

COVID Data Tracker

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

COVID-19 Home >



Effective September 29, 2023, weekly updates to maps, charts, and data provided by CDC for COVID Data Tracker will occur on Fridays by 12 p.m. ET. This change aligns with the timing of CDC's weekly updates for respiratory viruses (<https://www.cdc.gov/respiratory-viruses/index.html>).

United States at a Glance

Collapse

Trend in % Test Positivity

-0.8% in most recent week

Trend in Hospital Admissions

-8.2% in most recent week

Total Hospitalizations
6,405,961

Trend in % Emergency Department Visits

-17.7% in most recent week

Trend in % COVID-19 Deaths

-3.8% in most recent week

Total Deaths
1,147,253

CLICK TO VIEW OTHER PAGES:

Variants & Genomic Surveillance



< Back to Variants & Genomic Surveillance

Variant Proportions

Monitoring Variant Proportions

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.

To identify and track [SARS-CoV-2 variants](#), CDC uses [genomic surveillance](#). CDC's national genomic surveillance system collects SARS-CoV-2 specimens for sequencing through the National SARS-CoV-2 Strain Surveillance (NS3) 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 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-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 collection, specimen treatment, shipping, analysis, and upload into public databases.

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.

Nowcast estimates (provided for the most recent two two-week periods when the "Nowcast on" option is selected 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 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 performs frequent evaluations of Nowcast to inform performance improvements.

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 Friday.

On This Page

[Monitoring Variant Proportions](#)

[Nowcast](#)

[More About Variants](#)

[About These Data](#)

HHS Region:

USA

Data for the 2-Week Period

Ending on:

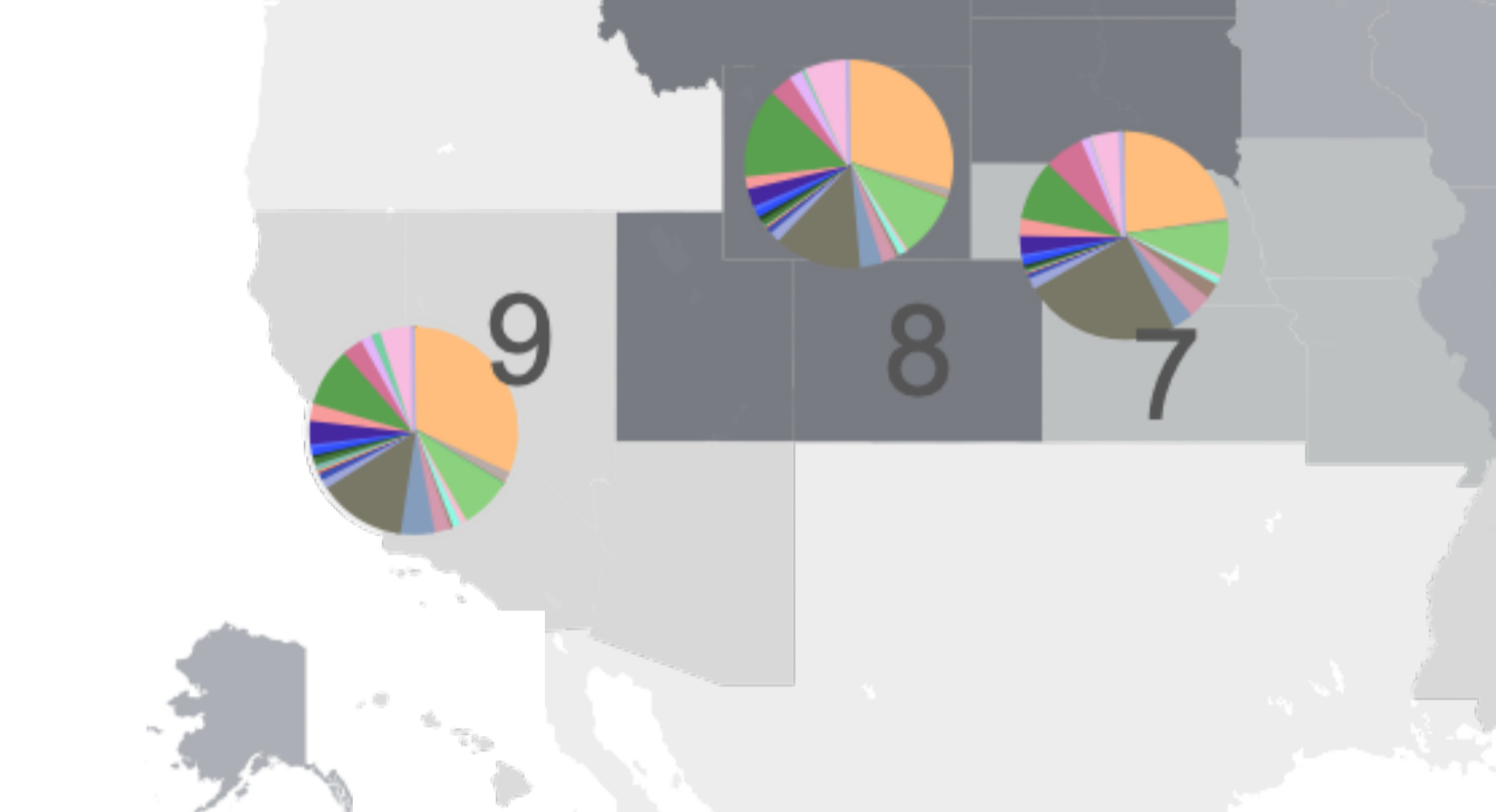
10/14/2023(Nowcast)

