

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

**Washington State Department of Health**

**May 25, 2022**

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*Washington State Department of*  
***Health***

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

## Washington State Department of Health

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Next generation sequencing 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. Sequencing allows public health officials to detect clusters of cases, and monitor new lineages. Groups of same-species viruses that share a set of genome mutations are referred to as a lineage. Some lineages may have characteristics such as the ability to spread more quickly, or cause more severe disease. These lineages are classified as variants of interest, variants being monitored, 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 humans.

### **At a glance (data through May 24, 2022)**

- During the month of April 2022, **15.5%** 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.
- **94,581 (8.7%)** 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 and BA 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, including against the Omicron variant.	22,115	Nov 29, 21	May 09, 22

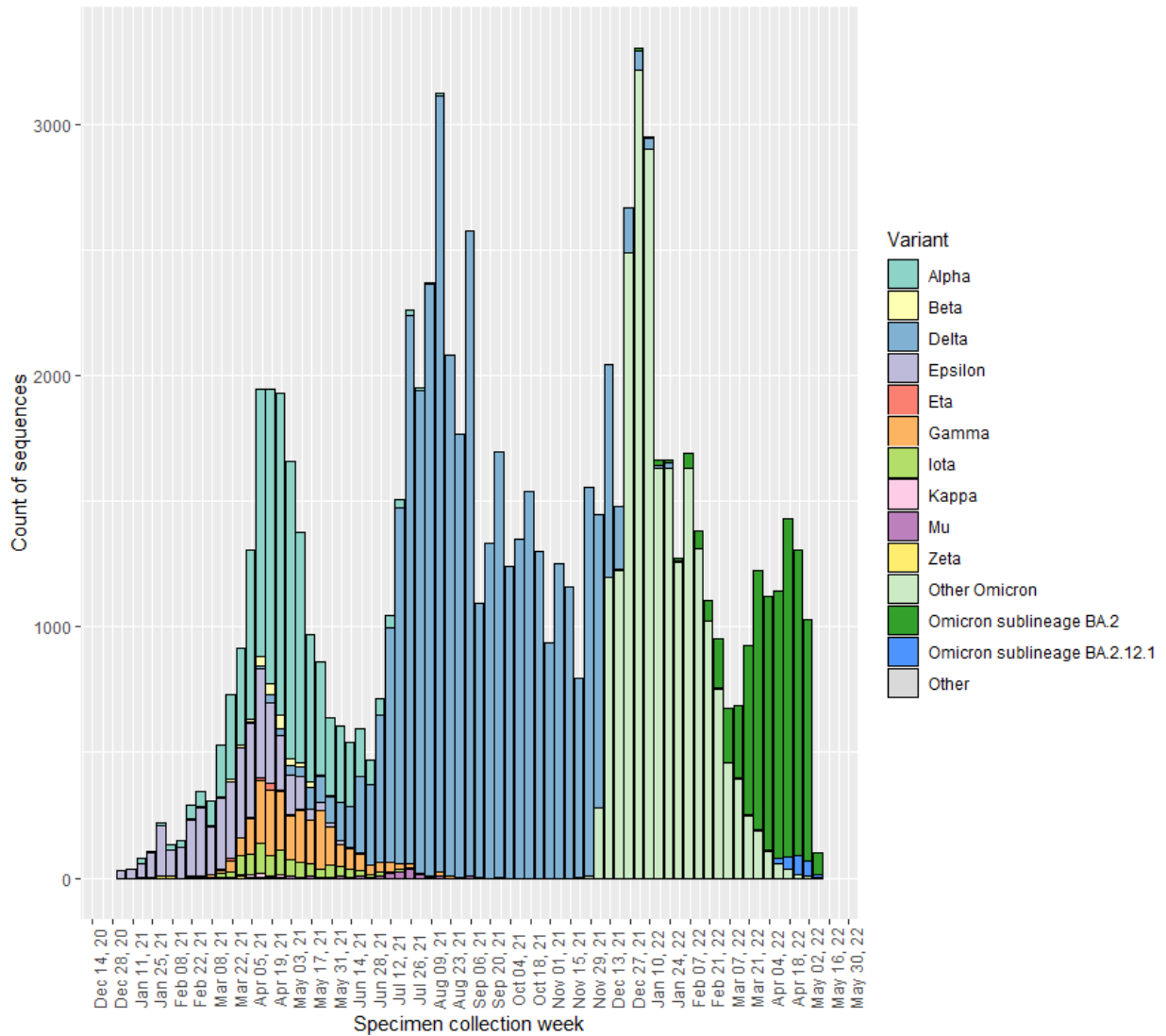
\*Detection dates are based on the date a sample is collected, it can take several weeks before a variant result is completed and added to the report

