

S1 Table. Standard curve relationship between genome equivalents and Ct values. Synthetic T7 RNA transcripts corresponding to a 1,363 base pair segment of the SARS-CoV-2 nucleocapsid gene were serially diluted from 10^6 - 10^0 and evaluated in duplicate with RT-qPCR. The best-fit linear regression of the average Ct on the log₁₀-transformed standard values had slope -3.60971 and intercept 40.93733 ($R^2 = 0.99$).

Standard (GE/ul)	Replicate 1 (Ct)	Replicate 2 (Ct)	Average Ct
10^6	19.3	19.7	19.5
10^5	23.0	21.2	22.1
10^4	26.9	26.7	26.8
10^3	30.6	30.4	30.5
10^2	34.0	34.0	34.0
10^1	37.2	36.6	36.9
10^0	N/A	39.9	39.9