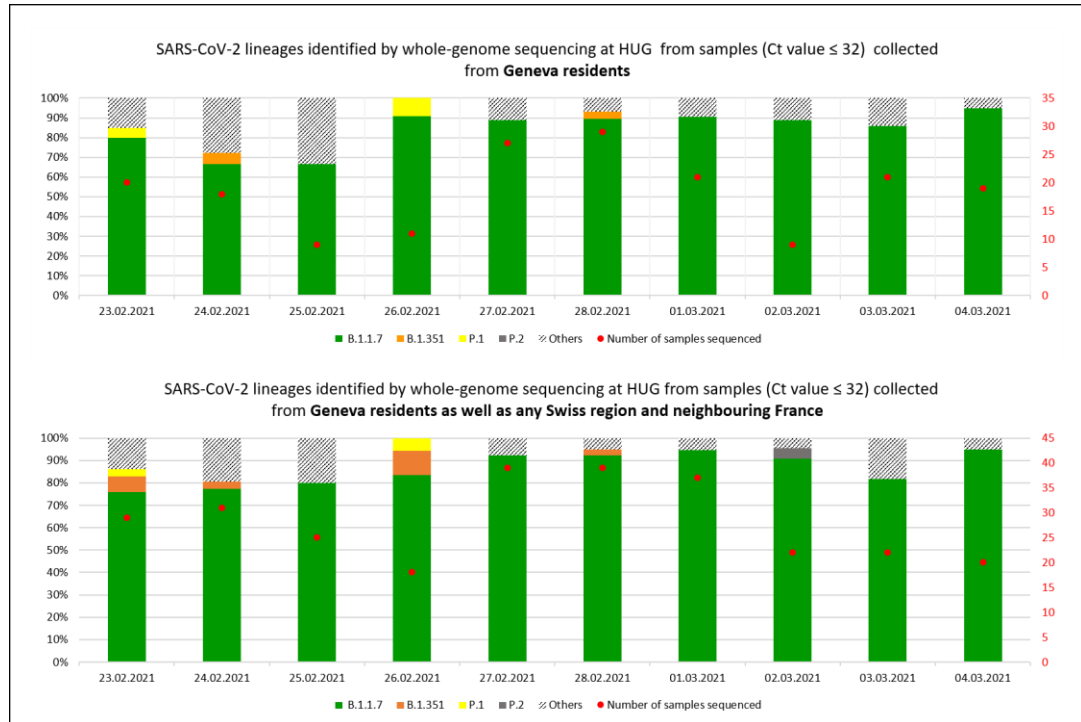
Specimens analyzed in our laboratory come from the community (majority), from hospital workers (systematic screening in case of any symptoms and cluster investigations), from asymptomatic travelers, and from hospitalized patients.

**501Y and 484K mutation screening by RT-PCR among SARS-CoV-2 positive samples collected in GE and sent to our laboratory for primary diagnosis**



Almost all new positive cases are due to a variant carrying the 501Y mutation. Only few samples carrying the 484K mutations (P.1 Brazil and B.1.351 South-Africa) are identified each week. Some samples, displaying the 484K without the 501Y mutation has been detected, and correspond to the P.2 variant. This combination is still rarely observed in Geneva.

## Most recent whole genome sequencing results performed on SARS-CoV-2 positive samples collected in GE and sent to our laboratory



WGS is carried out in close collaboration with the Health 2030 Genome Center in Geneva and is based on a daily random sampling of SARS-CoV-2 positive specimens by RT-PCR with as only selection criterion a Ct value ≤ 32. This graph displays the sequences with 95% of positions covered ≥ 15x and submitted to GISAID (282 sequences obtained from samples collected from February 23 to March 4, 2021).

B.1.1.7 is now generating almost all new SARS-CoV-2 infections, as confirmed by whole genome sequencing. Few B.1.351 are also circulating at a low level. P.1 sequences are only rarely retrieved. P.2 variant sequences have been confirmed in two samples in the Geneva area, between February 23 and March 3, 2021.

### Conclusions

- The B.1.1.7 variant is representing almost all new SARS-CoV-2 contaminations in the Geneva area since the end of February.
- Only few samples carrying the 484K mutation (Brazilian P.1 or South Africa B.1.351) are detected each week. Rare P.2 sequences are also identified.
- The absolute number of new positive cases and the proportion of positive cases is slightly increasing over the last 2 weeks.

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