This shows weighted and Nowcast estimates for the United States. The table and map show estimates for the 2-week period ending on 10/14/2023(Nowcast) if available.

Weighted and Nowcast Estimates in United States for 2-Week Periods in 6/25/2023 – 10/14/2023

Nowcast Estimates in United States for 10/1/2023 – 10/14/2023

Hover over (or tap in mobile) any lineage of interest to see the amount of uncertainty in that lineage's estimate.

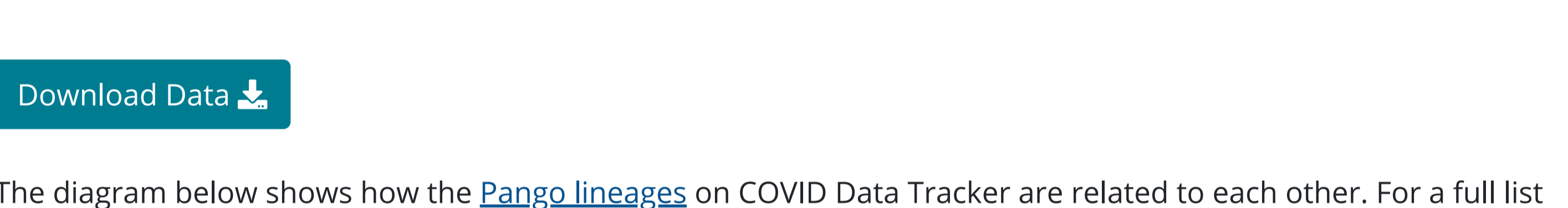


WHO label	Lineage #	% Total	95%PI
Omicron	EG.5	23.6%	21.2-26.3%
	HV.1	19.5%	16.8-22.6%
	FL.1.5.1	13.5%	10.8-16.7%
	XBB.1.16.6	10.3%	9.1-11.8%
	HK.3	4.9%	3.6-6.7%
	XBB.2.3	4.1%	3.4-4.9%
	XBB.1.16.11	3.1%	2.5-3.9%
	XBB.1.16	2.8%	2.4-3.3%
	XBB.1.16.1	2.2%	1.7-2.7%
	XBB.1.16.15	1.8%	1.3-2.4%
	HF.1	1.7%	1.2-2.4%
	GK.1.1	1.6%	1.3-2.1%
	XBB	1.4%	1.2-1.7%
	GE.1	1.4%	1.0-1.9%
	XBB.1.5.70	1.2%	0.9-1.8%
	CH.1.1	0.2%	0.1-0.3%
	GK.2	0.9%	0.7-1.2%
	XBB.1.5	0.9%	0.7-1.0%
	EG.6.1	0.8%	0.6-1.2%
	XBB.1.9.1	0.8%	0.6-1.0%
	XBB.1.5.72	0.6%	0.4-0.8%
	XBB.1.5.68	0.5%	0.3-0.8%
	XBB.1.9.2	0.5%	0.4-0.7%
	XBB.1.42.2	0.5%	0.3-0.8%
	BA.2	0.3%	0.1-0.8%
	XBB.1.5.10	0.3%	0.2-0.4%
	CH.1.1	0.2%	0.1-0.3%
	XBB.2.3.8	0.2%	0.1-0.3%
	XBB.1.5.59	0.1%	0.1-0.2%
	FD.1.1	0.1%	0.1-0.1%
	FE.1.1	0.1%	0.0-0.1%
	XBB.1.5.1	0.0%	0.0-0.0%
	EU.1.1	0.0%	0.0-0.0%
	BQ.1	0.0%	0.0-0.0%
	FE.1.1.529	0.0%	0.0-0.0%
	FD.2	0.0%	0.0-0.0%
	Other	0.0%	0.0-0.1%

* Enumerated lineages are US VOC and lineages circulating above 1% nationally in at least one 2-week period. "Other" represents the aggregation of lineages which are circulating <1% nationally during all 2-week periods displayed.

