

SARS-CoV-2 Sequencing and Variants in Washington State

Washington State Department of Health

March 29, 2023



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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 March 28, 2023)

- During the month of February 2023, **12.8%** 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.
- **139,195 (9.9%)** COVID-19 cases in Washington state have sequencing information available since January 2021.

Please note the following information are no longer being presented in this report:

- *S-Gene Target Failure (SGTF)*: The Molecular Epidemiology Program has been using the SGTF data as a proxy for variant tracking, but due to differences in lab gene amplification cut offs, recent months of SGTF data has resulted in variable data. We have determined that this data is not as informative as during the initial Omicron wave.
- *Variant proportion amongst sentinel versus vaccine breakthrough cases*: We will not be sharing specific variant proportions due to several factors that affect our ability to interpret breakthrough case data:
 - At-home tests are used more frequently, and most results are not routinely reported to the Washington State Department of Health

- The potential for people who are vaccinated and boosted to be more likely to be tested
 - A previous SARS-CoV-2 infection may provide some immunity from a reinfection for those who are unvaccinated
 - Individuals with underlying health conditions potentially being more likely to get vaccinated boosted, tested, and also experience severe outcomes.
- *Variant proportion amongst sentinel versus reinfection cases:* Due to increasing challenges with case ascertainment, we lack the specificity to accurately classify cases as a primary SARS-CoV-2 infection or a reinfection with SARS-CoV-2. Given these challenges with accurate population classification, we will not share specific variant proportions within those populations.

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	70,147	Nov 29, 21	Mar 15, 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:

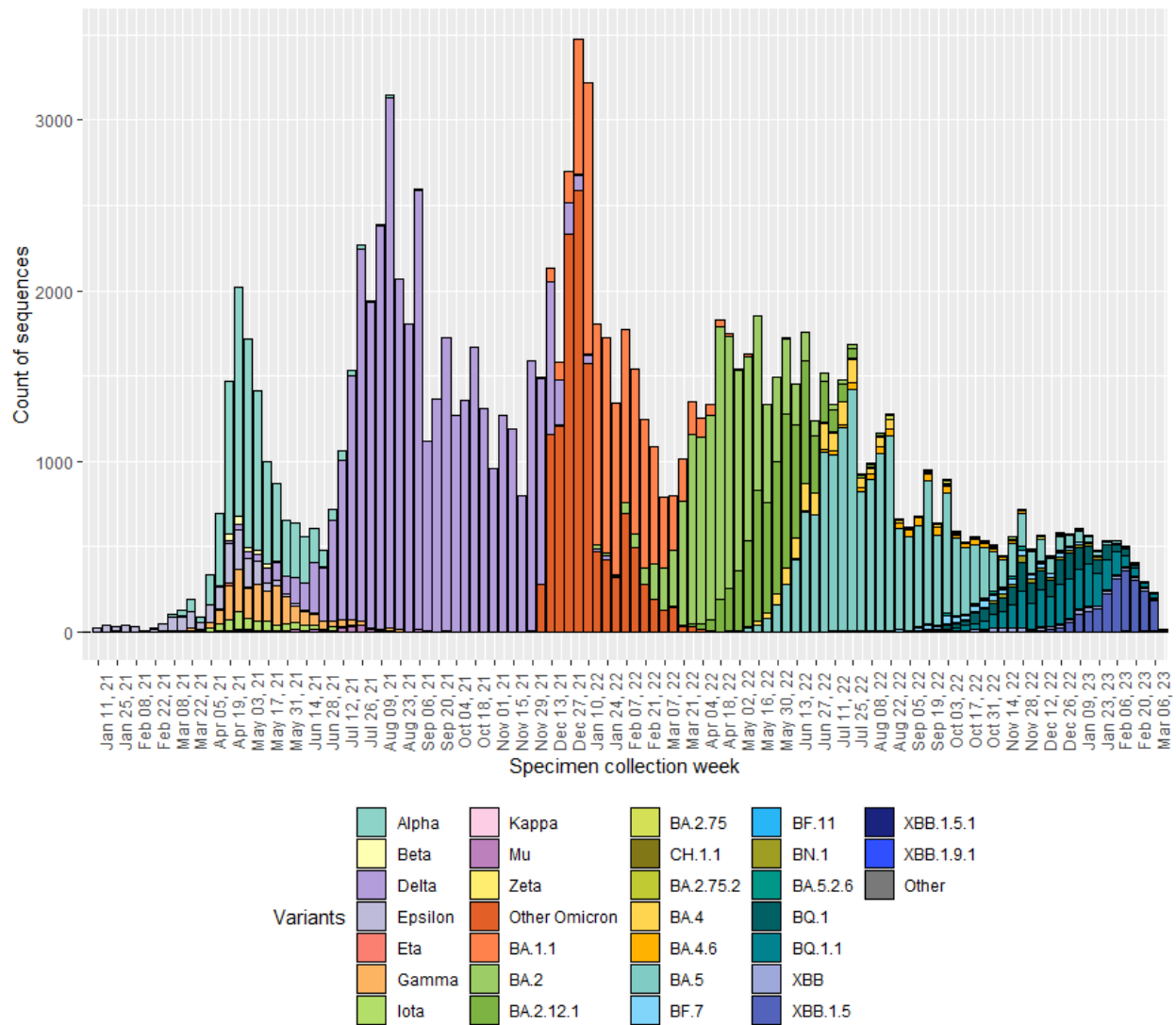
Omicron grouping	Inclusion
Other Omicron	Includes B.1.1.529, BA.1.X, BA.3.X
BA.1.1	Includes BA.1.1.X
BA.2	Includes BA.2.X except BA.2.12.1 and BA.2.75.X
BA.2.12.1	Includes BA.2.12.1.X
BA.2.75	Includes BA.2.75.X except BA.2.75.2 and BA.2.75.5.1
CH.1.1	Includes CH.1.1.X
BA.2.75.2	Includes BA.2.75.2.X
BN.1	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 all XBB.X except XBB.1.5.X and XBB.1.9.1
XBB.1.5	Includes all XBB.1.5.X except XBB.1.5.1
XBB.1.5.1	Includes XBB.1.5.1.X
XBB.1.9.1	Includes XBB.1.9.1.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

