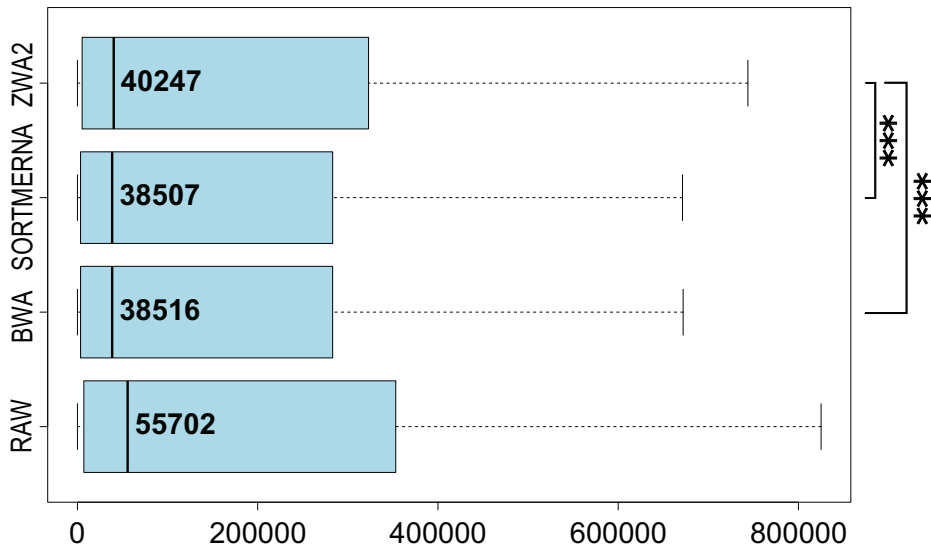


Virus mapped reads



Supplementary figure 2 Comparison of the total number of reads mapped on 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 median values for this metric are displayed within the bar plots. 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 < 0.001).