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Division of Infectious  
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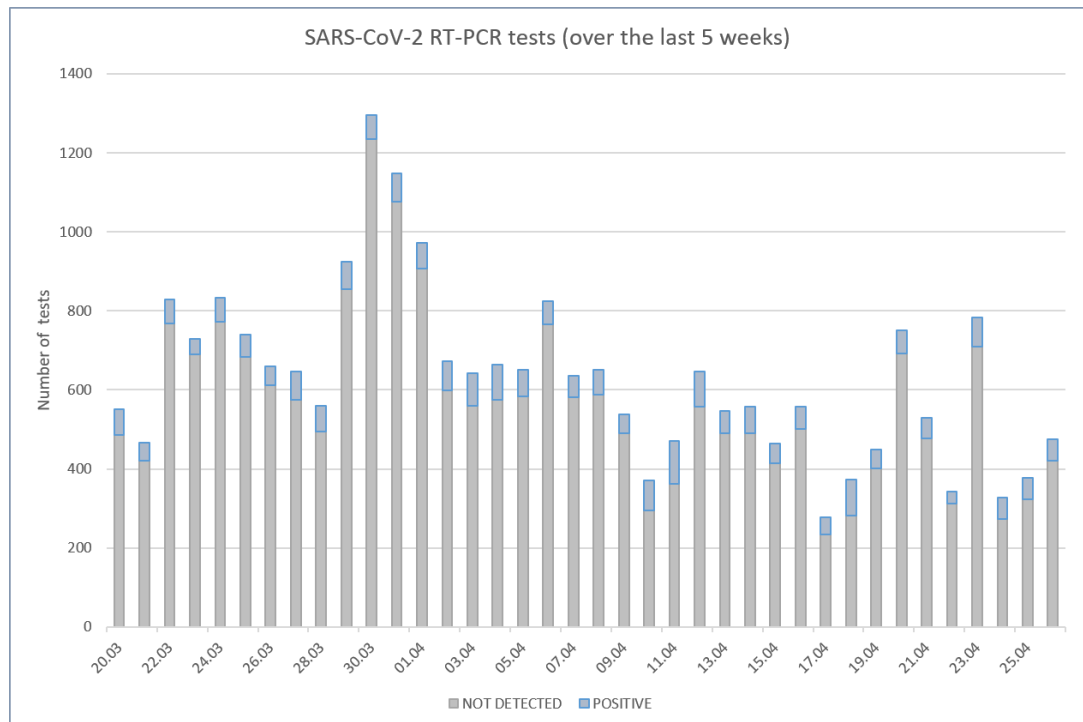
Diagnostic Department

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

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

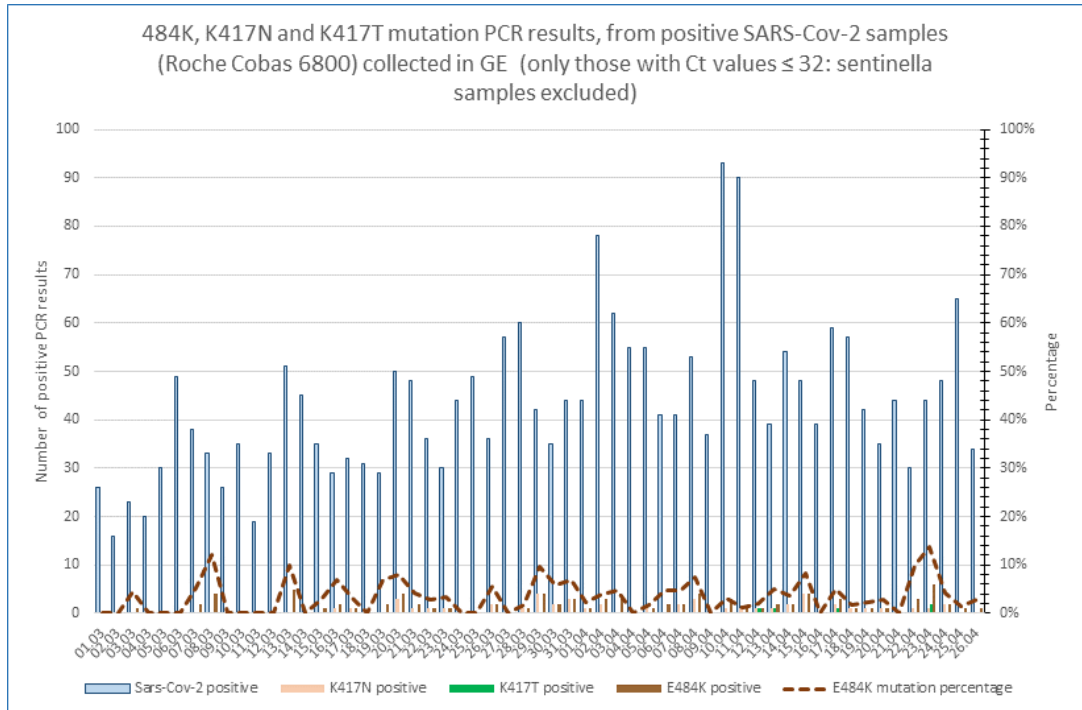
The number of tests performed at the laboratory of virology of Geneva University Hospitals represents around 1/3 of the total number of tests performed in the canton of Geneva. Specimens analyzed in our laboratory come from the community (the majority), from hospital workers (systematic screening in case of any symptoms, cluster investigations and asymptomatic HCWs as part of hospital surveillance system), from asymptomatic travelers needing a screening test, and from hospitalized patients. All tests performed at our outpatient testing center (located in the Hospital but open to anyone from the community) are PCR-based and not Antigen-based; of course many centers in the canton are using Antigen-based tests for primary screening.

