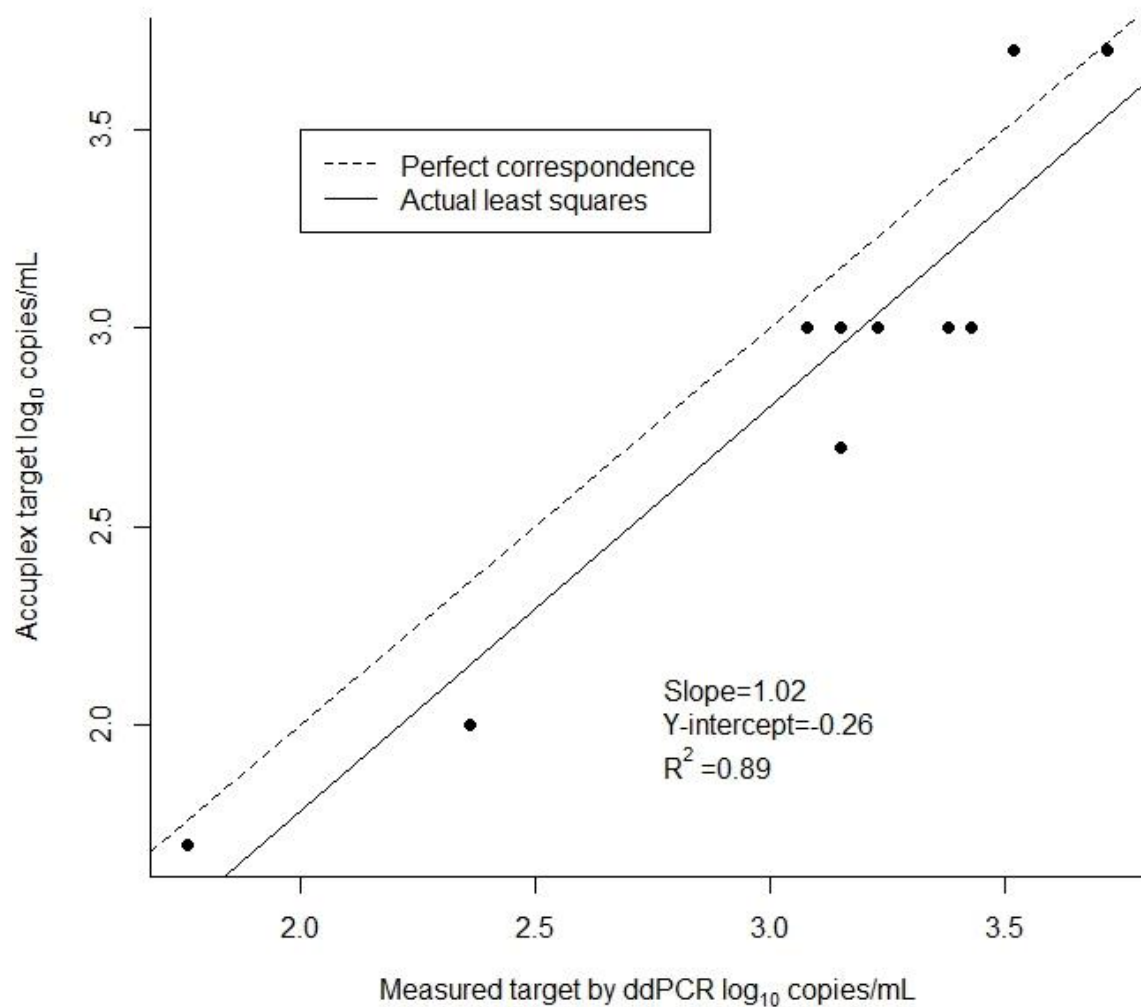
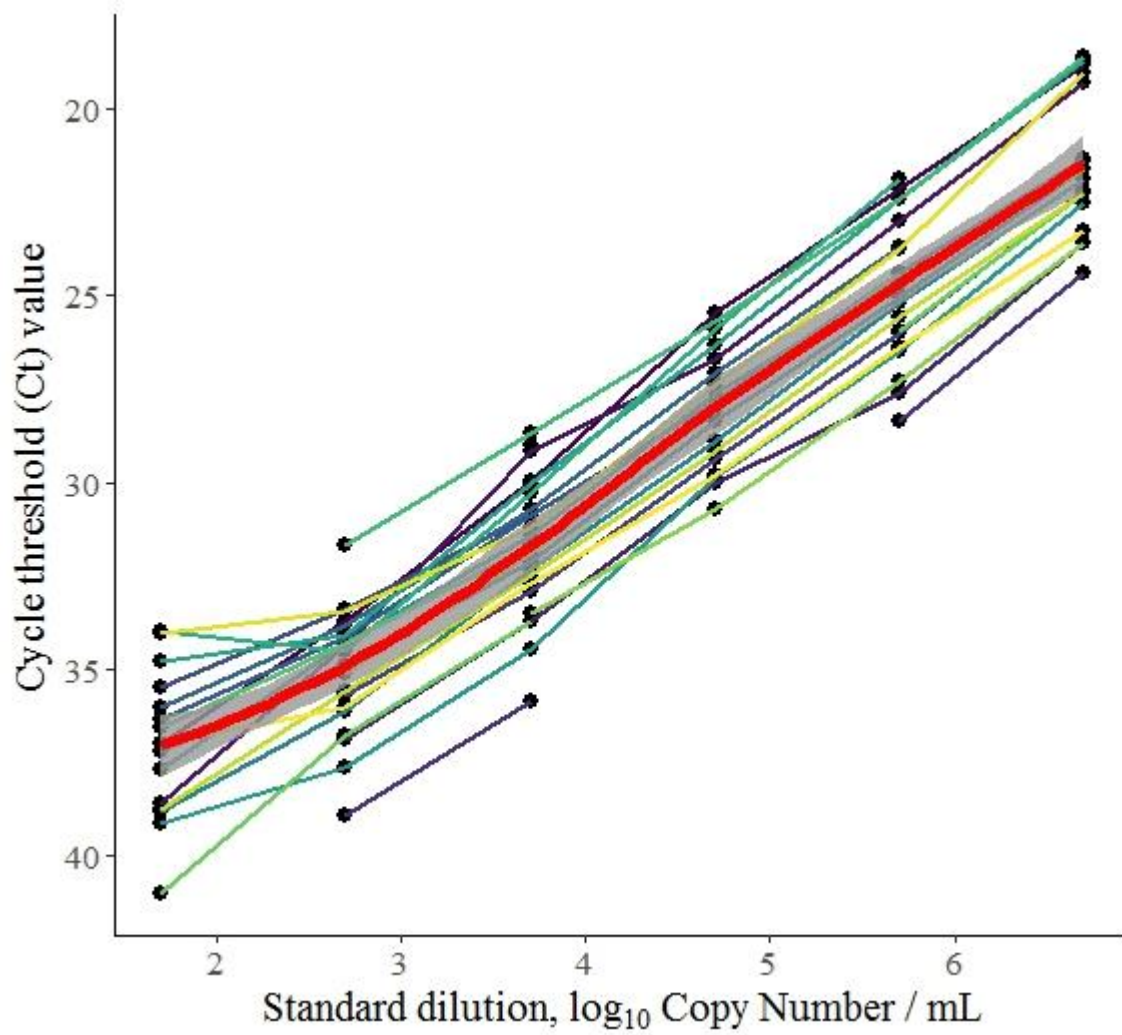
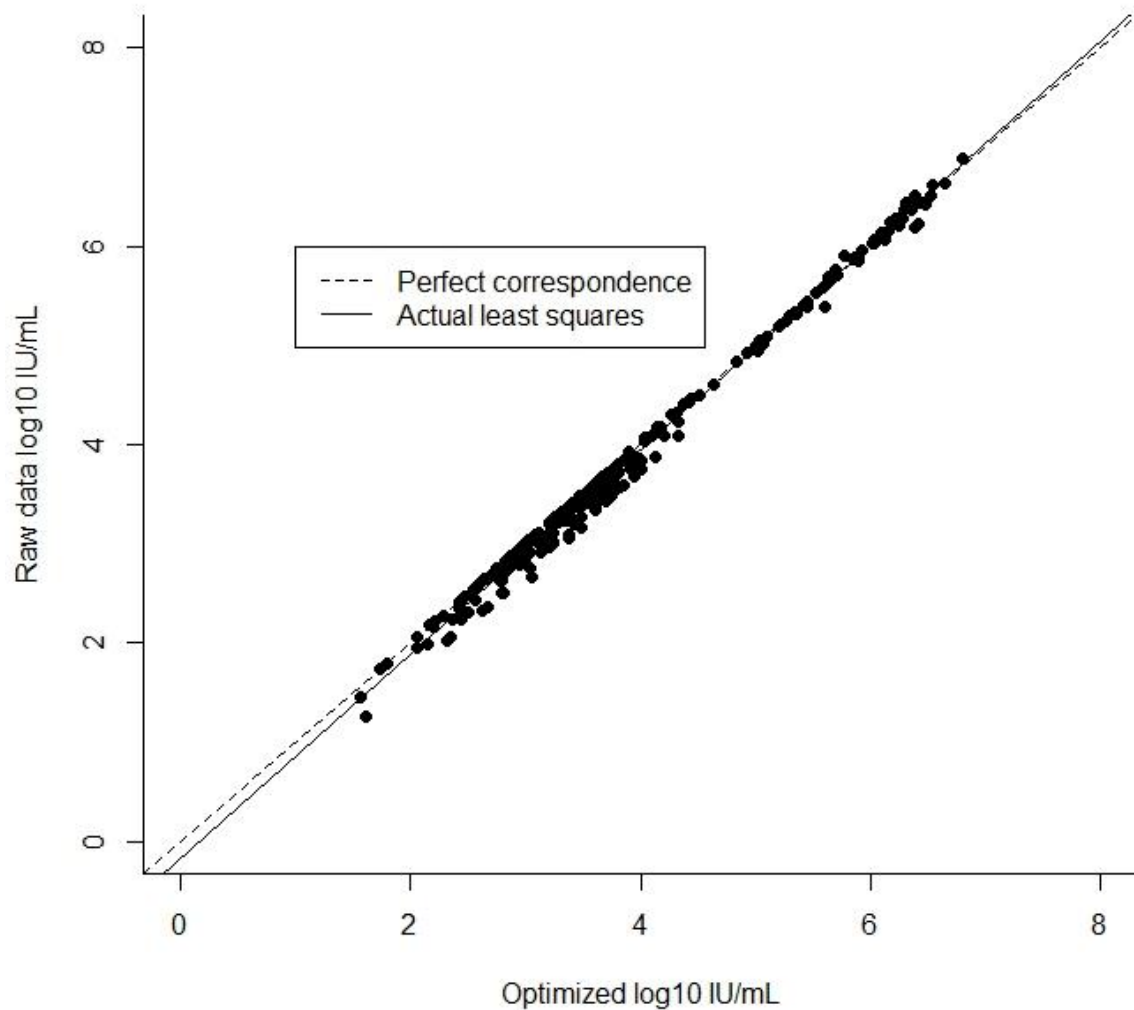




