ddPCR: a more sensitive and accurate tool for SARS-CoV-2

2 detection in low viral load specimens

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- Word count (abstract): 246

30 Word count (main text): 2114

Abstract

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Background: Real-Time PCR (RT-PCR) is widely used as the gold standard for

clinical detection of SARS-CoV-2. However, due to the low viral load in patient

throat and the limitation of RT-PCR, significant numbers of false negative reports are

inevitable, which should not be ignored.

37 **Methods:** We explored the feasibility of droplet digital PCR (ddPCR) to detect

38 SARS-CoV-2 from 57 clinical pharyngeal swab samples and compared with RT-PCR

in terms of the sensitivity and accuracy. Among 57 samples, all of which were

40 reported as negative nucleic acid by officially approved clinical RT-PCR detection, 43

samples were collected from suspected patients with fever in clinic, and 14 were from

42 supposed convalescents who were about to discharge after treatment. The experiment

43 was double-blind.

44 **Results:** The lower limit of detection of the optimized ddPCR is at least 500 times

45 lower than that of RT-PCR. The overall accuracy of ddPCR for clinical detection is

46 94.3 %. 33 out of 35 negative pharyngeal swab samples checked by RT-PCR were

47 correctly judged by ddPCR based on the follow-up investigation. In addition, 9 out of

48 14 (64.2 %) supposed convalescents with negative nucleic acid test twice by RT-PCR

were positive by ddPCR detection.

50 Conclusions: ddPCR shows superiority for clinical detection of SARS-CoV-2 to

51 reduce the false negatives, which could be a powerful complement to the current

52 standard RT-PCR. Before the ddPCR to be approved for diagnosis, the current clinical

53 practice that the convalescent continues to be quarantined for 2 weeks is reasonable

and necessary.

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Key words: SARS-CoV-2; droplet digital PCR; RT-PCR; clinical detection

Introduction

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The recent outbreak of coronavirus disease 2019 (COVID-19) caused by the infection of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) poses a great threat to public health all over the world. 1,2 On February 28, 2020, the world health organization (WHO) has upgraded the global risk level of this viral pneumonia from "high" to "very high". According to WHO and Chinese Center for Disease Control and Prevention (CDC), the current gold standard for the diagnosis of SARS-CoV-2 infection is based on the real-time fluorescent quantitative PCR (RT-PCR), which means that the nucleic acid of SARS-CoV-2 could be detected in patient specimens using RT-PCR.^{3,4} However, the disadvantages of insufficient detection of RT-PCR are more and more prominent, especially the problem of detection dynamic range in the clinical application. At present, it has been found in clinical practice that some patients had fever, and chest CT showed symptoms of suspected viral pneumonia such as lower lobe lesions of the lungs, but the nucleic acid test of pharyngeal swab did not show positive results until 5-6 days after the onset of viral pneumonia. It was estimated that only 30 %-60 % positive results can be obtained among COVID-19 patients that further confirmed by chest CT.⁵ This might be explained by the relatively low viral load in the throat of patients and the sensitivity limitation of RT-PCR technology, which inevitably produced the false negatives during the clinical diagnosis, leading to a potential risk of viral transmission. Besides, supposed convalescent, who is about to discharge, also need multiple tests with negative results for confirmation. Therefore, it is a pressing needs for a more sensitive and accurate detection method for the pathogenic detection. Digital PCR is based on the principles of limited dilution, end-point PCR, and Poisson statistics, with absolute quantification as its heart.⁶ It has broader dynamic range without external interference and robustness to variations in PCR efficiency. 7-9 In 2011, Hindson developed the droplet digital PCR (ddPCR) technology based on traditional digital PCR. 10 The reaction mixture can be divided into tens of thousands of nanodroplets during the process. These vast and highly consistent oil droplets

