

SARS-CoV-2 Sequencing and Variants in Washington State

Washington State Department of Health

January 25, 2023



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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 (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 January 24, 2023)

- During the month of December 2022, **7.6%** 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.
- **132,847 (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	66,729	Nov 29, 21	Jan 16, 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
BQ.1.1	Includes BQ.1.1.X
XBB	Includes XBB.X except XBB.1.5
XBB.1.5	Includes XBB.1.5.X

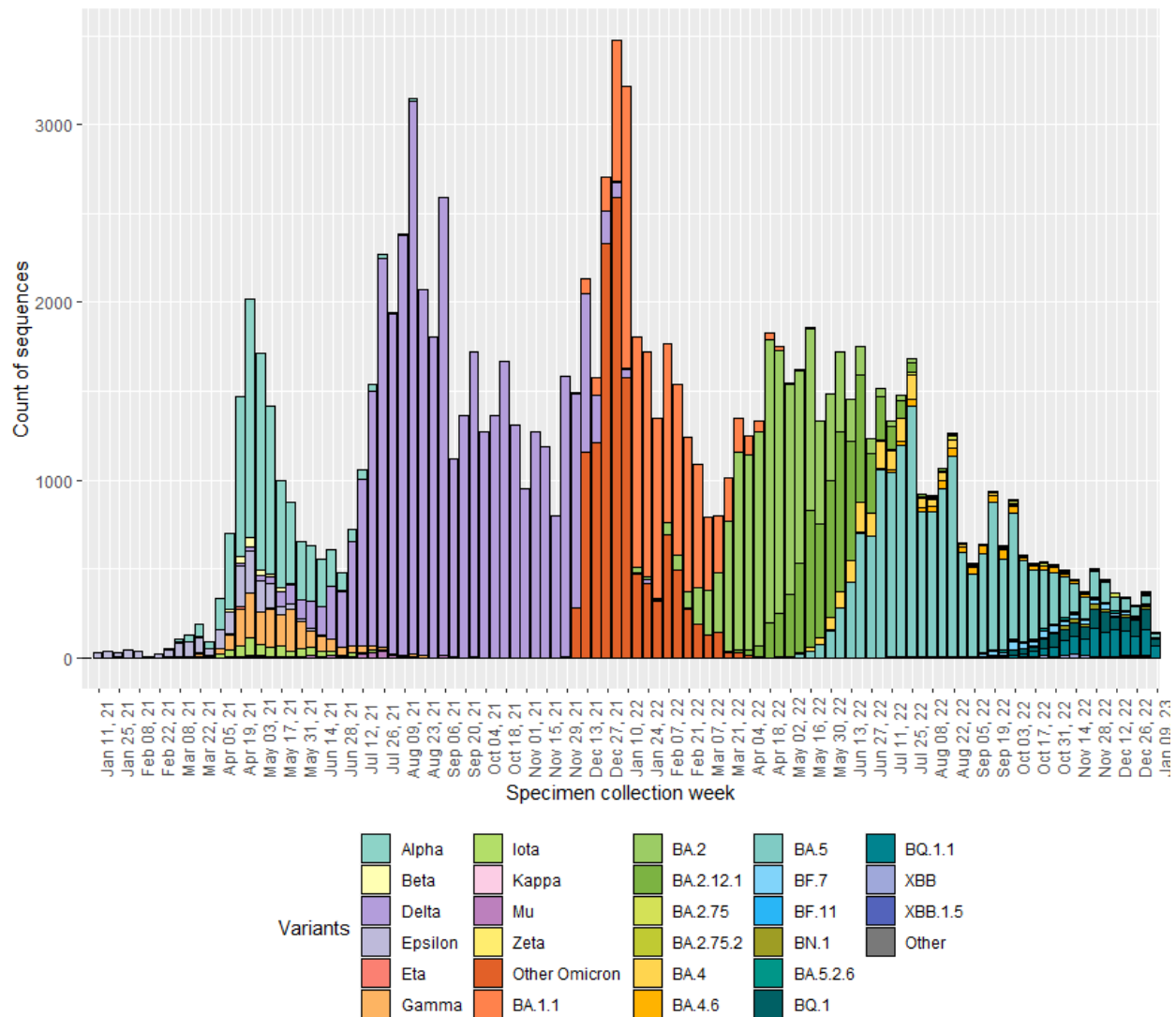
Variants Being Monitored

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

Variant	Area first detected	Cumulative Washington cases detected	First detection in Washington*	Most recent detection in Washington*
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

