

SARS-CoV-2 Sequencing and Variants in Washington State

Washington State Department of Health

December 01, 2021



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For more information or additional copies of this report:

Disease Control and Health Statistics
Public Health Outbreak Coordination, Informatics, and Surveillance
1610 NE 150th Street, MS: K17-9
Shoreline, WA 98155

Phone: 206-418-5700 (24-hour contact for local health jurisdictions only)

Email: CommDisEpi@doh.wa.gov

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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.

Washington State has increased sequencing capacity, and is currently sequencing at least 5% of positive specimens, which [ranks among the best](#) in the nation according to the Centers for Disease Control and Prevention (CDC).

At a glance (data through November 30, 2021)

- During the month of October 2021, **9.3%** 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.
- **50,900 (11.9%)** 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 of emergence	Background	Cumulative Washington cases detected	First detection in Washington*	Most recent detection in Washington*
Delta (B.1.617.2)	India	Delta is currently the dominant variant in Washington State. Delta has been found to be more transmissible than other variants such as Alpha, and some research indicates greater risk of hospitalization. Approved vaccines are effective at preventing severe disease and death, including against the Delta variant.	28,517	Feb 12, 21	Nov 20, 21

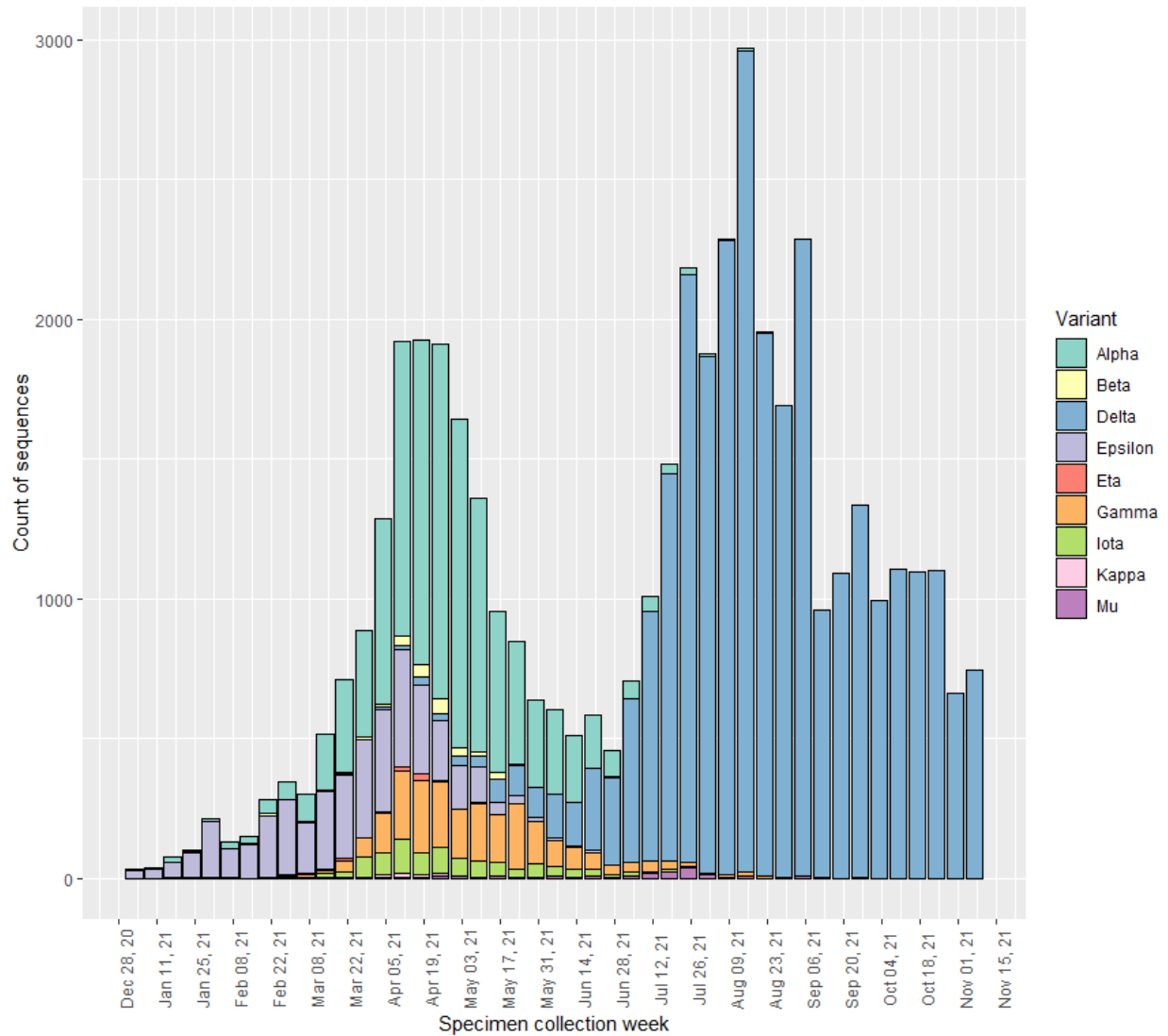
*Detection dates are based on the date a sample is collected, it can take several weeks before a variant result is completed and added to the report

