

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

**Washington State Department of Health**

**May 31, 2023**

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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 (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 May 30, 2023)**

- During the month of April 2023, **7.5%** 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.
- **140,825 (9.9%)** 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 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	70,433	Nov 29, 21	May 09, 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:

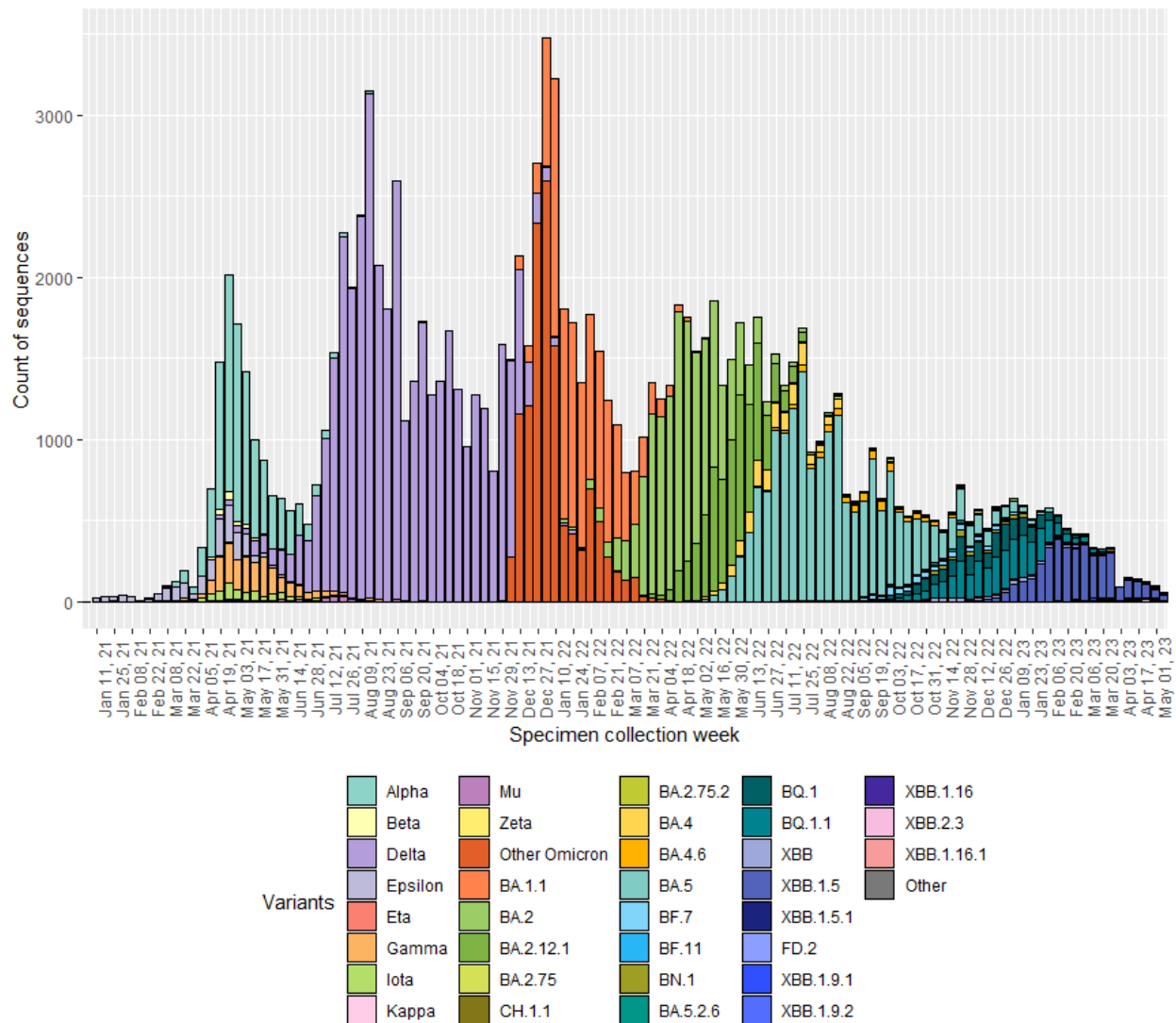
Omicron grouping	Inclusion
Other Omicron	Includes B.1.1.529, BA.1.X, BA.3.X
BA.1.1	Includes BA.1.1.X
BA.2	Includes BA.2.X except BA.2.12.1 and BA.2.75.X
BA.2.12.1	Includes BA.2.12.1.X
BA.2.75	Includes BA.2.75.X except BA.2.75.2 and BA.2.75.5.1
CH.1.1	Includes CH.1.1.X
BA.2.75.2	Includes BA.2.75.2.X
BN.1	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 XBB.X except XBB.1.5 and XBB.1.9.1
XBB.1.5	Includes XBB.1.5.X except XBB.1.5.1
XBB.1.5.1	Includes XBB.1.5.1.X
FD.2	Includes FD.2.X
XBB.1.9.1	Includes XBB.1.9.1.X
XBB.1.9.2	Includes XBB.1.9.2.X
XBB.2.3	Includes XBB.2.3.X
XBB.1.16	Includes XBB.1.16.X except XBB.1.16.1
XBB.1.16.1	Includes XBB.1.16.1X

