Weekly update on Variants of Concern (VOC)

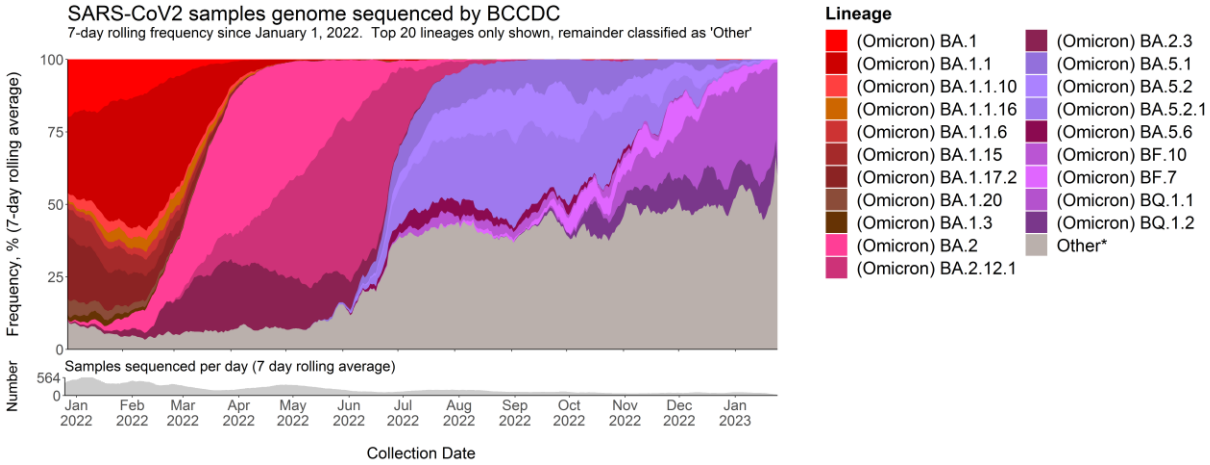
2 February, 2023

Of all positive samples sequenced* in epi week 3 (January 15 - January 21) in BC, all were were confirmed Variants of Concern (VOCs). Over time, the distribution of variants demonstrate the temporality and changing nature of VOCs circulating as shown in Figure 1. Detection of BA.5, including all descendant sublineages, has remained relatively stable in BC.

Due to the large diversity in BA.5 sublineages (>100 descendants), the total sequenced for each individual descendant strain is low and collapsed in the 'Other' category in Figure 1. Lineages sequenced in the most recent week of data available categorized as 'Other' are listed in the footnote of the figure. This report provides more detail for the breakdown of sequenced samples in the most recent six weeks of data available (Figure 5).

Data from epi week 3 may reflect partial data; estimates are expected to change as more specimens are received and sequenced.

Figure 1. Twenty most prevalent lineages in British Columbia, January 1, 2022 - January 21, 2023**



*Other, in the most recent week of data, includes:
BA.5.10.1, BA.5.2.34, BF.28, BF.7.*, BQ.1, BQ.1.1.*, BQ.1.2.*, BQ.1.3, BQ.1.5, BQ.1.8, BR.2.1, BW.1.1, CH.1.1, CK.1, CK.2.1.1
CM.8.1, DJ.1.1, XBB.1.5, XBF

Pangolin version: 4.2, Usher version: 1.18, Pango version: 1.18. Total Pango assignments: 20 886; Total Usher assignments: 50 251