Variants being monitored

Variant	Area of emergence	Cumulative Washington cases detected	First detection in Washington*	Most recent detection in Washington*
Alpha (B.1.1.7)	United Kingdom	9,799	Jan 07, 21	Sep 08, 21
Beta (B.1.351)	South Africa	270	Jan 29, 21	Jun 29, 21
Epsilon (B.1.427 / B.1.429)	California	3,982	Dec 11, 20	Jun 24, 21
Eta (B.1.525)	New York	83	Feb 02, 21	Jun 08, 21
Gamma (P.1)	Brazil	2,350	Feb 06, 21	Aug 27, 21
Iota (B.1.526)	New York	888	Jan 21, 21	Aug 20, 21
Kappa (B.1.617.1)	India	46	Mar 22, 21	Jun 14, 21
Mu (B.1.621)	Colombia	178	Apr 09, 21	Sep 26, 21

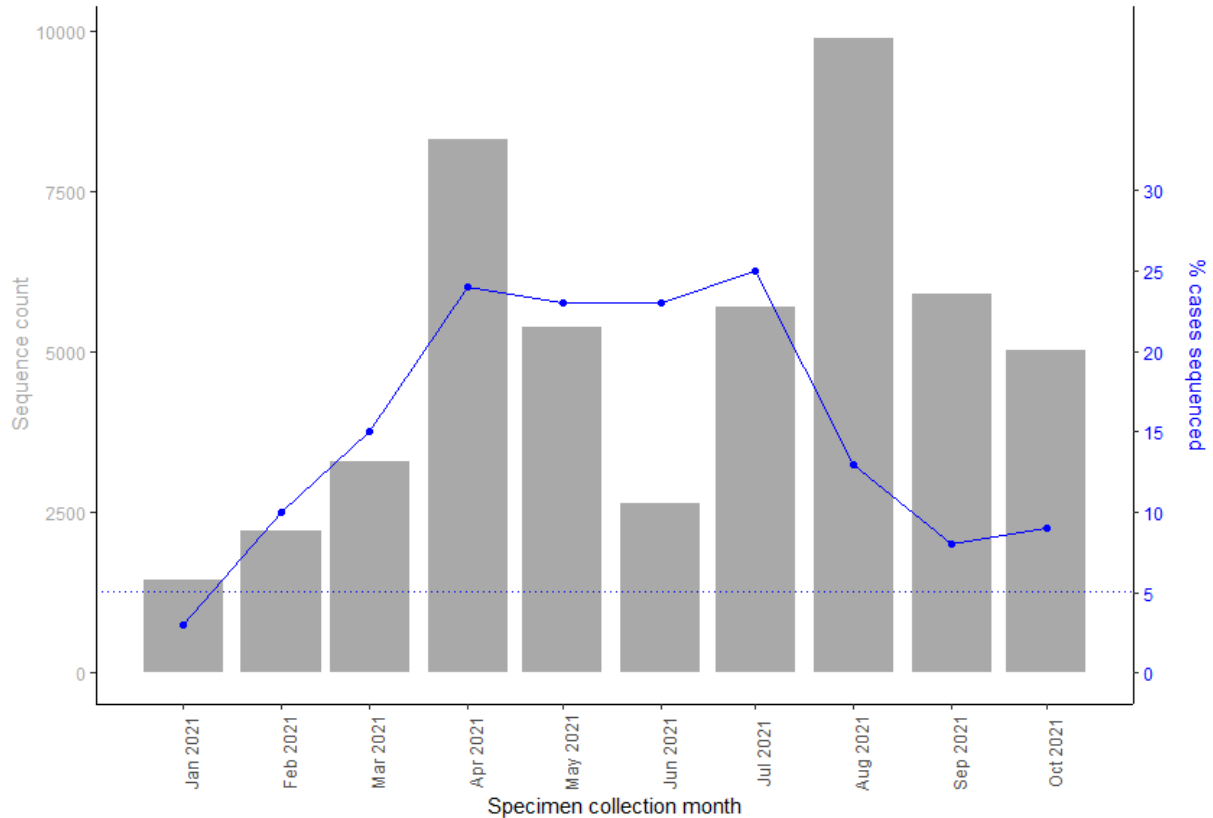
*Detection dates are based on the date a sample is collected, it can take several weeks before a variant result is completed and added to the report

