

-1% in most recent week

6,727,163

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Variants & Genomic Surveillance

Variant Proportions

COVID Data Tracker

Maps, charts, and data provided by CDC, updates Mondays and Fridays by 8 p.m. ET

COVID-19 Home

**United States at a Glance** Trend in % Test Positivity

Collapse

Trend in % Emergency Department Visits

-19% in most recent week

Trend in % COVID-19 Deaths

Trend in Hospital Admissions +10.3% in most recent week

-9.6% in most recent week **Total Hospitalizations Total Deaths** 

1,169,666

SARS-CoV-2, the virus that causes COVID-19, is constantly changing and accumulating mutations in its genetic code over time. New variants of SARS-CoV-2 are expected to continue to emerge. Some variants will emerge and disappear, while others will emerge and continue to spread and may replace previous variants.

< Back to Variants & Genomic Surveillance

### To identify and track <u>SARS-CoV-2 variants</u>, CDC uses <u>genomic surveillance</u>. CDC's national genomic surveillance system collects SARS-CoV-2 specimens for sequencing through the National SARS-CoV-2 Strain Surveillance (NS3)

**Monitoring Variant Proportions** 

lineage. The proportions of SARS-CoV-2 variants in a population are calculated nationally, by HHS region, and by jurisdiction. The sequences analyzed through CDC's national genomic sequencing and bioinformatics efforts fuel the comprehensive and population-based U.S. surveillance system established to identify and monitor the spread of variants. Rapid virus genomic sequencing data combined with phenotypic data are further used to determine whether COVID-

program, as well as SARS-CoV-2 sequences generated by commercial or academic laboratories contracted by CDC

and state or local public health laboratories. Virus genetic sequences are analyzed and classified as a particular

19 tests, treatments, and vaccines authorized or approved for use in the United States will work against emerging variants. Types of Variant Proportion Data CDC provides estimates of variant proportions for two-week periods. These proportions are calculated in two ways: weighted estimates and Nowcast estimates.

Weighted estimates (provided for all two-week periods except the most recent two, two-week periods) are variant proportions that are based on empirical (observed) genomic sequencing data. These estimates are not available for the most recent two-week periods because of the time it takes to generate the sequencing data, including sample

#### Lineages with weighted estimates less than 1% of all circulating variants are combined with their parent lineage. When the weighted estimate of a lineage crosses the 1% threshold and has substitutions in the spike protein that could affect vaccine efficacy, transmission, or severity, it may be separated from its parent lineage and displayed on

its own in the variant proportions data.

Friday.

On This Page

1/20/2024(Nowcast) if available.

that lineage's estimate.

genomic sequencing results

100%

80%

Weighted and Nowcast Estimates in United States for

Hover over (or tap in mobile) any lineage of interest to see the amount of uncertainty in

2-Week Periods in 10/1/2023 - 1/20/2024

Weighted Estimates: Variant proportions based on reported

**Monitoring Variant Proportions** 

collection, specimen treatment, shipping, analysis, and upload into public databases.

below) are model-based projections of variant proportions for the most recent two-week periods to enable timely public health action. CDC uses the Nowcast to forecast variant proportions before the weighted estimates are available for a given two-week period.

Projections for an emerging lineage with a high growth rate may have a higher degree of

performs frequent evaluations of Nowcast to inform performance improvements.

uncertainty (wider predictive interval) when it is just beginning to spread and still has low weighted

estimates. Projections may also be biased during times of delayed reporting (e.g., around holidays). CDC

Nowcast estimates (provided for the most recent two two-week periods when the "Nowcast on" option is selected

Nowcast estimates for a parent lineage include projected changes in its child lineages until a child lineage's weighted estimate crosses the 1% threshold. Once the weighted estimate crosses the 1% threshold for the two-week period with sequences available, the initial Nowcast projections for the child lineage proportion for the two recent two-week periods may be substantially higher than 1%.

