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 28, 2021

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

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 14.2% of the total number of cases identified in Switzerland were sequenced by the Surveillance program, yielding over 9486 sequences in September.

In September, COVID-19 cases numbers decreased in Switzerland, and were due almost exclusively to the B.1.617.2 (Delta) variant or its sub-lineages.

Circulation of all other variants has essentially stopped, with only around 10 sequenced samples, out of approximately 9000, that were not Delta (99.9% Delta); among these, B.1.1.318 was identified during week 35 but not afterwards.

Mutations can accumulate in the Delta background, and a large variety of sub-lineages have already been observed, although there is not much data available regarding any additional relevant properties. One Delta sub-lineage called AY.4.2 has recently been identified as a *Variant Under Monitoring* by both the ECDC and Public Health England, because of a preliminary observation of an increased growth rate in the UK compared to Delta. This variant was rarely identified during the month of September in Switzerland: among 9486 sequences retrieved during the surveilled period, 38 were AY 4.2.

No important geographical breakdown of a particular sub-lineage has been noticed.

Unsurprisingly, B.1.617.2 (Delta or its sub-lineages) was also the most frequent variant detected in wastewater during the month of September.

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 including Dianalabs, Polyanalytic, Dianalabs Valais, Proxilab and Bioanalytica ; Biolytix; Synlab Bioggio (TI); Labor Team W, Risch), cantonal-based laboratories (Hôpital du Valais – Institut Central), 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 30 to October 3 (weeks 35, 36, 37, 38, 39). 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

4 variants and their sub-lineages are currently considered VOCs by the WHO, B.1.1.7 (Alpha), B.1.351 (Beta), P.1 (Gamma), and B.1.617.2 (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.

One Delta sub-lineage, named AY.4.2, has recently been designated as a *Variant Under Monitoring* by both the ECDC and Public Health England, because of a slowly increasing proportion of cases in various countries like the UK, although its spread outside UK is less consistent. Its estimated transmission advantage in the UK is between 10 and 15%, although this is less clear in other countries where the sub-variant is less frequent, due to a small dataset. It is too soon however to conclude that this indicates that this sub-lineage is intrinsicly more transmissibile, or that there is increased spread caused by behavioral events. Within the UK, no difference in hospitalization rate or severity has been noted.

During the meeting of the Swiss Surveillance Coordination meeting, the Health 2030 Genome Center highlighted a potential issue in a genomic region of the SARS-CoV-2, which may lead to a misclassification of Delta AY* sub-lineages. This led to the sharing of this issue on virological.org (https://virological.org/t/missing-g21987a-mutation-in-sars-cov-2-delta-variants-due-to-non-specific-amplification-by-artic-v3-primers/764). Of note, characteristics mutations of the AY 4.2 mutations are located outside of the amplification primer, and this issue should not affect the identification of AY 4.2.

In addition to the typical Delta mutations in the spike protein, AY.4.2 contains the mutations Y145H and A222V. The Y145H mutation was also observed sporadically in Alpha but never spread. In EU1, A222V did not appear to have a major effect as assessed by monoclonal antibody binding or pseudo-typed virus titers. It appeared repeatedly in larger clades and might convey a slight advantage or have a stabilizing/permissive effect. Both mutations are in the N-terminal region, which is the second most dominant antigenic epitope after the RBD. No data suggests that they affect neutralization of this strain. However, more data are needed, and more information will follow. Finally, AY.4.2 carries a third additional substitution on the ORF1ab gene (A2529V), which is also present in other variants.

Other spike mutations spotted across various Delta sub lineages include:

- K417N: This mutation arose independently within lineages AY.1 and AY.2, but these lineages have decreased in frequency since their first identification. Notably, position 417 is mutated in VOCs Beta (to amino acid `N`) and Gamma (to `T`) and has been associated with reduced neutralization in some subjects.
- Q613H: This mutation arose independently several times in Delta. 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 by mRNA vaccines has been shown to be remain high against all VOCs, although reduced effectiveness against infection and mild symptoms has been observed for Beta and Delta over time (*https://www.who.int/publications/m/item/weekly-epidemiological-update-on-covid-19---21-september-2021*). Transmissibility in vaccinated populations is greatly reduced (see report of the month of June). No data are yet available regarding vaccine effectiveness against AY 4.2.

Impact on diagnostic tests
Nucleic acid detection may be affected by mutations in the RNA sequence of target regions. 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, and various rapid diagnostic tests analytical sensitivity was conserved in detecting all variants, including Delta. (*Bekliz et al. MedRxiv. 2021*).