Epidemiologic curve of variants being monitored and variants of concern by week of specimen collection date from January 01 to November 13, 2021



- 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 through October 2021.

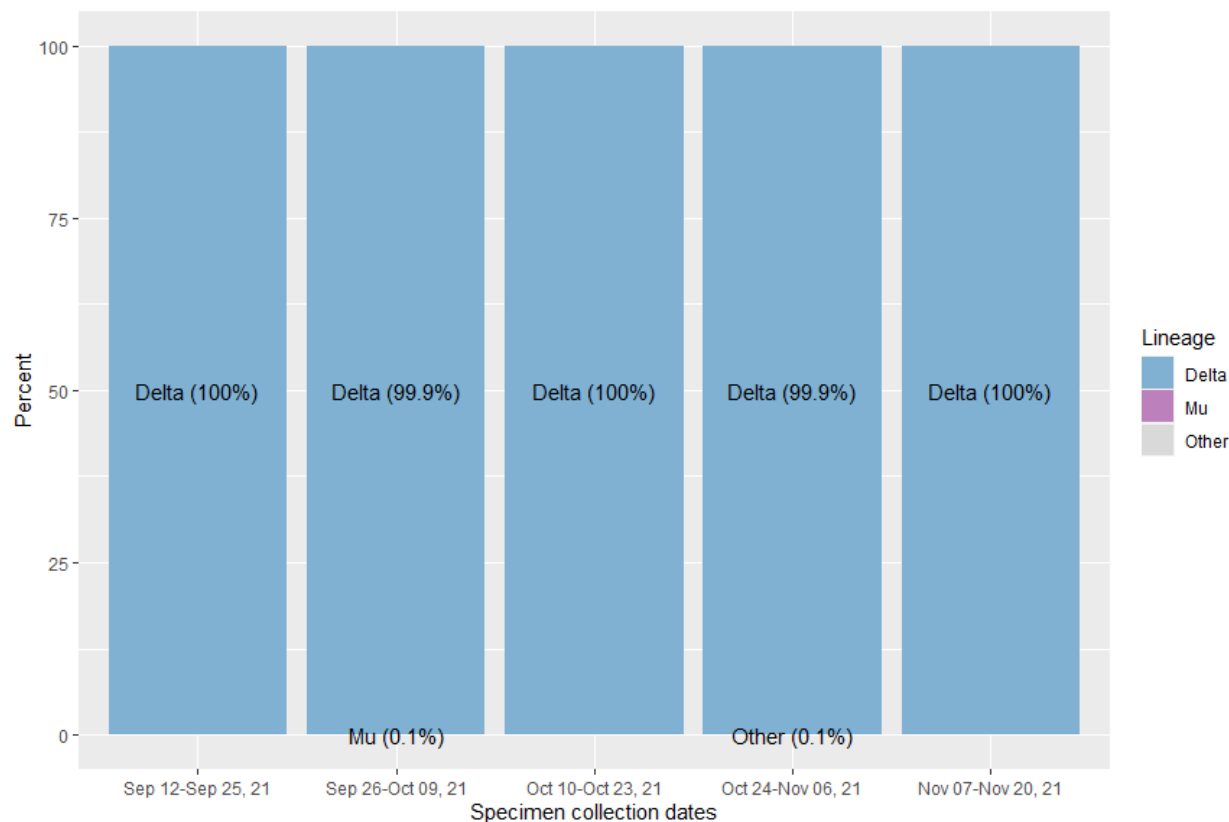


- Samples are not sequenced for every confirmed COVID-19 case. The above graph shows the total number of specimens sequenced (gray bars) and the percent of all confirmed cases (blue line) that have had sequencing performed each month. Data from the previous month may still be incomplete.
- Sequencing 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 with shared characteristics, allowing them to be grouped together. There are many different virus lineages that are not variants of concern or variants being monitored. These are grouped together as 'Other' on this chart. 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 two-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.

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