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substantially improve the detection dynamic range and accuracy of digital PCR in a low-cost and practical format.¹¹ In recent years, this technology has been widely used, such as analysis of absolute viral load from clinical samples, analysis of gene copy number variation, rare allele detection, gene expression, microRNA analysis and genome edit detection et al. 12,13,14,15 Here, taking the advantages of ddPCR, we optimized the preparation of pharyngeal swab samples, and develop a workflow of ddPCR to detect SARS-CoV-2 using Chinese CDC approved primer and probe sets. Based on the results of this optimized ddPCR system, we showed that the overall accuracy of the ddPCR for clinical pathogen detection is 94.3 %, and 64.2 % of supposed convalescents with two consecutive negative nucleic acid tests by RT-PCR still carry SARS-CoV-2. **Materials and methods Ethics statement** This study was approved by the Ethics Committee of the Renmin Hospital and Zhongnan Hospital of Wuhan University. The analysis was performed on existing samples collected during standard diagnostic tests, posing no extra burden to patients, as described previously.² **Specimen collection and RNA extraction** Pharyngeal swab samples were obtained from clinical suspected patients with fever or rehabilitation quasi-discharged patients of COVID-19 at Renmin Hospital and Zhongnan Hospital of Wuhan University according to the interim guidance of WHO. Pharyngeal swabs were soaked in 500 µl PBS and vortexed with diameter of 3 mm beads (Novastar, China) for 15 seconds immediately. Total RNA was extracted from the supernatant using QIAamp viral RNA mini kit (Qiagen) following manufacturer's instruction. First strand cDNA was synthesized using PrimeScript RT Master Mix (TakaRa) with random primer and oligo dT primer.

118 **Primers and probes** 119 The primers and probes targeted the ORF1ab and N of SARS-CoV-2 according to 120 Chinese CDC. Target 1 (ORF1ab), forward: 5'-CCCTGTGGGTTTTACACTTAA-3', 121 reverse: 5'-ACGATTGTGCATCAGCTGA-3', probe: 122 5'-FAM-CCGTCTGCGGTATGTGGAAAGGTTATGG-BHQ1-3'; 123 Target 2 (N), forward: 5'-GGGGAACTTCTCCTGCTAGAAT-3', 124 reverse: 5'-CAGACATTTTGCTCTCAAGCTG-3', probe: 5'-FAM-TTGCTGCTGCTTGACAGATT-TAMRA-3'. 16 125 126 127 **Droplet Digital PCR workflow** 128 All the procedure follow the manufacture instructions of the QX200 Droplet Digital 129 PCR System using supermix for probe (no dUTP) (Bio-Rad). Briefly, the TaqMan 130 PCR reaction mixture was assembled from a 2× supermix for probe (no dUTP) 131 (Bio-Rad), 20× primer and probes (final concentrations of 900 and 250 nM, 132 respectively) and template (variable volume) in a final volume of 20 µl. Twenty 133 microliters of each reaction mix was converted to droplets with the QX200 droplet 134 generator (Bio-Rad). Droplet-partitioned samples were then transferred to a 96-well 135 plate, sealed and cycled in a T100 Thermal Cycler (Bio-Rad) under the following 136 cycling protocol: 95 °C for 10 min (DNA polymerase activation), followed by 40 cycles of 94 °C for 30 s (denaturation) and 60 °C for 1 min (annealing) followed by an 137 infinite 4-degree hold. The cycled plate was then transferred and read in the FAM 138 139 channels using the QX200 reader (Bio-Rad). 140 RT-PCR 141 142 The primers and probes used in ddPCR are also used in RT-PCR. A 30-µl reaction was 143 set up containing 10 µl of RNA, 18.5 µl of reaction buffer provided with the one step 144 RT-PCR system and 1.5 µl enzyme mix (BGI BIOTECHNOLOGY). Thermal cycling 145 was performed at 50 °C for 20 min for reverse transcription, followed by 95°C for 10 min and then 40 cycles of 95 °C for 15 s, 60 °C for 30 s in BIO-RAD CFX96 Touch 146

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RT-PCR system.

Data statistical analysis

Analysis of the ddPCR data was performed with Quanta Soft analysis software v.1.7.4.0917 (Bio-Rad) that accompanied the droplet reader calculate the concentration of the target DNA sequences, along with their Poisson-based 95 % confidence intervals. The positive populations for each primer/probe are identified using positive and negative controls with single (i.e., not multiplexed) primer–probe sets. The concentration reported by QuantaSoft equals copies of template per microliter of the final 1× ddPCR reaction, which was also used in all the results. In addition, plots of linear regression were conducted with GraphPad Prism 7.00, and probit analysis for lower limit of detection (LLoD) was conducted with StatsDirect software v3.2.9. Lower limit of quantitation (LLoQ) and LLoD were defined as the lowest concentration at which 95 % and 50 % of positive samples were detected, respectively.

