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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.

Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. 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
☐	☒	An indication of 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 statistics 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
☐	☒	Clearly defined error bars *State explicitly what error bars represent (e.g. SD, SE, CI)*

Our web collection on statistics for biologists may be useful.

Software and code

Policy information about availability of computer code

Data collection	No commercial or open source was collected and used. All data was collected through experimental findings.
Data analysis	All statistical analyses were performed using GraphPad Prism version 5.00 or 8.00 for Windows (GraphPad Software, La Jolla, CA). The n values in the figure legend indicate the number of independent experiments and each experiment was conducted with two to three technical replicates. Where appropriate, column analyses were performed using an unpaired, two-tailed t-test. P values less than 0.05 (95% confidence interval) were considered significant). RNA seq data were analyzed using CLC (QIAGEN) with p<0.05 and QIAGEN's IPA (QIAGEN). The canonical pathways and functional processes Pathway enrichment p-values (Fisher's exact test) and activation z-scores were calculated by IPA.

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 upon request. 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 relevant data are available from the authors.

Field-specific reporting

Please select 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/authors/policies/ReportingSummary-flat.pdf

Life sciences study design

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

Sample size	No statistical method was used to predetermine sample size. Sample sizes were selected based on previous experience to obtain statistical significance and reproducibility.
Data exclusions	No data has been excluded.
Replication	All experiments were performed with at least three biological triplicates. All the experimental findings were reliably reproduced.
Randomization	Samples were allocated into experimental groups according to their genotype. For all animal studies, mice and ferrets were randomly assigned to each group but by age.
Blinding	The investigators were not blinded to group allocation during the collection of specimens from animal, but were binded to data analysis.

Reporting for specific materials, systems and methods

Materials & experimental systems

n/a	Involved in the study
☒	☐ Unique biological materials
☐	☒ Antibodies
☐	☒ Eukaryotic cell lines
☒	☐ Palaeontology
☐	☒ Animals and other organisms
☒	☐ Human research participants

Methods

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

Antibodies

Antibodies used	Primary antibody: in-house generated NP monoclonal antibody against SFTSV Second antibody : HRP-conjugated anti mouse Ig G antibody (cat #115-035-146, lot # 126768, Jackson ImmunoResearch). Antibody was used at 1:1000 for IHC.
Validation	Primary NP antibody was made in our laboratory and was validated through western blotting and immuno fluorescence assay. Anti-mouse antibody validated by Jackson ImmunoResearch was from Jackson ImmunoResearch. Each antibody was used at 1:1000 dilution for IHC.

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	Vero E6 cells (ATCC No. CRL-1586; American Type Culture Collection, Manassas, VA) were cultured in Dulbecco's Modified Eagle Medium (DMEM; Gibco, Grand Island, NY) containing 2% fetal bovine serum (FBS; Gibco) with penicillin (100 U/ml) and streptomycin (100 µg/ml; P/S, Gibco) placed in 37°C incubator supplemented with 5% CO2.
Authentication	Vero E6 cells were purchased from ATCC (No. CRL-1586; American Type Culture Collection, Manassas, VA)
Mycoplasma contamination	All cells were mycoplasma-free.
Commonly misidentified lines (See ICLAC register)	No commonly misidentified cell lines were used.

Animals and other organisms

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

Laboratory animals	Eight-week-old or aged (≥20 months) female mice (n=17) of each strain (BALB/c, C3H, C57BL/6, and FVB) were used for SFTSV infection. Young adults (20-24 months, ≤2Y) and aged ferrets (48-50 months), ≥4 Y) were also used for SFTSV infections (14 male and 32 female ferrets were used for this study) . All animal experiment protocols were approved by the Medical Research Institute, a member of Laboratory Animal Research Center of Chungbuk National University (LARC) (approval number: CBNUA-986-16-01), and conducted in BSL3 facility (KCDC-14-3-07).
Wild animals	No wild animal was used in this study
Field-collected samples	This study did not involves samples collected from the field.