nature portfolio

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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	BioRad Image Lab(software version 1.2.0.12) for Western blot assay; BioRad CFX Manager Version(software version 3.1.1517.0823.) for qRT-PCR assay; Leica Application Suite X (software version 3.1.3.8976 for signals of fluorescence, and Leica LAS V4.10 for signals without fluorescence) for microscope observation; Thermo Xcalibur (software version 3.0.63) for Mass Spectrometry assay.
Data analysis	We fully described the software availability and data analysis method in the manuscript's Methods and materials part. For RNA-Seq: Sequencing was performed on an Illumina NovaSeq 6000. After sequencing, Clean reads were aligned to Arabidopsis reference genome (TAIR10)(https://www.arabidopsis.org/) using Tophat (version 2.1.1) with default parameters. Then, the number of uniquely mapped reads were counted by HTSeq (version 0.11.2). The Counts Per Million (CPM) were calculated and DEGs were identified using edgeR. Genes with normalized expression level of more or equal to 1 CPM in at least one sample were selected as expressed genes. The differentially expressed genes (DEGs) were those with a FDR value less than 0.05. GO enrichment analysis was performed using clusterProfiler (version 3.6.0). The heatmap and venn diagram were drawn by R packages(ClusterProfiler3.0), in which the p value was calculated by Fisher' exact test, and was adjusted by Benjamini-Hochbery method(https://www.ncbi.nlm.nih.gov/sra/?term=PRJNA700788)(OMICS 2012 May;16(5):284-7. doi: 10.1089/omi.2011.0118). For Mass Spectrometry assay:The data were analyzed using a pre-release version of Thermo Scientific Proteome DiscovererTM software version 1.4. The proteome sequences for Arabidopsis downloaded from TAIR were used for the database searching and the mass tolerance was set to 0.05 Da. Excel (software version office 2007), Adobe Illustrator CS6 (software version 16.0)and Graphpad Prism(software version 8.0.1(244)) were used for graphs data presentation.

Image J version (software version 1.51j) for Root gravitropism VGI statistical assay.

Adobe Photoshop CS6 (software version 13.0 X64) was used to process and organize pictures.

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

a.The RNA-seq data have been deposited in the Sequence Read Archive (SRA) database under accession numbers PRJNA700788(https://www.ncbi.nlm.nih.gov/sra/?term=PRJNA700788).
b.Source gel data for all immunoblots and radiograms (Fig. 3a, b, c, d, e, g and h; Extended fig. 8f, g and i) are provided in Supplementary Fig. 1.
c. Source data for all graphs (Fig. 1c, e and f; Fig. 2e, g and h; Extended fig. 1d and f; Extended fig. 2b and f; Extended fig. 3a-e; Extended fig. 4b; Extended fig. 6b, d and e; Extended fig. 7a and b; Extended fig. 8a, d and g; Extended fig. 9h, j and l) are also provided in Supplementary Table 2.
d. Source data for LC-MS/MS Analysis is provided in Supplementary Fig. 2.
e. Primers used in this research are provided in Supplementary Table 3.

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	We used three biological replicates for RNA-Seq, following the common practice in the field. All the samples for mRNA expression, protein abundance, ChIP experiments were treated the same way, each experiment was analyzed at least with three biological replicates. Sample sizes are indicated in the main text, Figures and legends. We confirmed that the sample sizes that we used in this study were adequate by performing biological replicates and obtaining similar results.
Data exclusions	No data were excluded from the analysis.
Replication	All experiments were replicated independently and showed similar results. Number of repeats is provided in the figure legends where appreciate. The main findings were repeated by different people in the laboratory, as well as in different laboratory.
Randomization	Where possible, plants were randomly selected from the larger pools which were grown in identical conditions. Different genotypes were randomly positioned in the growth chambers. All samples were exposed to similar growth conditions and controls without any selection criteria. Large populations of genetically individuals were taken to minimize bias. For instance, in protein blotting, biochemical and qRT-PCR experiments, samples were randomly allocated to 3 groups as 3 independent biological replicates.
Blinding	The key phenotype and confocal analysis were confirmed by double-blind. For RNA-Seq experiments, they were carried out without prior knowledge of experimental outcome, therefore, blinding was not applied. For biochemical analysis, since the authors performed the experiments also analyzed the data, the blinding was not applied. However, these data have been verified by other authors in the manuscript as well as by other members in the laboratory.