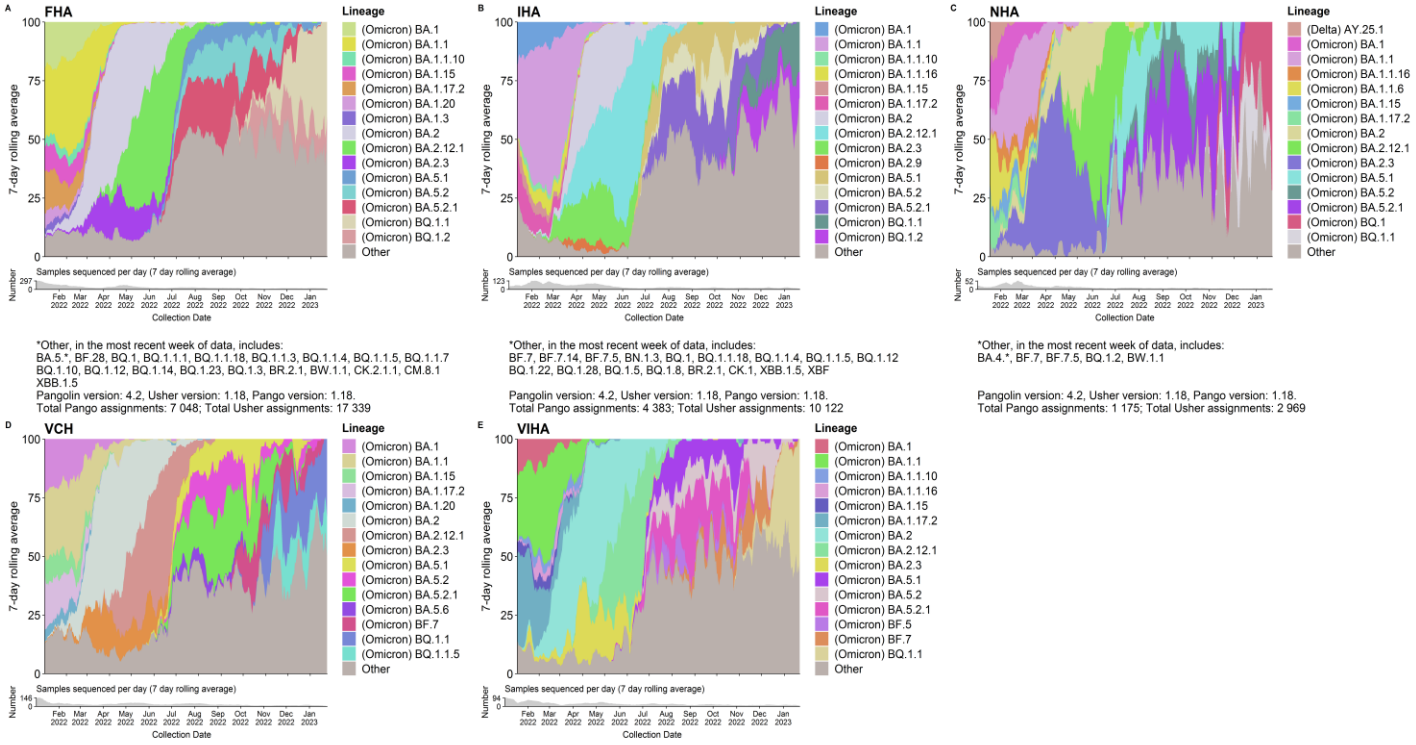
*Lineages in the Other category listed with an asterisk * comprise of descendants within the parent variant.*

**Data from the PLOVER system at the BCCDC Public Health Lab.*

***Dashed lines indicate the time of changes in whole genome sequencing (WGS) sampling strategy (epi week 22: all positive samples; epi week 36: transition from full sequencing to sequencing a subset of 10% of representative samples in addition to all targeted samples, while keeping a monthly census of all positive samples on the first week of the month; epi week 46: transition to WGS of all positive samples; epi week 51: transition from full sequencing to sequencing a subset of representative positive samples in addition to priority cases (including outbreaks, long-term care, vaccine escape, travel-related, hospitalization).*

As shown in Figure 2, Omicron sub-lineages have different prevalence distribution in each health authority. Lineages sequenced in the most recent week of data available categorized as 'Other' are listed in the footnote of the figure.