The table below shows the number of variants of concern (VOC) and variants being monitored (VBM) detected by county of home address since January 2021.

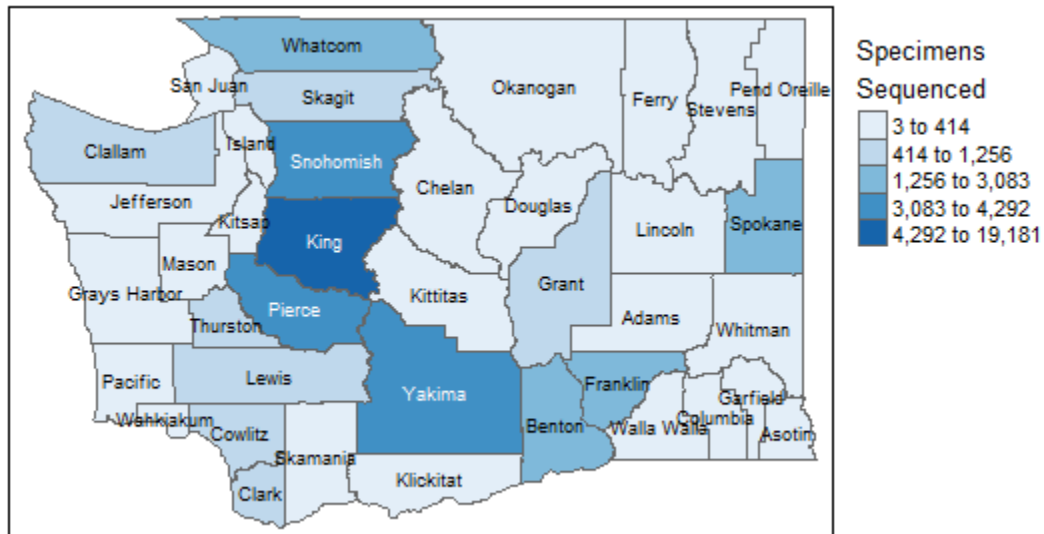
	VOC	VBM								
County	Delta	Alpha	Beta	Gamma	Epsilon	Eta	Iota	Kappa	Mu	Total specimens sequenced
Adams	231	35	0	3	18	0	2	0	0	289
Asotin	42	8	0	0	0	0	1	0	0	51
Benton	1,869	414	1	85	229	23	71	0	17	2,709
Chelan	243	29	0	2	7	0	0	0	0	281
Clallam	484	75	0	19	5	0	1	0	21	605
Clark	498	79	1	36	29	0	3	0	0	646
Columbia	2	0	0	0	0	0	0	0	0	2
Cowlitz	486	41	0	42	27	0	1	0	0	597
Douglas	156	22	0	0	3	0	4	0	0	185
Ferry	10	3	0	0	1	0	0	0	0	14
Franklin	1,416	317	4	107	167	12	35	0	11	2,069
Garfield	4	0	0	0	0	0	0	0	0	4
Grant	590	63	0	13	26	0	6	0	0	698
Grays Harbor	265	46	2	15	21	0	0	0	0	349
Island	199	33	0	7	2	0	0	0	0	241
Jefferson	97	28	0	0	6	0	3	0	0	134
King	8,684	4,990	190	1,038	1,808	32	438	37	67	17,284
Kitsap	274	59	2	6	33	0	6	0	2	382
Kittitas	287	29	1	15	7	0	1	0	6	346
Klickitat	96	7	0	1	1	0	5	0	0	110
Lewis	648	74	0	8	22	0	0	0	0	752
Lincoln	44	5	0	2	1	0	1	0	0	53
Mason	120	23	1	3	3	0	3	0	0	153
Okanogan	127	15	0	0	2	0	0	0	1	145