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. It is based on a daily random sampling of SARS-CoV-2 positive specimens by RT-PCR with a Ct value  $\leq 32$  as the only selection criterion. In some instances, sequencing can be done in specimens sent by other laboratories in Switzerland.



The overall positivity rate is stable, and is between 10 and 15%.

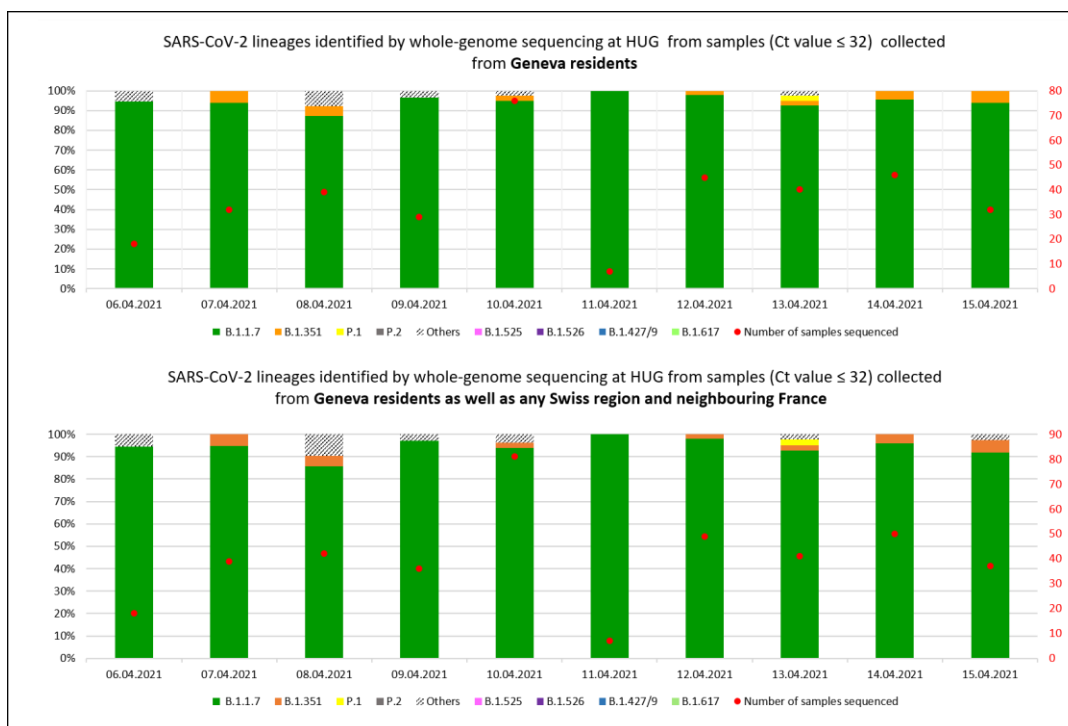
### 484K mutation screening by RT-PCR among SARS-CoV-2 positive samples collected in GE and sent to our laboratory for primary diagnosis



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 mutations by specific RT-PCR assays. Specimens carrying the 484K and the 501Y mutations are subsequently tested for the 417N/T mutation. Starting date of E484K mutation screening: January, 27, 2021. Starting date of 417N/T mutation screening: March, 3, 2021.