CDC provides updated variant proportions for weighted estimates and Nowcast estimates every other week on

**Nowcast More About Variants About These Data** 

**HHS Region:** Data for the 2-Week Period **Ending on:** USA 1/20/2024(Nowcast)  $\blacksquare$ This shows weighted and Nowcast estimates for the United States. The table and map show estimates for the 2-week period ending on

Nowcast:

of variant

proportions

Model-based

projected estimates

WHO label

Omicron

Lineage #

JN.1

HV.1

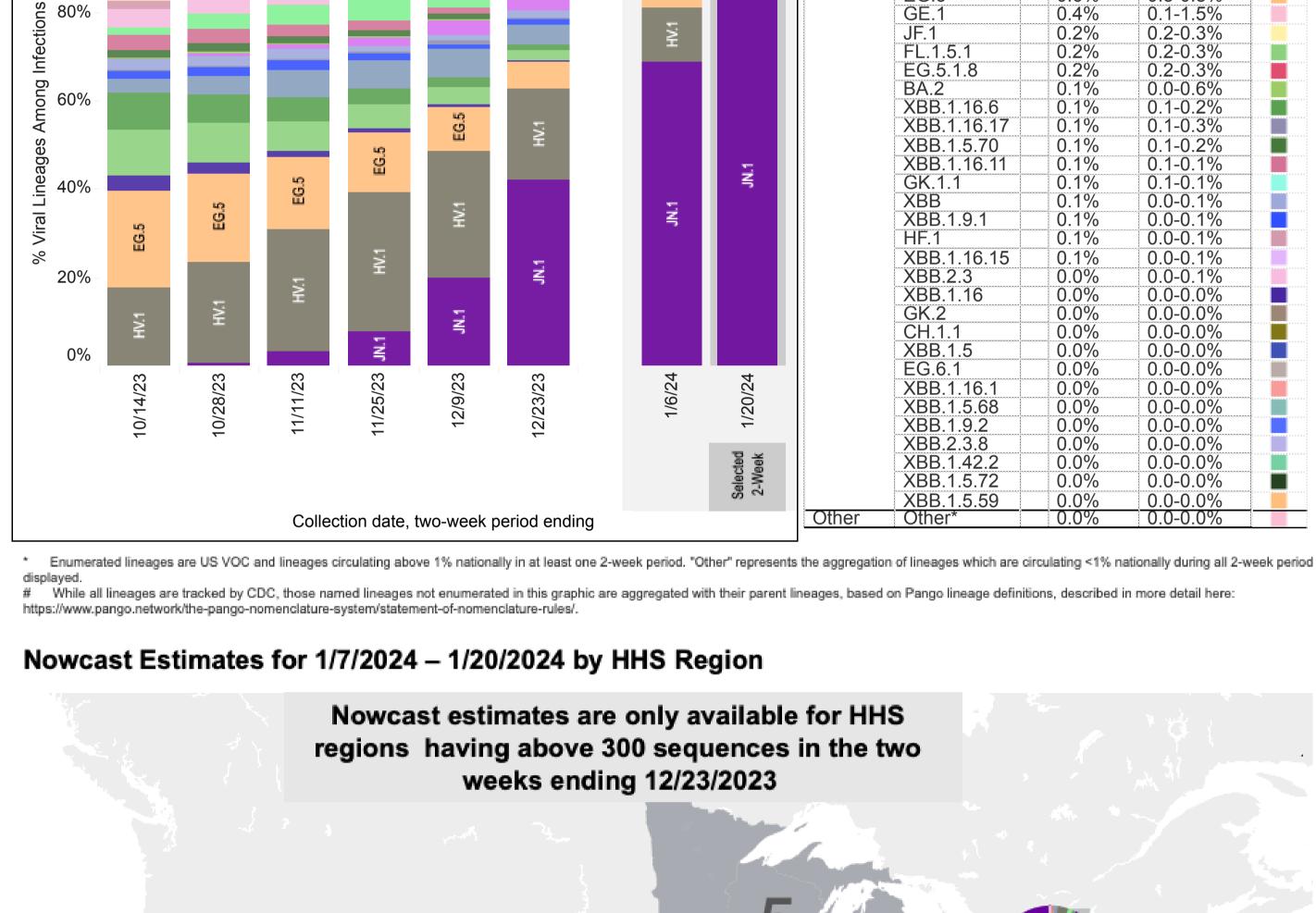
