

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

- ☐ ☒ 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 All analyses were conducted with R version 3.6.0 and the VGAM package 1.1.1.

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

Anonymized raw data and R syntax to reproduce all the analyses, figures, tables and supplementary tables in the published article are available at: [Dryad link pending].

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

Life sciences study design

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

Sample size	We estimated a priori the sample size to be 300 participants. The primary outcome of the study was the reduction in the exhaled virus concentration of normal tidal breathing by wearing face mask in terms of total virus by RT-PCR as a proxy for infectious virus particle. We expected that a 1-log reduction in exhaled virus particle by face mask intervention would have a clinically relevant effect in reducing the probability of transmission. Except for influenza, there was no quantitative data available from exhaled breath samples from respiratory virus-infected individuals before the present study. If the standard deviation of exhaled virus concentration was 1 log copies/ml (Milton et al., PLoS Pathog 2013), we would detect a difference of >1 log copies/ml in the mask vs control group as long as we have >15 participants with a specific respiratory virus. For example, if our study included 23 participants with rhinovirus detectable in exhaled breath without a mask, we will have 80% power and 0.05 significance level to identify differences in viral shedding in aerosols of 1.28 log ₁₀ copies associated with the use of face masks, assuming a standard deviation of 1.54 log ₁₀ copies based on data from nasal and throat swab (Lu et al., J Clin Microbiol 2008). We expected from 300 individuals with ARI, at least 150 to have a respiratory virus, and at least 20-30 to have each of rhinovirus, coronavirus, adenovirus and parainfluenza plus small numbers of other respiratory viruses, assuming the Viral Panel would detect respiratory viruses in 60% of participants including 10% by influenza (since we partly recruited during the influenza seasons) and the other 50% made up of rhinovirus, coronavirus, adenovirus and parainfluenza virus.
Data exclusions	As described in the Results section and Supplementary Figure 1, only participants who provided exhaled breath samples and randomized to mask intervention were included; and final analyses were performed only for participants with either coronavirus, influenza virus or rhinovirus infection, which had sufficient sample size for comparison between mask intervention.
Replication	Samples from a subset of participants identified with a coronavirus, influenza or rhinovirus infection were re-tested by RT-PCR with consistent results. R syntax is available to reproduce all the analyses, figures, tables and supplementary tables in the published article.
Randomization	Prior to the exhaled breath collection, each participant was randomly allocated in a 1:1 ratio to either wearing a surgical face mask or not during the exhaled breath collection using a computer-generated sequence. The allocation was concealed to the study staff performing the exhaled breath collection before allocation of the mask intervention.
Blinding	Blinding to the participant and the study staff for the mask intervention was not possible. The study staff performing the statistical analyses was also involved in the data collection. We expected there would be minimal bias due to unblinding since data collection for questionnaires was done before randomization to mask intervention, and viral load from a sample measured by RT-PCR is an objective measurement.

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
☒	☐ Animals and other organisms
☐	☒ Human research participants
☐	☒ Clinical data

Methods

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

Eukaryotic cell lines

Policy information about [cell lines](#)

Cell line source(s)	Madin-Darby Canine Kidney (MDCK) cells
Authentication	European Collection of Authenticated Cell Cultures.
Mycoplasma contamination	We confirm that all cell lines tested negative for mycoplasma contamination.
Commonly misidentified lines (See ICLAC register)	Nil

Human research participants

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

Population characteristics	As described in the Results section, Table 1a and Supplementary Table 1, there were some differences in characteristics of participants with the different viruses. Overall, most participants were younger adults and 5% were age 11-17 years, but there were more children with influenza virus and no children in the subgroup with coronavirus infection. Overall, 59% were female, but there were more females among the subgroup with coronavirus infection. The majority of participants did not have underlying medical conditions and overall 9% had received influenza vaccination for the current season but only 2% among those with influenza virus infection. The majority of participants were sampled within 24–48 or 48–72 hours of illness onset. 24% of participants had a measured fever $\geq 37.8^{\circ}\text{C}$, with influenza patients more than twice as likely than coronavirus and rhinovirus-infected patients to have a measured fever. Coronavirus-infected participants coughed the most with an average of 17 (SD 30) coughs during the 30-minute exhaled breath collection. The profile of the participants randomized to with-mask vs without-mask groups were similar.
Recruitment	As described in the Methods section, participants were recruited year-round from March 2013 through May 2016 in a general outpatient clinic of a private hospital in Hong Kong. As routine practice, clinic staff screened all individuals attending the clinics for respiratory and any other symptoms regardless of the purpose of the visit at the triage. Study staff then approached immediately those who reported at least one of the following symptoms of acute respiratory illness (ARI) for further screening: fever $\geq 37.8^{\circ}\text{C}$, cough, sore throat, runny nose, headache, myalgia and phlegm. Individuals who reported ≥ 2 ARI symptoms, within 3 days of illness onset and ≥ 11 years of age were eligible to participate.
Ethics oversight	As described in the Methods section, the study protocol was approved by the Institutional Review Board of The University of Hong Kong and the Clinical and Research Ethics Committee of Hong Kong Baptist Hospital.

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	The present study was not registered in clinical trials registries, as it was a laboratory-based study of detection of viruses in exhaled breath and the effect of wearing surgical facemasks on virus detection. It was not a Phase II/III clinical trial.
Study protocol	Not available in clinical trials registries (as above). Study protocol will be made available to editors and peer reviewers if requested.
Data collection	As described in the Methods section, participants were recruited year-round from March 2013 through March 2016 in a general outpatient clinic of a private hospital in Hong Kong. Data collection for questionnaires and exhaled breath sample collection was done face-to-face with the participant by trained study staff at the same clinic on the day of participant enrolment.
Outcomes	As pre-specified in the study protocol, the primary outcomes of the study were the virus generation rate in the tidal breathing of participants infected by different respiratory viruses, and the efficacy of face mask in preventing virus dissemination in exhaled breath especially at the aerosol fraction. As pre-specified in the study protocol, one of the secondary outcomes was to provide indirect evidence for relative importance of different transmission routes of influenza and other respiratory viruses. In this regard, in the present manuscript we examined the correlation between viral shedding in nose swabs, throat swabs, respiratory droplets and aerosols, and factors affecting viral shedding in respiratory droplets and aerosols. As described in the Discussion section in the present manuscript about the limitation of our study, there was large proportion of participants with undetectable viral shedding in exhaled breath for each of the viruses studied, and therefore we were unable to examine the exhaled respiratory virus reduction proportion by chi-squared test, nor the exhaled respiratory virus reduction volume (i.e. viral load) by t-test and linear regression as pre-specified in the study protocol. Instead, we have used Fisher's exact test and Tobit regression for the same purposes respectively.