Hôpitaux Universitaires Genève

UNIVERSITÉ DE GENÈVE
FACULTÉ DE MÉDECINE

Federal Office of Public Health FOPH
Public Health Directorate Communicable
Diseases Division

Schwarzenburgstrasse 157
3003 Bern
Switzerland

Geneva, October 06, 2021

Swiss national SARS-CoV-2 genomic and variants surveillance program: report of the month of August

Geneva Centre for Emerging Viral Diseases

Division of Infectious Diseases

Department of Medicine

Laboratory of virology

Division of Laboratory Medicine

Diagnostic Department

1. Summary

Over 16% of the total number of cases identified in Switzerland were sequenced by the Surveillance program, yielding over 10'580 sequences in August.

In August, COVID-19 cases numbers continued to rise in Switzerland, due almost entirely to the B.1.617.2 (Delta) variant.

Numerous Delta sub-lineages have been identified, but data is not concrete enough to make any conclusions at this time. There is no evidence that any clade within Delta is of greater concern at this time. Some mutations however can accumulate in the Delta background, and more information is expected to follow.

Other VOCs have only rarely been detected during the surveilled period:
- Alpha has been replaced by Delta, and was rarely detected during the surveilled period
- B.1.351 (Beta) circulation has essentially ceased in August (2 cases)
- P.1 (Gamma) circulation has essentially ceased in August (5 cases)

Other variants of interest or variants under monitoring were also rarely identified:
- B.1.621 (Mu), circulation has essentially ceased in August (1 case)
- B.1.1.318 circulation sharply decreased after week 31, with only 6 later cases.
- Lastly, C.37 (Lambda), was not detected in August.

No important geographical breakdown of a particular variant has been noticed.

Unsurprisingly, B.1.617.2 (Delta) was also the most frequent variant detected in wastewater during the month of August.

laurent.kaiser@hcuge.ch | T. +41 (0)22 372 98 00 | F. +41(0)22 372 98 30 | hug-ge.ch

2. Description of the Swiss national SARS-CoV-2 genomic and variants surveillance program.

The overall goal of the program is to provide epidemiological trends and to highlight meaningful observations.

Because greater transmissibility and/or immune escape potential of the different VOCs and VOIs can result in new surges in COVID-19 numbers despite the vaccination campaign, this program aims to closely monitor each variant displaying mutations known to be linked with either increased transmissibility or immune escape potential.

Currently, 15 diagnostic laboratories have joined the program, including university hospital centres in Switzerland (Geneva, Lausanne, Bern, Basel, Zurich, St-Gall, Ticino), in addition to private laboratories (Viollier, Medisupport CH Romande including Dianalabs, Biolytix, Synlab Bioggio (TI), Labor Team W, Risch), cantonal-based laboratories (Hôpitaux du Valais), Spital Region Oberaargau (Bern, Solothurn, Aargau, Luzern), and 3 high-throughput sequencing platforms (Health 2030 Genome Centre in Geneva, Functional Genomics Centre Zurich run by ETH Zürich and University of Zürich, Genomics Facility Basel run by ETH Zürich and University of Basel).

Processed sequencing data are shared openly within 14 days from positive PCR result through the GISAID platform (https://www.gisaid.org) and eventually through the Swiss Pathogen Surveillance Platform (SPSP). The centralized analysis of this National Surveillance will be performed by the groups of Pr. Neher, Pr. Stadler and Dr. Althaus, where variants of concern are counted, analyzed and all sequences scanned for new variants with potential changes in antibody-Spike interactions (https://nextstrain.org/groups/swiss, https://covariants.org/per-country, https://cov-spectrum.ethz.ch). This work is done in close collaboration with the Swiss National COVID-19 Science Task Force and the Swiss Institute of Bioinformatics (SIB).

In order to complement the genomic surveillance based on patient samples, sequencing of SARS-CoV-2 in wastewater samples is also performed, initially funded for 6 months. Samples are collected daily in six wastewater treatment plants (WWTP), under the coordination of Eawag. Up to 50 samples per week over the first 26 weeks have been performed. The sequencing and analysis of these samples, including detection of variants, is done under the coordination of Prof Niko Beerenwinkel. It started in December 2020 for Lausanne and Zurich, and in February 2021 for all six WWTP (https://bsse.ethz.ch/cbg/research/computational-virology/sarscov2-variants-wastewater-surveillance.html). The analysis of wastewater samples is envisaged to run until the end of the surveillance program on 31.3.2022.

Immunological characterization of the variants within the surveillance program is coordinated by Professor Trono's team at EPFL.

This report has been produced by Marc Friedli, Pauline Vetter, Samuel Cordey, Erik Boehm, Richard Neher, Christian Althaus, Martina Reichmuth, Cornelius Römer, Niko Beerenwinkel, Chaoran Chen, Tanja Stadler, Priscilla Turelli, Didier Trono, Emma Hodcroft, Nadja Wipf, Damir Perisa, and Laurent Kaiser. The list of the participants and collaborators of the program can be found at the end of this report in the appendix.

This report covers the period of August 2 to August 29 (weeks 31, 32, 33, 34). All data presented in this report are based on the sampling date.

3. Variants of concern (VOCs), variant of interest (VOI) and other surveilled variants: brief summary and special focus

Currently, 4 variants are considered VOCs by the WHO, B.1.1.7 (VOC Alpha), B.1.351 (VOC Beta), P.1 (VOC Gamma), and B.1.617.2 (VOC Delta). Of note, while still a VOC for WHO, the European Centre for Disease Prevention and Control de-escalated Alpha as a VOC.

Similarly only 2 variants are still considered variants of interest by WHO: the C.37 (Lambda) variant first identified in Peru, and the B.1.621 (Mu) variant, first identified in Colombia.

For most purposes, given Delta's dominance, only new lineages that can displace it are of practical concern. There is currently no data indicating that those 2 VOIs may outcompete Delta.

