

7 **Figure S1.** DMSO decreases negative droplet intensity in RT-ddPCR assays. The RT-  
8 ddPCR reactions containing 0%, 2.5%, or 5% DMSO were performed for a Chelex-lowTE sample  
9 prepared with the ATCC SARS-CoV-2 virions and 293FT cells using N1 and cRPP30 (left panel) or N2  
10 and RPP30 (right panel). The grey clusters represent negative droplets; blue and green clusters  
11 represent Fam and Hex positive droplets, respectively; and orange clusters represent double positive  
12 droplets.

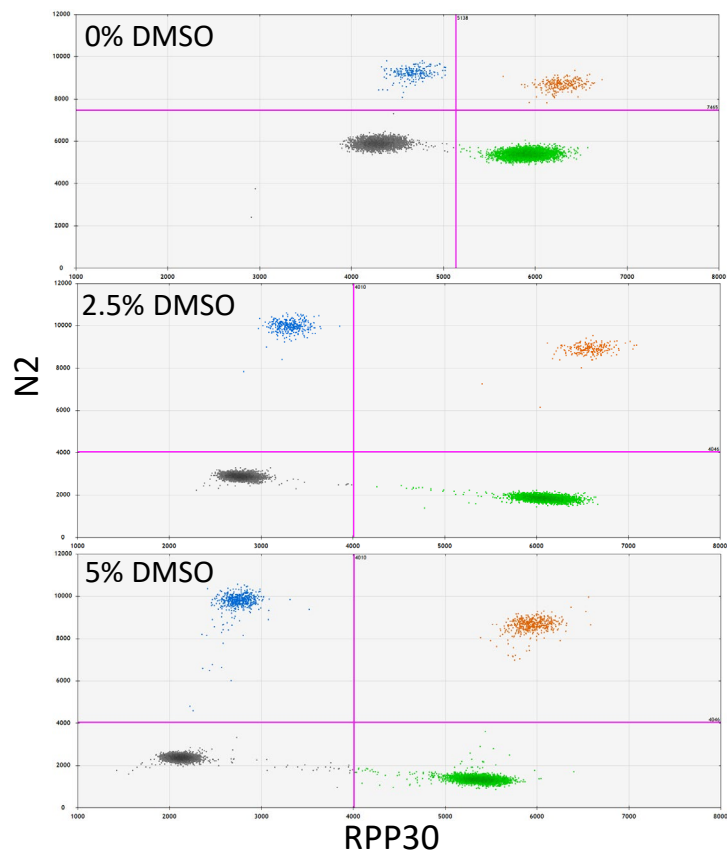
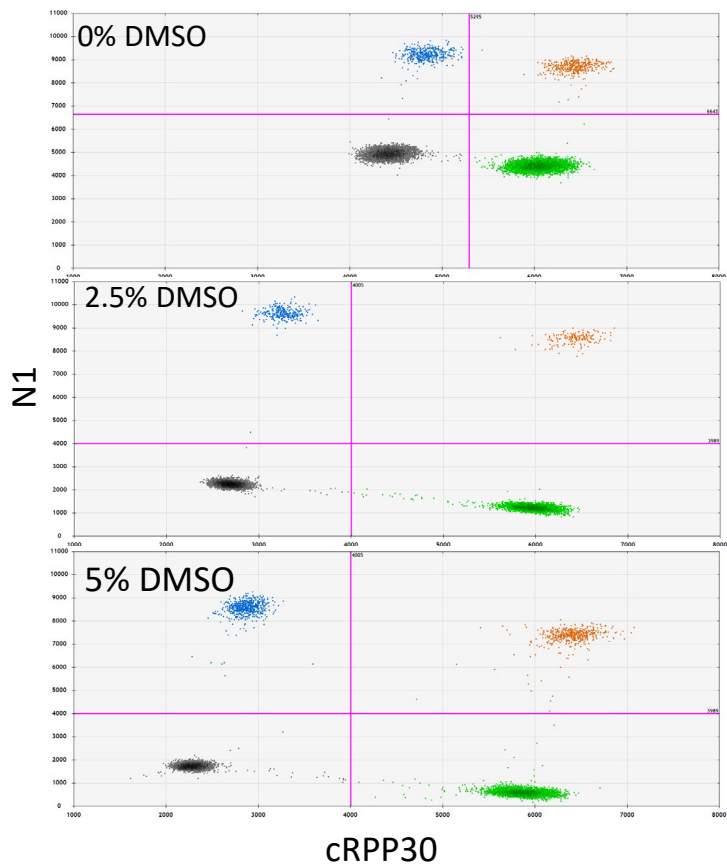
13 **Figure S2.** SARS-CoV-2 prepared in different buffers used for RT-qPCR without RNA-  
14 extraction. **(A)** Samples were diluted in H<sub>2</sub>O as indicated at the bottom. Expected\_Ct refers to Ct  
15 calculated based on Ct from extracted RNA normalized with added virion numbers after dilution using the  
16  $\Delta$ Ct method. **(B)** Buffer compatibility in RT-qPCR. Sample RNA, not heated and 5  $\mu$ l of which contained  
17 materials extracted from 6,250 virions. Other samples were heated in the presence of Chelex, of which  
18 undiluted samples also contained 6,250 virions per 5  $\mu$ l. Samples were diluted in H<sub>2</sub>O. Samples with  
19 undetermined Ct values were plotted as Ct 40. The NEB Luna RT-qPCR kit and NEB-Luna-Program I  
20 was used. NTC, no-template control.