## 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	10,336	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	38,738	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	2,499	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

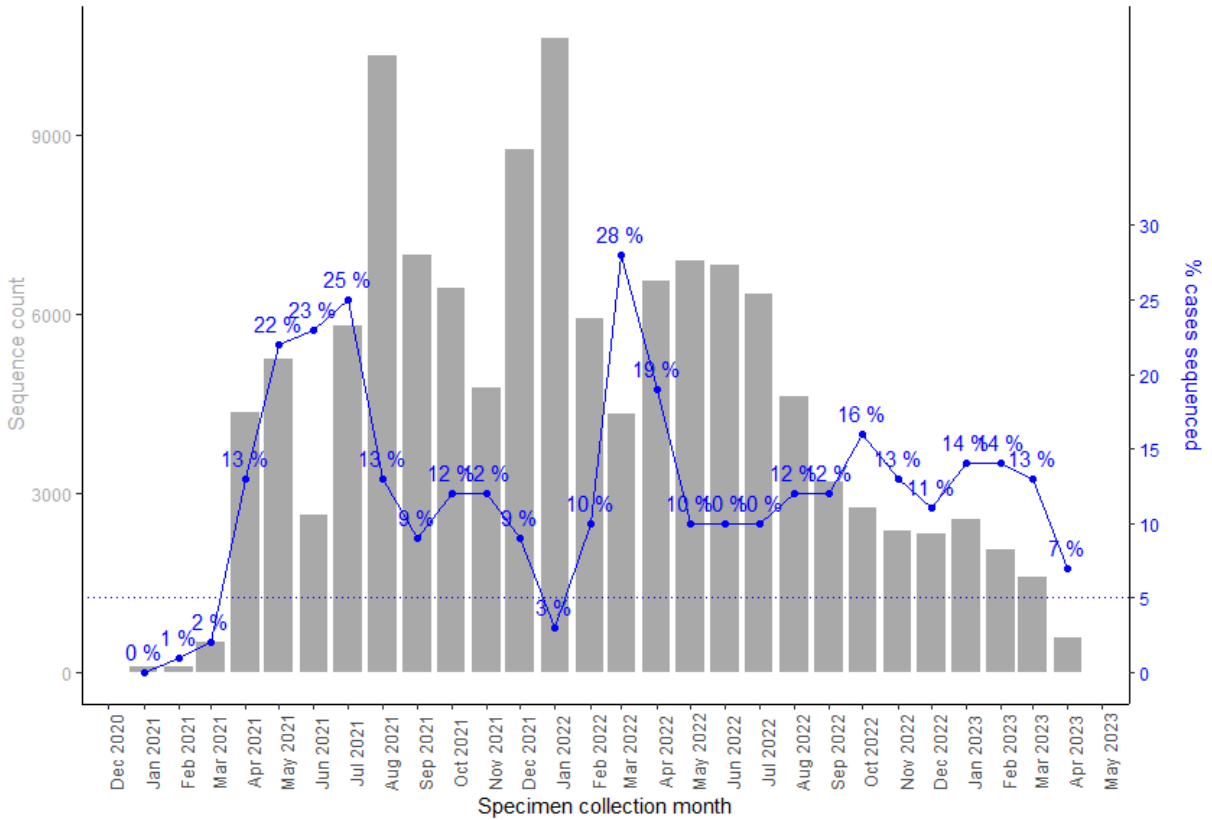
\*Detection dates are based on the date a sample is collected, it can take several weeks before a variant result is completed and added to the report

