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Reporting Summary

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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 All analyses involved standard Python or R libraries used for basic data processing, statistics, machine learning, and plotting.

Data analysis

```

Python 3.9.12
gprofiler-official==1.0.0
lifelines==0.27.3
matplotlib==3.5.1
numpy==1.21.5
pandas==1.4.2
scikit-learn==1.0.2
scipy==1.10.0
statsmodels==0.13.5

R 4.1.2
metafor==4.2.0
  
```

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](#)

All data are available upon reasonable request with formal applications submitted to respective cohort committees to protect patient sensitive data. Stanford data (including Stanford-ADRC, SAMS, BPD, SCMD) can be requested at <https://web.stanford.edu/group/adrc/cgi-bin/web-proj/datareq.php>. Data from specific Stanford cohorts can be requested to the following cohort leaders: ADRC, Tony Wyss-Coray (twc@stanford.edu); SAMS, Beth Mormino (bmormino@stanford.edu) or Anthony Wagner (awagner@stanford.edu); BPD and SCMD, Kathleen Poston (klposton@stanford.edu). Knight-ADRC proteomics data were generated by the laboratory of principal investigator Carlos Cruchaga (cruchaga@wustl.edu) and are available upon reasonable request at <https://knightadrc.wustl.edu/professionals-clinicians/request-center-resources/submit-a-request/>. ADNI data can be requested at the ADNI database (<https://adni.loni.usc.edu/>). DIAN data can be requested at <https://dian.wustl.edu/our-research/for-investigators/diantu-investigator-resources/dian-tu-biospecimen-request-form/>. Pseudonymized BioFINDER2 data can be shared to qualified academic researchers after request to cohort leader Oskar Hansson (oskar.hansson@med.lu.se) for the purpose of replicating procedures and results presented in the study. Data transfer must be performed in agreement with EU legislation regarding general data protection regulation and decisions by the Ethical Review Board of Sweden and Region Skåne. Kuopio data can be requested and accessed via a repository on Terra https://app.terra.bio/#workspaces/marsh-terra-inph/INPH_Proteomics_Workspace. ROSMAP data can be requested at <https://www.radc.rush.edu> and www.synapse.org. ARIC proteomics data is available through the NHLBI Biologic Specimen and Data Repository Information Coordinating Center (<https://biolincc.nhlbi.nih.gov/studies/aric/>). Additional ARIC requests for clinical or proteomic data from individual investigators may be submitted to the ARIC steering committees and will be reviewed to ensure that data can be shared without compromising patient confidentiality or breaching intellectual property restrictions. Participant-level demographic, clinical and proteomic data may be partially restricted based on previously obtained participant consent. Data sharing restrictions may also be applied to ensure consistency with confidentiality or privacy laws and considerations (<https://sites.csc.unc.edu/aric/>).

Here are links and citations to gprofiler39 (<https://biit.cs.ut.ee/gprofiler/gost>) Gene Ontology40,41 database (<https://geneontology.org/>) and SynGO42 database (<https://www.syngoportal.org/>).

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

Cohorts were generally age-sex matched between AD cases and controls. Sex was included as a covariate for all major regression models. The YWHAG:NPTX2 ratio changes with cognitive impairment, similarly in both sexes.

Reporting on race, ethnicity, or other socially relevant groupings

Race and other cohort demographics are provided in Supplementary Tables 1 (CSF) and 10 (plasma)

Population characteristics

PARTICIPANTS

Age, sex, race, APOE4 genotype, PTau181:AB42 distributions for each cohort are provided in Supplementary Tables 1 (CSF) and 10 (plasma). Sporadic AD cohorts were made up of participants of ages around 50-90. DIAN, the autosomal dominant AD cohort, was made up of participants around ages 20-60.

Stanford (ADRC, SAMS, BPD, SCMD)

Plasma and CSF collection, processing, and storage for all Stanford cohorts followed a single standard procedure. All studies were approved by the Institutional Review Board of Stanford University and written informed consent or assent was obtained from all participants or their legally authorized representative.

Blood collection and processing followed a rigorous standardized protocol to minimize variation. Briefly, about 10cc of whole blood was collected in 4 vacutainer ethylenediaminetetraacetic acid (EDTA) tubes (Becton Dickinson) and spun at 1800 x g for 10 minutes to separate out plasma, leaving 1cm of plasma above the buffy coat to avoid contamination. Plasma was aliquoted into polypropylene tubes and stored at -80°C. Processing took approximately one hour draw to freezing and storage. All draws occurred in the morning to minimize circadian effects.