## 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	9,937	Jan 07, 21	Sep 08, 21
Beta (B.1.351)	South Africa	272	Jan 29, 21	Jun 29, 21
Delta (B.1.617.2 and AY lineages)	India	38,171	Apr 03, 21	Feb 28, 22
Epsilon (B.1.427 / B.1.429)	California	4,047	Dec 11, 20	Jun 24, 21
Eta (B.1.525)	New York	83	Feb 02, 21	Jun 08, 21
Gamma (P.1)	Brazil	2,401	Feb 06, 21	Dec 02, 21
Iota (B.1.526)	New York	896	Jan 21, 21	Aug 20, 21
Kappa (B.1.617.1)	India	46	Mar 22, 21	Jun 14, 21
Mu (B.1.621)	Colombia	184	Apr 09, 21	Dec 20, 21
Zeta (P.2)	Brazil	44	Jan 18, 21	Apr 20, 21

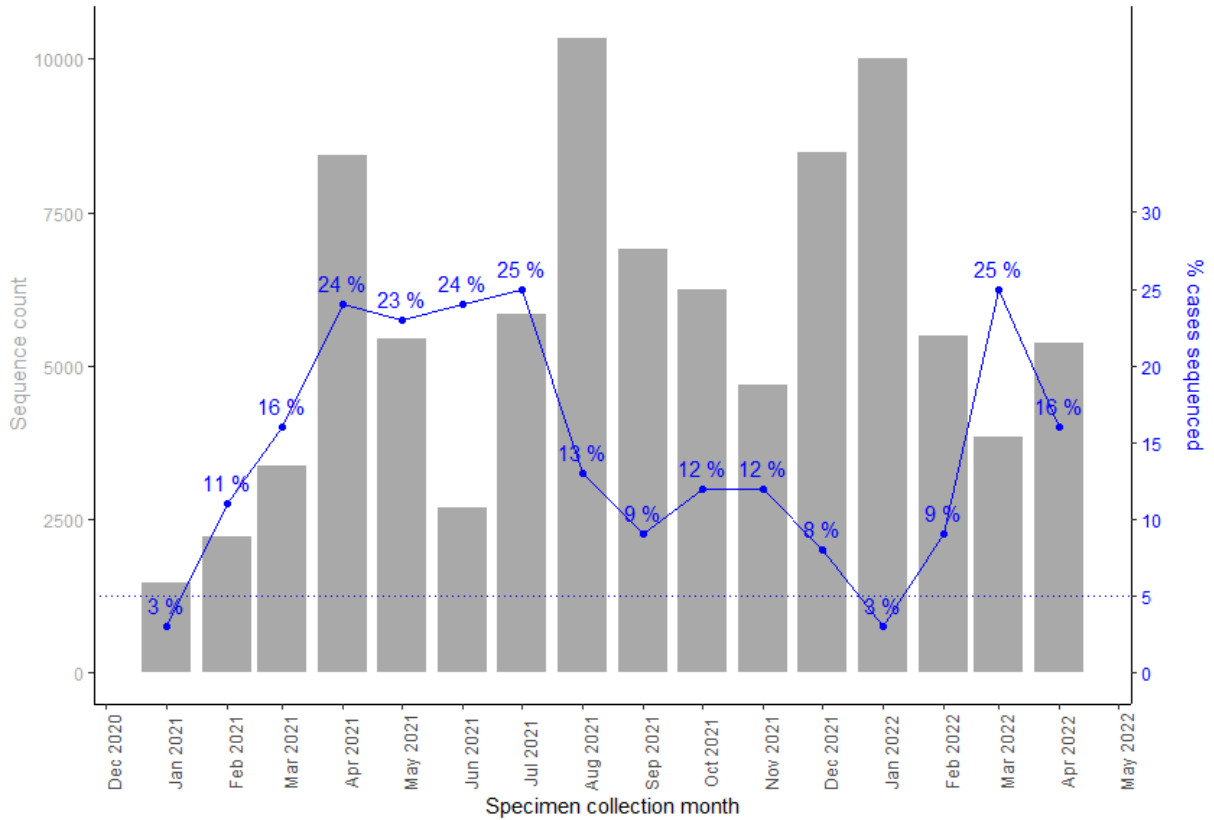
\*Detection dates are based on the date a sample is collected, it can take several weeks before a variant result is completed and added to the report

