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

Hawaii Department of Health

2023-02-14

Contents

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 refer 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 Centers for Disease Control and Prevention (CDC) as Variants of Concern (VOC) and others as Variants Being Monitored (VBM), because of their attributes, which, for example, can be increased transmissibility, decreased neutralization by antibodies generated during previous infection or vaccination, and/or increased severity of disease. The 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. According to the CDC, more than 7% of PCR-positive cases in the State of Hawaii have been sequenced since testing began (https://covid.cdc.gov/covid-data-tracker/#published-sars-cov-2-sequences).

Acknowledgements

This report integrates genomes sequenced since 1 Jan 2021 by:

Institution	Program/partner	Count	Percent
State Laboratories Division		17547	74.891%
Centers for Disease Control and Prevention	National SARS-CoV-2 Strain Surveillance (NS3)	412	1.758%
	Quest Diagnostics Incorporated	1483	6.329%
	Laboratory Corporation of America	1604	6.846%
	Aegis Sciences Corporation	379	1.618%
	Helix/Illumina	182	0.777%
	Infinity Biologix	16	0.068%
	Mako Medical	20	0.085%
	Fulgent Genetics	8	0.034%
Tripler Army Medical Center		691	2.949%
University of Hawaii		861	3.675%
Aegis Sciences Corporation*		227	0.969%
Total		**23430**	**100.000%**

County distribution of genomes sequenced by:

State Laboratories Division (since 1 Jan 2021)

Honolulu County	Maui County	Hawaii County	Kauai County	unknown	Total
10089	3529	2785	787	357	17547

University of Hawaii (22 Jan 2022 – 23 Aug 2022)

Honolulu County	Maui County	Hawaii County	Kauai County	unknown	Total
508	67	221	17	48	861

Aegis Sciences Corporation* (since 14 Sep 2022)

Honolulu County	Maui County	Hawaii County	Kauai County	unknown	Total
54	11	3	0	159	227

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 257 additional SARS-CoV-2 genome sequences since the previous report was generated (31 Jan 2023).
- CDC programs/partners reported 34 additional SARS-CoV-2 genome sequences from the State of Hawaii since the previous report was generated.
- Aegis Sciences Corporation reported 2 additional SARS-CoV-2 genome sequences from the State of Hawaii 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. An asterisk following the dot of a lineage designation (e.g., BA.*, BA.5.*, BA.5.1.*) signifies only inclusion of lineages with an additional numerical suffix that follows the respective dot.
- Lineages called using pangolin v4.2, pangolin-data v1.18, and usher v0.5.4.
- Omicron has represented 100% of sequenced variants in the State of Hawaii since 28 Jan 2022.
- Changes in the statewide estimated variant proportions compared to the previous reporting period include decreases in BQ.1* (-9%) and BQ.1.1* (-4%), and increases in XBB.1.5 (+12%) and BA.5* (+4%). CH.1.1* is now being tracked separately (was previously aggregated with BA.2.75*) and represents ~5% of the statewide estimated variant proportions for the latest period. XBF is no longer being tracked separately under estimated variant proportions and is now aggregated with the Omicron X* variant category.
- Due to a shift away from laboratory-based PCR testing to self-administered antigen testing, the availability of clinical specimens has decreased statewide, resulting in smaller sample sizes for SARS-CoV-2 sequencing and variant reporting. Therefore, estimated variant proportions may not be truly representative, particularly for counties with low sequencing numbers (e.g., Maui, Hawaii, and Kauai counties).

Variants of Concern (VOC) and Variants Being Monitored (VBM)

Evidence to date shows that vaccination generally leads to milder cases, not requiring hospitalization, for all VOC and VBM that are described here, even if the efficacy of antibodies is diminished against these variants compared to the original version of the virus.

Also, *none* of these variants are classified as a *"Variant of High Consequence (VOHC)"*, according to CDC variant classifications (https://www.cdc.gov/coronavirus/2019-ncov/variants/variant-classifications.html), which is a category that would imply a variant has the ability to evade diagnosis, significantly reduce vaccine effectiveness and protection against severe disease, significantly reduce susceptibility to treatments, or lead to more severe disease and increased hospitalizations.

Variants of Concern in the State of Hawaii

Omicron (B.1.1.529, BA.*, BE.*, BF.*, BG.*, BK.*, BL.*, BM.*, BN.*, BQ.*, BR.*, BY.*, BW.*, CA.*, CB.*, CH.*, CK.*, CM.*, CP.*, CQ.*, DB.*, DC.*, DF.*, DG.*, DN.*, DR.*, XAC, XAS, XBB*, XBC*, and XBF 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 WHO labeled it "Omicron" on 26 Nov 2021.

B.1.1.529 is the parent lineage of Omicron; primary sub-lineages of B.1.1.529 have BA.* designations (e.g., BA.1, BA.2, BA.5). Primary sub-lineages of BA.2.12.1, BA.2.3.20, BA.2.75.1, BA.2.75.2, BA.2.75.3, BA.2.75.4, BA.2.75.5, BA.2.75.6, BA.2.75.9, and BA.4.6.5 have BG.*, CM.*, BL.*, CA.*, BM.*, BR.*, BN.*, BY.*, CB.*, and DC.* designations, respectively. Primary sub-lineages of BA.5.1.10, BA.5.2.1, BA.5.2.6, BA.5.2.24, BA.5.2.25, BA.5.3.1, BA.5.6.2, and BA.5.10.1 have BK.*, BF.*, CP.*, CK.*, DB.*, BE.*, BW.*, and DF.* designations, respectively. Primary sub-lineages of BE.1.1.1, BE.4.1.1, BM.4.1.1, and CK.2.1.1 have BQ.*, CQ.*, CH.*, and DG.* designations, respectively. Primary sub-lineages of BQ.1.1.3 and BQ.1.1.5 have DR.* and DN.* designations, respectively. SARS-CoV-2 recombinants that receive a PANGO classification have an X* lineage designation. 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. XAC is derived from BA.1* and BA.2*, XAS is derived from BA.5* and BA.2*, XBB is derived from BJ.1 (a primary sub-lineage of BA.2.10.1) and BM.1.1.1, XBC is derived from BA.2* and B.1.617.2 (Delta), and XBF is derived from BA.5.2.3 and CJ.1 (a primary sub-lineage of BM.1.1.1). Omicron variants correspond to Nextstrain clades 21M, 21K, 21L, 22A, 22B, 22C, 22D, 22E, 22F, and 23A (https://ncov-clades-schema.vercel.app/).

Due to acquired mutations within the spike protein, successively dominant Omicron variants (BA.1*, BA.2*, BA.2.12.1*, BA.5*, and BQ.1*/BQ.1.1*) have been increasingly better at evading antibodies elicited by vaccinations and/or prior infections; notable information regarding their defining mutations can be found at https://covariants.org/variants (21K, 21L, 22C, 22B, and 22E, respectively). Furthermore, due to prevalence of antibody-resistant Omicron variants, monoclonal antibody products (e.g., Bebtelovimab and Evusheld) are no longer authorized for emergency use against COVID-19 (https://health.hawaii.gov/coronavirusdisease2019/for-clinicians/covid-19-treatment/).

Variants Being Monitored 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 Alpha have the Q.* designation. As of Mar 2022, Alpha is considered as a previously circulating variant of concern by the WHO. 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. As of Mar 2022, Beta is considered as a previously circulating variant of concern by the WHO. 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. As of Mar 2022, Gamma is considered as a previously circulating variant of concern by the WHO. 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. As of Jun 2022, Delta is considered as a previously circulating variant of concern by the WHO. Delta variants 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. As of Jul 2021, Epsilon is considered as a previously circulating variant of interest by the WHO. 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. As of Jul 2021, Zeta is considered as a previously circulating variant of interest by the WHO. 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. As of Sep 2021, Iota is considered as a previously circulating variant of interest by the WHO. 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. As of Mar 2022, Mu is considered as a previously circulating variant of interest by the WHO. The MU variant corresponds to Nextstrain clade 21H.