## Epidemiologic curve of variants being monitored and variants of concern by week of specimen collection date from January 01, 2021 to May 19, 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 April 2023.**



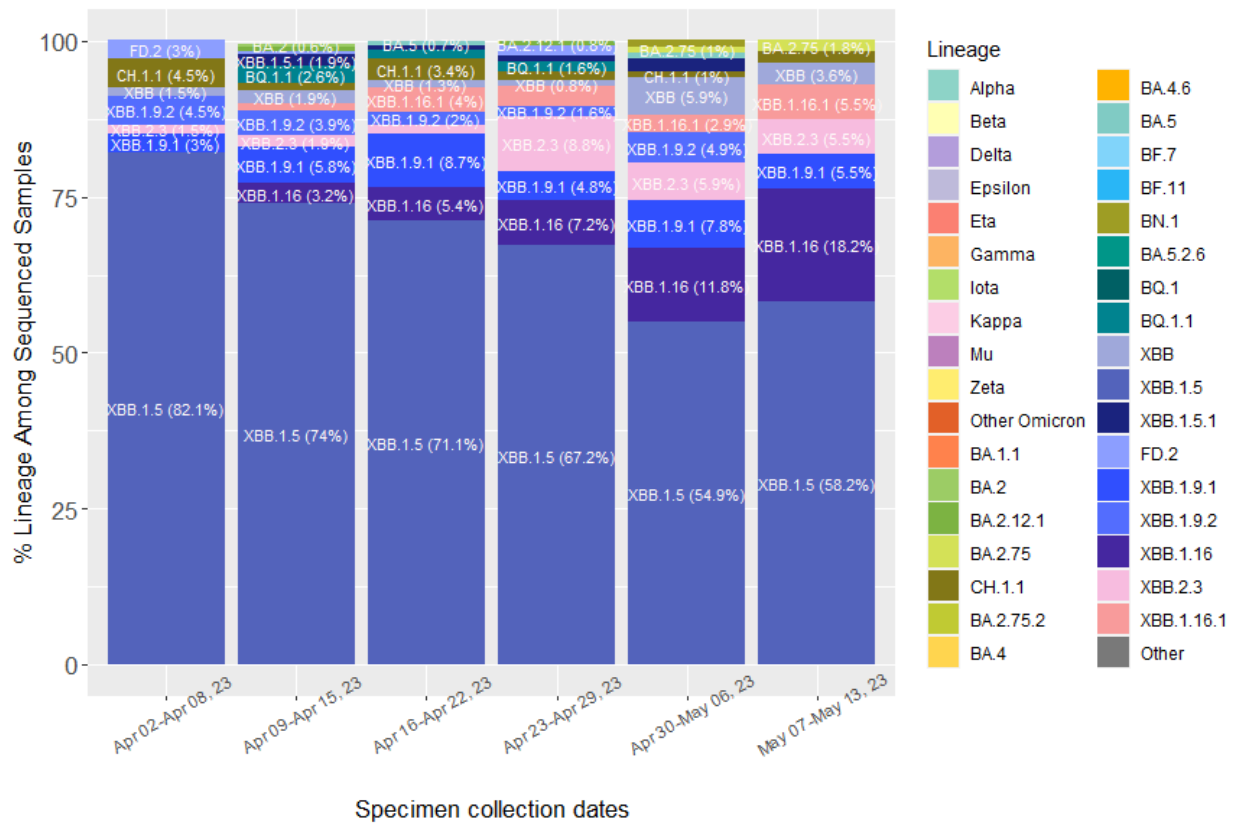
- Samples are not sequenced for every confirmed COVID-19 case. The above graph shows the total number of specimens sequenced (gray bars) and the percent of all confirmed cases (blue line) that have had sequencing performed each month. Data from the previous month may still be incomplete.
- Sequencing 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. Since this figure represents the share of all sequences that a particular lineage represents, as the proportion of sequences assigned to one lineage increases, the proportion of sequences assigned to other lineages will decrease.

