

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

- fluorescence and absorption measurements in bacterial lysate: Tecan i-control v3.3
- size-exclusion chromatography: UNICORN 7.3 SP1 software
- fluorescence anisotropy and reporter-gene data: CLARIOstar 5.21R2
- fluorescence micrographs acquisition and evaluation: Nikon Elements Advanced Research software, ImageJ 1.8.0 and MATLAB 2019a.

Data analysis

- data analysis: Fit-O-Mat v0.741, Microsoft Excel v. 16.26, GraphPad Prism 7.0a

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

The data that support the findings of this study are available from the corresponding author upon reasonable request.

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](https://www.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	For all measurements, at least three biological replicates (i.e. independent samples) were analyzed and averaged. No statistical tests were used to determine sample size. Based on the resultant standard deviation across measurements, this sample size was considered appropriate.
Data exclusions	No data were excluded for biochemical analyses and membrane translocation experiments. Outliers for light-regulated gene expression were statistically determined and excluded as described in Jacobs JL, Dinman JD (2004) Systematic analysis of bicistronic reporter assay data. <i>Nucleic Acids Res</i> 32(20):e160–e160
Replication	Experiments were replicated as indicated. All replications yielded similar results; no replication failed.
Randomization	Not relevant, because the study did not involve experiments on animals or humans. All experiments were conducted with purified components, in bacterial lysate or in mammalian cell culture.
Blinding	Not relevant, because the study did not involve experiments on animals or humans. All experiments were conducted with purified components, in bacterial lysate or in mammalian cell culture.

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	Included in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> Antibodies
<input type="checkbox"/>	<input checked="" type="checkbox"/> Eukaryotic cell lines
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology
<input checked="" type="checkbox"/>	<input type="checkbox"/> Animals and other organisms
<input checked="" type="checkbox"/>	<input type="checkbox"/> Human research participants
<input checked="" type="checkbox"/>	<input type="checkbox"/> Clinical data

Methods

n/a	Included 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

Eukaryotic cell lines

Policy information about [cell lines](#)

Cell line source(s)	Chinese hamster ovary cells (CHO-K1; DSMZ, 497 Braunschweig, Germany); Mouse fibroblasts (NIH-3T3)
Authentication	Authentication by DSMZ employee; NIH-3T3 fibroblasts were authenticated by confirming morphology.
Mycoplasma contamination	Cell lines from DSMZ were bought without Mycoplasma contamination at DSMZ ; NIH-3T3 cell lines tested negative for mycoplasma contamination.
Commonly misidentified lines (See ICLAC register)	None