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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 Authors & Referees 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 commercial or open source databases used.
Data analysis	Short sequence read alignment using Burrows-Wheeler transform, Li & Durbin. Bioinformatics 2009; 25: 1754; Genome consensus generated using Geneious ver 11.1.4; Percentages of nucleotides at each position of the genome using bam-readcount (https://github.com/genome/bam-readcount)

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

GenBank accession numbers MT215193, MT215194, MT215195, MT270814, MT270815 and MT276600. Data will be released 1st May 2020

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 study design

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

Sample size	15 dogs, 7 cats and four human patients. All eligible subjects during study period 10th Feb - 27th March 2020 were included. Sample size calculation is not relevant.
Data exclusions	No data exclusions
Replication	RT-PCR assays have been done independently in two different laboratories with up to 6 different gene targets. All positive results were confirmed by re-extraction and repeat PCR on the original specimen.
Randomization	Not relevant. An observational study. No intervention investigated
Blinding	Not relevant. An observational study. No intervention investigated

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)	Vero-E6 cells (ATCC CRL-1586)
Authentication	Cell lines obtained from ATCC. Original cell stocks maintained in liquid N2 storage and each thawed aliquot discarded after 20 cell passages.
Mycoplasma contamination	Confirmed to be free of mycoplasma using two methods. A cell culture based kit from Invivogen. PlasmoTest™ - Mycoplasma Detection Kit and a PCR assay from ABM. https://www.abmgood.com/pcr-mycoplasma-detection-kit-g238.html
Commonly misidentified lines (See ICLAC register)	No commonly misidentified cell lines used.

Animals and other organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research

Laboratory animals	None
Wild animals	None
Field-collected samples	Samples collected by veterinarians of the Department of Agriculture, Fisheries and Conservations as part of routine management of the animals
Ethics oversight	Agriculture, Fisheries and Conservation Department

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

Human research participants

Policy information about studies involving human research participants

Population characteristics	Retrieving virus sequence data from four patients in contact with the dogs
Recruitment	Humans in two households diagnosed with COVID-19 in contact with the infected dogs.
Ethics oversight	Part of the routine public health epidemic response and also Institutional Review Board approval UW20-168, University of Hong Kong Hospital Authority of Hong Kong West Cluster.

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	This is not a clinical trial
Study protocol	This is an emergency public health response during a pandemic.
Data collection	Epidemiological data collected as part of routine outbreak investigation during the period 10th February - 27th March 2020.
Outcomes	Relevant outcomes reported in manuscript.