



Supplementary Result Figure 2: The median length of all contigs with a minimum length of 500bp is higher in samples from the Illumina method

The number of contigs with a minimum length of 500bp is plotted on the x-axis in a log 2 scale. Each point represents one contig and is plotted in a scatterplot with the median values shown as a red line. The Kruskal-Wallis test was used to test whether the means differed significantly between the same sample for the three different bait capture methods and the P value is shown in the two red boxes on the left of the figure. Dunn's multiple comparison test was used to show significant differences between the three different bait capture methods for each sample. All significant mean differences are shown with * <0.05, ** <0.01, ***<0.001 and **** <0.0001. A P value marked with *, **, ***, or **** always means that the mean rank was significantly higher than other samples marked with the letters "I" for Illumina method, "A" for Ampheus = veSEQ method, and "H" for inHouse = RVI-seq method. For example, ****A *H in the Illumina dataset for Corona 229E NL63 OC43 mix samples means that the mean rank for the Illumina sample is significantly higher than the mean rank for the Ampheus samples (A****) and also significantly higher than the mean rank for the inHouse samples with (H*).

Abbreviations: hCoV = non SARS-CoV-2 human coronavirus, SC2 = SARS-CoV-2, neg = negative, pos = positive, hPIV1 = human parainfluenza virus 1, 1M, 100K, 10K, 1K = number of Twist synthetic RNA copies used as input into workflow