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Correspondence

Erratum: Correction of Text in the Article "Evidence of Long-Distance Droplet Transmission of SARS-CoV-2 by Direct Air Flow in a Restaurant in Korea"

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▸ This corrects the article "Evidence of Long-Distance Droplet Transmission of SARS-CoV-2 by Direct Air Flow in a Restaurant in Korea" in volume 35, number 46, e415.

To the Editor:

The authors regret that there was an important error in the methods section. The genome sequencing preparation section in methods was not approved to publish by the original researchers. The 4 sentences ("In total, … were generated.") related with genome sequencing preparation in 'Personal factor investigation' section should be removed.

Content of corrections:

1. The contents of the last 4 sentences were removed in the 'Personal factor investigation section' of METHODS.
2. The reference number 8 is used as a reference of the previous sentence of removed contents.

Before

METHODS

Personal factor investigation

The epidemiological investigation was implemented according to the 'Infectious Diseases Control and Prevention Act' (Act number 16725) in Korea and the guidelines for response to COVID-19 by the Korea Disease Control and Prevention Agency (KDCA).[4] Data comprising patient's personal statements by interview, medical institution usage history, credit card record, closed-circuit television (CCTV) images, cell phone location data, and other associated information were secured by an epidemiological investigation team.[5] The Epidemic Investigation Support System (EISS) developed by KDCA was also used for location tracking of confirmed cases and hot-spot analysis.[6] Nasopharyngeal specimens of cases and close contacts were collected and tested using real-time reverse transcription polymerase chain reaction (rRT-PCR) by Jeollabuk-do Institute of Health & Environment Research, and genome sequencing analysis for verifying association between cases was performed by the KDCA.[7] In total, 10–100 ng of the extracted viral RNA with a maximum volume of 8.5 μL was

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subjected to target enrichment using a Truseq RNA library prep for enrichment (Illumina, San Diego, CA, USA) and Truseq RNA Enrichment (Illumina). Dual-index filtering and adapter trimming were conducted on the sequences using our in-house scripts. Hybridization probes were designed to cover the whole genome of SARS-CoV-2 using the Wuhan-Hu-1 strain.[8] The biotinylated probes were 120 base pair in length with 3 × tiling (Celemics, Inc. Seoul, Korea). In total, 745 conserved probes were generated.

After

METHODS

Personal factor investigation

The epidemiological investigation was implemented according to the 'Infectious Diseases Control and Prevention Act' (Act number 16725) in Korea and the guidelines for response to COVID-19 by the Korea Disease Control and Prevention Agency (KDCA).[4] Data comprising patient's personal statements by interview, medical institution usage history, credit card record, closed-circuit television (CCTV) images, cell phone location data, and other associated information were secured by an epidemiological investigation team.[5] The Epidemic Investigation Support System (EISS) developed by KDCA was also used for location tracking of confirmed cases and hot-spot analysis.[6] Nasopharyngeal specimens of cases and close contacts were collected and tested using real-time reverse transcription polymerase chain reaction (rRT-PCR) by Jeollabuk-do Institute of Health & Environment Research, and genome sequencing analysis for verifying association between cases was performed by the KDCA.[7,8]

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