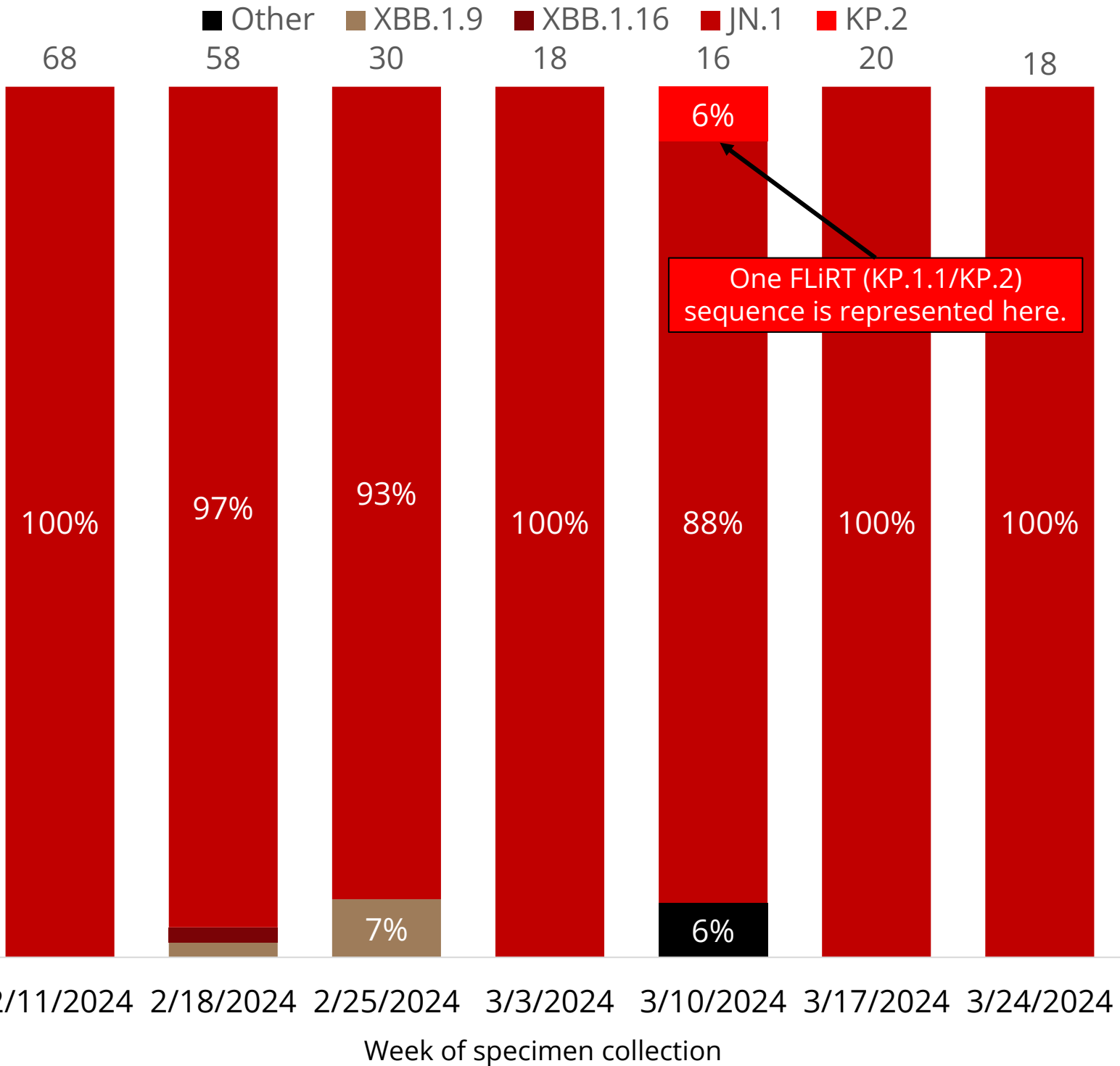


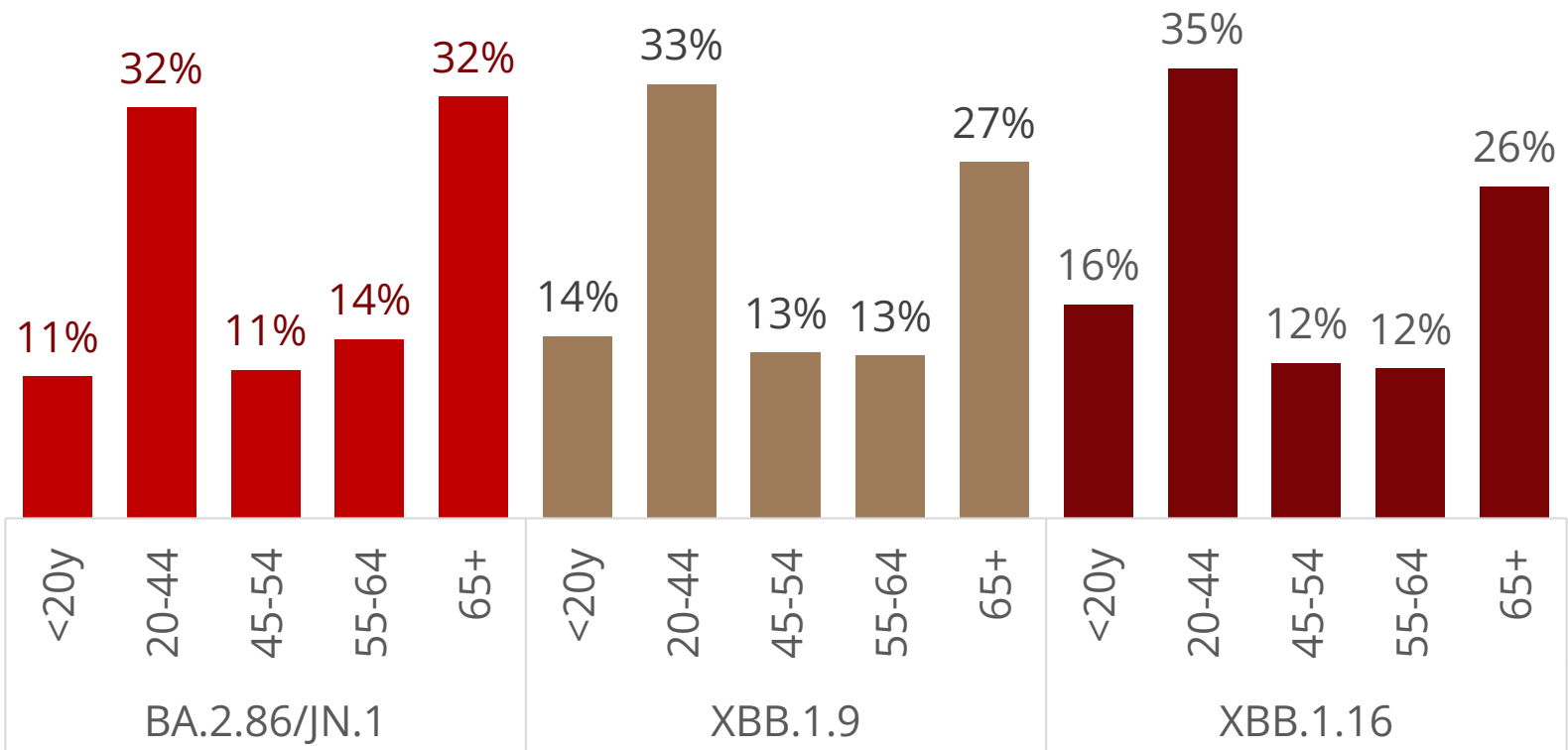
[Click here for GISAID data](#)

The Omicron lineage JN.1 is the dominant variant in Arizona through 2024.



