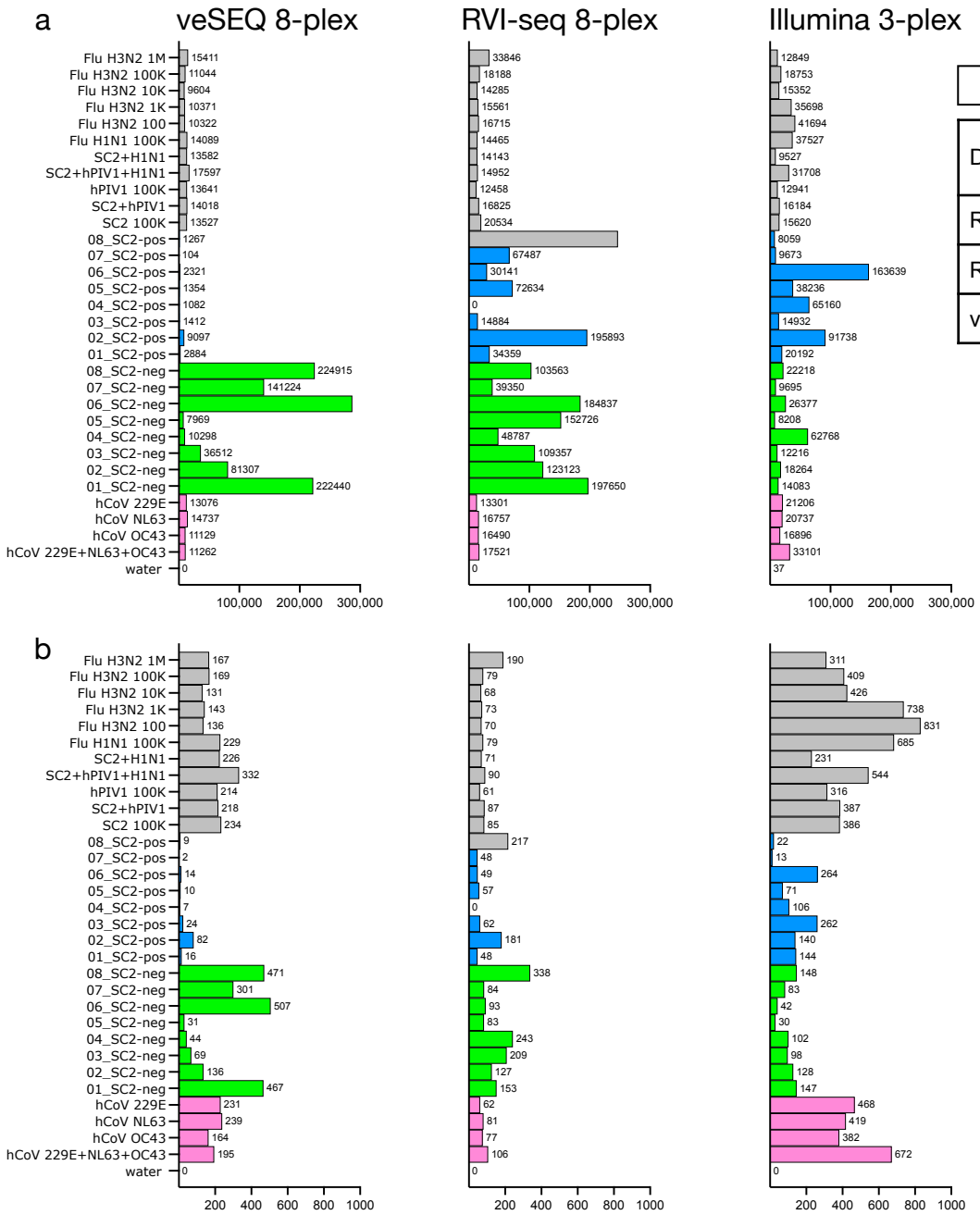

Number contigs ≥ 0 bp

Dunn's multiple comparisons test	Rank sum diff.	Adjusted P Value
RVI-seq# contigs (≥0kb) vs. veSEQ# contigs (≥0kb)	28.00	0.0009
RVI-seq# contigs (≥0kb) vs. Ill# contigs (≥0kb)	8.000	0.9051
veSEQ# contigs (≥0kb) vs. Ill# contigs (≥0kb)	-20.00	0.0295

Number contigs ≥ 1 kbp

Dunn's multiple comparisons test	Rank sum diff.	Adjusted P Value
RVI-seq# contigs (≥1kb) vs. veSEQ# contigs (≥1kb)	-3.000	>0.9999
RVI-seq# contigs (≥1kb) vs. Ill# contigs (≥1kb)	-21.00	0.0201
veeSEQ# contigs (≥1kb) vs. Ill# contigs (≥1kb)	-18.00	0.0604

Number contigs ≥ 5 kbp

Dunn's multiple comparisons test	Rank sum diff.	Adjusted P Value
RVI-seq# contigs (≥5kb) vs. veSEQ# contigs (≥5kb)	-7.000	>0.9999
RVI-seq# contigs (≥5kb) vs. Ill# contigs (≥5kb)	-8.000	0.9051
veSEQ# contigs (≥5kb) vs. Ill# contigs (≥5kb)	-1.000	>0.9999

Supplementary Result Figure 1: Number of contigs differs between bait capture methods in Pilot 1 study

HQ paired-end short reads with a minimum length of 100bp were de-novo assembled using MetaSPAdes and the quality of the contigs was assessed using MetaQuast. The total number of contigs was determined with no minimum length (a), with a minimum length of 1kb (b), 5kb (c) and 25kb (d). Clinical positve and negative SARS-CoV-2 are coloured with blue and green, respectively. Non SARS-CoV-2 human corona virus are colour coded with pink. The number of contigs is shown on the x-axis, with some differences noted between the three different bait capture methods. 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, RVI-seq (inHouse), veSEQ, and Ill are the different bait capture methods used in pilot 1 study