Figure 2. Fifteen most prevalent lineages in British Columbia by Health Authority, January 1, 2022 - January 21, 2023



*Other, in the most recent week of data, includes:
BA.5.*, BF.28, BQ.1, BQ.1.1.1, BQ.1.1.18, BQ.1.1.3, BQ.1.1.4, BQ.1.1.5, BQ.1.1.7
BQ.1.10, BQ.1.12, BQ.1.14, BQ.1.23, BQ.1.3, BR.2.1, BW.1.1, CK.2.1.1, CM.8.1
XBB.1.5
Pangolin version: 4.2, Usher version: 1.18, Pango version: 1.18.
Total Pango assignments: 7 048; Total Usher assignments: 17 339

*Other, in the most recent week of data, includes:
BF.7, BF.7.14, BF.7.5, BN.1.3, BQ.1, BQ.1.1.18, BQ.1.1.4, BQ.1.1.5, BQ.1.12
BQ.1.22, BQ.1.28, BQ.1.5, BQ.1.8, BR.2.1, CK.1, XBB.1.5, XBF

Pangolin version: 4.2, Usher version: 1.18, Pango version: 1.18.
Total Pango assignments: 4 383; Total Usher assignments: 10 122

*Other, in the most recent week of data, includes:
BA.4.*, BF.7, BF.7.5, BQ.1.2, BW.1.1

Pangolin version: 4.2, Usher version: 1.18, Pango version: 1.18.
Total Pango assignments: 1 175; Total Usher assignments: 2 969

*Other, in the most recent week of data, includes:
BQ.1, BQ.1.1.18, BQ.1.1.23, BQ.1.12, BQ.1.14, BQ.1.2, BQ.1.22, BQ.1.3, CH.1.1
CM.8.1, DJ.1.1, XBF

Pangolin version: 4.2, Usher version: 1.18, Pango version: 1.18.
Total Pango assignments: 2 961; Total Usher assignments: 9 516

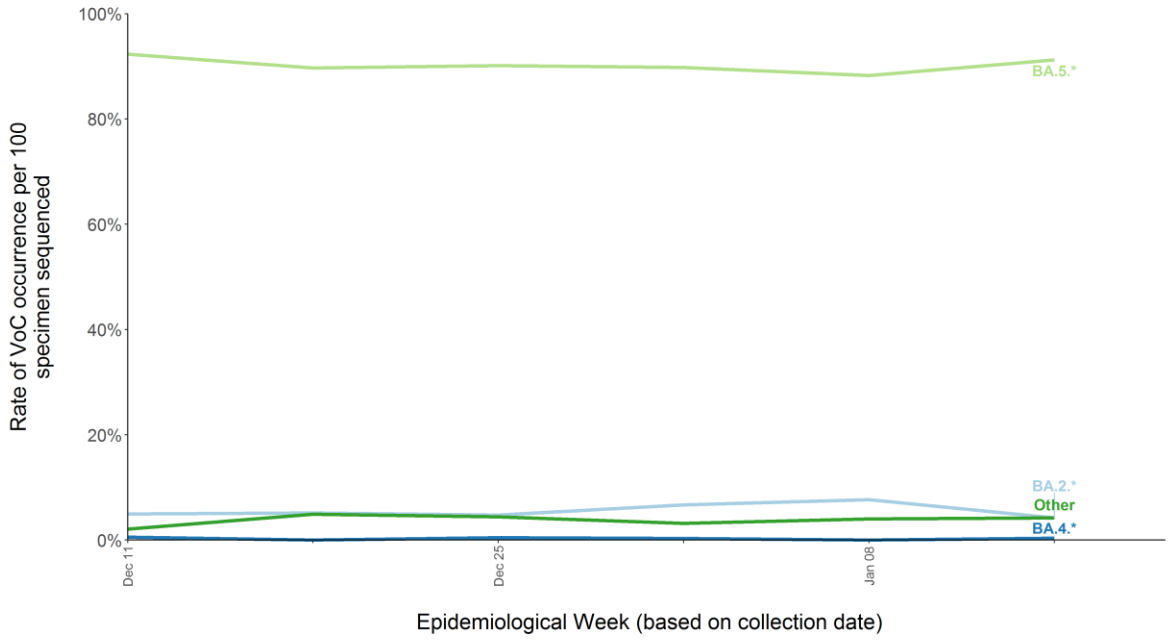
*Other, in the most recent week of data, includes:
BA.5.*, BQ.1, BQ.1.1.18, BQ.1.1.28, BQ.1.1.31, BQ.1.1.5, BQ.1.11, BQ.1.12, BQ.1.2
BR.2.1, BU.1, BW.1.1, other BA.2.*, XBB.1.5