Data timeframe represented above: 2/11/2024 to 3/30/2024

# Sequenced COVID-19 cases, by variant, for each age group and county



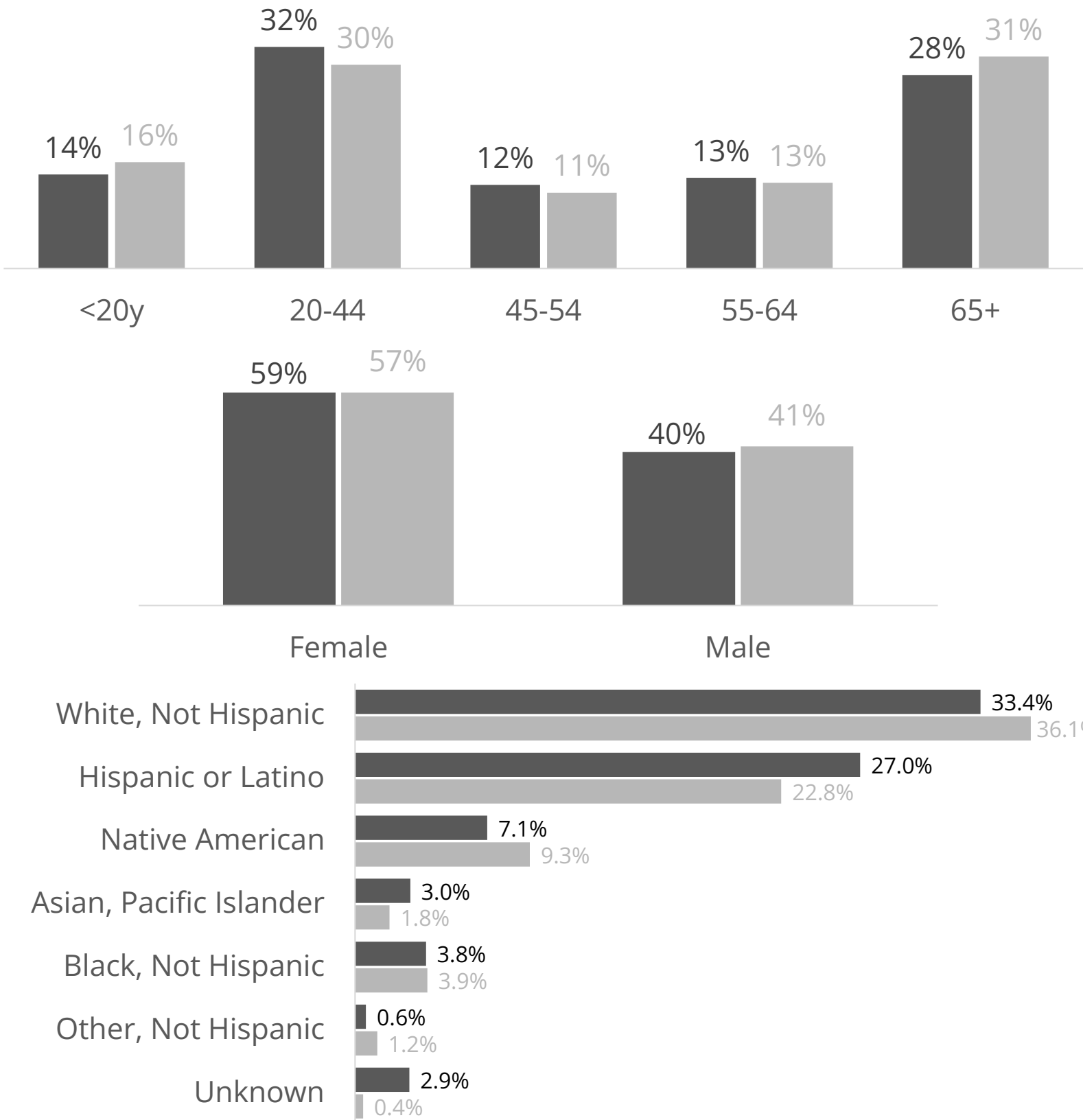
County of Residence	XBB.1.5	XBB.1.9	XBB.1.16	BA.2.86/JN.1	Total XBB Sequenced
Apache	0.0%	100.0%	0.0%	0.0%	2
Cochise	4.2%	56.2%	8.3%	31.2%	144
Coconino	0.0%	33.3%	16.7%	50.0%	6
Gila	0.0%	50.0%	25.0%	25.0%	8
Graham	4.7%	33.3%	52.4%	9.5%	42
Greenlee	0.0%	42.8%	42.8%	14.3%	7
La Paz	0.0%	0.0%	0.0%	0.0%	0
Maricopa	6.9%	48.0%	11.6%	33.5%	1028
Mohave	6.7%	40.0%	14.3%	39.0%	105
Navajo	28.6%	28.6%	0.0%	42.9%	7
Pima	6.3%	47.7%	14.1%	31.9%	348
Pinal	9.4%	44.9%	15.0%	30.7%	127
Santa Cruz	0.0%	0.0%	0.0%	0.0%	0
Yavapai	0.0%	25.0%	0.0%	75.0%	4
Yuma	0.0%	66.7%	33.3%	0.0%	3
Totals	122	870	243	596	1,831

