

# **SARS-CoV-2 Sequencing and Variants in Washington State**

**Washington State Department of Health**

**February 22, 2023**

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# SARS-CoV-2 Sequencing and Variants in Washington State

## Washington State Department of Health

**February 22, 2023**

Next Generation Sequencing (NGS) is a set of laboratory methods that scientists use to scan a viral genome to determine the genome sequence of a virus. A genome sequence of a virus is referred to as its “genomic fingerprint,” and can reveal mutations in a virus that make it unique. Mutations are changes in a genome sequence and occur naturally over time.

Scientists compare viral genomes to better understand how viruses can spread from person to person. NGS technology allows public health officials to detect clusters of cases and monitor new variant viruses. Groups of same-species viruses that share a set of genome mutations are referred to as a lineage. Some variants belonging to specific lineages may have characteristics such as the ability to spread more quickly, cause more severe disease, or impact clinical therapy such as treatment with monoclonal antibodies. These variants may be classified as variants of interest, variants being monitored, variants of concern or variants of high concern.

Throughout this report, we refer to the scientific name of the virus SARS-CoV-2 that causes COVID-19. Sequencing can only be performed on samples that are processed in laboratories and where swabs are stored in liquid that is compatible with sequencing, which means only samples used for molecular tests (such as PCR) can be included. For this reason, this report is limited to confirmed cases only. The genomes that are sequenced and compared are those of the virus, not of humans.

### **At a glance (data through February 21, 2023)**

- During the month of January 2023, **11.4%** of all confirmed molecular COVID-19 cases were sequenced. This number is preliminary and will change over time as additional specimens are received from the previous month.
- **136,103 (9.8%)** COVID-19 cases in Washington state have sequencing information available since January 2021.

CDC currently categorizes variants as Variants of High Consequence (VOHC), Variants of Concern (VOC), Variants of Interest (VOI) and Variants Being Monitored (VBM). There are currently no VOHC and VOI so only VOC and VBM are detailed in this report.

## Variants of Concern

Variant	Area first detected	Background	Cumulative Washington cases detected	First detection in Washington*	Most recent detection in Washington*
Omicron (B.1.1.529, BA.1, BA.1.1, BA.2, BA.3, BA.4 and BA.5 lineages)	South Africa	Early research indicates evidence for increased transmissibility, immune evasion, and lower risk of hospitalization and death, relative to Delta. Approved vaccines are effective at preventing severe disease and death against Omicron variants	69,258	Nov 29, 21	Feb 06, 23

\*Detection dates are based on the date a sample is collected, it can take several weeks before a variant result is completed and added to the report

Note: Omicron lineages in this report are defined as below:

Omicron grouping	Inclusion
Other Omicron	Includes B.1.1.529, BA.1.X, BA.3.X
BA.1.1	Includes BA.1.1.X
BA.2	Includes BA.2.X except BA.2.12.1 and BA.2.75.X
BA.2.12.1	Includes BA.2.12.1.X
BA.2.75	Includes BA.2.75.X except BA.2.75.2 and BA.2.75.5.1
BA.2.75.2	Includes BA.2.75.2.X
BN.1	Includes BA.2.75.5.1.X (Alias of B.1.1.529.2.75.5.1)
BA.4	Includes BA.4.X except BA.4.6.X
BA.4.6	Includes BA.4.6.X
BA.5	Includes BA.5.X except BF.7 and BA.5.2.6
BA.5.2.6	Includes BA.5.2.6.X
BF.7	Includes BF.7.X (Alias of B.1.1.529.5.2.1.7)
BF.11	Includes BF.11.X (Alias of B.1.1.529.5.2.1.11)
BQ.1	Includes BQ.1 (Alias of BA.5.3.1.1.1.1.1) except BQ.1.1

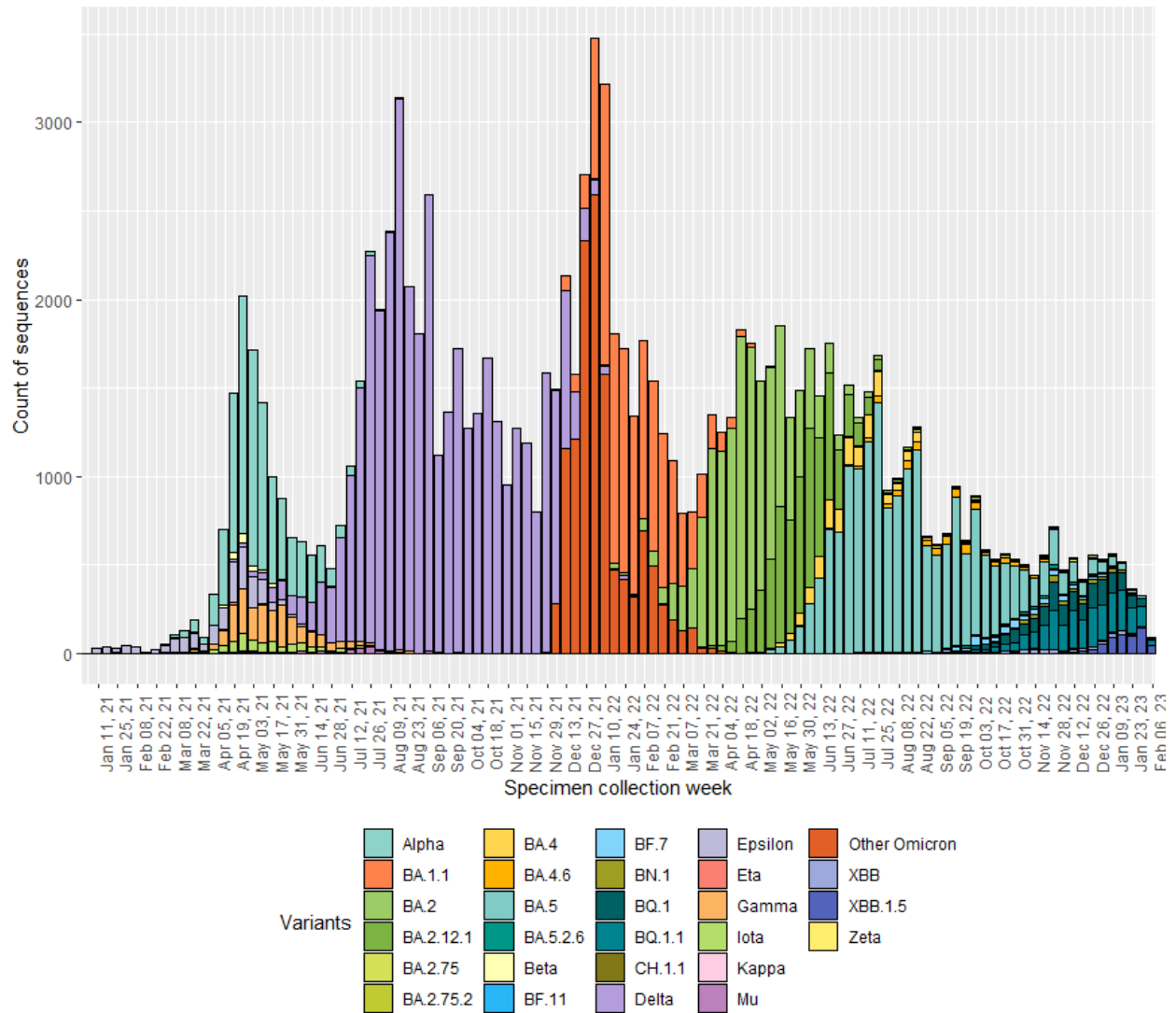
Omicron grouping	Inclusion
BQ.1.1	Includes BQ.1.1.X
XBB	Includes XBB.X except XBB.1.5
XBB.1.5	Includes XBB.1.5.X
CH.1.1	Includes CH.1.1.X