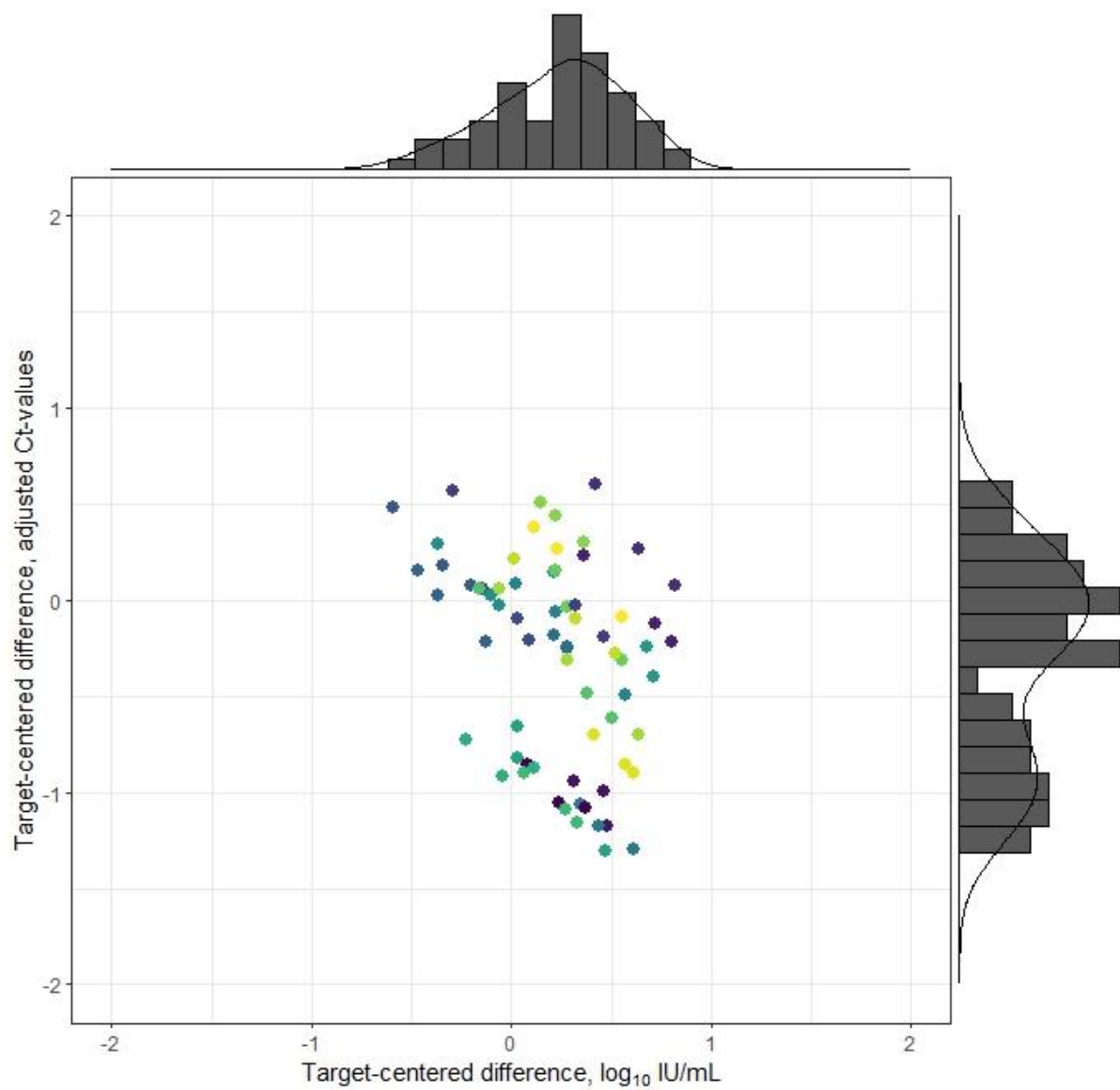
Supplemental Figure 1. Validation of reference test material prepared for ring trials. The association between the predicted target dilution of a standard SARS-CoV-2 vRNA reference genome (SeraCare Accuplex) and the actual dilution measured by digital PCR (“dPCR”). The dashed line indicates perfect correspondence (slope = 1, y-intercept = 0) and the least squares regression is shown by a solid line.