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
☒	☐ Human research participants
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

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

Antibodies

Antibodies used

anti-GFP(Provided by Roche,Cat#11814460001, dilution 1:1000 for western blot);anti-TOR(dilution 1:1000 for western blot, dilution 1:500 for TOR immunoprecipitation); anti-HA(Provided by Roche, Cat#11583816001, dilution 1:3000 for western blot, dilution 1:500 for AD-TOR immunoprecipitation);anti-GFP(Provided by Abcam,Cat# ab290, dilution 1:400 for ChIP);GFP-Trap magnetic agarose(Provided by Chromotek,Cat# gta-20, dilution 1:500 for PLT2-YFP immunoprecipitation); Myc antibody conjugated to agarose(Provided by Sigma-Aldrich,Cat# A7470, dilution 1:500 for BD-PLT2 immunoprecipitation);anti-Myc(Provided by Abcam,Cat# ab32, dilution 1:3000 for western blot);anti-Phospho-S/T(42H4) (Provided by Cell Signaling Technology,Cat #9386, dilution 1:3000 for western blot);anti-MBP(Provided by New England Biolabs,Cat #E8032L, dilution 1:5000 for western blot);Amylose Resin(Provided by New England Biolabs,Cat #E8021L, dilution 1:500 for MBP-PLT2 immunoprecipitation).

Validation

The anti-TOR antibody was validated in Arabidopsis for Western blot in Xiong and Sheen, 2012, J Biol Chem (DOI:10.1074/jbc.M111.300749). Applied Biological Chemistry, 2019, 62(1)(DOI:10.1186/s13765-019-0475-8).

Concerning other commercial antibody specificity, we kindly refer to the supplier's websites and datasheets to find statements on specificity and citations for the use of the antibodies.

The commercial anti-GFP antibody (Roche,Cat#11814460001) link: https://www.sigmaaldrich.cn/CN/zh/product/roche/11814460001?context=product.

The commercial anti-HA antibody (Roche, Cat#11583816001) link: https://www.sigmaaldrich.cn/CN/zh/search/11583816001?focus=products&page=1&perPage=30&sort=relevance&term=11583816001&type=product. https://www.sigmaaldrich.cn/CN/zh/technical-documents/technical-article/protein-biology/western-blotting/anti-ha.

The commercial anti-GFP antibody (Abcam,Cat# ab290) link: https://www.abcam.com/gfp-antibody-ab290.html.

The commercial GFP-Trap magnetic agarose (Chromotek,Cat# gta-20) link: https://www.chromotek.com/search/?L=0&id=16&tx_solr%5Bq%5D=gta-20.

The commercial Myc antibody conjugated to agarose (Sigma-Aldrich,Cat# A7470) link: https://www.sigmaaldrich.cn/CN/zh/product/sigma/a7470?context=product.

The commercial anti-Myc antibody (Abcam,Cat# ab32) link: https://www.abcam.com/myc-tag-antibody-9e10-ab32.html.

The commercial Amylose Resin antibody (New England Biolabs,Cat #E8021L) link: https://www.neb.com/products/e8021-amylose-resin#Product%20Information.

The commercial anti-MBP antibody (New England Biolabs,Cat #E8032L) link: https://www.neb.com/products/e8032-anti-mbp-monoclonal-antibody#Product%20Information.

The commercial anti-Phospho-S/T(42H4) antibody (Cell Signaling Technology,Cat #9386) link: https://www.cellsignal.cn/products/primary-antibodies/phospho-threonine-42h4-mouse mab/9386;jsessionid=0fcyeiuans1p1k2bt-5innib9eu9of8mklh6xbj1.prod_store03?N=4294956287&Ntt=9386&_requestid=1795082&fromPage=plp&site-search-type=Products.

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)

The human NSCLC cell line HCC827 was obtained from the American Type Culture Collection and cultured following the manufacturer's instructions.

Authentication

The HCC827 cells were authenticated using short-tandem repeat (STR) profiling.

Mycoplasma contamination

All cell lines testd negative for mycoplasma contamination.

Commonly misidentified lines
(See ICLAC register)

No commonly misidentified cell lines were used in the study.