## Epidemiologic curve of variants being monitored and variants of concern by week of specimen collection date from January 01, 2021 to May 14, 2022



- 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.

**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 April 2022.**

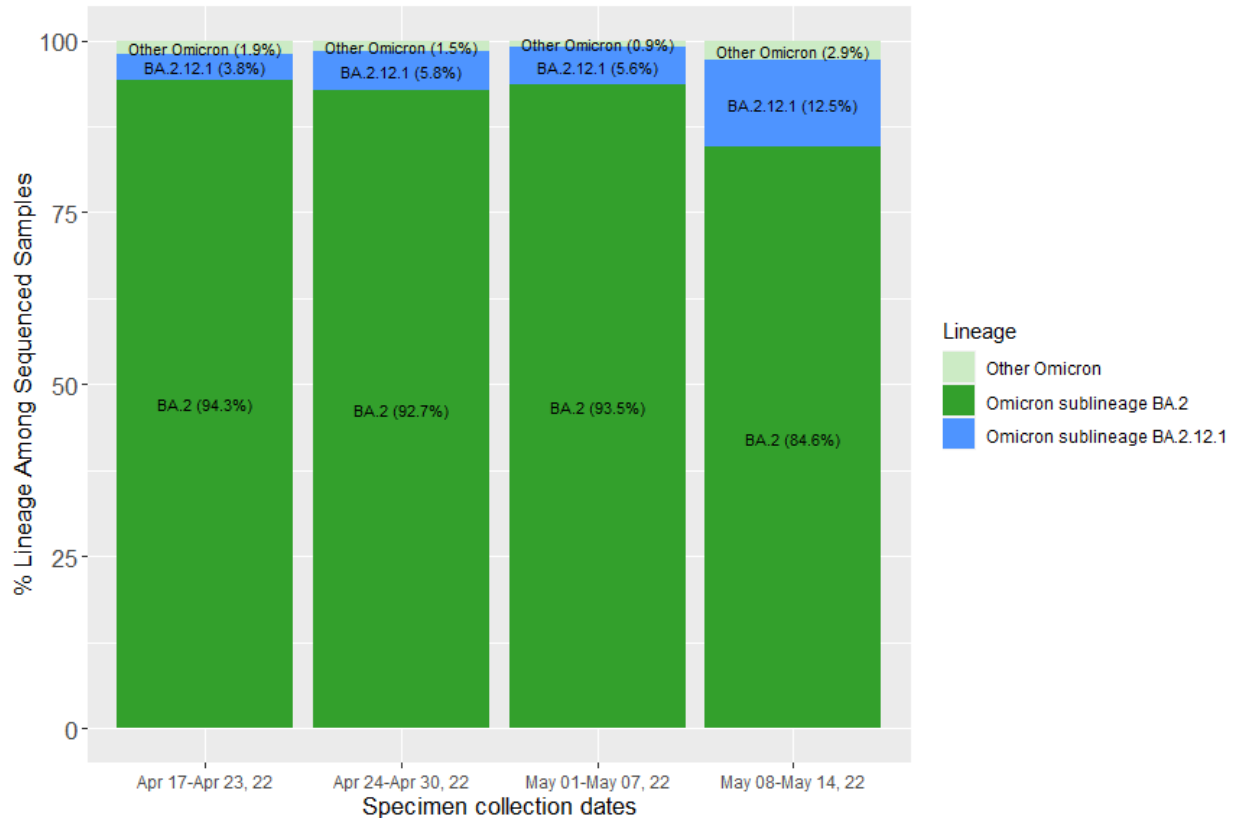


- Samples are not sequenced for every confirmed COVID-19 case. The above graph shows the total number of specimens sequenced (gray bars) and the percent of all confirmed cases (blue line) that have had sequencing performed each month. Data from the previous month may still be incomplete.
- Sequencing 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 table below shows the current number of variants of concern (VOC) detected by county of home address since January 2022.

County	VOC			Total VOC specimens sequenced
	Other Omicron	BA.2	BA.2.12.1	
