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CORRIGENDUM

Corrigendum to: Epidemiology of Severe Acute Respiratory Syndrome Coronavirus 2 Emergence Amidst Community-Acquired Respiratory Viruses

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In "Epidemiology of Severe Acute Respiratory Syndrome Coronavirus 2 Emergence Amidst Community-Acquired Respiratory Viruses" by Leuzinger et al. [*J Infect Dis* 2020; 222(8): 1270–1279], there were two designation errors regarding the reverse-transcription quantitative nucleic acid amplification (RT-QNAT) assays used.

First, the amplicon size of the Basel-S-gene assay is 112 bp and hence should be called Basel-SCoV2-S-112bp (see corrected Supplementary Table 1).

Second, the Basel-N-gene should be called Basel-SCoV2-ORF8-97bp as this assay targets sequences immediately upstream of the N-gene in the ORF8 gene of SARS-CoV-2 (see corrected Supplementary Table 1).

This assay was designed in January at the beginning of the COVID-19 pandemic when the number of complete genome sequences of SARS-CoV-2 was limited to less than 20 in public databases. The authors therefore used the SARS-CoV-1 Urbani strain (accession number: AY278741) as reference, which is approximately 200 nt shorter than the SARS-CoV-2 genome (Wuhan-1 strain, accession number: NC_045512, 29'903 nt). The discrepancy in length of the two genomes led to an erroneous initial attribution of the target sequences as being located in the N-gene. Although primer and probe annotations in the manuscript were correctly depicted and used, the name of the assay was not changed to reflect the correct target, namely the ORF8 gene and the amplicon size of 97bp.

Thus, when referring to the N-gene assay in the publication indicated above, readers should be aware of the correct target being the ORF8 of SARS-CoV-2.

The authors regret this naming error.

Table S1. Forward primers, reverse primers and probes of the SARS-CoV-2 RT-QNATs

Gene	Primer/Probe	Sequence (5′→3′)	Position[1]
Spike glycoprotein	Forward primer	GGTTATCTTCAACCTAGGAC	22364 - 22383
(Basel-SCoV2-S-112bp)	Reverse primer	ATTTCAACGTACACTTTGTT	22475 - 22456
	Probe	TGTAGACTGTGCACTTGACCCTCTCTC	22426 - 22452
ORF8	Forward primer	ATCGGTAATTATACAGTTTCC	28119 - 28139
(Basel-SCoV2-ORF8-97bp)	Reverse primer	AGTCTTCATAGAACGAACAA	28215 - 28196
	Probe	TGCCAGGAACCTAAATTGGGTAGTCT	28161 - 28186

[1]Position according to SARS-CoV-2 isolate Wuhan-Hu-1 (acc. no. NC_045512.2)

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SARS-COV-2 REVERSE TRANSCRIPTION QUANTITATIVE NUCLEIC ACID TESTING

For the Roche assay, the extraction control was included as specified by the manufacturer, while the Basel assays were spiked with unrelated nucleic acids. Both assays were run on independent plates in parallel for all NOPS tested. Concordant negative results were interpreted as confirmed, while concordant positive and discordant results were retested using the laboratory-developed RT-QNAT targeting the viral ORF8 gene (Basel-SCoV2-ORF8-97bp). The Roche-E-gene was run on the CFX96 RT-PCR (Bio-Rad Laboratories, Cressier, Switzerland) as specified by the manufacturer. The Basel-SCoV2-S-112bp and Basel-SCoV2- ORF8-97bp used the RT Takyon MMX containing uridine and the uracil-N-glycosylase for amplicon decontamination (Eurogentec, Liège, Belgium), 300 nmolar end concentration of the primers and probe for the Basel-SCoV2-S-112bp QNAT, and 900 nmolar end concentration of the primers and 100 nmolar probe for the Basel-SCoV2- ORF8-97bp QNAT (Supplementary Table S1). The Basel assays had a reaction volume of 25 µL and 5 µL of extracted TNA run on an ABI7500 Fast Real-Time PCR system (Thermo Fisher Scientific, Massachusetts, United States). The single-step reverse transcription and cycling conditions for the RT-QNATs were 50 °C for 10 min; 95 °C for 5 min; and 45 cycles of 95 °C for 30 s and 60°C for 60 s.