Palaeontology and Archaeology

Specimen provenance

Provide provenance information for specimens and describe permits that were obtained for the work (including the name of the issuing authority, the date of issue, and any identifying information). Permits should encompass collection and, where applicable, export.

Specimen deposition

Indicate where the specimens have been deposited to permit free access by other researchers.

Dating methods

If new dates are provided, describe how they were obtained (e.g. collection, storage, sample pretreatment and measurement), where they were obtained (i.e. lab name), the calibration program and the protocol for quality assurance OR state that no new dates are provided.

☐ Tick this box to confirm that the raw and calibrated dates are available in the paper or in Supplementary Information.

Ethics oversight

Identify the organization(s) that approved or provided guidance on the study protocol, OR state that no ethical approval or guidance was required and explain why not.

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

Animals and other organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research

Laboratory animals

For laboratory animals, report species, strain, sex and age OR state that the study did not involve laboratory animals.

Wild animals

Provide details on animals observed in or captured in the field; report species, sex and age where possible. Describe how animals were caught and transported and what happened to captive animals after the study (if killed, explain why and describe method; if released, say where and when) OR state that the study did not involve wild animals.

Field-collected samples

For laboratory work with field-collected samples, describe all relevant parameters such as housing, maintenance, temperature, photoperiod and end-of-experiment protocol OR state that the study did not involve samples collected from the field.

Ethics oversight

Identify the organization(s) that approved or provided guidance on the study protocol, OR state that no ethical approval or guidance was required and explain why not.

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

Human research participants

Policy information about studies involving human research participants

Population characteristics

Describe the covariate-relevant population characteristics of the human research participants (e.g. age, gender, genotypic information, past and current diagnosis and treatment categories). If you filled out the behavioural & social sciences study design questions and have nothing to add here, write "See above."

Recruitment

Describe how participants were recruited. Outline any potential self-selection bias or other biases that may be present and how these are likely to impact results.

Ethics oversight

Identify the organization(s) that approved the study protocol.

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

Clinical data

Policy information about clinical studies

All manuscripts should comply with the ICMJE guidelines for publication of clinical research and a completed CONSORT checklist must be included with all submissions.

Clinical trial registration

Provide the trial registration number from ClinicalTrials.gov or an equivalent agency.

Study protocol

Note where the full trial protocol can be accessed OR if not available, explain why.

Data collection

Describe the settings and locales of data collection, noting the time periods of recruitment and data collection.

Outcomes

Describe how you pre-defined primary and secondary outcome measures and how you assessed these measures.

Dual use research of concern

Policy information about dual use research of concern

Hazards

Could the accidental, deliberate or reckless misuse of agents or technologies generated in the work, or the application of information presented in the manuscript, pose a threat to:

No	Yes	
☐	☐	Public health
☐	☐	National security
☐	☐	Crops and/or livestock
☐	☐	Ecosystems
☐	☐	Any other significant area

Experiments of concern

Does the work involve any of these experiments of concern:

No	Yes	
☐	☐	Demonstrate how to render a vaccine ineffective
☐	☐	Confer resistance to therapeutically useful antibiotics or antiviral agents
☐	☐	Enhance the virulence of a pathogen or render a nonpathogen virulent
☐	☐	Increase transmissibility of a pathogen
☐	☐	Alter the host range of a pathogen
☐	☐	Enable evasion of diagnostic/detection modalities
☐	☐	Enable the weaponization of a biological agent or toxin
☐	☐	Any other potentially harmful combination of experiments and agents

ChIP-seq

Data deposition

☐ Confirm that both raw and final processed data have been deposited in a public database such as GEO.

☐ Confirm that you have deposited or provided access to graph files (e.g. BED files) for the called peaks.

Data access links *May remain private before publication.*	*For "Initial submission" or "Revised version" documents, provide reviewer access links. For your "Final submission" document, provide a link to the deposited data.*
Files in database submission	*Provide a list of all files available in the database submission.*
Genome browser session (e.g. UCSC)	*Provide a link to an anonymized genome browser session for "Initial submission" and "Revised version" documents only, to enable peer review. Write "no longer applicable" for "Final submission" documents.*