Data timeframe represented above: 10/1/2023 to 3/30/2024

NOTE: Variants: BA.5, BQ.1 & BA.2 are not included

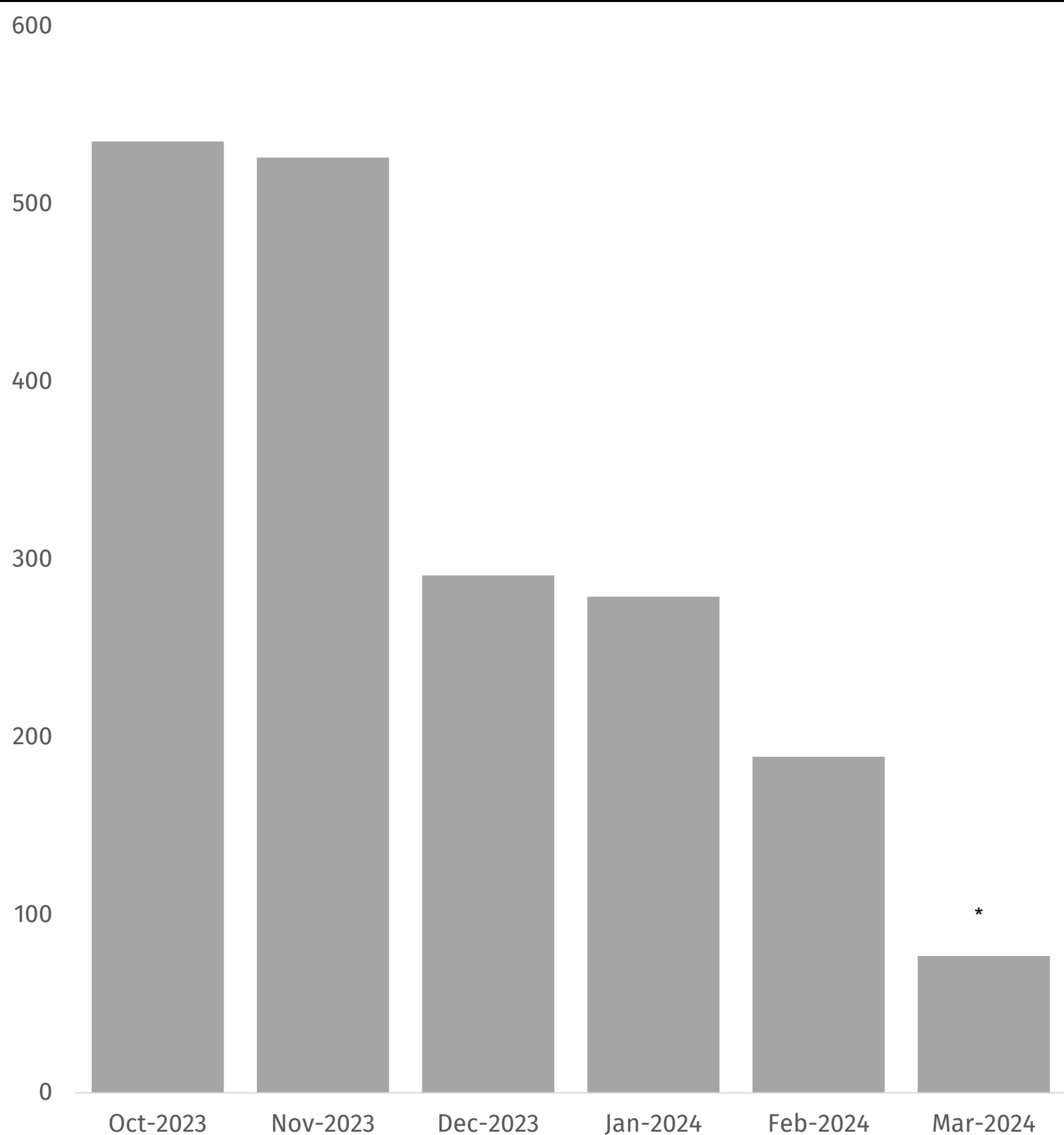
# Proportion of COVID-19 cases sequenced compared to case demographics

Demographics for Arizona's sequenced cases resemble cases from October 1<sup>st</sup>, 2023 through March 30<sup>th</sup>, 2024 COVID-19 cases, although a higher proportion of cases aged 20-44 years have been sequenced.



