

## 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<br><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<br><i>Give <math>P</math> 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 Thermo Xcalibur 3.0.63 (LC-MS)

Data analysis The following softwares were used in this study: GraphPad Prism 8.0.3, Origin 7 SR4 v7.0552(B552) HKL2000, XDS (Version March 15, 2019), HKL2MAP, phenix.mr, phenix.autosol, phenix.refine in the PHENIX program suite (version 1.14-3260), phnix.map in the PHENIX program suite (version 1.19.2-4158), PyMOL (version 2.2.0), Proteome Discoverer 1.4.0.288, PEAKS Studio 10.0 build 20190129.

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](#)

Coordinates and structure factors have been deposited in the Protein Data Bank under accession codes 7F9F[<https://www.rcsb.org/structure/7F9F>] (nThC), 7F91[<https://www.rcsb.org/structure/7F91>] (Met substituted rThC), 7F9G[<https://www.rcsb.org/structure/7F9G>] (rThC in complex with Ca<sup>2+</sup> and fucose), 7FBL[<https://www.rcsb.org/structure/7FBL>] (rThC in complex with Ca<sup>2+</sup> and mannose), and 7F9J[<https://www.rcsb.org/structure/7F9J>] (rThC Q25K in complex with Ca<sup>2+</sup>). All

other data are available in the main text or the supplementary materials. SwissProt accession number: C0HM62 for Thrombocorticin was assigned. Source data are provided with this paper.

## 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	More than three experiments are performed to gain statistical data. This sample size was used in our previous experiments, for example Blood 127, 1307-1316 (2016).
Data exclusions	No data were excluded
Replication	All measurements are replicated with at least three sets of experiments. P values, 95% confidence intervals, or table of analysis are given either in main text or supporting information.
Randomization	Cells were randomly allocated from the culture flask to multi well plates to perform cell proliferation experiments.
Blinding	Not relevant to this study. All data collected are either controlled (cell proliferation assays), or quantitative (X-ray diffraction, LC-MS), and no subjective judgments are required. All the data used in this paper are provided in the paper, supporting information, source data and public databases.

## 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 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 type="checkbox"/>            | <input checked="" 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                          |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Dual use research of concern           |

### 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 |

## Antibodies

Antibodies used	phospho-JAK2 Cell Signaling Technology #3771 Dilution 1:1000 phospho-STAT5 Cell Signaling Technology #9359 Dilution 1:1000 phospho-ERK1/2 Cell Signaling Technology #9101 Dilution 1:1000 phospho-AKT Cell Signaling Technology #4060 Dilution 1:1000 JAK2 Cell Signaling Technology #3230 Dilution 1:2000 STAT5 Cell Signaling Technology #94205 Dilution 1:2000 ERK1/2 Cell Signaling Technology #9102 Dilution 1:2000 AKT Cell Signaling Technology #9271 Dilution 1:2000 MPL Merck Millipore #06-044 Dilution 1:2000 b-actin Cell Signaling Technology #4967 Dilution 1:20000
Validation	Validated by manufacturer. Details are provided in source data

## Eukaryotic cell lines

Policy information about [cell lines](#)

Cell line source(s)	Ba/F3 cells , gift from Nissan Chemical Co. Ltd and Dr. Megumi Funakoshi-Tago at Faculty of Pharmacy, Keio University. iPS cells were from our previous study (Br J Haematol. 2018 Jun;181(6):791-802.)
Authentication	Not authenticated
Mycoplasma contamination	cell line was not tested for Mycoplasma contamination
Commonly misidentified lines (See <a href="#">ICLAC</a> register)	not relevant to this study

## Animals and other organisms

Policy information about [studies involving animals](#); [ARRIVE guidelines](#) recommended for reporting animal research

Laboratory animals	No laboratory animals were used.
Wild animals	The marine sponge Corticium sp. was collected using SCUBA. The specimen was frozen immediately after collection and identified as indicated in our previous publication in ref 12. All sponge material was used for isolation of the lectin.
Field-collected samples	The sponge specimen was kept frozen at -20 degree until use.
Ethics oversight	The sponge specimen was collected under permission of Chuuk State Department of Marine Resources.

Note that full information on the approval of the study protocol must also be provided in the manuscript.