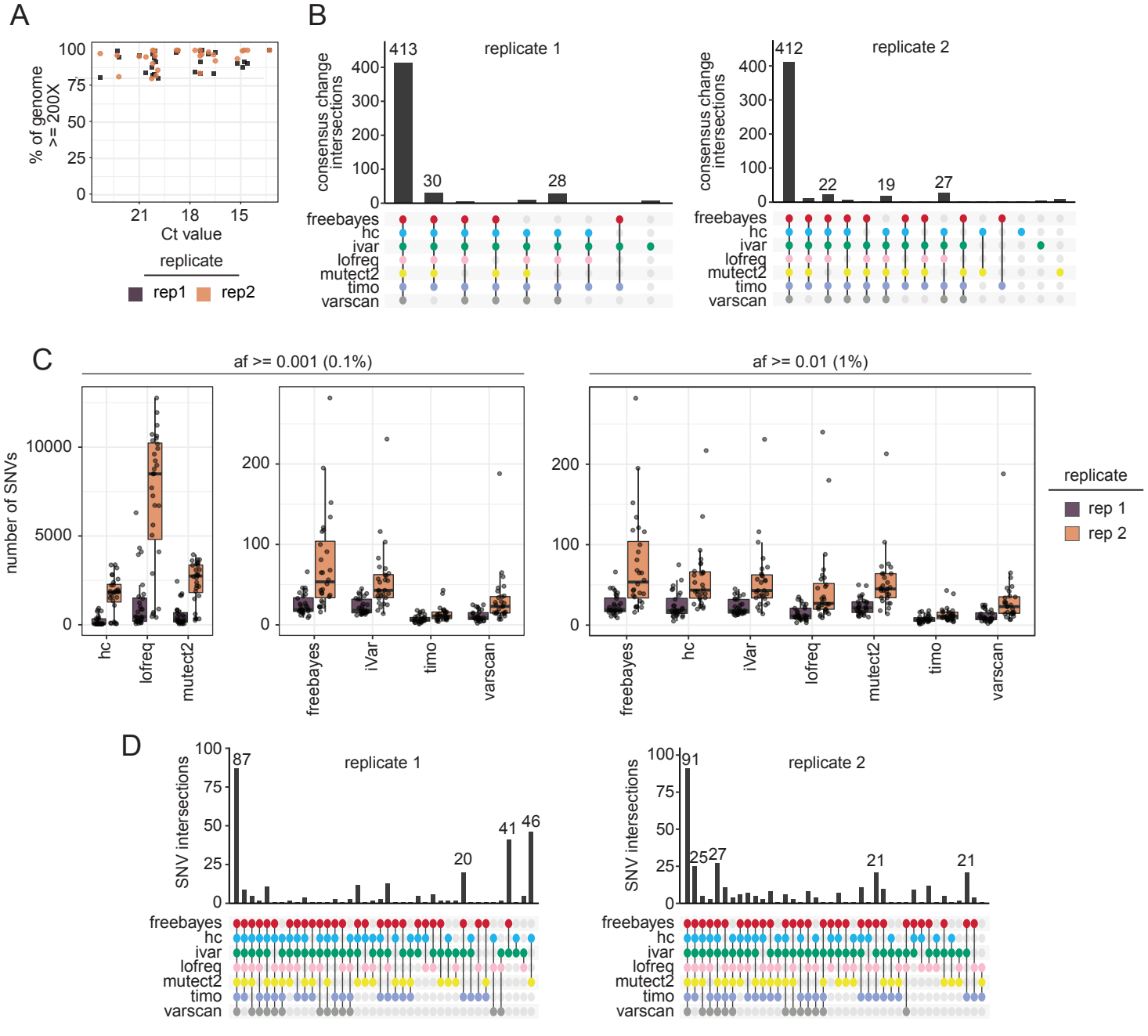

Figure S6. Quantification of majority and minority variants identified in data from SARS-CoV-2 clinical specimens. **(A)** Scatter plot showing Ct value against percentage of genome with coverage over 200x after filtering for only samples with 80% of the genome over the 200x cutoff. **(B)** Upset plot showing agreement of consensus changes between variant callers in each replicate using an allele frequency cutoff of 0.50 (≥50%) and coverage cutoff of 5x. Vertical bars indicate the size of the shared set of changes while dots and connecting lines show which callers share a given set of identified changes. **(C)** Box and whisker plot showing number of minor variants with indicated allele frequency cutoffs found in replicate 1 and replicate 2 sequencing data. Points represent individual samples. Boxes and whiskers show min, first quartile, median, third quartile and max for each replicate. Tools are grouped due to differences in scale on the y-axis. **(D)** Upset plot showing agreement of minority variants between all variant callers in each replicate using an allele frequency cutoff of 0.03 (3%) and coverage cutoff of 200x. Vertical bars indicate the size of the shared set of variants while dots and connecting lines show which callers share a given set of identified variants.