

# State of Hawaii SARS-CoV-2 Sequencing and Variant Report

Hawaii Department of Health

2023-10-03

## Introduction

Whole genome sequencing (WGS) involves a set of laboratory methods used to determine the full genome sequence of an organism or virus, which, in the case of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2)—the virus that causes Coronavirus Disease 2019 (COVID-19), is approximately 30,000 letters, each letter a nucleotide code denoted as A, C, G, or T.

The genome sequence of a virus can reveal mutations that make it unique. Mutations are changes in a genome sequence (usually one-letter changes) that occur naturally over time. A viral genome that contains one or more mutations is referred to as a variant.

Collecting the genome sequences of virus specimens can reveal information about the relatedness of viruses and the similarities shared among groups of viruses. A closely related group of viruses derived from a common ancestor is referred to as a lineage.

Sequencing of viral genomes allows scientists to better understand virus transmission and evolution, and how each may impact public health. Sequencing also allows public health officials to monitor and characterize outbreaks and clusters, detect new variants, and conduct genomic surveillance (analysis of trends, similarities, and differences in circulating variants).

Some SARS-CoV-2 variants are classified by the U.S. government SARS-CoV-2 Interagency Group (SIG) as either Variants of Concern (VOC), Variants of Interest (VOI), or Variants Being Monitored (VBM) based on their attributes (e.g., transmissibility and/or severity of disease) and prevalence. The Centers for Disease Control and Prevention (CDC) has extensive information about SARS-CoV-2 variant classification that is updated as new evidence becomes available (<https://www.cdc.gov/coronavirus/2019-ncov/variants/variant-classifications.html>).

Sequencing can only be performed on specimens that contain SARS-CoV-2 RNA, which means only specimens used for molecular tests such as PCR can be included. Therefore, this report is limited to confirmed PCR-positive cases only. The genomes that are sequenced and compared are those of the virus, not humans.

Sequencing can be performed on stored specimens at any time. Therefore, the dataset used for this report is dynamic and batches of stored specimens that are newly sequenced will be added to the dataset as sequencing occurs, thus trends based on historical data can change over time.

In February 2021, State Laboratories Division, Hawaii Department of Health increased sequencing efforts done on PCR-positive specimens to improve the State's ability to detect new variants and conduct genomic surveillance of SARS-CoV-2.

## Acknowledgements

This report integrates genomes sequenced since 1 Jan 2021 by:

Institution	Program/partner	Count	Percent
State Laboratories Division		22282	78.100%
Centers for Disease Control and Prevention	National SARS-CoV-2 Strain Surveillance (NS3)	412	1.444%
	Quest Diagnostics Incorporated	1670	5.853%
	Laboratory Corporation of America	1639	5.745%
	Aegis Sciences Corporation	379	1.328%
	Helix/Illumina	185	0.648%
	Infinity Biologix	16	0.056%
	Mako Medical	20	0.070%
	Fulgent Genetics	8	0.028%
	UW Virology Lab	4	0.014%
Tripler Army Medical Center		822	2.881%
University of Hawaii at Manoa		861	3.018%
Aegis Sciences Corporation*		232	0.813%
<b>Total</b>		<b>28530</b>	<b>100.000%</b>

County distribution of genomes sequenced by institution:

	Honolulu County	Maui County	Hawaii County	Kauai County	unknown	Total
State Laboratories Division (since 1 Jan 2021)	13857	3801	3405	852	367	22282
University of Hawaii at Manoa (22 Jan 2022 – 23 Aug 2022)	508	67	221	17	48	861
Aegis Sciences Corporation* (since 14 Sep 2022)	54	11	3	0	164	232

Notes:

- In support of genomic surveillance efforts, PCR-positive specimens are routinely provided to State Laboratories Division (SLD) by commercial/clinical laboratories that operate throughout the State of Hawaii, including Clinical Labs of Hawaii (CLH), Diagnostic Laboratory Services, Inc. (DLS), Kaiser Permanente Hawaii, and S&G Labs Hawaii. The specimens are then processed, sequenced, and analyzed by the Laboratory Preparedness and Response Branch (LPRB) within SLD.
- In coordination with SLD, the School of Life Sciences, University of Hawaii at Manoa provided sequencing and analysis services for 861 PCR-positive specimens processed by the LPRB.
- As of 14 Sep 2022, Aegis Sciences Corporation\* reports SARS-CoV-2 genome sequences independently of the Centers for Disease Control and Prevention (CDC).
- County information is not provided for specimens sequenced by CDC programs/partners and by Tripler Army Medical Center.

## Summary and key notes

- This report reflects sequenced PCR-positive specimens only, and not all PCR-positive cases in the State of Hawaii are sequenced.
- Each successfully sequenced specimen produces one consensus SARS-CoV-2 genome sequence that is further analyzed to determine the variant.
- State Laboratories Division reported 816 additional SARS-CoV-2 genome sequences since the previous report was generated (5 Sep 2023).
- CDC programs/partners reported 3 additional SARS-CoV-2 genome sequences from the State of Hawaii since the previous report was generated.
- There were 3 historical SARS-CoV-2 genome sequences from UW Virology Lab (under CDC programs/partners) added since the previous report was generated.
- SARS-CoV-2 variant nomenclature is defined by a World Health Organization (WHO) label (letters of the Greek Alphabet, e.g., Alpha, Beta, Gamma, Delta, etc.), Phylogenetic Assignment of Named Global Outbreak (PANGO) lineage (alphabetical prefix and a numerical suffix), and/or Nextstrain clade (year of emergence followed by the next available letter in the alphabet, e.g., 20A, 20B, etc.). In this report, variant counts are reported using the WHO label and PANGO lineage nomenclatures only.
- For PANGO lineage nomenclature, ‘the numerical suffix has three hierarchical levels (primary, secondary, and tertiary). Each full stop (period or dot) within the numerical suffix represents “descendant of”. Descendants of lineages with tertiary suffixes are assigned to the next available alphabetical prefix, in alphabetical order.’ More details can be found at <https://www.pango.network/the-pango-nomenclature-system/statement-of-nomenclature-rules/>.
- In this report, an asterisk (\*) following a lineage designation (e.g., BA.5\*) signifies inclusion of the respective lineage (e.g., BA.5) and its sub-lineages (or descendants, e.g., BA.5.\*) unless otherwise specified.
- Due to the decreasing trend in the number of PCR tests being conducted, the availability of PCR-positive specimens has decreased statewide, resulting in smaller sample sizes for SARS-CoV-2 sequencing and variant reporting. Estimated variant proportions may not be truly representative for counties with low sequencing numbers.
- FL.1.5.1\* (includes its sub-lineage HN.1), XBB.1.16.6, XBB.1.6.11, and HV.1 are now tracked separately under estimated variant proportions. FL.1.5.1\* was previously aggregated to XBB.1.9.1\*. XBB.1.16.6 and XBB.1.16.11 were previously aggregated to XBB.1.16\*. HV.1 was previously aggregated to EG.5.1\*.
- BA.2.86, a lineage that has recently raised global concern, has been detected in Honolulu County. BA.2.86 is a ‘saltation’ lineage in that it exhibits a large evolutionary jump (possesses a large number of mutations) in relation to its most recently known ancestor, BA.2 (<https://virological.org/t/sars-cov-2-evolution-post-omicron/911>). BA.2.86 also harbors numerous mutations that are distinct from those found in currently circulating variants and experimental evidence suggests that BA.2.86 may be even more immune evasive as a result; however, it is not yet clear if BA.2.86 or its descendants pose(s) greater risks to the community in terms of clinical severity or whether it will outcompete currently circulating variants ([https://www.thelancet.com/journals/laninf/article/PIIS1473-3099\(23\)00588-1/fulltext](https://www.thelancet.com/journals/laninf/article/PIIS1473-3099(23)00588-1/fulltext) | [https://www.thelancet.com/journals/laninf/article/PIIS1473-3099\(23\)00575-3/fulltext](https://www.thelancet.com/journals/laninf/article/PIIS1473-3099(23)00575-3/fulltext) | [https://www.thelancet.com/journals/laninf/article/PIIS1473-3099\(23\)00573-X/fulltext](https://www.thelancet.com/journals/laninf/article/PIIS1473-3099(23)00573-X/fulltext)). Because only a single specimen with BA.2.86 has been found in Hawaii to date, it is not tracked separately under estimated variant proportions (graphs on pages 8 and 12).

## Variant Classifications

As SARS-CoV-2 continues to evolve, variants receive Variants of Concern (VOC), Variants of Interest (VOI), and Variants Being Monitored (VBM) classifications by the U.S. government SARS-CoV-2 Interagency Group (SIG) based on their attributes (e.g., transmissibility and/or severity of disease) and prevalence. VBM are variants circulating at very low levels or that are no longer detected, and thus do not pose an impending risk to public health. Therefore, a VOC or a VOI may be downgraded to a VBM after a significant and sustained decrease in prevalence over time. Currently, no SARS-CoV-2 variants are classified as VOI in the U.S. More information regarding these classifications can be found at <https://www.cdc.gov/coronavirus/2019-ncov/variants/variant-classifications.html>.

### Variants of Concern (VOC) in the State of Hawaii

#### Omicron (B.1.1.529 and descendant lineages)

B.1.1.529 was first detected in specimens collected on 11 Nov 2021 in Botswana and on 14 Nov 2021 in South Africa; the World Health Organization (WHO) labeled it “Omicron” on 26 Nov 2021. In the U.S., Omicron lineages were classified as VOC on 30 Nov 2021.

BA.1 and BA.2 emerged as the dominant primary descendants (sub-lineages) of B.1.1.529. BA.2 later outcompeted BA.1 and gave rise to BA.2.12.1, BA.2.75, BA.4, BA.5, and XBB, all of which have since given rise to their own descendants. As Omicron continues to evolve, new lineages and their sub-lineages constantly emerge. Some rapidly expand to outcompete those previously dominant due to acquired mutations that confer enhanced infectivity and/or immune resistance, and thus increased transmissibility. The co-circulation of different Omicron lineages/sub-lineages over time has also given rise to numerous recombinant variants. A recombinant forms when the genomes of two lineages (infecting a person simultaneously) undergo recombination during the viral replication process, producing a variant that is distinct from both parent lineages. Recombinants that expand and later receive a PANGO nomenclature have an X\* lineage designation (e.g., XBB). The major parental Omicron lineages correspond to Nextstrain clades 21M (B.1.1.529), 21K (BA.1), 21L (BA.2), 22A (BA.4), 22B (BA.5), 22C (BA.2.12.1), 22D (BA.2.75), 22E (BQ.1), 22F (XBB), 23A (XBB.1.5), 23B (XBB.1.16), 23C (CH.1.1), 23D (XBB.1.9), 23E (XBB.2.3), and 23F (EG.5.1); a diagram of their evolutionary relationship can be viewed at <https://ncov-clades-schema.vercel.app/>. Detailed information about Nextstrain clades and their relationship to various lineages can be found at <https://covariants.org/variants>.