JG.3 HK.3

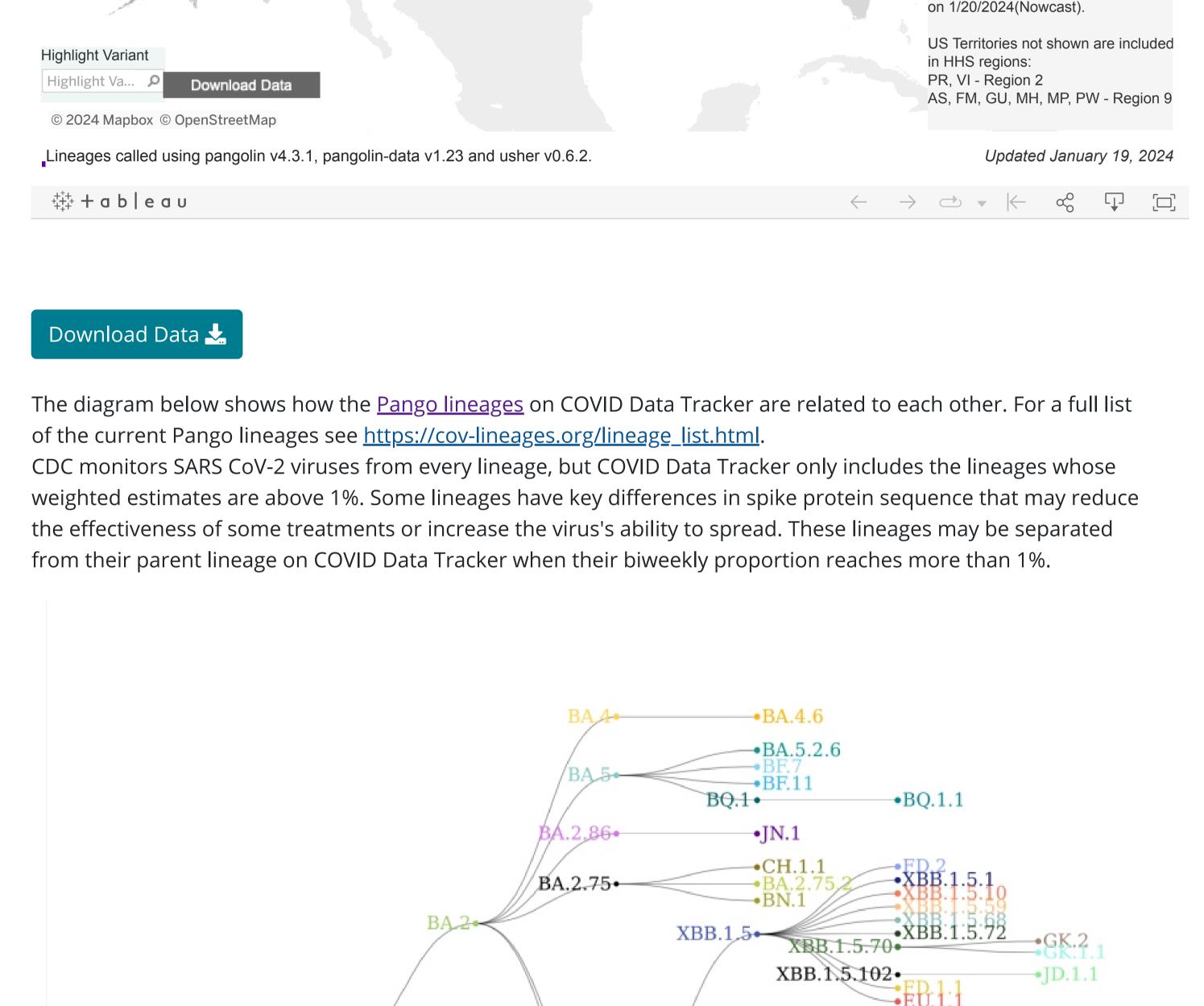
EG.5

GE.1

JD.1.1

BA.2.86





XBB.1.9.1

XBB.1.9.2

XBB. 16:6.

•JG.3

•EG.5.1.8

XBB.1,9.2.5,1.3.

BA. 12.1

# ‡‡ + a b | e a u

Origin Strain•

B.1.1,529

What You Need to Know about Variants

CDC's Role in Tracking Variants

**About These Data** 

Published SARS-CoV-2 Sequences

**Genomic Surveillance for SARS-CoV-2 Variants** 

Science Brief: Emerging SARS-CoV-2 Variants

All Variants in the United States

SARS-CoV-2 Variant Classifications and Definitions

-B.1.61 ₹.2

BA.1.

