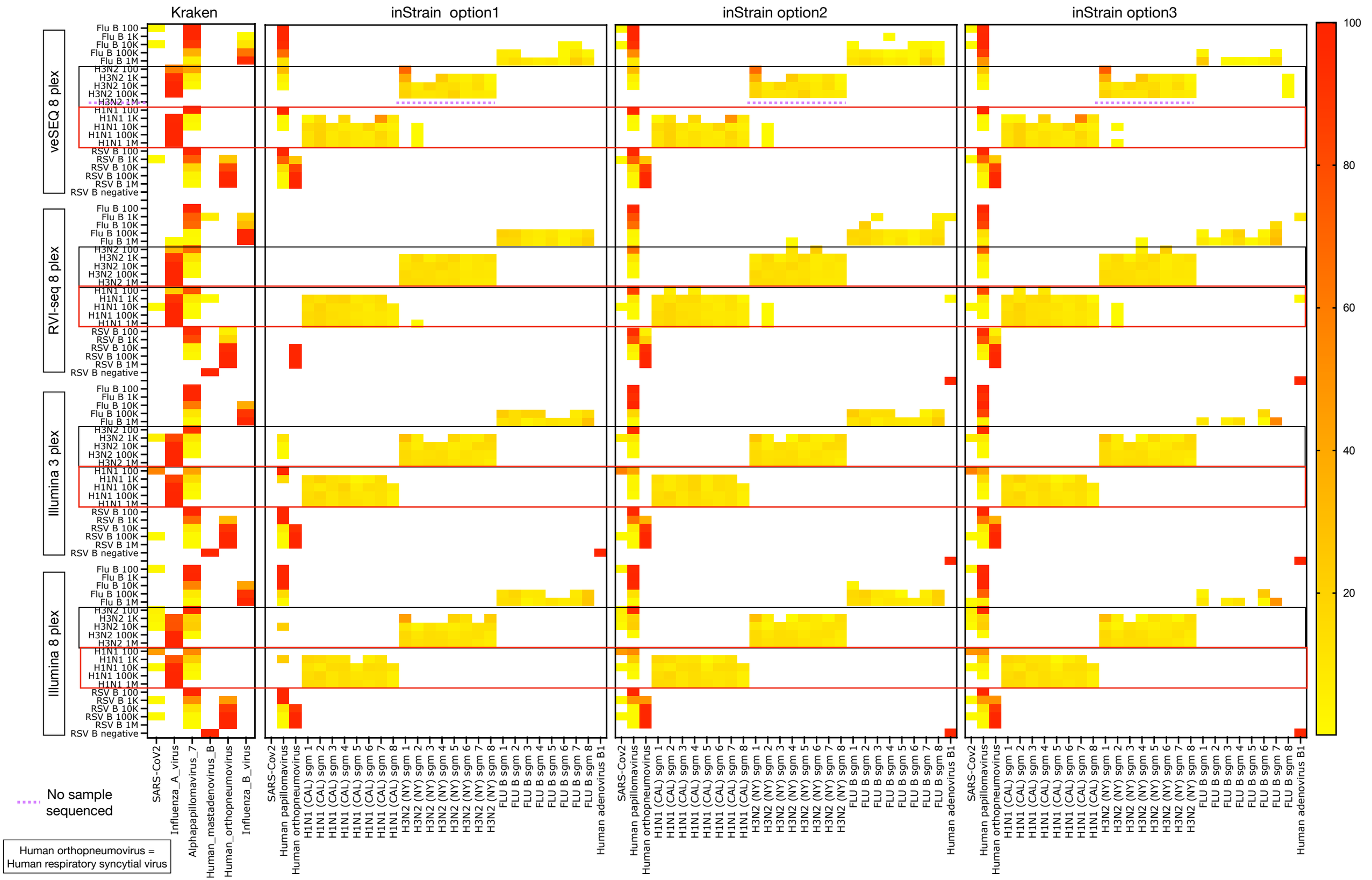

Supplementary Result Figure 8: NIBSC Flu sample analysis with Kraken and three different inStrain options

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.