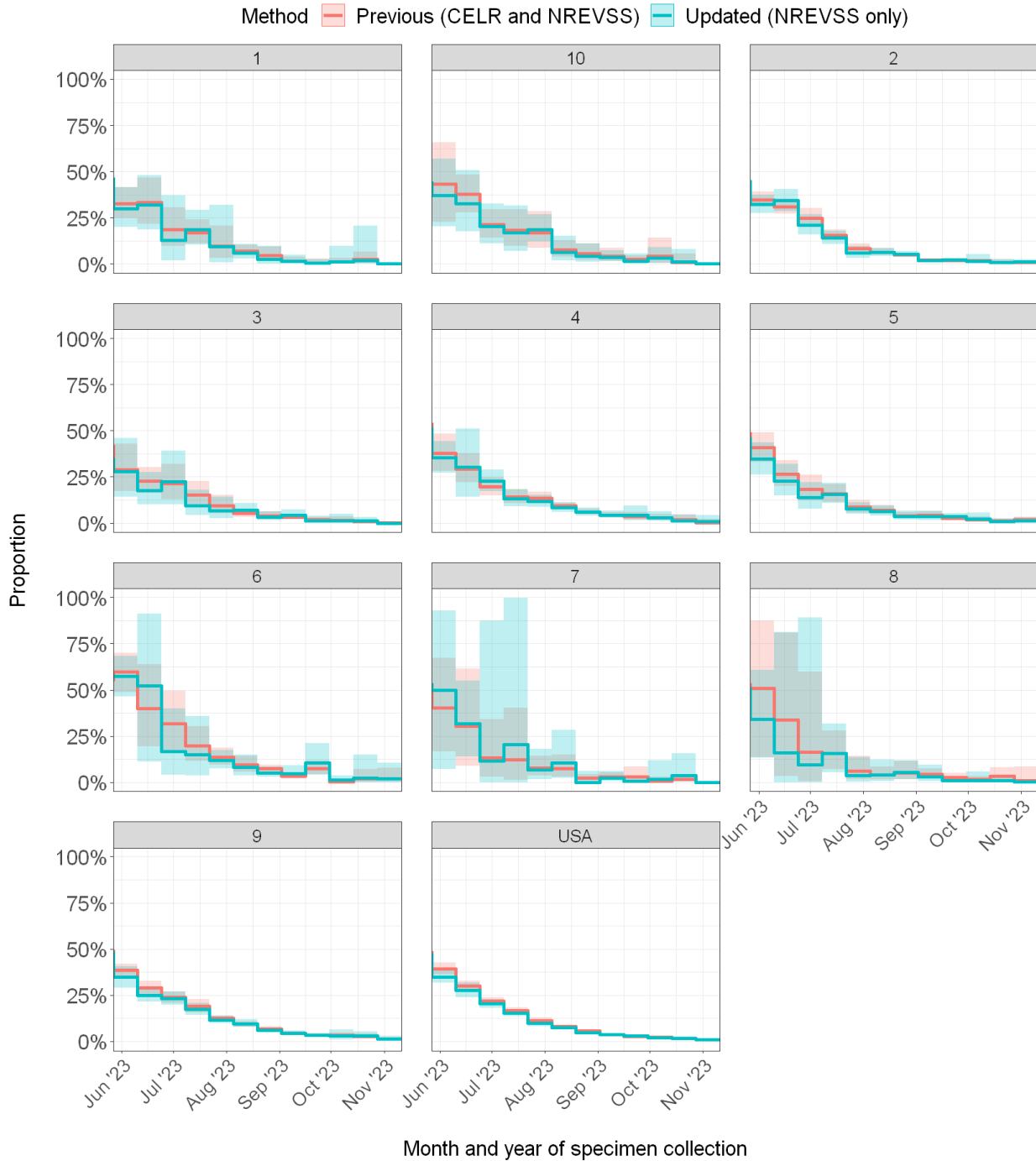
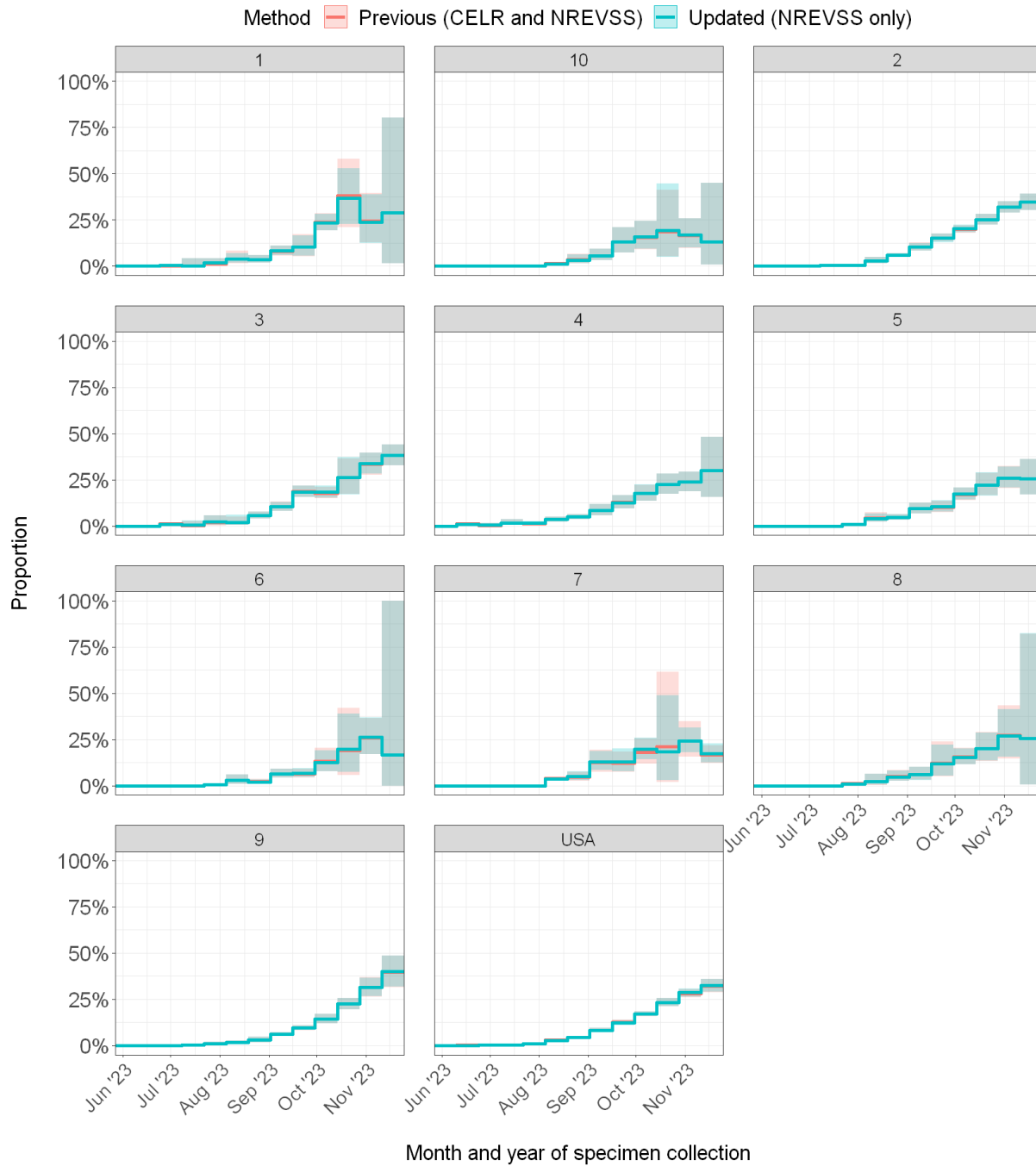