CSF was collected via lumbar puncture using a 20-22 G spinal needle that was inserted in the L4-L5 or L5-S1 interspace. CSF samples were immediately centrifuged at 500 x g for 10 minutes, aliquoted in polypropylene tubes, and stored at -80°C.

Plasma from all Stanford cohorts were sent to Somalogic for proteomics (v4.1 SOMAscan, ~7,000 proteins) in the same batch. CSF samples from all Stanford cohorts were sent to Somalogic for proteomics (v4.0 SOMAscan, ~5,000 proteins) in the same batch. Core CSF AD biomarkers Aβ42, Aβ40, and pTau181 were measured using the fully automated Lumipulse G 1200 instrument (Fujirebio US, Malvern, PA) as previously described^{1,2}. Descriptions for each cohort are provided below.

A total of 1160 plasma samples (738 participants, longitudinal sampling) and 371 CSF samples (371 participants, 1 sample from each) from Stanford were included in this study. Per-cohort sample sizes are as follows: ADRC plasma n=827 (423 participants), CSF n=113; SAMS plasma n=222 (215 participants), CSF n=169. BPD plasma n=55 (55 participants), CSF n=68. SCMD plasma n=45 (45 participants), CSF n=21.

Stanford- Alzheimer's Disease Research Center (ADRC)

Samples were acquired through the National Institute on Aging (NIA)-funded Stanford-ADRC, a longitudinal observational study of clinical dementia subjects and age-sex-matched nondemented subjects. Healthy control participants were deemed cognitively unimpaired during a clinical consensus conference that included board-certified neurologists and neuropsychologists. Cognitively impaired subjects underwent Clinical Dementia Rating and standardized neurological and neuropsychological assessments, including procedures of the National Alzheimer's Coordinating Center (<https://naccdata.org/>), to determine cognitive and diagnostic status. Cognitive status was determined in a clinical consensus conference that included neurologists and neuropsychologists. All participants were free from acute infectious diseases and in good physical condition.

Stanford Aging and Memory Study (SAMS)

SAMS is an ongoing longitudinal study of healthy aging. Blood and CSF collection/processing and neurological/neuropsychological assessments were performed by the same team and followed the same protocol as in Stanford-ADRC. All SAMS participants had CDR=0 and a neuropsychological test score within the normal range; all SAMS participants were deemed cognitively unimpaired during a clinical consensus conference that included neurologists and neuropsychologists.

Stanford Biomarkers in Parkinson's Disease Study (BPD)

The BPD cohort³ was a Michael J Fox Foundation for Parkinson's Research (MJFF) funded longitudinal study of biomarkers associated with cognitive decline in Parkinson's disease (PD). Research participants were recruited from the Stanford Movement Disorders Center between 2011-2015 with a PD diagnosis according to UK Brain Bank criteria and required bradykinesia with muscle rigidity and/or rest tremor. All participants completed baseline cognitive, motor, neuropsychologic, imaging, and biomarkers assessments (plasma and optional CSF) including Movement Disorders Society-revised Unified Parkinson's Disease Rating Scale (MDS-UPDRS). Age-match Healthy Controls (HC) were also recruited to control for age-associated biomarker changes. After comprehensive neuropsychological battery all participants were given a cognitive diagnosis of no cognitive impairment, mild cognitive impairment, or dementia, according to published criteria.

Stanford Center for Memory Disorders Cohort Study (SCMD)

The SCMD was an NIA-funded cross-sectional study of people across the cognitive continuum. Participants with mild dementia due to Alzheimer's (AD) and amnesic mild cognitive impairment (aMCI) were recruited from the Stanford Center for Memory Disorders between 2011-2015. Participants were included if they had a diagnosis of probable AD dementia (amnesic presentation) according to the National Institute on Aging-Alzheimer's Association⁴ (NIA-AA) criteria and a Clinical Dementia Rating (CDR) score of 0.5 or 1, or a diagnosis of MCI according to the NIA-AA criteria⁴, a score of 1.5 SDs below age-adjusted normative means on at least one test of episodic memory, and a CDR score of less than 1. Healthy older controls (HC) were recruited from the community, were selected to have a similar average age as enrolled patients, and were required to have normal neuropsychological performance and CDR of 0. Participants completed cognitive, neuropsychologic, imaging, and biomarker assessments with plasma.