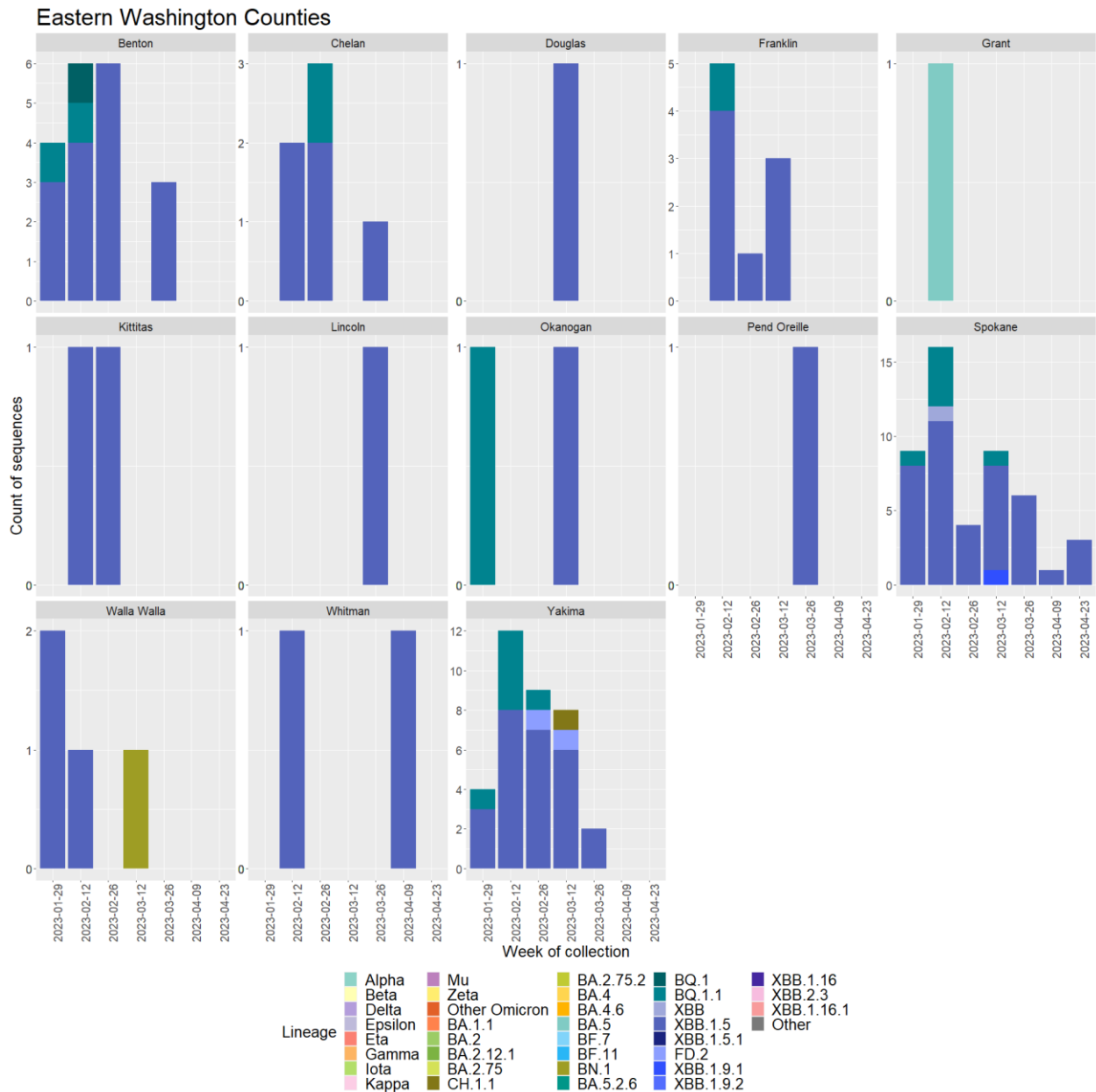
NOTE: The data on this graph come from cases that are randomly selected for sequencing statewide, Cases sequenced because they were part of an outbreak or were otherwise manually selected for sequencing are excluded, as this could cause a lineage to appear overrepresented.



