



**Supplementary Result Figure 3:**  
**MetaQUAST metrics for de-novo**  
**assembled metagenomes differed**  
**slightly between viral bait capture**  
**methods.**

HQ paired-end short reads for all SARS-CoV-2 samples, with a minimum length of 100bp, were de-novo assembled using MetaSPAdes and the quality of the contigs was assessed using MetaQUAST and the SARS-CoV-2 reference strain 'Wuhan MN908947.3'. The length of the largest contigs (a), the total aligned length (b), the assembly accuracies determined for mismatches per 100 kbp (c) and INDELS per 100 kbp (d), and the fraction of the genome sequenced (e) are shown on the x-axis.

SARS-CoV-2 positive and negative samples are coloured blue and green respectively. Synthetic SARS-CoV-2 RNA samples alone or mixed with hPIV1 and/or Flu H1N1 are coloured grey. Total aligned length is the total number of aligned bases in the assembly, which may be longer than the largest alignment itself.

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, - - - = No sequence data obtained