### Variants Being Monitored (VBM) in the State of Hawaii

#### Alpha (B.1.1.7 and Q.\* lineages)

B.1.1.7 was first identified in the United Kingdom in Sep 2020; the WHO labeled it “Alpha” on 31 May 2021. B.1.1.7 is the parent lineage of Alpha; sub-lineages of B.1.1.7 have the Q.\* designation. In the U.S., Alpha lineages were classified as VOC on 29 Dec 2020 and downgraded to VBM on 21 Sep 2021. The Alpha variant corresponds to Nextstrain clade 20I.

#### Beta (B.1.351 and B.1.351.\* lineages)

B.1.351 was first identified in South Africa in May 2020; the WHO labeled it “Beta” on 31 May 2021. In the U.S., Beta lineages were classified as VOC on 29 Dec 2020 and downgraded to VBM on 21 Sep 2021. The Beta variant corresponds to Nextstrain clade 20H.

#### Gamma (P.1 and P.1.\* lineages)

P.1 was first identified in Brazil in Nov 2020; the WHO labeled it “Gamma” on 31 May 2021. In the U.S., Gamma lineages were classified as VOC on 29 Dec 2020 and downgraded to VBM on 21 Sep 2021. The Gamma variant corresponds to Nextstrain clade 20J.

**Delta (B.1.617.2 and AY.\* lineages)**

B.1.617.2 was first identified in India in Oct 2020; the WHO labeled it “Delta” on 31 May 2021. B.1.617.2 is the parent lineage of Delta; sub-lineages of B.1.617.2 have the AY.\* designation. In the U.S., Delta lineages were classified as VOC on 15 Jun 2021 and downgraded to VBM on 14 Apr 2022. The major lineages of Delta correspond to Nextstrain clades 21A, 21I, and 21J.

**Epsilon (B.1.429 and B.1.427 lineages)**

The closely related lineages B.1.429 and B.1.427 were first identified in California in Mar 2020; the WHO labeled them “Epsilon” on 31 May 2021. In the U.S., Epsilon lineages were classified as VOC on 19 Mar 2021, and downgraded to VOI on 29 Jun 2021 and then to VBM on 21 Sep 2021. The Epsilon variant corresponds to Nextstrain clade 21C.

**Zeta (P.2 lineage)**

P.2 was first identified in Brazil in Apr 2020; the WHO labeled it “Zeta” on 31 May 2021. In the U.S., P.2 (Zeta) was classified a VOI on 26 Feb 2021 and downgraded to a VBM on 21 Sep 2021. The Zeta variant corresponds to Nextstrain clade 20B/S.484K.

**Iota (B.1.526 lineage)**

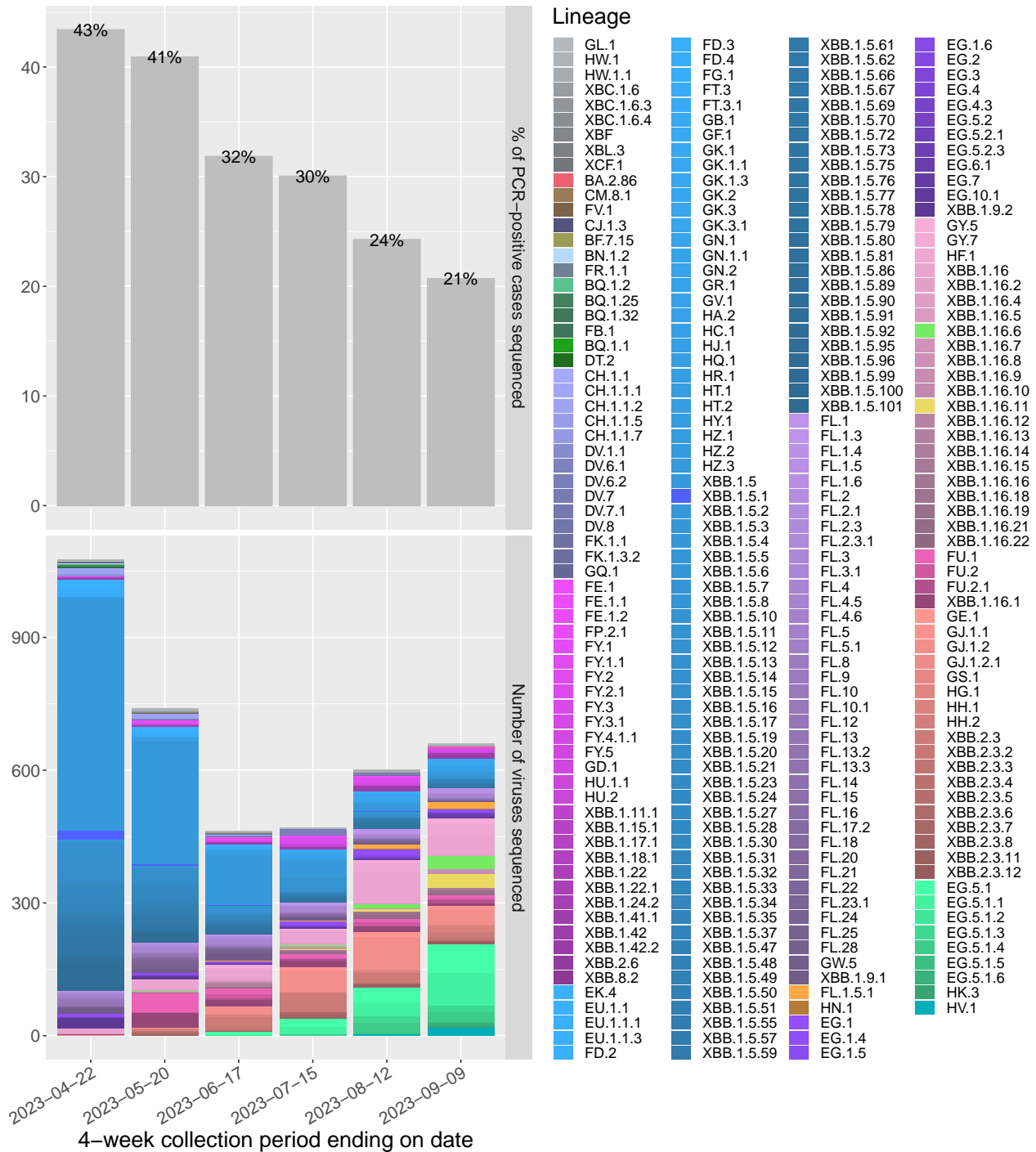
B.1.526 was first identified in New York in Nov 2020; the WHO labeled it “Iota” on 31 May 2021. In the U.S., B.1.526 (Iota) was classified a VOI on 26 Feb 2021 and downgraded to a VBM on 21 Sep 2021. The Iota variant corresponds to Nextstrain clade 21F.

**Mu (B.1.621 and B.1.621.1 lineages)**

Lineage B.1.621 was first identified in Columbia in Jan 2021; the WHO labeled “MU” on 30 Aug 2021. In the U.S., Mu lineages were classified as VBM on 21 Sep 2021. The MU variant corresponds to Nextstrain clade 21H.