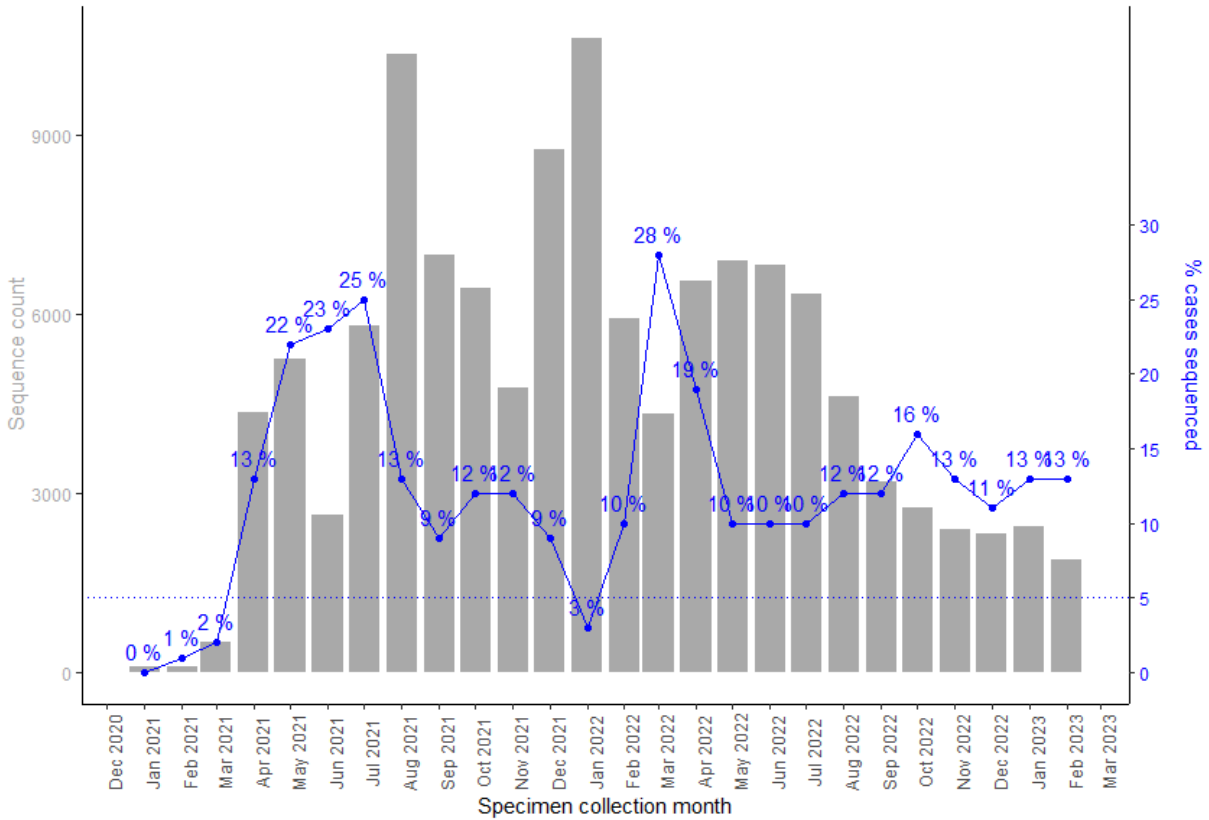
*Detection dates are based on the date a sample is collected, it can take several weeks before a variant result is completed and added to the report

