



Supplementary figure 3 Comparison of the coverage of viral sequences, as calculated after the implementation of each method (RAW, BWA, SORTMERA and ZWA2) separately on the examined RNA-seq samples and subsequent mapping of the treated RNA-seq data on the corresponding viral genes/genomes by BWA. The dotted lines connecting the colorful dots on the graph depict the fluctuations of the viral coverage rates for the same RNA-seq sample, treated separately by each method. A small subsection of the diagram (viral coverage rates between 95% and 100%) is zoomed in for representation purposes, clearly displaying the corresponding plotted data on the right side. The statistical analysis of the mean differences across the studied methods was performed by RM-ANOVA and Tukey's multiple comparison testing, and the output statistical significance of ZWA2 is indicated by (* p -value < 0.05).