	VOC	VBM								
County	Delta	Alpha	Beta	Gamma	Epsilon	Eta	Iota	Kappa	Mu	Total specimens sequenced
Pacific	143	20	0	7	28	0	0	0	1	199
Pend Oreille	70	2	0	2	0	0	3	0	0	77
Pierce	1,522	865	24	147	458	2	76	0	18	3,112
San Juan	16	6	0	0	0	0	0	0	0	22
Skagit	764	177	1	35	20	0	1	0	0	998
Skamania	12	3	0	0	0	0	2	0	0	17
Snohomish	2,108	1,155	21	220	351	6	40	6	10	3,917
Spokane	1,972	186	1	127	56	4	52	1	0	2,399
Stevens	125	14	0	3	1	0	2	1	0	146
Thurston	937	139	4	12	47	0	6	0	1	1,146
Wahkiakum	19	7	0	2	0	0	0	0	0	28
Walla Walla	193	9	0	5	12	1	3	0	10	233
Whatcom	1,363	475	6	254	37	2	21	1	5	2,164
Whitman	255	71	0	12	13	0	6	0	0	357
Yakima	2,069	249	10	108	492	1	92	0	8	3,029

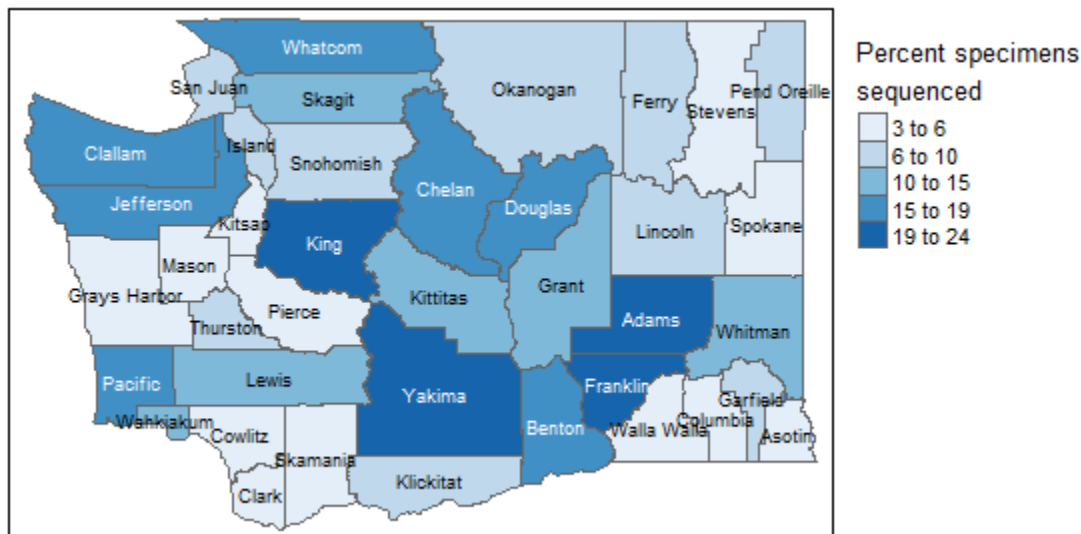
Geographic Coverage of Sequencing

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.



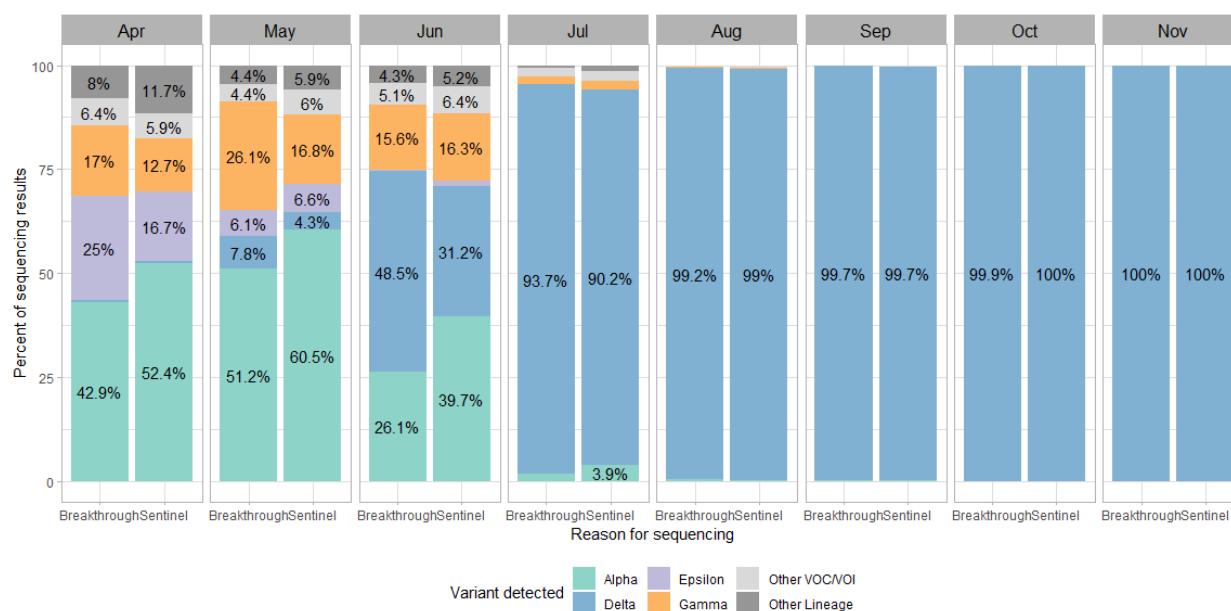
Vaccine Breakthrough

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	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov
Alpha	134	151	97	28	8	1	0	0
Delta	2	23	180	1,544	2,722	1,594	1,566	433
Epsilon	78	18	1	0	0	0	0	0
Gamma	53	77	58	32	6	0	0	0
Other VOC/VOI	20	13	19	31	5	3	0	0
Other Lineage	25	13	16	12	4	0	1	0

Symptom information

Public Health gathers information from patients during interviews and records information about what symptoms people experience during their illness. Not all patients are able to be interviewed, so the symptom status is 'unknown' for many cases of illness. When there are a lot of infections, it is more challenging to contact each person, which is why some variants such as Delta have information available for a smaller percentage of cases. Information in the tables below is only presented for variants with at least 100 cases identified.