New Spike mutations have been spotted across various Delta sub lineages, which deserve mention:

- Y145H: This mutation recently emerged in a sub lineage of AY.4 together with A222V. Position 145 is in the NTD next to the prominent deletion 144 in VoC Alpha. This position is mutated to `N` in VOI Mu (21H). Within Delta, this mutation has increased in frequency in the UK, now above 5%. It was previously observed sporadically across Europe. The UK data is compatible with a growth advantage of approximately 10%. Outside the UK, growth signals for this mutations are mixed. Notably, this mutations was also observed sporadically in Alpha but never spread.
- A222V: The mutation SA222V was a characteristic mutation of B.1.177 (EU1). It has appeared multiple times independently in Delta, see: https://nextstrain.org/groups/neherlab/ncov/europe?c=gt-S_222&f_region=Europe&label=clade:21A%20%28Delta%29. It is part of one large clade branching off at the base of Delta that has been circulating since May. Recently, it appeared together with Y145N in a sub lineage of AY.4 (see above). In EU1, A222V did not appear to have a major effect on spike conformation as assessed by binding assays with monoclonal antibodies or pseudo-typed virus titers. It has, however, appeared repeatedly in larger clades and might convey a slight advantage or have a stabilizing/permissive effect.
- K417N: Mutation K417N has arisen independently within lineages AY.1 and AY.2, but both of these lineages are rare and have not been observed lately. While not currently a concern, position 417 is mutated in VOCs Beta (to `N`) and Gamma (to `T`) and has been associated with a reduction in neutralization in some subjects.
- Q613H: Has arisen at least several times independently with Delta, including twice within the AY.33 sub-lineage. It is most prevalent and increasing in Canada, but has decreased in prevalence in Europe in recent weeks. Growth signals that were initially present in the data have weakened and it is hence unclear whether it has a consistent growth advantage across countries. Notably, it is adjacent to the D614G mutation that became dominant early in the pandemic.

Vaccines effectiveness:
Protection against severe disease has been shown to be remain high against all VOCs. However, reduced protection against symptomatic disease and infection has been observed against Beta and Delta. A review of the last evidence processed by WHO concluded to the "evidence that vaccine effectiveness of mRNA vaccines against severe disease outcomes due to Delta is high, with evidence of no-to-minimal waning for these severe outcomes to date" *https://www.who.int/publications/m/item/weekly-epidemiological-update-on-covid-19---21-september-2021*); while recent studies have suggested that the Moderna vaccine might be more effective against Delta infections than the Pfizer vaccine (to be interpreted with caution because of numerous potential biases).

Transmissibility
Delta appears to be the most transmissible variant detected so far, and has largely displaced all other variants, although Mu and Lambda still retain a strong presence in some South American countries. Viral titers for Delta appear to be higher. As Delta has demonstrated some immune escape, it is unclear how much this explains its current transmissibility advantage. Of note, transmissibility in vaccinated populations is greatly reduced (see report of the month of June).

Impact on diagnostic tests
Nucleic acid detection may be affected by mutations in the RNA sequence of target regions. S-gene dropout, as seen with variant Alpha, is an example of this. Another significant example is the lower sensitivity of the Genexpert® (Cepheid) for the N2 target for the Delta variant (*https://www.fda.gov/medical-devices/coronavirus-covid-19-and-medical-devices/sars-cov-2-viral-mutations-impact-covid-19-tests*). However, as RT-PCR tests use multiple targets, those mutations have not been reported yet to cause diagnostic failure.

Rapid antigen tests, theoretically may be affected by amino acid mutations in the N protein. However, diagnostic efficacy of antigenic tests appears to be relatively unaffected thus far (*Bekliz et al. Lancet Microbe. 2021*). As the potential exists, this will continue to be monitored.

Considering potential transmissibility, immune escape, and diagnostic issues, the variants presented below will be particularly surveilled:

- variants classified as VOCs by the WHO: B.1.1.7 (Alpha), B.1.351 (Beta), P.1 (Gamma), B.1.617.2 (Delta) – and their sub-lineages
- new variants (until sufficient monitoring suggests they do not have a replicative/escape advantage) that include E484K + N501Y: higher transmissibility, immune escape risk, resistance to mAbs, such as B.1.621 (Mu).
- variants with E484K alone due to immune escape risk and resistance to mAbs, such as B.1.620.
- variants that include L452R: increased transmissibility, resistance to mAbs, such as: B.1.617.2 (Delta) and C.37 (Lambda)

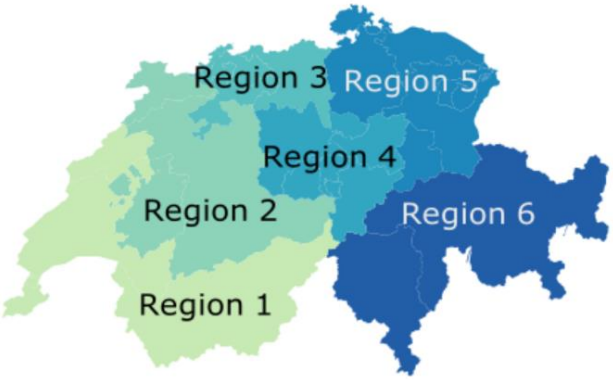
4. Epidemiology in Switzerland and number and origin of sequences produced through the program during the surveilled period

Data in this report comes from 3 sources: 1) The publicly available data on COVID-19 as reported by the FOPH (https://www.covid19.admin.ch), including data that is declared to the FOPH by the different laboratories in Switzerland; 2) data originating from laboratories participating in the surveillance program; and 3) sequences submitted to GISAID, for which the corresponding infected person was in Switzerland (resident or recent travel history to Switzerland).

General caveat: the numbers and denominators are fluid and variable over time; and are subject to change depending notably on the different databases used, and variable declaration delays. All data generated by this program is also submitted to SPSP.

The number and origin of sequences submitted to GISAID by each laboratory during January and February, 2021, prior to the start of the surveillance program can be found in the first report covering the months of March and April 2021.

Data will be presented here by regions, using the same region definitions that are used for the influenza sentinel surveillance system in Switzerland. Data are presented according to residency post-code.



Region 1 includes the cantons of Geneva, Neuchatel, Vaud and Wallis

Region 2 includes the cantons of Bern, Fribourg and Jura

Region 3 includes the cantons of Aargau, Basel (Basel-Stadt and Basel-Land) and Solothurn

Region 4 includes the cantons of Luzern, Unterwalden (Obwalden and Niedwalden), Schwitz, Uri and Zug

Region 5 includes the cantons of Appenzell (Appenzell Ausserrhoden and Appenzell Innerrhoden), Glarus, Sankt Gallen, Schaffhausen, Thurgau and Zurich.

Region 6 includes the cantons of Graubünden and Ticino.