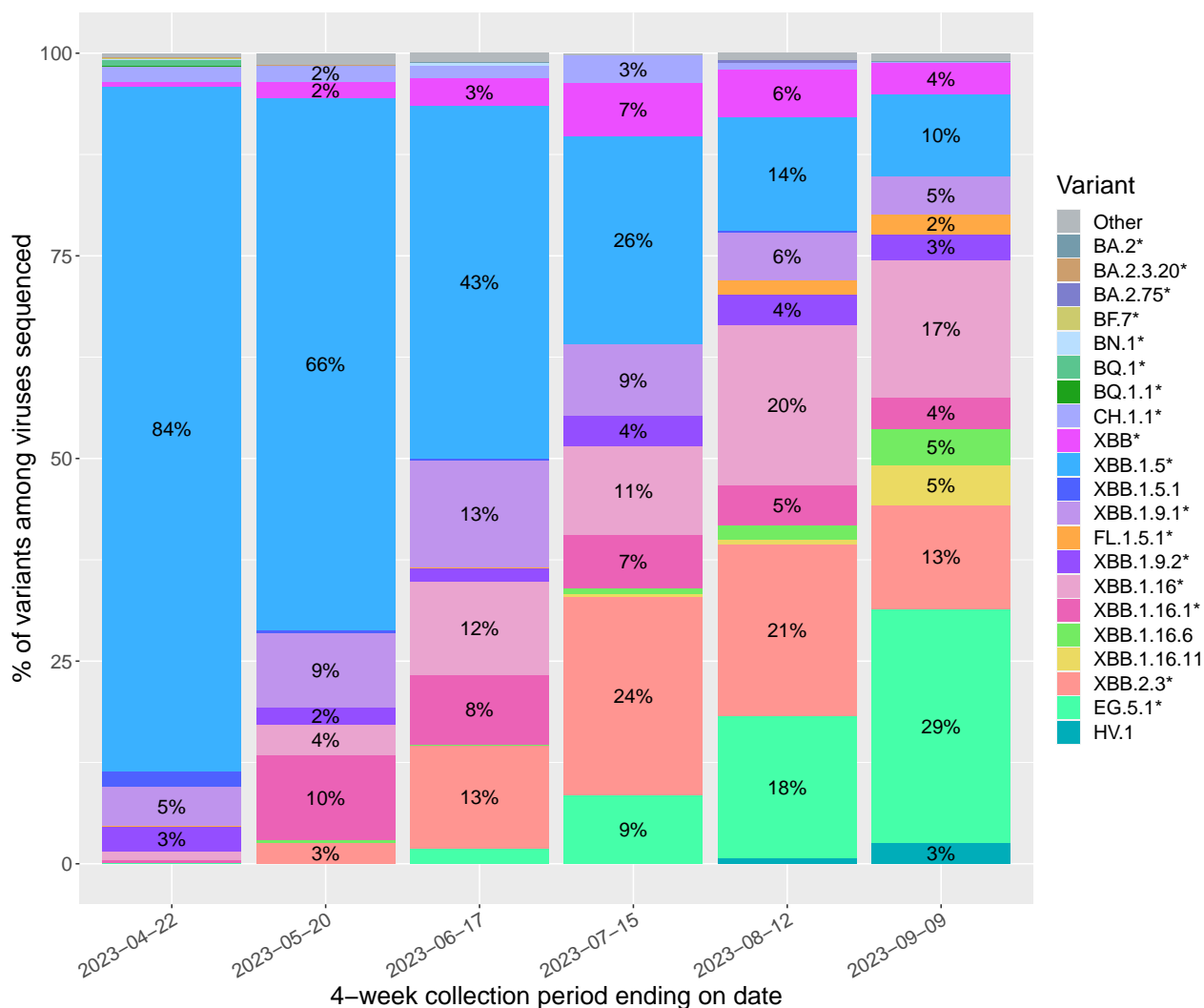
# State of Hawaii

## Total variants identified



**Figure Notes:** Graph depicts SARS-CoV-2 variants by lineage identified in the State of Hawaii in the 4-week collection periods ending on dates shown (based on when the specimen was collected from a patient). Upper (gray) bars represent the percentage of PCR-positive cases from each period that were sequenced. Lower (color) bars represent the number of sequenced viruses from each period (numbers may change over time as additional sequences are reported; one sequenced virus equates to one PCR-positive case). This graph does not estimate prevalence in the population.

## Estimated variant proportions for the State of Hawaii



**Figure Notes:** Graph depicts estimated SARS-CoV-2 variant proportions (percentages rounded to the nearest integer) for the State of Hawaii, grouped in 4-week collection periods (based on the date of specimen collection). Not all positive SARS-CoV-2 specimens are sequenced and sequenced specimens are not a random selection of all COVID-19 cases. Graph only includes specimens selected randomly for surveillance. Percentage estimates based on historical data may change over time as additional sequences are reported. Each variant is defined by the parental lineage shown; an asterisk (\*) indicates inclusion of respective sub-lineages. “Other” includes lineages not belonging to the other variant categories shown.



## Variants of Concern in the State of Hawaii

WHO label	Lineage	Earliest specimen collection date	Latest specimen collection date	Cumulative sequences
Omicron				20573
	Other	01 Apr 2023	31 Oct 2022	5642
	BA.1.1	27 Nov 2021	19 Jun 2022	1675
	BA.2.12.1	21 Mar 2022	29 Sep 2022	1613
	BA.2	18 Jan 2022	01 Aug 2022	1577
	XBB.1.5	13 Dec 2022	06 Sep 2023	1542
	BA.5.2.1	31 May 2022	03 Jan 2023	1039
	BA.2.3	06 Jan 2022	14 Nov 2022	837
	BA.1.1.2	06 Dec 2021	01 Apr 2022	588
	BG.5	09 Apr 2022	21 Aug 2022	533
	BA.5.2	17 Jun 2022	11 Jan 2023	486
	BA.1.15	30 Nov 2021	09 Apr 2022	425
	BQ.1.1	27 Sep 2022	27 Mar 2023	421
	BA.5.1	07 Jun 2022	29 Jan 2023	405
	BA.5.5	03 May 2022	28 Oct 2022	362
	BQ.1	16 Sep 2022	13 Feb 2023	314
	BA.5.6	21 May 2022	03 Dec 2022	253
	BA.2.3.17	25 Jan 2022	15 Jun 2022	208
	XBB.1.16	20 Mar 2023	05 Sep 2023	194
	BF.5	16 Jun 2022	19 Dec 2022	176
	GJ.1.2	03 May 2023	03 Sep 2023	173
	BA.4.1	04 May 2022	29 Nov 2022	169
	BA.1	07 Dec 2021	11 Apr 2022	164
	BA.5.1.1	14 May 2022	02 Dec 2022	162
	BA.2.9	25 Jan 2022	25 Jul 2022	161
	BA.4.6	21 Jun 2022	20 Jan 2023	156
	EG.5.1	21 Apr 2023	08 Sep 2023	127
	EG.5.1.1	31 May 2023	10 Sep 2023	123
	BA.1.1.18	10 Dec 2021	30 Mar 2022	100
	BA.2.18	21 Mar 2022	11 Jul 2022	96
	BF.10	05 Jun 2022	12 Jan 2023	94
	XBB.2.3	15 May 2023	31 Aug 2023	94
	BQ.1.5	02 Oct 2022	18 Jan 2023	91
	XBB.1.5.91	21 Jan 2023	04 May 2023	88
	XBB.1.16.1	30 Mar 2023	08 Sep 2023	86
	FU.1	02 Apr 2023	01 Sep 2023	85
	BA.5.1.23	23 Jun 2022	27 Oct 2022	82
	BQ.1.1.3	01 Nov 2022	20 Feb 2023	78
	BA.5.2.9	20 Jun 2022	02 Dec 2022	77
	XBB.1.5.15	05 Jan 2023	05 Sep 2023	76
	BA.2.86	06 Sep 2023	06 Sep 2023	1

*Table Notes:*

- Lineage “Other” represents an aggregation of different Omicron lineages in which each alone accounts for <0.4% of the cumulative Omicron sequences from the State of Hawaii; excludes BA.2.86.

## Variants Being Monitored in the State of Hawaii

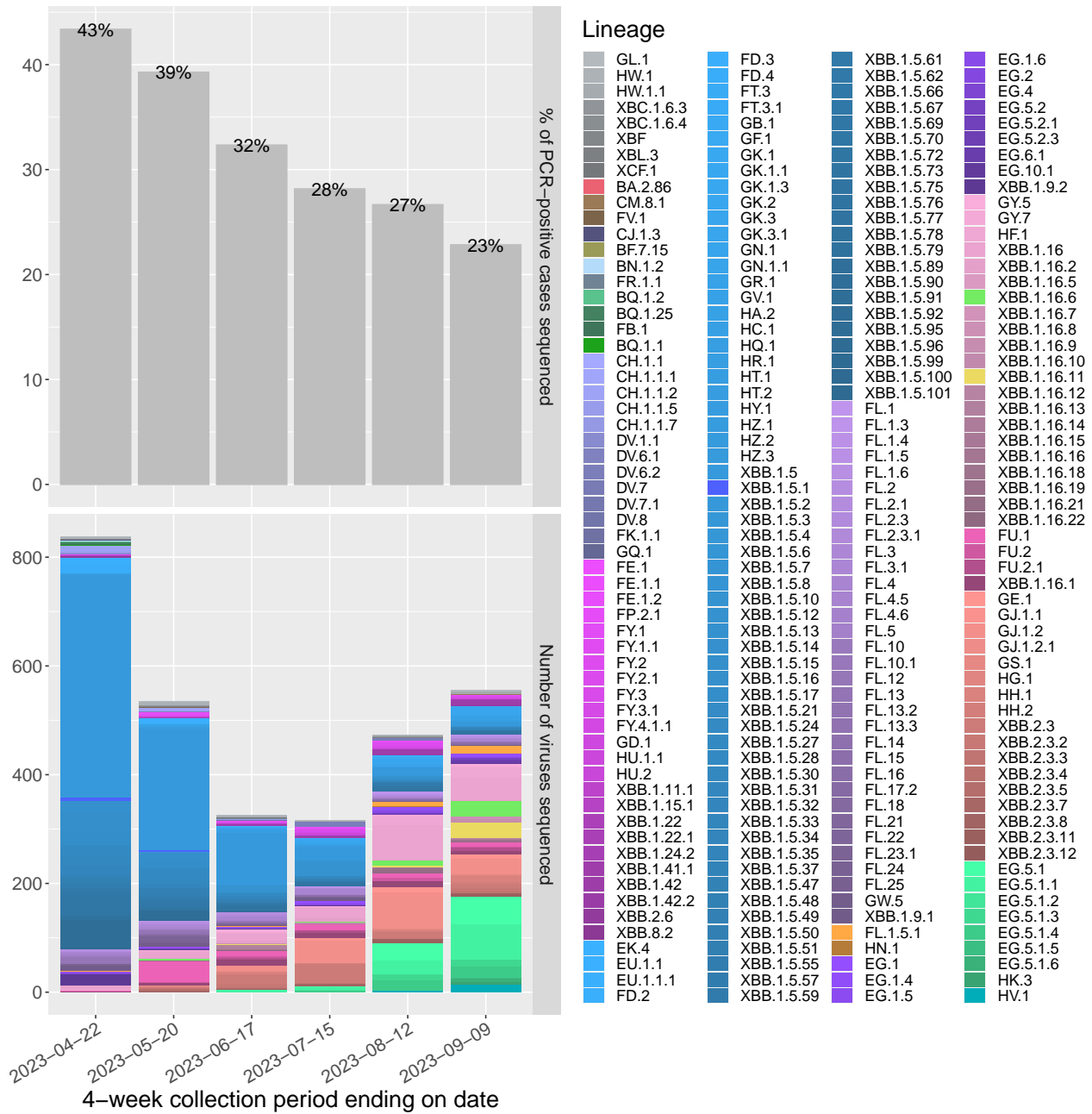
WHO label	Lineage	Earliest specimen collection date	Latest specimen collection date	Cumulative sequences
Alpha				797
	B.1.1.7	21 Jan 2021	14 Aug 2021	745
	Q.3	21 Mar 2021	02 Sep 2021	52
Beta	B.1.351	16 Feb 2021	22 Sep 2021	20
Gamma				191
	P.1.10	24 Apr 2021	14 Jul 2021	84
	P.1	24 Mar 2021	21 Jul 2021	54
	P.1.12	21 Mar 2021	28 Apr 2021	20
	P.1.17	29 Mar 2021	21 Jul 2021	18
	P.1.13	03 May 2021	28 Jun 2021	15
Delta				5623
	AY.103	21 May 2021	12 Jan 2022	1227
	AY.44	07 Jun 2021	19 Jan 2022	1038
	Other AY.*	01 Aug 2021	30 Jul 2021	617
	AY.3	24 Jun 2021	02 Jan 2022	562
	AY.25	21 Jun 2021	20 Jan 2022	534
	AY.54	23 Jun 2021	21 Nov 2021	367
	AY.100	17 Jul 2021	12 Dec 2021	196
	AY.25.1	08 Jul 2021	27 Jan 2022	196
	AY.1	30 Jun 2021	30 Nov 2021	185
	AY.119	06 Jul 2021	21 Dec 2021	136
	AY.26	07 Jun 2021	28 Dec 2021	132
	AY.117	15 Jul 2021	17 Dec 2021	127
	AY.122	09 Jul 2021	26 Nov 2021	107
	B.1.617.2	28 May 2021	16 Dec 2021	101
	AY.47	21 Jul 2021	07 Dec 2021	98
Epsilon				781
	B.1.429	31 Dec 2020	03 Jun 2021	723
	B.1.427	07 Dec 2020	05 Jun 2021	58
Zeta	P.2	06 Feb 2021	08 Feb 2021	2
Iota	B.1.526	06 Feb 2021	23 Jul 2021	128
Mu				58
	B.1.621	03 Jun 2021	17 Sep 2021	45
	B.1.621.1	27 May 2021	24 Aug 2021	13

*Table Notes:*

- Lineage “Other AY.\*” represents an aggregation of different AY.\* lineages in which each alone accounts for <2% of the cumulative Delta sequences from the State of Hawaii.

