**Interpreting Nextclade quality metrics**

Alt-text Figure 8 - Nextclade input page

Screenshot of Nextclade input page. Red rectangles highlight the "sequence data you've added" box and the "run" button. Detailed description in the main text.

Alt-text Figure 9 - Nextclade run output

Screenshot of Nextclade run output. Detailed description in the main text.

Alt-text Figure 10 - Nextclade output: additional information

Screenshot of Nextclade output. It highlights a box of additional information about the analysed sequences: Missing data, mixed sites, private mutations, mutation clusters, frame shifts and stop codons.

Alt-text Figure 11 - Nextclade output: nucleotide substitutions

Screenshot of Nextclade output. It shows a list of nucleotide substitutions compared to the reference sequence, amino acid substitutions, private mutations and unclassified mutations.

Alt-text Figure 12 - Nextclade output: amino acid translation

Screenshot of a Nextclade output. It highlights a box that indicates the amino acid and nucleotide changes in a sequence, as well as their correspondent positions in the sequence.

Alt-text Figure 13 - Nextclade export window

Screenshot of a Nextclade export window. The output can be exported in different formats including CSV, ZIP, FASTA, and others.