Epidemiologic curve of variants being monitored and variants of concern by week of specimen collection date from January 01, 2021 to March 17, 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.X, and BA.3.X 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 February 2023.

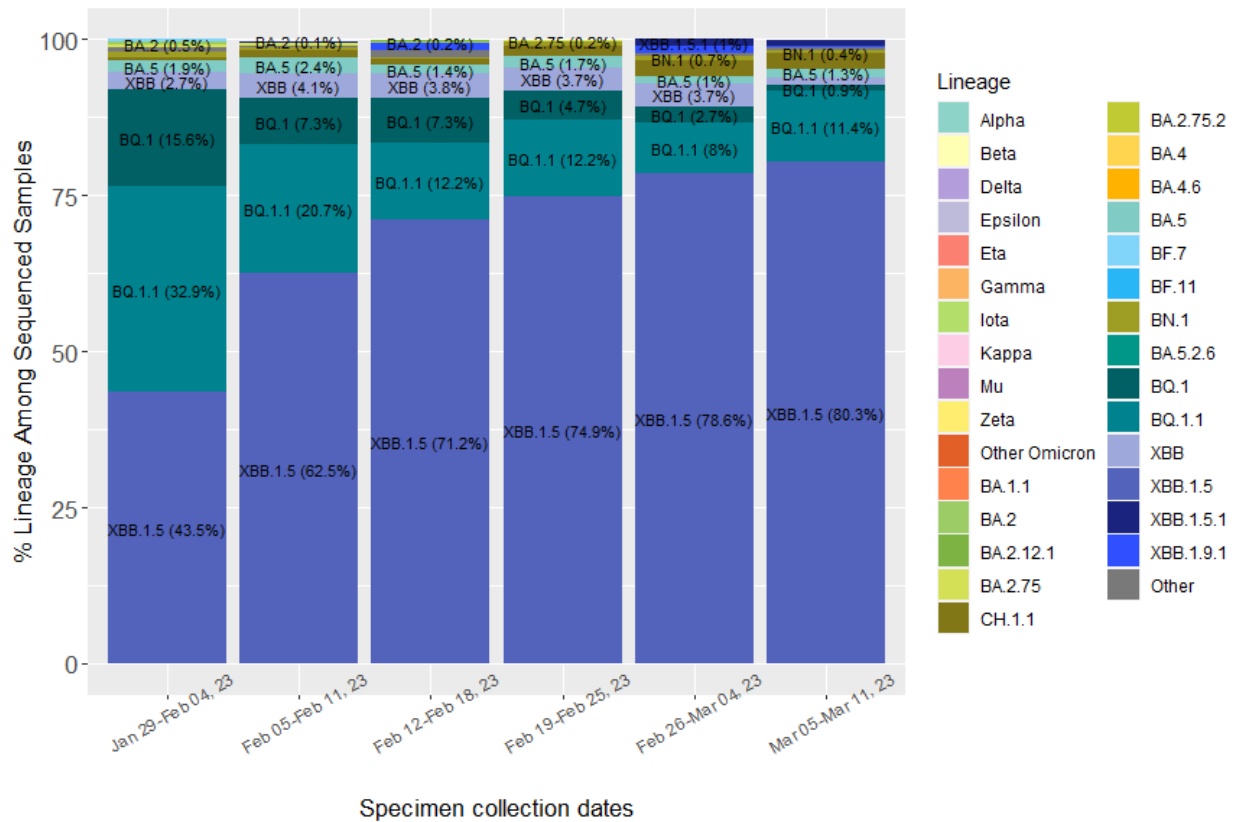


- Samples are not sequenced for every confirmed COVID-19 case. The above graph shows the total number of specimens sequenced (gray bars) and the percent of all confirmed cases (blue line) that have had sequencing performed each month. Data from the previous month may still be incomplete.
- Sequencing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

