

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 (<i>n</i>) 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 <i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i>
☐	☒ 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. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted <i>Give P values as exact values whenever suitable.</i>
☒	☐ 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 <i>d</i> , Pearson's <i>r</i>), 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	Attune Cytometric v5.3.0 was used to collect flow cytometry data.
Data analysis	Applied Biosystems Design & Analysis 2.8.0 was used to analyze RT-qPCR data. FlowJo 10.8.0 was used to analyze Flow Cytometry data. FIJI 1.53q was used to quantify Western Blot images. GraphPad Prism 11.0.0 was used to generate graphs and perform statistical tests.

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](#)

qPCR CT values and Western blot images are provided in the Supplementary Data file. All other data is available upon reasonable request from B.W.

Research involving human participants, their data, or biological material

Policy information about studies with [human participants or human data](#). See also policy information about [sex, gender \(identity/presentation\), and sexual orientation](#) and [race, ethnicity and racism](#).

Reporting on sex and gender	N/A
Reporting on race, ethnicity, or other socially relevant groupings	N/A
Population characteristics	N/A
Recruitment	N/A
Ethics oversight	N/A

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	No sample size calculation was performed. In general we performed 3 biological replicates so that we could perform statistical tests since this is the minimum number of samples necessary to perform a test
Data exclusions	No data were excluded
Replication	Results were replicated across three biological replicates across different days by the same investigator. All data reported are robust and reproducible. Biological replicate is defined in this study as cells plated and treated with Cas protein in a cell culture dish. For 3 replicates, the cells were plated and treated on 3 separate days.
Randomization	All experiments were performed with human cell lines. The order in which flow cytometry samples were measured were randomized by masking the label until it is placed on the flow cytometer. qPCR data could not be randomized because knowledge of well position is needed to determine sample results. Allocation was decided by biological treatment and could therefore not be randomized. Our negative controls were performed at the same time as the test samples to control for other variables such as room temperature or cell passage number.
Blinding	Researchers were not blinded because experiments involved conditions with objectively measured outcomes and predefined treatment groups.

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
☒	☐ Plants

Methods

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

Antibodies

Antibodies used	BRCA1 (Santa Cruz Biotechnology sc-6954, 1:100), Mre-11 (Novus NB-100-142, 1:5000), and β -tubulin (Cell Signaling #2128, 1:1000), anti-mouse IgG HRP (Cell Signaling #7076, 1:5000), anti-rabbit IgG Alexa Fluor 647 (Invitrogen A21245, 1:1000)
Validation	Antibodies were used for immunoblot and the manufacturers validated all these antibodies for immunoblot use. We additionally validated the antibodies based on band size. Correct band size was confirmed by literature evidence and manufacturer reporting.

Eukaryotic cell lines

Policy information about [cell lines and Sex and Gender in Research](#)

Cell line source(s)	HEK 293T cells were received from ATCC (CRL-3216)
Authentication	None of the cell lines used were authenticated.
Mycoplasma contamination	All cell lines tested negative for Mycoplasma.
Commonly misidentified lines (See ICLAC register)	None were used.

Plants

Seed stocks	N/A
Novel plant genotypes	N/A
Authentication	N/A

Flow Cytometry

Plots

Confirm that:

- ☒ The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).
- ☒ The axis scales are clearly visible. Include numbers along axes only for bottom left plot of group (a 'group' is an analysis of identical markers).
- ☒ All plots are contour plots with outliers or pseudocolor plots.
- ☒ A numerical value for number of cells or percentage (with statistics) is provided.

Methodology

Sample preparation	Cells were detached from dish with trypsin, quenched with cell culture media, then pelleted and resuspended in ice cold 1X Hank's buffered salt saline and kept on ice until analyzed.
Instrument	Attune NxT Acoustic Focusing Cytometer (Applied Biosystems Model number AFC2)
Software	FlowJo software (version 10.8.1)
Cell population abundance	Cells were not sorted and entire live cell population was analyzed.
Gating strategy	Gating strategy can be found in Supplementary Figure S2. Cells were selected with FSC-H/SSC-A gates, then single cells were selected with SSC-H and SSC-A gates, then GFP and mCherry positive gates were drawn based on blank cell location in the YL2-H and BL1-H gates.

- ☒ Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information.