Adams	1	2	0	67
Asotin	0	0	0	13
Benton	11	40	0	597
Chelan	3	18	0	190
Clallam	0	113	2	316
Clark	1	168	1	513
Columbia	0	1	0	7
Cowlitz	8	26	0	344
Douglas	1	9	0	121
Ferry	0	1	0	10
Franklin	6	16	0	405
Grant	2	2	0	266
Grays Harbor	15	64	0	475
Island	0	68	2	138
Jefferson	0	14	0	81
King	35	4,981	152	11,472
Kitsap	2	133	0	401
Kittitas	0	9	0	76
Klickitat	0	3	0	21
Lewis	13	10	1	252
Lincoln	0	1	0	7
Mason	1	18	0	112
Okanogan	1	3	0	127
Pacific	6	5	0	122
Pend Oreille	0	0	0	13
Pierce	11	445	4	1,677



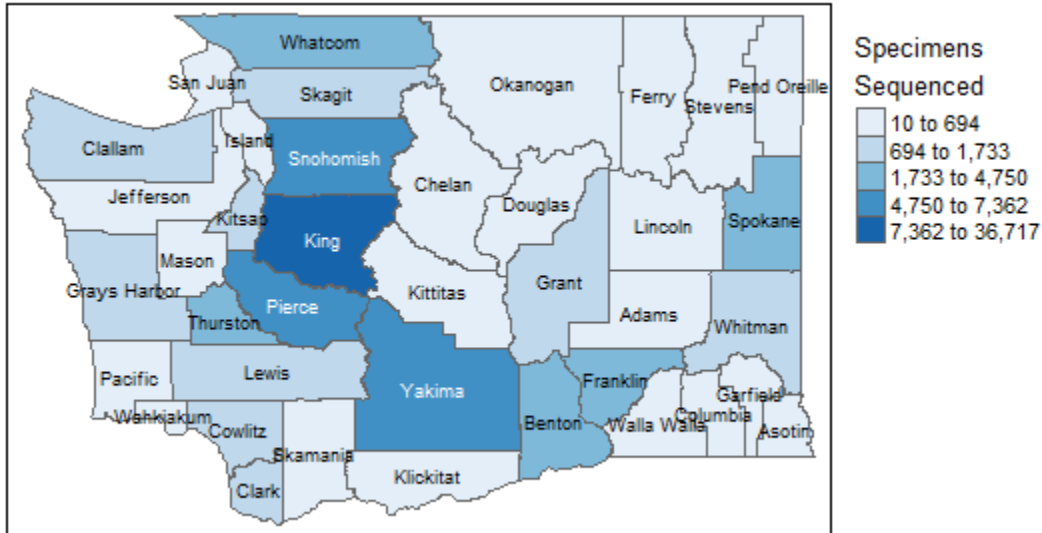
County	VOC			Total VOC specimens sequenced
	Other Omicron	BA.2	BA.2.12.1	
San Juan	0	3	0	19
Skagit	0	169	10	343
Skamania	0	1	0	6
Snohomish	4	896	23	1,996
Spokane	15	94	1	806
Stevens	1	2	0	30
Thurston	14	127	2	1,374
Wahkiakum	0	3	0	10
Walla Walla	1	14	1	179
Whatcom	2	837	38	1,507
Whitman	1	25	1	211
Yakima	11	44	2	1,368