21 **Figure S3.** Tris EDTA and DMSO containing buffers. **(A)** RT-qPCR of samples with heat-  
22 inactivated ATCC SARS-CoV-2 virions. 5  $\mu$ l of samples were used for one reaction in RT-qPCR except  
23 that samples in MEM  $\alpha$  were diluted 1:1 with H<sub>2</sub>O. Samples with undetermined Ct values were plotted as  
24 Ct 40. The NEB Luna RT-qPCR kit and NEB-Luna-Program I was used. **(B)** RT-ddPCR of saliva samples  
25 with heat-inactivated ATCC SARS-CoV-2 virions. The Chelex was prepared in H<sub>2</sub>O, lowTE or TED99

1 (lowTE with 99% DMSO). RNA-kit refers to RNA extracted with the RNeasy Protect Saliva Mini Kit. NTC,  
2 no-template control.

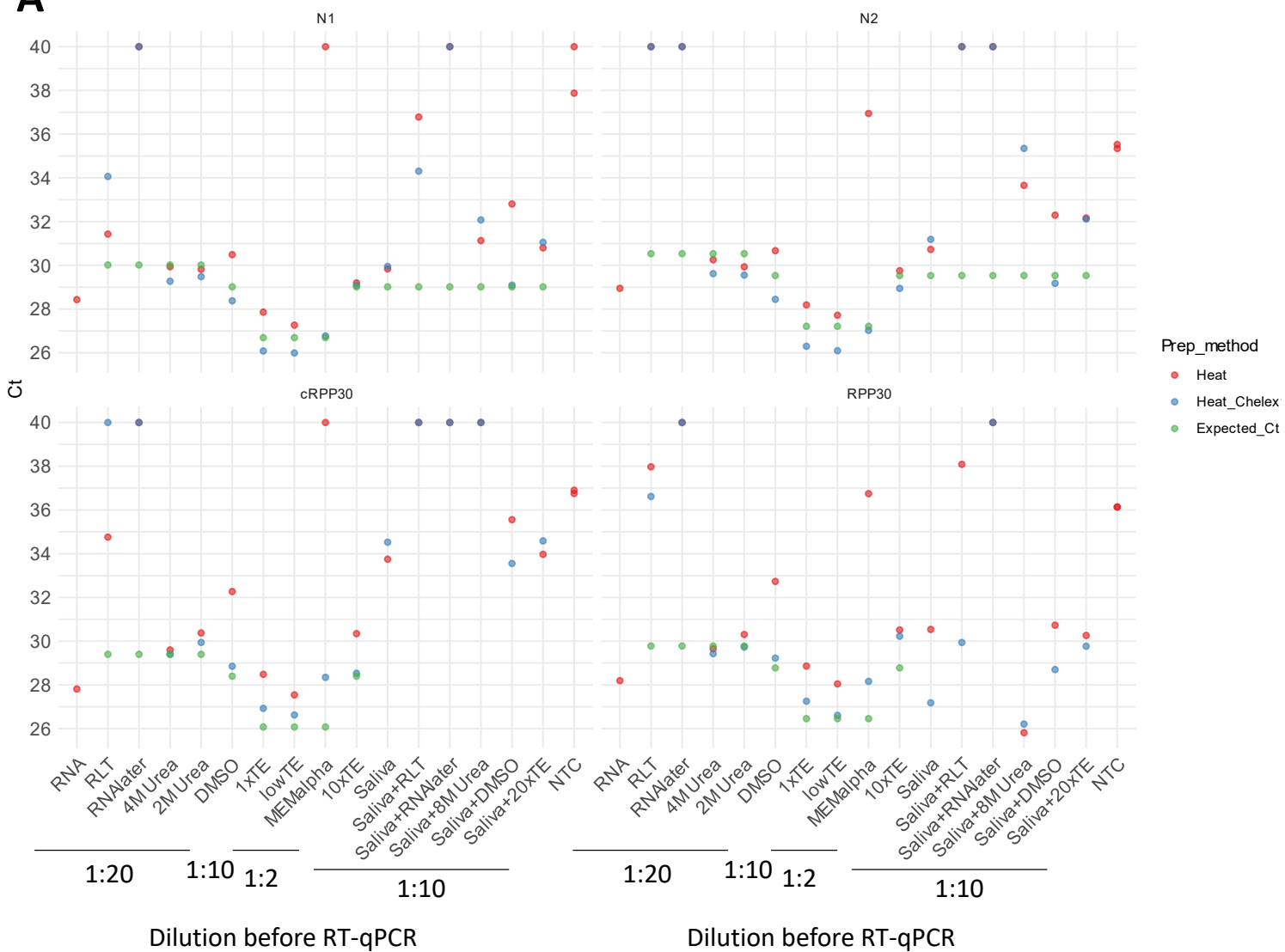
3 **Figure S4.** Optimization of the NEB Luna RT-qPCR assay. Extracted RNA samples were  
4 serial diluted and assayed either using 2.5 µl sample in a 10 reaction volume or 5 µl in a 20 µl reaction,  
5 and using a longer PCR protocol (I: 10 seconds of denature and 40 seconds of annealing/extension) or a  
6 shorter PCR protocol (II: 5 seconds of denature and 20 seconds of annealing/extension). NTC, no-  
7 template control.

# Figure S1

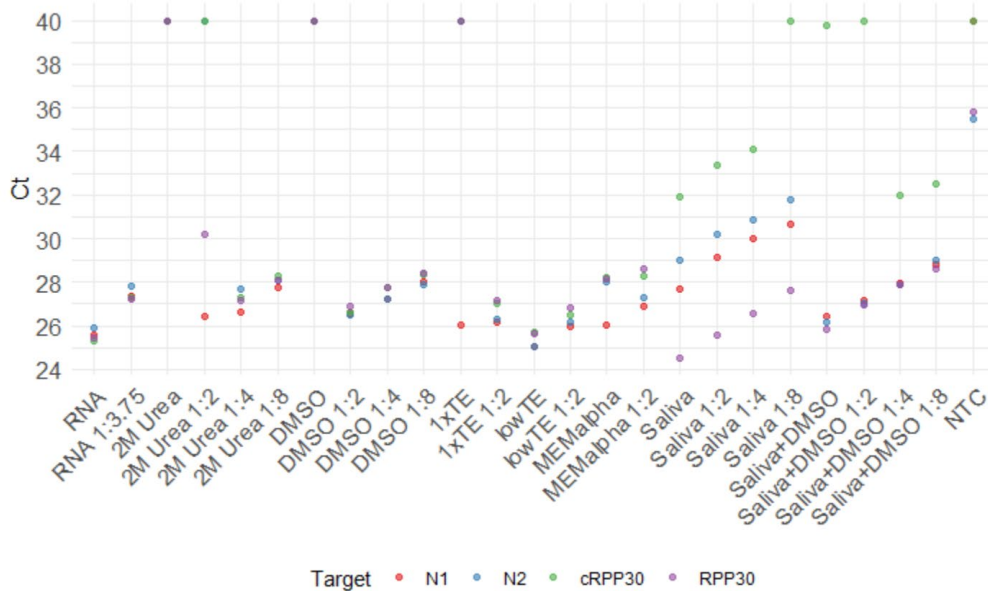


# Figure S2

**A**



**B**





## Figure S4