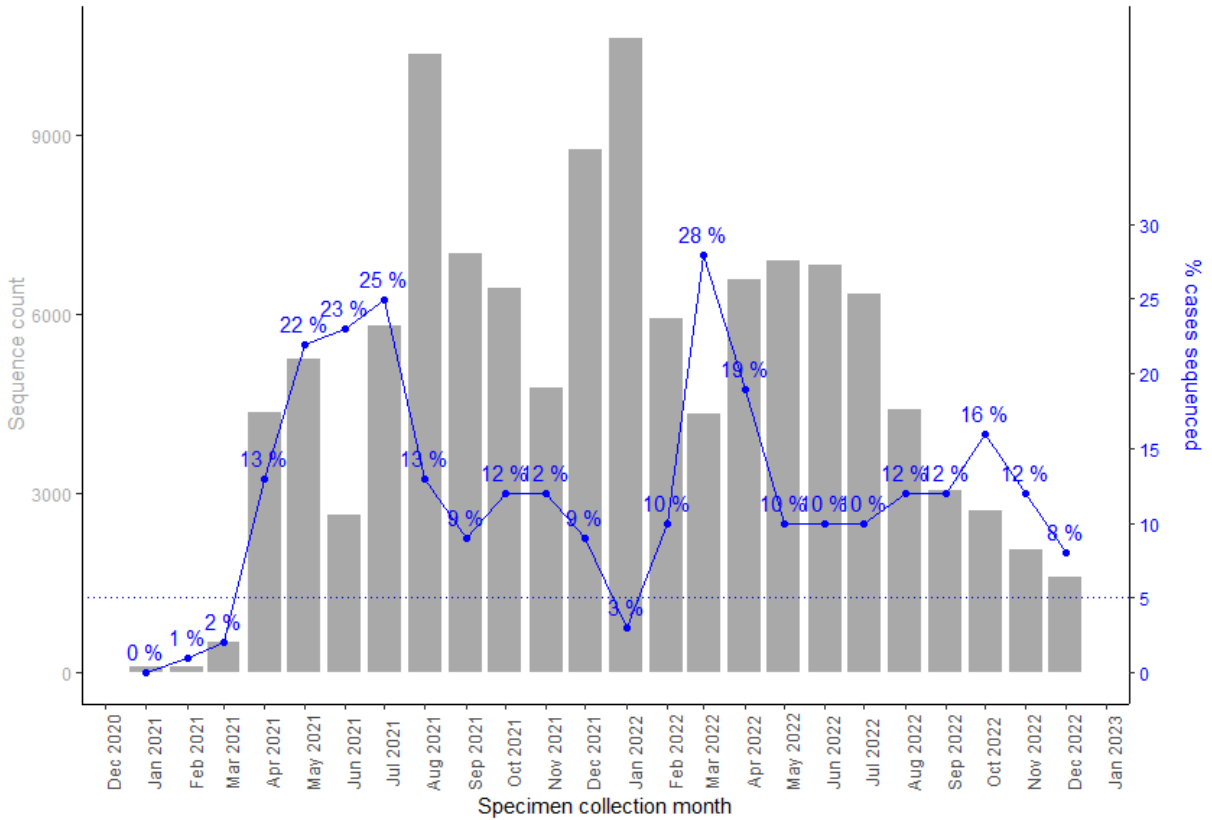
*Detection dates are based on the date a sample is collected, it can take several weeks before a variant result is completed and added to the report

Epidemiologic curve of variants being monitored and variants of concern by week of specimen collection date from January 01, 2021 to January 13, 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 December 2022.