BA.1, BA.3 and their sublineages (except BA.1.1 and its sublineages) are aggregated with B.1.1.529. Except BA.2.12.1, BA.2.75, XBB and their sublineages, BA.2 sublineages are aggregated with BA.2. Except BA.2.75.2, CH.1.1 and BN.1, BA.2.75 sublineages are aggregated with BA.2.75. Except BA.4.6, sublineages of BA.4 are aggregated to BA.4. Except BF.7, BF.11, BA.5.2.6, BQ.1 and BQ.1.1, sublineages of BA.5 are aggregated to BA.5. Except the lineages shown and their sublineages, sublineages of XBB are aggregated to XBB. Except XBB.1.5.1, XBB.1.5.10, FD.2, EU.1.1, XBB.1.5.68 and XBB.1.5.70 sublineages of XBB.1.5 are aggregated to XBB.1.5. Except FL.1.5.1, sublineages of XBB.1.16.1 are aggregated to XBB.1.16.1. Except XBB.1.16.1, XBB.1.16.15 sublineages of XBB.1.16 are aggregated to XBB.1.16. Sublineages of XBB.1.42.2 are aggregated to XBB. Except FE.1.1, sublineages of XBB.1.18.1 are aggregated to XBB. For all the other lineages listed, their sublineages are aggregated to the listed parental lineages respectively. Previously, FL.1.5.1, OE.1, EG.6.1 and HV.1, FD.1.1, XBB.2.3.8, HF.1, GK.1.1, HK.3 was aggregated to XBB.1.9.1, XBB.2.3.10, XBB.1.9.2, XBB.1.5.15, XBB.2.3, XBB.1.16.13, XBB.1.5.70 and XBB.1.9.2.3.1.1 respectively. Lineages BA.2.75.2, XBB, XBB.1.5, XBB.1.5.1, XBB.1.5.10, FD.2, XBB.1.5.1, XBB.1.9.2, XBB.1.16, XBB.1.16.1, XBB.2.3, BN.1, BA.4.6, BF.7, BF.11, BA.5.2.6, BQ.1.1, EU.1.1, XBB.1.5.68, FE.1.1, EG.5, XBB.1.5.72, FL.1.5.1, OE.1, EG.6.1, XBB.1.16.11, FD.1.1, XBB.2.3.8, HV.1, XBB.1.42.2, GK.2, HF.1, XBB.1.16.15, GK.1.1 and HK.3 contain the spike substitution R346T.

Nowcast Estimates for 10/1/2023 – 10/14/2023 by HHS Region



Highlight Variant

Highlight V...

Download Data

© 2023 Mapbox © OpenStreetMap

Updated October 13, 2023

Lineages called using pangolin v4.3.1, pangolin-data v1.22 and usher v0.6.2.

Download Data

The diagram below shows how the [Pango lineages](#) on COVID Data Tracker are related to each other. For a full list of the current Pango lineages see https://cov-lineages.org/lineage_list.html. CDC monitors SARS CoV-2 viruses from every lineage, but COVID Data Tracker only includes the lineages whose weighted estimates are above 1%. Some lineages have key differences in spike protein sequence that may reduce the effectiveness of some treatments or increase the virus's ability to spread. These lineages may be separated from their parent lineage on COVID Data Tracker when their biweekly proportion reaches more than 1%.



Origin Strain

B.1.1.529

B.1.617.2

BA.1

BA.2

BA.4

BA.5

BA.6

BA.7

BA.8

BA.9

BA.10

BA.11

BA.12

BA.13

BA.14

BA.15

BA.16

BA.17

BA.18

BA.19

BA.20

BA.21

BA.22

BA.23

BA.24

BA.25

BA.26

BA.27

BA.28

BA.29

BA.30

BA.31

BA.32

BA.33

BA.34

BA.35

BA.36

BA.37

BA.38

BA.39

BA.40

BA.41

BA.42

BA.43

BA.44

BA.45

BA.46

BA.47

BA.48

BA.49

BA.50

BA.51

BA.52

BA.53

BA.54

BA.55

BA.56

BA.57

BA.58

BA.59

BA.60

BA.61

BA.62

BA.63

BA.64

BA.65

BA.66

BA.67

BA.68

BA.69

BA.70

BA.71

BA.72

BA.73

BA.74

BA.75

BA.76

BA.77

BA.78

BA.79

BA.80

BA.81

BA.82

BA.83

BA.84

BA.85

BA.86

BA.87

BA.88

BA.89

BA.90

BA.91

BA.92

BA.93

BA.94

BA.95

BA.96

BA.97

BA.98

BA.99

BA.100

BA.101

BA.102

BA.103

BA.104

BA.105

BA.106

BA.107

BA.108

BA.109

BA.110

BA.111

BA.112

BA.113

BA.114

BA.115

BA.116

BA.117

BA.118

BA.119

BA.120

BA.121

BA.122

BA.123

BA.124

BA.125

BA.126

BA.127

BA.128

BA.129

BA.130

BA.131

BA.132

BA.133

BA.134

BA.135

BA.136

BA.137

BA.138

BA.139

BA.140

BA.141

BA.142

BA.143

BA.144

BA.145

BA.146

BA.147

BA.148

BA.149

BA.150

BA.151

BA.152