Results

Comparison of the lower limit between ddPCR and the standard RT-PCR

Using a manual threshold to define positivity, 9 % of negative controls (3/32) were scored as positive due to one single positive droplet (data not shown). The presence of two positive droplets or more was not observed for negative controls. Serial dilutions of a positive control DNA fragment of SARS-CoV-2 were tested with primers/probe sets targeting ORF1ab and N of SARS-CoV-2, respectively for ddPCR. It shows good linearity (R2: 0.9932 and 0.9824, respectively) (Fig. 1A and 1B). Reportable range of ddPCR is from 10 copies/μl to 2500 copies/μl for both ORF1ab and N primes/probe sets. In contrast, the dynamic range of RT-PCR is from 50 copies/μl to 10⁵ copies/μl for both ORF1ab and N primes/probe sets (Fig. 1C and 1D). To define the limit of quantification of ddPCR, five low concentrations of plasmid control were analyzed with 8 replicates. The lower limit of quantitation (LLoQ) of the optimized ddPCR is 1.003 copies/μl and 0.415 copies/μl for ORF1ab and N primers/probe sets, respectively. The lower limit of detection (LLoD) of the optimized ddPCR is 0.109

178 copies/ul and 0.021 copies/ul for ORF1ab and N primers/probe sets, respectively (Fig. 179 2), which is at least 500 times lower than the RT-PCR detection kit used in current 180 clinical test. Therefore, the ddPCR is more sensitive for samples with low level 181 analyte. 182 Detection of SARS-CoV-2 from patient specimens with ddPCR 183 184 57 clinical pharyngeal swab samples (Fig. 3), which were judged to be negative by 185 both officially approved clinical RT-PCR detection and the commercial RT-PCR detection kit for double check (generally referred to as RT-PCR), were tested with 186 187 ddPCR in double-blind. We did not know any information, results of clinical 188 diagnosis and status of enrolled patients during the tests. The follow-up investigation 189 revealed those information after ddPCR tests. Compared with the information and 190 clinical diagnosis, our results show that the overall accuracy of the optimized ddPCR is 94.3 % and 64.2 % of supposed convalescents are still carrying SARS-CoV-2. 191 192 Details are as follows (Fig. 3) (Table 1 and 2): 193 Firstly, among 27 febrile suspected patients whose SARS-CoV-2 nucleic acid were 194 negative initially tested by RT-PCR, 25 out of 27 were detected with ddPCR as 195 positive and 2 out of 27 were negative. However, all 27 patients were diagnosed with SARS-CoV-2 infection by chest CT as well as RT-PCR in subsequent follow-up 196 197 investigations, and all of them were hospitalized. As a result, 92.6 % of patients with false negative nucleic acid test could be identified as positive by the optimized ddPCR 198 199 (Table 1). Secondly, pharyngeal swabs of 8 febrile patients with negative results tested by 200 RT-PCR were also tested negative by ddPCR. In the follow-up investigation 201 202 COVID-19 was excluded based on the normal results of chest CT and RT-PCR (Table 203 1). 204 Thirdly, pharyngeal swabs collected from 8 febrile suspected patients in the clinic 205 recently with negative nucleic acid tests by RT-PCR, were detected positive by ddPCR. However, chest CT of these 8 patients did not show any abnormalities upon 206

their first visit the clinic. According to official clinical guidelines, these 8 patients

208 were home guarantined and no further followed-up by us (Table 1). 209 Finally, pharyngeal swabs of 14 supposed convalescent were tested negative in two 210 consecutive tests by RT-PCR (Table 2). However, using ddPCR, 9 out of 14 were 211 positive with a positive rate of 64.2 %. Therefore, the current clinical practice that the 212 convalescent continues to be quarantined for 2 weeks is reasonable and necessary. 213 In conclusion, compared with RT-PCR, ddPCR show superiority for clinical detection 214 of SARS-CoV-2 to reduce the false negatives, which could be a powerful complement 215 to the current standard RT-PCR. 216 217 Discussion 218 More and more nucleic acid detection kits have been developed for SARS-CoV-2 219 recently based on RT-PCR to meet the requirement of large-scale clinical molecular 220 diagnosis. It has been reported that 6 kinds of RT-PCR detection kits were compared 221 and analyzed for their detection performance. Results showed that there are 222 differences in the detection ability of these kits for weakly positive samples, and the accuracy, sensitivity and reproducibility of some reagents are not ideal 17 In the 223 224 meantime, many efforts have been focusing on developing better and complementary 225 technology for clinical diagnosis of SARS-CoV-2, due to the limited sensitivity and 226 precision of RT-PCR for viral quantitation. Different from RT-PCR that the data are 2.2.7 measured from a single amplification curve and a Cq value, which is highly dependent on reaction efficiency, primer dimers and sample contaminants, ddPCR is 228 229 measured at reaction end point which virtually eliminates these potential pitfalls. 230 Results in this work proved that ddPCR is more sensitive (Fig. 1) and accurate for low 231 viral load diagnosis (Fig. 2), which can greatly reduce the false negatives detection 232 (Fig 3). 233 Based on two primers/probe sets targeting ORF1ab and N of SARS-CoV-2, results 234 showed that N primers/probe set was more sensitive compared to that of ORF1ab. 235 Among 42 samples that were judged as positive with ddPCR, 40 in 42 were detected 236 as positive by N primers/probe set, and 12 in 42 were detected as positive by ORF1ab 237 primers/probe set. This could be explained by the subgenomic RNA discontinuous