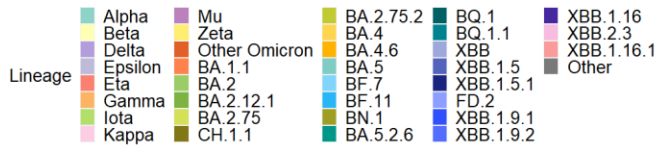
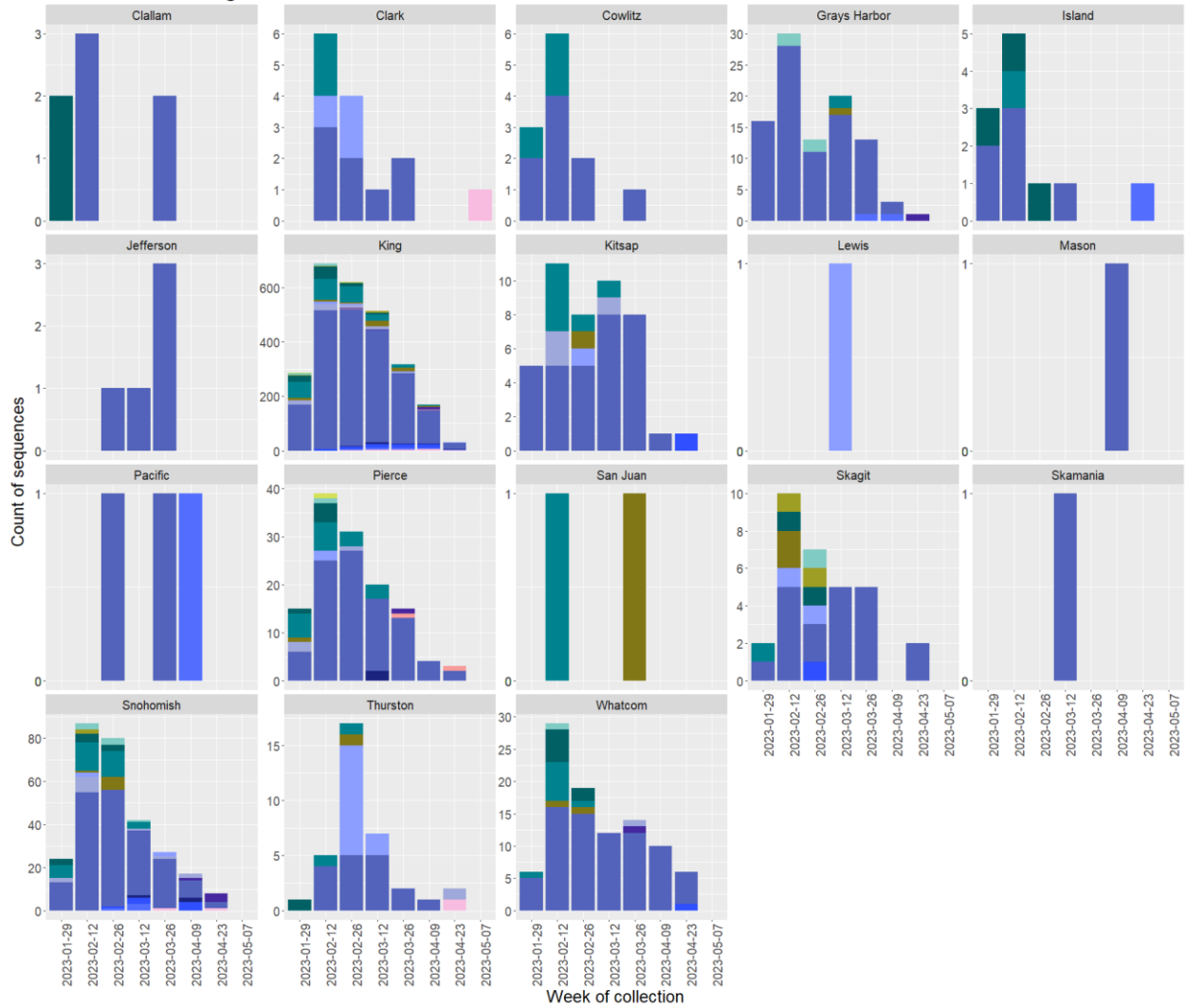
The chart above shows the proportions of the most common SARS-CoV-2 lineages circulating in Washington grouped in one-week intervals. Proportions are calculated using data which are subject to change over time and will be updated as more data becomes available, including data from prior time periods. **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 figures below show the current number of variants of concern (VOC) detected by county of home address since four months prior stratified by Eastern and Western Washington; data is from the Washington Disease Reporting System (WDRS).