Data timeframe represented above: 10/1/2023 to 3/30/2024

# Number of COVID-19 cases sequenced, by month of specimen collection



Data timeframe represented above: 10/1/2023 to 3/30/2024

\*Please note that March 2024 includes data up to the 30th

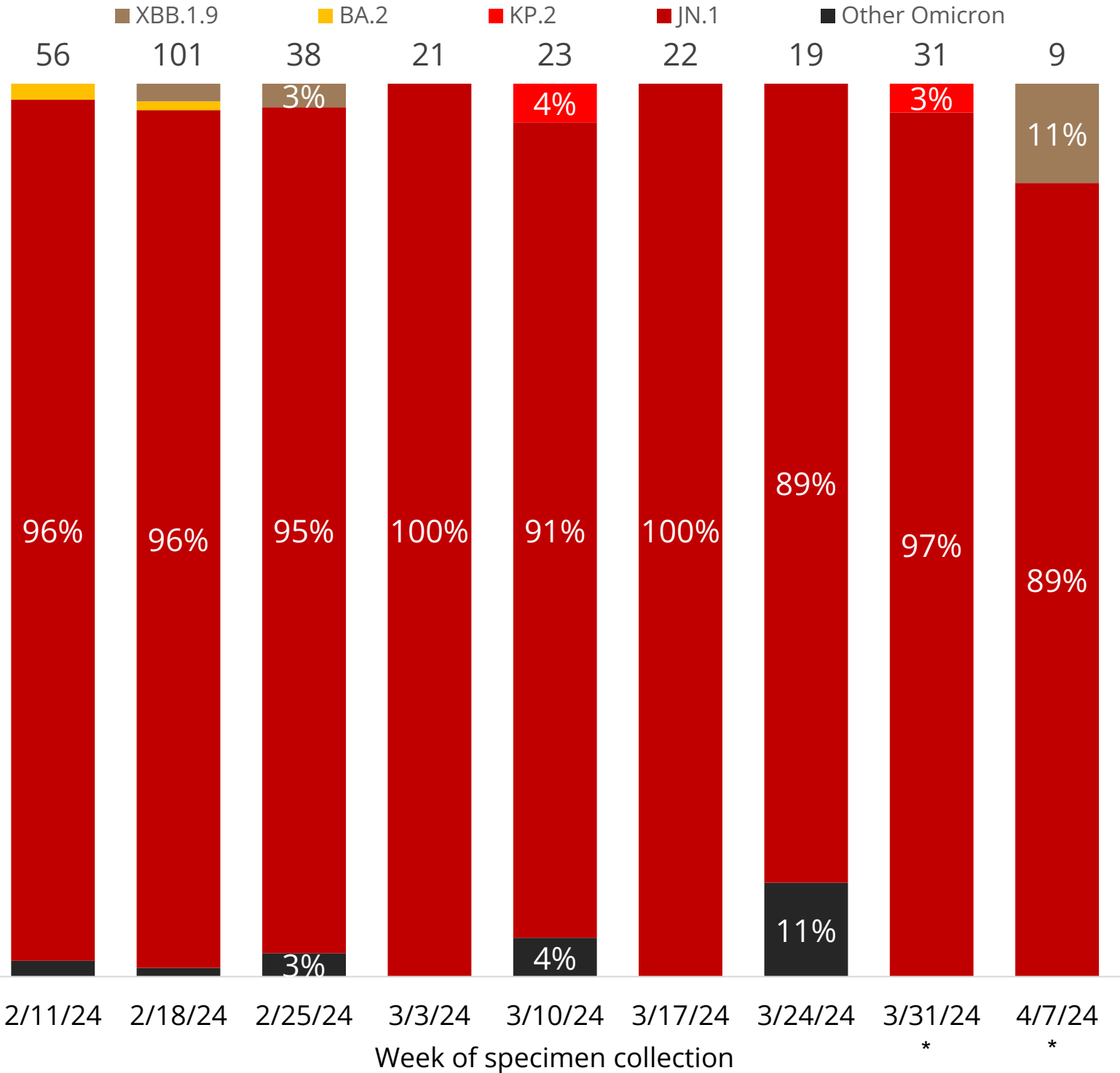
## About the data for *ARIZONA – COVID-19 Sequenced Cases*:

- Facilities performing laboratory tests for COVID-19 report positive COVID-19 test results to ADHS pursuant to Arizona Administrative Code R9-6-204.
- Laboratories collect specimens from across the state. Sequencing is performed by specialized laboratories on a sample of specimens. The sequencing results are sent to ADHS and matched to case data.
- The sequencing data shown in this report represent lineage data that has been matched to reported and confirmed COVID-19 cases. Only one sequencing result is shown for a case with multiple results.
- Formal nomenclature for SAR-CoV-2 is constantly changing due to its rapid mutation rate. Grouping of the variants is based on CDC denoted variants of concern format. All sequenced variants are represented within this report.
- The data time frame on page 1 (cases with sequenced specimens collected within a rolling 7-week period) was selected to better show the prevalence of current circulating variants. The lineages shown will vary to best reflect recent variants of concern circulating in Arizona. In this week's report:
  - BA.2.86/JN.1 includes all sub-variants (BA.2.86.1, JN.1.4, etc.)
  - XBB.1.5 includes all sub-variants respectively (XBB.1.5.1, etc.).
  - XBB.1.9 includes all sub-variants respectively (XBB.1.9.5, etc.).
  - XBB.1.16 includes all sub-variants respectively (XBB.1.16.1, etc.).
  - Other XBB includes all other sub-variants of XBB (XBB.1.2, etc.).
- The remainder of the report includes the total accumulated cases with sequenced specimens collected October 1, 2023 to March 30, 2024.
  - This data was compiled, verified, and matched by ADHS.
- Sequencing data is derived from whole genome sequencing performed on a proportion of positive COVID-19 samples in Arizona. Not every positive sample for COVID-19 is sequenced.
- ADHS receives data from various partners, affecting the timing of when summarized sequencing data will be available for any given period. Samples are collected, tested for COVID-19, delivered to the respective laboratories then sequenced. ADHS partners validate the quality of the data and report the results. There is time between each step of the process for matching sequence data to case data.
- COVID-19 sequencing data is reported to ADHS at a rapid rate. Interpretation of the data presented should consider that sequencing data is continuously updated.
- Please consult with public health if making clinical decisions based on circulating variant proportions.



[Click here for case linked data](#)

The variant data shown on this page is not linked to case data as in the figures above.  
\*The two most recent weeks shown may not be a complete representation of variant proportions and are subject to change with additional samples uploaded.



Data timeframe represented above: 2/11/2024 to 4/13/2024

## About the Data *ARIZONA – COVID-19 GISAID Specimens:*

- Data presented in this report is sourced from the SARS-CoV-2 WGS repository on [GISAID.org](https://gisaid.org).
  - GISAID is an open source, public repository for storing and documenting raw pathogen WGS data including but not limited to SARS-CoV-2.
  - Submission to GISAID is voluntary, and cadence of submissions is determined on the basis of each individual sequencing labs.
- The purpose of this report is to visualize the circulating variants of submitted sequenced samples to GISAID and is meant to serve as a public situational awareness of the most up-to-date sequencing efforts of SARS-CoV-2.
  - The differences in the lag time between the data represented in the GISAID report & the data presented in the ARIZONA – COVID-19 Sequenced Cases report is due to the reporting of the cases to ADHS, and the cadence of voluntarily submissions of sequencing labs to GISAID.
  - This report differs from the ARIZONA – COVID-19 Sequenced Cases report released by ADHS in not representing demographic data or associated case data.
  - This report can serve as a reference for ADHS sequencing laboratory partners to validate their test kit libraries and add contextual knowledge for the sequencing labs in their WGS efforts for the state.

## About this report:

- Sequencing laboratories may collect specimens from across the state.
- The timeframe of the data presented in this report is a rolling 9-week period, in order to demonstrate the changes in the distribution of the current circulating variants.
- The lineages shown will vary in order to best reflect recent variants of concern sequenced by ADHS lab partners. In this report, variants are represented as the following:
  - JN.1 includes all sub-variants (JN.1.7, JN.1.16, etc.), except KP.2.
  - XBB.\* includes all sub-variants respectively.
  - Other omicron includes all other B.1.1.529 sub-variants.

## About GISAID:

- Sequencing is performed by specialized laboratories on clinical specimens. Sequencing results (virus characterization/variant), state/county of sample collection, dates of collection/submission, and submitter names is uploaded onto GISAID.
  - This data is anonymous and NOT linked to any patient or case data.
  - Data pulled from GISAID differs from MEDSIS data. WGS data sourced from GISAID are NOT matched to public health case data.
  - Due to the data quality of a public repository, duplicates might be included. However, these duplicates are filtered out within the ADHS data presented in other pages of this report.
  - Upload dates may differ from sample collection dates and sequencing dates.