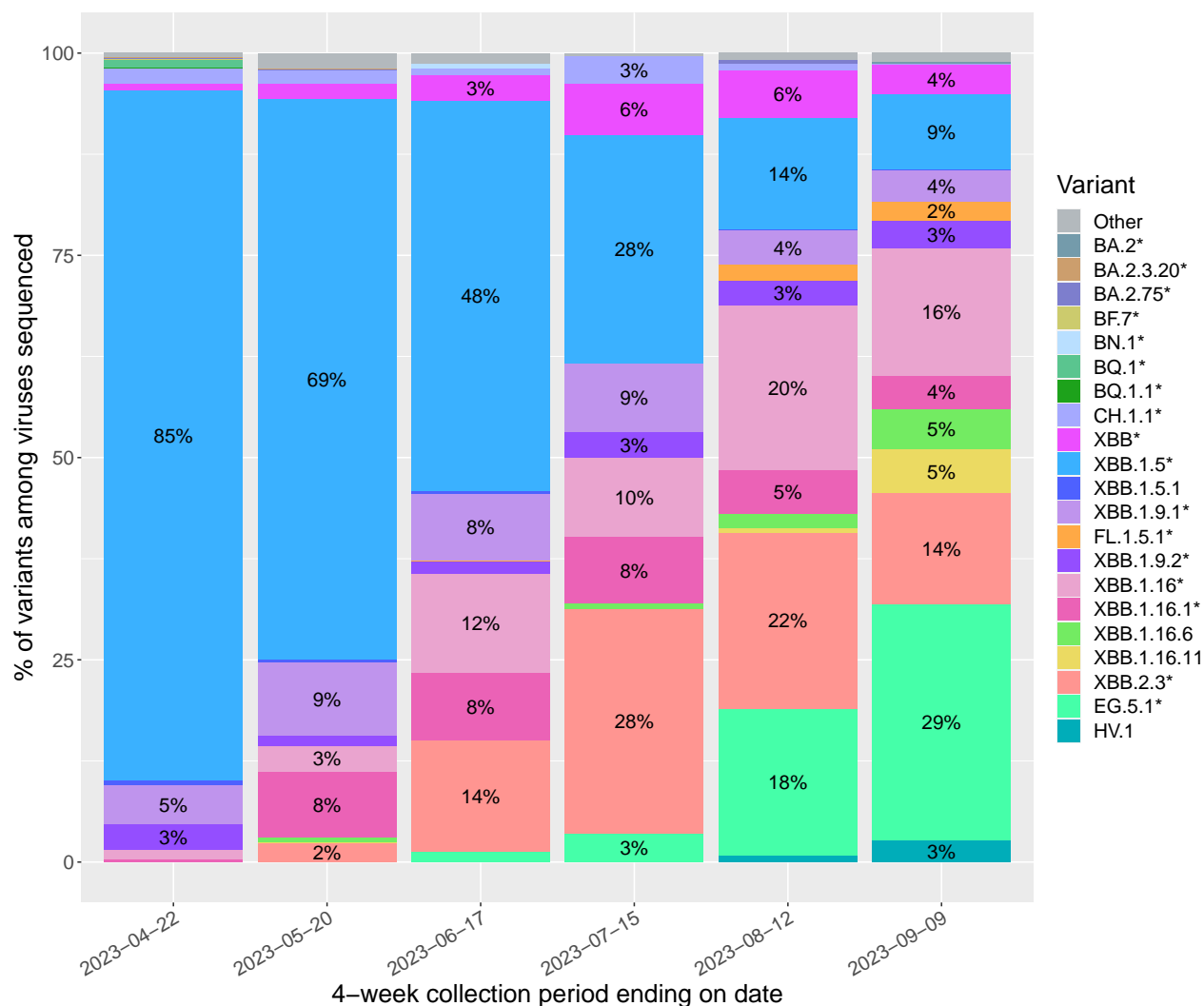
# Honolulu County

## Total variants identified



**Figure Notes:** Graph depicts SARS-CoV-2 variants by lineage identified in Honolulu County in the 4-week collection periods ending on dates shown (based on when the specimen was collected from a patient). Upper (gray) bars represent the percentage of PCR-positive cases from each period that were sequenced. Lower (color) bars represent the number of sequenced viruses from each period (numbers may change over time as additional sequences are reported; one sequenced virus equates to one PCR-positive case). This graph does not estimate prevalence in the population.

## Estimated variant proportions for Honolulu County



**Figure Notes:** Graph depicts estimated SARS-CoV-2 variant proportions (percentages rounded to the nearest integer) for Honolulu County, grouped in 4-week collection periods (based on the date of specimen collection). Not all positive SARS-CoV-2 specimens are sequenced and sequenced specimens are not a random selection of all COVID-19 cases. Graph only includes specimens selected randomly for surveillance. Percentage estimates based on historical data may change over time as additional sequences are reported. Each variant is defined by the parental lineage shown; an asterisk (\*) indicates inclusion of respective sub-lineages. “Other” includes lineages not belonging to the other variant categories shown.

## Variants of Concern in Honolulu County

WHO label	Lineage	Earliest specimen collection date	Latest specimen collection date	Cumulative sequences
Omicron				10644
	Other	01 Apr 2023	31 Oct 2022	3278
	XBB.1.5	17 Dec 2022	05 Sep 2023	1159
	BA.1.1	27 Nov 2021	11 May 2022	658
	BA.2	27 Jan 2022	08 Jul 2022	627
	BA.2.12.1	21 Mar 2022	29 Sep 2022	504
	BA.5.2.1	05 Jun 2022	03 Jan 2023	465
	BA.2.3	30 Jan 2022	14 Nov 2022	366
	BA.1.1.2	06 Dec 2021	31 Mar 2022	309
	BG.5	09 Apr 2022	21 Aug 2022	303
	BQ.1.1	07 Oct 2022	27 Mar 2023	250
	BA.5.2	22 Jun 2022	09 Jan 2023	232
	BQ.1	04 Oct 2022	13 Feb 2023	191
	BA.5.1	11 Jun 2022	29 Jan 2023	169
	BA.5.5	29 May 2022	28 Oct 2022	168
	BA.1.15	30 Nov 2021	07 Apr 2022	163
	XBB.1.16	20 Mar 2023	05 Sep 2023	161
	GJ.1.2	03 May 2023	03 Sep 2023	149
	BA.5.6	18 Jun 2022	04 Nov 2022	134
	BA.2.3.17	05 Feb 2022	02 Jun 2022	121
	EG.5.1.1	31 May 2023	10 Sep 2023	98
	BA.4.6	26 Jun 2022	09 Dec 2022	86
	EG.5.1	13 Jun 2023	08 Sep 2023	86
	BA.4.1	22 May 2022	29 Nov 2022	82
	BA.5.1.1	14 May 2022	02 Dec 2022	76
	FU.1	02 Apr 2023	01 Sep 2023	76
	XBB.1.5.91	17 Mar 2023	04 May 2023	76
	XBB.2.3	15 May 2023	31 Aug 2023	74
	BA.2.9	14 Mar 2022	29 Jun 2022	70
	BQ.1.5	02 Oct 2022	18 Jan 2023	67
	BF.5	17 Jun 2022	19 Dec 2022	61
	XBB.1.5.15	10 Feb 2023	10 Aug 2023	56
	XBB.1.5.17	22 Jan 2023	05 Jun 2023	55
	XBB.1.5.69	18 Mar 2023	25 Apr 2023	49
	XBB.1.16.1	30 Mar 2023	08 Sep 2023	48
	BQ.1.1.69	30 Nov 2022	30 Jan 2023	47
	BA.1	07 Dec 2021	14 Mar 2022	43
	EG.5.1.4	30 Jun 2023	07 Sep 2023	43
	XBB.1.5.10	24 Mar 2023	16 Aug 2023	43
	BA.2.86	06 Sep 2023	06 Sep 2023	1

*Table Notes:*

- Lineage “Other” represents an aggregation of different Omicron lineages in which each alone accounts for <0.4% of the cumulative Omicron sequences from Honolulu County; excludes BA.2.86.

