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Corresponding author(s): Hegde

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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	Mass spectrometry data were collected using a Q Exactive Plus hybrid quardrupole-Orbitrap mass spectrometer (Thermo Fisher Scientific) equipped with a nanospray ion source. Phosphorimaging of radioactive samples was acquired on Typhoon FLA7000 (GE Healthcare). Flow cytometry data were collected using Becton Dickinson LSRII instrument.
Data analysis	ImageJ (version 2.0.0-rc-69/1.52p) was used to display densitometry of autoradiographs. FlowJo (version 10.6.2 for Mac OS X operating system) was used to plot flow cytometry data. Mass spectrometry raw files were processed using Proteome Discoverer (version 2.1, Thermo Scientific). MS/MS spectra were searched against mammals, UniProt Fasta database using Mascot (version 2.4, Matrix Science) search engine. Scaffold 4 Version 4.8.9 (www.proteomesoftware.com) was used to analyze mass spectrometry data.

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

No datasets were generated or analysed during the current study.

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 performed. Biochemical experiments were repeated on independent days to verify reproducibility with no further statistical testing.
Data exclusions	No data were excluded from the analysis.
Replication	Biochemical experiments were replicated to verify reproducibility. No attempts at replication failed. Details are provided in the "Statistics and Reproducibility" section of the Methods.
Randomization	Randomisation is not relevant to this study which reports biochemical analyses.
Blinding	Blinding is not relevant to this study which reports biochemical 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	Involved in the study
☐	☒ Antibodies
☐	☒ Eukaryotic cell lines
☒	☐ Palaeontology
☒	☐ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☐	☒ Flow cytometry
☒	☐ MRI-based neuroimaging

Antibodies

Antibodies used	CCDC47 antibody #1 (A305-100A-1) and CCDC47 antibody #2 (A305-101A-1) were obtained from Bethyl-laboratories and each was used at 1:5,000 for immunoblotting and 1:500 for IPs. FLAG immunoprecipitations (IPs) were performed using FLAG-M2 affinity gel (Sigma, Lot # SLBW6125) and used at 1:100 dilution for IPs. Anti-HA antibody (1:500 for IPs) was generated in house and has been described (Itakura et al., 2016, Mol. Cell, 63:21-33). Signal Peptide Peptidase (SPP) antibody was purchased from Bethyl Laboratories (Lot # A304-404A-1) and used at 1:250 dilution for IPs. Anti-Asterix (WDR83OS) antibody was purchased from Sigma/Human Protein Atlas (HPA065685, Lot # A304-404A-1) and used at 1:1,000 for immunoblotting and 1:250 for IPs. Anti-UBQLN2 antibody was clone 5F5 obtained from Sigma (WH0029978M3, Lot # FB261-5F5) and used at 1:250 for IPs. Anti-SRP54 was from BD Biosciences (610940, Lot # 7157596) and used at 1:200 for IPs. Custom antibodies against Sec61-beta (1:10,000 for immunoblotting, 1:500 for IPs), TRAP-alpha (1:5,000 for immunoblotting, 1:500 for IPs), and TRAM (1:5,000 for immunoblotting, 1:500 for IPs) have been described previously (Fons et al., 2003, J. Cell Biol.,160:529-30). Custom antibody against Sec61-alpha (1:5,000 for immunoblotting, 1:500 for IPs) has been described previously (Song et al., 2000, Cell, 100:333-343). Custom antibody against SPC12 (1:5,000 for immunoblotting) has been described previously (Gorlich and Rapoport, 1993, Cell, 75:615-630). Custom antibody against Sec63 (1:2,000 for immunoblotting) has been described previously (Garrison et al., 2005, Nature, 436:285-289). Calnexin antibody (1:5,000 for immunoblotting) was from Enzo Lifesciences (#ADI-SPA-865). BiP antibody (1:1,000 for immunoblotting) was from BD Biosciences (#610978). PDI antibody (1:1,000 for immunoblotting) was from Enzo Lifesciences (#ADI-SPA-890). EMC5 antibody (1:1,000 for immunoblotting) was from Abcam (#Ab174366).
Validation	Antibodies were not validated. Specificity controls are displayed within the figures of the manuscript.

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	HEK293 FRT/TO TRex cells from Invitrogen.
Authentication	The validity of this cell line was ensured by the antibiotic resistance markers within its genome and by its unique FRT site downstream of a doxycycline-inducible promoter.
Mycoplasma contamination	Cell lines were negative for mycoplasma. They are tested monthly.
Commonly misidentified lines (See ICLAC register)	None used.

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	Cells were washed with PBS and trypsinised. After inhibiting trypsin, cells were collected into 1.5 ml tubes, spun at 5,000 rpm for 3 min at 4°C, washed with 1 ml of ice cold PBS, spun again and resuspended in 500 µl of ice cold PBS for immediate analysis by flow cytometry.
Instrument	LSRII instrument (Becton Dickinson).
Software	FlowJo software (version 10.6.2 for Mac OS X operating system).
Cell population abundance	No staining was performed and no sorting was performed. All transfected live cells were counted in the analysis. Transfection was judged by GFP reporter expression. Cell viability was judged by the absence of DAPI staining.
Gating strategy	No gating or sorting was performed. All transfected live cells were counted in the analysis. Transfection was judged by GFP reporter expression. Cell viability was judged by the absence of DAPI staining. Examples of dot plots representing the raw data used to generate the histograms are shown in Extended Data Fig. 6 and 7.

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