Knight- Alzheimer's Disease Research Center (ADRC)

The Knight-ADRC cohort is an NIA-funded longitudinal observational study of clinical dementia subjects and age-matched controls. Research participants undergo longitudinal cognitive, neuropsychologic, imaging and biomarker assessments including Clinical Dementia Rating (CDR). AD cases corresponded to those with a diagnosis of dementia of the Alzheimer's type (DAT) using criteria equivalent to the National Institute of Neurological and Communication Disorders and Stroke-Alzheimer's Disease and Related Disorders Association for probable AD, and AD severity was determined using the Clinical Dementia Rating (CDR) at the time of lumbar puncture (for CSF samples) or blood draw (for plasma samples). Controls received the same assessment as the cases but were nondemented (CDR=0).

Blood samples were collected in EDTA tubes (Becton Dickinson vacutainer purple top) at the visit time, immediately centrifuged at 1,500g for 10min, aliquoted on two-dimensional barcoded Micronic tubes (200ul per aliquot) and stored at -80°C. The plasma was stored in monitored -80°C freezer until it was pulled and sent to Somalogic (SOMAScan7k) for data generation. Proteomics data from 2,112 plasma samples from each of 2,122 participants were included in this study.

CSF samples were collected through lumbar puncture from participants after an overnight fast. Samples were processed and stored at -80 °C until they were sent for protein measurement. Proteomics data from 927 CSF samples from each of 927 participants were included in this study. CSF samples from Knight-ADRC, ADNI, and DIAN were sent for proteomics using the SOMAScan platform (SOMAScan7k) in the same batch. CSF Aβ₄₂, Aβ₄₀, and pTau181 were measured using the LUMIPULSE G1200 immunoassay platform according to the manufacturer's specifications.

The Institutional Review Board of Washington University School of Medicine in St. Louis approved the study and research was performed in accordance with the approved protocols.

Alzheimer's Disease Neuroimaging Initiative (ADNI)

ADNI is a longitudinal multi-center study designed to develop early biomarkers of AD. All data used in this study were accessed from the ADNI database <https://adni.loni.usc.edu/>. ADNI investigators assessed and diagnosed subjects as either cognitively normal (CN; Mini Mental State Examination [MMSE] ≥ 24, Clinical Dementia Rating [CDR]=0, non-depressed), mildly cognitively impaired (MCI; MMSE ≥ 24, CDR=0.5, objective memory-impairment on education-adjusted Wechsler Memory Scale II, preserved activities of daily living) or demented (MMSE = 20-26, CDR > 0.5, NINCDS/ADRDA criteria for probable AD). Comprehensive details on study design, data acquisition, ethics, and policies can be found above. CSF Aβ₄₂, pTau181 were measured using the xMAP immunoassay platform according to the manufacturer's specifications. Proteomics data from 725 CSF samples from each of 725 participants were included in this study.

Dominantly Inherited Alzheimer Network (DIAN)

DIAN, led by Washington University School of Medicine in St. Louis, is a family-based long-term observational study designed to understand the earliest changes of autosomal dominant AD (ADAD). All participants undergo clinical and cognitive batteries (i.e. Clinical Dementia Rating – Global). Comprehensive details on study design, data acquisition, ethics, and policies can be found at <https://dian.wustl.edu/>. The data used in this study are from data freeze 15 (DF15). CSF Aβ₄₂, pTau181 were measured using the LUMIPULSE G1200 platform according to the manufacturer's specifications. Proteomics data from 455 CSF samples from each of 455 participants were included in this study.

BioFINDER2

BioFINDER2 is a Swedish prospective cohort study (NCT03174938) on age-related neurodegenerative diseases. AD was diagnosed based on the Diagnostic and Statistical Manual of Mental Disorders (5th edition) and Aβ positivity (CSF Aβ42:Aβ40). Proteomics data from a total of n=829 participants, consisting of n=480 cognitively unimpaired, n=213 with mild cognitive impairment and n=136 with AD dementia were included in this study. CDR-Global scores were not measured in BioFINDER2, so for estimation, AD participants were subdivided according to Mini-Mental State Examination (MMSE) thresholds defined in Pernecky et. al.⁵: 21–25 for mild dementia (CDR=1), 11–20 for moderate dementia (CDR=2), 0–10 for severe dementia (CDR=3). The participants were recruited at Skåne University Hospital and the Hospital of Ångelholm, Sweden. The study was approved by the Regional Ethical Committee in Lund, Sweden, and all participants gave written informed consent.

