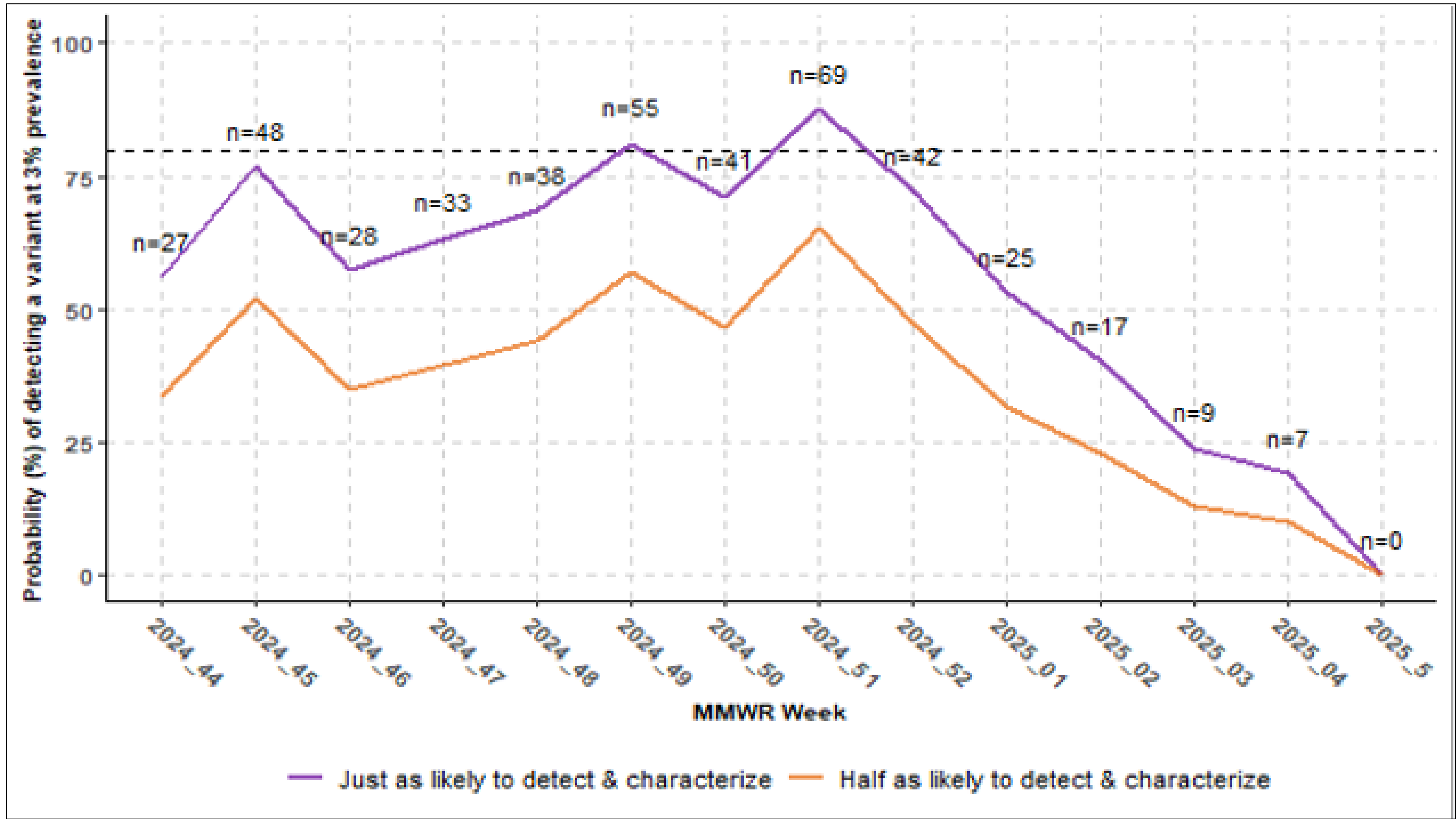


# Example SARS-CoV-2 Sequencing Surveillance Report Outputs

## Probability of Detection analysis

Figure 1. Probability of Detecting a Variant at 3 Percent Prevalence by Week  
Massachusetts, 10/27/2024-02/01/2025



**Interpretation:** Probability estimates assume that sampling is homogenous and representative statewide across the time period. This plot and the table to the right present the probability of detecting a variant at 3% prevalence statewide under two detection scenarios. We believe our current situation is that we are just as likely to detect and characterize a variant of interest compared to other circulating variants, represented in purple. We also present data for an alternate scenario where we are only half as likely to detect a variant of interest compared to other circulating variants due to potential changes in virus biology, represented in orange.