Divisions of the different regions, from https://covariants.org/per-country

Number of cases processed by the laboratories participating in the surveillance program

During the period covered by the present report, the FOPH reported a total of over 64,000 confirmed SARS-CoV-2 cases in Switzerland, indicating a substantial rise in the number of infections. Supplementary Table 1 provides an overview of the number and incidence of confirmed cases, the effective reproduction number R_e, the number and incidence of tests, test positivity, the number and proportion of sequenced samples, and the number and proportion of VOCs by canton, region and for Switzerland overall.

The laboratories participating in this program reported 25,534 positive tests during the surveilled program, which represents about 39.5% of the total number of cases reported in Switzerland (including both PCR and antigen-based tests). Detailed data regarding the total number of tests performed each week by the laboratories participating in the surveillance program (including negative and positive tests numbers, and the number of the positive tests that have been sequenced) are available in appendix Table 3. Of note, antigen-based tests are by definition excluded from the surveillance, which applies only to PCR tests (although antigen positive cases may be asked to be re-tested by RT-PCR).

Number of SARS-CoV-2 sequences produced through the surveillance program

A total number of 10,583 SARS-CoV-2 sequences have been submitted to GISAID during this period. This represents around 16.4% of all cases detected in Switzerland during the surveilled period (see Supplementary Table 2 and 3 in Appendix for details). Of note, this number includes sequences from samples received from other laboratories in order to ensure sequencing of post-vaccination infections.

Table 1 shows the number of sequences successfully submitted to GISAID through the surveillance program during the surveilled period by calendar week.

Week	Date	Number of sequences successfully submitted to GISAID
31	Aug 2 to Aug 8	2428
32	Aug 9 to Aug 15	3174
33	Aug 16 to Aug 22	3116
34	Aug 23 to Aug 29	1866
	Total	10583

Table 1: number of sequences submitted to GISAID through the surveillance program

The total number of SARS-CoV-2 sequences submitted to GISAID by each laboratory during the month of August is available in Supplementary Table 3 in the appendix.

Covering of sequencing in Switzerland and contribution of the national SARS-CoV-2 surveillance sequencing program

As shown in Figure 1, the total number of SARS-CoV-2 sequences submitted per week progressively increased during the month of August (weeks 31 to 34), reflecting the increase in cases within Switzerland. Almost all of the sequences available in GISAID (green curve) and those on which the surveillance is conducted, come from the national surveillance program.

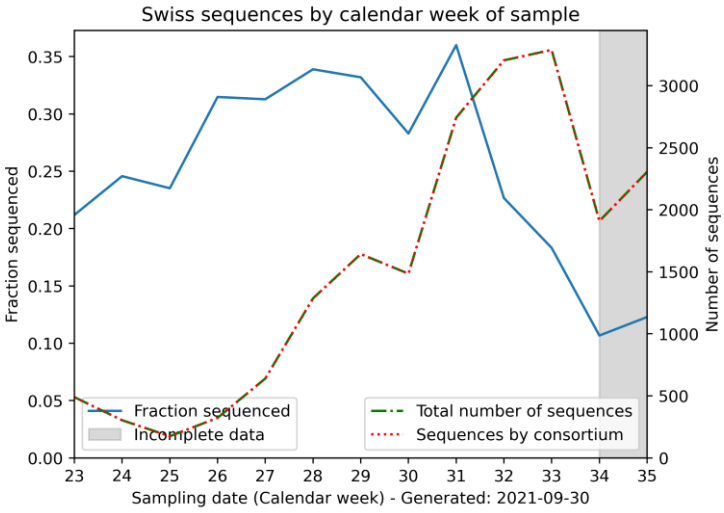


Figure 1: Number of SARS-CoV-2 sequences available for Switzerland (total available Swiss sequences in GISAID in green, Swiss sequences submitted through the program in dotted orange) and fraction of the total number of positive cases declared to the FOPH that have been sequenced (blue curve). The grey indicates an incomplete data period.

During the surveilled period, the total proportion of positive sequenced cases was on average around 16%, largely above the aim of the program. The drop in week 34 was probably due to a low submission rate from region 3 labs and/or GISAID submission delays. Submission delays are identified and are currently being monitored to ensure timely share of sequences.

Figure 2 displays the number and fraction of SARS-CoV-2 cases sequenced for each Swiss region. Regions 4 and 6 continued to have the lowest total number of sequences and the lowest fraction of cases sequenced, however, the regional fractions of sequenced cases were all above the 10% overall goal.

Figure 3 shows the sequencing coverage among the different Swiss cantons over the last 3 months, presented by fraction of cases sequenced relative to the total number of reported cases in the canton.

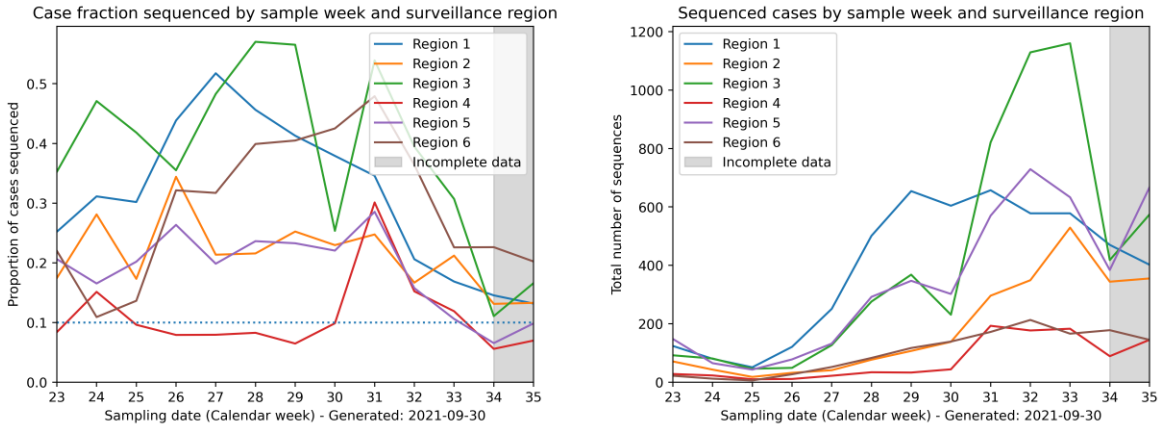


Figure 2: Sequencing coverage among the different Swiss regions per week, presented by fraction of cases sequenced (left) and by number of sequences (right). The grey indicates an incomplete data period.