## Variants Being Monitored in Honolulu County

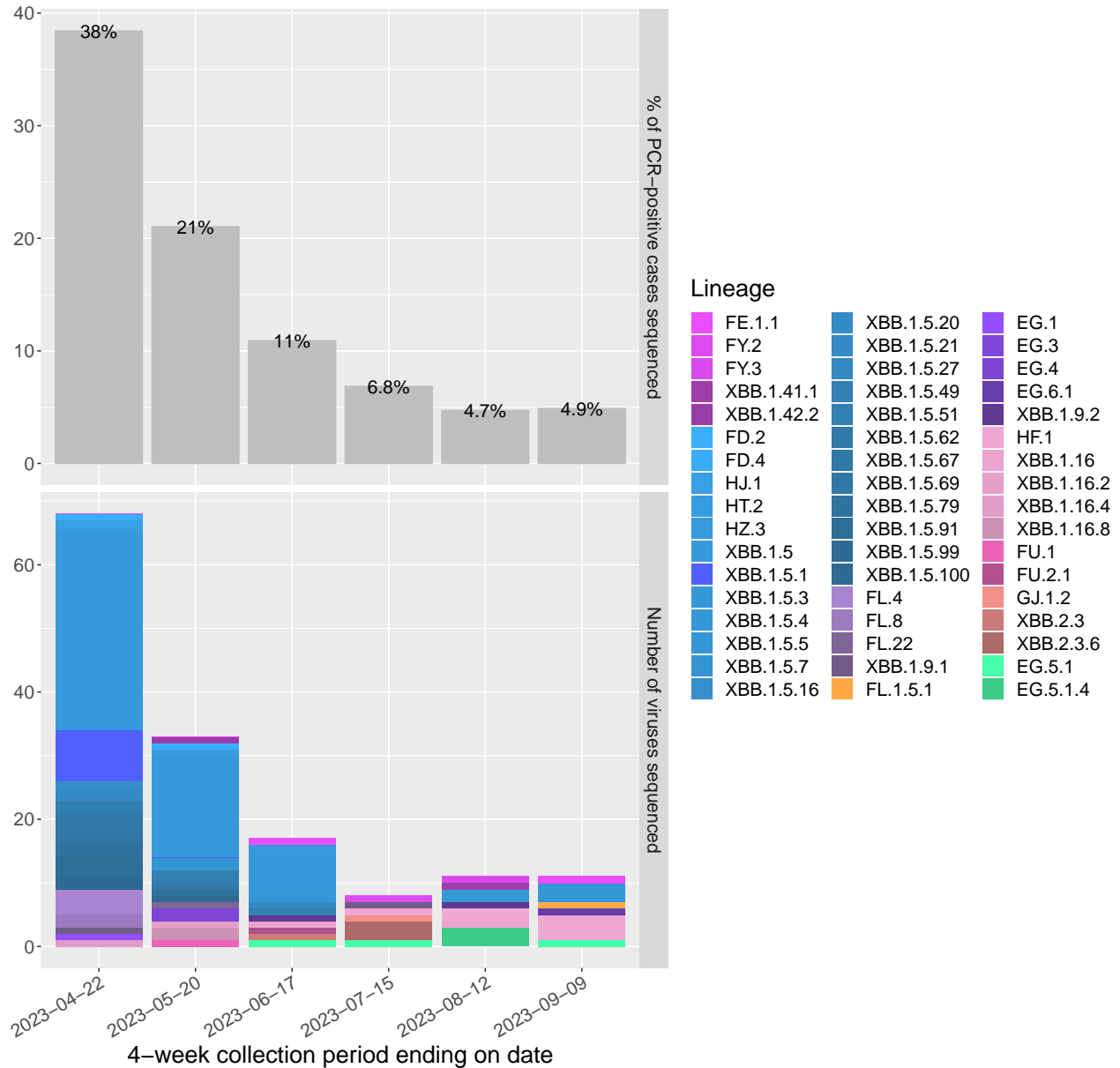
WHO label	Lineage	Earliest specimen collection date	Latest specimen collection date	Cumulative sequences
Alpha				514
	B.1.1.7	21 Jan 2021	14 Aug 2021	481
	Q.3	03 Apr 2021	02 Sep 2021	33
Beta	B.1.351	16 Feb 2021	22 Sep 2021	17
Gamma				98
	P.1.10	24 Apr 2021	13 Jul 2021	53
	P.1	24 Mar 2021	11 Jul 2021	15
	P.1.13	03 May 2021	28 Jun 2021	15
	P.1.17	29 Mar 2021	20 Jul 2021	14
	P.1.12	03 Apr 2021	03 Apr 2021	1
Delta				2635
	AY.103	20 Jun 2021	18 Dec 2021	732
	AY.44	07 Jun 2021	22 Dec 2021	416
	Other AY.*	01 Aug 2021	30 Nov 2021	289
	AY.54	23 Jun 2021	21 Nov 2021	259
	AY.3	24 Jun 2021	17 Dec 2021	237
	AY.25	21 Jun 2021	04 Jan 2022	201
	AY.1	30 Jun 2021	30 Nov 2021	107
	AY.100	23 Jul 2021	12 Dec 2021	88
	AY.117	15 Jul 2021	11 Nov 2021	73
	AY.26	07 Jun 2021	21 Nov 2021	69
	AY.25.1	18 Jul 2021	11 Dec 2021	64
	AY.119	06 Jul 2021	13 Dec 2021	50
	B.1.617.2	28 May 2021	25 Oct 2021	50
Epsilon				351
	B.1.429	05 Jan 2021	29 May 2021	320
	B.1.427	07 Jan 2021	05 Jun 2021	31
Zeta	P.2	06 Feb 2021	08 Feb 2021	2
Iota	B.1.526	08 Feb 2021	23 Jul 2021	26
Mu				25
	B.1.621	03 Jun 2021	28 Jul 2021	19
	B.1.621.1	27 May 2021	24 Aug 2021	6

*Table Notes:*

- Lineage “Other AY.\*” represents an aggregation of different AY.\* lineages in which each alone accounts for <2% of the cumulative Delta sequences from Honolulu County.

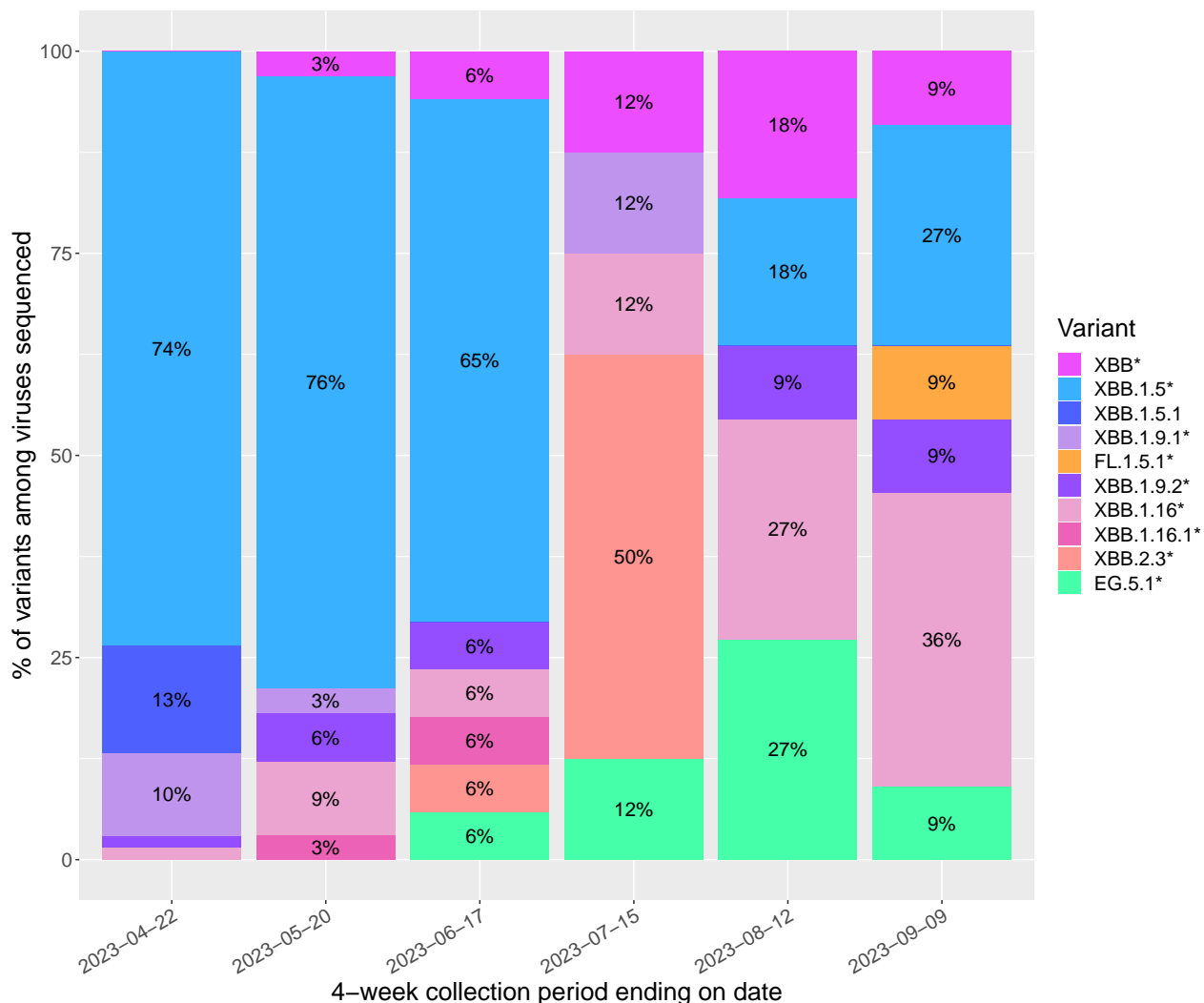
# Maui County

## Total variants identified



**Figure Notes:** Graph depicts SARS-CoV-2 variants by lineage identified in Maui County in the 4-week collection periods ending on dates shown (based on when the specimen was collected from a patient). Upper (gray) bars represent the percentage of PCR-positive cases from each period that were sequenced. Lower (color) bars represent the number of sequenced viruses from each period (numbers may change over time as additional sequences are reported; one sequenced virus equates to one PCR-positive case). This graph does not estimate prevalence in the population.

## Estimated variant proportions for Maui County



**Figure Notes:** Graph depicts estimated SARS-CoV-2 variant proportions (percentages rounded to the nearest integer) for Maui County, grouped in 4-week collection periods (based on the date of specimen collection). Not all positive SARS-CoV-2 specimens are sequenced and sequenced specimens are not a random selection of all COVID-19 cases. Graph only includes specimens selected randomly for surveillance. Percentage estimates based on historical data may change over time as additional sequences are reported. Each variant is defined by the parental lineage shown; an asterisk (\*) indicates inclusion of respective sub-lineages.