Methodology

Replicates	*Describe the experimental replicates, specifying number, type and replicate agreement.*
Sequencing depth	*Describe the sequencing depth for each experiment, providing the total number of reads, uniquely mapped reads, length of reads and whether they were paired- or single-end.*
Antibodies	*Describe the antibodies used for the ChIP-seq experiments; as applicable, provide supplier name, catalog number, clone name, and lot number.*
Peak calling parameters	*Specify the command line program and parameters used for read mapping and peak calling, including the ChIP, control and index files used.*
Data quality	*Describe the methods used to ensure data quality in full detail, including how many peaks are at FDR 5% and above 5-fold enrichment.*
Software	*Describe the software used to collect and analyze the ChIP-seq data. For custom code that has been deposited into a community repository, provide accession details.*

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	*Describe the sample preparation, detailing the biological source of the cells and any tissue processing steps used.*
Instrument	*Identify the instrument used for data collection, specifying make and model number.*
Software	*Describe the software used to collect and analyze the flow cytometry data. For custom code that has been deposited into a community repository, provide accession details.*
Cell population abundance	*Describe the abundance of the relevant cell populations within post-sort fractions, providing details on the purity of the samples and how it was determined.*
Gating strategy	*Describe the gating strategy used for all relevant experiments, specifying the preliminary FSC/SSC gates of the starting cell population, indicating where boundaries between "positive" and "negative" staining cell populations are defined.*

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

Magnetic resonance imaging

Experimental design

Design type	*Indicate task or resting state; event-related or block design.*
Design specifications	*Specify the number of blocks, trials or experimental units per session and/or subject, and specify the length of each trial or block (if trials are blocked) and interval between trials.*
Behavioral performance measures	*State number and/or type of variables recorded (e.g. correct button press, response time) and what statistics were used to establish that the subjects were performing the task as expected (e.g. mean, range, and/or standard deviation across subjects).*

Acquisition

Imaging type(s)	*Specify: functional, structural, diffusion, perfusion.*
Field strength	*Specify in Tesla*
Sequence & imaging parameters	*Specify the pulse sequence type (gradient echo, spin echo, etc.), imaging type (EPI, spiral, etc.), field of view, matrix size, slice thickness, orientation and TE/TR/flip angle.*
Area of acquisition	*State whether a whole brain scan was used OR define the area of acquisition, describing how the region was determined.*

Diffusion MRI ☐ Used ☐ Not used

Preprocessing

Preprocessing software	*Provide detail on software version and revision number and on specific parameters (model/functions, brain extraction, segmentation, smoothing kernel size, etc.).*
Normalization	*If data were normalized/standardized, describe the approach(es): specify linear or non-linear and define image types used for transformation OR indicate that data were not normalized and explain rationale for lack of normalization.*
Normalization template	*Describe the template used for normalization/transformation, specifying subject space or group standardized space (e.g. original Talairach, MNI305, ICBM152) OR indicate that the data were not normalized.*
Noise and artifact removal	*Describe your procedure(s) for artifact and structured noise removal, specifying motion parameters, tissue signals and physiological signals (heart rate, respiration).*

Volume censoring

Define your software and/or method and criteria for volume censoring, and state the extent of such censoring.

Statistical modeling & inference

Model type and settings

Specify type (mass univariate, multivariate, RSA, predictive, etc.) and describe essential details of the model at the first and second levels (e.g. fixed, random or mixed effects; drift or auto-correlation).

Effect(s) tested

Define precise effect in terms of the task or stimulus conditions instead of psychological concepts and indicate whether ANOVA or factorial designs were used.

Specify type of analysis: ☐ Whole brain ☐ ROI-based ☐ Both

Statistic type for inference
(See Eklund et al. 2016)

Specify voxel-wise or cluster-wise and report all relevant parameters for cluster-wise methods.

Correction

Describe the type of correction and how it is obtained for multiple comparisons (e.g. FWE, FDR, permutation or Monte Carlo).

Models & analysis

n/a	Involved in the study
☐	☐ Functional and/or effective connectivity
☐	☐ Graph analysis
☐	☐ Multivariate modeling or predictive analysis

Functional and/or effective connectivity

Report the measures of dependence used and the model details (e.g. Pearson correlation, partial correlation, mutual information).

Graph analysis

Report the dependent variable and connectivity measure, specifying weighted graph or binarized graph, subject- or group-level, and the global and/or node summaries used (e.g. clustering coefficient, efficiency, etc.).

Multivariate modeling and predictive analysis

Specify independent variables, features extraction and dimension reduction, model, training and evaluation metrics.