## Variants Being Monitored

Variant	Area first detected	Cumulative Washington cases detected	First detection in Washington*	Most recent detection in Washington*
Alpha (B.1.1.7)	United Kingdom	10,337	Jan 07, 21	Sep 08, 21
Beta (B.1.351)	South Africa	282	Jan 29, 21	Jun 29, 21
Delta (B.1.617.2 and AY lineages)	India	38,729	Apr 03, 21	Sep 02, 22
Epsilon (B.1.427 / B.1.429)	California	4,191	Dec 11, 20	Jun 24, 21
Eta (B.1.525)	New York	92	Feb 02, 21	Jun 08, 21
Gamma (P.1)	Brazil	2,498	Feb 06, 21	Dec 02, 21
Iota (B.1.526)	New York	933	Jan 21, 21	Aug 20, 21
Kappa (B.1.617.1)	India	46	Mar 22, 21	Jun 14, 21
Mu (B.1.621)	Colombia	219	Apr 09, 21	Dec 20, 21
Zeta (P.2)	Brazil	45	Jan 18, 21	Apr 20, 21

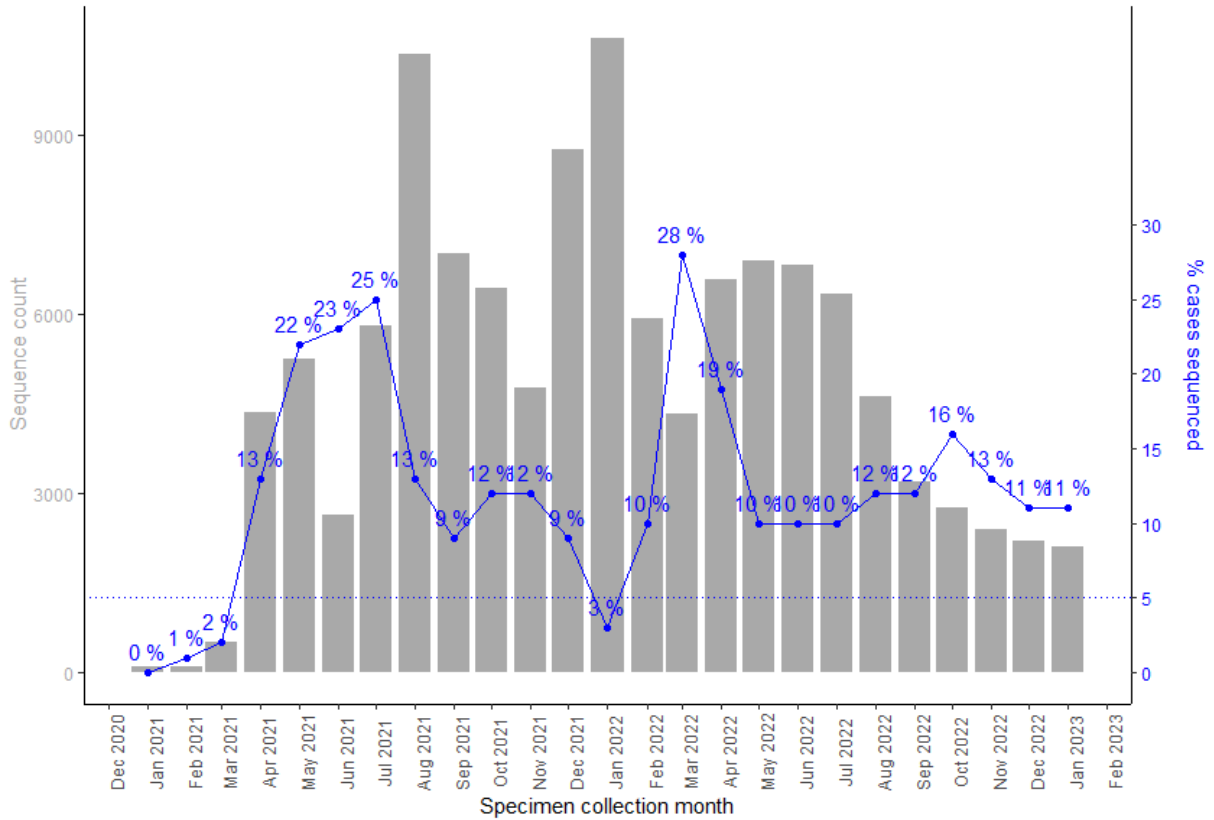
\*Detection dates are based on the date a sample is collected, it can take several weeks before a variant result is completed and added to the report