Pangolin version: 4.2, Usher version: 1.18, Pango version: 1.18.
Total Pango assignments: 2 503; Total Usher assignments: 7 080

Pangolin designation beyond three sub-lineages (e.g. BA.5.x.x.x) results in the assignment of a new naming convention whereby a new lineage (e.g. BE) is assigned. These new designations (e.g. BE, BM, etc.) are collapsed in their parental lineage (e.g. BA.5*) in Figure 3.

Recombinants (e.g. XBB.1.5) are collapsed in the 'Other' category.

Figure 3. Proportion of lineages [#] sequenced over the past 6 weeks from 04 December, 2022 to January 21, 2023

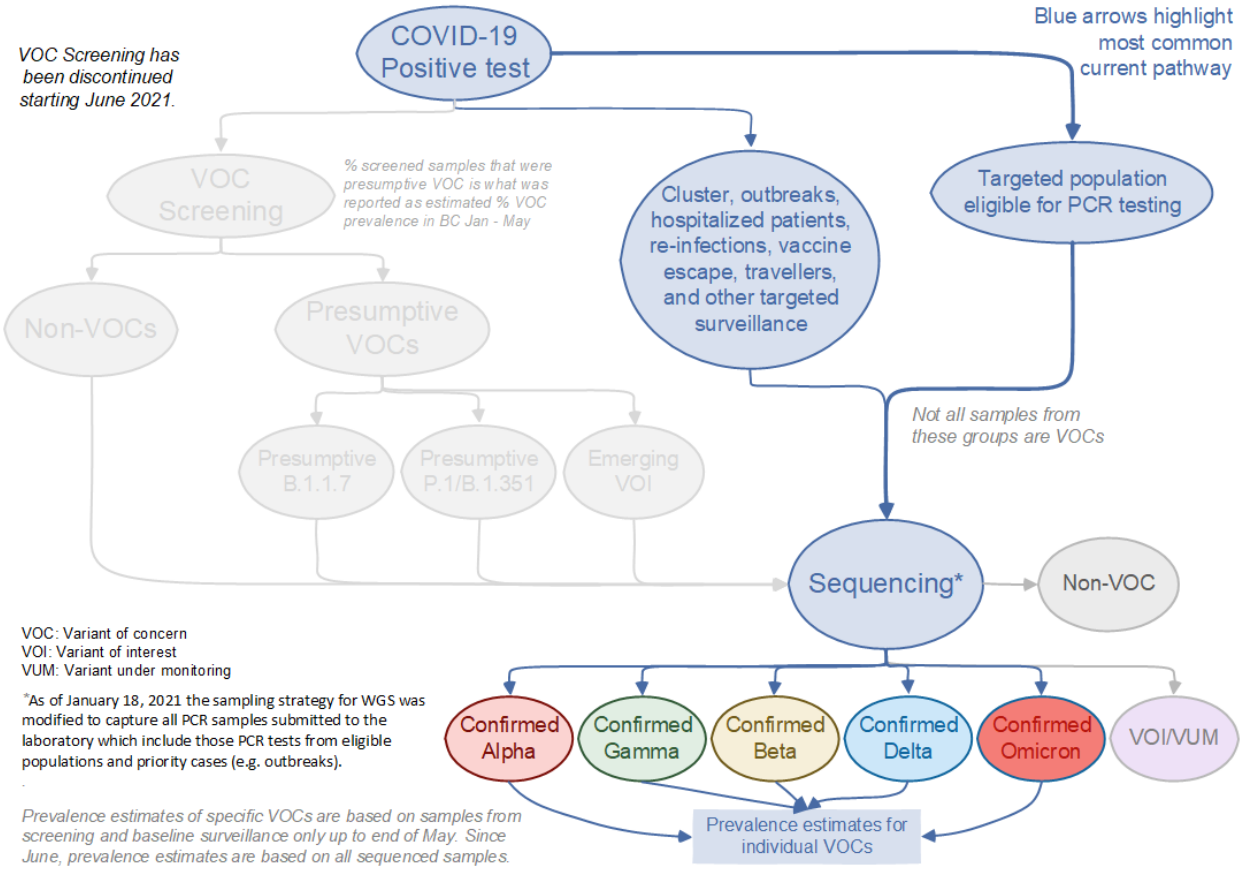


[#] *See appendix for the definitions of VOC lineages*

Monitoring of Variants

BCCDC Public Health Laboratory is continuously monitoring for both VOCs and VOIs and it is tracking a regularly updated Variants Under Monitoring (VUMs) by adapting and optimizing its sampling strategy. To address the latest VOC, Omicron, sequencing of all positives samples was resumed with retrospective specimens collected from November 15th 2021 - December 20th 2021. The sampling