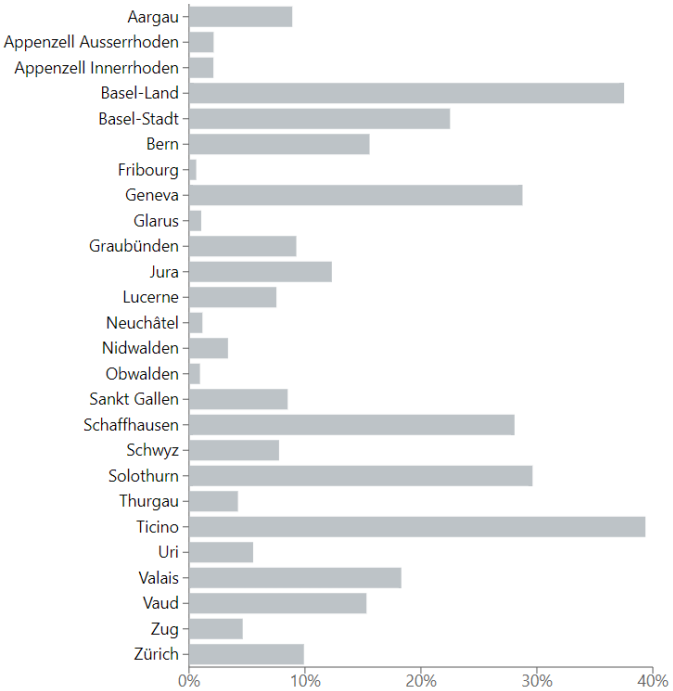


Figure 3: Sequencing coverage among the different Swiss cantons over the last 3 months, presented by fraction of cases sequenced. Screenshot form CoVspectrum website. Online dynamic navigation is available at https://cov-spectrum.ethz.ch/explore/Switzerland/AllSamples/Past3M/sequencing-coverage

5. Variants circulating in Switzerland since January 2021, with a focus on the surveilled period

Determination of the proportion of total number of sequences over time falling into defined variant groups is done by Emma Hodcroft's team and displayed on the CoVariant website (https://covariants.org/per-country). Those results are based on the total number of sequences submitted to GISAID over the time period for Switzerland. Those data mainly, but not exclusively, come from the national genomic surveillance program since its beginning (see Figure 1).

The B.1.617.2 Delta variant (in green in Figure 4) was almost exclusively retrieved during the month of August all over Switzerland, accounting for around 99% of the submitted sequences (see Figures 5 and 6). See Table 2 below for the number of the main VOCs/VOIs by region. Neither Mu neither Lambda seem to be able to outcompete Delta in countries where they were circulating. Mu was rarely retrieved in Switzerland during the month of August, while Lamba was not retrieved at all (table 2).

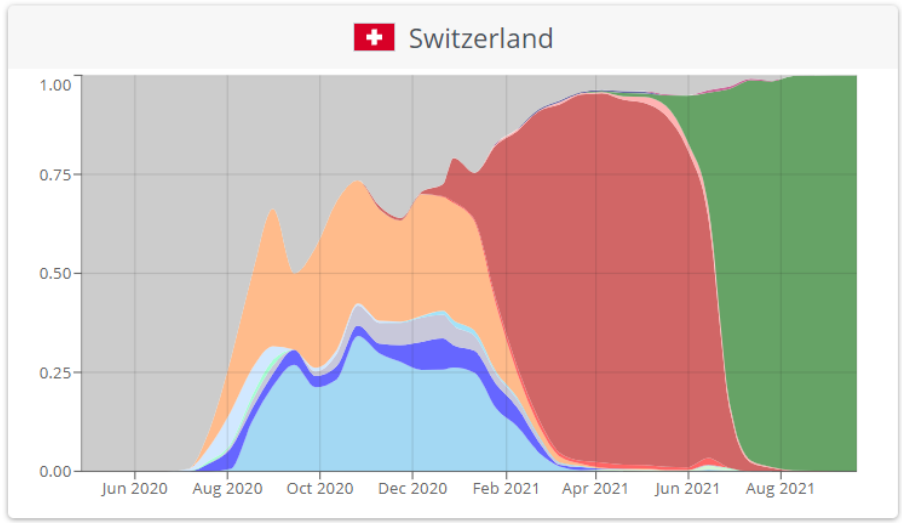
Region	Alpha	Beta	Delta	Gamma	Mu	others	sequences	cases	% sequenced
All	27	2	13258	4	2	155	13448	76335	0.176
1	6	0	2659	0	0	20	2685	14418	0.186
2	4	0	1844	1	0	24	1873	11078	0.169
3	9	2	4014	0	0	77	4102	15399	0.266
4	3	0	776	1	0	7	787	7017	0.112
5	4	0	2959	1	1	18	2983	25240	0.118
6	1	0	862	1	1	9	874	3183	0.275

Table 2: number of sequences corresponding to selected variants in each region of Switzerland during the month of August 2021.

AY* lineages (Delta sublineages) are very new, and their definitions are still in flux, we chose not to elaborate on their proportion within the country at this time. Indeed, any changes in prevalence should be considered very carefully, as the definition of those sublineages are not clearly assigned.

A summary of the main new Spike mutations spotted across various Delta sub-lineages is available in section 3 of this report, describing the main VOC/VOIs.

An estimate of the total number of VOCs circulating in Switzerland, corrected by taking in account the 12.5 % fraction of sequencing in Switzerland is available through the covSPECTRUM program developed at ETHZ at https://cov-spectrum.ethz.ch/explore/Switzerland.



Nextstrain Clade	Pango Lineage	WHO name
20I/501Y.V1	B.1.1.7	Alpha
20H/501Y.V2	B.1.351	Beta
20J/501Y.V3	P.1	Gamma
21A/S:478K	B.1.617.2	Delta
20C/S.452R	B.1.427/B.1.429	Epsilon
20A/S: 484K	B.1.525	Eta
20C/S: 484K	B.1.526	Iota
21A/S: 154K	B.1.617.1	Kappa
21G	C.37	Lambda
20A/S:439K	B.1.258	
20A/S:98F	B.1.221	
20E (EU1)	B.1.177	
20A.EU2	B.1.160	
21H	B.1.621	

Figure 4: proportion of total number of sequences (not cases), over time, that fall into defined variant groups, for Switzerland. Screenshot from CoVariant website. Dynamic navigation is available at https://covariants.org/per-country. Dark green indicates lineage B.1.617.2 (Delta). Note the rapid increase in prevalence and rise to dominance. Dark Red indicates B.1.1.7 (Alpha), the previously dominant lineage in Switzerland.