## Epidemiologic curve of variants being monitored and variants of concern by week of specimen collection date from January 01, 2021 to February 10, 2023



- The above graph shows the total number of variants detected by the week the specimen was collected from a patient.
- Sequencing can be performed on stored patient specimens at any time, so these numbers may change as additional specimens are sequenced.
- This graph shows all specimens sequenced, including specimens sequenced during outbreaks and other targeted sequencing efforts.
- “Other Omicron “ includes B.1.1.529, BA.1 and BA.3 sublineages

**Number of specimens sequenced, and percent of Washington State confirmed COVID-19 cases that have been sequenced by specimen collection date from January 2021 through January 2023.**

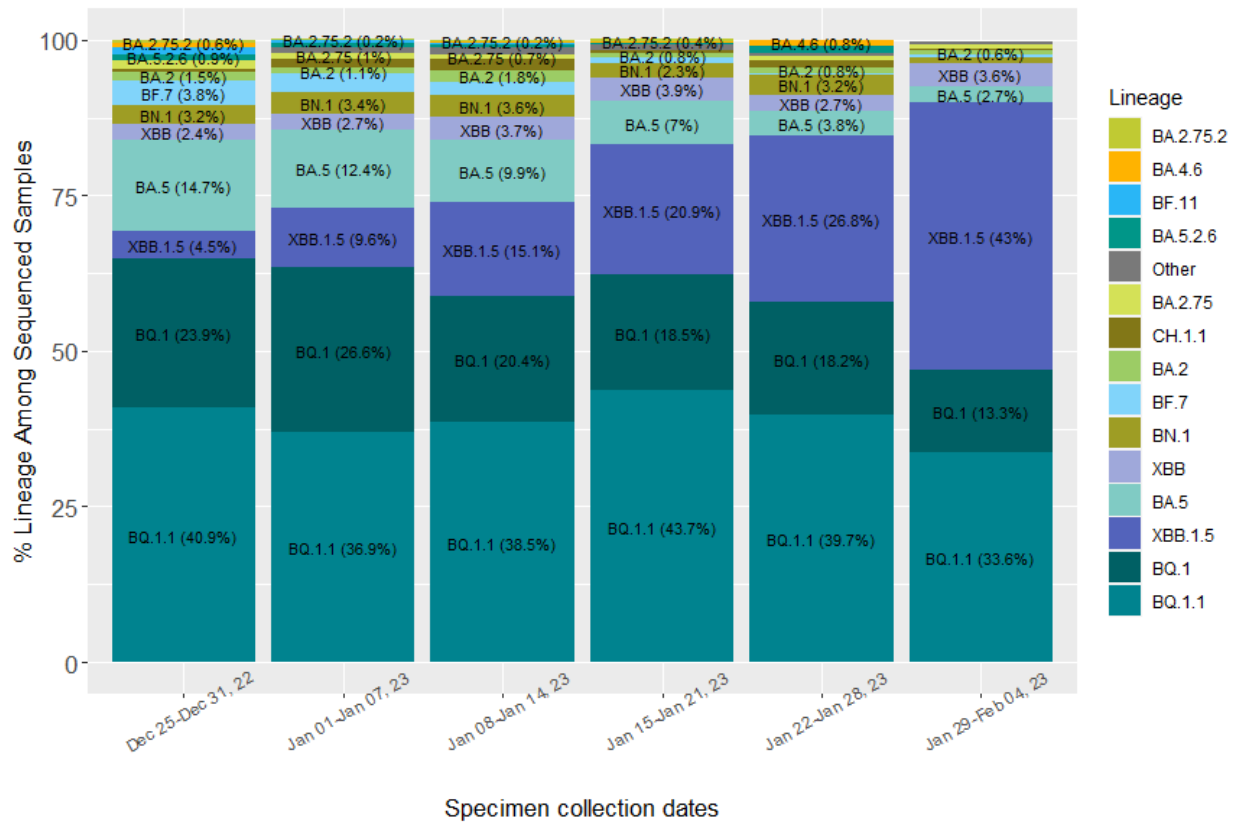


- Samples are not sequenced for every confirmed COVID-19 case. The above graph shows the total number of specimens sequenced (gray bars) and the percent of all confirmed cases (blue line) that have had sequencing performed each month. Data from the previous month may still be incomplete.
- Sequencing can be performed on stored specimens at any time, so numbers from past months may change if stored specimens are sequenced.

## SARS-CoV-2 Lineages Circulating in Washington State

The graph below shows the change in proportion of select SARS-CoV-2 lineages by time period. A viral lineage is a group of viruses that descend from a common ancestor with shared genetic characteristics, allowing them to be grouped together. As the proportions of variants increase, the proportion of other lineages will decrease.

NOTE: The data on this graph come from cases that are randomly selected for sequencing statewide, Cases sequenced because they were part of an outbreak or were otherwise manually selected for sequencing are excluded.



The chart above shows the proportions of the most common SARS-CoV-2 lineages circulating in Washington grouped in one-week intervals. Proportions are calculated using data which are subject to change over time and will be updated as more data becomes available, including data from prior time periods. **Due to the time it takes to complete sequencing, the most recent time period is based on a very small number of sequences and likely to be adjusted over time.**

To see the national trends, visit the CDC's [variant proportions page](#).