CSF samples were collected close in time after baseline clinical examination and handled according to established preanalytical protocols, previously described in detail⁶. All analyses were performed by technicians blinded to all clinical and imaging data. CSF P-tau181, Aβ42 and Aβ40 was measured using Elecsys assays in accordance with the manufacturer's instructions (Roche Diagnostics International Ltd). CSF Aβ42/Aβ40 was used to define Aβ positivity according to previously established cutoffs of < 0.087. CSF samples from the BioFINDER2 cohort were analyzed with liquid chromatography-tandem mass spectrometry (LC-MS/MS), previously described in detail⁸.

Tau-PET was performed using [¹⁸F]RO948. Standardized uptake value ratio (SUVR) images were created for the 70–90 min post-injection interval using the inferior cerebellar cortex as reference region. A composite corresponding to a Braak I-IV meta-region of interest was used to represent AD-related tau tangle pathology.

Kuopio University Hospital

The Kuopio Normal Pressure Hydrocephalus (NPH) and AD Registry and Tissue Bank includes patients from the Eastern Finnish population who were referred to the KUH neurosurgical unit for suspected NPH. The registry's inclusive criteria encompass a wide range of hydrocephalic conditions and comorbidities: patients must exhibit one to three symptoms potentially associated with NPH (such as impaired gait, cognition, or urinary continence) along with enlarged brain ventricles (Evans' index > 0.3) as seen on computer tomography (CT) or magnetic resonance imaging (MRI), and no other clear cause that alone explains the observed findings and symptoms. Preoperative comorbidities and conditions were recorded at baseline, and patients underwent a systematic differential diagnostic workup followed by a CSF tap test paired with gait evaluation.

Diagnostic right frontal cortical brain biopsy was taken from all the patients during shunt surgery from the insertion site of the intraventricular catheter. A neuropathologist (TR) analyzed immunoreactivity for Aβ and hyperphosphorylated tau with light microscopy and the results were graded as present or absent. The patients were then further classified into groups by the presence of the pathology of Aβ and/or HPT observed in the frontal cortical biopsies⁹. Follow-up was conducted on all operated patients, with optimal shunt function ensured through valve adjustment, brain imaging, shunt valve tapping, lumbar infusion testing, and shunt revision if necessary. CDR-Global scores were not measured in Kuopio, so the CERAD cognitive score¹⁰ including MMSE was used instead. The latest follow-up MMSE score <26 was considered as at least mild dementia⁹.

Lumbar CSF proteomics was performed using high-throughput tandem mass tag (TMT)-labelling mass spectrometry, previously described in detail¹¹. Data from 90 subjects with CSF proteomics and cognitive scoring performed within 1 year were included in this study.

The study was conducted according to the Declaration of Helsinki and all patients provided informed consent. The Research Ethics Committee of the Northern Savo Hospital District (decision No 276/13.02.00/2016).

Religious Order Study and Rush Memory and Aging Project (ROSMAP)

All ROSMAP participants enrolled without known dementia and agreed to detailed clinical evaluation and brain donation at death¹². Both studies were approved by an Institutional Review Board of Rush University Medical Center (ROS IRB# L91020181, MAP IRB# L86121802). Both studies were conducted according to the principles expressed in the Declaration of Helsinki. Each participant signed an informed consent, Anatomic Gift Act, and an (Rush Alzheimer's Disease Center) RADC Repository consent (IRB# L99032481) allowing their data and biospecimens to be repurposed. All MAP participants and a subset of ROS have blood drawn during an annual home visit. For plasma, blood is drawn in a lavender (purple) top EDTA tube. For out of town ROS sites, they were spun, aliquoted into nunc vials, stored in dry ice and sent to the RADC by FedEx where they were transferred to -80°C. Samples collected in the northeastern Illinois were brought to the RADC laboratory and processed there with the same procedures. A total of 1046 55ul samples were shipped to Stanford, then to Somalogic for proteomics (SOMAScan7k). 973 samples passed quality control.

Clinical and neuropathologic data collection has been reported in detail^{13–17}. Regarding clinical diagnosis, an actuarial decision tree designed to mimic expert clinical judgment was implemented by computer to inform several clinical diagnoses, including dementia and AD. It combines data reduction techniques for the cognitive performance testing with a series of discrete clinical judgments made in series by a neuropsychologist and a clinician. Presumptive diagnoses of dementia and AD are calculated that conform to accepted clinical criteria. The clinician is asked to agree or disagree with the decisions. An algorithm uses these decisions to provide diagnoses of MCI and amnesic MCI. Persons with MCI are judged to have cognitive impairment by the neuropsychologist without a diagnosis of dementia by the clinician. Persons without dementia or MCI are categorized as having no cognitive impairment (NCI).