State of Hawaii

Total variants identified

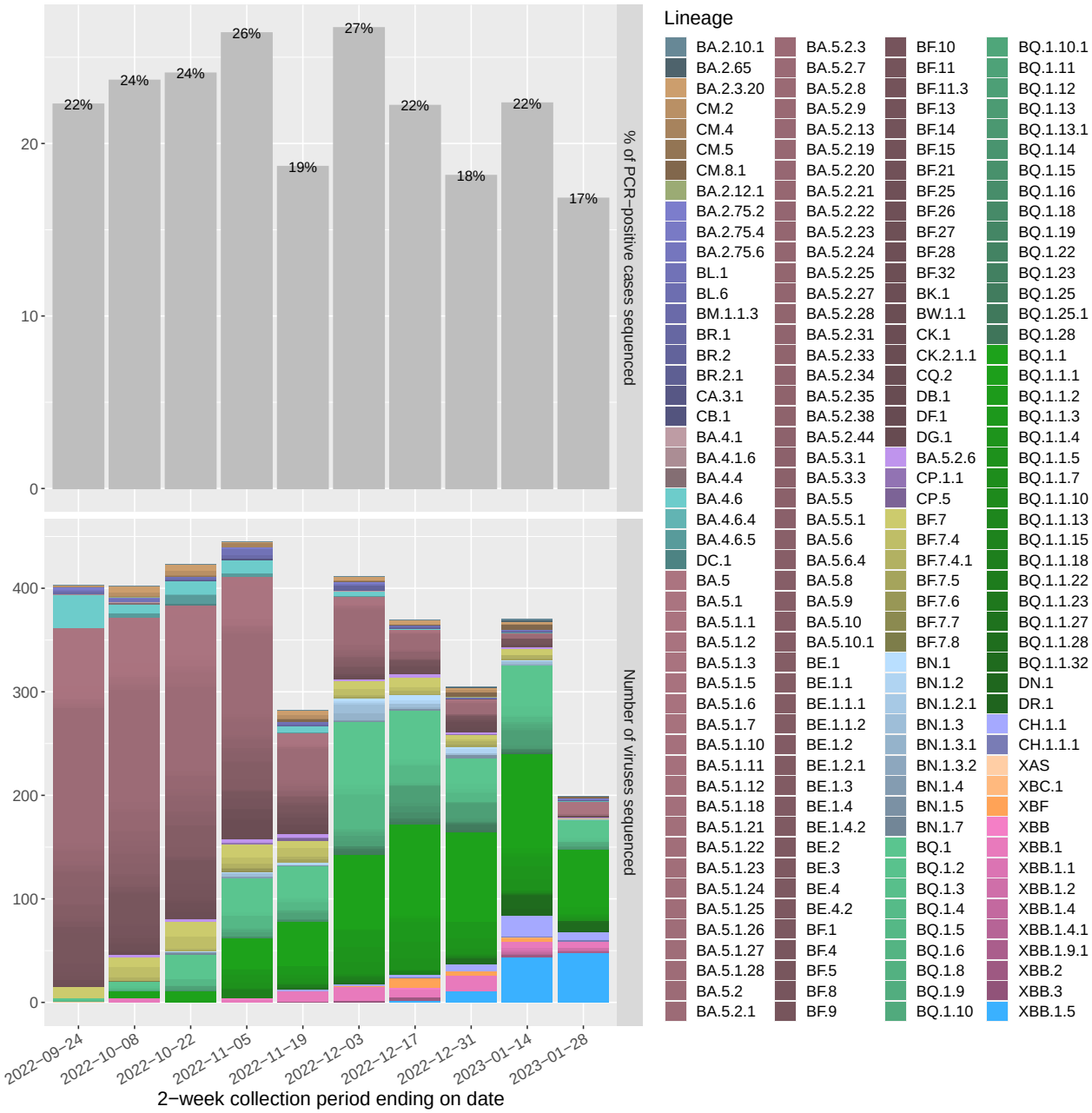

Figure Notes:

- Graph depicts SARS-CoV-2 variants by lineage identified in the State of Hawaii in the 2-week collection periods ending on the 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

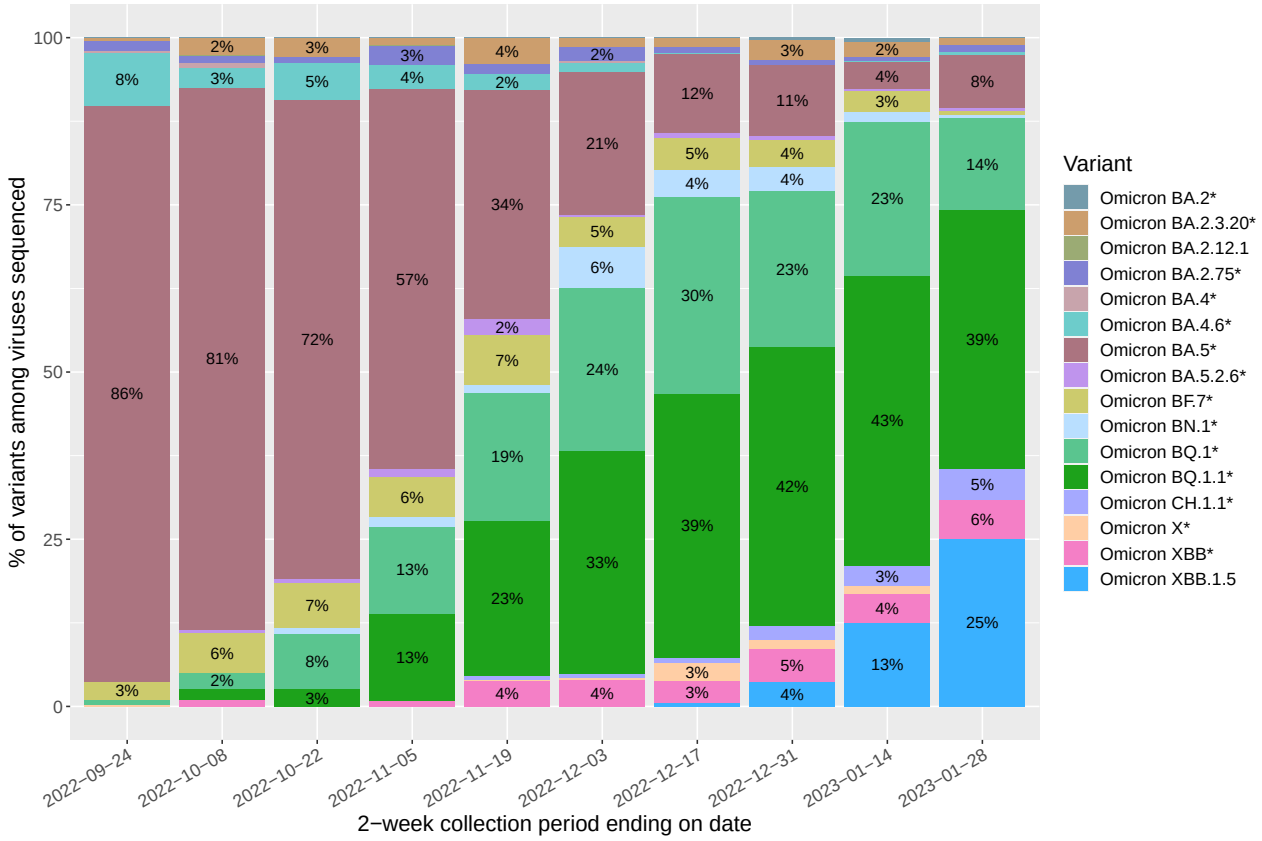

Figure Notes:

- Graph depicts estimated SARS-CoV-2 variant proportions (percentages rounded to the nearest integer) for the State of Hawaii, grouped in 2-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. This graph was generated by only counting specimens that were selected randomly for the purpose of surveillance.
- Percentage estimates based on historical data may change over time as additional sequences are reported.
- Omicron BA.2* includes BA.2 and its sub-lineages (BA.2.*); excludes BA.2.3.20*, BA.2.12.1*, and BA.2.75*.
- Omicron BA.2.3.20* includes BA.2.3.20 and its sub-lineages (CM.*).
- Omicron BA.2.75* includes BA.2.75 and its sub-lineages (BA.2.75.*, BL.*, BM.*, BR.*, BY.*, CA.*, CB.*, CH.*); excludes CH.1.1*.
- Omicron BA.4* includes BA.4 and its sub-lineages (BA.4.*); excludes BA.4.6.
- Omicron BA.4.6* includes BA.4.6 and its sub-lineages (BA.4.6.*, DC.*).
- Omicron BA.5* includes BA.5 and its sub-lineages (BA.5.*, BE.*, BF.*, BK.*, BW.*, CK.*, CQ.*, DB.*, DF.*, DG.*); excludes BA.5.2.6* and BF.7*.
- Omicron BA.5.2.6* includes BA.5.2.6 and its sub-lineages (CP.*).
- Omicron BF.7* includes BF.7 and its sub-lineages (BF.7.*).
- Omicron BN.1* includes BN.1 and its sub-lineages (BN.1.*).
- Omicron BQ.1* includes BQ.1 and its sub-lineages (BQ.1.*); excludes BQ.1.1*.
- Omicron BQ.1.1* includes BQ.1.1 and its sub-lineages (BQ.1.1.*, DN.*, DR.*).
- Omicron CH.1.1* includes CH.1.1 and its sub-lineages (CH.1.1.*)
- Omicron X* includes Omicron recombinants except for XBB*.
- Omicron XBB* includes XBB and its sub-lineages (XBB.*); excludes XBB.1.5.

Variants of Concern in the State of Hawaii

WHO label	Lineage	Area of emergence	Cumulative sequences	Earliest specimen collection date	Most recent specimen collection date
Omicron			15477		
	Other	Various	2482	01 Aug 2022	31 Oct 2022
	BA.1.1	South Africa/Botswana	1740	27 Nov 2021	19 Jun 2022
	BA.2.12.1	USA/Canada	1614	21 Mar 2022	29 Sep 2022
	BA.2	South Africa/Botswana	1573	18 Jan 2022	06 Sep 2022
	BA.5.2.1	South Africa/UK/USA	1074	31 May 2022	20 Jan 2023
	BA.2.3	Philippines	839	06 Jan 2022	22 Jul 2022
	BA.1.1.2	Japan	569	06 Dec 2021	01 Apr 2022
	BG.5	USA	533	09 Apr 2022	21 Aug 2022
	BQ.1.1	Global	495	27 Sep 2022	05 Feb 2023
	BA.5.2	South Africa/UK/USA	475	17 Jun 2022	11 Jan 2023
	BA.5.1	Portugal	446	07 Jun 2022	29 Jan 2023
	BA.1.15	USA	426	30 Nov 2021	09 Apr 2022
	BA.5.5	USA	363	03 May 2022	28 Oct 2022
	BQ.1	Nigeria	286	16 Sep 2022	02 Feb 2023
	BA.5.6	USA	253	21 May 2022	03 Dec 2022
	BA.2.3.17	USA	208	25 Jan 2022	15 Jun 2022
	BA.1	South Africa/Botswana	187	07 Dec 2021	11 Apr 2022
	BF.5	Israel	177	16 Jun 2022	19 Dec 2022
	BA.4.1	South Africa	168	04 May 2022	29 Nov 2022
	BA.2.9	Europe	161	25 Jan 2022	25 Jul 2022
	BA.5.1.1	USA	161	14 May 2022	02 Dec 2022
	BA.4.6	USA/UK/Denmark	154	21 Jun 2022	09 Dec 2022
	XBB.1.5	USA	125	13 Dec 2022	03 Feb 2023
	BA.1.1.18	USA	95	10 Dec 2021	30 Mar 2022
	BF.7	UK/Belgium/Denmark	95	19 Jul 2022	21 Jan 2023
	BF.10	USA	94	05 Jun 2022	12 Jan 2023
	BA.2.18	UK	93	21 Mar 2022	11 Jul 2022
	BQ.1.5	Global	90	02 Oct 2022	14 Jan 2023
	BA.5.1.23	Spain	82	23 Jun 2022	27 Oct 2022
	BA.5.2.9	USA	79	20 Jun 2022	02 Dec 2022
	BQ.1.1.3	UK	75	01 Nov 2022	16 Jan 2023
	BE.1.1	Germany	68	18 Jun 2022	29 Dec 2022
	BQ.1.1.4	Global	68	24 Oct 2022	15 Jan 2023
	XBB.1	Bangladesh/Singapore	65	30 Sep 2022	24 Jan 2023
	BA.5.2.21	Indonesia	64	07 Jul 2022	14 Nov 2022

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.