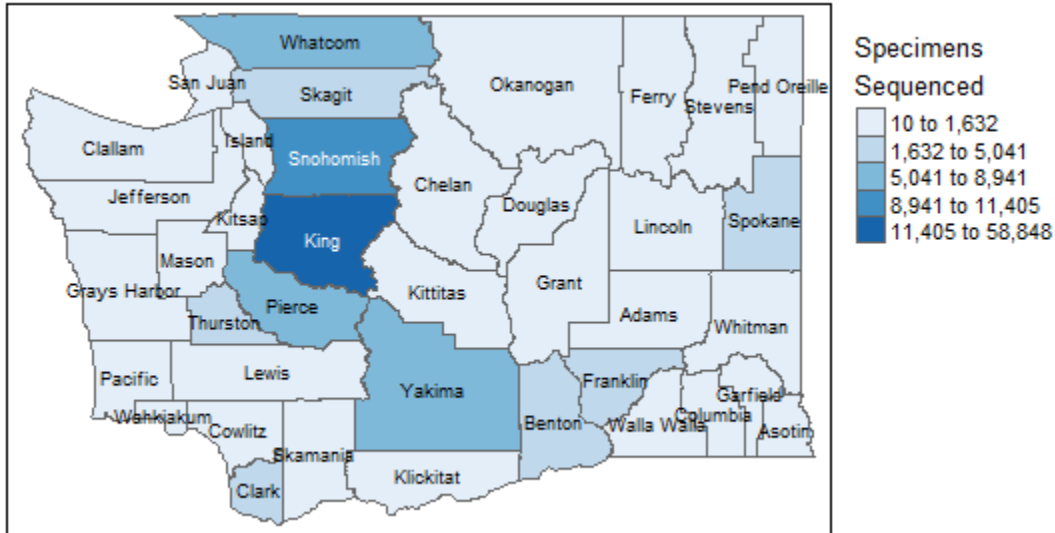
The figure below shows the current number of variants of concern (VOC) detected by county of home address since four months prior; data is from the Washington Disease Reporting System (WDRS).



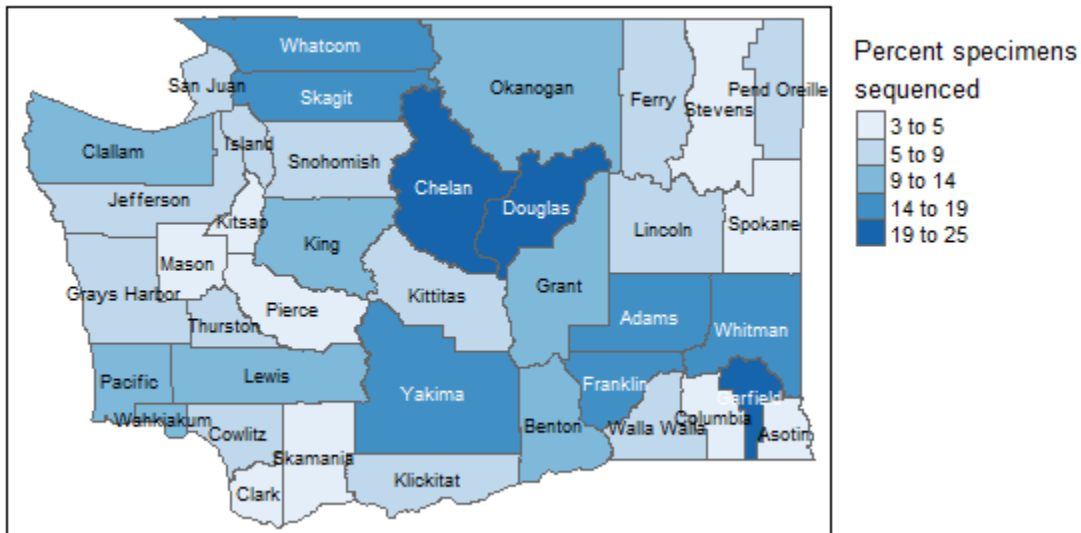
## Geographic Coverage of Sequencing

Efforts are made to sequence specimens from all geographic areas of Washington State. The number of sequences and the percent of cases sequenced vary based on several factors including number of cases in that region and which laboratories conduct the majority of testing in each locality.

The map below shows the number of specimens sequenced by county of home address since January 1, 2021.



The map below shows the percent of COVID-19 cases with at least one specimen sequenced by county of home address since January 1, 2021.