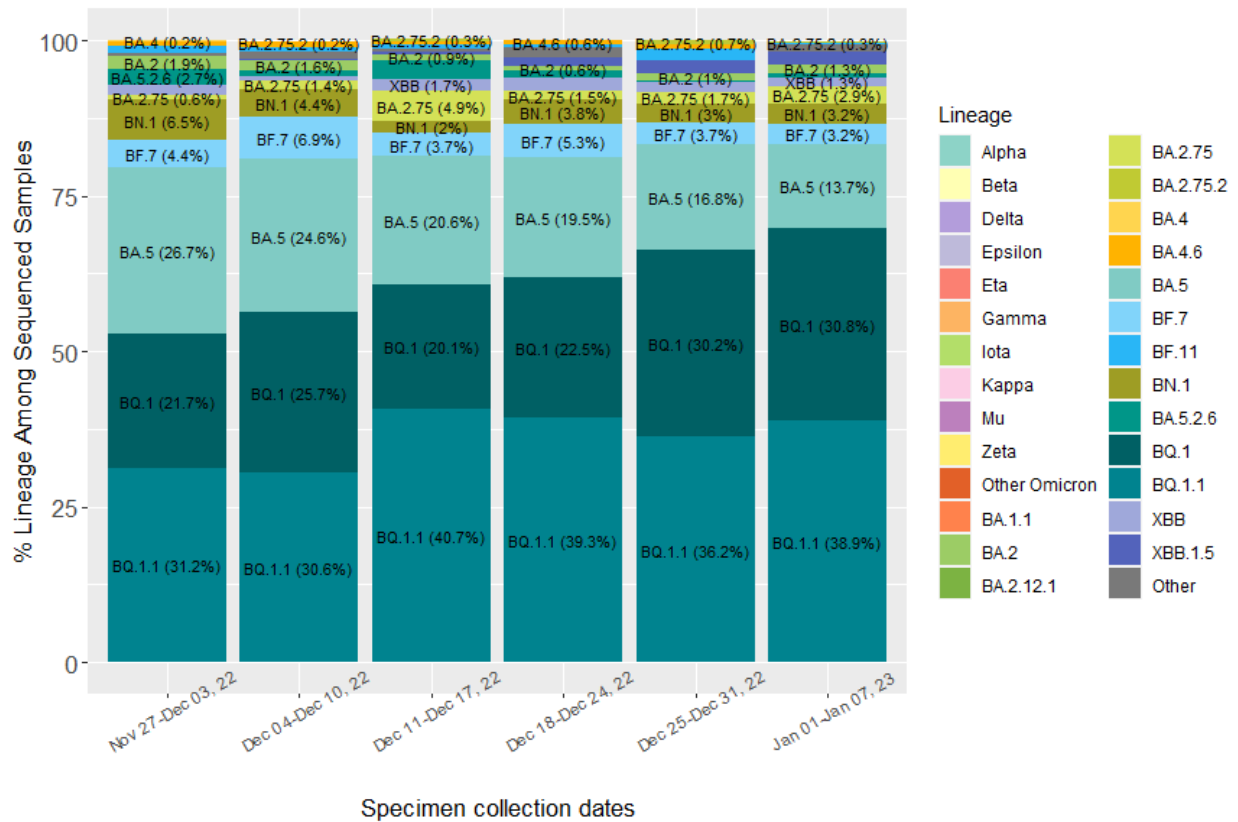


- Samples are not sequenced for every confirmed COVID-19 case. The above graph shows the total number of specimens sequenced (gray bars) and the percent of all confirmed cases (blue line) that have had sequencing performed each month. Data from the previous month may still be incomplete.
- Sequencing 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; data is from the Washington Disease Reporting System (WDRS).

County	VOC															Total current VOC specimens sequenced
	Other Omicron	BA.2	BA.2.12.1	BA.2.75	BA.2.75.2	BN.1	BA.4	BA.4.6	BA.5	BF.7	BA.5.2.6	BQ.1	BQ.1.1	XBB	XBB.1.5	
Adams	30	3	6	0	0	0	0	0	15	0	0	0	1	0	0	91
Asotin	1	1	4	0	0	0	2	0	10	0	0	0	1	0	0	32
Benton	260	102	98	1	1	1	20	8	303	3	1	10	9	0	0	1,116
Chelan	45	61	95	0	1	0	22	7	241	11	6	6	6	1	0	632
Clallam	25	175	61	0	0	1	22	8	184	5	1	1	0	1	0	669
Clark	141	300	195	1	1	1	36	9	315	11	1	12	13	0	0	1,261
Columbia	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	8
Cowlitz	115	87	66	1	0	0	8	1	134	2	1	4	16	0	0	646
Douglas	24	45	40	1	0	0	5	0	141	3	2	4	6	1	0	363
Ferry	1	2	3	0	0	0	0	0	0	0	0	0	0	0	0	15
Franklin	167	39	39	0	2	0	25	3	367	3	3	2	2	1	0	977
Garfield	0	1	1	0	0	0	0	0	1	0	0	0	0	0	0	3
Grant	55	26	32	0	0	0	6	0	66	2	0	1	3	0	0	405
Grays Harbor	167	97	51	0	0	0	9	24	141	4	0	4	15	0	1	751
Island	31	120	42	0	0	1	8	7	69	4	0	1	9	0	0	334
Jefferson	26	12	7	0	0	0	0	0	17	0	0	1	0	0	0	105

