

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

n/a

Data analysis

STAR-aligner, DESeq2 (R), FeatureCounts (R), EnhancedVolcano (R)

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](#)

The RNA sequencing data described in this work is available on SRA.

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

The methods and results do not preferentially pertain to or affect one sex or gender.

Reporting on race, ethnicity, or other socially relevant groupings

The manuscript does not report on race, ethnicity or any other socially relevant groupings.

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 calculations were required for this study.

Data exclusions

No data were excluded from the analyses

Replication

A minimum of 3 biological replicates were performed for each experiment. If any technical replicates were performed, these were averaged and used as 1 biological replicate for that data point.

Randomization

No randomization was applied for any methods or analyses

Blinding

No blinding was applied for any methods or analyses.

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	<input type="checkbox"/> Involved in the study <input type="checkbox"/> Antibodies <input type="checkbox"/> Eukaryotic cell lines <input checked="" type="checkbox"/> Palaeontology and archaeology <input checked="" type="checkbox"/> Animals and other organisms <input checked="" type="checkbox"/> Clinical data <input checked="" type="checkbox"/> Dual use research of concern <input checked="" type="checkbox"/> Plants
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Methods

n/a	<input type="checkbox"/> Involved in the study <input checked="" type="checkbox"/> ChIP-seq <input checked="" type="checkbox"/> Flow cytometry <input checked="" type="checkbox"/> MRI-based neuroimaging
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Antibodies

Antibodies used

CDK4 anti-rabbit (Cell Signalling Technologies – D9G3E), β -actin anti-mouse (Invitrogen – 10515215), pRB anti-rabbit(Ser807/811, Cell Signalling Technology), and Total Rb anti-mouse (Cell Signalling Technology). Corresponding HRP-conjugated secondary antibodies (anti-rabbit: Cell Signalling Technologies – 7074S, anti-mouse: Invitrogen – A16078) were used for detection.

Eukaryotic cell lines

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

Cell line source(s)	HEK293 (ECACC), MCF-7 (ECACC) and MDA-MB-231 (ECACC)
Authentication	None of the cell lines used were authenticated.
Mycoplasma contamination	All cell lines were tested and found not to be contaminated by Mycoplasma
Commonly misidentified lines (See ICLAC register)	n/a

Plants

Seed stocks	n/a
Novel plant genotypes	n/a
Authentication	n/a