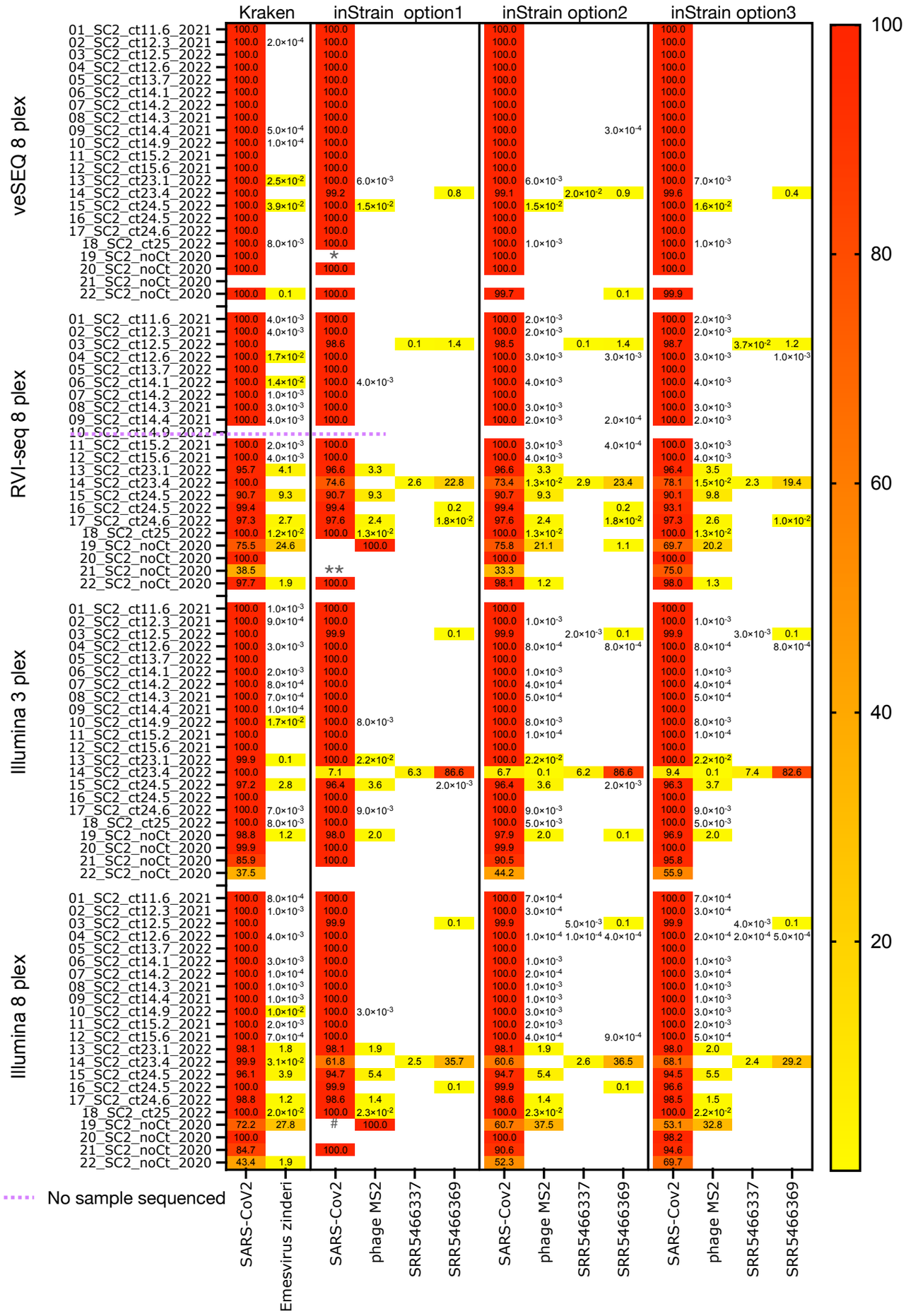

Supplementary Result Figure 7: Kraken and inStrain analysis for clinical SARS-CoV-2 positive samples

HQ paired end short reads downsampled to maximum 1 million reads were taxonomically analysed by Kraken2/Bracken and with inStrain using three different parameters. The three different inStrain options were: option 1 “with database mode, min genome coverage 1, min read average nucleotide identity (ani) of (0.92) and skip mm profiling”, option 2 'no database mode, min genome coverage 0, min read ani of 0.9’, option 3 (default) “no database mode, min genome coverage 0, min read ani 0.95”. Only taxa with a minimum read number of 1000 and with a minimum relative abundance of 2% in at least one sample are shown. Cell value are colour coded with a minimum abundance of 0.01%.

Classification notes:

The spiked phage MS2 is named Emesvirus zinderi in the Kraken database. SRR5466337 and SRR5466369 are ssRNA phage.

Abbreviation:

SC2 = SARS-CoV-2, ct = cycle threshold value for PCR detection of SARS-CoV-2