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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	Invitrogen Attune NxT software
Data analysis	Graph Prism 7.0 Flowjow 10.5.2 MAGeCK 0.5.4 RIGER, as implemented in GENE-E version 3.0.215(https://software.broadinstitute.org/GENE-E/)

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

All data will be available on request from the authors.

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	No experiments presented in this study required sample size to be determined
Data exclusions	No data were excluded
Replication	All cell culture experiments were repeated at least two independent times. For these experiments cells were inoculated with different multiplicity of infection (MOI) and data presented in figures showed results for one representative MOI in the linear range of infection. All attempts at replication were successful
Randomization	No experiments presented in this study required randomization
Blinding	No experiments presented in this study required blinding

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
[ ]	[x] Antibodies
[ ]	[x] Eukaryotic cell lines
[x]	[ ] Palaeontology
[ ]	[x] Animals and other organisms
[ ]	[x] Human research participants
[x]	[ ] Clinical data

Methods

n/a	Involved in the study
[x]	[ ] ChIP-seq
[ ]	[x] Flow cytometry
[x]	[ ] MRI-based neuroimaging

Antibodies

Antibodies used	anti-FHL1 mAb (ref MAB5938, Biotchene), polyclonal anti-FHL1 rabbit Ab (ref NBP1-88745, Novus Biologicals) anti-GAPDH mAb (ref SC-47724, Santa Cruz Biotechnology), polyclonal rabbit anti-HA (ref 3724, Cell Signaling Technology), anti-FLAG M2 mAb (ref F1804, SIGMA), anti-RFP (ref 6G6, Chromotek), anti-CHIKV E2 mAb (3E4 was provided by V. Choumet, Insitut Pasteur), anti-alphavirus E2 mAb (CHIK-265 was provided by Michael Diamonds, University school of medicine, St Louis, USA), anti-vimentin antibody (ab24525, abcam), anti-EEEV E1 mAb (ref MAB8754, Sigma), anti-pan-flavivirus E protein mAb (4G2), anti-dsRNA J2 mAb (Scicons), Alexa FluorTM 488-conjugated goat anti-rabbit IgG (A11034, Invitrogen), Alexa FluorTM-647-conjugated goat anti-chicken IgG (ab150175, abcam), Alexa FluorTM 488-conjugated goat anti-mouse IgG (115-545-003, Jackson ImmunoResearch), Alexa FluorTM 647-conjugated goat anti-mouse IgG (115-606-062, Jackson ImmunoResearch), peroxydase-conjugated donkey anti-rabbit IgG (711-035-152, Jackson ImmunoResearch), and anti-mouse/HRP (P0260, Dako Cytomotion)
Validation	Anti-FHL1 antibody was validated by Western Blot and immunofluoresence assay. All the antibody used in this study have been already validated by manufacturers.

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	HAP1 cells were purchased from Horizon Discovery. 293FT were purchased from Thermo Fisher Scientific (R70007). HEK-293T and VeroE6 were purchased from ATCC. HepG2 and BHK21 were provided by Olivier Schwartz, (Institut Pasteur, France). Primary myoblasts and primary fibroblasts were provided by G. Bonne, R. Ben Yaou and A. Bertrand Legout (Institut de Myologie, France). Human placenta choriocarcinoma Bewo cells were provided by M. Lecuit (Institut Pasteur, France). AP61 mosquito (Aedes pseudoscutellaris) cells were provided by P. Despres (Institut Pasteur, France)
Authentication	none
Mycoplasma contamination	All cell lines were tested negative for mycoplasma contamination using the MycoAlert Myoplasma detection kit from Lonza Primary cell lines were not tested
Commonly misidentified lines (See ICLAC register)	No misidentified cell lines were used in this study

Animals and other organisms

Policy information about studies involving animals; ARRIVE guidelines