**Targets:** The target we would like to meet is 80% probability of detecting a variant at 3% prevalence each week. This target could be achieved with a weekly sample size of n=53-105 successfully sequenced samples.

\* These data are presented for specimens reported to the Massachusetts Virtual Epidemiologic Network (MAVEN), where n = the number of successfully sequenced, confirmed cases each week.

\* Dates are based on the earliest date a patient tested positive for COVID-19. This date may differ slightly from the sequencing specimen collection date. Data are current as of 6 February 2025.

Table 1. Probability of Detecting a Variant at 3 Percent Prevalence by Week and  
Change in Number of Samples Needed to Meet Surveillance Targets  
Massachusetts, 10/27/2024-02/01/2025

MMWR Week	Number of Sequenced Cases	Probability of detecting a variant at 3% prevalence (detection ratio=1)	Change needed in the number of samples to meet target of n=53 (detection ratio=1)	Probability of detecting a variant at 3% prevalence (detection ratio=0.5)	Change needed in the number of samples to meet target of n=105 (detection ratio=0.5)
2024_44	27	56.1%	+26 samples	33.9%	+78 samples
2024_45	48	76.8%	+5 samples	52.1%	+57 samples
2024_46	28	57.4%	+25 samples	34.9%	+77 samples
2024_47	33	63.4%	+20 samples	39.7%	+72 samples
2024_48	38	68.6%	+15 samples	44.2%	+67 samples
2024_49	55	81.3%	No change	57.0%	+50 samples
2024_50	41	71.3%	+12 samples	46.7%	+64 samples
2024_51	69	87.8%	No change	65.3%	+36 samples
2024_52	42	72.2%	+11 samples	47.5%	+63 samples
2025_01	25	53.3%	+28 samples	31.9%	+80 samples
2025_02	17	40.4%	+36 samples	23.0%	+88 samples
2025_03	9	24.0%	+44 samples	12.9%	+96 samples
2025_04	7	19.2%	+46 samples	10.2%	+98 samples
2025_05	.	.	.	.	.