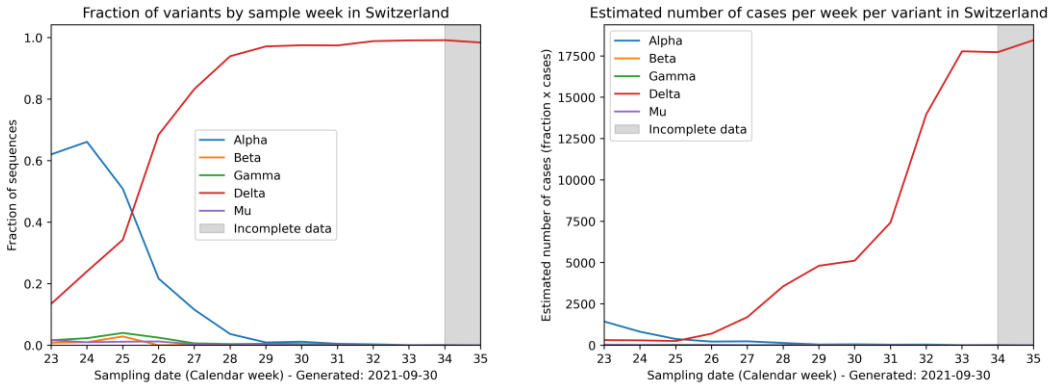


Figure 5: (Left): Percentage of circulating VOCs and VOIs in Switzerland by week, over the 35 first weeks of 2021 (total number of B.1.1.7 (Alpha), B.1.351 (Beta), P.1 (Gamma), B.1.617.2 (Delta) and B.1.1.318 (AZ) sequences from Switzerland and successfully submitted to GISAID are shown here). The grey indicates an incomplete data period. (Right): Estimated number of sequences of the main VOCs/VOIs and variants under monitoring retrieved during the surveilled period. The grey indicates an incomplete data period.*

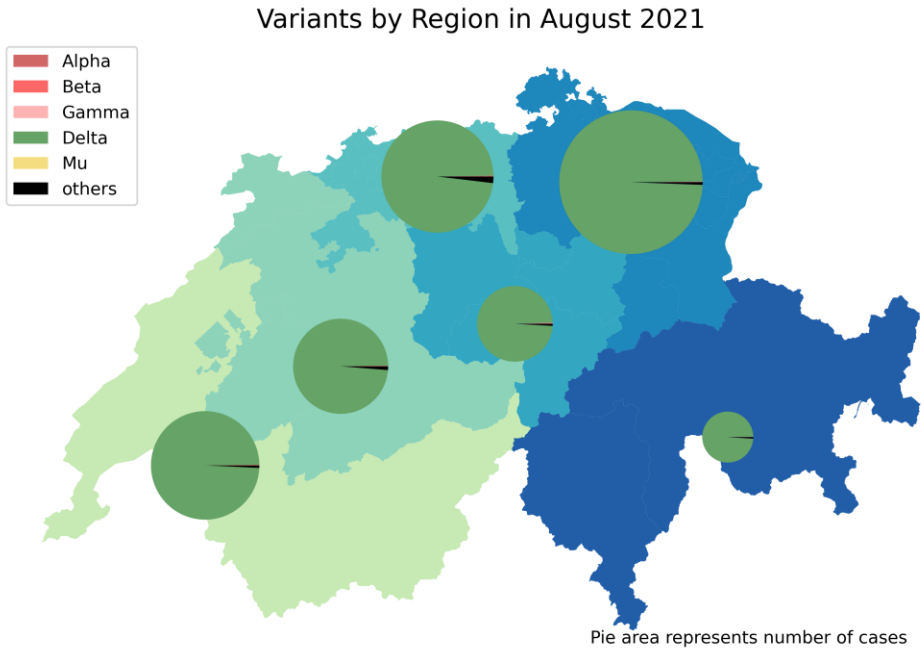


Figure 6: Distribution of variants per region, for August 2021, shown on a map. The total number of sequences in that month, in the region, is shown in parentheses next to each region name. The size of the pie chart corresponds to the total number of sequences. Note the dominance of Delta in all regions.

6. Assessment of the competition between the different variants in Switzerland

The competition between different SARS-CoV-2 variants can be modelled using multinomial logistic regression. The analysis by Dr. Althaus' group is based on sequences retrieved from CovSPECTRUM. The results confirmed that Delta remains the only dominant SARS-CoV-2 variant in Switzerland in August 2021.