strategy for WGS was modified starting December 21st 2021 to capture a subset of representative positive specimens in addition to the priority cases (including outbreaks, long-term care, vaccine escape, travel-related, hospitalization). Reflecting the current testing guidelines, most sequencing is now through positive PCR samples as shown in Figure 4. As of October, 2022 priority cases no longer include travel testing due to the ending of COVID-19 emergency border measures.

Figure 4. Overview of the screening and sequencing process applied to positive COVID-19 tests in BC, Jan 2023.



Please note the turnaround time sequencing which takes approximately 7-11 days, but it could also take longer if there are lab backlogs or if there are delays in receiving current positive samples from frontline laboratories.

Whole genome sequencing (WGS)

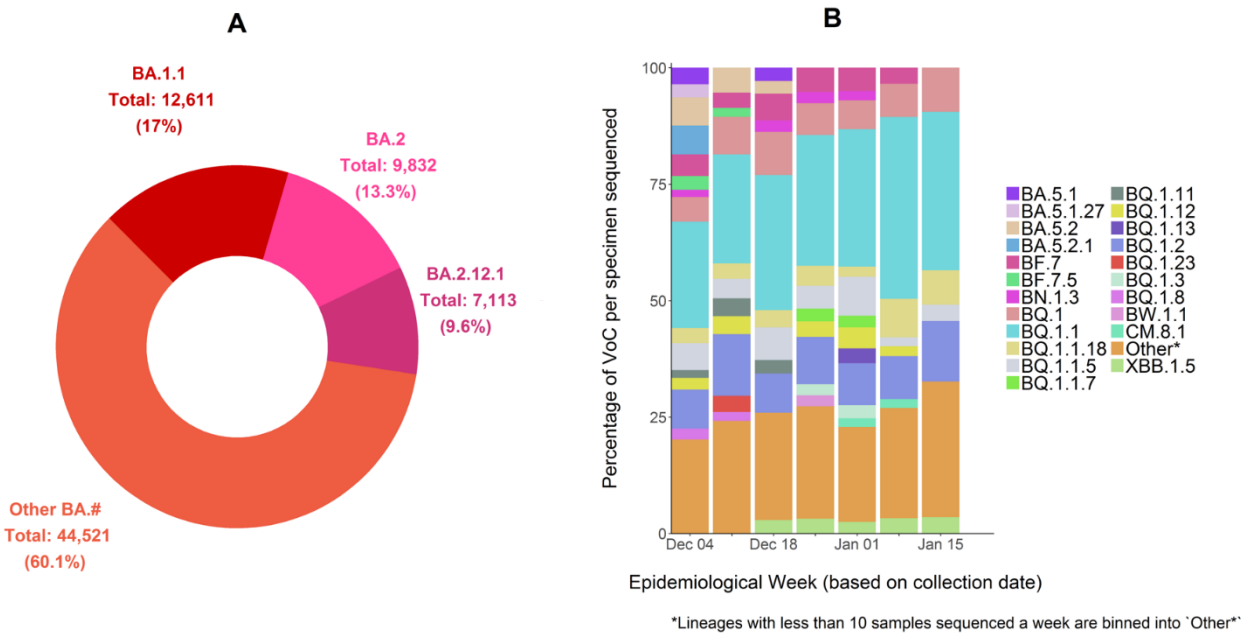
Whole genome sequencing (Illumina only) was performed on 186,033 specimens up to epi week 3 (January 15 - January 21) in BC. Figure 4 above illustrates BC's whole genome sequencing strategy of COVID cases.