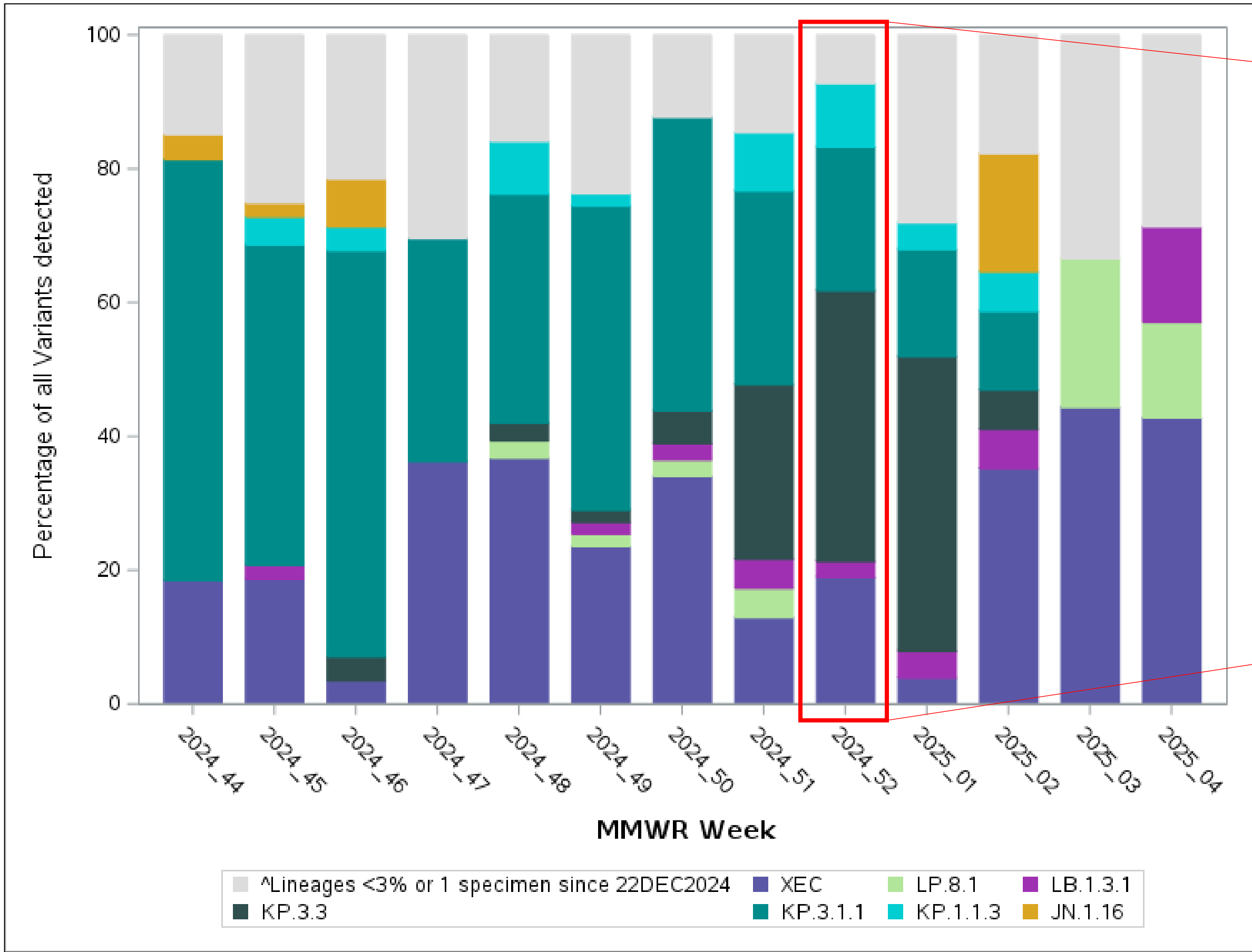
\* These data are presented for specimens reported to the Massachusetts Virtual Epidemiologic Network (MAVEN) and include only successfully sequenced, confirmed cases.

\* Dates are based on the earliest date a patient tested positive for COVID-19. This date may differ slightly from the sequencing specimen collection date. Data are current as of 6 February 2025.

\* Virus biology adaptations can impact variant detection and/or genomic characterization by affecting test sensitivity, ability to successfully sequence, asymptomatic rate, and the likelihood of testing for infections. The `Just as likely to detect` scenario (detection ratio=1) reflects the probability of detecting and characterizing a variant in situations where there are no differences in detection or ability to genomically characterize between a variant of interest and other circulating variants. `Half as likely to detect` (detection ratio=0.5) reflects the probability of detecting and characterizing a variant in situations where detection or characterization of a variant of interest is half as likely to be successful compared to other circulating variants.

## Variant Prevalence analysis

Figure 2. Lineages Detected by Whole Genome Sequencing  
Massachusetts, 10/27/2024-02/01/2025



Lineage	Prevalence (95% CI) Week 52 (n=42)
KP.3.3	40.5% (25.7%-55.3%)
XEC	19% (7.1%-30.9%)
KP.3.1.1	21.4% (9%-33.8%)
KP.1.1.3	9.5% (0.6%-18.4%)
LB.1.3.1	2.4% (0%-7%)
Other lineages <3% or n=1 since 22DEC2024	7.2% (0%-15%)

\* Lineages detected by Whole Genome Sequencing (WGS) are presented for specimens reported to the Massachusetts Virtual Epidemiologic Network (MAVEN) for successfully sequenced, confirmed cases, and are updated, when available, with data from the Global Initiative on Sharing All Influenza Data (GISAID) or the National Center for Biotechnology Information (NCBI).

\* Dates are based on the earliest date a patient tested positive for COVID-19. This date may differ slightly from the sequencing specimen collection date. Data are current as of 6 February 2025.

\* Lineages detected at less than 3% or in 1 specimen in the last 6 weeks are grouped together, for ease of interpretation.