As shown by the brown dotted-line, variants carrying the 484K mutation (mainly B.1.351, see below for details) have been circulating at a low level in the community in the Geneva area since mid-March. The proportion of variants carrying the 484K mutation is stable over time, and these don't seem to be able to outcompete B.1.1.7 so far.

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



This graph displays the sequences with 95% of positions covered  $\geq 15x$  and submitted to GISAID (400 sequences obtained from samples collected from April, 6 to April, 15, 2021).

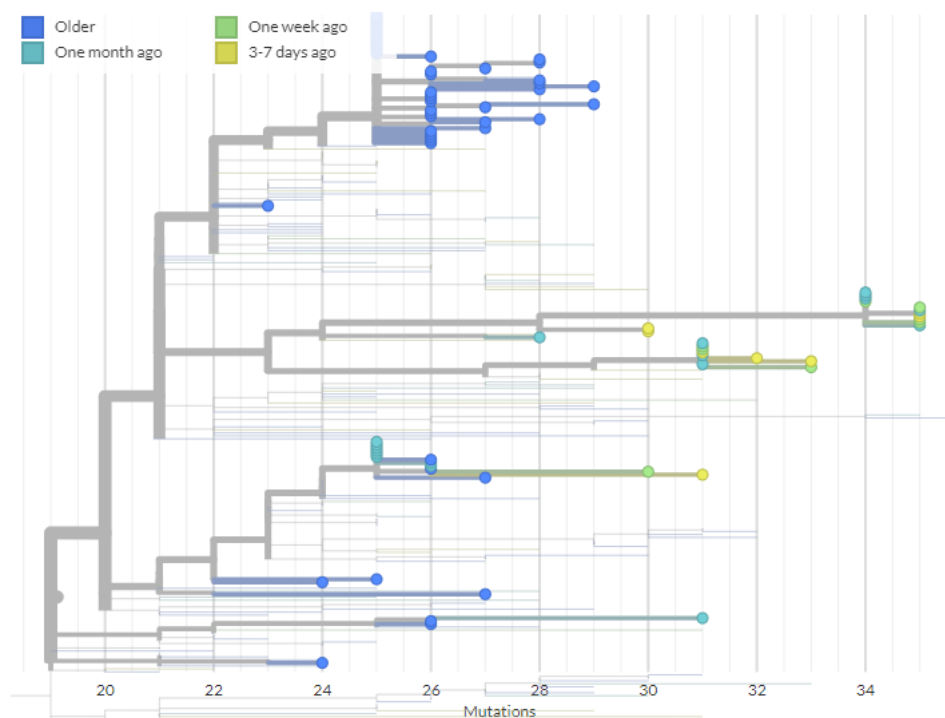
B.1.1.7 has been causing almost all new SARS-CoV-2 infections since the end of February, as confirmed by whole genome sequencing.

B.1.351 is still circulating at a low level in the community.

A single P.1 sequence was identified.

No other VOC/VOI has been identified over this period of time.

### Phylogenetic analysis of SARS-CoV-2 genomes retrieved in the Geneva area in their context (data shown for the B.1.351 lineage)



[https://nextstrain.org/groups/swiss/ncov/501Y-V2?c=recency&f\\_country=Switzerland&f\\_division=Geneva&label=mlabel:20C/C28253T&m=div](https://nextstrain.org/groups/swiss/ncov/501Y-V2?c=recency&f_country=Switzerland&f_division=Geneva&label=mlabel:20C/C28253T&m=div)

Phylogenetic analysis data are produced by Nextstrain, in collaboration with Richard Neher's group at the University of Basel.

### Conclusions

- The B.1.1.7 variant still represents almost all new SARS-CoV-2 infections in the Geneva area.
- Variants carrying the 484K mutation are currently not able to outcompete B.1.1.7.
- A single P.1 sequence has been identified in the Geneva area and no other VOCs/VOIs have been identified over the last period of surveillance.
- In particular, no B.1.617 has been detected in the area so far.

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