County	VOC															Total current VOC specimens sequenced
	Other Omicron	BA.2	BA.2.12.1	BA.2.75	BA.2.75.2	BN.1	BA.4	BA.4.6	BA.5	BF.7	BA.5.2.6	BQ.1	BQ.1.1	XBB	XBB.1.5	
King	3,181	7,735	3,318	135	29	136	724	357	8,763	293	74	760	925	87	16	30,380
Kitsap	96	228	121	2	0	1	25	12	314	5	1	7	10	0	0	1,009
Kittitas	18	17	5	0	0	0	2	0	9	0	0	3	2	0	0	107
Klickitat	3	7	3	0	0	0	0	0	7	0	0	0	0	0	0	37
Lewis	60	24	23	0	0	0	4	5	51	0	0	0	1	0	0	358
Lincoln	2	4	0	0	0	0	1	0	23	0	0	0	1	0	0	35
Mason	26	37	23	0	0	0	5	9	157	1	3	0	0	0	0	353
Okanogan	41	15	34	0	0	0	0	4	13	0	0	0	0	0	0	210
Pacific	53	13	22	0	0	1	3	0	14	1	0	0	2	0	0	167
Pend Oreille	2	2	2	0	0	0	0	0	3	0	0	0	0	0	0	20
Pierce	537	815	493	4	0	5	98	39	1,037	19	10	37	62	4	0	3,957
San Juan	5	5	3	0	0	0	0	0	1	0	0	2	0	0	0	29
Skagit	46	318	135	6	0	0	48	15	427	12	2	24	40	2	0	1,199
Skamania	2	0	3	0	0	0	0	0	5	2	0	0	0	0	0	16
Snohomish	522	1,471	703	23	9	19	117	65	1,641	48	18	89	112	11	3	5,517
Spokane	181	173	139	0	0	0	35	14	316	2	4	7	16	0	0	1,424
Stevens	7	4	2	0	0	0	0	0	12	0	0	0	0	0	0	45
Thurston	643	267	165	3	0	1	21	12	374	10	3	20	15	1	1	2,176
Wahkiakum	2	6	2	0	0	0	1	0	0	0	0	0	0	0	0	16

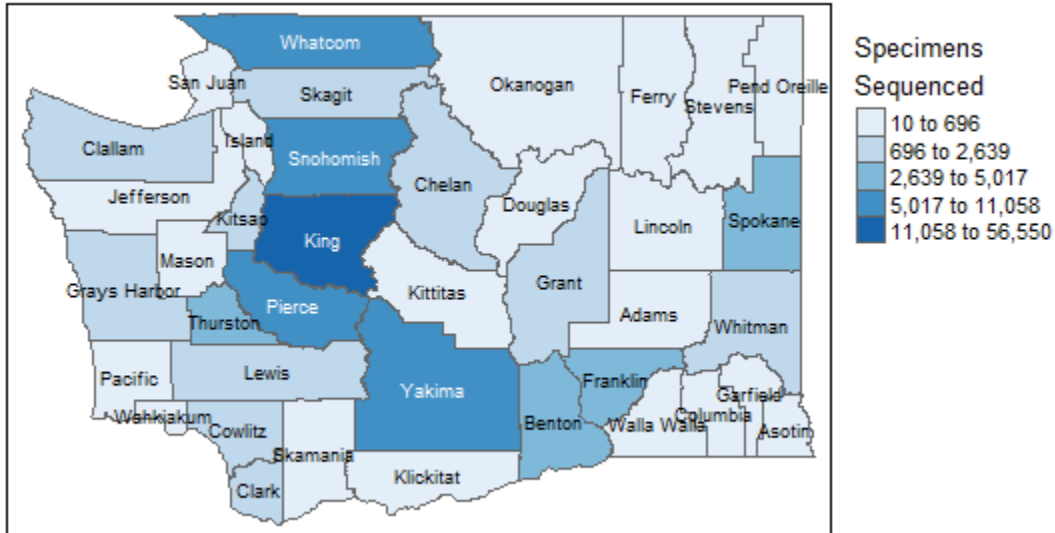
County	VOC															Total current VOC specimens sequenced
	Other Omicron	BA.2	BA.2.12.1	BA.2.75	BA.2.75.2	BN.1	BA.4	BA.4.6	BA.5	BF.7	BA.5.2.6	BQ.1	BQ.1.1	XBB	XBB.1.5	
Walla Walla	39	27	64	0	0	0	3	12	44	0	0	1	3	0	0	325
Whatcom	201	1,297	648	4	0	2	120	38	1,101	25	9	53	52	4	2	3,997
Whitman	40	58	25	0	0	1	2	1	46	0	0	0	0	0	0	321
Yakima	595	132	116	1	1	1	51	11	506	3	0	9	8	0	1	2,184

