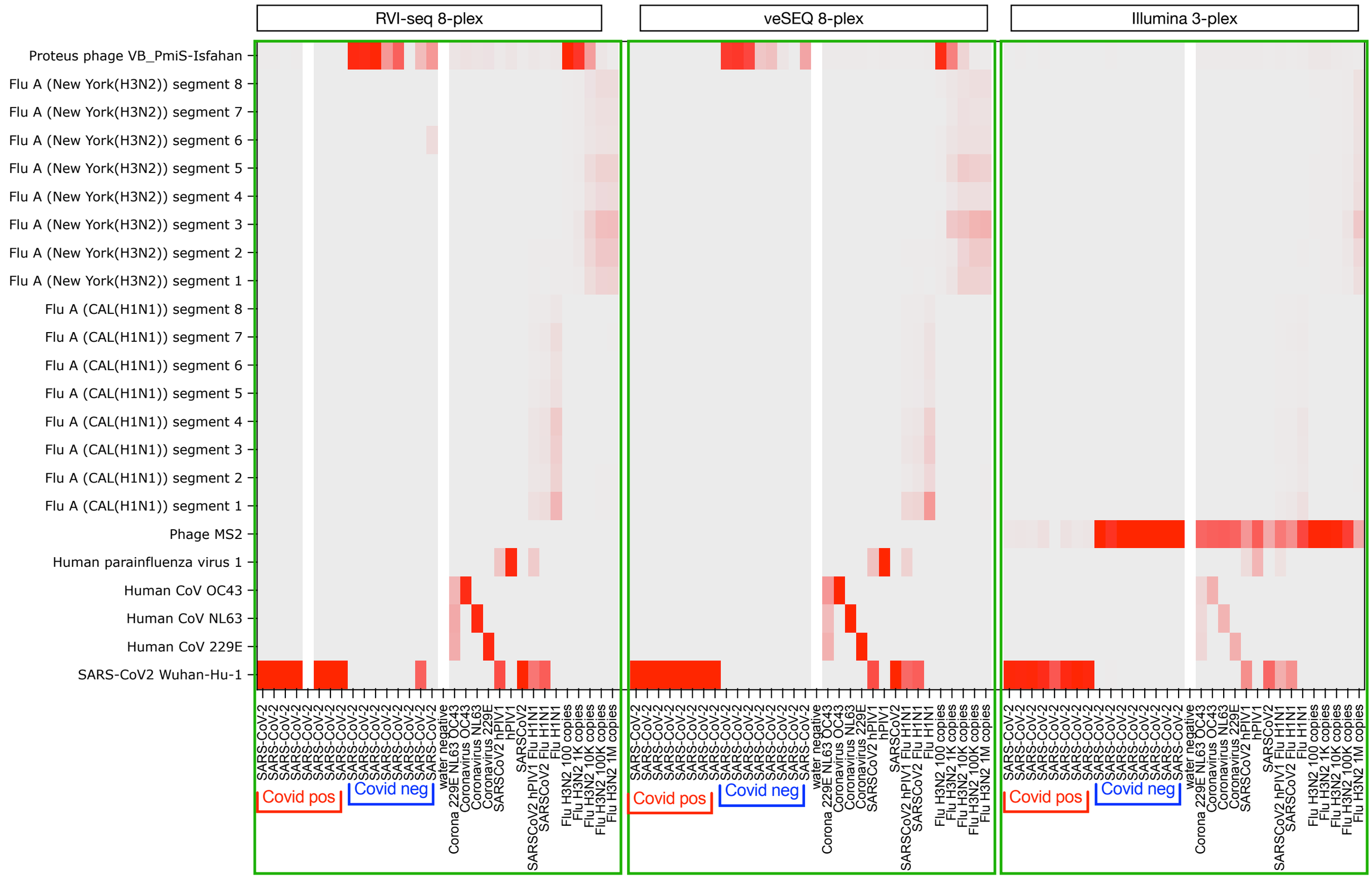

Figure S4 - Pilot 1 - Viral Bait Capture inStrain analysis demonstrating the high abundance of spiked-in phage MS2 in the Illumina dataset

Paired end reads of a minimum length of 100 bp were used for taxonomic classification with inStrain. Only viral taxa n=22/61 with a minimum abundance of 0.07% are presented; this encompasses 99.93% of all viral hits. The strong signal of the spike phage MS2 in the Illumina dataset accounted for a large proportion of sequences, which resulted in a markedly weaker signal for the influenza A virus and human seasonal coronavirus. The clinical positive SARS-CoV-2 samples exhibited less impact from the spike MS2 phage. Due to the impact of the MS2 spike on viral signal strength and to standardise with the AMPHEUS and RVI-seq methods, we did not spike MS2 into any further experiments.