- In this table, "Other Omicron" includes all B.1.1.529 and BA.1, BA.3, BA.4 and BA.5 sublineages

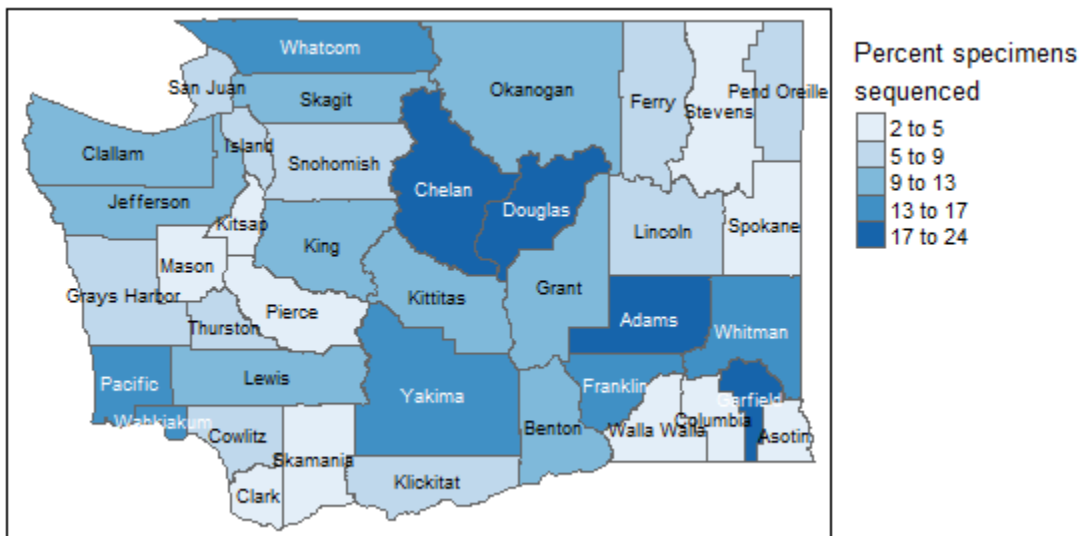
## Geographic Coverage of Sequencing

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 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.