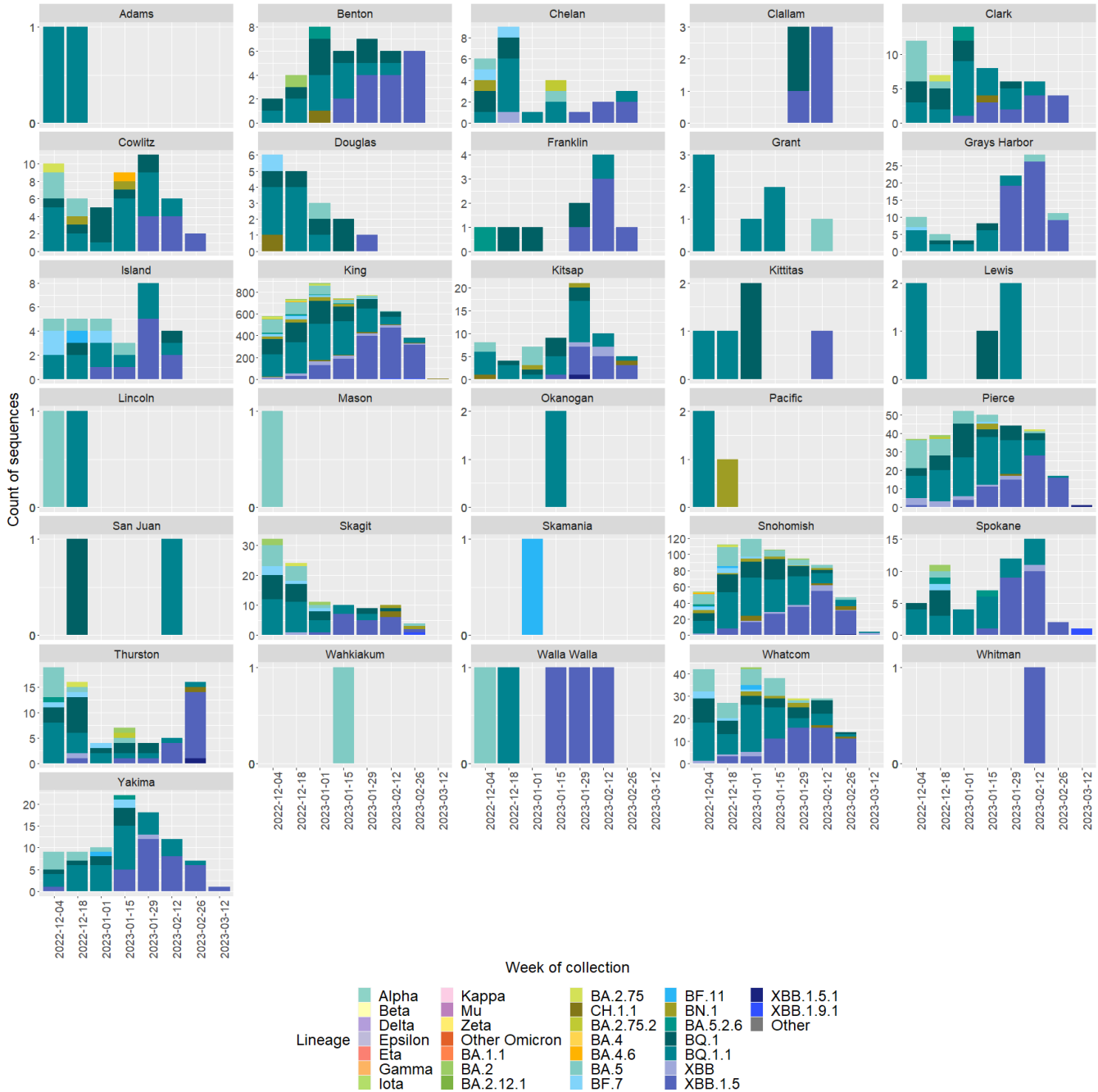
NOTE: The data on this graph come from cases that are randomly selected for sequencing statewide, Cases sequenced because they were part of an outbreak or were otherwise manually selected for sequencing are excluded.