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

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

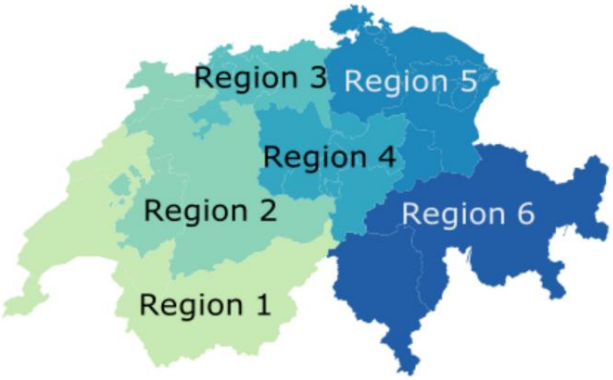
4. Epidemiology in Switzerland and number and origin of sequences produced through the program during the surveilled period

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

Caveat: For the month of September, there are substantial delays in reporting/declaring data or there is substantial underreporting by some laboratories participating in the program. Data are only available for 10 of 15 laboratories (detailed data can be found in Supplementary Table 2). Submission delays are being identified and actions will be taken to ensure timely sharing of sequences.

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 66 576 confirmed SARS-CoV-2 cases in Switzerland. 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.

As of the writing of this report, the laboratories participating in this program reported 23,118 positive tests during the surveilled program, which represents about 35% of the total number of cases reported in Switzerland (including both PCR and antigen-based tests). Because of reporting delays, this number may be underestimated. 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.

Number of declared SARS-CoV-2 sequences produced through the surveillance program (presented by submission date, further declarations are still ongoing)

A total number of 7,742 SARS-CoV-2 sequences have been declared to have been submitted to GISAID during this period. However, more than 9,400 sequences are available for this period on GISAID, which illustrates the reporting delays and the delay between sampling and submission.

This represents around 12% of all cases detected in Switzerland during the surveilled period (see Supplementary Table 2 and 3 in the 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 (data is incomplete)

Week	Date	Number of sequences declared and successfully submitted to GISAID
35	Aug 30 to Sep 5	1593
36	Sep 6 to Sep 12	1697
37	Sep 13 to Sep 19	1601
38	Sep 20 to Sep 26	1702
39	Sep 27 to Oct 3	1149
	Total	7742

Table 1: number of sequences submitted to GISAID through the surveillance program during the surveilled period, by all laboratories in the program. Note these data are not by sampling date but rather by submission to GISAID date. Data are incomplete due to late reporting by multiple laboratories

The total number of SARS-CoV-2 sequences declared and submitted to GISAID by each laboratory during the month of September 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 generally declined during the month of September (weeks 35 to 39), reflecting the decline 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.

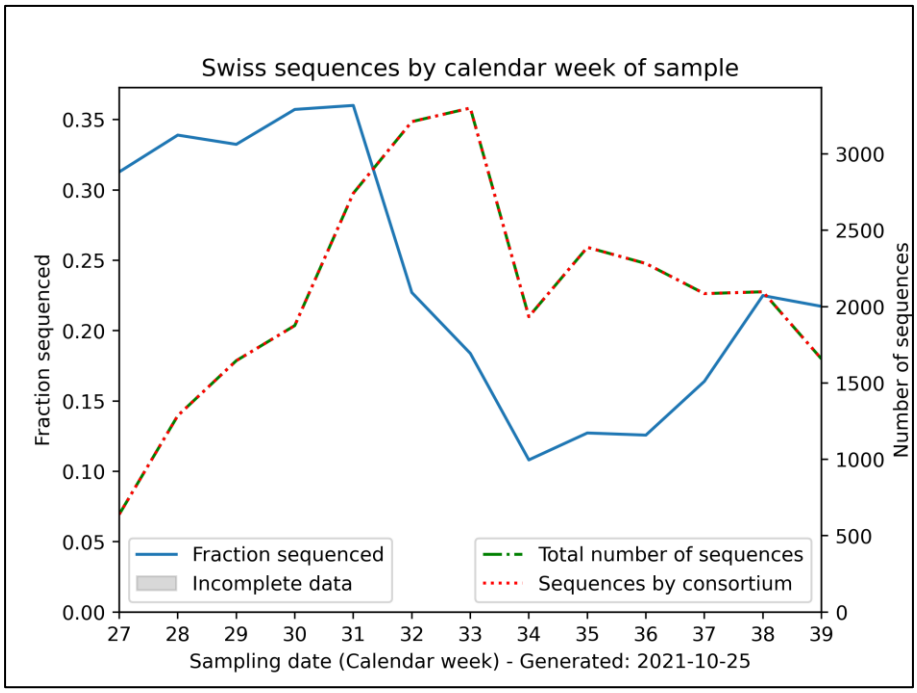


Figure 1: Number of SARS-CoV-2 sequences available for Switzerland (total available Swiss sequences in GISAID in green, Swiss sequences submitted through the program in dotted orange) and fraction of the total number of positive cases declared to the FOPH that have been sequenced (blue curve).

During the surveilled period, the total proportion of positive sequenced cases increased from between just above 10% to 20%, with a mean of 15%, largely above the aim of the program.