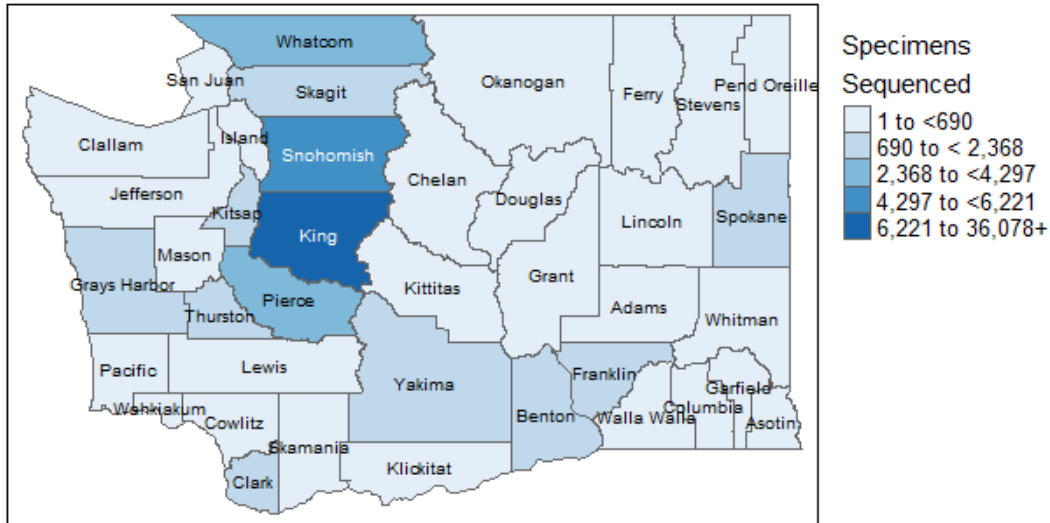
# Western Washington Counties



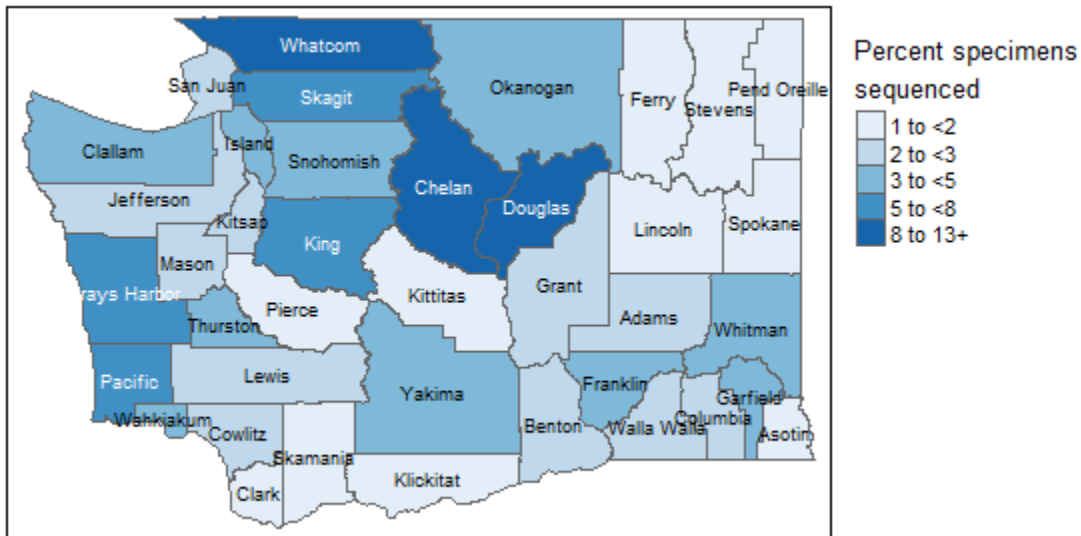
## Geographic Coverage of Sequencing

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%	4,252	1.3%	38,590	17.2%
BA.5	2.1%	2,083	0.4%	17,663	9.2%
BA.2	1.2%	1,154	0.2%	13,779	8.2%
Other Omicron	1.2%	1,150	0.3%	12,344	14.1%
BA.1.1	2.4%	2,356	0.8%	11,248	15.1%
Alpha	3.4%	3,438	0.6%	10,298	12.7%
BA.2.12.1	1.7%	1,722	0.3%	6,795	10.3%
Other	2.6%	2,590	0.8%	5,329	17.4%
Epsilon	2.6%	2,565	0.7%	4,133	17%
XBB.1.5	3.1%	3,148	0.4%	3,463	3.7%
BQ.1.1	2.6%	2,637	0.2%	2,996	6.3%
Gamma	6.8%	6,847	1.8%	2,483	17.6%
BQ.1	2%	2,025	0.2%	1,827	5.4%
BA.4	1.9%	1,874	0.3%	1,441	3.7%
Iota	3.2%	3,226	1.3%	930	30%
BA.4.6	2.9%	2,894	0.6%	691	5%
BF.7	3.2%	3,202	0.8%	531	23.5%
XBB	0.6%	567	0%	353	0%
BN.1	1.4%	1,361	0.3%	294	25%
Beta	6.8%	6,786	1.1%	280	15.8%
Mu	2.8%	2,752	1.8%	218	33.3%
BA.2.75	1.1%	1,058	0%	189	0%
BA.5.2.6	2.4%	2,367	0.6%	169	25%
CH.1.1	2.4%	2,381	0%	126	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%	38,590
BA.5	12%	28%	26%	20%	12%	3%	0%	17,663
BA.2	19%	32%	24%	15%	8%	2%	0%	13,779
Other Omicron	24%	33%	23%	13%	5%	1%	0%	12,344
