

Figure 1-figure supplement 1

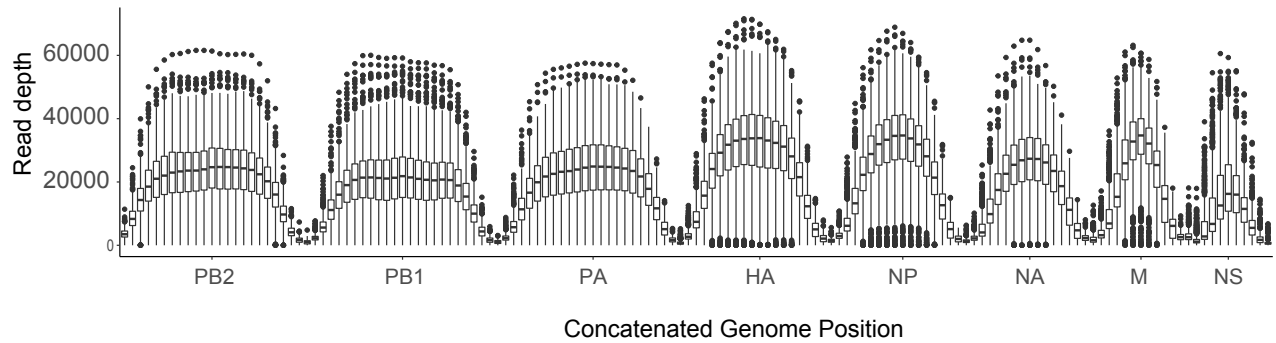


Figure 1-figure supplement 1. Sequence coverage for all samples. For each sample, the sliding window mean coverage was calculated using a window size of 200 and a step of 100. The distributions of these means are plotted as box plots (median, 25th and 75th percentiles, whiskers extend to most extreme point within median $\pm 1.5 \times \text{IQR}$) where the y-axis represents the read depth and the x-axis indicates the position of the window in a concatenated IAV genome.