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, while regions 4 and 5 continued to have the lowest fraction of cases sequenced, and were under the 10% goal for weeks 35 and 36. The rest of the regions were all above the 10% sequencing goal.

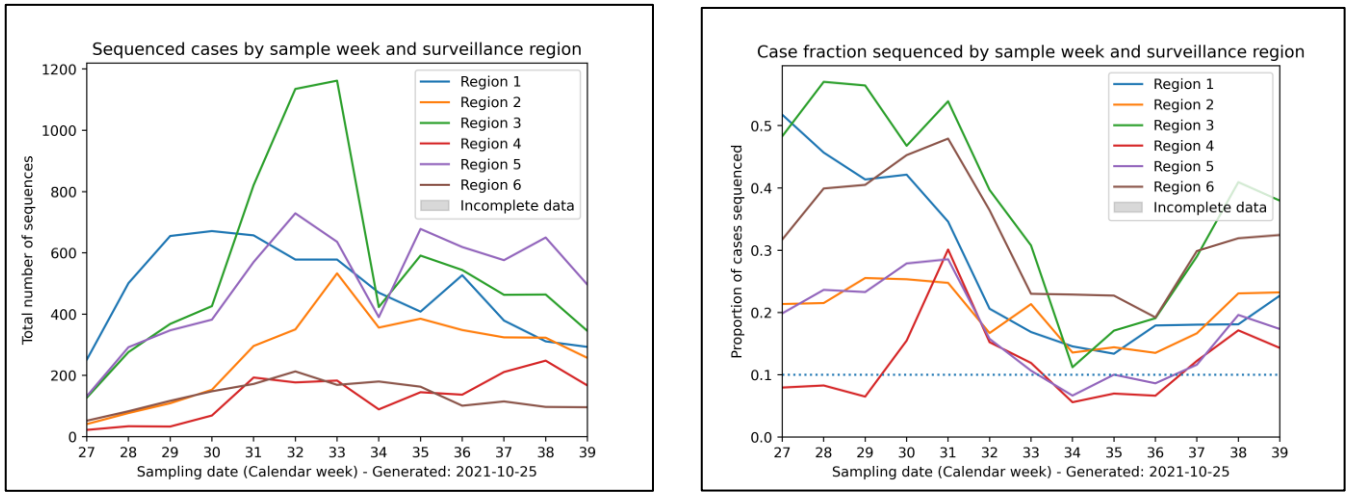


Figure 2: Sequencing coverage among the different Swiss regions per week, presented by fraction of cases sequenced (left) and by number of sequences (right).

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) and its sub-lineages were almost exclusively retrieved during the month of September all over Switzerland, accounting for around 99.97% of the submitted sequences (see Figures 5 and 6). See Table 2 below for details. Neither Mu nor Lambda were retrieved at all in Switzerland during the surveilled period (table 2).

Region	Delta	AY.4.2	Others	sequences	cases	% sequenced
All	9483	38	3	9486	66576	14.2
1	1781	3	1	1782	11106	16.0
2	1524	7	0	1524	9704	15.7
3	2062	7	1	2063	9953	20.7
4	823	3	0	823	8489	9.7
5	2700	18	1	2701	25095	10.8
6	547	0	0	547	2229	24.5

Table 2: number of sequences corresponding to selected variants in each region of Switzerland during the month of September 2021. No Alpha, Beta, Gamma, Lambda, Mu, etc. were identified, according to data received by October 19.

Some sequences are AY* lineages (Delta sub-lineages), which are still poorly defined. AY.4 is the most common sub-lineage in Switzerland, at over 48%. 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.

Within Delta-sub-lineages, AY.4.2 has rarely been identified during the month of September in Switzerland: among 9486 sequences retrieved during the surveilled period, 38 were AY 4.2.