- In this table, “Other Omicron” includes all B.1.1.529, BA.1, and BA.3 sublineages

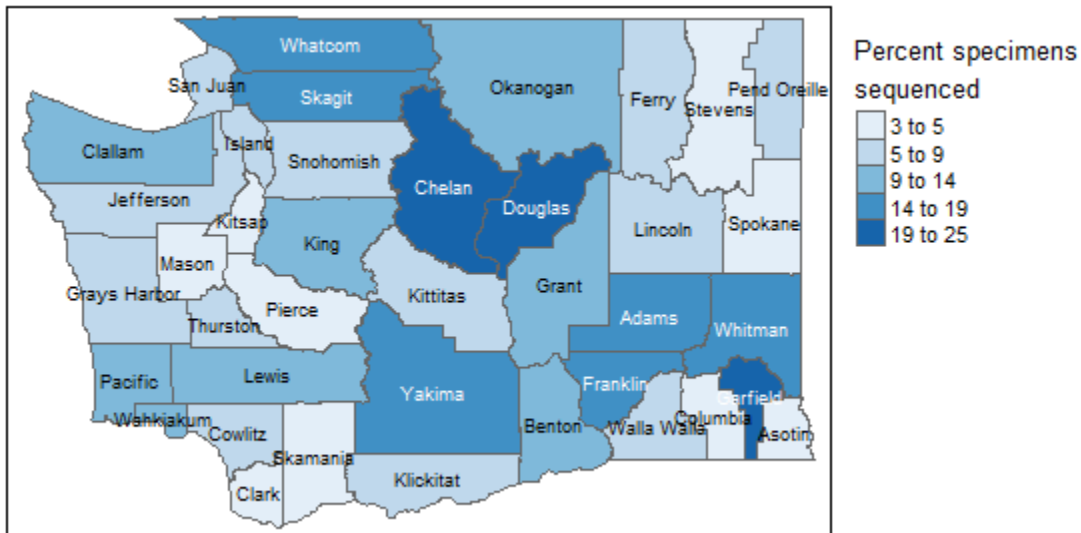
Geographic Coverage of Sequencing

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 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.