Variants Being Monitored in the State of Hawaii

WHO label	Lineage	Area of emergence	Cumulative sequences	Earliest specimen collection date	Most recent specimen collection date
Alpha			797		
	B.1.1.7	UK	743	21 Jan 2021	14 Aug 2021
	Q.3	USA	52	21 Mar 2021	02 Sep 2021
	Q.4	South Africa/Botswana	2	28 Apr 2021	29 Apr 2021
Beta	B.1.351	South Africa	20	16 Feb 2021	22 Sep 2021
Gamma			191		
	P.1.10	USA	84	24 Apr 2021	14 Jul 2021
	P.1	Brazil	54	24 Mar 2021	21 Jul 2021
	P.1.12	Peru	20	21 Mar 2021	28 Apr 2021
	P.1.17	USA/Mexico	18	29 Mar 2021	21 Jul 2021
	P.1.13	USA	15	03 May 2021	28 Jun 2021
Delta			5622		
	AY.103	USA	1228	21 May 2021	12 Jan 2022
	AY.44	USA	1039	07 Jun 2021	19 Jan 2022
	Other AY.*	Various	612	01 Aug 2021	30 Jul 2021
	AY.3	USA	562	24 Jun 2021	02 Jan 2022
	AY.25	USA	532	21 Jun 2021	20 Jan 2022
	AY.54	USA	367	23 Jun 2021	21 Nov 2021
	AY.100	South Africa/Botswana	197	17 Jul 2021	12 Dec 2021
	AY.25.1	South Africa/Botswana	196	08 Jul 2021	27 Jan 2022
	AY.1	Europe	186	30 Jun 2021	30 Nov 2021
	AY.119	USA	136	06 Jul 2021	21 Dec 2021
	AY.26	USA/Mexico	132	07 Jun 2021	28 Dec 2021
	AY.117	USA	128	15 Jul 2021	17 Dec 2021
	AY.122	South Africa/Botswana	107	09 Jul 2021	26 Nov 2021
	B.1.617.2	India	102	28 May 2021	16 Dec 2021
	AY.47	USA	98	21 Jul 2021	07 Dec 2021
Epsilon			781		
	B.1.429	USA	722	31 Dec 2020	03 Jun 2021
	B.1.427	USA	59	07 Dec 2020	05 Jun 2021
Zeta	P.2	Brazil	2	06 Feb 2021	08 Feb 2021
Iota	B.1.526	USA	128	06 Feb 2021	23 Jul 2021
Mu			58		
	B.1.621	Columbia	45	03 Jun 2021	17 Sep 2021
	B.1.621.1	USA	13	27 May 2021	24 Aug 2021

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

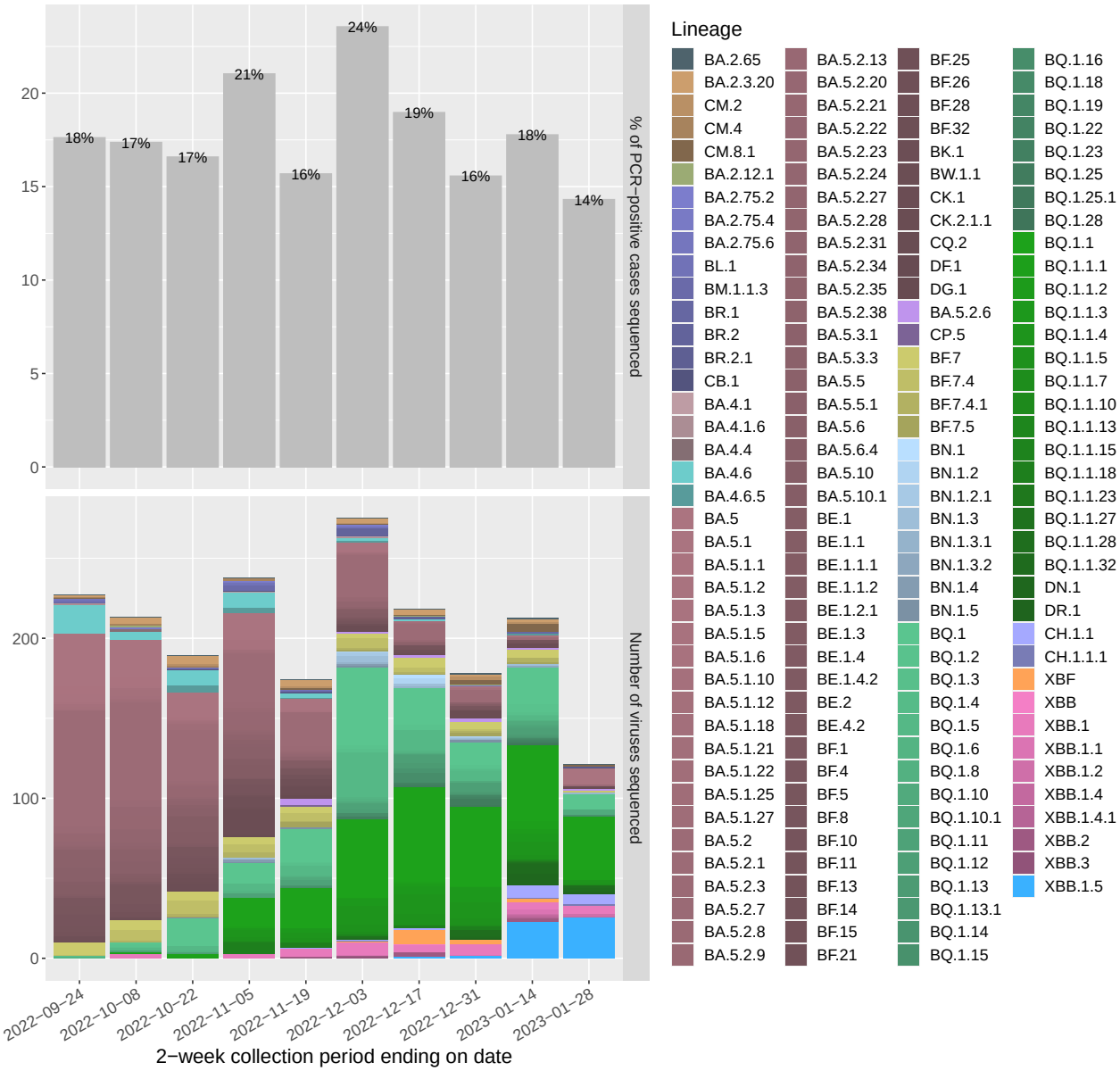

Figure Notes:

- Graph depicts SARS-CoV-2 variants by lineage identified in Honolulu County in the 2-week collection periods ending on the 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