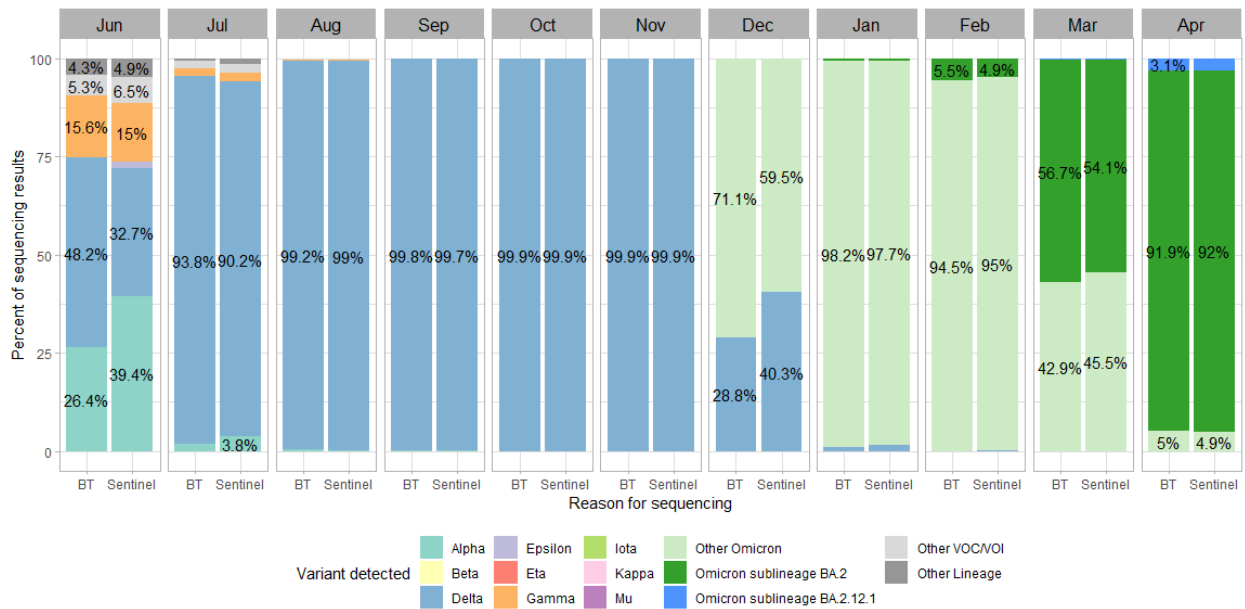
## Vaccine Breakthrough Cases

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 at least 14 days after their final dose of SARS-CoV-2 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**



## Breakthrough cases by variant table

Variant	Jun	Jul	Aug	Sep	Oct	Nov	Dec	Jan	Feb	Mar	Apr
Alpha	105	30	9	1	0	0	0	0	0	0	0
Delta	192	1,659	2,938	2,016	2,178	1,655	1,294	56	0	0	0
Epsilon	1	0	0	0	0	0	0	0	0	0	0
Gamma	62	33	6	0	0	0	1	0	0	0	0
Other Omicron	0	0	0	0	0	1	3,189	5,269	2,959	1,172	193
Omicron sublineage BA.2	0	0	0	0	0	0	0	39	171	1,546	3,559
Omicron sublineage BA.2.12.1	0	0	0	0	0	0	0	0	0	6	120

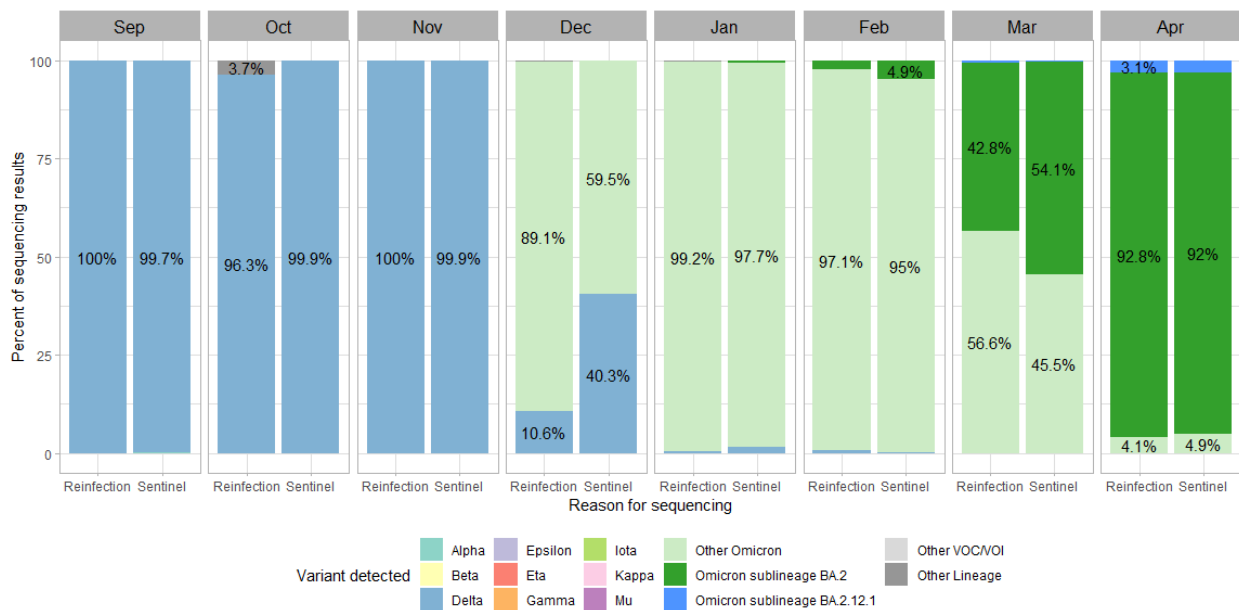
Variant	Jun	Jul	Aug	Sep	Oct	Nov	Dec	Jan	Feb	Mar	Apr
Other VOC/VOI	21	34	6	3	0	0	0	0	0	0	0
Other Lineage	17	13	4	0	2	1	3	4	2	5	1

