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☒ Initial submission ☐ Revised version ☐ Final submission

Life Sciences Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form is intended for publication with all accepted life science papers and provides structure for consistency and transparency in reporting. Every life science submission will use this form; some list items might not apply to an individual manuscript, but all fields must be completed for clarity.

For further information on the points included in this form, see Reporting Life Sciences Research. For further information on Nature Research policies, including our data availability policy, see Authors & Referees and the Editorial Policy Checklist.

Experimental design

1. Sample size

Describe how sample size was determined.

Samples sizes were based on standards in the field, typically 3 independent biological replicates, with each replicate assayed in technical duplicate or triplicate.

2. Data exclusions

Describe any data exclusions.

N/A

3. Replication

Describe whether the experimental findings were reliably reproduced.

Yes, for examples, CRISPR screening hits were readily validated by independent CRIPSR targeting experiments. Antiviral phenotypes were confirmed in multiple cell backgrounds and in multiple biological replicates.

4. Randomization

Describe how samples/organisms/participants were allocated into experimental groups.

N/A

5. Blinding

Describe whether the investigators were blinded to group allocation during data collection and/or analysis.

One replicate of electron microscopy experiments was blinded so that analysis was done on individual samples prior to knowing the identify of the samples.

Note: all studies involving animals and/or human research participants must disclose whether blinding and randomization were used.

6. Statistical parameters

For all figures and tables that use statistical methods, confirm that the following items are present in relevant figure legends (or in the Methods section if additional space is needed).

n/a	Confirmed
☐	☒ The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement (animals, litters, cultures, etc.)
☐	☒ A description of how samples were collected, noting whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☐	☒ A statement indicating how many times each experiment was replicated
☐	☒ The statistical test(s) used and whether they are one- or two-sided (note: only common tests should be described solely by name; more complex techniques should be described in the Methods section)
☐	☒ A description of any assumptions or corrections, such as an adjustment for multiple comparisons
☐	☒ The test results (e.g. *P* values) given as exact values whenever possible and with confidence intervals noted
☐	☒ A clear description of statistics including central tendency (e.g. median, mean) and variation (e.g. standard deviation, interquartile range)
☐	☒ Clearly defined error bars

See the web collection on statistics for biologists for further resources and guidance.

Software

Policy information about availability of computer code

7. Software

Describe the software used to analyze the data in this study.	Prism 7

For manuscripts utilizing custom algorithms or software that are central to the paper but not yet described in the published literature, software must be made available to editors and reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). *Nature Methods* guidance for providing algorithms and software for publication provides further information on this topic.

Materials and reagents

Policy information about availability of materials

8. Materials availability

Indicate whether there are restrictions on availability of unique materials or if these materials are only available for distribution by a for-profit company.	No restrictions

9. Antibodies

Describe the antibodies used and how they were validated for use in the system under study (i.e. assay and species).	FLAG-M2 (Sigma #F2426), J2 dsRNA antibody (Scicons, 1:200), anti-GFP antibody (Abcam #6556), anti-HA antibody (BioLegend #901501), anti-IFI6 polycolonal antibody (ProSci, custom generated), anti-beta Actin (ab6276 Abcam), anti-HSPA5 (ThermoFisher PA5-34941), anti-calnexin (Enzo Life Sciences #ADI-SPA-860-D). Antibodies were validated by western blot or immunofuorescence using mock-transfected cells as controls. Alternatively, antibodies to host proteins were validated by showing that CRIPSR-targeted cells lacked expression of the protein target.

10. Eukaryotic cell lines

a. State the source of each eukaryotic cell line used.	Cell lines were obtained from colleagues (C.Rice, M.Diamond, JL.Casanova, N.Alto, N. Conrad)
b. Describe the method of cell line authentication used.	Common human cells lines wereauthenticated with STR analysis using the ATCC Cell Line Authentication service.
c. Report whether the cell lines were tested for mycoplasma contamination.	All cell lines are routinely tested for mycoplasma using a PCR based assay. (Vendor GeM Mycoplasma Detection Kit from Sigma Cat.#MP0025-1KT).
d. If any of the cell lines used are listed in the database of commonly misidentified cell lines maintained by ICLAC, provide a scientific rationale for their use.	No commonly misidentified cell lines were used.

Animals and human research participants

Policy information about studies involving animals; when reporting animal research, follow the ARRIVE guidelines

11. Description of research animals

Provide details on animals and/or animal-derived materials used in the study.	No animals were used.

Policy information about studies involving human research participants

12. Description of human research participants

Describe the covariate-relevant population characteristics of the human research participants.	The study did not involve human research participants.