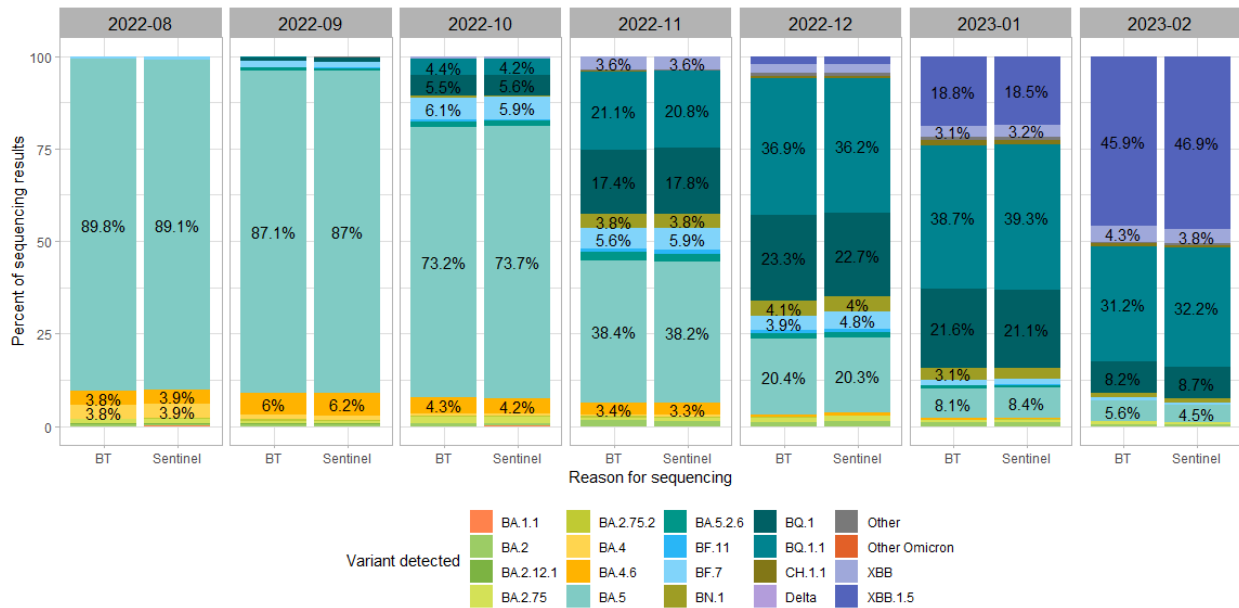
## Vaccine Breakthrough Cases

A complete report on vaccine breakthrough cases can be found in the reports section of the [DOH data dashboard](#).

A vaccine breakthrough case is defined as someone who tests positive for SARS-CoV-2 (either a PCR test or antigen test) at least 14 days after a person received their last recommended dose of an authorized, age-appropriate COVID-19 vaccine. DOH is monitoring sequencing results for vaccine breakthrough cases. This can help scientists determine whether any specific variants of the virus are causing more breakthrough cases than expected.

The table and chart below show vaccine breakthrough cases based on lineages. Lineages not designated as VOC, VOI or VBM are marked as 'Other'.

**Proportion of variants identified among vaccine breakthrough cases (Breakthrough) with sequencing results compared to variants identified among randomly selected COVID-19 cases (Sentinel) during the same time frame. This shows if breakthrough cases are enriched for particular variant(s) compared to the unbiased sentinel controls.**



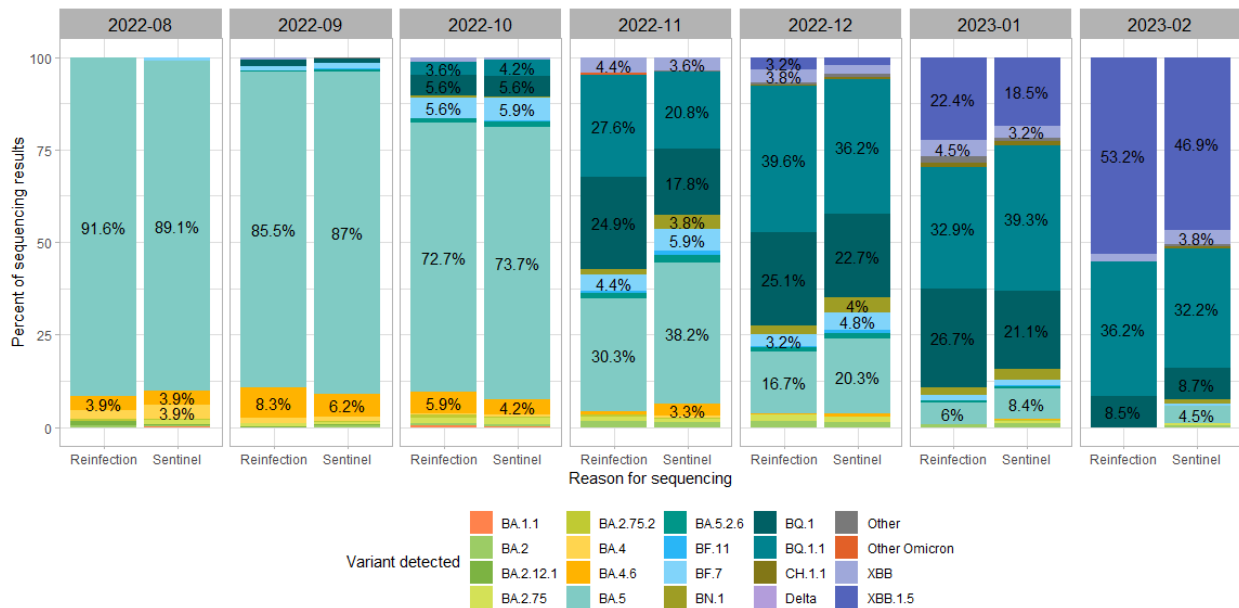
## Breakthrough cases by variant table

Variant	2022-08	2022-09	2022-10	2022-11	2022-12	2023-01	2023-02
BA.2	4	10	19	29	18	16	1
BA.2.12.1	5	7	0	0	0	0	0
BA.2.75	13	19	35	15	22	12	2
BA.2.75.2	1	9	11	8	4	2	0
BA.4	46	29	14	6	0	0	0
BA.4.6	46	150	97	67	12	6	0
BA.5	1,084	2,176	1,665	749	362	140	13
BA.5.2.6	1	18	32	42	29	13	0
BF.11	0	3	9	18	11	2	0
BF.7	6	41	139	110	70	26	2
BN.1	0	0	10	75	73	54	3
BQ.1	0	26	125	340	413	372	19
BQ.1.1	0	4	100	412	654	668	72
CH.1.1	0	0	1	1	11	22	2
Delta	0	1	0	0	0	0	0
Other	1	4	1	6	15	14	1
Other Omicron	0	0	0	1	0	0	0
XBB	0	1	16	70	42	54	10
XBB.1.5	0	0	1	2	37	325	106

## Reinfection

In general, reinfection means a person was infected once with the virus that causes COVID-19, recovered, and then later became infected again. We are still learning about COVID-19 and the duration and strength of immunity following infection with this virus. Based on what we know from similar respiratory viruses, we expect some COVID-19 reinfections to occur. For disease surveillance purposes, a person with a reported reinfection is an individual with two positive COVID-19 test results (molecular or antigen) reported to DOH where the tests were performed at least 90 days apart. In addition, if genetic sequencing of respiratory samples from a patient's first (or primary) infection and most recent infection identifies different variants, they are considered a confirmed reinfection regardless of the amount of time between positive tests. Washington State Department of Health adopted this definition on September 1, 2021.