CDR-Global scores were not assessed in ROSMAP. Rather, participants underwent a battery of 21 cognitive performance tests, 17 of which were combined into a measure of global cognition which was z-scored based on the mean and standard deviation of all participants from baseline¹⁸. For estimation participants were subdivided according to Global Cognition z-scores: cognitively normal = z-score > 0, mild cognitive impairment = -1 < z-score < 0, mild dementia = -2 < z-score < -1, moderate dementia -3 < z-score < -2, and severe dementia z-score < -3. These cutoffs were set based on distributions of Global Cognition z-scores per clinical diagnosis. Details on cognitive scores, neuropathology, and other patient info are

described at <https://www.radc.rush.edu/documentation.htm>. Proteomics data from 973 plasma samples from each of 890 participants were included in this study.

Global Neurodegeneration Proteomics Consortium (GNPC)

The GNPC19 is a major neurodegenerative disease biomarker discovery effort, which hosts the largest collection of SomaScan data (over 40,000 patient samples from over 20 international research groups) from patient samples across healthy aging, Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis (ALS), and frontotemporal dementia (FTD). All cohorts and data are anonymized. Cohorts that measured CDR-Global cognitive scores were included in this study.

Atherosclerosis Risk in Communities (ARIC) Study

ARIC is a prospective epidemiologic study conducted in four U.S. communities: Forsyth County, NC; Jackson, MS; the northwest suburbs of Minneapolis, MN; and Washington County, MD. The ARIC study enrolled 15,792 mostly white and black participants aged 45-64 between 1987-1989/20. After initial enrollment, participants had four additional in-person visits: Visit 2 (1990-1992), Visit 3 (1993-1995), Visit 4 (1996-1999), Visit 5 (2011-2013). Participants were invited back for Visit 6 (2016-2017) after five years, and Visit 7 (2018-2019) immediately thereafter. Additional follow-up visits are ongoing. Blood was drawn for proteomic analysis at Visits 2 and 5. For this manuscript, late-life (8-year) dementia risk was assessed between Visit 5 and 7. Plasma was collected using standardized protocols and frozen at -80°C until analysis. Proteins were measured using the SomaScan v4.0 assay; protein QC steps have been described in detail previously²¹.

Dementia was adjudicated through cognitive assessment tests, telephone screening, informant ratings, hospital records, and death record review, as previously described²². From Visits 2 through 4, a 3-instrument cognitive assessment was applied (delayed word recall task, digit symbol substitution from the Wechsler Adult Intelligence Scale -Revised, and a letter fluency task). At Visits 5 through 7, a surveillance approach was employed, where participants received a comprehensive cognitive exam and a functional assessment that included the Clinical Dementia Rating Scale and Functional Activities Questionnaire. With these data, dementia was classified based on the National Institute on Aging and Alzheimer's Association and the Diagnostic and Statistical Manual of Mental Disorder – Fifth Edition criteria. In the time between Visit 5 and 6, participants were contacted annually via phone and administered the SIS, a brief cognitive assessment. If participants received a low score on the SIS, or if they were unable to participate in the screening via phone, the Ascertain Dementia 8 (AD8) was administered to the participant's informant. For participants who received a dementia diagnosis at visit 6 or 7, SIS, AD8, hospital discharge, and death certificate codes were used to define the date of dementia onset. For participants who did not attend visits 6 or 7, SIS, AD8, hospital discharge, and death certificate codes were used to define dementia diagnosis and date of dementia onset.

ARIC study protocols were approved by IRBs at each participating center: University of North Carolina at Chapel Hill, Chapel Hill, NC; Wake Forest University, Winston-Salem, NC; Johns Hopkins University, Baltimore, MD; University of Minnesota, Minneapolis, MN; and University of Mississippi Medical Center, Jackson, MS. All ARIC participants gave written informed consent at each study visit; proxies provided consent for participants who were judged to lack capacity.

Recruitment

Patient recruitment is detailed per cohort in the methods

Ethics oversight

All cohorts and studies were approved by appropriate ethics boards

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

All samples with CSF/plasma proteomics data and cognitive impairment information were assessed. No other sample size calculations were performed.

Data exclusions

CSF/plasma proteomics data and cognitive impairment information were necessary.

Replication

Multi-cohort study (6 for CSF, 9 for plasma). All attempts at replication were successful.

Randomization

NA, no treatment group

Blinding

NA, no treatment group

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

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, mosaicism, off-target gene editing) were examined.