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N/réf : LK/MS/PV

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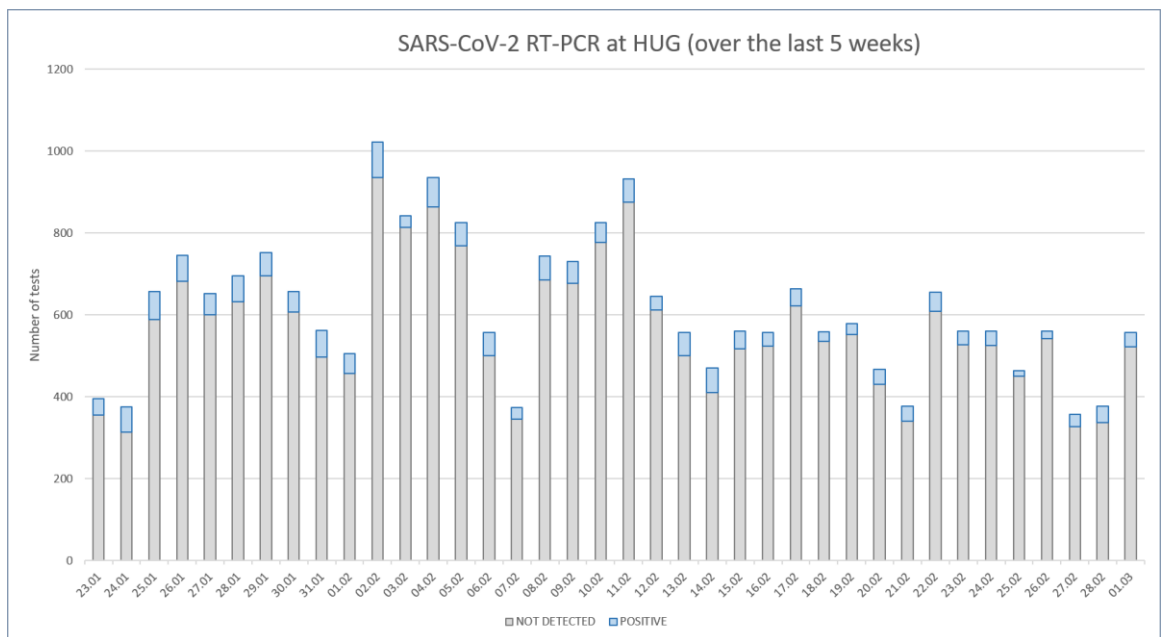
Laboratory of virology

Division of Laboratory
Medicine

Diagnostic Department

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

SARS-CoV-2 testing at HUG



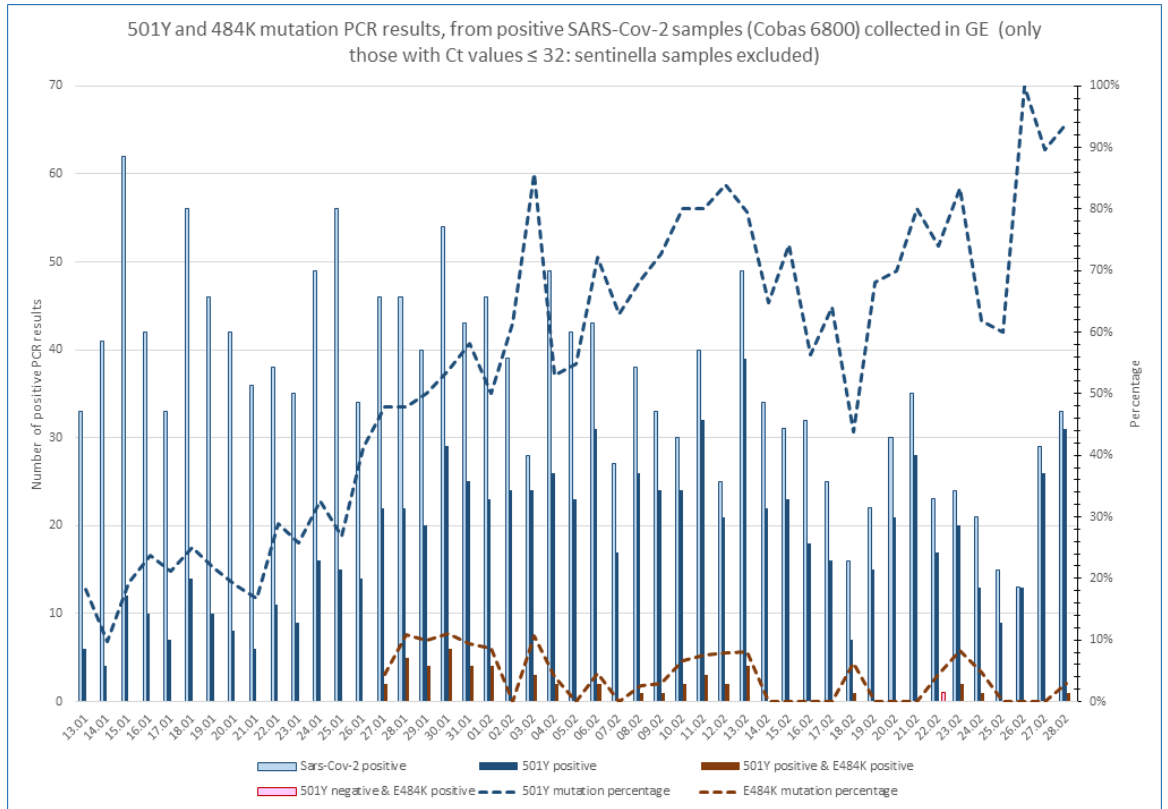
Among all SARS-CoV-2 RT-PCR-positive samples identified in our laboratory, all those with a Ct value ≤ 32 are subsequently screened for the 501Y and 484K mutation by specific RT-PCR assays.