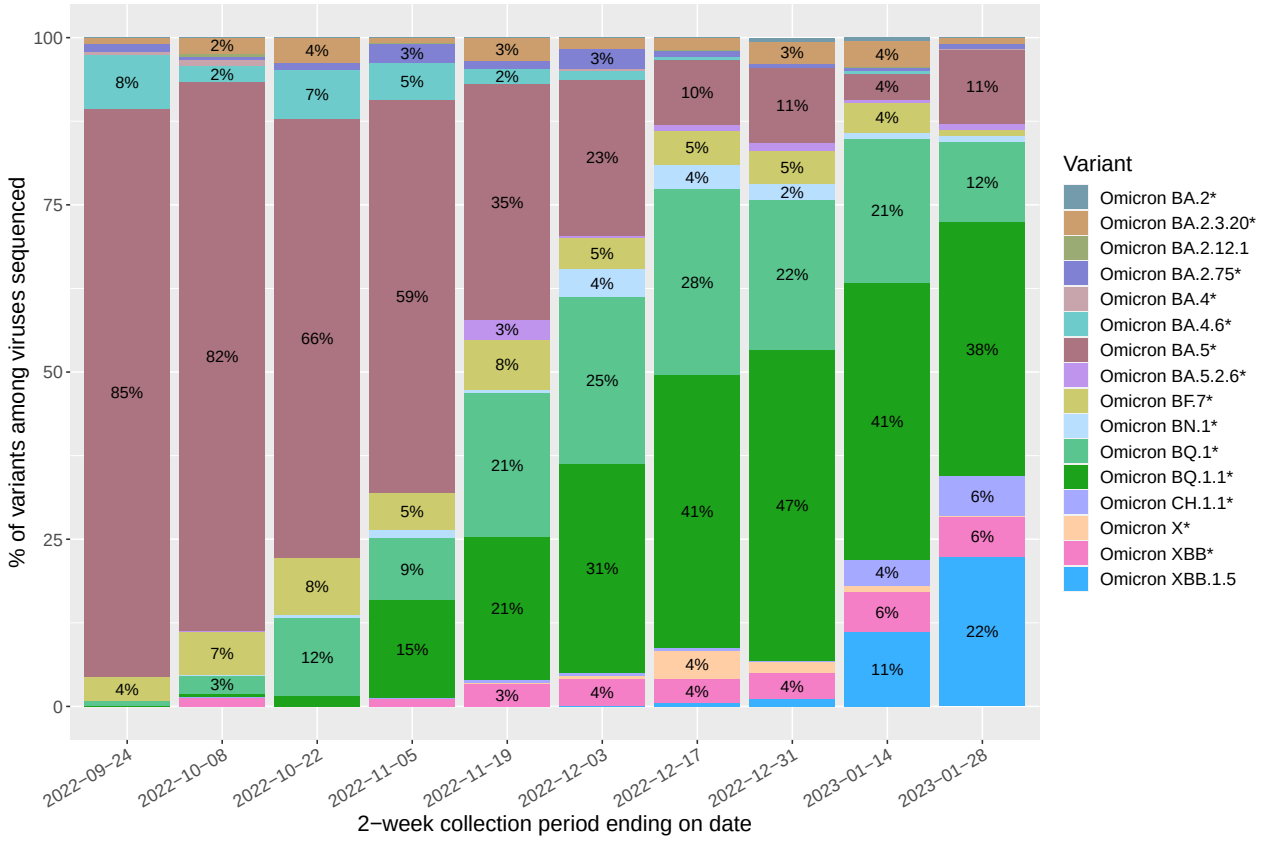

Figure Notes:

- Graph depicts estimated SARS-CoV-2 variant proportions (percentages rounded to the nearest integer) for Honolulu County, grouped in 2-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. This graph was generated by only counting specimens that were selected randomly for the purpose of surveillance.
- Percentage estimates based on historical data may change over time as additional sequences are reported.
- Omicron BA.2* includes BA.2 and its sub-lineages (BA.2.*); excludes BA.2.3.20*, BA.2.12.1*, and BA.2.75*.
- Omicron BA.2.3.20* includes BA.2.3.20 and its sub-lineages (CM.*).
- Omicron BA.2.75* includes BA.2.75 and its sub-lineages (BA.2.75.*, BL.*, BM.*, BR.*, BY.*, CA.*, CB.*, CH.*); excludes CH.1.1*.
- Omicron BA.4* includes BA.4 and its sub-lineages (BA.4.*); excludes BA.4.6.
- Omicron BA.4.6* includes BA.4.6 and its sub-lineages (BA.4.6.*, DC.*).
- Omicron BA.5* includes BA.5 and its sub-lineages (BA.5.*, BE.*, BF.*, BK.*, BW.*, CK.*, CQ.*, DB.*, DF.*, DG.*); excludes BA.5.2.6* and BF.7*.
- Omicron BA.5.2.6* includes BA.5.2.6 and its sub-lineages (CP.*).
- Omicron BF.7* includes BF.7 and its sub-lineages (BF.7.*).
- Omicron BN.1* includes BN.1 and its sub-lineages (BN.1.*).
- Omicron BQ.1* includes BQ.1 and its sub-lineages (BQ.1.*); excludes BQ.1.1*.
- Omicron BQ.1.1* includes BQ.1.1 and its sub-lineages (BQ.1.1.*, DN.*, DR.*).
- Omicron CH.1.1* includes CH.1.1 and its sub-lineages (CH.1.1.*)
- Omicron X* includes Omicron recombinants except for XBB*.
- Omicron XBB* includes XBB and its sub-lineages (XBB.*); excludes XBB.1.5.

Variants of Concern in Honolulu County

WHO label	Lineage	Area of emergence	Cumulative sequences	Earliest specimen collection date	Most recent specimen collection date
Omicron			6877		
	Other	Various	1256	01 Aug 2022	31 Oct 2022
	BA.1.1	South Africa/Botswana	683	27 Nov 2021	11 May 2022
	BA.2	South Africa/Botswana	623	27 Jan 2022	20 Jul 2022
	BA.2.12.1	USA/Canada	504	21 Mar 2022	29 Sep 2022
	BA.5.2.1	South Africa/UK/USA	475	05 Jun 2022	20 Jan 2023
	BA.2.3	Philippines	367	30 Jan 2022	24 Jun 2022
	BG.5	USA	303	09 Apr 2022	21 Aug 2022
	BA.1.1.2	Japan	300	06 Dec 2021	31 Mar 2022
	BQ.1.1	Global	295	07 Oct 2022	01 Feb 2023
	BA.5.2	South Africa/UK/USA	236	22 Jun 2022	09 Jan 2023
	BA.5.1	Portugal	190	11 Jun 2022	29 Jan 2023
	BQ.1	Nigeria	176	04 Oct 2022	02 Feb 2023
	BA.5.5	USA	169	29 May 2022	28 Oct 2022
	BA.1.15	USA	164	30 Nov 2021	07 Apr 2022
	BA.5.6	USA	134	18 Jun 2022	04 Nov 2022
	BA.2.3.17	USA	121	05 Feb 2022	02 Jun 2022
	BA.4.6	USA/UK/Denmark	86	26 Jun 2022	09 Dec 2022
	BA.4.1	South Africa	81	22 May 2022	29 Nov 2022
	BA.5.1.1	USA	76	14 May 2022	02 Dec 2022
	BA.2.9	Europe	70	14 Mar 2022	29 Jun 2022
	BQ.1.5	Global	66	02 Oct 2022	06 Jan 2023
	XBB.1.5	USA	66	17 Dec 2022	02 Feb 2023
	BF.5	Israel	62	17 Jun 2022	19 Dec 2022
	BF.7	UK/Belgium/Denmark	53	19 Jul 2022	21 Jan 2023
	BQ.1.1.4	Global	52	24 Oct 2022	15 Jan 2023
	BA.1	South Africa/Botswana	43	07 Dec 2021	14 Mar 2022
	BE.1.1	Germany	41	18 Jun 2022	29 Dec 2022
	BF.10	USA	40	09 Jul 2022	05 Dec 2022
	XBB.1	Bangladesh/Singapore	39	04 Oct 2022	24 Jan 2023
	BA.5.1.23	Spain	36	24 Jun 2022	16 Aug 2022
	BA.1.1.18	USA	35	10 Dec 2021	30 Mar 2022
	BF.7.4	Europe	35	28 Sep 2022	21 Dec 2022

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 Honolulu County.

Variants Being Monitored in Honolulu County

WHO label	Lineage	Area of emergence	Cumulative sequences	Earliest specimen collection date	Most recent specimen collection date
Alpha			514		
	B.1.1.7	UK	481	21 Jan 2021	14 Aug 2021
	Q.3	USA	33	03 Apr 2021	02 Sep 2021
Beta	B.1.351	South Africa	17	16 Feb 2021	22 Sep 2021
Gamma			98		
	P.1.10	USA	53	24 Apr 2021	13 Jul 2021
	P.1	Brazil	15	24 Mar 2021	11 Jul 2021
	P.1.13	USA	15	03 May 2021	28 Jun 2021
	P.1.17	USA/Mexico	14	29 Mar 2021	20 Jul 2021
	P.1.12	Peru	1	03 Apr 2021	03 Apr 2021
Delta			2635		
	AY.103	USA	732	20 Jun 2021	18 Dec 2021
	AY.44	USA	417	07 Jun 2021	22 Dec 2021
	Other AY.*	Various	283	01 Aug 2021	30 Nov 2021
	AY.54	USA	259	23 Jun 2021	21 Nov 2021
	AY.3	USA	237	24 Jun 2021	17 Dec 2021
	AY.25	USA	200	21 Jun 2021	04 Jan 2022
	AY.1	Europe	107	30 Jun 2021	30 Nov 2021
	AY.100	South Africa/Botswana	88	23 Jul 2021	12 Dec 2021
	AY.117	USA	74	15 Jul 2021	11 Nov 2021
	AY.26	USA/Mexico	69	07 Jun 2021	21 Nov 2021
	AY.25.1	South Africa/Botswana	64	18 Jul 2021	11 Dec 2021
	B.1.617.2	India	55	28 May 2021	25 Oct 2021
	AY.119	USA	50	06 Jul 2021	13 Dec 2021
Epsilon			351		
	B.1.429	USA	320	05 Jan 2021	29 May 2021
	B.1.427	USA	31	07 Jan 2021	05 Jun 2021
Zeta	P.2	Brazil	2	06 Feb 2021	08 Feb 2021
Iota	B.1.526	USA	26	08 Feb 2021	23 Jul 2021
Mu			25		
	B.1.621	Columbia	19	03 Jun 2021	28 Jul 2021
	B.1.621.1	USA	6	27 May 2021	24 Aug 2021

