Figure S1. Sequencing coverage of the 30 intra-cDNA and inter-cDNA replicates. Sequencing coverage of the 98 ARTIC V3 panel amplicons for the 30 intra-cDNA and inter-cDNA replicates generated from five COVID-19-positive swab samples. Green bars represent the amplicons generated using the ARTIC original primer set, and orange bars show the amplicons generated using the alternative V3 primers.

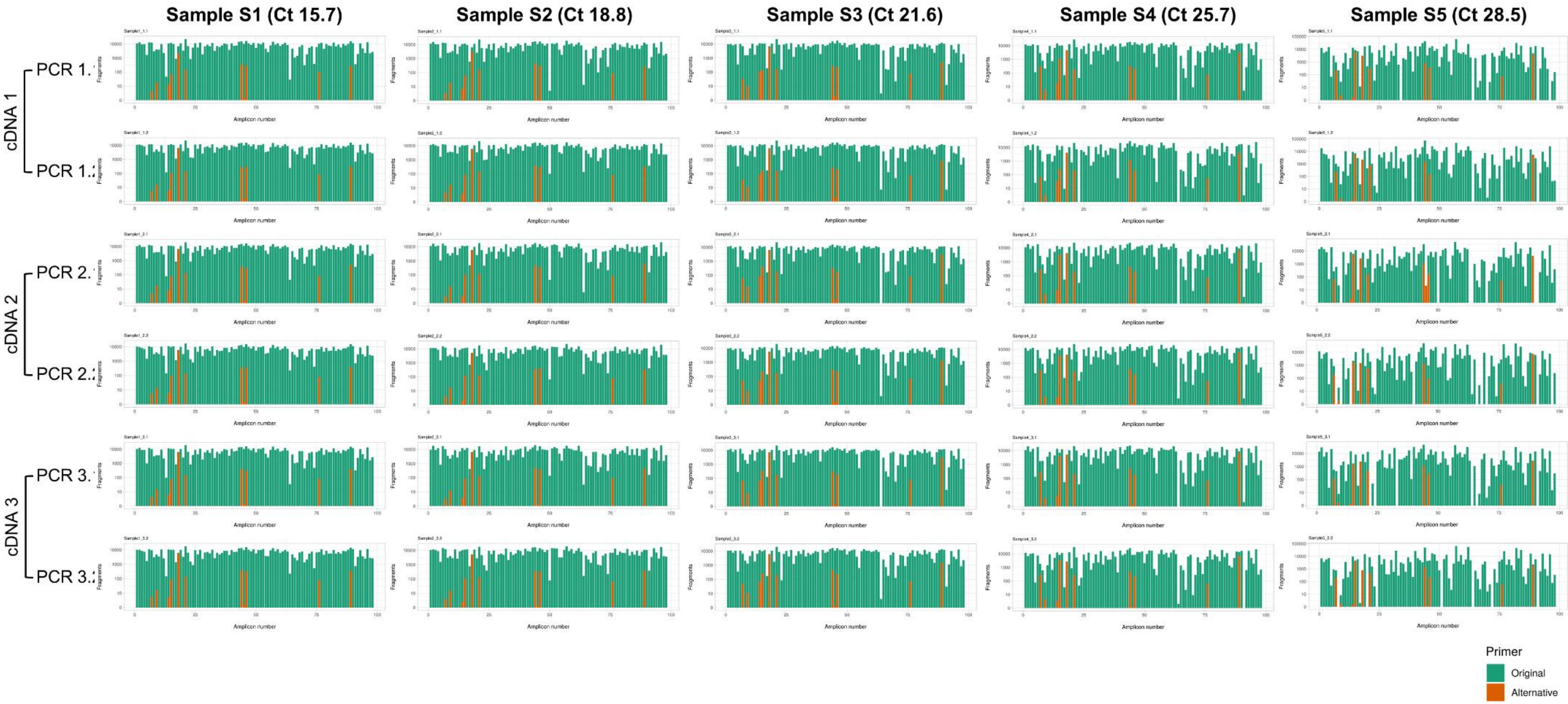

Figure S2. Coverage and genotypability are similar when amplifying higher cDNA volumes or pooling distinct replicates. (A) Ct frequency distribution of the 20 COVID-19-positive samples analyzed in (B) and (C). Ct values are rounded to the closest integer number. **(B)** Coverage and **(C)** genotypability when analyzing a single replicate generated from 10 µL cDNA or after merging the sequencing results of two replicates generated from 5 µL cDNA.

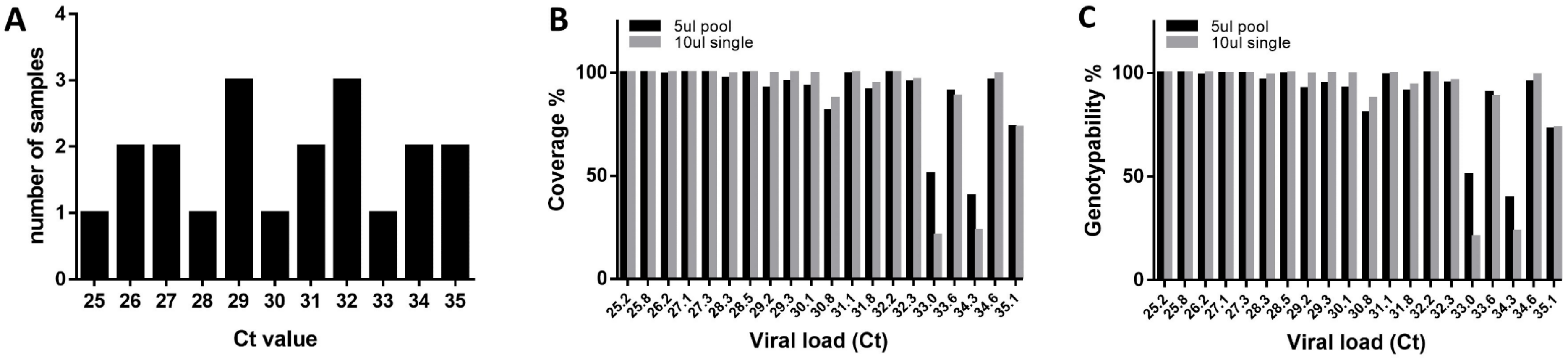

Figure S3. Distribution of Ct values across a cohort of 170 COVID-19 swab samples. The graph shows the frequency of COVID-19 swab samples showing a certain Ct (determined by RT-qPCR) in the cohort analyzed in Figure 5. Ct values are rounded to the closest integer number.