The VOCs represent a cumulative 85.5% of all the variants that were detected in the province since the start of the pandemic (see WGS frequency of lineages table on BCCDC website). The Delta (n = 57,837) and Omicron (n = 74,077) variants account for largest proportion of the VOCs. Omicron includes B.1.1.529, the parent lineage, and BA sub-lineages (Figure 5 and appendix Table).

BQ.1.1.* is the most predominantly sequenced variant in the past 6 weeks.

Figure 5. Distribution of Omicron**

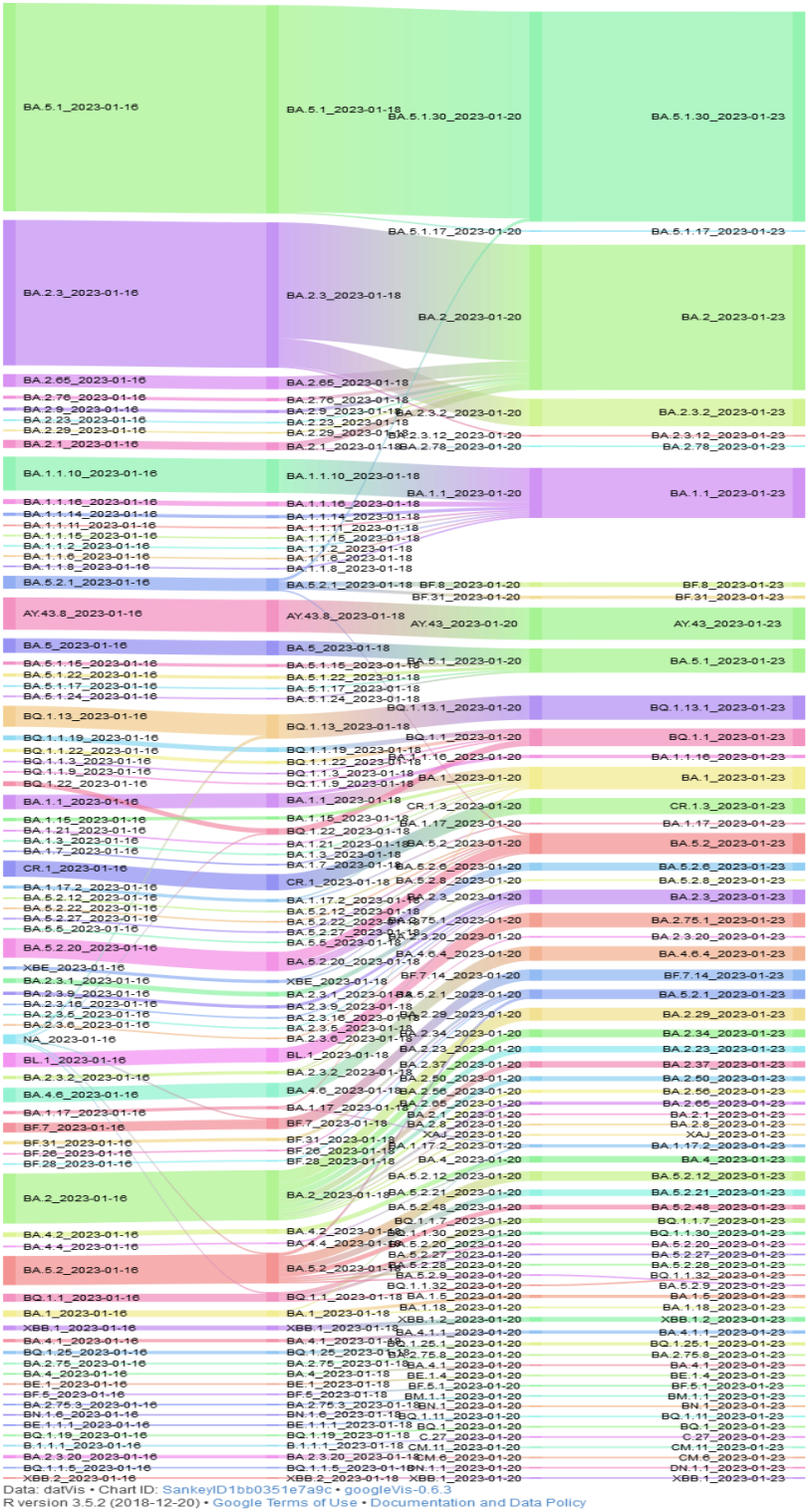
Panel A: three most prevalent lineages cumulatively; Panel B: sublineages in the past 6 weeks