DOH is monitoring sequencing results for reinfection cases. This can help scientists determine whether any specific variants of the virus are causing more reinfection cases than expected. The table and chart below show reinfection cases based on lineages. Lineages not designated as VOC, VOI or VBM are marked as 'other'. Proportion of variants identified among reinfection cases (Reinfection) with sequencing results compared to variants identified among randomly selected COVID-19 cases (Sentinel) during the same time frame.



## Reinfection cases by variant table

Please note - data for the most recent month are incomplete

Variant	2022-08	2022-09	2022-10	2022-11	2022-12	2023-01	2023-02
BA.1.1	0	0	1	0	0	0	0
BA.2	1	0	2	5	6	3	0
BA.2.12.1	2	1	0	0	0	0	0
BA.2.75	0	3	5	3	7	0	0
BA.2.75.2	1	0	2	2	0	0	0
BA.4	4	4	1	0	0	0	0
BA.4.6	7	28	18	3	1	0	0
BA.5	164	290	221	90	62	24	0
BA.5.2.6	0	1	4	5	4	2	0
BF.11	0	0	0	1	1	0	0
BF.7	0	4	17	13	12	6	0
BN.1	0	0	1	5	9	8	0
BQ.1	0	6	17	74	93	107	4
BQ.1.1	0	0	11	82	147	132	17
CH.1.1	0	0	0	0	1	4	0
Other	0	0	0	0	2	7	0
Other Omicron	0	0	0	1	0	0	0
XBB	0	2	4	13	14	18	1
XBB.1.5	0	0	0	0	12	90	25

The hospitalization table below includes sequencing data since January 1, 2021 and does not account for factors that can influence hospitalization rates such as age and vaccination status, which may be different across variants. This means that hospitalization rates are not necessarily comparable between variants.

### Hospitalizations and deaths by variant

Variant	Percent cases who were hospitalized	Cases who were hospitalized per 100,000	Cases who died from COVID-19	Total cases	Percent of hospitalized cases who died from COVID-19
Delta	4.3%	4,256	1.3%	38,601	17.2%
BA.5	2%	2,032	0.3%	17,568	9.2%
BA.2	1.1%	1,090	0.2%	13,764	8%
Other Omicron	1.1%	1,127	0.3%	12,339	13.7%
BA.1.1	2.3%	2,348	0.8%	11,245	14.4%
Alpha	3.5%	3,454	0.6%	10,307	12.6%
BA.2.12.1	1.7%	1,708	0.3%	6,790	10.3%
Other	2.6%	2,585	0.8%	5,299	16.8%
Epsilon	2.6%	2,588	0.7%	4,135	16.8%
Gamma	6.8%	6,849	1.7%	2,482	17.6%
BQ.1.1	2.5%	2,524	0.1%	2,338	3.4%
BQ.1	1.8%	1,772	0.5%	1,580	10.7%
BA.4	1.9%	1,882	0.3%	1,435	3.7%
Iota	3.2%	3,226	1.3%	930	30%
BA.4.6	2.9%	2,899	0.6%	690	5%
XBB.1.5	1.6%	1,579	0.4%	570	11.1%
BF.7	3.2%	3,220	0.8%	528	23.5%
Beta	7.1%	7,117	1.1%	281	15%
BN.1	1.6%	1,575	0.4%	254	25%
XBB	0.8%	844	0%	237	0%
Mu	2.8%	2,752	1.8%	218	33.3%
BA.2.75	1.1%	1,111	0%	180	0%

Variant	Percent cases who were hospitalized	Cases who were hospitalized per 100,000	Cases who died from COVID-19	Total cases	Percent of hospitalized cases who died from COVID-19
BA.5.2.6	2.4%	2,367	0.6%	169	25%
Eta	1.1%	1,087	1.1%	92	100%
BF.11	1.7%	1,667	0%	60	0%
Kappa	2.2%	2,174	0%	46	0%
Zeta	2.2%	2,222	0%	45	0%



