nature portfolio

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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	ImageLab software version 5.2.1 (Bio-Rad), Zeiss ZEN,
Data analysis	GraphPad Prism, Proteome Discoverer 2.1, Scaffold 4 Q+S, Alphafold (v2.3.2)

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

All the data can be found in either the main text or the supplementary materials. Source data are provided with this paper. The mass spectrometry proteomics data have been deposited to the ProteomeXchange with the dataset identifier PXD050108.

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	The number of samples was selected to ensure sufficient power for detecting statistically significant differences, based on standard calculations.
Data exclusions	No data were excluded from the analyses
Replication	Experiments were independently replicated to evaluate reproducibility and were confirmed to be reproducible. The methods employed are detailed in the manuscript.
Randomization	No randomization was required.
Blinding	The investigators were blinded to group allocation during data collection and/or analysis.

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	anti-WSTF (BAZ1B) antibody (ab51256, Abcam), (sc-514287, Santa Cruz Biotechnology), (#2152, Cell Signaling); anti-WDR48 (UAF1) antibody (sc-514473, Santa Cruz Biotechnology); anti-beta Tubulin antibody (ab15568, abcam); anti-FLAG antibody (F3165, Sigma); anti-SNF2H (SMARCA5) antibody (ab3749, Abcam); anti-GAPDH antibody (sc-32233, Santa Cruz Biotechnology); anti-Lamin B1 antibody (ab16048, Abcam); anti-V5 antibody (V8137, Sigma); anti-Histone H2A.X S139ph (phospho Ser139) antibody (GTX127340, GeneTex); anti-RFC4 antibody (ab182145, Abcam); anti-BRD4 antibody (A301-985A50, Bethyl); anti-PCNA antibody (sc-56, Santa Cruz

Biotechnology) (ab70472, abcam); anti-Ubiquityl-PCNA (Lys164) antibody (#13439, Cell Signaling); anti-USP1 antibody (A301-700A, Bethyl); anti-MBP antibody (sc-13564, Santa Cruz Biotechnology); anti-HSV tag antibody (ab19355, abcam); anti-Phospho-CHK1 (Ser345) antibody (#2348, Cell Signaling); anti-CHK1 antibody (#2360, Cell Signaling); anti-Phospho-CHK2 (Thr68) antibody (#2197, Cell Signaling); anti-CHK2 antibody (sc-17747, Santa Cruz Biotechnology); anti-casein kinase IIα' antibody (sc-514403, Santa Cruz Biotechnology); anti-RFC1 (sc-271656, Santa Cruz Biotechnology); anti-Histone H3 antibody (07-690, Merck); anti-Histone H2A.X antibody (#2595, Cell Signaling);

Validation

In the case of commercial antibodies, validations are available on manufacturer's website. Antibodies are further validated by ourselves using siRNA knockdown coupled with immunoblotting or purified protein binding.

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s)	Human embryonic kidney (HEK) 293T cells (CRL-3216), HeLa(CCL-2) and U2OS cells (HTB-96) (purchased from American Type Culture Collection (Manassas, VA)).
Authentication	none of cell lines used were authenticated
Mycoplasma contamination	Cells are not contaminated with Mycoplasma
Commonly misidentified lines (See ICLAC register)	No commonly misidentified cell lines were used in the study

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	Cell lines expressing ATAD5 Wild-type and B1m mutant in ATAD5 knock-out 293AD cells were labeled with 10mM EdU for 30 minutes before harvesting. For flow cytometry analysis, samples were prepared using the Click-iT™ Plus EdU Alexa Fluor™ 647 Flow Cytometry Assay Kit (Invitrogen) according to the manufacturer's instructions.
Instrument	FACSVerse™ flow cytometer (BD Biosciences)
Software	BD FACSuite™ software (BD Biosciences), FlowJo software (Tree Star)
Cell population abundance	N/A
Gating strategy	N/A

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