Symptom status by variant

	VOC	VBM						
Symptoms	Delta	Alpha	Beta	Epsilon	Gamma	Iota	Mu	Other*
Yes	89%	91%	86%	91%	92%	93%	85%	92%
No	11%	9%	14%	9%	8%	7%	15%	8%
Unknown	49%	34%	31%	35%	31%	36%	39%	37%
Total cases	28440	9773	269	3933	2336	885	178	5270

Symptoms by variant among cases reporting symptoms

	VOC	VBM						
Symptom	Delta	Alpha	Beta	Epsilon	Gamma	Iota	Mu	Other*
Total symptomatic	13012	5853	159	2329	1481	525	93	3052
Fever	48%	33%	19%	26%	38%	31%	27%	30%
Muscle aches	44%	32%	21%	28%	35%	29%	28%	33%
Sore throat	37%	27%	20%	21%	27%	29%	27%	24%
Cough	37%	27%	20%	21%	27%	29%	27%	24%
Shortness of breath	17%	12%	10%	11%	14%	9%	13%	12%
Nausea or vomiting	18%	12%	10%	10%	14%	13%	10%	11%
Headache	53%	38%	25%	33%	39%	34%	43%	39%
Abdominal pain	11%	8%	8%	7%	8%	5%	8%	9%
Diarrhea	18%	12%	6%	10%	13%	10%	12%	12%
Loss of taste or smell	42%	21%	16%	24%	24%	24%	31%	29%

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

The hospitalization table below 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

	VOC	VBM						
Outcome	Delta	Alpha	Beta	Epsilon	Gamma	Iota	Mu	Other*
Cases who were hospitalized	4%	3%	6%	2%	7%	3%	3%	3%
Cases who died from COVID-19	1%	1%	0%	1%	1%	1%	2%	1%
Total cases	28440	9773	269	3933	2336	885	178	5270

Age distribution by variant

	VOC	VBM						
Age group	Delta	Alpha	Beta	Epsilon	Gamma	Iota	Mu	Other*
Age 0-19	23%	27%	29%	24%	21%	25%	22%	24%
Age 20-34	30%	32%	35%	31%	35%	33%	37%	30%
Age 35-49	21%	22%	21%	22%	23%	24%	20%	23%
Age 50-64	14%	12%	11%	14%	11%	12%	12%	15%
Age 65-79	7%	3%	2%	4%	4%	4%	6%	5%
Age 80+	2%	1%	0%	1%	3%	1%	1%	2%
Unknown	2%	2%	1%	2%	2%	1%	2%	2%
Total cases	28440	9773	269	3933	2336	885	178	5270

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

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:

University of Washington Virology Lab
Laboratory Corporation of America
Washington State Department of Health Public Health Laboratories
Seattle Flu Study
Fulgent Genetics
Northwest Laboratory
Incyte Diagnostics Spokane
Atlas Genomics
Altius Institute for Biomedical Sciences
Interpath Laboratory
Northwest Laboratories
Central Washington Hospital
Quest Diagnostics Incorporated
Providence Regional Medical Center Everett
Aegis Sciences Corporation
Overlake Hospital
Kaiser Permanente Washington Health Research Institute
OHSU Lab Services Molecular Microbiology Lab
Providence Sacred Heart Medical Center
Swedish Medical Center, Seattle, WA, USA
Evergreen Healthcare
Helix/Illumina
FidaLab
Gravity Diagnostics, LLC
Infinity Biologix

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

University of Washington Virology Lab

Seattle Flu Study

Centers for Disease Control and Prevention

Washington State Department of Health Public Health Laboratories

Altius Institute for Biomedical Research

Providence St. Joseph Health Molecular Genomics Laboratory

Oregon SARS-CoV-2 Genome Sequencing Center

Atlas Genomics

Institute for Systems Biology

Gravity Diagnostics, LLC

Ginkgo Bioworks Clinical Laboratory

The Jackson Laboratory