

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 |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> 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> |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> A description of all covariates tested |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> 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) |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> For null hypothesis testing, the test statistic (e.g. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted <i>Give P values as exact values whenever suitable.</i> |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> 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

Data analysis

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 atomic coordinates and structure factors have been deposited in the Protein Data Bank with the access code of 8CZJ (<https://www.rcsb.org/structure/unreleased/8CZJ>). The structural data cited in this study are available online under PDB ID: 5TSB (<https://www.rcsb.org/structure/5tsb>), PDB ID: 5TSA (<https://www.rcsb.org/structure/5tsa>) and PDB ID: 7Z6N (<https://www.rcsb.org/structure/7Z6N>). All data needed to evaluate the conclusions in the paper are present in the main text and/or in the Supplementary Information. The source data underlying Figures 5c, 5d, 7a, 7b, 8a, 8b, 9c and Supplementary Figures S4a, S8, S12 are provided as a Source Data file. Additional data related to this paper may be requested from the authors.

Human research participants

Policy information about [studies involving human research participants and Sex and Gender in Research](#).

Reporting on sex and gender

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

In one transport assay, three biological replicates were included for each condition/variant, which follows the convention of the field, and 2-3 independent experiments were conducted for each variant/condition. For other biochemical assays, one sample was included for each condition/variant in one experiment, and 2-3 independent experiments were conducted for each condition/variant. The results of independent experiments are similar and consistent.

Data exclusions

No data were excluded unless there is strong evidence showing experiment failure, for instance, cell culture contamination.

Replication

In one transport assay, three biological replicates were included for each condition/variant, which follows the convention in the field, and 2-3 independent experiments were conducted for each variant/condition. For other biochemical assays, one sample was included for each condition/variant in one experiment, and 2-3 independent experiments were conducted for each condition/variant. The results of independent experiments are similar and consistent.

Randomization

In transport assay, the same batch of cells cultured in different subwells in the same plate behave similarly and gave consistent results. Accordingly, there is no need of randomization. For other experiments, there was no process of selecting samples from a pool of candidates, so randomization was not applicable.

Blinding

As there was no process of selecting samples from a pool of candidates, blinding cannot be applied in this work. For all the experiments presented in this study, one person is usually responsible for one type of experiment from beginning till the end. For key experiments, the results have been confirmed by a second person.

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 |
|-------------------------------------|---|
| <input type="checkbox"/> | <input checked="" type="checkbox"/> Antibodies |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> Eukaryotic cell lines |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Palaeontology and archaeology |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Animals and other organisms |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Clinical data |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Dual use research of concern |

Methods

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

Antibodies

Antibodies used

Anti-Histag: Invitrogen, Catalog # 37-2900, Lot# WC318953
 Anti-HA: Thermo Fisher Scientific, Cat#26183, Lot# WJ331634
 Anti-beta actin: Cell Signaling Technology, Cat# 4970, Lot# 19
 Custom anti-BbZIP monoclonal antibody, generated by Creative Biolabs, Inc. using purified BbZIP as antigen.
 HRP-conjugated Horse anti-mouse IgG at 1:5000 from Cell Signaling Technology, Product # 7076S, Lot# 36
 HRP-conjugated Goat anti-rabbit IgG at 1:5000 from Cell Signaling Technology, Product # 7074S, Lot# 30
 Note: as this study has been conducted since 2017, the lot# of antibodies have been changed for multiple times and some records were missing. Only the Lot#s that are from the most recent experiments are reported.

Validation

Anti-Histag: Invitrogen, Catalog # 37-2900, Clone# 4A12E4. <https://www.thermofisher.com/antibody/product/6x-His-Tag-Antibody-clone-4A12E4-Monoclonal/37-2900>
 Anti-HA. Thermo Fisher Scientific (Invitrogen), Cat#26183, Clone# 2-2.2.14. <https://www.thermofisher.com/antibody/product/HA-Tag-Antibody-clone-2-2-2-14-Monoclonal/26183>
 Anti-beta-actin: Cell Signaling Technology, Cat# 4970, Clone# 13E5. <https://www.cellsignal.com/products/primary-antibodies/b-actin-13e5-rabbit-mab/4970>
 Custom anti-BbZIP monoclonal antibody, validation data is shown in Supplementary Figure 12.

Eukaryotic cell lines

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

Cell line source(s)

HEK293T from Human

Authentication

Purchased from ATCC, Catalog# CRL-3216

Mycoplasma contamination

The cell line is free of mycoplasma contamination.

Commonly misidentified lines
(See [ICLAC](#) register)

HEK293T is not listed in the misidentified lines.