## Reinfection

A complete report on reinfection cases can be found in the reports section of the DOH data dashboard.

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	Sep	Oct	Nov	Dec	Jan	Feb	Mar	Apr
Delta	32	52	46	28	2	2	0	0
Other Omicron	0	0	0	236	619	297	82	8
Omicron sublineage BA.2	0	0	0	0	1	7	62	180

Variant	Sep	Oct	Nov	Dec	Jan	Feb	Mar	Apr
Omicron sublineage BA.2.12.1	0	0	0	0	0	0	1	6
Other Lineage	0	2	0	1	2	0	0	0

The hospitalization table below includes 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	Cases who were hospitalized	Cases who died from COVID-19	Total cases
Other Omicron	1.3%	0.5%	22,086
BA.2	0.5%	0.1%	8,366
BA.2.12.1	0.4%	0%	240
Alpha	3.4%	0.5%	9,910
Beta	6.3%	0.4%	271
Delta	4.2%	1.3%	38,074
Epsilon	2.6%	0.7%	3,996
Gamma	6.7%	1.6%	2,386
Iota	3.1%	1.1%	893
Mu	3.3%	2.2%	183
Other	2.5%	0.7%	4,814

### Age distribution by variant

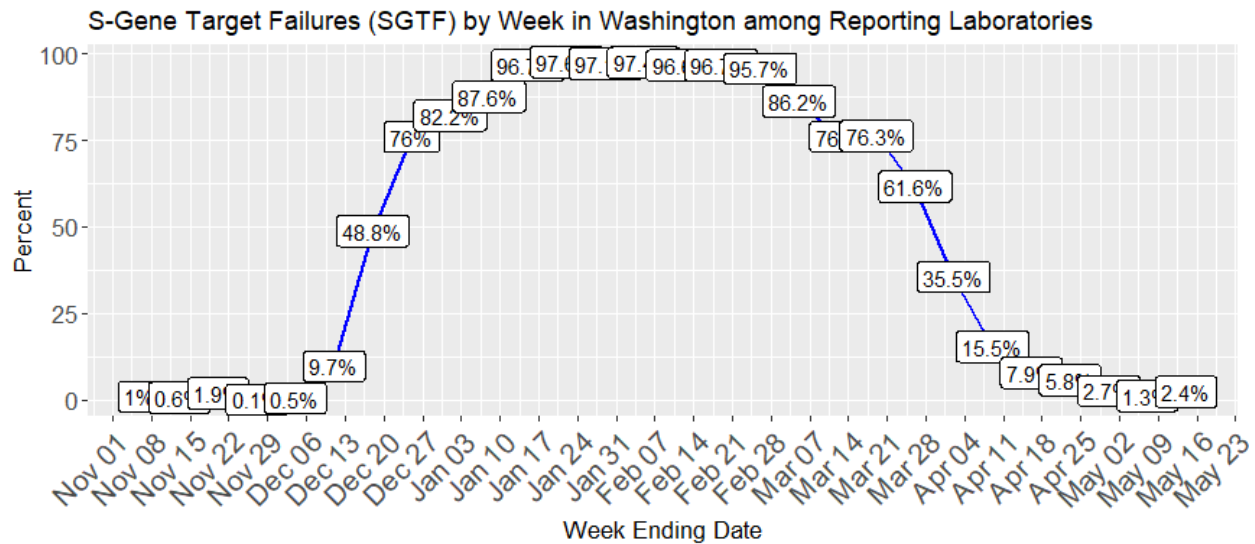
Variant	Age 0-19	Age 20-34	Age 35-49	Age 50-64	Age 65-79	Age 80+	Unknown	Total cases
Other Omicron	24%	32%	22%	13%	5%	2%	2%	22,086
//BA.2	19%	33%	23%	14%	7%	2%	2%	8,366
BA.2.12.1	22%	30%	18%	14%	10%	2%	4%	240
Alpha	27%	32%	22%	12%	3%	1%	2%	9,910
Beta	30%	35%	21%	11%	3%	0%	1%	271
Delta	23%	29%	22%	14%	7%	2%	2%	38,074
Epsilon	25%	31%	22%	14%	4%	1%	2%	3,996
Gamma	22%	35%	23%	11%	4%	3%	2%	2,386
Iota	25%	32%	24%	12%	4%	1%	1%	893
Mu	23%	37%	19%	12%	7%	1%	2%	183
Other	24%	29%	23%	15%	5%	2%	2%	4,814

\*Other includes all 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. BA.2 and BA.2.12.1 do not carry this mutation. 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. Additionally, the Omicron sub-lineage BA.2 and BA.2.12.1 do not carry this mutation.