## Age distribution by variant

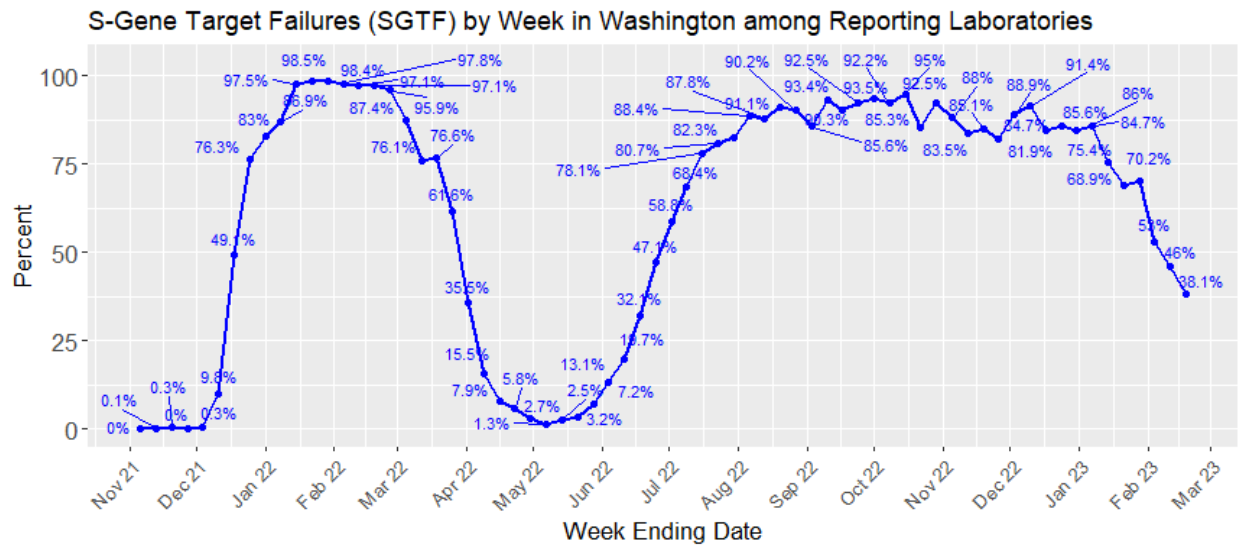
Variant	Age 0-19	Age 20-34	Age 35-49	Age 50-64	Age 65-79	Age 80+	Unknown	Total cases
Delta	23%	29%	23%	15%	8%	2%	0%	38,601
BA.5	12%	28%	26%	20%	12%	3%	0%	17,568
BA.2	19%	32%	24%	15%	8%	2%	0%	13,764
Other Omicron	24%	33%	23%	13%	5%	1%	0%	12,339
BA.1.1	24%	30%	22%	14%	7%	2%	0%	11,245
Alpha	27%	32%	23%	13%	3%	1%	0%	10,307
BA.2.12.1	15%	32%	24%	17%	9%	3%	0%	6,790
Other	24%	29%	24%	16%	5%	2%	0%	5,299
Epsilon	25%	31%	24%	14%	4%	1%	0%	4,135
Gamma	22%	35%	24%	12%	4%	3%	0%	2,482
BQ.1.1	12%	27%	28%	19%	11%	3%	0%	2,338
BQ.1	12%	27%	26%	20%	12%	3%	0%	1,580
BA.4	17%	31%	26%	16%	8%	2%	0%	1,435
Iota	25%	33%	25%	12%	4%	1%	0%	930
BA.4.6	13%	31%	24%	16%	13%	2%	0%	690
XBB.1.5	15%	27%	28%	18%	9%	2%	0%	570
BF.7	10%	26%	22%	23%	13%	5%	0%	528
Beta	29%	34%	21%	12%	3%	0%	0%	281
BN.1	6%	25%	31%	19%	14%	4%	0%	254
XBB	11%	34%	24%	22%	8%	1%	0%	237
Mu	22%	37%	22%	11%	6%	1%	0%	218
BA.2.75	11%	26%	31%	17%	14%	1%	0%	180
BA.5.2.6	11%	30%	25%	16%	15%	2%	0%	169
Eta	32%	28%	25%	10%	5%	0%	0%	92
BF.11	12%	27%	23%	28%	8%	2%	0%	60
BA.2.75.2	8%	38%	27%	21%	6%	0%	0%	48
CH.1.1	4%	30%	30%	22%	11%	2%	0%	46

Variant	Age 0-19	Age 20-34	Age 35-49	Age 50-64	Age 65-79	Age 80+	Unknown	Total cases
Kappa	20%	41%	26%	9%	4%	0%	0%	46
Zeta	29%	22%	31%	18%	0%	0%	0%	45

\*Other includes all variant viruses that are not categorized as VOC or VBM

## Tracking Omicron Using Clinical Tests

WA DOH is tracking the Omicron variant using sequencing. One challenge is that the sequencing process can take up to a few weeks, so we use another testing marker known as ‘S gene target failure (SGTF)’ to identify possible Omicron cases carrying this mutation rapidly and inform public health action. Variants with SGTF include BA.1, BA.3, BA.4 and BA.5 and BA.5 sub-lineages BQ.1 and BQ.1.1. Variants without this mutation that do have S-gene target presence include BA.2 and sub-lineages BA.2.12.1, BA.2.75, CH.1.1, XBB and XBB.1.5. While SGTF does not always mean that a case will be finalized as Omicron, greater than 95% of these results are predicted to finalize as Omicron. Many laboratories are sharing this data with WA DOH to help track the spread of Omicron.



A small number of other SARS-CoV-2 viruses other than Omicron can cause SGTF, these can be seen in the small numbers (0-3) seen weekly prior to the week of November 28th.

First Day of Week	Last Day of Week	Total Positives	Total SGTF	Percent SGTF
2021-10-31	2021-11-06	1,086	0	0%
2021-11-07	2021-11-13	1,093	1	0.1%
2021-11-14	2021-11-20	1,129	3	0.3%
2021-11-21	2021-11-27	1,267	0	0%
2021-11-28	2021-12-04	2,414	8	0.3%
2021-12-05	2021-12-11	2,342	229	9.8%
2021-12-12	2021-12-18	3,162	1,552	49.1%
2021-12-19	2021-12-25	4,528	3,456	76.3%
2021-12-26	2022-01-01	5,033	4,178	83%
2022-01-02	2022-01-08	10,893	9,469	86.9%

First Day of Week	Last Day of Week	Total Positives	Total SGTF	Percent SGTF
2022-01-09	2022-01-15	13,481	13,149	97.5%
2022-01-16	2022-01-22	11,754	11,581	98.5%
2022-01-23	2022-01-29	8,363	8,233	98.4%
2022-01-30	2022-02-05	4,686	4,581	97.8%
2022-02-06	2022-02-12	2,696	2,619	97.1%
2022-02-13	2022-02-19	1,372	1,332	97.1%
2022-02-20	2022-02-26	627	601	95.9%
2022-02-27	2022-03-05	478	418	87.4%
2022-03-06	2022-03-12	355	270	76.1%
2022-03-13	2022-03-19	334	256	76.6%
2022-03-20	2022-03-26	375	231	61.6%
2022-03-27	2022-04-02	332	118	35.5%
2022-04-03	2022-04-09	381	59	15.5%
2022-04-10	2022-04-16	544	43	7.9%
2022-04-17	2022-04-23	762	44	5.8%
2022-04-24	2022-04-30	1,143	31	2.7%
2022-05-01	2022-05-07	1,190	15	1.3%
2022-05-08	2022-05-14	1,419	36	2.5%
2022-05-15	2022-05-21	1,602	51	3.2%
2022-05-22	2022-05-28	1,516	109	7.2%
2022-05-29	2022-06-04	1,295	169	13.1%
2022-06-05	2022-06-11	1,270	250	19.7%
2022-06-12	2022-06-18	1,167	375	32.1%
2022-06-19	2022-06-25	1,236	582	47.1%
2022-06-26	2022-07-02	1,092	642	58.8%
2022-07-03	2022-07-09	1,122	767	68.4%
2022-07-10	2022-07-16	999	780	78.1%
2022-07-17	2022-07-23	1,032	833	80.7%
2022-07-24	2022-07-30	979	806	82.3%
2022-07-31	2022-08-06	658	582	88.4%