SUPPLEMENTARY FIGURE 2. Comparison of proportions* of Omicron lineage XBB.1.5 (A) and HV.1 (B) with 95% CIs,[†] nationally and by U.S. Department of Health and Human Services Regions 1–10,[§] estimated with COVID-19 electronic reporting and National Respiratory and Enteric Virus Surveillance System–derived weights[¶] versus National Respiratory and Enteric Virus Surveillance System alone — United States, May 14, 2023–November 11, 2023

A. Omicron lineage XBB.1.5



B. Omicron lineage HV.1



Abbreviations: CELR = COVID-19 electronic laboratory reporting; NREVSS = National Respiratory and Enteric Virus Surveillance System; NS3 = National SARS-CoV-2 Strain Surveillance program.

* Sequences are reported to CDC through NS3, contract laboratories, public health laboratories, and other U.S. institutions. Variant proportion estimation methods use a complex survey design and statistical weights to account for the probability that a specimen is sequenced. <https://covid.cdc.gov/covid-data-tracker/#variant-proportions>

† 95% CIs for estimates are shown by shaded areas.

[§] <https://www.hhs.gov/about/agencies/iea/regional-offices/index.html>

[¶] Between May 11, 2023, and November 16, 2023, a combination of data sources was used to estimate survey design weights. The percentage of positive SARS-CoV-2 nucleic acid amplification test results by HHS Region was obtained from the National Respiratory and Enteric Virus Surveillance System, and the number of positive specimens by HHS Region was obtained from COVID-19 electronic laboratory reporting. Percentages of positive test results from NREVSS and CELR correlated well (<https://doi.org/10.15585/mmwr.mm7219e2>). Beginning November 17, 2023, survey design weights were changed to rely solely on NREVSS data.