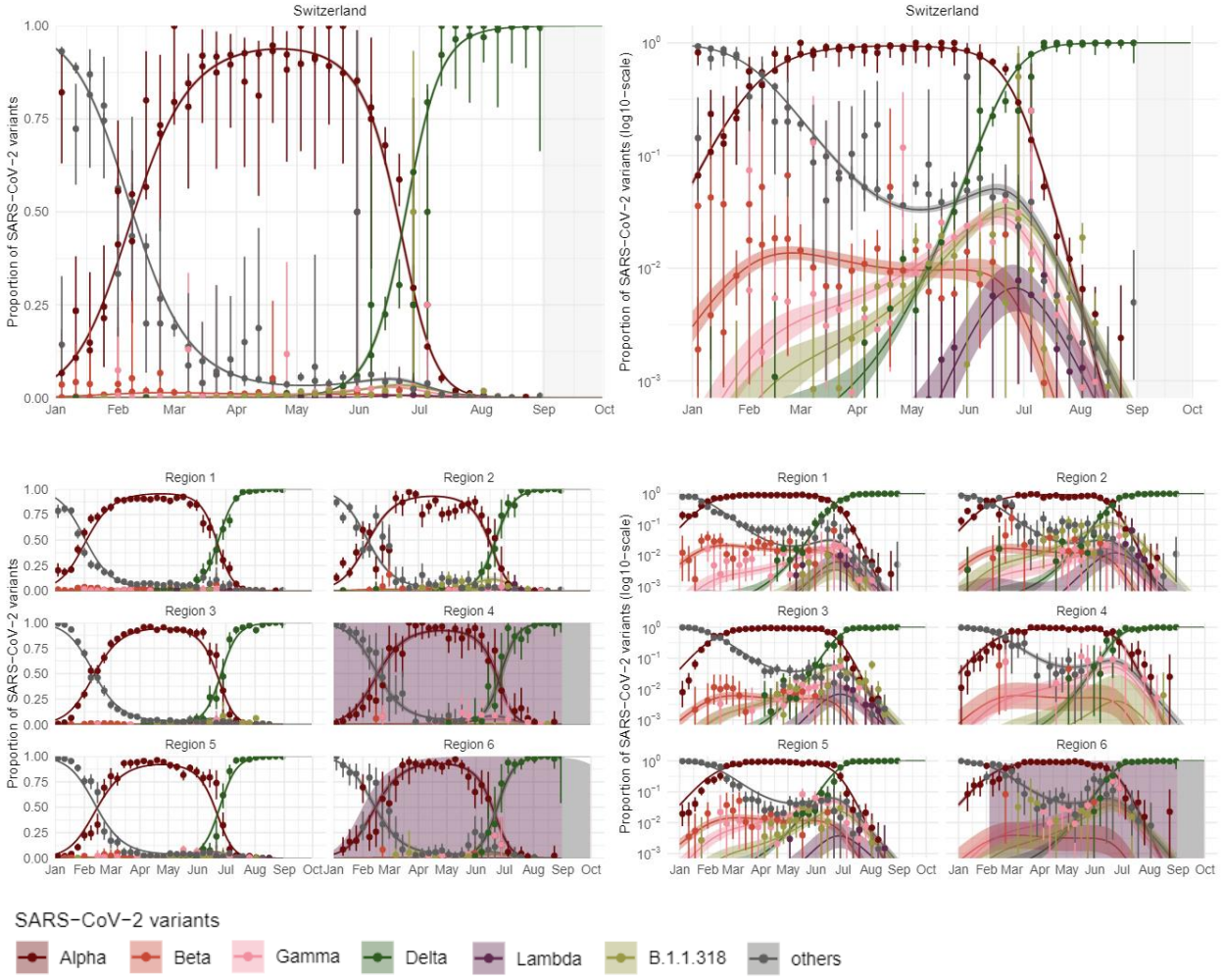


Figure 7: Observed and modeled proportion of SARS-CoV-2 variants over time in Switzerland. In April and May 2021, Gamma and Delta started to replace Alpha, with Delta now outcompeting all other variants. At the end of August, more than 95% of the retrieved sequences in Switzerland were due to Delta. No new variants appear to be displacing Delta. Model fits are based on a multinomial logistic regression with splines.

7. Wastewater surveillance program

Since February, an increased prevalence of the B.1.1.7 (Alpha) variant has been observed over time in all of the six wastewater treatment plants (WWTPs) that are tested on a daily basis. The B.1.617.2 (Delta) variant started to appear around the beginning of June in all WWTPs. By the end of July it had reached the highest levels in all catchment areas of the respective WWTPs. Notably, detection of variants in wastewater can be challenging if the prevalence is low due to low RNA concentrations, as was the case in June and July. In this situation, it is especially difficult to distinguish related lineages that share variant-defining mutations. This is the case, for example, among the sub-clades of B.1.617*. During the month of August, the dominance of B.1.617.2 (Delta) was obvious in all surveyed WWTPs.

Figure 8: Prevalence of variants of SARS-CoV-2 estimated from wastewater samples collected daily until August 31 or later (except Lausanne: July 31) in WWTPs located in 7 different Swiss cantons. B.1.617.2 (Delta) is represented in in dark green, B.1.617.1 in light green (Kappa), B.1.617.3 in purple, B.1.1.7 (Alpha) in dark red, B.1.351 (Beta) in light red, P.1 (Gamma) in pink. From the website of ETH Zürich. Online dynamic navigation available at https://bsse.ethz.ch/cbg/research/computational-virology/sarscov2-variants-wastewater-surveillance.html.

Data from the Canton of Zurich are presented here, although this data comes from a separate effort and is not part of the national surveillance program.

8. Immunological characterization of variants

A basic immunological characterization effort is part of the Swiss national SARS-CoV-2 genomic and the variants surveillance program. This characterization involves testing viral Spike variations (i.e. significant sequence deviation in spike-coding region) for their sensitivity to neutralization by sera from previously infected or vaccinated individuals and by therapeutic / preventive monoclonal antibodies, some already FDA approved and some in development. For this, their spike proteins (the target of neutralizing antibodies) are synthesized based on its sequence and analyzed in neutralization assays. Of note, cell-free surrogate neutralization assays also provide semi-quantitative information on the relative affinity of each spike variants for the ACE2 viral receptor, which likely plays an important role in viral infectivity and transmission.

In the month of August, Spike proteins harboring either the full combination of mutations found in VOCs Alpha, Beta, Gamma and Delta, in the Lambda VOI, and in variants under monitoring (VUM) Eta, Kappa and Epsilon, or Spike proteins harboring one of each of the mutations found in the Delta VOC have been produced. The purified Spike variants have been used in the S^3-ACE2 neutralization assay to monitor the neutralization potential of 2 FDA-approved Regeneron® antibodies (RGN10933 casirivimab and RGN10987 imdevimab) as well as 3 in house developed monoclonal antibodies (P5C3-LS, mAb2 and mAb3). A substantial decrease in neutralization is observed for the Spikes of the Beta, Delta and, to a lesser extent, Gamma VOCs. Meanwhile only a modest variability in neutralization is observed for the Spike proteins of all other tested VOCs, VOIs or VUMs. This agrees with results previously obtained in the live virus-based assay and results published in the literature with convalescent serum. In the case of the Delta variant, the L452R mutation alone seems to be the major determinant of the neutralization escape.