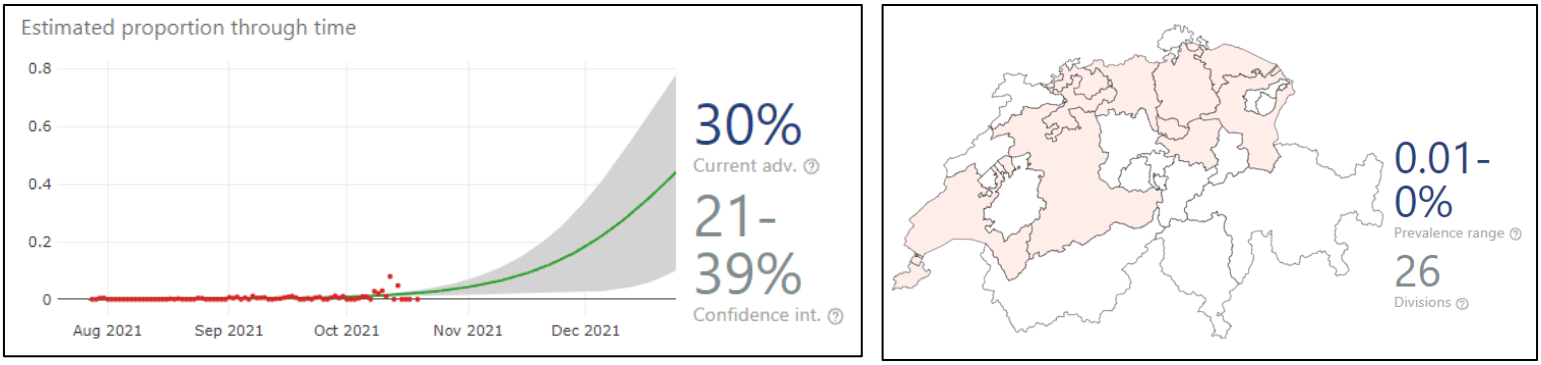


Figure 3: AY.4.2 estimated transmission advantage over time compared to co-circulating strains (left) and geographic distribution across Switzerland and average proportion during the surveilled period (right). Dynamic navigation available at https://cov-spectrum.ethz.ch/explore/Switzerland.

Among other sequences identified in Switzerland during the surveilled period, very few other lineages were recorded as of data received by October 25. These sequences included:

- 1 B.1.617.1 (Kappa) sequence
- 1 B.1.576 sequence (week 35)
- 1 B.1.620 sequence
- 1 B.1 sequence (week 35)
- 8 B.1.1.318 sequences (5 week 35)

Note that additional sequences received between 19 and 25 October may explain the difference with available numbers in Table 2.