BA.1.1	24%	30%	22%	14%	7%	2%	0%	11,248
Alpha	27%	32%	23%	13%	3%	1%	0%	10,298
BA.2.12.1	15%	32%	24%	17%	10%	3%	0%	6,795
Other	24%	29%	24%	16%	5%	2%	0%	5,329
Epsilon	25%	31%	24%	14%	4%	1%	0%	4,133
XBB.1.5	13%	28%	26%	19%	12%	3%	0%	3,463
BQ.1.1	13%	26%	27%	19%	11%	3%	0%	2,996
Gamma	22%	35%	24%	12%	4%	3%	0%	2,483
BQ.1	11%	27%	26%	20%	12%	3%	0%	1,827
BA.4	17%	31%	26%	16%	8%	2%	0%	1,441
Iota	25%	33%	25%	12%	4%	1%	0%	930
BA.4.6	13%	31%	24%	16%	13%	2%	0%	691
BF.7	10%	27%	23%	23%	13%	5%	0%	531
XBB	10%	35%	25%	20%	9%	1%	0%	353
BN.1	11%	24%	30%	18%	13%	3%	0%	294
Beta	29%	34%	21%	12%	3%	0%	0%	280
Mu	22%	37%	22%	11%	6%	1%	0%	218
BA.2.75	10%	25%	31%	19%	14%	1%	0%	189
BA.5.2.6	11%	29%	26%	15%	15%	2%	0%	169
CH.1.1	12%	32%	25%	17%	11%	4%	0%	126

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

**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  
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  
Grittmann 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 Army Medical Research Institute of Infectious Diseases

University of Washington Virology Lab

Washington State Department of Health Public Health Laboratories

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