#### region, hover pointer to that variant in the specific region in U.S. map (a table showing proportions of other variants will also show up). **Nowcasting:** The default setting for the chart, table, and U.S. map is to display <u>CDC's Nowcast estimates</u>. Because

### statistical weights for these estimates that are based on the total number of reverse transcription polymerase chain reaction (RT-PCR) tests and number of SARS-CoV-2-positive RT-PCR test results received, stratified by state, specimen collection date, and by genomic surveillance data source. Variant proportions are estimated based on

sequencing data, which are published 2-3 weeks later.

genomic sequences obtained through CDC (NS3 and CDC-funded sequencing contracts) and tagged baseline surveillance sequencing submitted to public repositories by state, local, academic, or commercial laboratories. Sequences used in this analysis are intended to be a representative sample of all cases during the selected timeframe and location. They may not match cases reported by states, territorial, tribal, and local officials. Estimates of weighted variant proportions are subject to change, as sequence data from specimens previously collected continues to increase over time. The variant data reported for the jurisdiction-level estimates are limited to those designated as a <u>variant of concern</u> (VOC), variant of interest (VOI), or variant being monitored (VBM) by the U.S. government SARS-CoV-2 Interagency Group (SIG). Differences in the number of SARS-CoV-2 positive RT-PCR tests, sources of sequence data, and number of sequences available during a period affects the degree of certainty in the weighted proportion estimates. Confidence intervals are provided to describe these uncertainties. These data will be updated every other week on Friday.

**Instructions**: Data in the chart and table show the estimated variant proportions for the most common variants

and timeframe. The U.S. map shows the estimated biweekly proportions of the most common SARS-CoV-2 variants

circulating in the United States, divided by HHS regions. Data can be filtered by timeframe (two-week periods), and

national or HHS region from the drop-down controls on the top. If a specific timeframe is selected in the chart, the

data will change in the table and map to reflect the selected timeframe. If a specific region is selected in the U.S.

map, the data will change in the table and map to reflect the selected region. For example, if Region 4 is selected,

variant can be highlighted in all figures by selecting it in the "Highlight Variant" box in the left bottom corner of U.S.

data will reflect estimates based on reported results from MS, GA, AL, TN, KY, NC, SC, and FL. Data for a specific

intervals/prediction intervals for all the common variants in the specific timeframe, hover pointer over a bar

(timeframe) in the chart. To see the change of the proportion of a variant in different timeframes in a specific

it can take 2-3 weeks from the time a specimen is collected to when its sequence data is available for analysis,

Nowcast is an important tool that can estimate variant proportions for more recent time intervals. Nowcast does

not predict future spread of the virus, but it does help estimate current prevalence of variants, based on genomic

surveillance data from previous weeks. Estimates of variant proportions for previous two-week period may change

as more data are reported. Nowcast estimates consistently align with the weighted proportions based on reported

school) and may skew proportions within its larger jurisdiction. Using a survey-design-based approach, CDC uses

map, or in the chart, table or pie chart in the U.S. map. To see the proportions and their confidence

Visit the <u>SARS-CoV-2 Variant Classifications and Definitions</u> page to learn more about variant attributes and their classifications.

How is CDC using genomic sequencing to track SARS-CoV-2 variants?

Want to know more about variants of the virus that causes COVID-19?

**Email Address: Email Address** 

**Cite COVID Data Tracker** 

**COVID Data Tracker** 

Weekly Review

Centers for Disease Control and Prevention. COVID Data Tracker. Atlanta, GA: U.S. Department of Health and Human Services, CDC; 2024, January 20.

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Nowcast Estimates in United States for 1/7/2024 - 1/20/2024 **USA** 

95%PI

82.9-88.2%

4.4-6.4%

1.4-2.0%

1.1-2.1%

1.2-1.9%

1.2-1.8% 0.5-0.8%

%Total

85.7%

5.3%

1.6%

1.5%

1.5%

1.5%

0.6%

Regional proportions from specimens collected in the 2-week period ending

# More About Variants

To provide more representative national, regional, and jurisdiction-level estimates of variant proportions, calculations are included to account for sampling of data over time and across or within states. For example, sequences generated from outbreak investigations are often from a very narrow geographical region (such as a

Weighted Proportions

Why do we use genomic surveillance to monitor SARS-CoV-2 variants? Visit the Genomic Surveillance for SARS-CoV-2 Variants page to learn more

Visit CDC's Role in Tracking Variants page to learn more

Visit the About Variants of the Virus that Causes COVID-19 page to learn more

What SARS-CoV-2 variants are being monitored?

What's this?

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U.S. Department of Health & Human Services