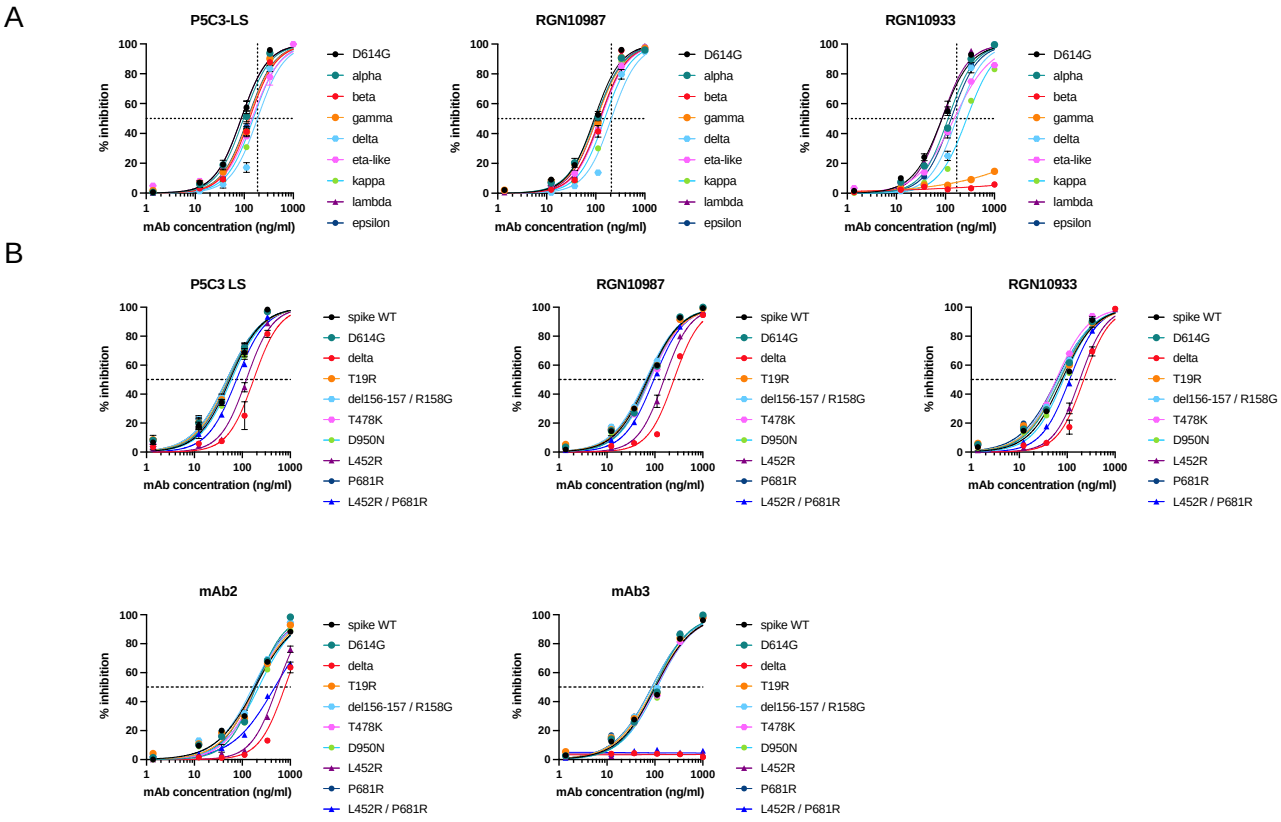


Figure 9: The neutralization potential of individual monoclonal antibodies varies with Spike mutants. Indicated Spike variants (A) or Spikes with each of the mutations found on the Delta VOC (B) were used to test the neutralization potential of REGEN-CoV-2 (RGN10987 and RGN10933) and in house developed monoclonal antibodies (P5C3-LS, mAb2 and mAb3) with the S^3-ACE2 *neutralization assay.*

Conclusion

In August, over 10,000 sequences were obtained through this surveillance program. Each week since this surveillance program started, it has contributed almost all of the Swiss SARS-CoV-2 sequences available on GISAID. In August, around 16% of the cases reported in Switzerland were sequenced, down from the month before. This reflects an increase in case numbers as well as a decrease in sequences. Region 4 and 6 are still the least represented geographical areas.

It continues to be nearly exclusively B.1.617.2 (Delta) variant (and its sub lineages) that circulate, with a relatively homogenous representation over the different Swiss regions, accounting for around 99% of the sequences identified in August. Numerous sub-lineages are increasingly detected, with no particular significance identified for any particular sub lineage so far. Despite this, there are four new spike mutations identified across these sub lineages, which have independently arisen multiple times and may confer slight advantages. Of note, the sub lineage definition and characterization are still ongoing, and any reported prevalence changes should therefore be considered carefully.

No additional diagnostic issues were noted for any variant in August.

All other variants were only rarely detected, both in clinical samples and in the wastewater surveillance part of the program:

- B.1.351 (Beta) was only detected twice in August.
- P.1 (Gamma) was only detected 5 times in August.
- The B.1.621 variant, (considered a VOI), was only detected once in August.
- B.1.1.318, circulation sharply decreased after week 31, with only 6 cases in weeks 32&33.
- C.37 (Lambda), another VOI, was not detected in August.

No important geographical breakdown of a particular variant has been noticed.

An estimate of the total number of VOCs circulating in Switzerland, corrected by taking in account the fraction of sequencing in Switzerland is available at https://cov-spectrum.ethz.ch/explore/Switzerland.

As the number of cases of SARS-CoV-2 increases due to the Delta variant, and as Delta diversifies, an effort will be made to identify any concerning sub-lineages. Furthermore, an effort will be made to add more laboratories to the program in order to maintain representative sequencing throughout the country.

This resurgence in the number of new COVID-19 cases raises concerns regarding a new wave of hospitalization especially in unvaccinated population. Vaccination keeps a high effectiveness against severe disease due to the Delta variant and should be promoted.

Acknowledgements:

https://bsse.ethz.ch/cevo/research/sars-cov-2/swiss-sars-cov-2-sequencing-consortium.html

Marc Friedli, Pauline Vetter, Samuel Cordey, Erik Boehm, Richard Neher, Christian Althaus, Emma Hodcroft, Tanja Stadler, Philippe Lemercier, Ioannis Xenarios, Lorenzo Cerutti, Louis Du Plessis, Nadja Wipf, Damir Perisa, Laurent Kaiser, for the Swiss national SARS-CoV-2 genomic and variants surveillance program coordination committee.

Appendix :

SARS-CoV-2 epidemiology in Switzerland:

We used publicly available data on COVID-19 as reported by FOPH (https://www.covid19.admin.ch) and sequence data submitted to GISAID to provide a summary of the SARS-CoV-2 epidemiology in Switzerland.

sup_table_overview_Aug.xlsx

Supplementary Table 1: Epidemiological data for Switzerland, its regions and cantons in August 2021: population, number and incidence of confirmed cases, effective reproduction number R_e, number and incidence of tests, test positivity, number and proportion of sequenced samples, and number and proportion of VOCs. R_e by region is represented as the median and range of the daily R_e values for all cantons within a region.

week	date	Total PCR tests	Positive tests	Sequenced	% positives	% positives sequenced
31	Aug 2 to Aug 8	44 998	3 824	2428	8.50%	63.49%
32	Aug 9 to Aug 15	49 553	6 175	3174	12.46%	51.40%
33	Aug 16 to Aug 22	56 607	7 737	3116	13.67%	40.27%
34	Aug 23 to Aug 29	63 235	7 799	1866	12.33%	23.92%
	Total	214 394	25 534	10 583	11.91%	41.45%

Supplementary Table 2: Total number of tests performed by the laboratories participating in the surveillance program from July 5 to August 1, 2021.