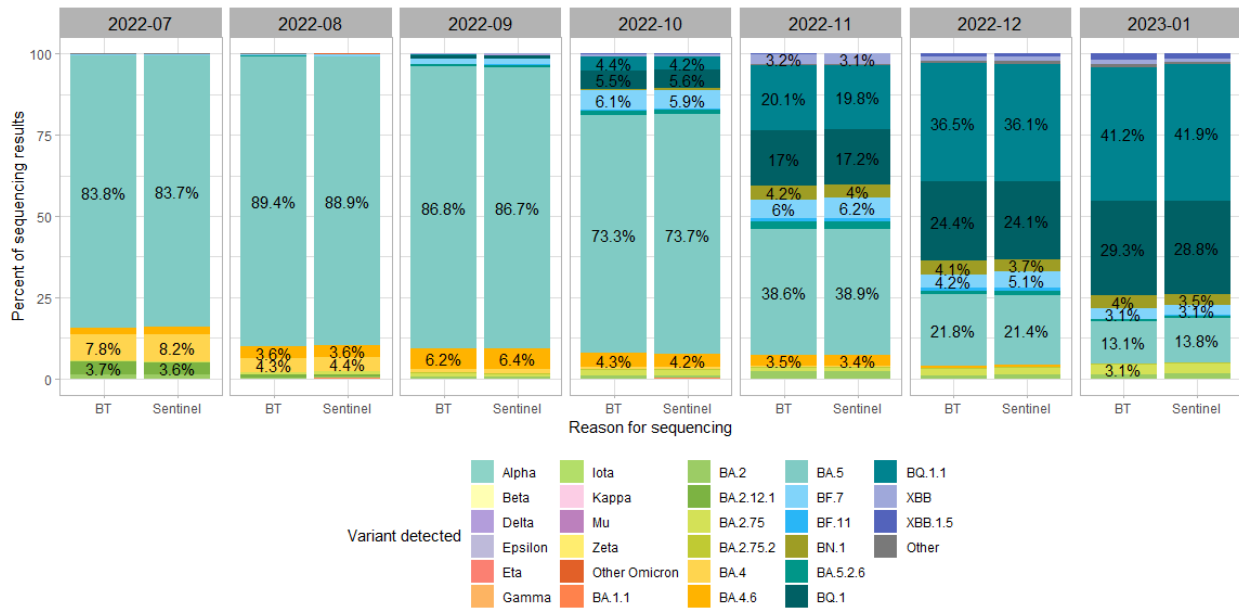
Vaccine Breakthrough Cases

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.



