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Corresponding author(s): Mohammad Rubayet Hasan

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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	No software was used
Data analysis	No software was used

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

All data generated or analysed during this study are included in this published article (and its supplementary information files).

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	No statistical methods were used to predetermine sample size. Nasopharyngeal swab (NPS) specimens that meets the inclusion criteria for the study were collected for a total of 6 months. A total of 207 NPS specimens were collected of which 115 were from adults and 92 were from children from a total of 92 families. For paired T-test analysis of ACE2 gene expression for a sample size of 92 (adult vs children) with mean Ct difference =-1.785, SD=4.506 and alpha=0.05, the resulting power is 0.964, confirming that sample sizes were sufficient.
Data exclusions	No data were excluded. For paired data analysis, each of the children were paired with their mothers with the exception of such cases where mother was negative for COVID-19 or no specimen was available from the mother. Data for the additional adult members of the family were excluded on in the paired analysis.
Replication	Repeat measures of ACE2 and TMPRSS2 gene expression in a set of NPS specimens at the optimization phase of the study were reproducible.
Randomization	NPS specimens from study subjects were grouped based on their age group (Adult and children) and COVID-19 infection status.
Blinding	Blinding was not possible at the time of specimen collection because subjects were chosen based on their fulfillment of study inclusion criteria. Also, gene expression analysis of paired samples were performed simultaneously to ensure that the results were not affected by subtle variation in experimental conditions.

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

Human research participants

Policy information about studies involving human research participants

Population characteristics	Data were collected on age, gender and SARS-CoV-2 infection status of all participants. Simple and multivariate regression analysis was performed with age, gender and ACE2 and TMPRSS2 gene expression data as independent variables and SARS-CoV-2 infection status as dependent (outcome) variable.
Recruitment	During the period of June to December 2020, residual NPS specimens were collected based on specific inclusion criteria: i) at least one member of the family was positive for COVID-19 by RT-qPCR; ii) paired NPS specimens were available for the child and at least one of the accompanying adult family members; and iii) at least 0.5 ml of specimen was available for gene expression analysis. No other selection bias was expected.
Ethics oversight	The study was approved by Sidra Medicine IRB

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

Clinical data

Policy information about clinical studies

All manuscripts should comply with the ICMJE guidelines for publication of clinical research and a completed CONSORT checklist must be included with all submissions.

Clinical trial registration	*Provide the trial registration number from ClinicalTrials.gov or an equivalent agency.*
Study protocol	*Note where the full trial protocol can be accessed OR if not available, explain why.*
Data collection	*Describe the settings and locales of data collection, noting the time periods of recruitment and data collection.*
Outcomes	*Describe how you pre-defined primary and secondary outcome measures and how you assessed these measures.*