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](#).

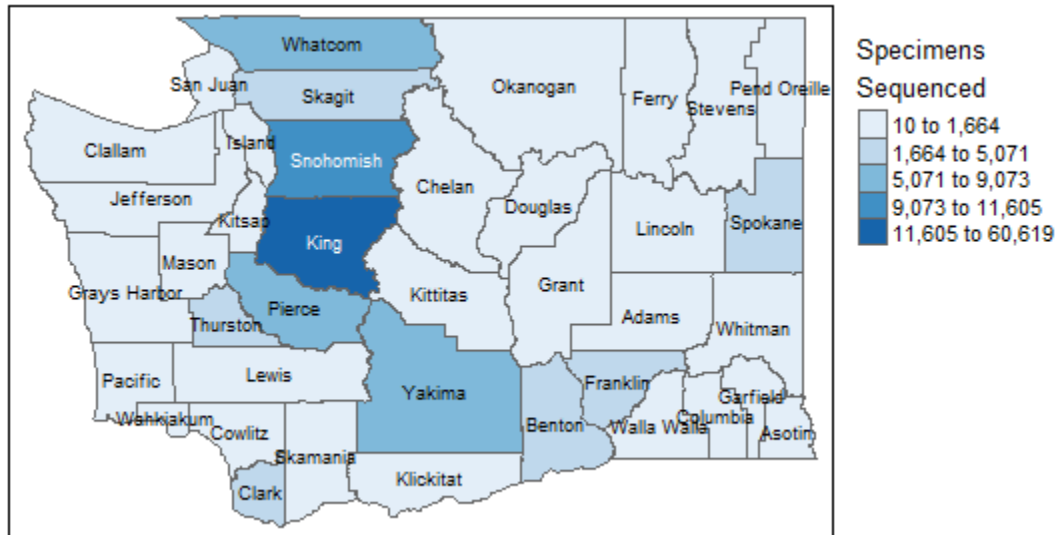
The figure below shows the current number of variants of concern (VOC) detected by county of home address since four months prior; data is from the Washington Disease Reporting System (WDRS).



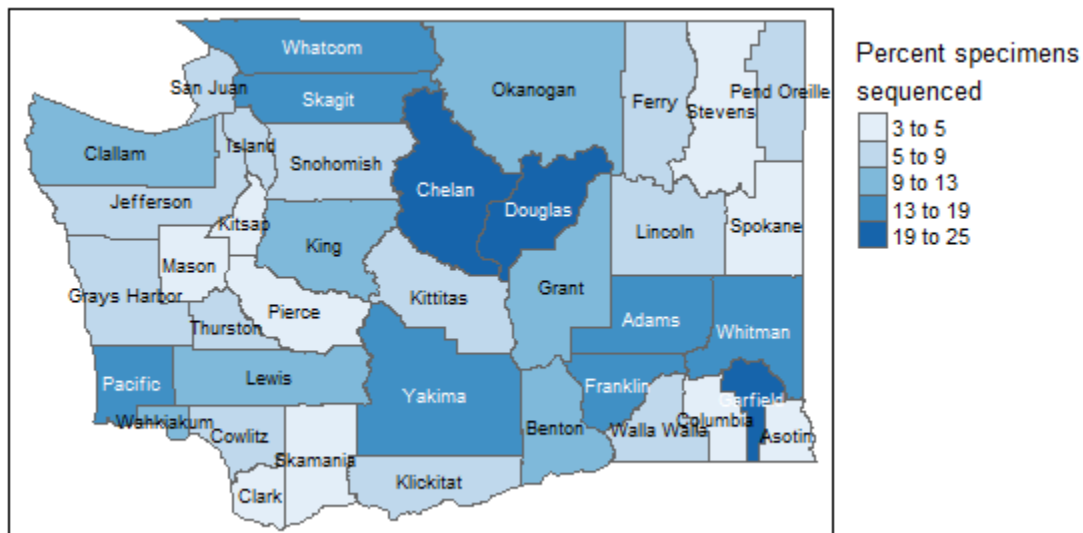
Geographic Coverage of Sequencing

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.