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

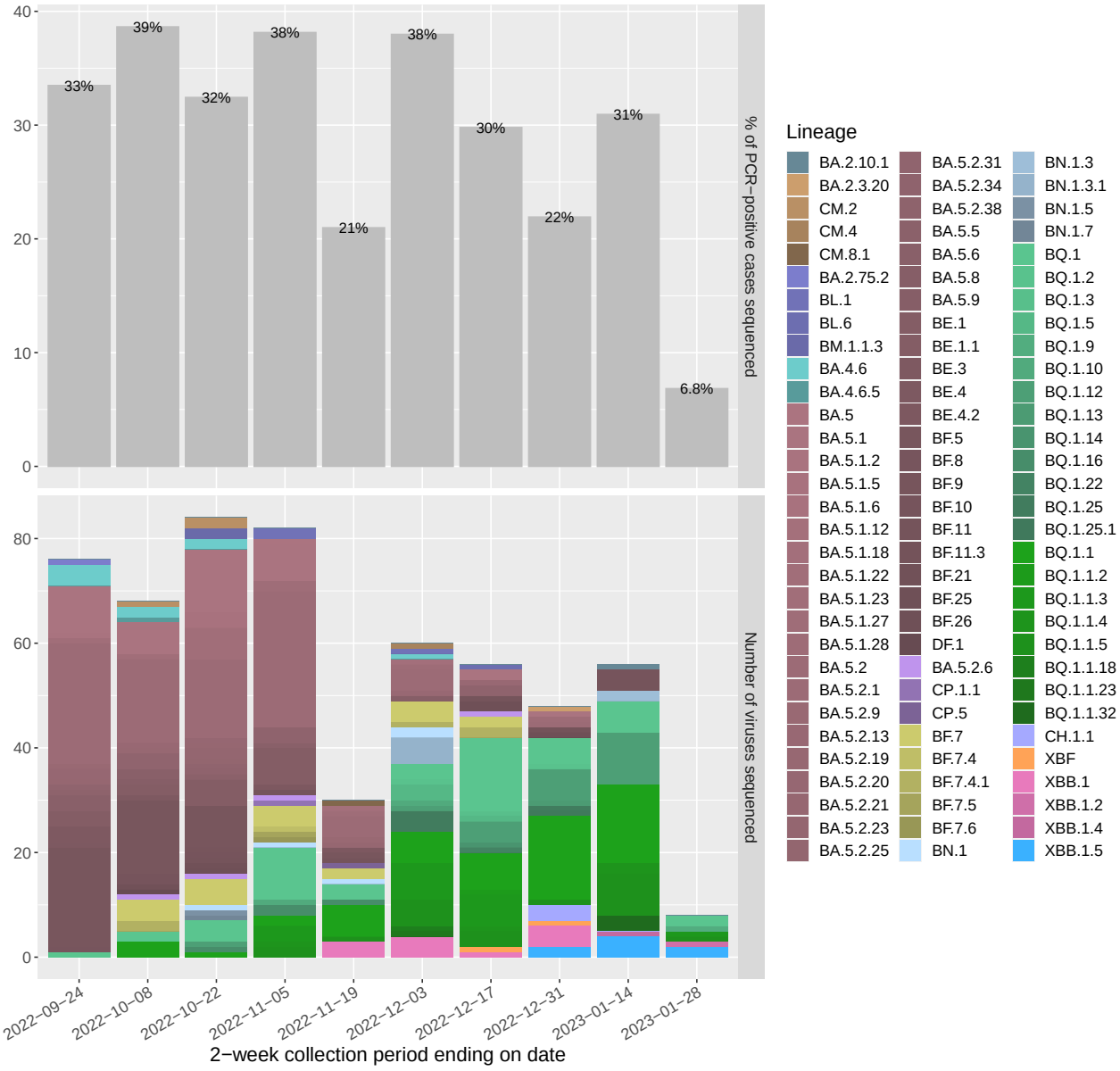

Figure Notes:

- Graph depicts SARS-CoV-2 variants by lineage identified in Maui County in the 2-week collection periods ending on the 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

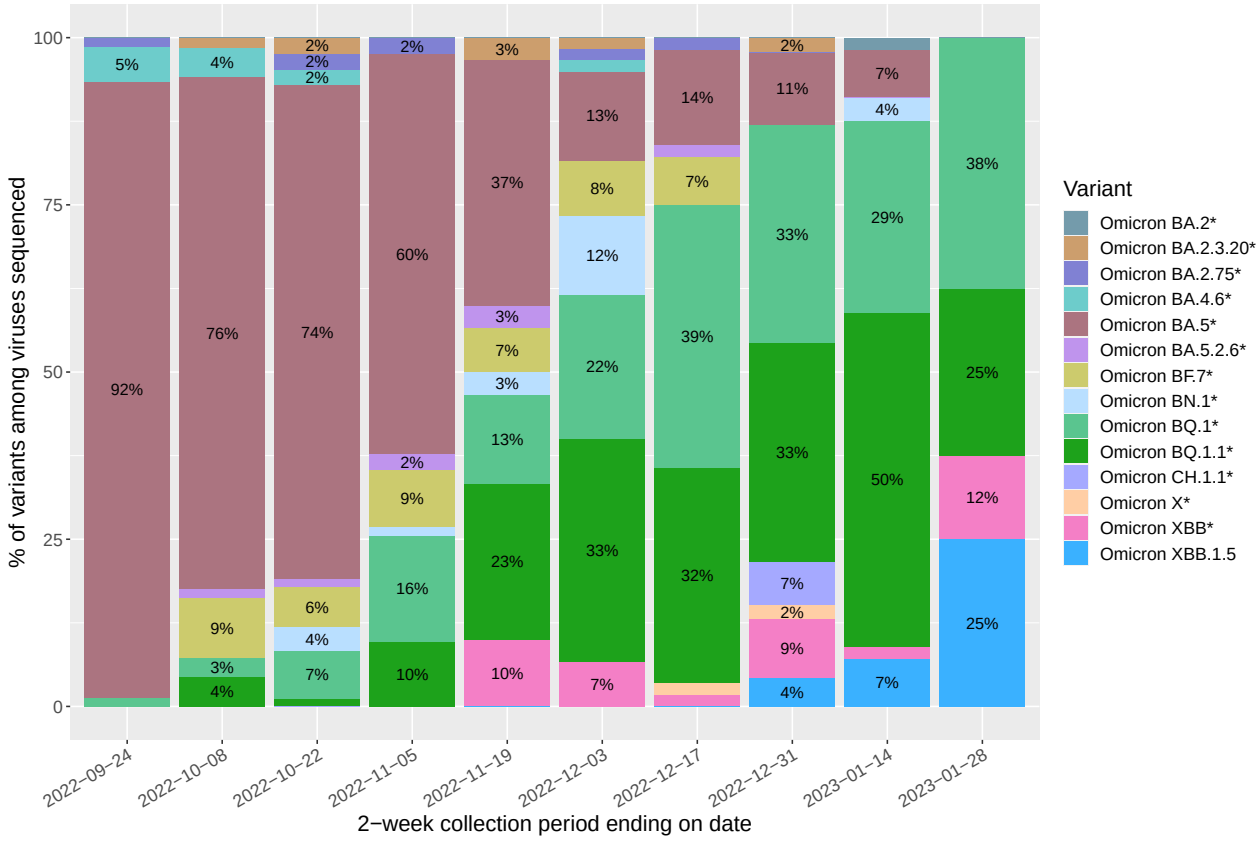

Figure Notes:

- Graph depicts estimated SARS-CoV-2 variant proportions (percentages rounded to the nearest integer) for Maui County, grouped in 2-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. This graph was generated by only counting specimens that were selected randomly for the purpose of surveillance.
- Percentage estimates based on historical data may change over time as additional sequences are reported.
- Omicron BA.2* includes BA.2 and its sub-lineages (BA.2.*); excludes BA.2.3.20*, BA.2.12.1*, and BA.2.75*.
- Omicron BA.2.3.20* includes BA.2.3.20 and its sub-lineages (CM.*).
- Omicron BA.2.75* includes BA.2.75 and its sub-lineages (BA.2.75.*, BL.*, BM.*, BR.*, BY.*, CA.*, CB.*, CH.*); excludes CH.1.1*.
- Omicron BA.4.6* includes BA.4.6 and its sub-lineages (BA.4.6.*, DC.*).
- Omicron BA.5* includes BA.5 and its sub-lineages (BA.5.*, BE.*, BF.*, BK.*, BW.*, CK.*, CQ.*, DB.*, DF.*, DG.*); excludes BA.5.2.6* and BF.7*.
- Omicron BA.5.2.6* includes BA.5.2.6 and its sub-lineages (CP.*).
- Omicron BF.7* includes BF.7 and its sub-lineages (BF.7.*).
- Omicron BN.1* includes BN.1 and its sub-lineages (BN.1.*).
- Omicron BQ.1* includes BQ.1 and its sub-lineages (BQ.1.*); excludes BQ.1.1*.
- Omicron BQ.1.1* includes BQ.1.1 and its sub-lineages (BQ.1.1.*, DN.*, DR.*).
- Omicron CH.1.1* includes CH.1.1 and its sub-lineages (CH.1.1.*)
- Omicron X* includes Omicron recombinants except for XBB*.
- Omicron XBB* includes XBB and its sub-lineages (XBB.*); excludes XBB.1.5.