238 replication and transcription model of coronavirus. The genome RNA of 239 SARS-CoV-2 encodes single copy of ORF1ab and N, respectively. In contrast, a 240 nested set of around 10 subgenomic RNAs (sgRNAs), each of which encodes one 241 copy of N, are synthesized by viral replication and transcription complex in a manner of discontinuous transcription .^{18,19,20} Therefore, the copy numbers of N gene is 242 significantly higher than that of ORF1ab gene in SARS-CoV-2 infected cells. 243 244 Although 2 patients, who were clinically confirmed by chest CT and RT-PCR 245 subsequently, were reported as negative nucleic acid in pharyngeal swabs by our ddPCR, leading to 2 false negative reports by ddPCR in 35 cases (5.7 % missing rate), 246 247 the overall accuracy of SARS-CoV-2 detection is significantly improved, which will 248 benefit to the early diagnosis, intervention and treatment. 249 Notably, 64.2 % supposed convalescent patients, who are negative for pharyngeal 250 swab nucleic acid tests twice by RT-PCR, are still carrying SARS-CoV-2 based on our 251 work. Although there is no evidence that such COVID-19 convalescent carrying 252 SARS-CoV-2 will be infectious to other healthy person, the risk still exists. Therefore, 253 the current clinical practice that the convalescent continues to be quarantined for 2 254 weeks is reasonable and necessary. And we recommend that ddPCR could be a 255 complement to the current standard RT-PCR to re-confirm the convalescent, which 256 will benefit to reduce the risk of the SARS-CoV-2 epidemic and social panic. 257 **Author Contributions** 258 259 YC, KL conceptualized the study design. TS, WH, LD, TC, YX, and GC recruited the 260 patients, collected specimens, collected demographic, clinical data; XL, MG, QZ, XW, 261 YY, MS, DG and ZH did the laboratory tests. JF, YL and QZ plotted the figures; XL, 2.62 MG, JF and YC analyzed the data; ZH, XK, YL, YlL and YC interpreted the 263 results; JF wrote the initial drafts of the manuscript; YC and KL revised the 264 manuscript and FL and KX commented on it. All authors read and approved the final 265 report. 266

Funding

268 This study was supported by National Science and Technology Major Project 269 (#2018ZX10733403 and #2018YFA0900801), China NSFC grants (#81672008) and 270 Hubei Natural Science Foundation (#2018CFA035), Basic Scientific Research 271 Foundation of Central Universities (#2042019gf0026), Ministry of Science and 2.72 Technology of China, the National Mega Project on Major Infectious Disease Prevention (#2017ZX10103005) and National Key Research and Development 273 274 Program of China (#2018YFE0204500). None of the funders had any role in the study 275 design and the collection, analysis, and interpretation of data or in the writing of the 276 article and the decision to submit it for publication. The researchers confirm their independence from funders and sponsors. 2.77 278 279 Acknowledgement 280 We are grateful to Taikang Insurance Group Co., Ltd and Beijing Taikang Yicai 281 Foundation for their great support to this work. 282 **Declaration of interests** 283 284 No authors have received research funding from the company whose commercial 285 products were used in this work. All authors report no competing interests. All authors 286 have completed the Unified Competing Interest form. 287 Reference 288 289 Wu F, Zhao S, Yu B, et al. A new coronavirus associated with human 290 respiratory disease in China. Nature 2020; 291 https://doi.org/10.1038/s41586-020-2008-3 292 2. Chen L, Liu W, Zhang Q, et al. RNA based mNGS approach identifies a novel 293 human coronavirus from two individual pneumonia cases in 2019 Wuhan 294 outbreak. Emerg Microbes Infect 2020;9(1):313–9. 295 3. World Health Organization. Laboratory testing for 2019 novel coronavirus