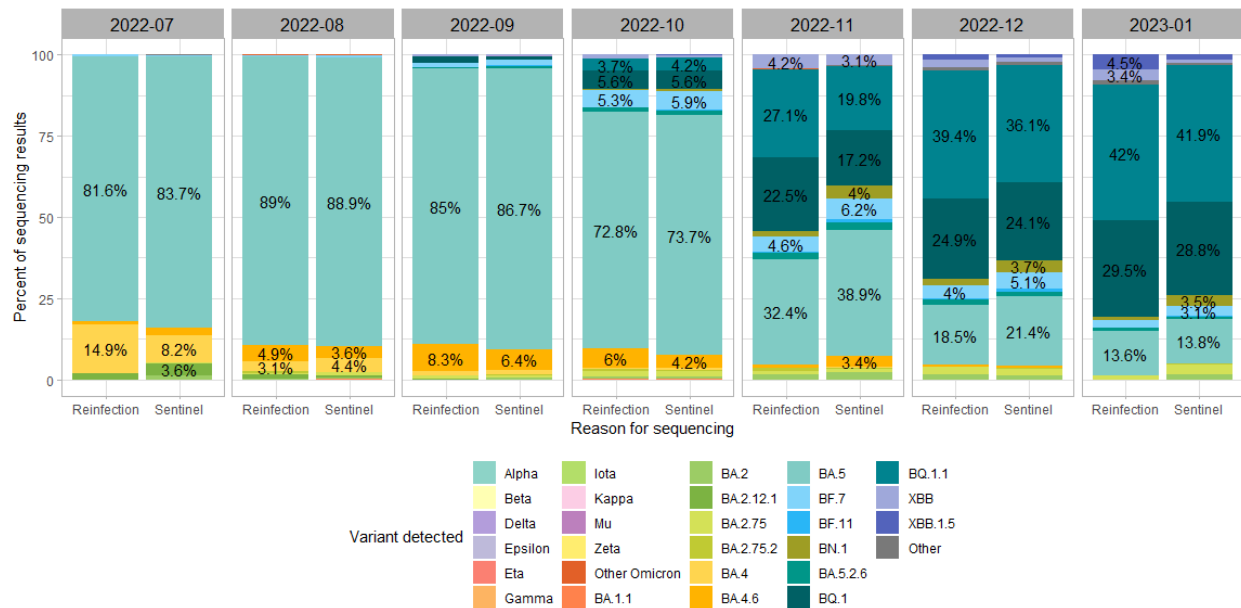
Breakthrough cases by variant table

Variant	2022-07	2022-08	2022-09	2022-10	2022-11	2022-12	2023-01
BA.2	17	10	9	19	36	12	5
BA.2.12.1	47	26	7	0	0	0	0
BA.2.75	7	22	19	34	15	23	13
BA.2.75.2	0	5	9	11	7	4	1
BA.4	99	141	27	13	5	0	0
BA.4.6	27	120	147	95	58	10	0
BA.5	1,059	2,940	2,061	1,630	634	269	55
BA.5.2.6	0	7	17	30	37	16	2
BF.11	0	0	3	9	17	10	1
BF.7	3	14	40	135	98	52	13
BN.1	0	0	0	10	69	50	17
BQ.1	0	0	25	123	280	301	123
BQ.1.1	0	0	4	99	330	451	173
Delta	1	0	1	0	0	0	0
Other	3	3	4	1	4	10	4
Other Omicron	0	0	0	0	1	0	0
XBB	0	0	1	15	52	16	5
XBB.1.5	0	0	0	1	1	10	8

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	2022-07	2022-08	2022-09	2022-10	2022-11	2022-12	2023-01
BA.1.1	0	0	0	1	0	0	0
BA.2	0	1	0	2	4	4	0
BA.2.12.1	4	6	1	0	0	0	0
BA.2.75	0	2	3	5	3	6	1
BA.2.75.2	0	2	0	2	2	0	0
BA.4	30	14	4	1	0	0	0
BA.4.6	2	22	26	18	3	1	0
BA.5	164	398	267	219	85	46	12
BA.5.2.6	0	0	1	4	5	4	1
BF.11	0	0	0	0	1	1	0
BF.7	1	1	4	16	12	10	2
BN.1	0	0	0	1	5	5	1
BQ.1	0	0	6	17	59	62	26
BQ.1.1	0	0	0	11	71	98	37
Other	0	0	0	0	0	2	1
Other Omicron	0	1	0	0	1	0	0
XBB	0	0	2	4	11	6	3
XBB.1.5	0	0	0	0	0	4	4

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%	4,266	1.3%	38,609	17.2%
BA.5	2%	1,998	0.3%	16,869	9.5%
BA.2	1.1%	1,077	0.2%	13,744	8.1%
Other Omicron	1.1%	1,127	0.3%	12,337	13.7%
BA.1.1	2.3%	2,348	0.8%	11,244	14.4%
Alpha	3.5%	3454	0.6%	10,308	12.6%
BA.2.12.1	1.7%	1,708	0.3%	6,790	10.3%
Other	2.6%	2,578	0.8%	5,276	16.9%
Epsilon	2.6%	2,588	0.7%	4,135	16.8%
Gamma	6.8%	6,849	1.7%	2,482	17.6%
BA.4	1.9%	1,897	0.3%	1,423	3.7%
BQ.1.1	2.3%	2,331	0.2%	1,330	6.5%
BQ.1	1.3%	1,323	0.3%	1,058	14.3%
Iota	3.2%	3,226	1.3%	930	30%
BA.4.6	3%	3,026	0.6%	661	5%
BF.7	2.8%	2,772	0.9%	469	30.8%
Beta	7.1%	7,117	1.1%	281	15%
Mu	2.8%	2,752	1.8%	218	33.3%
BA.2.75	1.1%	1,099	0%	182	0%
BA.5.2.6	2.9%	2,878	0.7%	139	25%
Eta	1.1%	1,087	1.1%	92	100%
BF.11	1.9%	1,923	0%	52	0%
Kappa	2.2%	2,174	0%	46	0%
Zeta	2.2%	2,222	0%	45	0%