Variants of Concern in Maui County

WHO label	Lineage	Area of emergence	Cumulative sequences	Earliest specimen collection date	Most recent specimen collection date
Omicron			2793		
	Other	Various	439	01 Dec 2022	31 May 2022
	BA.2.12.1	USA/Canada	413	06 Apr 2022	26 Aug 2022
	BA.5.2.1	South Africa/UK/USA	276	31 May 2022	01 Dec 2022
	BA.1.1	South Africa/Botswana	257	16 Dec 2021	19 Jun 2022
	BA.2	South Africa/Botswana	254	13 Feb 2022	12 Jul 2022
	BA.5.2	South Africa/UK/USA	114	19 Jun 2022	28 Dec 2022
	BA.5.1	Portugal	112	17 Jun 2022	27 Dec 2022
	BA.5.5	USA	95	02 Jun 2022	12 Oct 2022
	BA.1.15	USA	86	14 Dec 2021	09 Apr 2022
	BA.2.3	Philippines	72	28 Jan 2022	14 Jul 2022
	BF.5	Israel	69	16 Jul 2022	19 Nov 2022
	BQ.1.1	Global	56	06 Oct 2022	12 Jan 2023
	BQ.1	Nigeria	51	16 Sep 2022	31 Jan 2023
	BA.5.6	USA	44	27 May 2022	25 Oct 2022
	BA.5.2.9	USA	41	01 Jul 2022	06 Nov 2022
	BG.5	USA	37	19 Apr 2022	16 Jul 2022
	BA.4.1	South Africa	35	09 May 2022	06 Sep 2022
	BA.5.1.23	Spain	31	23 Jun 2022	19 Oct 2022
	BA.1	South Africa/Botswana	26	17 Dec 2021	25 Feb 2022
	BA.4.6	USA/UK/Denmark	26	08 Jul 2022	23 Nov 2022
	BA.5.1.1	USA	25	17 Jun 2022	17 Aug 2022
	BF.7	UK/Belgium/Denmark	25	01 Aug 2022	07 Dec 2022
	BA.1.1.2	Japan	23	13 Dec 2021	15 Feb 2022
	BF.10	USA	23	23 Jun 2022	12 Jan 2023
	BQ.1.12	North America/Europe	22	16 Oct 2022	13 Jan 2023
	BQ.1.1.5	Global	21	03 Nov 2022	19 Jan 2023
	BA.2.9	Europe	20	08 Mar 2022	25 Jul 2022
	BA.2.42	Australia	19	24 Apr 2022	23 Jun 2022
	BA.1.1.18	USA	17	30 Dec 2021	22 Feb 2022
	BE.3	USA	17	28 Jun 2022	29 Sep 2022
	BQ.1.1.3	UK	17	01 Nov 2022	15 Jan 2023
	BA.2.29	Japan	15	08 Apr 2022	16 May 2022
	BE.1.1	Germany	15	13 Jul 2022	27 Oct 2022

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

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

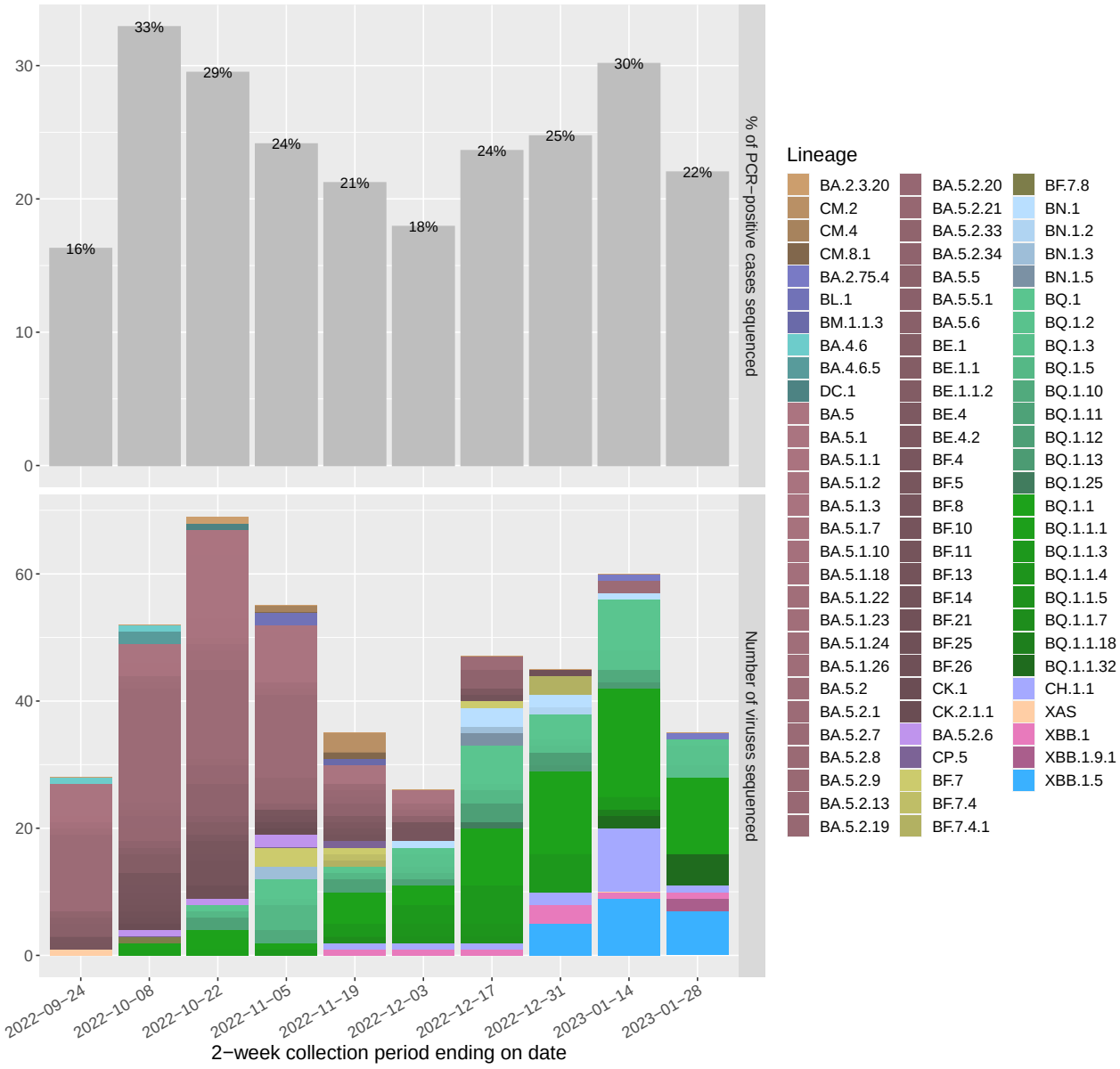

Figure Notes:

- Graph depicts SARS-CoV-2 variants by lineage identified in Hawaii County in the 2-week collection periods ending on the 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

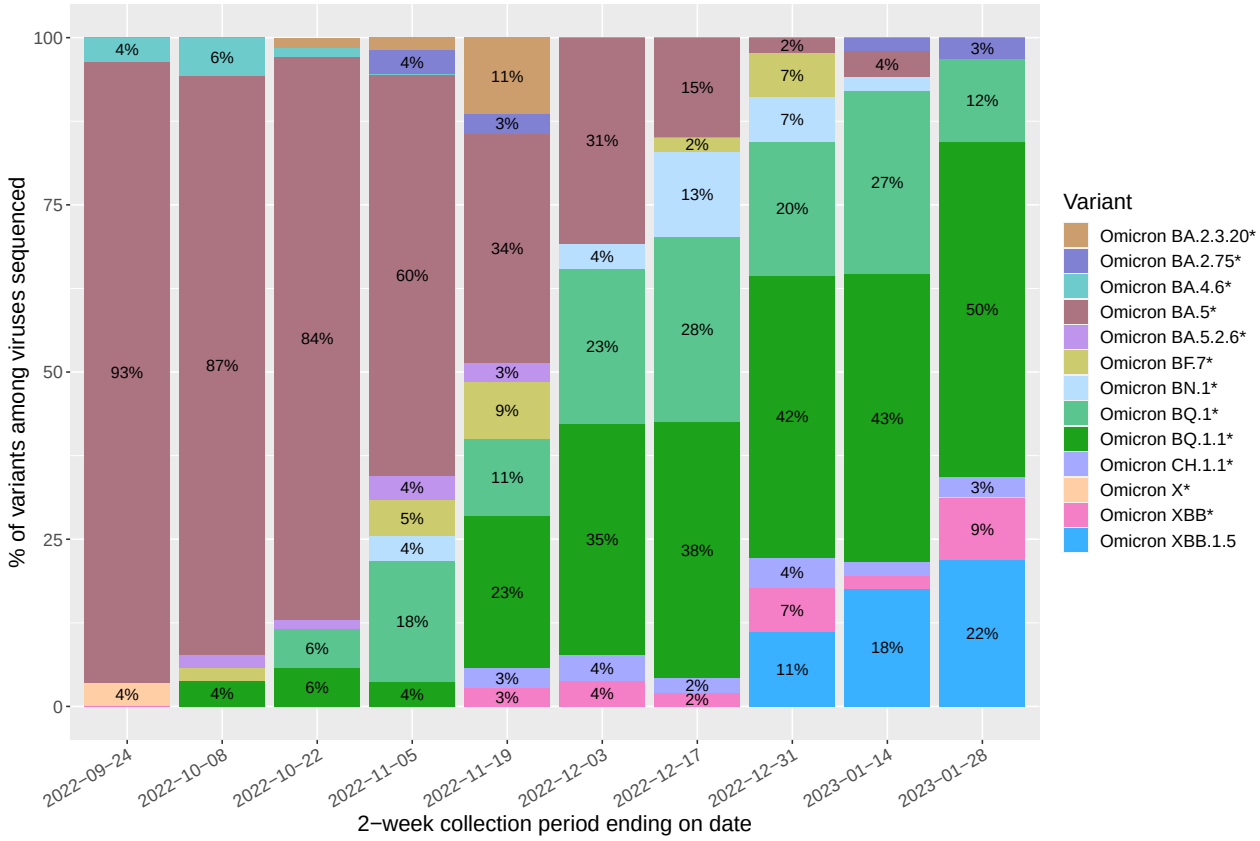

Figure Notes:

- Graph depicts estimated SARS-CoV-2 variant proportions (percentages rounded to the nearest integer) for Hawaii County, grouped in 2-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. This graph was generated by only counting specimens that were selected randomly for the purpose of surveillance.
- Percentage estimates based on historical data may change over time as additional sequences are reported.
- Omicron BA.2.3.20* includes BA.2.3.20 and its sub-lineages (CM.*).
- Omicron BA.2.75* includes BA.2.75 and its sub-lineages (BA.2.75.*, BL.*, BM.*, BR.*, BY.*, CA.*, CB.*, CH.*); excludes CH.1.1*.
- Omicron BA.4.6* includes BA.4.6 and its sub-lineages (BA.4.6.*, DC.*).
- Omicron BA.5* includes BA.5 and its sub-lineages (BA.5.*, BE.*, BF.*, BK.*, BW.*, CK.*, CQ.*, DB.*, DF.*, DG.*); excludes BA.5.2.6* and BF.7*.
- Omicron BA.5.2.6* includes BA.5.2.6 and its sub-lineages (CP.*).
- Omicron BF.7* includes BF.7 and its sub-lineages (BF.7.*).
- Omicron BN.1* includes BN.1 and its sub-lineages (BN.1.*).
- Omicron BQ.1* includes BQ.1 and its sub-lineages (BQ.1.*); excludes BQ.1.1*.
- Omicron BQ.1.1* includes BQ.1.1 and its sub-lineages (BQ.1.1.*, DN.*, DR.*).
- Omicron CH.1.1* includes CH.1.1 and its sub-lineages (CH.1.1.*)
- Omicron X* includes Omicron recombinants except for XBB*.
- Omicron XBB* includes XBB and its sub-lineages (XBB.*); excludes XBB.1.5.