Week	Date	Basic Surveillance							Augmented Surveillance						Sentinella Laboratories		
		EOC	St-Gallen	Labor Team W *	Risch	SRO	Synlab	Biolytix *	UBS	IFIK	Diana labs GE	CHUV	UZH	ICH-VS	HUG	ETH/ Viollier	All
31	Aug 2 to Aug 8	97	42	186	ND.	22	15	21	192	52	88	79	125	74	242	1034	2118
32	Aug 9 to Aug 15	90	44	186	ND.	43	44		222	52	127	50	187	91	237	1391	2565
33	Aug 16 to Aug 22	79	48	186	ND.	37	37		120	37	78	47	205	89	276	1578	2575
34	Aug 23 to Aug 29	92	48	186	ND.	70	70	46	125	118	84	66	138	91	254	372	1461
	Total	358	182	744	0	172	137	67	659	259	377	242	655	345	1009	4375	9581

*Supplementary Table 3: number of sequences submitted to GISAID by each laboratory during the surveilled period (August 2 to August 29, 2021). *including sequencing sent to high-throughput platforms ND. = No data/ missing data.*

Contact list as of 28.6.21 :

Coordination committee mailing list	
Name	e-mail address
Laurent Kaiser	Laurent.Kaiser@hcuge.ch
Samuel Cordey	Samuel.Cordey@hcuge.ch
Marc Friedli	marc.friedli@epfl.ch
Richard Neher	richard.neher@unibas.ch
Tanja Stadler	tanja.stadler@bsse.ethz.ch
Emma Hodcroft	emma.hodcroft@ispm.unibe.ch
Christian Althaus	christian.althaus@ispm.unibe.ch
Ioannis Xenarios	ioannis.xenarios@unil.ch
Philippe Le Mercier	Philippe.Lemercier@sib.swiss
Pauline Vetter	Pauline.Vetter@hcuge.ch
Erik Boehm	Erik.Boehm@hcuge.ch
Lorenzo Cerutti	lorenzo.cerutti@health2030.ch
Damir Perisa	Damir.Perisa@bag.admin.ch
Nadja Wipf	Nadja.wipf@bag.admin.ch

Laboratories mailing list		
Laboratory	Name	e-mail address
HUG	Laurent Kaiser	Laurent.Kaiser@hcuge.ch
HUG	Samuel Cordey	Samuel.Cordey@hcuge.ch
HUG	Pauline Vetter	Pauline.Vetter@hcuge.ch
HUG	Erik Boehm	Erik.Boehm@hcuge.ch
CHUV	Gilbert Greub	Gilbert.Greub@chuv.ch
CHUV	Claire Bertelli	Claire.Bertelli@chuv.ch
Universtätsspital Basel	Adrian Egli	Adrian.Egli@usb.ch
Universtätsspital Basel	Tim Roloff	Tim.Roloff@usb.ch
IFIK UNIBE	Alban Ramette	alban.ramette@ifik.unibe.ch
UZH	Alexandra Trkola	trkola.alexandra@virology.uzh.ch
UZH	Michael Huber	huber.michael@virology.uzh.ch
EOC Bellinzona	Gladys Martinetti Luchini	Gladys.MartinettiLucchini@eoc.ch
Zlsmg St-Gallen	Oliver Nolte	Oliver.Nolte@zlmsg.ch
Zlsmg St-Gallen	Yannick Gerth	Yannick.Gerth@zlmsg.ch
Viollier laboratories	Tanja Stadler	tanja.stadler@bsse.ethz.ch
Viollier laboratories	Christiane Beckmann	christiane.beckmann@viollier.ch
Viollier laboratories	Henriette Kurth	Henriette.Kurth@viollier.ch
Hopitaux du Valais	Alexis Dumoulin	Alexis.Dumoulin@hopitalvs.ch
Dianalabs	Nadia Liassine	Nadia.liassine@dianalabs.ch
Dianalabs	Katia Jaton	Katia.jaton@dianalabs.ch
Dianalabs	Géraldine Jost	Geraldine.jost@dianalabs.ch
Dianalabs (Genesupport)	Tanguy Araud	Tanguy.araud@genesupport.ch
labor team w ag	Andreas Lindauer	andreas.lindauer@team-w.ch
Synlab CH-I	Etleva Lleshi	Etleva.Lleshi@synlab.com
Spital Region Oberaargau	Alexander Imhof	a.imhof@sro.ch
Laboratory Risch	Nadia Wohlwend	nadia.wohlwend@risch.ch

BAG mailing list:	
Name	e-mail address
Damir Perisa	Damir.Perisa@bag.admin.ch
Katrin Schneider	katrin.schneider@bag.admin.ch
Martine Bourqui	Martine.Bourqui@bag.admin.ch
Fosca Gattoni	Fosca.Gattoni-Losey@bag.admin.ch
Ulrich Kihm	Ulrich.Kihm@bag.admin.ch
Natalia Krempaska	natalia.krempaska@bag.admin.ch
Selina Schwegler	Selina.schwegler@bag.admin.ch
Michael Bel	Michael.Bel@bag.admin.ch
Mirjam Mäusezahl	Mirjam.Mäusezahl@bag.admin.ch
Oliver Caliaro	oliver.caliaro@bag.admin.ch
Tobias Schuster	tobias.schuster@bag.admin.ch
Nadja Wipf	Nadja.wipf@bag.admin.ch

Sequencing centers:		
Center	Name	e-mail address
Health 2030 Genome Center	Keith Harshman	keith.harshman@health2030.ch
Health 2030 Genome Center	Ioannis Xenarios	ioannis.xenarios@health2030.ch
Genomics Facility Basel-ETH Zurich	Christian Beisel	christian.beisel@bsse.ethz.ch
The Functional Genomics Center Zurich (FGCZ)- ETHZ and UZH	Ralph Schlapbach	ralph.schlapbach@fgcz.ethz.ch

Wastewater surveillance program mailing list:	
Name	e-mail address
Niko Beerenwinkel	niko.beerenwinkel@bsse.ethz.ch

Immunological characterization program of the variant mailing list:	
Name	e-mail address
Priscilla Turelli	priscilla.turelli@epfl.ch
Didier Trono	didier.trono@epfl.ch