*** These counts represent the total number of samples (not cases) sequenced.*

BCCDC Public Health Laboratory updates the lineage assignment tool (Pangolin), on an at least weekly basis, to reflect current lineage classification changes as shown in Figure 6.

Figure 6. Lineage assignment changes* in Pangolin



Appendix – VOC Lineages*** Table

VOC	Associated Lineages
Alpha	B.1.1.7, Q.*
Beta	B.1.351, B.1.351.*
Gamma	P.1, P.1.*
Delta	B.1.617.2, AY.*
Omicron**	B.1.1.529, BA.*, BA, BC, BD, BE, BF, BG, BH, BJ, BK, BL, BM, BN, BP, BQ, BR, BS, BT, BU, BV, BW, BY, BZ, CA, CB, CC, CD, CE, CF, CG, CH, CJ, CK, CL, CM, CN, CP, CQ, CR, CS, CT, CU, CV, CW, CY, CZ, DA, DB, DC, DD, DE, DF, DG, DH, DJ, DK, DL, DM, DN, DP, DQ, DR, DS, DT, DU, XE, XG, XH, XJ, XK, XL, XM, XN, XP, XQ, XR, XT, XU, XV, XW, XY, XZ, XAA, XAB, XAC, XAD, XAE, XAF, XAG, XAH, XAJ, XAK, XAL, XAM, XAN, XAP, XAQ, XAR, XAS, XAT, XAU, XAV, XAW, XAZ, XBB, XBC, XBD, XBE, XBF, XBG, XBH, XBJ, XBK, XBL, XBM

** Indicates an additional numerical value (e.g. Q.1).*

*** Lineages starting with X indicate a recombination of Omicron variants.*

**** Lineage assignments are based on the use of Pangolin, an epidemiological lineage assignment tool (github.com/cov-lineages/pangolin); these may change with time as new SARS-CoV-2 genomic data becomes available.*