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Reporting Summary

Nature Portfolio 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 Portfolio 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 in the data collection.
Data analysis	Sequenced data was assembled with the reference sequences in database using CLC Genomic Workbench v21. The sequence alignment and annotation were performed using CLC Genomic Workbench v21.Phylogenetic trees were reconstructed with nucleotide sequences using IQ-TREE (v1.6.12) with GTR+G as the best-fit substitution model and 1,000 bootstrap replicates. MAFFT method was used for sequence alignment. Maps were produced using ArcGIS Desktop 10.6.

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 Portfolio 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 description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our policy

Provide your data availability statement here.

Human research participants

Policy information about studies involving human research participants and Sex and Gender in Research.

Reporting on sex and gender	The patients' information was obtained from medical records. A standardized questionnaire was used to obtain the information of the close contacts. The term sex was used in the study.
Population characteristics	The patient was a 4-year-old boy living with his father, grandparents, brother and sister, who are otherwise healthy, in Shangcai County, Zhumadian City of Henan province, China. Throat swabs were also collected from 6 close contacts (60-year-old grandfather, 60-year-old grandmother, 32-year-old father, 36-year-old aunt, 8-year-old brother, and 6-year-old sister of the patient).
Recruitment	In April 2022, as part of hospital surveillance of febrile patients in Zhumadian Central Hospital, Henan province, China, a febrile pediatric patient with recurrent fever of unknown cause was screened. Following the identification of infection with an avian influenza virus, an epidemiological investigation was performed on the patient and his close-contact family members and relatives using a standard questionnaire, which included demographic information, pre-existing underlying diseases and the exposure history before the onset of illnesses.
Ethics oversight	According to the regulations and guidelines of the NHFPC of China, data collection on this patient was part of the routine surveillance and outbreak investigation, and was therefore exempt from the oversight by institutional review board.

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

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	The patient was a 4-year-old boy living with his father, grandparents, brother and sister, who are otherwise healthy, in Shangcai County, Zhumadian City of Henan province, China. Throat swabs and blood samples were collected from five close-contact family members (grandfather, grandmother, father, eight-year-old brother, and six-year-old sister) who lived together with the patient, and the aunt who had close contact with the patient while he was ill.
Data exclusions	No data was excluded in the analyses.
Replication	Reproducibility of experimental findings was not applicable because our study is observational.
Randomization	Randomization used to allocate participates into experimental groups was not applicable because our study is observational.
Blinding	Blinding was not applicable because our study is observational.

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
☐	☒ Clinical data
☒	☐ Dual use research of concern

Methods

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

Animals and other research organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research, and Sex and Gender in Research

Laboratory animals	No laboratory animal was used in the study.
Wild animals	No wild animal was used in the study.
Reporting on sex	Sex of animals was not considered in study design.
Field-collected samples	To infer the possible infection source of the patient, we performed field investigation in the residence of the patient and the village. The 63 animal and environmental samples were collected, including nasopharyngeal swabs, anal swabs, faecal and blood samples collected from companion animals, livestock and poultry, environmental samples that included the surface swabs, drinking water, sewage, and water in a pool close to the family.
Ethics oversight	According to the regulations and guidelines of the NHFPC of China, data collection on this patient was part of the routine surveillance and outbreak investigation, and was therefore exempt from the oversight by institutional review board. Written informed consent was obtained from the guardian of the patient and all the participating subjects.

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	Clinical trial registration was not applicable.
Study protocol	The full study protocol was already included in the main text.
Data collection	In April 2022, as part of hospital surveillance of febrile patients in Zhumadian Central Hospital, Henan province, China, a febrile pediatric patient with recurrent fever of unknown cause was screened. Following the identification of infection with an avian influenza virus, an epidemiological investigation was performed on the patient and his close-contact family members and relatives using a standard questionnaire, which included demographic information, pre-existing underlying diseases and the exposure history before the onset of illnesses. To infer the possible infection source of the patient, we performed field investigation in the residence of the patient and the village on April 13.
Outcomes	A standardized questionnaire was used to obtain the patients' information from medical records, including demographic data, underlying medical conditions, symptoms and signs, routine blood test results, radiographic findings, and disease outcome.