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%	4,251	1.3%	38,601	17.2%
BA.5	2%	2,047	0.4%	17,637	9.7%
BA.2	1.1%	1,096	0.2%	13,773	7.9%
Other Omicron	1.1%	1,102	0.3%	12,342	14%
BA.1.1	2.3%	2,339	0.8%	11,246	14.4%
Alpha	3.5%	3,454	0.6%	10,306	12.6%
BA.2.12.1	1.7%	1,708	0.3%	6,792	10.3%
Other	2.6%	2,598	0.8%	5,312	16.7%
Epsilon	2.6%	2,588	0.7%	4,134	16.8%
BQ.1.1	2.6%	2,566	0.2%	2,845	9.6%
Gamma	6.8%	6,849	1.7%	2,482	17.6%
XBB.1.5	1.9%	1,882	0.5%	2,072	2.6%
BQ.1	2.1%	2,058	0.6%	1,798	10.8%
BA.4	1.9%	1,880	0.3%	1,436	3.7%
Iota	3.2%	3,226	1.3%	930	30%
BA.4.6	2.9%	2,886	0.6%	693	5%
BF.7	3.2%	3,195	0.8%	532	23.5%
XBB	0.9%	926	0%	324	0%
Beta	6.8%	6,786	1.1%	280	15.8%
BN.1	1.5%	1,455	0.4%	275	25%
Mu	2.8%	2,752	1.8%	218	33.3%
BA.2.75	1.1%	1,064	0%	188	0%
BA.5.2.6	2.4%	2,353	0.6%	170	25%
Eta	1.1%	1,087	1.1%	92	100%
CH.1.1	2.4%	2,353	0%	85	0%
BF.11	1.6%	1,639	0%	61	0%
Kappa	2.2%	2,174	0%	46	0%
Zeta	2.2%	2,222	0%	45	0%

Age distribution 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
	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%	17,637	
BA.2	19%	32%	24%	15%	8%	2%	0%	13,773	
Other Omicron	24%	33%	23%	13%	5%	1%	0%	12,342	
BA.1.1	24%	30%	22%	14%	7%	2%	0%	11,246	
Alpha	27%	32%	23%	13%	3%	1%	0%	10,306	
BA.2.12.1	15%	32%	24%	17%	9%	3%	0%	6,792	
Other	24%	29%	24%	16%	5%	2%	0%	5,312	
Epsilon	25%	31%	24%	14%	4%	1%	0%	4,134	
BQ.1.1	12%	27%	27%	20%	11%	3%	0%	2,845	
Gamma	22%	35%	24%	12%	4%	3%	0%	2,482	
XBB.1.5	12%	29%	26%	20%	11%	3%	0%	2,072	
BQ.1	11%	27%	26%	20%	12%	3%	0%	1,798	
BA.4	17%	31%	26%	16%	8%	2%	0%	1,436	
Iota	25%	33%	25%	12%	4%	1%	0%	930	
BA.4.6	13%	31%	24%	16%	13%	2%	0%	693	
BF.7	10%	27%	23%	23%	13%	5%	0%	532	
XBB	10%	33%	24%	21%	10%	1%	0%	324	
Beta	29%	34%	21%	12%	3%	0%	0%	280	
BN.1	8%	25%	30%	18%	13%	4%	0%	275	
Mu	22%	37%	22%	11%	6%	1%	0%	218	
BA.2.75	10%	26%	30%	19%	14%	1%	0%	188	
BA.5.2.6	11%	29%	25%	16%	15%	2%	0%	170	
Eta	32%	28%	25%	10%	5%	0%	0%	92	
CH.1.1	7%	33%	26%	16%	12%	6%	0%	85	
BF.11	11%	28%	23%	28%	8%	2%	0%	61	
BA.2.75.2	8%	38%	26%	22%	6%	0%	0%	50	
Kappa	20%	41%	26%	9%	4%	0%	0%	46	
Zeta	29%	22%	31%	18%	0%	0%	0%	45	
XBB.1.9.1	17%	8%	8%	50%	17%	0%	0%	12	
XBB.1.5.1	14%	43%	14%	29%	0%	0%	0%	7	

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

We gratefully acknowledge the laboratories that tested and sequenced the specimens for reporting the sequencing metadata including the linages 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
Avero Diagnostics
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
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
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 Lauring Laboratory
United States Arm Medical Research Institute of Infectious Diseases
University of Washington Virology Lab
Washington State Department of Health Public Health Laboratories
