



Figure S1: Linearity (A) and agreement (B) of the SARS-CoV-2 signal in the E- and N-gene triplex RT-PCRs. Two EQA-samples with pre-known SARS-CoV-2 load were diluted in a SARS-CoV-2 free human respiratory sample to obtain clinical specimens with defined SARS-CoV-2 copies/ml. Mean threshold cycle (Ct) values (and standard deviations) from up to six runs are given (A). The Bland-Altman-Plot (B) shows the bias (mean difference between the Ct values of both methods, solid line) with the 95% limits of agreement (dashed lines).