(2019-nCoV) in suspected human cases. [Internet]. 2020; Available from:

https://www.who.int/emergencies/diseases/novel-coronavirus-2019/technical-g

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- 298 uidance/laboratory-guidance
- 4. General Office of the National Health and Health Commission O of the SA of
- TCM. Diagnosis and treatment of pneumonitis with a new type of coronavirus
- infection (trial version 5) [Internet]. 2020; Available from:
- http://bgs.satcm.gov.cn/zhengcewenjian/2020-02-06/12848.html
- 303 5. Wu Z, McGoogan JM. Characteristics of and Important Lessons From the
- Coronavirus Disease 2019 (COVID-19) Outbreak in China: Summary of a
- Report of 72 □ 314 Cases From the Chinese Center for Disease Control and
- Prevention. JAMA [Internet] 2020;2019:25–8. Available from:
- 307 http://www.ncbi.nlm.nih.gov/pubmed/32091533
- 308 6. Vogelstein B, Kinzler KW. Digital PCR. Proc Natl Acad Sci U S A
- 309 1999;96(16):9236–41.
- 7. Pohl G, Shih I-M. Principle and applications of digital PCR. Expert Rev Mol
- 311 Diagn 2004;4(1):41–7.
- 312 8. Sanders R, Mason DJ, Foy CA, Huggett JF. Evaluation of Digital PCR for
- Absolute RNA Quantification. PLoS One 2013;8(9):e75296.
- 9. White RA, Blainey PC, Fan HC, Quake SR. Digital PCR provides sensitive
- and absolute calibration for high throughput sequencing. BMC Genomics
- 316 2009;10(1):110–6.
- 317 10. Hindson BJ, Ness KD, Masquelier DA, et al. High-throughput droplet digital
- PCR system for absolute quantitation of DNA copy number. Anal Chem
- 319 2011;83(22):8604–10.
- 320 11. Hindson CM, Chevillet JR, Briggs HA, et al. Absolute quantification by
- droplet digital PCR versus analog real-time PCR. Nat Methods
- 322 2013;10(10):1003–5.
- 323 12. Brunetto GS, Massoud R, Leibovitch EC, et al. Digital droplet PCR (ddPCR)
- for the precise quantification of human T-lymphotropic virus 1 proviral loads
- in peripheral blood and cerebrospinal fluid of HAM/TSP patients and
- identification of viral mutations. J Neurovirol 2014;20(4):341–51.
- 327 13. Caviglia GP, Abate ML, Tandoi F, et al. Quantitation of HBV cccDNA in

328 anti-HBc-positive liver donors by droplet digital PCR: A new tool to detect 329 occult infection. J Hepatol 2018;69(2):301–7. Available from: https://doi.org/10.1016/j.jhep.2018.03.021 330 331 Postel M, Roosen A, Laurent-Puig P, Taly V, Wang-Renault S-F. 332 Droplet-based digital PCR and next generation sequencing for monitoring 333 circulating tumor DNA: a cancer diagnostic perspective. Expert Rev Mol 334 Diagn 2018;18(1):7–17. 15. Miyaoka Y, Mayerl SJ, Chan AH, Conklin BR. Detection and Quantification of 335 HDR and NHEJ Induced by Genome Editing at Endogenous Gene Loci Using 336 337 Droplet Digital PCR [Internet]. In: Karlin-Neumann G, Bizouarn F, editors. 338 Digital PCR: Methods and Protocols. New York, NY: Springer New York; 339 2018. p. 349–62. Available from: 340 https://doi.org/10.1007/978-1-4939-7778-9_20 341 16. National Institute For viral Disease Control and prevention of PRC. Specific 342 primers and probes for detection 2019 novel coronavirus [Internet]. 2020; 343 Available from: http://www.chinaivdc.cn/kyjz/202001/t20200121 211337.html 344 17. Guo Y., Wang K., Zhang Y., Zhang W., Wang L. LP. Comparison and analysis 345 of the detection performance of six new coronavirus nucleic acid detection 346 reagents. Chongqing Med 2020;14(0):1671–8348. 347 18. Thiel V, Ivanov KA, Putics Á, et al. Mechanisms and enzymes involved in SARS coronavirus genome expression. J Gen Virol 2003;84(9):2305–15. 348 349 19. Hussain S, Pan J, Chen Y, et al. Identification of Novel Subgenomic RNAs and 350 Noncanonical Transcription Initiation Signals of Severe Acute Respiratory 351 Syndrome Coronavirus. J Virol 2005;79(9):5288–95. 352 20. Chen Y, Liu Q, Guo D. Emerging coronaviruses: Genome structure, replication, 353 and pathogenesis. J Med Virol 2020;(January):1–6. 354 355 356