First Day of Week	Last Day of Week	Total Positives	Total SGTF	Percent SGTF
2022-08-07	2022-08-13	576	506	87.8%
2022-08-14	2022-08-20	551	502	91.1%
2022-08-21	2022-08-27	449	405	90.2%
2022-08-28	2022-09-03	341	292	85.6%
2022-09-04	2022-09-10	271	253	93.4%
2022-09-11	2022-09-17	331	299	90.3%
2022-09-18	2022-09-24	333	308	92.5%
2022-09-25	2022-10-01	429	401	93.5%
2022-10-02	2022-10-08	296	273	92.2%
2022-10-09	2022-10-15	200	190	95%
2022-10-16	2022-10-22	150	128	85.3%
2022-10-23	2022-10-29	160	148	92.5%
2022-10-30	2022-11-05	184	162	88%
2022-11-06	2022-11-12	182	152	83.5%
2022-11-13	2022-11-19	222	189	85.1%
2022-11-20	2022-11-26	216	177	81.9%
2022-11-27	2022-12-03	262	233	88.9%
2022-12-04	2022-12-10	185	169	91.4%
2022-12-11	2022-12-17	190	161	84.7%
2022-12-18	2022-12-24	160	137	85.6%
2022-12-25	2022-12-31	163	138	84.7%
2023-01-01	2023-01-07	114	98	86%
2023-01-08	2023-01-14	138	104	75.4%
2023-01-15	2023-01-21	151	104	68.9%
2023-01-22	2023-01-28	121	85	70.2%
2023-01-29	2023-02-04	115	61	53%
2023-02-05	2023-02-11	126	58	46%
2023-02-12	2023-02-18	113	43	38.1%

We thank the reporting laboratories: University of Washington Virology, Avero Diagnostics, The Vancouver Clinic, Atlas Laboratories, Evergreen Health, FidaLab

We gratefully acknowledge the laboratories that tested and sequenced the specimens for reporting the sequencing metadata including the lineages to WA DOH. We also thank the GISAID initiative as the whole genome sequencing data stored in their repository has helped us validate the submissions we receive from laboratories.

**The following clinical laboratories have contributed specimens for sequencing:**

Aegis Sciences Corporation  
Allenmore Hospital Laboratory  
Altius Institute for Biomedical Sciences  
Atlas Genomics  
BioReference Laboratories Inc.  
Cascade Valley Hospital  
Central Washington Hospital  
Columbia Basin Hospital  
Curative Labs Inc.  
Dayton General Hospital  
Deaconess Hospital  
Diatherix Laboratories  
Dynacare Northwest Inc.  
East Adams Rural Hospital  
Everett Clinic Microbiology  
Evergreen Healthcare  
Ferry County Hospital  
FidaLab  
Forks Community Hospital  
Fulgent Genetics  
Gravity Diagnostics, LLC  
Harborview Medical Center  
Healthquest Esoterics  
Helix/Illumina

Incyte Diagnostics Spokane  
Infinity Biologix  
Interpath Laboratory  
Jefferson Healthcare  
Kaiser Permanente Washington Health Research Institute  
Labcorp  
Laboratories Northwest  
Laboratory Corporation of America  
Legacy Laboratory  
Magnolia Diagnostics, LLC  
Mann-Grandstaff VA Medical Center  
Mason General Hospital Laboratory  
Mid Valley Hospital  
Molecular Testing Labs  
MultiCare  
Avero Diagnostics  
OHSU Lab Services Molecular Microbiology Lab  
Olympic Medical Center  
Overlake Hospital  
PeaceHealth  
Polyclinic  
Premier Medical Laboratory  
Providence Medical Group  
Public Health Seattle-King County Laboratory  
Quest Diagnostics Incorporated  
Samaritan Hospital Lab  
Seattle & King County Public Health Lab  
Seattle Children's Hospital  
Seattle Flu Study

Skagit Valley Hospital Laboratory  
St. Francis Hospital  
St. Joseph Medical Center Microbiology  
St. Michael Medical Center Laboratory  
Swedish Medical Center  
Tacoma General Hospital  
The Vancouver Clinic  
Tomorrow's Health, LLC  
TridentCare Laboratory  
TridentCare Laboratory  
University of Washington Virology Lab  
Virginia Mason Franciscan Health Microbiology  
Washington State Department of Health Public Health Laboratories

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**The following labs have reported sequencing data that is included in this report:**

Aegis Laboratory  
Altius Institute for Biomedical Research  
Atlas Genomics  
Boise VA Medical Center  
Centers for Disease Control and Prevention  
Curative  
Flow Diagnostics  
Fulgent Genetics  
Ginkgo Bioworks Clinical Laboratory  
Gravity Diagnostics, LLC  
Grittman Medical Center  
Grubaugh Lab  
Helix Laboratories  
Idaho Bureau of Laboratories



Infinity Biologix  
Institute for Systems Biology  
Kaiser Permanente  
Laboratory Corporation of America  
Montana Public Health Laboratory  
Naval Health Research Center  
Oregon SARS-CoV-2 Genome Sequencing Center  
Oregon State Public Health Laboratory  
Providence St. Joseph Health Molecular Genomics Laboratory  
Quest Diagnostics  
Seattle Flu Study  
The Jackson Laboratory  
The Luring Laboratory  
United States Arm Medical Research Institute of Infectious Diseases  
University of Washington Virology Lab  
Washington State Department of Health Public Health Laboratories

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