Age distribution by variant

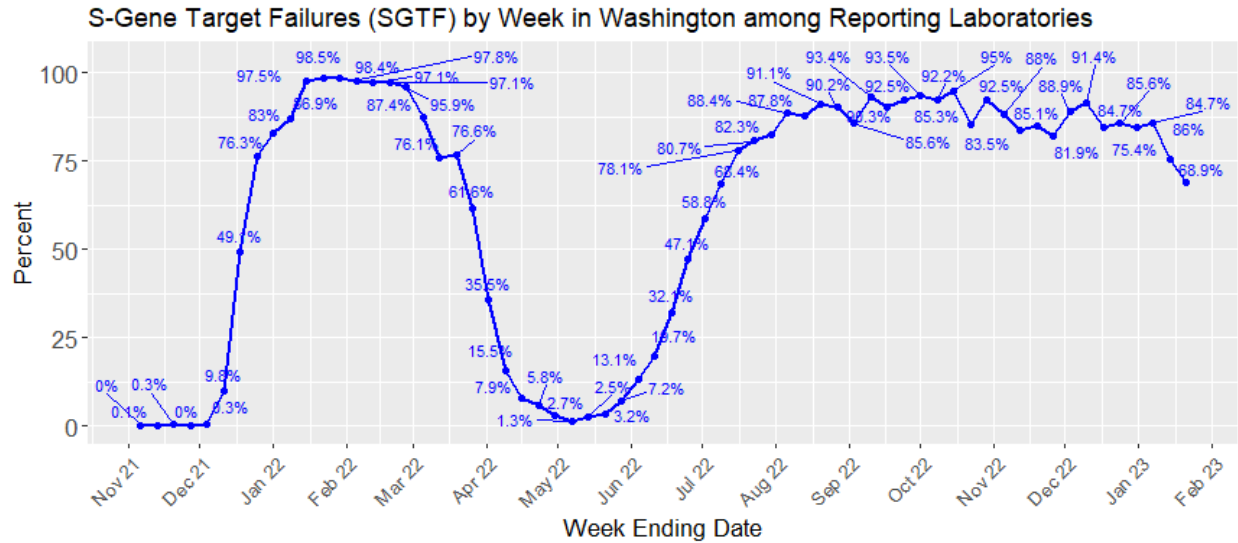
Variant	Age 0-19	Age 20-34	Age 35-49	Age 50-64	Age 65-79	Age 80+	Unknown	Total cases
Delta	23%	29%	23%	15%	8%	2%	0%	38,609
BA.5	12%	29%	25%	20%	12%	3%	0%	16,869
BA.2	19%	32%	24%	15%	8%	2%	0%	13,744
Other Omicron	24%	33%	23%	13%	5%	1%	0%	12,337
BA.1.1	24%	30%	22%	14%	7%	2%	0%	11,244
Alpha	27%	32%	23%	13%	3%	1%	0%	10,308
BA.2.12.1	15%	32%	24%	17%	9%	3%	0%	6,790
Other	24%	29%	24%	16%	5%	2%	0%	5,276
Epsilon	25%	31%	24%	14%	4%	1%	0%	4,135
Gamma	22%	35%	24%	12%	4%	3%	0%	2,482
BA.4	17%	31%	26%	16%	8%	2%	0%	1,423
BQ.1.1	10%	27%	27%	20%	12%	3%	0%	1,330
BQ.1	10%	29%	27%	20%	12%	3%	0%	1,058
Iota	25%	33%	25%	12%	4%	1%	0%	930
BA.4.6	13%	31%	24%	16%	13%	2%	0%	661
BF.7	10%	27%	23%	23%	12%	5%	0%	469
Beta	29%	34%	21%	12%	3%	0%	0%	281
Mu	22%	37%	22%	11%	6%	1%	0%	218
BA.2.75	11%	23%	33%	18%	13%	1%	0%	182
BN.1	8%	24%	34%	16%	13%	3%	0%	171
BA.5.2.6	12%	33%	24%	17%	14%	1%	0%	139
XBB	14%	32%	29%	21%	4%	0%	0%	113
Eta	32%	28%	25%	10%	5%	0%	0%	92
BF.11	13%	19%	25%	31%	10%	2%	0%	52
Kappa	20%	41%	26%	9%	4%	0%	0%	46
Zeta	29%	22%	31%	18%	0%	0%	0%	45
BA.2.75.2	7%	41%	25%	20%	7%	0%	0%	44

Variant	Age 0-19	Age 20-34	Age 35-49	Age 50-64	Age 65-79	Age 80+	Unknown	Total cases
XBB.1.5	21%	33%	17%	21%	8%	0%	0%	24

*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; these include BA.1, BA.3, BA.4 and BA.5 and sublineages. 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	1,086	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%
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%

First Day of Week	Last Day of Week	Total Positives	Total SGTF	Percent SGTF
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%
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%

First Day of Week	Last Day of Week	Total Positives	Total SGTF	Percent SGTF
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%

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

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