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

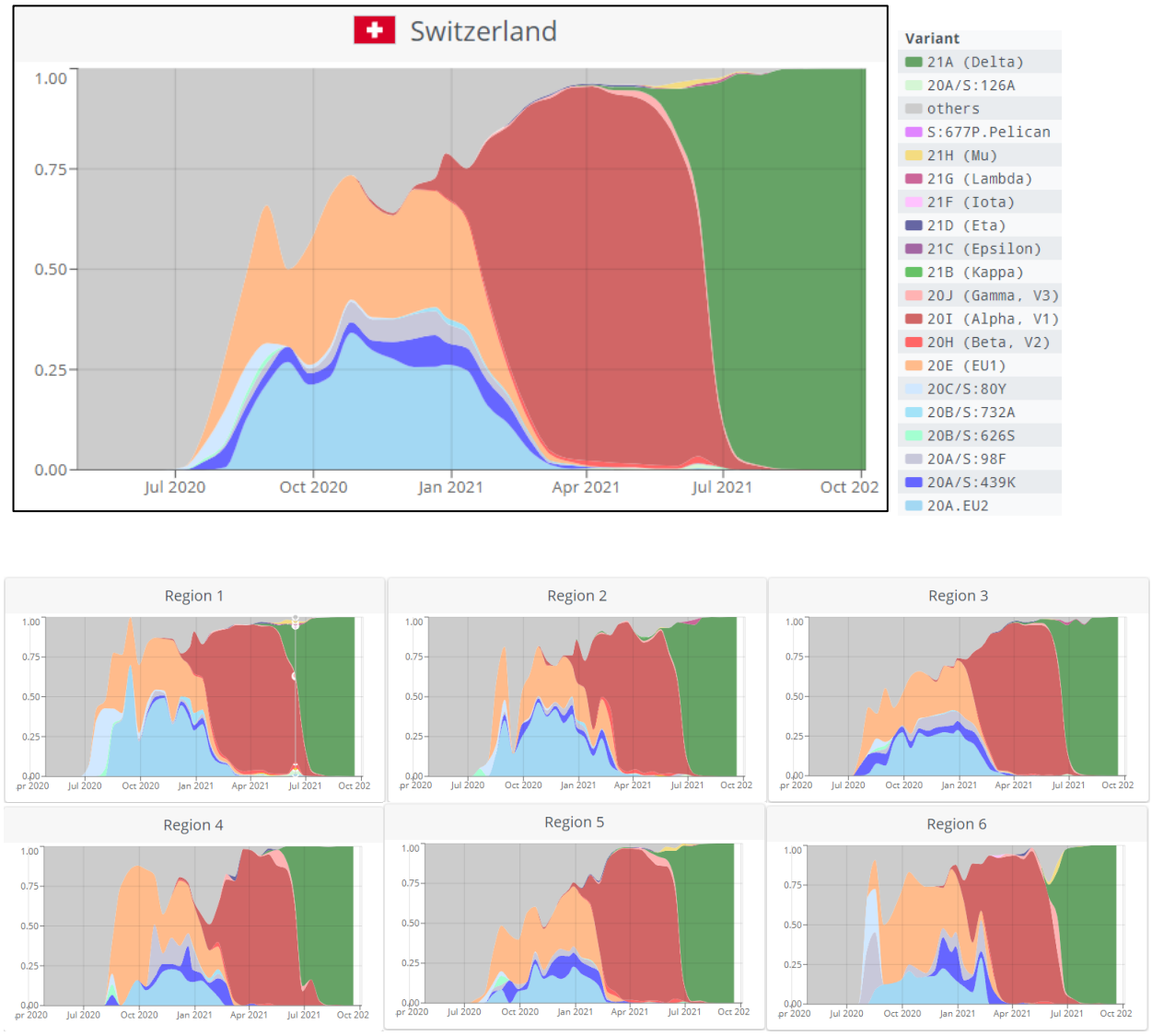


Figure 4: proportion of the total number of sequences (not cases), over time, that fall into defined variant groups, for Switzerland. Screenshot from CoVariant website. Dynamic navigation is available at https://covariants.org/per-country. Dark green indicates the currently dominant B.1.617.2 (Delta)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

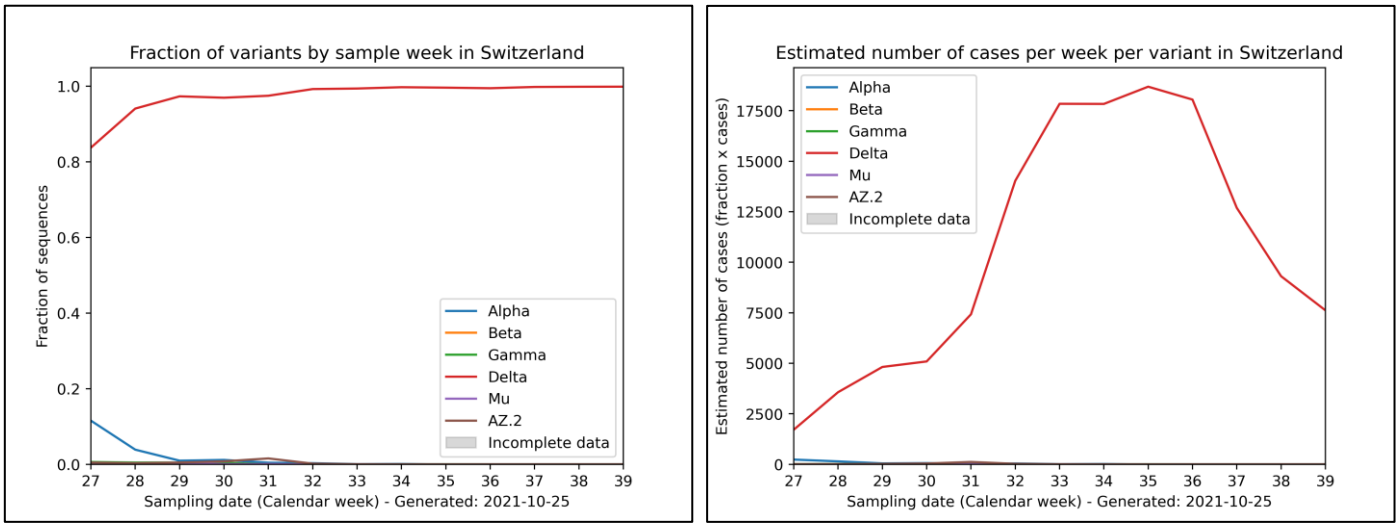


Figure 5: (Left): Percentage of circulating VOCs and VOIs in Switzerland by week, over the 39 first weeks of 2021 (total number of B.1.1.7 (Alpha), B.1.351 (Beta), P.1 (Gamma), B.1.617.2 (Delta) and B.1.621 (Mu) sequences from Switzerland and successfully submitted to GISAID are shown here).
(Right): Estimated number of sequences of the main VOCs/VOIs and variants under monitoring retrieved during the surveilled period.