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Figure legends Figure 1. Plot of results from a linearity experiment to determine reportable range of ddPCR and RT-PCR targeting for ORF1ab and N of SARS-CoV-2. (A and B) Expected values (converted to log10) were plotted on the X axis versus measured values (converted to log10) on the Y axis using Graph Pad Prism for ddPCR targeting ORF1ab and N. (C and D) Expected values (converted to log10) were plotted on the X axis versus measured Ct values on the Y axis using Graph Pad Prism for RT-PCR targeting ORF1ab and N. Data are representative of three independent experiments with 3 replicates for each concentration. Figure 2. Probit analysis sigmoid curve reporting the lower limit of quantitation (LLoQ) and the lower limit of detection (LLoD) of ddPCR. Replicate reactions of SARS-CoV-2 (A) ORF1ab and (B) N were done at concentrations around the detection end point determined in preliminary dilution experiments. The X axis shows expected concentration (copies/µl). The Y axis shows fraction of positive results in all parallel reactions performed. The inner line is a probit curve (dose-response rule). The outer lines are 95 % CI. Data are representative of three independent experiments with 8 replicates for each concentration. Figure 3. Information diagram of detection results with ddPCR and subsequent clinical diagnosis for both convalescent and febrile suspected patients.

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TablesTable 1. Detection results of ddPCR for febrile and suspected patients of COVID-19.

		Result of official	Result of nucleic	Result of o	dPCR			
Patient	Patient status	nucleic acid test by	acid test by	(copies	s/µl)	Judgment result of	Result of chest	Disposition of
Number		RT-PCR	RT-PCR in lab	ORF1ab	N	ddPCR	СТ	Hospital ធំ ឧ
P1	Fever, suspected	Negative	Negative	0	0.1	Positive	Viral pneumonia	Hospitalized
P2	Fever, suspected	Negative	Negative	0	0.1	Positive	Viral pneumonia	Hospitalized
Р3	Fever, suspected	Negative	Negative	0	0.1	Positive	Viral pneumonia	Hospitalized
P4	Fever, suspected	Negative	Negative	0	0.09	Positive	Viral pneumonia	Hospitalized
P5	Fever, suspected	Negative	Negative	0	0.07	Positive	Viral pneumonia	Hospitalized
P6	Fever, suspected	Negative	Negative	0	0.18	Positive	Viral pneumonia	Hospitalized
P7	Fever, suspected	Negative	Negative	0.15	0.68	Positive	Viral pneumonia	Hospitalized
P8	Fever, suspected	Negative	Negative	0.08	0.66	Positive	Viral pneumonia	Hospitalized

P9	Fever, suspected	Negative	Negative	0	0.08	Positive	Viral pneumonia	Hospitalized
P10	Fever, suspected	Negative	Negative	0	0.18	Positive	Viral pneumonia	Hospitalized
P11	Fever, suspected	Negative	Negative	0	0.23	Positive	Viral pneumonia	Hospitalized
P12	Fever, suspected	Negative	Negative	0.1	0.19	Positive	Viral pneumonia	Hospitalized
P13	Fever, suspected	Negative	Negative	0	0.18	Positive	Viral pneumonia	Hospitalized
P14	Fever, suspected	Negative	Negative	0	0.09	Positive	Viral pneumonia	Hospitalized
P15	Fever, suspected	Negative	Negative	0	0.37	Positive	Viral pneumonia	Hospitalized
P16	Fever, suspected	Negative	Negative	0	0.09	Positive	Viral pneumonia	Hospitalized
P17	Fever, suspected	Negative	Negative	0	0.16	Positive	Viral pneumonia	Hospitalized
P18	Fever, suspected	Negative	Negative	0.19	0.09	Positive	Viral pneumonia	Hospitalized
P19	Fever, suspected	Negative	Negative	0.1	0	Positive	Viral pneumonia	Hospitalized
P20	Fever, suspected	Negative	Negative	0	0.1	Positive	Viral pneumonia	Hospitalized
P21	Fever, suspected	Negative	Negative	0	0.33	Positive	Viral pneumonia	Hospitalized