First Day of Week	Last Day of Week	Total Positives	Total SGTF	Percent SGTF
2021-10-31	2021-11-06	1,249	13	1%
2021-11-07	2021-11-13	1,231	8	0.6%
2021-11-14	2021-11-20	1,240	24	1.9%
2021-11-21	2021-11-27	1,363	2	0.1%
2021-11-28	2021-12-04	2,578	13	0.5%
2021-12-05	2021-12-11	2,483	242	9.7%
2021-12-12	2021-12-18	3,304	1,614	48.8%
2021-12-19	2021-12-25	5,200	3,951	76%
2021-12-26	2022-01-01	6,484	5,329	82.2%
2022-01-02	2022-01-08	15,588	13,657	87.6%
2022-01-09	2022-01-15	16,599	16,050	96.7%

First Day of Week	Last Day of Week	Total Positives	Total SGTF	Percent SGTF
2022-01-16	2022-01-22	13,375	13,058	97.6%
2022-01-23	2022-01-29	8,895	8,640	97.1%
2022-01-30	2022-02-05	4,893	4,767	97.4%
2022-02-06	2022-02-12	2,794	2,700	96.6%
2022-02-13	2022-02-19	1,433	1,385	96.7%
2022-02-20	2022-02-26	674	645	95.7%
2022-02-27	2022-03-05	508	438	86.2%
2022-03-06	2022-03-12	367	279	76%
2022-03-13	2022-03-19	337	257	76.3%
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	664	16	2.4%

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

We gratefully acknowledge the GISAID initiative, original laboratories responsible for obtaining the specimens, as well as the submitting laboratories where the genome data were generated and shared via GISAID.

**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  
Northwest Laboratories  
Northwest Laboratories  
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  
Gritman 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 Loring 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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