nature portfolio

Corresponding author(s): Dr. Salla Koskela, Prof. Markus Linder

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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	No software was used
Data analysis	No software was used

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 data that support the findings of this study are available from the corresponding author upon request, and the source data are present.

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	This information has not been collected as the research did not involve these topics
Reporting on race, ethnicity, or other socially relevant groupings	See above
Population characteristics	See above
Recruitment	See above
Ethics oversight	See above

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 calculation was performed in the study. The sample sizes (minimum 3 replicates of each datapoint) were chosen to obtain sufficient data for calculation of average values and standard deviations when appropriate. Furthermore, all cultivations were performed with minimum three biological replicates with photographs of the representative flasks shown.
Data exclusions	As indicated within the description of the ELISA assay procedure in the materials and methods section, we have excluded all measured absorbance values, or B B0^-1 values <0.2 or >0.8 as they were outside the linear region of the standard curve. The data exclusion was performed strictly according to the manufacturer's instructions. No other data was excluded from the analyses.
Replication	The authors confirm that all the possible efforts were taken to replicate the experimental findings and all attempts at replication were successful. The key findings on cell-mediated protein gelation were replicated multiple times during the course of the study. The gelation was found successful in the replications of not only same cultivation volume but also across various cultivation volumes needed for different analyses.
Randomization	Not relevant as no statistical analysis was performed in this study
Blinding	Not relevant as no statistical analysis was performed in this study

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	1. Invitrogen 6x-His Tag Monoclonal Antibody (His.H8) HRP, REF MA1-21315-HRP, LOT AC410961.

2. BioLegend FITC anti-Ha.11 Epitope Tag, clone 16B12, Isotype Mouse IgG1, CAT 901507, LOT B363377.
3. Cayman Chemical His-Tag Detection ELISA kit, REF 10012445, Batch no. 0811395, containing His ELISA monoclonal antibody REF 400242, Batch/LOT 0800896-1; and Goat Anti-Mouse IgG coated plate, REF 400009, Batch/LOT 0800549-2

Validation

1. Invitrogen 6x-His Tag Monoclonal Antibody HRP, REF MA1-21315-HRP: The antibody has been validated by the manufacturer for use in Western blotting applications against proteins bearing 6x-His Tags. The antibody has been widely used with 46 reference publications, including that of proteins produced in Saccharomyces cerevisiae (Lee-Soety J. et al. 2012, Biochemical and Biophysical Research Communications 426,1:12-17).
2. BioLegend FITC anti-Ha.11 Epitope Tag, clone 16B12, Isotype Mouse IgG1, CAT 901507: Each lot of this antibody is quality control tested by immunofluorescent staining with flow cytometric analysis by the manufacturer. Its is ensured with extreme specificity that allows unambiguous identification and quantitative analysis of the tagged protein where the HA epitope is located in the middle of protein sequences as well as at the N- or C-terminus. Use of the antibody for FACS analysis with Saccharomyces cerevisiae has been reported (Kishkevich A. et al. 2025, ACS Synthetic Biology 14,9:3473-3486).
3. Cayman Chemicals, His ELISA monoclonal antibody REF 400242: The antibody has been formulated and tested to work with Cayman's ELISA kits. Use of the kit to detect recombinant proteins bearing His-tags has been reported (Zhang L. 2026, 102923 Cell Reports Medicine).

Plants

Seed stocks

Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.

Novel plant genotypes

Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.

Authentication

Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosiacism, off-target gene editing) were examined.

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

The surface display library was cultivated in liquid MM with 2% (w/v) glucose (30°C, 250 rpm). After 24 hours, the cell density (OD600) was determined, and ca. 10 million cells were collected by centrifugation (3000 g, 5 min). The growth medium was removed, and the cells resuspended in 500 µL of PBS, pH 7.4. The centrifugation and resuspension steps were repeated twice to fully remove the growth medium. The surface displayed proteins were probed and the cells stained with 1 µL anti-HA.11 epitope tag antibody conjugated to fluorescein isothiocyanate (FITC) (BioLegend, 1 mg/ml). After 20 min incubation on ice, the excess antibodies were removed by washing the cells twice in PBS. Prior the FACS analysis, the cells were resuspended in 1 ml of PBS. The empty control strain yAK003 was similarly cultivated and stained.

Instrument

FACSAria III ACDU 4L with temperature control, serial number P648282C200

Software

BD FACSDiva version 8.0

Cell population abundance

The dot plot of the surface display library contained in total 5812 events of which 238 were in the selected gate used in the sorting. The cells were sorted and in total 500 cells that passed through the defined gate were collected. All the collected cells were plated. The cells were plated under sterile conditions on selective MM agar plates without leucine. After incubation, the plates were visually observed to ensure they were free from contamination.

Gating strategy

Yeast cells were gated based on morphology (FSC-A vs SSC-A), followed by selection of single cells to prevent sorting of doublets (FSC-W vs FSC-H and SSC-W vs SSC-H). The gate P3 was generated in plot SSC-W vs SSC-H, but the outline of the gate was based on all three plots: FSC-A vs SSC-A, FSC-W vs FSC-H, and SSC-W vs SSC-H. Finally, P3 gated events with the highest fluorescence intensity were sorted from the “High” gate (FITC-A vs FSC-A).

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