P22	Fever, suspected	Negative	Negative	0.22	0.71	Positive	Viral pneumonia	Hospitalized
P23	Fever, suspected	Negative	Negative	0	0.16	Positive	Viral pneumonia	Hospitalized
P24	Fever, suspected	Negative	Negative	0	0.09	Positive	Viral pneumonia	Hospitalized ੂੁ ਨੂੰ
P25	Fever, suspected	Negative	Negative	0	0.16	Positive	Viral pneumonia	Hospitalized de
P26	Fever, suspected	Negative	Negative	0	0	Negative	Viral pneumonia	Hospitalized
P27	Fever, suspected	Negative	Negative	0	0	Negative	Viral pneumonia	Hospitalized er
P28	Fever, suspected	Negative	Negative	0	0.17	Positive	Normal	Home Quarantine
P29	Fever, suspected	Negative	Negative	0	0.06	Positive	Normal	Home Quarantine
P30	Fever, suspected	Negative	Negative	0	0.06	Positive	Normal	Home Quarantine
P31	Fever, suspected	Negative	Negative	0.08	0.2	Positive	Normal	Home Quarantine
P32	Fever, suspected	Negative	Negative	0	0.19	Positive	Normal	Home Quarantine.
P33	Fever, suspected	Negative	Negative	0	0.27 9	Positive	Normal	Home Quarantine

P34	Fever, suspected	Negative	Negative	0.15	8.0	Positive	Normal	Home Quarantine
P35	Fever, suspected	Negative	Negative	0	0.1	Positive	Normal	Home Quarantine
P36	Fever, suspected	Negative	Negative	0	0	Negative	Normal	Excluded =
P37	Fever, suspected	Negative	Negative	0	0	Negative	Normal	Excluded &
P38	Fever, suspected	Negative	Negative	0	0	Negative	Normal	Excluded Excluded
P39	Fever, suspected	Negative	Negative	0	0	Negative	Normal	Excluded er a
P40	Fever, suspected	Negative	Negative	0	0	Negative	Normal	Excluded Excluded Excluded
P41	Fever, suspected	Negative	Negative	0	0	Negative	Normal	
P42	Fever, suspected	Negative	Negative	0	0	Negative	Normal	Excluded Excluded Excluded
P43	Fever, suspected	Negative	Negative	0	0	Negative	Normal	Excluded all

Table 2. Detection results of ddPCR for supposed convalescent patients who is about to be discharged after treatment.

		Result of official	Result of ddPCR		Judgment result of		
Patient	Patient Patient status Number	nucleic acid test by	Result of nucleic	(copies/μl)		ddPCR	
Number		real time PCR	acid test by				
		(Positive/Negative)	RT-PCR in our lab	ORF1ab	N	(Positive/Negative)	
P44	Supposed convalescent	Negative	Negative	0	0.12	Positive	
P45	Supposed convalescent	Negative	Negative	0	0.11	Positive	
P46	Supposed convalescent	Negative	Negative	0.57	0.6	Positive	
P47	Supposed convalescent	Negative	Negative	0	0.45	Positive	
P48	Supposed convalescent	Negative	Negative	0	0.8	Positive	
P49	Supposed convalescent	Negative	Negative	0.09	0	Positive	
P50	Supposed convalescent	Negative	Negative	0	0.11	Positive	
P51	Supposed convalescent	Negative	Negative	0.19	5.3	Positive	
P52	Supposed convalescent	Negative	Negative	0.07	0.07	Positive	

P53	Supposed convalescent	Negative	Negative	0	0	Negative	
P54	Supposed convalescent	Negative	Negative	0	0	Negative	
P55	Supposed convalescent	Negative	Negative	0	0	Negative	
P56	Supposed convalescent	Negative	Negative	0	0	Negative	
P57	Supposed convalescent	Negative	Negative	0	0	Negative	