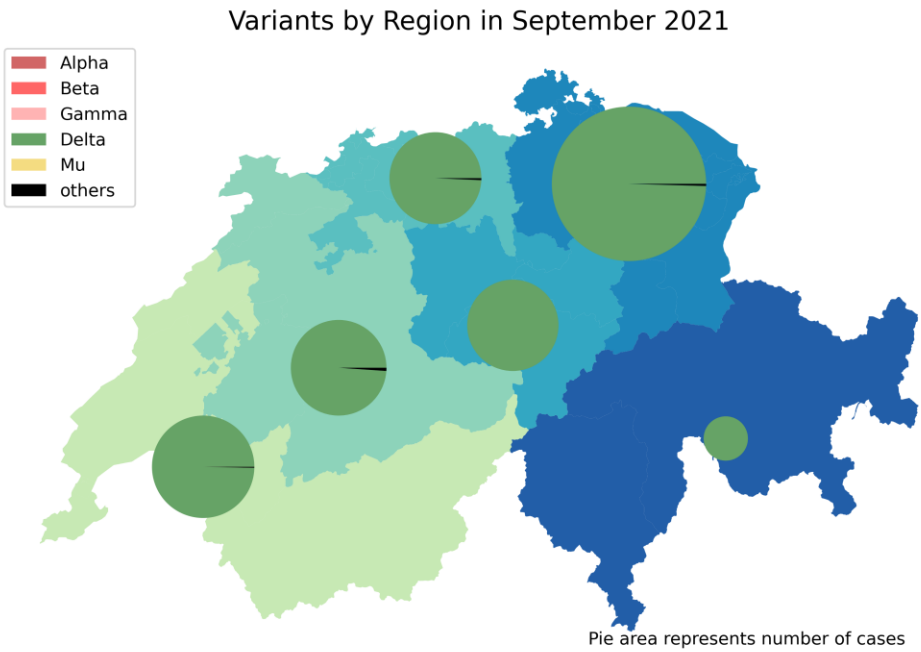


Figure 6: Distribution of variants per region, for September 2021, shown on a map. The size of the pie chart corresponds to the total number of sequences. Note the dominance of Delta in all regions.

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 September 2021.

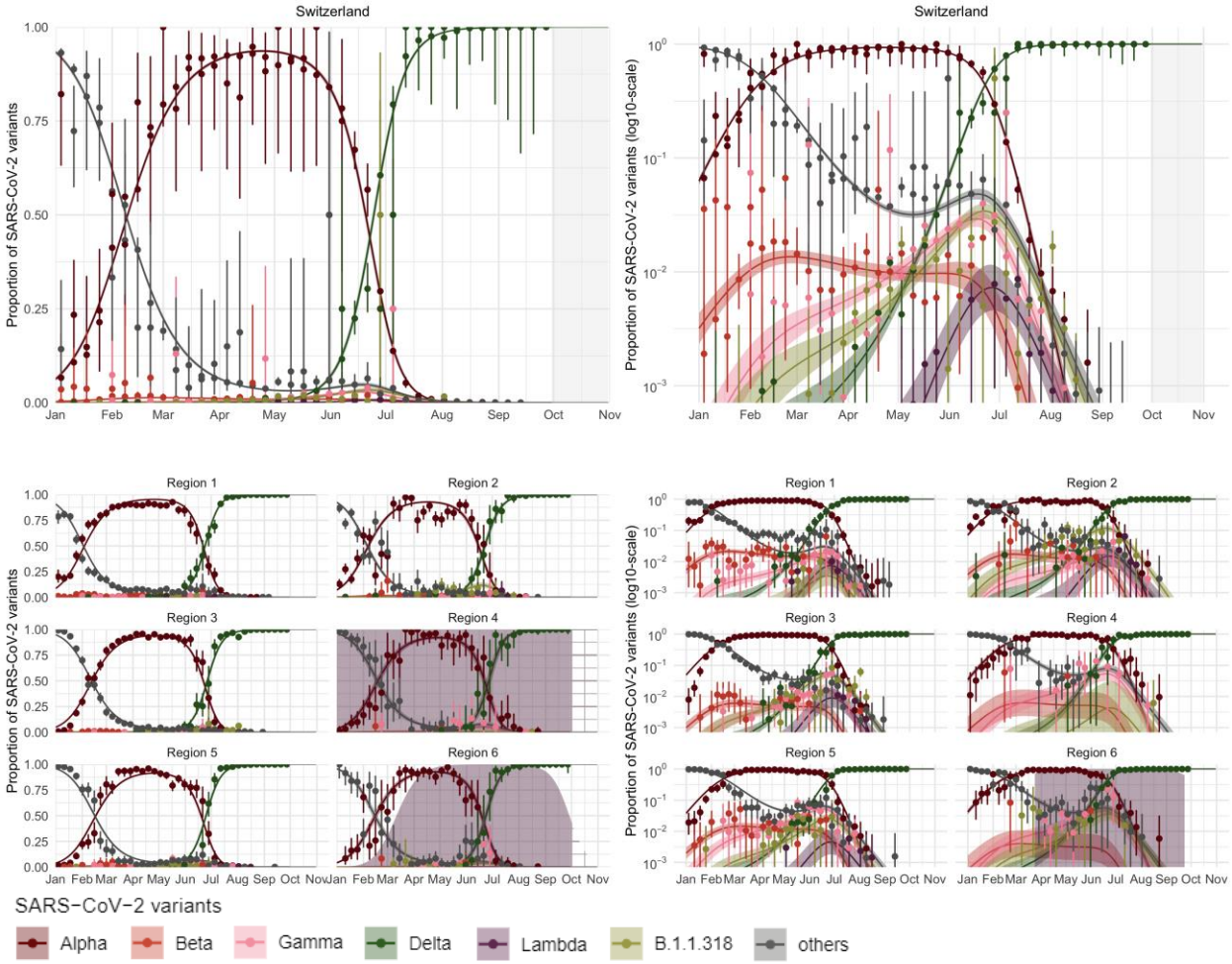


Figure 7: Observed and modeled proportion of SARS-CoV-2 variants over time in Switzerland. In April and May 2021, Gamma and Delta started to replace Alpha, with Delta now outcompeting all other variants. At the end of September, more than 999.9% of the retrieved sequences in Switzerland were due to Delta. No new variants appear to be displacing Delta. Model fits are based on a multinomial logistic regression with splines.