## Variants of Concern in Maui County

WHO label	Lineage	Earliest specimen collection date	Latest specimen collection date	Cumulative sequences
Omicron				3065
	Other	01 Dec 2022	31 May 2022	632
	BA.2.12.1	06 Apr 2022	26 Aug 2022	413
	BA.5.2.1	31 May 2022	01 Dec 2022	259
	BA.2	13 Feb 2022	12 Jul 2022	257
	BA.1.1	16 Dec 2021	19 Jun 2022	243
	BA.5.2	19 Jun 2022	28 Dec 2022	129
	BA.5.1	17 Jun 2022	15 Dec 2022	102
	BA.5.5	02 Jun 2022	12 Oct 2022	95
	XBB.1.5	27 Dec 2022	06 Jun 2023	92
	BA.1.15	14 Dec 2021	09 Apr 2022	86
	BA.2.3	28 Jan 2022	14 Jul 2022	72
	BF.5	16 Jul 2022	19 Nov 2022	69
	BQ.1	16 Sep 2022	31 Jan 2023	60
	BQ.1.1	06 Oct 2022	14 Mar 2023	48
	BA.5.6	27 May 2022	25 Oct 2022	44
	BA.5.2.9	01 Jul 2022	06 Nov 2022	39
	BG.5	19 Apr 2022	16 Jul 2022	37
	BA.4.1	09 May 2022	06 Sep 2022	35
	BA.5.1.23	23 Jun 2022	19 Oct 2022	31
	BQ.1.12	16 Oct 2022	08 Feb 2023	29
	BA.1	17 Dec 2021	25 Feb 2022	26
	BA.4.6	08 Jul 2022	23 Nov 2022	26
	BA.5.1.1	17 Jun 2022	17 Aug 2022	26
	BF.7	01 Aug 2022	17 Jan 2023	24
	BA.1.1.2	13 Dec 2021	15 Feb 2022	23
	BF.10	23 Jun 2022	12 Jan 2023	23
	BA.2.9	08 Mar 2022	25 Jul 2022	20
	DN.2	05 Nov 2022	19 Jan 2023	20
	BA.2.42	24 Apr 2022	23 Jun 2022	19
	BQ.1.1.3	01 Nov 2022	20 Feb 2023	19
	BA.1.1.18	30 Dec 2021	22 Feb 2022	17
	BE.3	28 Jun 2022	29 Sep 2022	17
	XBB.1	15 Nov 2022	10 Feb 2023	17
	XBB.1.5.1	23 Feb 2023	03 Apr 2023	16

*Table Notes:*

- Lineage “Other” represents an aggregation of different Omicron lineages in which each alone accounts for <0.5% of the cumulative Omicron sequences from Maui County.

## Variants Being Monitored in Maui County

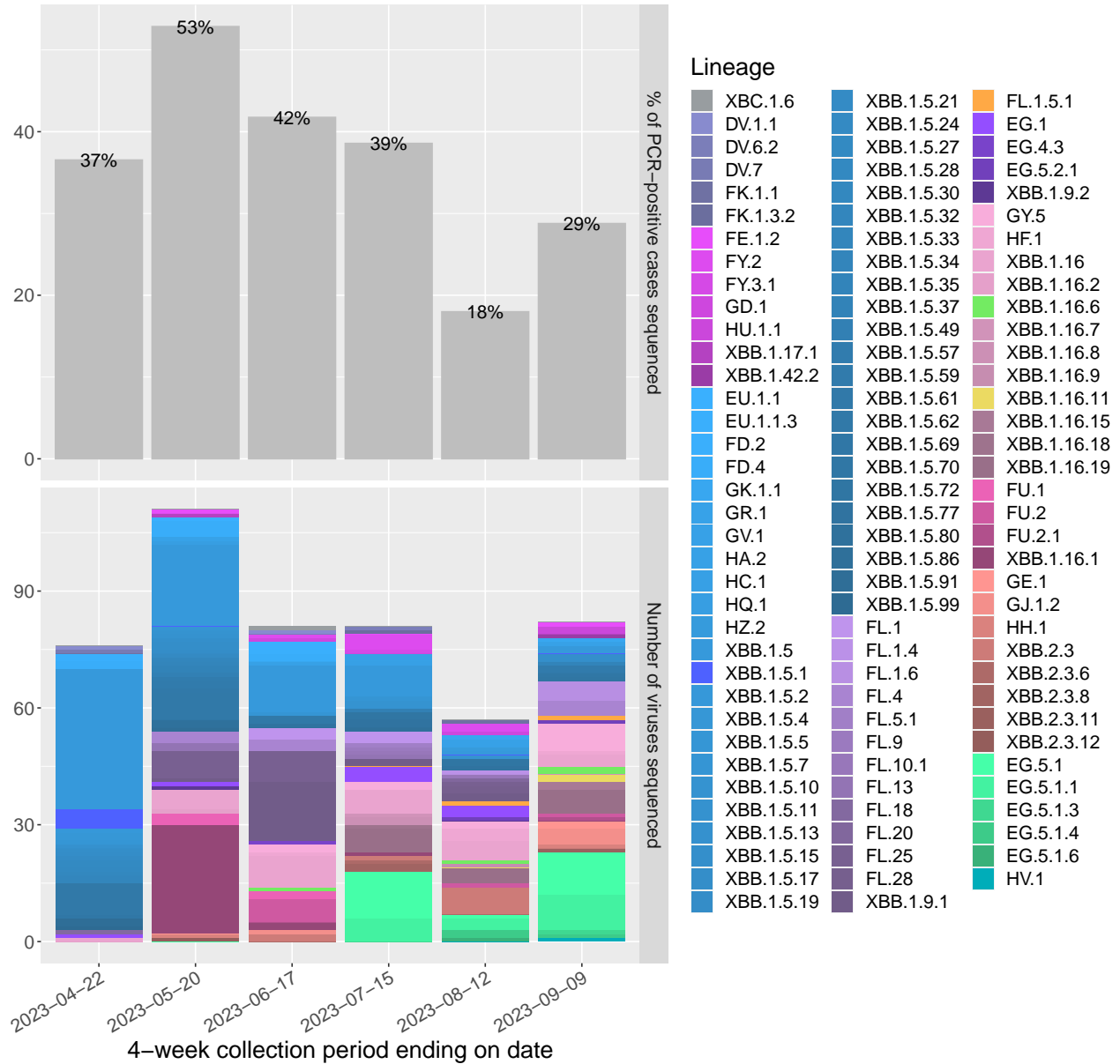
WHO label	Lineage	Earliest specimen collection date	Latest specimen collection date	Cumulative sequences
Alpha				41
	B.1.1.7	01 Mar 2021	11 Jul 2021	39
	Q.3	03 Apr 2021	28 May 2021	2
Beta	B.1.351	08 Jul 2021	08 Jul 2021	1
Gamma				43
	P.1	18 Apr 2021	20 Jun 2021	23
	P.1.12	21 Mar 2021	28 Apr 2021	19
	P.1.10	10 May 2021	10 May 2021	1
Delta				434
	AY.103	13 Jul 2021	23 Dec 2021	95
	AY.44	27 Jun 2021	27 Dec 2021	65
	AY.3	19 Jul 2021	01 Dec 2021	60
	Other AY.*	02 Aug 2021	30 Sep 2021	43
	AY.47	19 Aug 2021	07 Dec 2021	31
	AY.100	22 Jul 2021	18 Nov 2021	23
	AY.13	21 Jul 2021	13 Sep 2021	22
	AY.25	12 Aug 2021	19 Dec 2021	18
	AY.25.1	24 Jul 2021	10 Dec 2021	18
	AY.122	19 Jul 2021	01 Oct 2021	16
	AY.26	03 Aug 2021	28 Oct 2021	16
	AY.2	07 Jun 2021	06 Aug 2021	14
	AY.39	25 Sep 2021	31 Oct 2021	11
	B.1.617.2	02 Dec 2021	16 Dec 2021	2
Epsilon				273
	B.1.429	08 Jan 2021	18 May 2021	266
	B.1.427	27 Apr 2021	10 May 2021	7
Iota	B.1.526	12 Mar 2021	25 Jun 2021	16

### Table Notes:

- Lineage “Other AY.\*” represents an aggregation of different AY.\* lineages in which each alone accounts for <2% of the cumulative Delta sequences from Maui County.