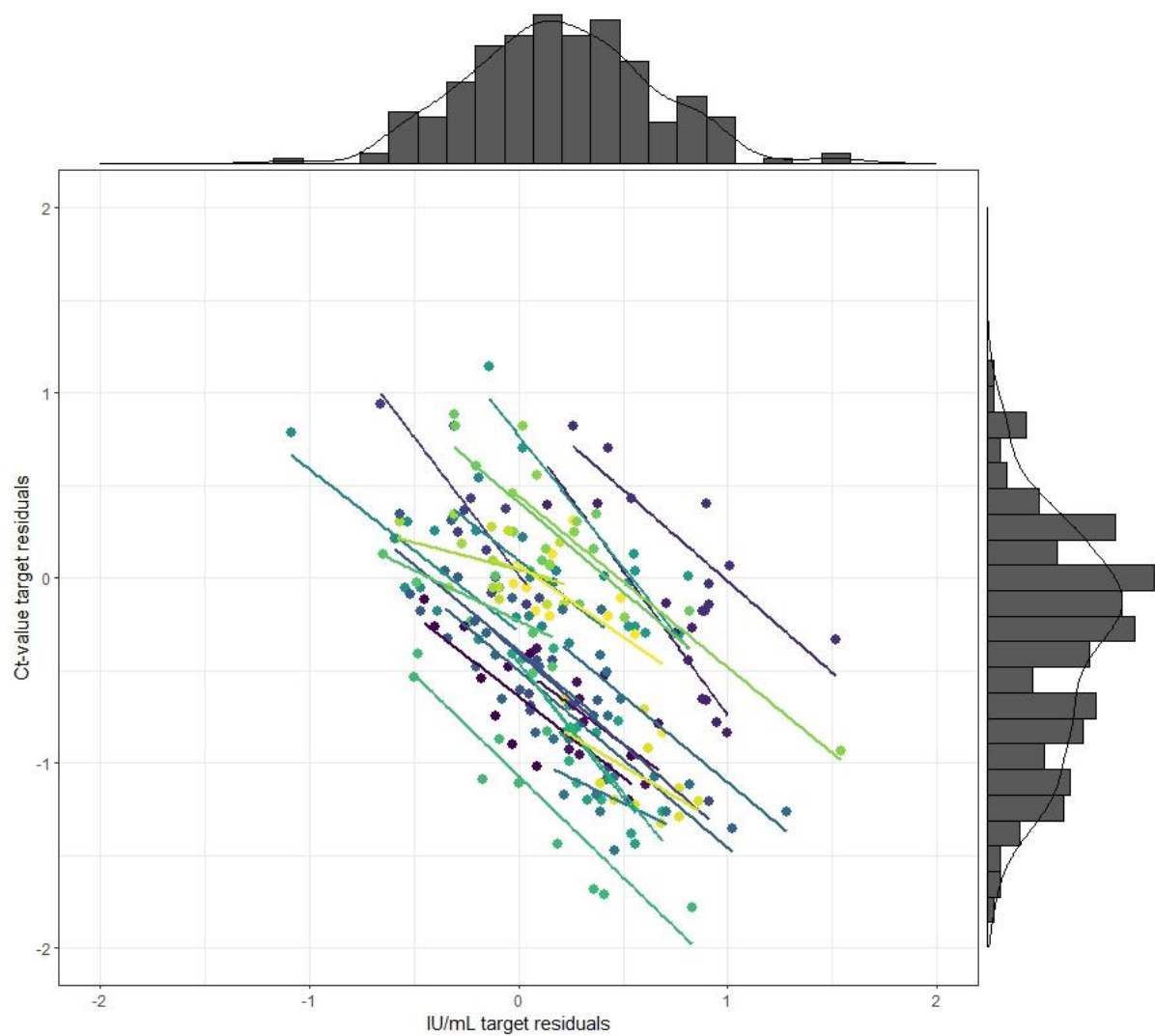
Supplemental Figure 2. Standard dilution curves from WHO reference standards by 9 laboratories using 15 unique test systems (23 curves) for the detection of SARS-CoV-2 vRNA. Curves from all 23 within-lab test systems are connected by lines and colored uniquely. A red line represents a loess curve fit of the data with a gray band representing the standard error of the curve.



Supplemental Figure 3. Estimation of the concentration (in copies per mL = IU/mL) of SARS-CoV-2 vRNA in clinical samples and in standard reference material based on a standard dilution curve. The conversion to IU/mL was performed on the lab-specific full curve (Figure S1) as well as on lab-specific optimized curves, wherein outliers were removed to obtain better fits. The dashed line shows a perfect correspondence between raw and optimized values (slope = 1, y-intercept = 0) and a solid line is drawn through the actual least squares fit.



Supplemental Figure 4. Target-centered Ct and IU/mL, scaled to log₁₀ copies, colored according to the 15 unique test systems in nine different participating laboratories for three clinical samples. The distribution of differences is shown on the upper and right axes as histograms with density plot overlays.



Supplemental Figure 5. Target-centered differences in Ct and IU/mL, scaled to $\log_{10}$ copies, colored according to the 15 unique test systems in nine different participating laboratories testing the concentration of SARS-CoV-2 vRNA in ten test samples containing a reference genome (SeraCare Accuplex) at various concentrations. The distribution of differences is shown on the upper and right axes as histograms with density plot overlays. Lines connect values of the ten samples from each of the 23 unique laboratory+test system combinations.