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Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Research policies, see our Editorial Policies and the Editorial Policy Checklist.

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	
☐	☒	The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement
☐	☒	A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☐	☒	The statistical test(s) used AND whether they are one- or two-sided *Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
☒	☐	A description of all covariates tested
☐	☒	A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
☐	☒	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)
☒	☐	For null hypothesis testing, the test statistic (e.g. *F*, *t*, *r*) with confidence intervals, effect sizes, degrees of freedom and *P* value noted *Give P values as exact values whenever suitable.*
☒	☐	For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
☒	☐	For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
☒	☐	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	A fluorescence plate reader and a real-time PCR system were used to record fluorescence signals from CRISPR-Cas detection of viral RNA. A real-time PCR system was used to record cycle threshold values for RNA standards and clinical RNA samples.
Data analysis	Microsoft Office Excel and Graphpad Prism were used to generate plots and kinetic curves.

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 and 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 main data supporting the results in this study are available within the paper and its supplementary information. Raw datasets generated and analysed during the study are available from the corresponding authors on reasonable request.

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

Life sciences study design

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

Sample size	Three biological replicates were performed unless noted otherwise. Minimal sample size for the validation of the CRISPR-based assay was determined prior to experimentation on the basis of sensitivity and specificity requirements for the diagnostic test set by the Department of Medical Sciences, Ministry of Public Health, Thailand.
Data exclusions	Technical failures were excluded based on pre-established criteria.
Replication	All attempts at replication were successful, and standard deviations were within the expected ranges.
Randomization	All COVID-19-positive clinical samples were obtained from a defined swab-collection time window, between 3 March and 10 April, 2020, at Siriraj.
Blinding	Samples were randomized upon giving them to the study staff, who were kept blinded to the SARS-CoV-2 RT-PCR results of the samples when they performed validation experiments for the CRISPR-based assay.

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	Involved in the study
☐	☒ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☒	☐ Animals and other organisms
☐	☒ Human research participants
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Antibodies

Antibodies used	Antibodies used in the lateral-flow strips include polyclonal (rabbit) anti-FITC antibody labelled with gold particles (for Hybridetect and Hybridetect 2T strips) and polyclonal (goat) digoxigenin antibody (for Hybridetect 2T strips). The antibodies were included as parts of the lateral-flow assay kit by Milenia Biotec.
Validation	Validation was performed by the supplier (Milenia Biotec).

Human research participants

Policy information about studies involving human research participants

Population characteristics	81 samples with known positive results from RT-PCR for SARS-CoV-2, 73 samples with known negative results from RT-PCR for SARS-CoV-2, and 3 known samples with positive results for human coronavirus OC43, NL63, and 229E were included for the validation of the assay. 380 samples were further collected as a part of pre-operative assessment of surgical patients.
Recruitment	Nasopharyngeal and throat swabs of patients with suspected SARS-CoV-2 infection were processed at the Diagnostic Molecular Laboratory, Department of Microbiology, Faculty of Medicine, Siriraj Hospital. No personally identifiable information was collected.
Ethics oversight	Ethical approval of the study was given by the Siriraj Institutional Review Board (COA: Si 339/2020 and Si 424/2020).

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