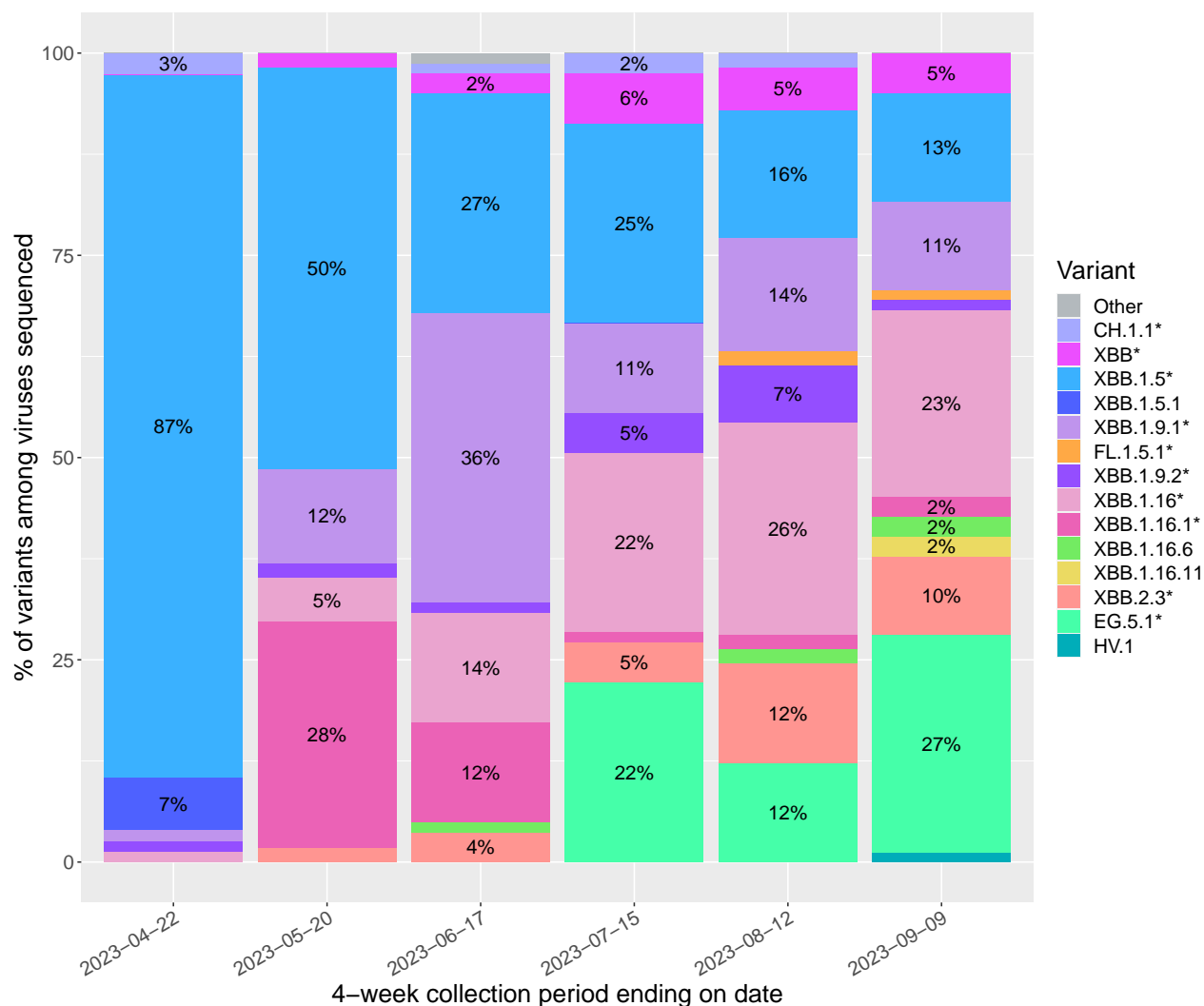
# Hawaii County

## Total variants identified



**Figure Notes:** Graph depicts SARS-CoV-2 variants by lineage identified in Hawaii County in the 4-week collection periods ending on dates shown (based on when the specimen was collected from a patient). Upper (gray) bars represent the percentage of PCR-positive cases from each period that were sequenced. Lower (color) bars represent the number of sequenced viruses from each period (numbers may change over time as additional sequences are reported; one sequenced virus equates to one PCR-positive case). This graph does not estimate prevalence in the population.

## Estimated variant proportions for Hawaii County



**Figure Notes:** Graph depicts estimated SARS-CoV-2 variant proportions (percentages rounded to the nearest integer) for Hawaii County, grouped in 4-week collection periods (based on the date of specimen collection). Not all positive SARS-CoV-2 specimens are sequenced and sequenced specimens are not a random selection of all COVID-19 cases. Graph only includes specimens selected randomly for surveillance. Percentage estimates based on historical data may change over time as additional sequences are reported. Each variant is defined by the parental lineage shown; an asterisk (\*) indicates inclusion of respective sub-lineages. “Other” includes lineages not belonging to the other variant categories shown.

## Variants of Concern in Hawaii County

WHO label	Lineage	Earliest specimen collection date	Latest specimen collection date	Cumulative sequences
Omicron				2435
	Other	01 Jul 2022	31 Oct 2022	649
	BA.2.12.1	13 Apr 2022	12 Aug 2022	213
	BA.2	19 Jan 2022	01 Aug 2022	182
	BA.5.2.1	12 Jun 2022	11 Dec 2022	163
	BA.1.1	13 Dec 2021	09 May 2022	156
	XBB.1.5	27 Dec 2022	06 Sep 2023	156
	BA.2.3	30 Jan 2022	22 Jul 2022	90
	BA.1.1.2	10 Dec 2021	01 Mar 2022	65
	BQ.1.1	07 Oct 2022	27 Feb 2023	65
	BA.5.1	07 Jun 2022	23 Nov 2022	64
	BA.5.2	17 Jun 2022	11 Jan 2023	55
	BA.5.1.1	14 May 2022	28 Sep 2022	41
	BA.5.6	21 May 2022	28 Sep 2022	32
	XBB.1.16.1	27 Apr 2023	26 Jun 2023	31
	XBB.1.16	31 Mar 2023	16 Aug 2023	28
	BA.5.5	03 May 2022	12 Sep 2022	27
	BQ.1	11 Oct 2022	23 Jan 2023	27
	BG.5	13 Apr 2022	12 Jul 2022	26
	BA.1	17 Dec 2021	02 Mar 2022	25
	BA.1.15	10 Dec 2021	22 Mar 2022	24
	EG.5.1	19 Jun 2023	07 Sep 2023	24
	BQ.1.1.3	04 Nov 2022	16 Feb 2023	22
	BA.2.9	28 Mar 2022	03 Jul 2022	21
	BF.5	07 Jul 2022	25 Nov 2022	20
	XBB.1.9.1	16 May 2023	21 Jul 2023	20
	BA.2.18	24 Apr 2022	24 Jun 2022	19
	EG.5.1.1	29 Jun 2023	01 Sep 2023	18
	XBB.1.5.62	16 Apr 2023	05 Jun 2023	17
	BA.4.1	16 Jun 2022	01 Sep 2022	16
	BQ.1.1.32	11 Jan 2023	07 Mar 2023	16
	CH.1.1	21 Nov 2022	16 Feb 2023	16
	FL.25	13 May 2023	31 Jul 2023	16
	XBB.1.16.19	29 Jun 2023	30 Aug 2023	16
	BA.4.6	11 Jul 2022	05 Oct 2022	13
	BA.5.2.34	07 Oct 2022	08 Dec 2022	13
	GY.5	25 May 2023	01 Sep 2023	13
	BA.2.3.17	24 Feb 2022	05 May 2022	12
	BF.10	06 Jul 2022	24 Oct 2022	12
	XBB.1.5.15	09 Jan 2023	05 Sep 2023	12

*Table Notes:*

- Lineage “Other” represents an aggregation of different Omicron lineages in which each alone accounts for <0.5% of the cumulative Omicron sequences from Hawaii County.

## Variants Being Monitored in Hawaii County

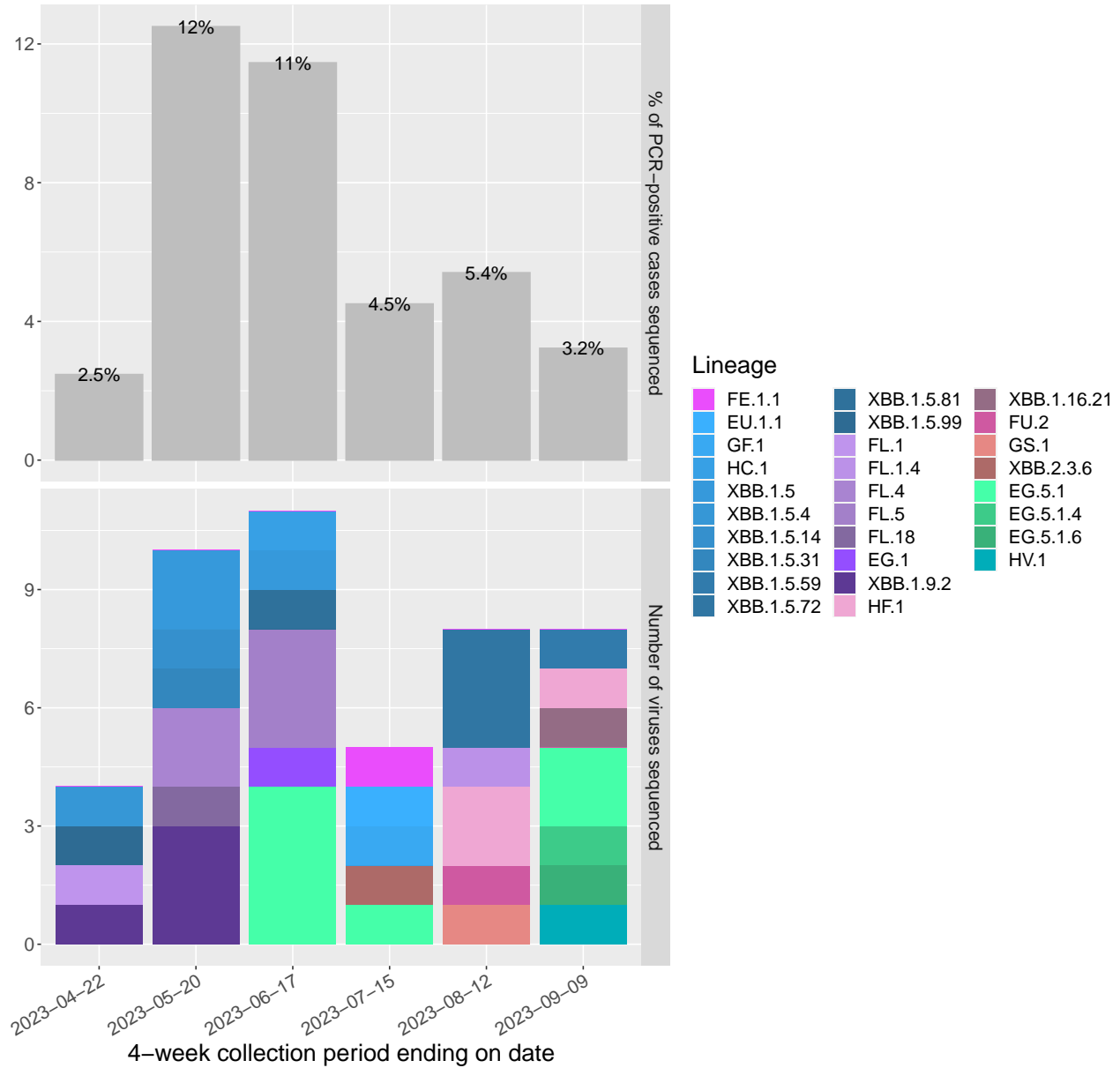
WHO label	Lineage	Earliest specimen collection date	Latest specimen collection date	Cumulative sequences
Alpha				71
	B.1.1.7	22 Feb 2021	22 Jul 2021	57
	Q.3	21 Mar 2021	20 Aug 2021	14
Gamma				17
	P.1.10	27 May 2021	13 Jun 2021	12
	P.1	10 May 2021	02 Jun 2021	4
	P.1.17	14 Jun 2021	14 Jun 2021	1
Delta				951
	AY.44	11 Jun 2021	16 Dec 2021	229
	AY.3	31 Jul 2021	16 Dec 2021	123
	AY.103	21 May 2021	16 Dec 2021	113
	AY.25	19 Jul 2021	09 Nov 2021	109
	Other AY.*	01 Jul 2021	30 Jul 2021	84
	AY.100	17 Jul 2021	12 Nov 2021	54
	AY.25.1	28 Jul 2021	17 Dec 2021	45
	AY.118	08 Jul 2021	27 Sep 2021	41
	AY.117	11 Aug 2021	17 Nov 2021	30
	AY.122	19 Jul 2021	22 Sep 2021	29
	AY.46.4	21 Jun 2021	06 Dec 2021	27
	AY.119	03 Aug 2021	24 Nov 2021	24
	AY.26	24 Jun 2021	03 Dec 2021	19
	AY.1	20 Jul 2021	03 Sep 2021	18
	B.1.617.2	06 Jul 2021	08 Nov 2021	6
Epsilon				44
	B.1.429	25 Jan 2021	26 May 2021	38
	B.1.427	04 Feb 2021	17 May 2021	6
Iota	B.1.526	06 Feb 2021	07 Jul 2021	73
Mu	B.1.621	13 Jun 2021	13 Jun 2021	1

### Table Notes:

- Lineage “Other AY.\*” represents an aggregation of different AY.\* lineages in which each alone accounts for <2% of the cumulative Delta sequences from Hawaii County.