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

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

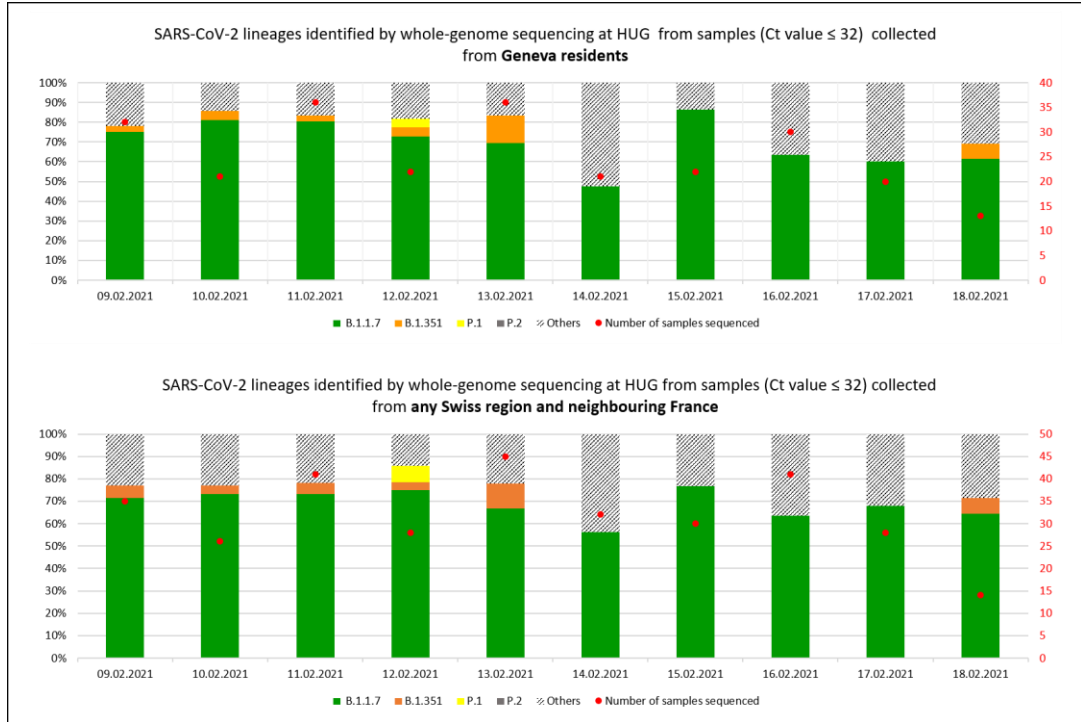
Specimens analyzed in our laboratory come from the community (majority), from hospital workers (systematic screening in case of any symptoms and cluster investigations), from asymptomatic travelers, and from hospitalized patients.

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 now due to a variant carrying the 501Y mutation. Only few samples carrying the 484K mutations (P.1 Brazil and B.1.351 South-Africa) have been identified over the past 7 days. One sample, displaying the 484K without the 501Y mutation has been detected, which is currently being sequenced. This combination is 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 (320 sequences obtained from samples collected from February 9 to February 18, 2021).

The predominant variant is still B.1.1.7, as confirmed by whole genome sequencing. Few B.1.351 are also circulating at a low level. P.1 sequences are only rarely retrieved.

Conclusions

The B.1.1.7 variant is now representing almost all new SARS-CoV-2 contaminations in the Geneva area. Only few samples carrying the 484K mutation (Brazilian P.1 or South Africa B.1.351) are detected each week.

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