

Reporting Summary

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Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

- | n/a | Confirmed |
|-------------------------------------|--|
| <input type="checkbox"/> | <input checked="" type="checkbox"/> The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> The statistical test(s) used AND whether they are one- or two-sided
<i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i> |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> A description of all covariates tested |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals) |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> For null hypothesis testing, the test statistic (e.g. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted
<i>Give P values as exact values whenever suitable.</i> |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Estimates of effect sizes (e.g. Cohen's d , Pearson's r), indicating how they were calculated |

Our web collection on [statistics for biologists](#) contains articles on many of the points above.

Software and code

Policy information about [availability of computer code](#)

Data collection

All fluorescence data were collected via the Hidex Sense 425-301 microplate reader (the emission-wavelength-optimization fluorescence data were collected via Tecan Spark 10M multimode microplate reader). Cycle threshold values for clinical samples were determined using quantitative RT-PCR from Seoul Clinical Laboratories.

Data analysis

All data were exported by Microsoft Excel 2016. Two-tailed Student's t -test were performed using Microsoft Excel 2016. The linear regression and the reported values for the coefficients of determination associated with the data were computed using SigmaPlot 12.0

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors/reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research [guidelines for submitting code & software](#) for further information.

Data

Policy information about [availability of data](#)

All manuscripts must include a [data availability statement](#). This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

The authors declare that all the data supporting the findings of this study are available within the paper and its Supplementary Information. Raw pre-processed data for Figs. 2–8 and Supplementary Figs. 1–9 are available from figshare with the identifier <https://doi.org/10.6084/m9.figshare.12547391>. Refseq mRNA of Homo sapiens (ftp://ftp.ncbi.nlm.nih.gov/refseq/H_sapiens) was used in the 'Primer Pair Specificity Checking Parameters' section of the primer-design process through Primer-BLAST.

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

Life sciences Behavioural & social sciences Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see [nature.com/documents/nr-reporting-summary-flat.pdf](https://www.nature.com/documents/nr-reporting-summary-flat.pdf)

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	Sample sizes were determined as per previous experimental experience, and are similar to those generally used in the field.
Data exclusions	No data were excluded.
Replication	Four biological replicates were performed for each experiment, except for Fig. 7 and Supplementary Fig. 9, which had two biological replicates each.
Randomization	Negative clinical samples were randomly picked to test for our experiment. Other samples were not randomized.
Blinding	No formal blinding was used.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involvement in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> Antibodies
<input checked="" type="checkbox"/>	<input type="checkbox"/> Eukaryotic cell lines
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology
<input checked="" type="checkbox"/>	<input type="checkbox"/> Animals and other organisms
<input type="checkbox"/>	<input checked="" type="checkbox"/> Human research participants
<input checked="" type="checkbox"/>	<input type="checkbox"/> Clinical data

Methods

n/a	Involvement in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> ChIP-seq
<input checked="" type="checkbox"/>	<input type="checkbox"/> Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/> MRI-based neuroimaging

Human research participants

Policy information about [studies involving human research participants](#)

Population characteristics	Clinical samples were obtained from subjects who were infected (or 'healthy' for the negatives) during COVID-19 in the Republic of Korea. The detailed characteristics and information of the clinical sample are provided in the Supplementary Table 6.
Recruitment	The clinical samples were recruited from Seoul Clinical Laboratories. A total of 40 samples (20 positives and 20 negatives) were obtained. The samples were remaining nasopharyngeal swab samples that had been tested for COVID-19 rRT-PCR by the Seoul Clinical Laboratory.
Ethics oversight	The informed-consent exemption and protocol were approved by the Institution Review Board of Seoul Clinical Laboratories under IRB-20-010.

Note that full information on the approval of the study protocol must also be provided in the manuscript.