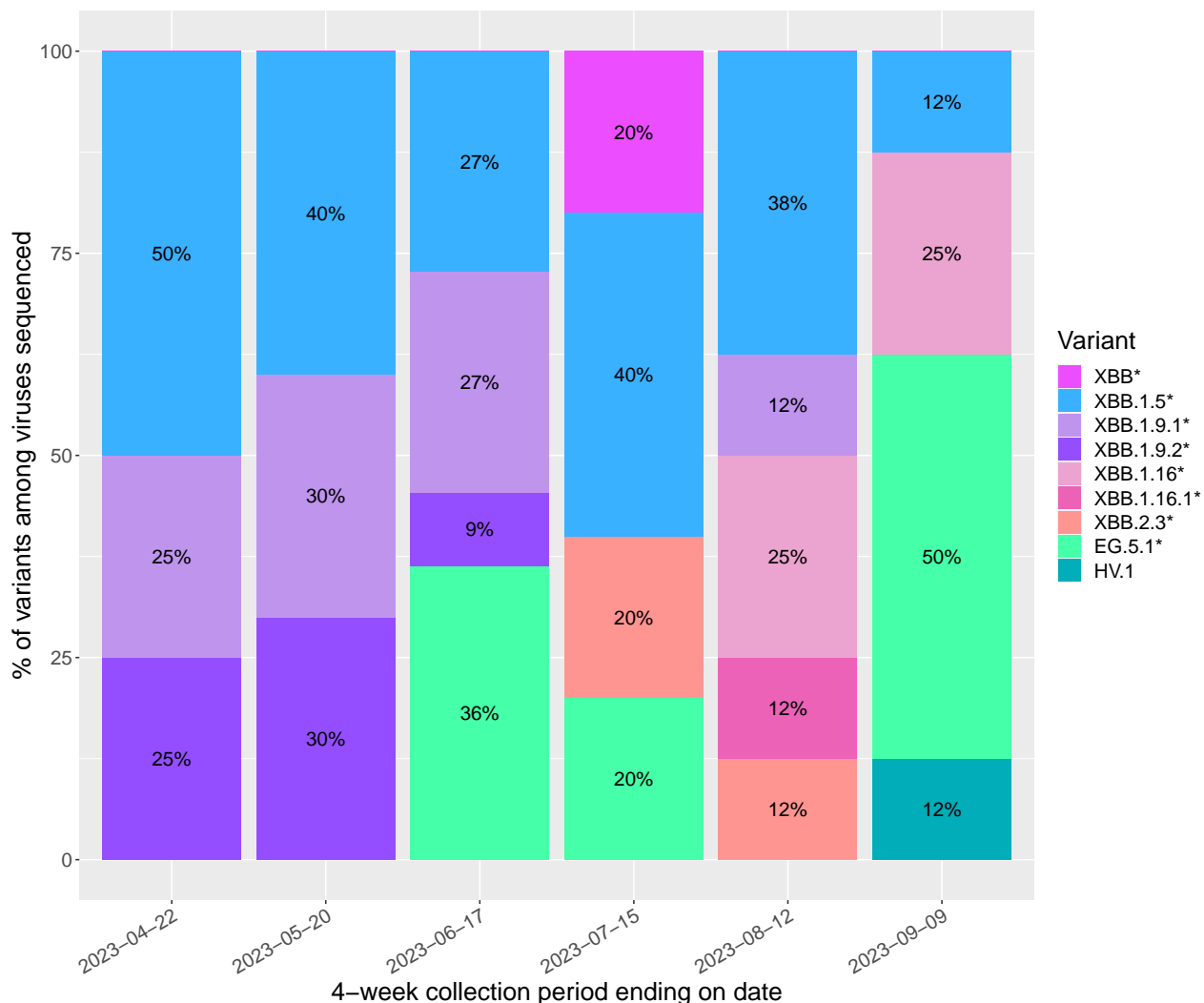
# Kauai County

## Total variants identified



**Figure Notes:** Graph depicts SARS-CoV-2 variants by lineage identified in Kauai County in the 4-week collection periods ending on dates shown (based on when the specimen was collected from a patient). Upper (gray) bars represent the percentage of PCR-positive cases from each period that were sequenced. Lower (color) bars represent the number of sequenced viruses from each period (numbers may change over time as additional sequences are reported; one sequenced virus equates to one PCR-positive case). This graph does not estimate prevalence in the population.

## Estimated variant proportions for Kauai County



**Figure Notes:** Graph depicts estimated SARS-CoV-2 variant proportions (percentages rounded to the nearest integer) for Kauai County, grouped in 4-week collection periods (based on the date of specimen collection). Not all positive SARS-CoV-2 specimens are sequenced and sequenced specimens are not a random selection of all COVID-19 cases. Graph only includes specimens selected randomly for surveillance. Percentage estimates based on historical data may change over time as additional sequences are reported. Each variant is defined by the parental lineage shown; an asterisk (\*) indicates inclusion of respective sub-lineages.



## Variants of Concern in Kauai County

WHO label	Lineage	Earliest specimen collection date	Latest specimen collection date	Cumulative sequences
Omicron				565
	Other	01 Mar 2023	31 Jan 2023	97
	BA.2	17 Mar 2022	28 Jun 2022	82
	BA.2.12.1	30 Mar 2022	29 Jun 2022	61
	BA.1.1	15 Dec 2021	19 Apr 2022	60
	BA.5.2.1	03 Jun 2022	02 Nov 2022	32
	BA.2.3	09 Mar 2022	24 May 2022	19
	BA.5.5	13 Jun 2022	31 Aug 2022	18
	BA.1.15	28 Dec 2021	23 Mar 2022	13
	BA.5.1	23 Jun 2022	29 Sep 2022	13
	BA.1	16 Dec 2021	07 Feb 2022	12
	BA.5.2	02 Jul 2022	17 Nov 2022	10
	XAC	28 Apr 2022	14 Jun 2022	9
	XBB.1.5	11 Jan 2023	14 Jun 2023	9
	BA.1.1.18	28 Dec 2021	21 Mar 2022	8
	BA.1.1.2	15 Dec 2021	09 Feb 2022	8
	BA.2.18	24 Apr 2022	16 Jun 2022	8
	BA.2.42	07 May 2022	02 Jul 2022	8
	BQ.1.1	04 Nov 2022	27 Jan 2023	8
	BG.5	03 May 2022	13 Jun 2022	7
	BQ.1	30 Sep 2022	06 Feb 2023	7
	EG.5.1	22 May 2023	25 Aug 2023	7
	BA.4.1	08 Jun 2022	26 Jun 2022	6
	BF.10	13 Jun 2022	19 Aug 2022	6
	BA.1.18	15 Dec 2021	04 Jan 2022	5
	BA.2.9	17 Mar 2022	09 May 2022	5
	BF.5	21 Jun 2022	17 Oct 2022	5
	BA.4.6	23 Aug 2022	04 Nov 2022	4
	BA.4.6.5	23 Aug 2022	04 Nov 2022	4
	BA.5.2.9	27 Jun 2022	30 Aug 2022	4
	BA.5.6	16 Jun 2022	29 Aug 2022	4
	BE.3	15 Jun 2022	17 Oct 2022	4
	XBB.1.9.2	14 Apr 2023	08 May 2023	4
	BA.2.1	25 May 2022	20 Jun 2022	3
	BA.5.1.10	06 Jul 2022	14 Oct 2022	3
	BA.5.1.30	23 Aug 2022	19 Oct 2022	3
	FL.5	24 May 2023	25 May 2023	3
	HF.1	09 Aug 2023	16 Aug 2023	3
	XBB.1.5.72	20 Jul 2023	02 Aug 2023	3

*Table Notes:*

- Lineage “Other” represents an aggregation of different Omicron lineages in which each alone accounts for <0.5% of the cumulative Omicron sequences from Kauai County.

## Variants Being Monitored in Kauai County

WHO label	Lineage	Earliest specimen collection date	Latest specimen collection date	Cumulative sequences
Alpha	B.1.1.7	05 Apr 2021	13 Jul 2021	20
Gamma				2
	P.1	31 May 2021	31 May 2021	1
	P.1.10	14 May 2021	14 May 2021	1
Delta				246
	AY.25	16 Jul 2021	10 Nov 2021	70
	AY.44	29 Jun 2021	21 Dec 2021	37
	AY.119	28 Aug 2021	21 Dec 2021	35
	Other AY.*	03 Nov 2021	30 Jun 2021	29
	AY.47	27 Jul 2021	29 Nov 2021	19
	AY.1	09 Aug 2021	30 Aug 2021	18
	AY.103	01 Aug 2021	15 Dec 2021	17
	AY.3	30 Sep 2021	15 Dec 2021	8
	AY.54	06 Jul 2021	09 Nov 2021	8
	B.1.617.2	06 Jun 2021	18 Oct 2021	5
Epsilon				31
	B.1.429	07 Jan 2021	08 May 2021	29
	B.1.427	27 Apr 2021	27 Apr 2021	2
Iota	B.1.526	14 Apr 2021	14 Apr 2021	1
Mu	B.1.621	29 Jun 2021	06 Jul 2021	2

*Table Notes:*

- Lineage “Other AY.\*” represents an aggregation of different AY.\* lineages in which each alone accounts for <2% of the cumulative Delta sequences from Kauai County.