7. Wastewater surveillance program

Since August, the B.1.617.2 (Delta) variant has been observed to be dominant over time in all of the seven wastewater treatment plants (WWTPs) that are tested on a daily basis. 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 September, the dominance of B.1.617.2 (Delta) was obvious in all surveyed WWTPs.

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.

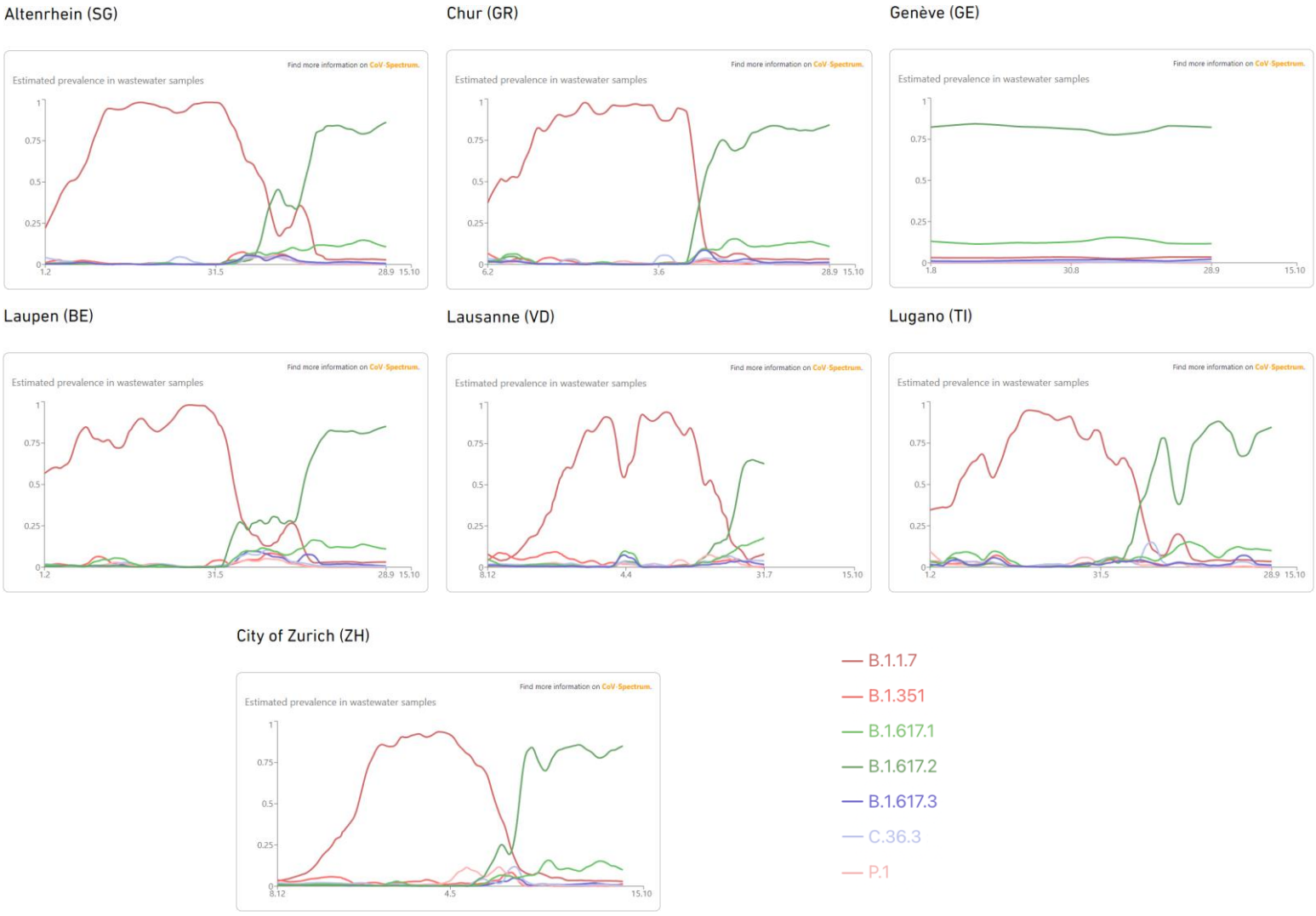


Figure 8: Prevalence of variants of SARS-CoV-2 estimated from wastewater samples collected daily until September 31 or later (except Lausanne: July 31) in WWTPs located in 7 different Swiss cantons. B.1.617.2 (Delta) is represented in in dark green, B.1.617.1 in light green (Kappa), B.1.617.3 in purple, 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..