Variants of Concern in Hawaii County

WHO label	Lineage	Area of emergence	Cumulative sequences	Earliest specimen collection date	Most recent specimen collection date
Omicron			1815		
	Other	Various	310	01 Aug 2022	31 Oct 2022
	BA.2.12.1	USA/Canada	213	13 Apr 2022	12 Aug 2022
	BA.2	South Africa/Botswana	182	19 Jan 2022	06 Sep 2022
	BA.5.2.1	South Africa/UK/USA	167	12 Jun 2022	11 Dec 2022
	BA.1.1	South Africa/Botswana	159	13 Dec 2021	09 May 2022
	BA.2.3	Philippines	90	30 Jan 2022	22 Jul 2022
	BQ.1.1	Global	67	07 Oct 2022	05 Feb 2023
	BA.5.1	Portugal	65	07 Jun 2022	23 Nov 2022
	BA.1.1.2	Japan	64	10 Dec 2021	01 Mar 2022
	BA.5.2	South Africa/UK/USA	50	17 Jun 2022	11 Jan 2023
	BA.5.1.1	USA	41	14 May 2022	28 Sep 2022
	BA.5.6	USA	32	21 May 2022	28 Sep 2022
	BA.5.5	USA	27	03 May 2022	12 Sep 2022
	BG.5	USA	26	13 Apr 2022	12 Jul 2022
	BA.1	South Africa/Botswana	25	17 Dec 2021	02 Mar 2022
	BQ.1	Nigeria	25	11 Oct 2022	16 Jan 2023
	BA.1.15	USA	24	10 Dec 2021	22 Mar 2022
	XBB.1.5	USA	24	27 Dec 2022	03 Feb 2023
	BA.2.9	Europe	21	28 Mar 2022	03 Jul 2022
	BF.5	Israel	20	07 Jul 2022	25 Nov 2022
	BQ.1.1.3	UK	20	04 Nov 2022	14 Jan 2023
	BA.2.18	UK	19	24 Apr 2022	24 Jun 2022
	BA.4.1	South Africa	16	16 Jun 2022	01 Sep 2022
	CH.1.1	India	16	11 Nov 2022	17 Jan 2023
	BA.5.2.34	Israel/USA	13	07 Oct 2022	08 Dec 2022
	BA.2.3.17	USA	12	24 Feb 2022	05 May 2022
	BA.4.6	USA/UK/Denmark	12	11 Jul 2022	05 Oct 2022
	BF.10	USA	12	06 Jul 2022	24 Oct 2022
	BQ.1.1.32	USA	12	11 Jan 2023	03 Feb 2023
	BQ.1.2	Global	11	26 Oct 2022	19 Jan 2023
	BA.5.1.23	Spain	10	27 Jun 2022	24 Oct 2022
	BA.5.2.21	Indonesia	10	25 Jul 2022	02 Nov 2022
	BE.1	South Africa/UK/Austria	10	22 Jul 2022	06 Oct 2022
	BE.3	USA	10	08 Jun 2022	07 Aug 2022

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	Area of emergence	Cumulative sequences	Earliest specimen collection date	Most recent specimen collection date
Alpha			71		
	B.1.1.7	UK	57	22 Feb 2021	22 Jul 2021
	Q.3	USA	14	21 Mar 2021	20 Aug 2021
Gamma			17		
	P.1.10	USA	12	27 May 2021	13 Jun 2021
	P.1	Brazil	4	10 May 2021	02 Jun 2021
	P.1.17	USA/Mexico	1	14 Jun 2021	14 Jun 2021
Delta			951		
	AY.44	USA	229	11 Jun 2021	16 Dec 2021
	AY.3	USA	123	31 Jul 2021	16 Dec 2021
	AY.103	USA	113	21 May 2021	16 Dec 2021
	AY.25	USA	108	19 Jul 2021	09 Nov 2021
	Other AY.*	Various	84	01 Jul 2021	30 Jul 2021
	AY.100	South Africa/Botswana	54	17 Jul 2021	12 Nov 2021
	AY.25.1	South Africa/Botswana	45	28 Jul 2021	17 Dec 2021
	AY.118	USA	41	08 Jul 2021	27 Sep 2021
	AY.117	USA	30	11 Aug 2021	17 Nov 2021
	AY.122	South Africa/Botswana	29	19 Jul 2021	22 Sep 2021
	AY.46.4	USA	27	21 Jun 2021	06 Dec 2021
	AY.119	USA	24	03 Aug 2021	24 Nov 2021
	AY.26	USA/Mexico	19	24 Jun 2021	03 Dec 2021
	AY.1	Europe	18	20 Jul 2021	03 Sep 2021
	B.1.617.2	India	7	06 Jul 2021	08 Nov 2021
Epsilon			44		
	B.1.429	USA	38	25 Jan 2021	26 May 2021
	B.1.427	USA	6	04 Feb 2021	17 May 2021
Iota	B.1.526	USA	73	06 Feb 2021	07 Jul 2021
Mu	B.1.621	Columbia	1	13 Jun 2021	13 Jun 2021

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

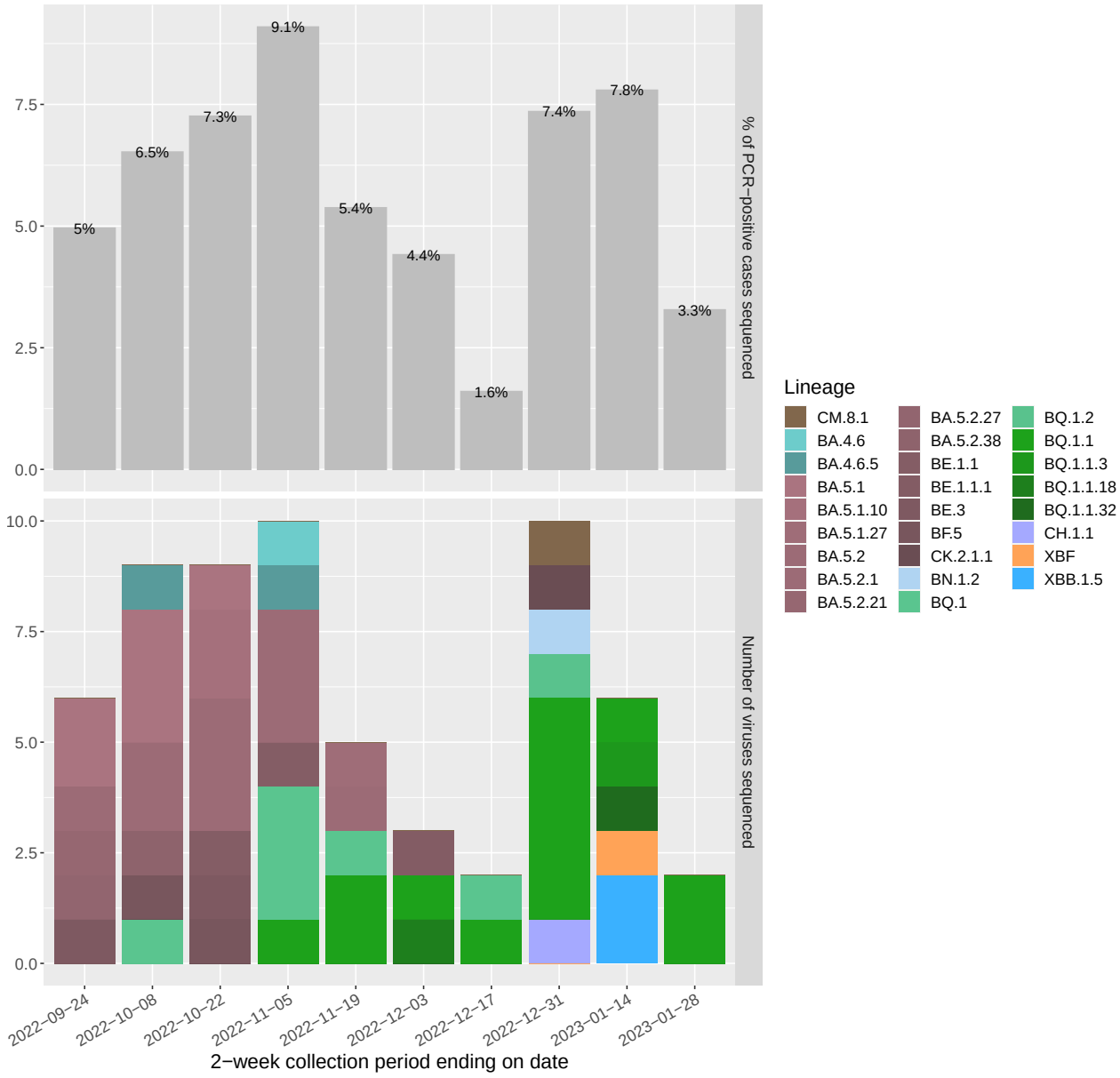

Figure Notes:

- Graph depicts SARS-CoV-2 variants by lineage identified in Kauai County in the 2-week collection periods ending on the 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

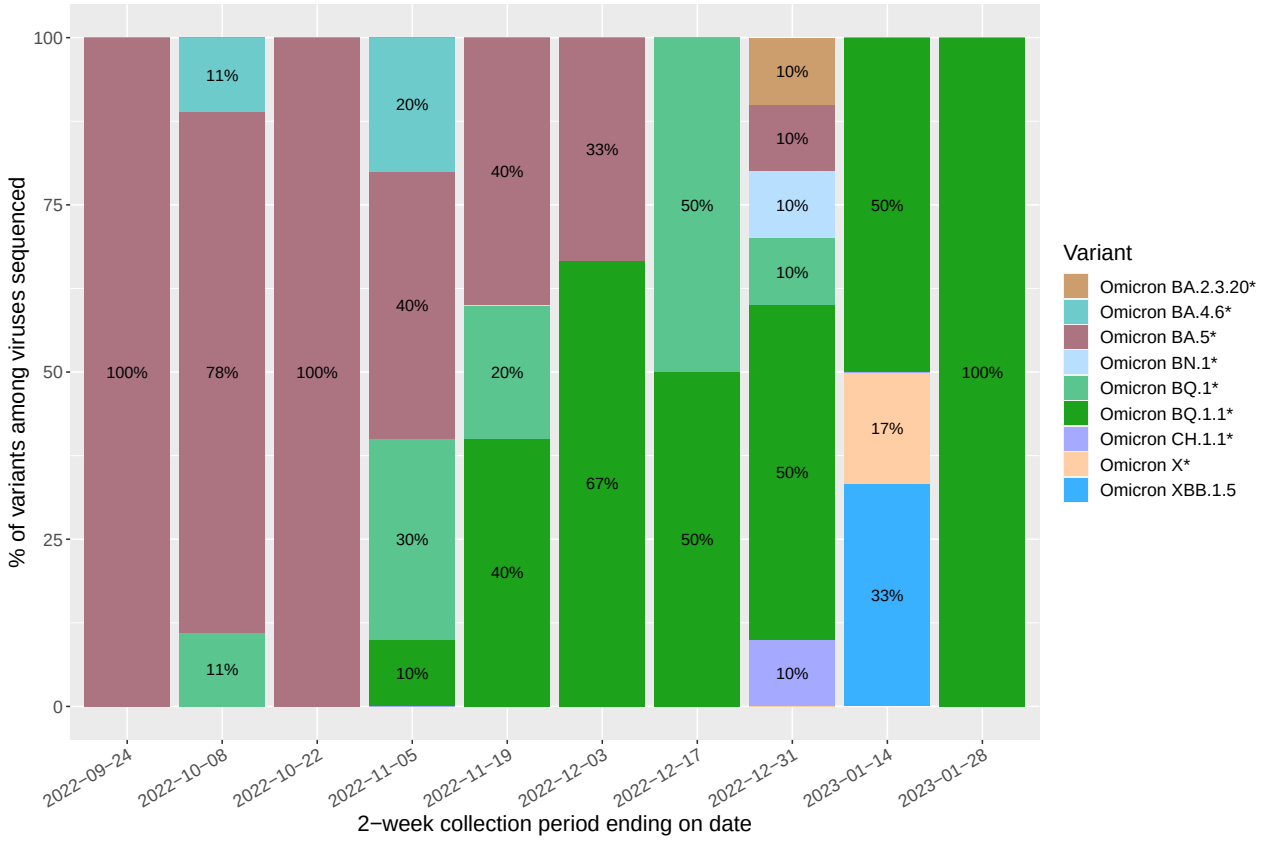

Figure Notes:

- Graph depicts estimated SARS-CoV-2 variant proportions (percentages rounded to the nearest integer) for Kauai County, grouped in 2-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. This graph was generated by only counting specimens that were selected randomly for the purpose of surveillance.
- Percentage estimates based on historical data may change over time as additional sequences are reported.
- Omicron BA.2.3.20* includes BA.2.3.20 and its sub-lineages (CM.*).
- Omicron BA.4.6* includes BA.4.6 and its sub-lineages (BA.4.6.*, DC.*).
- Omicron BA.5* includes BA.5 and its sub-lineages (BA.5.*, BE.*, BF.*, BK.*, BW.*, CK.*, CQ.*, DB.*, DF.*, DG.*); excludes BA.5.2.6* and BF.7*.
- Omicron BN.1* includes BN.1 and its sub-lineages (BN.1.*).
- Omicron BQ.1* includes BQ.1 and its sub-lineages (BQ.1.*); excludes BQ.1.1*.
- Omicron BQ.1.1* includes BQ.1.1 and its sub-lineages (BQ.1.1.*, DN.*, DR.*).
- Omicron CH.1.1* includes CH.1.1 and its sub-lineages (CH.1.1.*)
- Omicron X* includes Omicron recombinants except for XBB and its sub-lineages (XBB.*).

Variants of Concern in Kauai County

WHO label	Lineage	Area of emergence	Cumulative sequences	Earliest specimen collection date	Most recent specimen collection date
Omicron			501		
	BA.2	South Africa/Botswana	83	17 Mar 2022	26 Jul 2022
	BA.1.1	South Africa/Botswana	63	15 Dec 2021	19 Apr 2022
	BA.2.12.1	USA/Canada	62	30 Mar 2022	27 Jul 2022
	Other	Various	56	01 Aug 2022	30 Jan 2023
	BA.5.2.1	South Africa/UK/USA	32	03 Jun 2022	02 Nov 2022
	BA.2.3	Philippines	19	09 Mar 2022	24 May 2022
	BA.5.5	USA	18	13 Jun 2022	31 Aug 2022
	BA.5.1	Portugal	15	23 Jun 2022	19 Oct 2022
	BA.1.15	USA	13	28 Dec 2021	23 Mar 2022
	BQ.1.1	Global	13	04 Nov 2022	27 Jan 2023
	BA.1	South Africa/Botswana	12	16 Dec 2021	07 Feb 2022
	BA.5.2	South Africa/UK/USA	10	02 Jul 2022	17 Nov 2022
	XAC	USA/Canada	9	28 Apr 2022	14 Jun 2022
	BA.1.1.18	USA	8	28 Dec 2021	21 Mar 2022
	BA.1.1.2	Japan	8	15 Dec 2021	09 Feb 2022
	BA.2.18	UK	8	24 Apr 2022	16 Jun 2022
	BA.2.42	Australia	8	07 May 2022	02 Jul 2022
	BG.5	USA	7	03 May 2022	13 Jun 2022
	BA.4.1	South Africa	6	08 Jun 2022	26 Jun 2022
	BF.10	USA	6	13 Jun 2022	19 Aug 2022
	BQ.1	Nigeria	6	30 Sep 2022	07 Dec 2022
	BA.2.9	Europe	5	17 Mar 2022	09 May 2022
	BF.5	Israel	5	21 Jun 2022	17 Oct 2022
	BA.4.6	USA/UK/Denmark	4	23 Aug 2022	04 Nov 2022
	BA.4.6.5	Global	4	23 Aug 2022	04 Nov 2022
	BA.5.2.9	USA	4	27 Jun 2022	30 Aug 2022
	BA.5.6	USA	4	16 Jun 2022	29 Aug 2022
	BE.3	USA	4	15 Jun 2022	17 Oct 2022
	BA.2.1	UK	3	25 May 2022	20 Jun 2022
	BA.5.1.10	USA/Italy/UK	3	06 Jul 2022	14 Oct 2022
	XBB.1.5	USA	3	10 Jan 2023	31 Jan 2023

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	Area of emergence	Cumulative sequences	Earliest specimen collection date	Most recent specimen collection date
Alpha			20		
	B.1.1.7	UK	19	05 Apr 2021	13 Jul 2021
	Q.4	South Africa/Botswana	1	28 Apr 2021	28 Apr 2021
Gamma			2		
	P.1	Brazil	1	31 May 2021	31 May 2021
	P.1.10	USA	1	14 May 2021	14 May 2021
Delta			246		
	AY.25	USA	70	16 Jul 2021	10 Nov 2021
	AY.44	USA	37	29 Jun 2021	21 Dec 2021
	AY.119	USA	35	28 Aug 2021	21 Dec 2021
	Other AY.*	Various	25	03 Nov 2021	29 Nov 2021
	AY.47	USA	19	27 Jul 2021	29 Nov 2021
	AY.1	Europe	18	09 Aug 2021	30 Aug 2021
	AY.103	USA	17	01 Aug 2021	15 Dec 2021
	AY.3	USA	8	30 Sep 2021	15 Dec 2021
	AY.54	USA	8	06 Jul 2021	09 Nov 2021
	AY.67	South Africa/Botswana	7	06 Jun 2021	30 Jun 2021
	B.1.617.2	India	2	21 Sep 2021	18 Oct 2021
Epsilon			31		
	B.1.429	USA	29	07 Jan 2021	08 May 2021
	B.1.427	USA	2	27 Apr 2021	27 Apr 2021
Iota	B.1.526	USA	1	14 Apr 2021	14 Apr 2021
Mu	B.1.621	Columbia	2	29 Jun 2021	06 Jul 2021

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.