8. Immunological characterization of the variants

During the month of September, subject sera was assessed for antibody binding to 10 different Spike variants using the Luminex assay. Subject sera came from 50 previously infected individuals, 50 vaccinated individuals, and 50 individuals who were previously infected and then vaccinated (150 total). These assays continued into October, and are currently being analyzed. Results and analysis are expected to be presented in the report for the month of October.

Conclusion

In September, over 9,000 sequences were obtained through this surveillance program, in the midst of a gradual decline in case numbers. Each week since this surveillance program started, it has contributed almost all of the Swiss SARS-CoV-2 sequences available on GISAID. In September, around 14.2% 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 5 are still the least represented geographical areas, despite increasing efforts to recruit new laboratories in those regions.

It continues to be nearly exclusively the B.1.617.2 (Delta) variant (and its sub lineages) that circulates, with a relatively homogenous representation over the different Swiss regions, accounting for around 99.9% of the sequences identified in September. Numerous sub-lineages are increasingly detected, but sub-lineage definition and characterization are still ongoing. There are notably four new spike mutations identified across these sub-lineages, which have independently arisen multiple times and may confer slight advantages.

One Delta-sub-lineage called AY.4.2, recently identified as a Variant Under Monitoring by both ECDC and Public Health England, was rarely identified during the month of September in Switzerland, with 38 sequences retrieved during the surveilled period. This very low number precludes any solid conclusion on any increased trend of this variant in Switzerland at the time of the writing of this report.

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

Around 10 non-Delta sequences were identified by the sequencing program. Among other rare sequences identified over weeks 35 to 39 were: 1 B.1.617.1 (Kappa), 1 B.1.526, 1 B.1.620 and 8 B.1.1.318 sequences.

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

An issue in the detection of the G21987A mutation present in the Delta lineage, due to specifics of the usual protocols used in sequencing has been identified, and may result in the misclassification Delta sub-lineages. For this reason this mutation should not be considered for epidemiological tracing. No additional diagnostic issues were noted for any variant in September.

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.

Of note, for the month of September, 2021, substantial delays in reporting/declaring data and substantial GISAID submission delays by the laboratories were noted. Submission and declaration delays are being identified and actions will be implemented to ensure timely sharing of sequences and their interpretation.

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. Data presented here cover the period from August 30 to October 3.

sup_table_overview_Sep.xlsx

Supplementary Table 1: Epidemiological data for Switzerland, its regions and cantons in September 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
35	Aug 30 to Sep 5	42 787	6 730	1593	15.73%	23.67%
36	Sep 6 to Sep 12	43 682	6 404	1697	14.66%	26.50%
37	Sep 13 to Sep 19	40 420	4 335	1601	10.72%	36.93%
38	Sep 20 to Sep 26	34 805	3 167	1702	9.10%	53.74%
39	Sep 27 to Oct 3	29 811	2 482	1149	8.33%	46.29%
	Total	191 505	23 118	7 742	12.07%	33.49%

Supplementary Table 2: Total number of tests performed by the laboratories participating in the surveillance program from July 5 to September 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
35	Aug 30 to Sep 5	91	48	186*	ND	ND	ND	ND	128	55	94	ND	143	94*	183	851	1873
36	Sep 6 to Sep 12	57	48	186*	ND	ND	ND	ND	158	52	94	ND	244	94*	220	824	1977
37	Sep 13 to Sep 19	57	46	186*	ND	ND	ND	ND	131	45	94	ND	234	80*	144	850	1867
38	Sep 20 to Sep 26	36	48	186*	ND	ND	ND	ND	111	46	94	ND	211	64*	130	1026	1952
39	Sep 27 to Oct 3	35	48	186*	ND	ND	ND	ND	0	75	94	ND	192	32*	38	667	1367
	Total	276	238	930*	0	0	0	0	528	273	470	0	1024	364*	715	4218	9036

*Supplementary Table 3: number of sequences submitted to GISAID by each laboratory during the surveilled period (September 2 to September 29, 2021). *including sequencing sent to high-throughput platforms. ND = No 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 – Institut Central	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
Laboratoire Bioanalytica	Michael Naegele	michael.naegele@bioanlytica.ch
Laboratoire Bioanalytica	Livia Berlinger	livia.berlinger@bioanalytica.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
Nadja Wipf	Nadja.wipf@bag.admin.ch
Ursina Roder	ursina.roder@bag.admin.ch
Biagio Zaffora	biagio.zaffora@bag.admin.ch
Michael Bel	Michael.Bel@bag.admin.ch
Urs Mayr	urs.mayr@bag.admin.ch
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
Mirjam Mäusezahl	Mirjam.Mäusezahl@bag.admin.ch
Oliver Caliaro	oliver.caliaro@bag.admin.ch
Tobias Schuster	tobias.schuster@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