nature portfolio

Corresponding author(s): Ken Shirasu

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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	qPCR: MxPro - Mx3000P v4.10 (Stratagene), Western blotting: ImageQuant LAS 4000 1.2.0.101 (GE Healthcare), GUS activity: MikroWin 2000 (Berthold Technologies), GSH measurement: Magellan v7.2 (Tecan), Microscopy: ZEN 2.1 SP1 (ZEISS)
Data analysis	Microsoft Office Excel 2010 (Microsoft), GraphPad Prism 8.3.0 (GraphPad Software), Photoshop CC 2019 (Adobe), R statistical language version 2.11.1 with the Bioconductor package, edgeR version 1.6.15, Bowtie version 0.12.8, ImageJ 1.53e

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 in this study are available in the Article. Source data for Figs. 1-6 and Supplementary Figs. 2-4, 6-10 have been provided. RNA-seq data from this study have been deposited in NCBI's Gene Expression Omnibus and are accessible through GEO series accession number GSE154593. All other data are available from the corresponding author upon requests.

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 statistical methods were used to predetermine sample sizes. Required sample sizes were estimated based on our preliminary data and by published papers by other researchers.
Data exclusions	No data were excluded.
Replication	All experiments were replicated independently and showed similar results. Number of repeats is provided in the figure legends or material and methods.
Randomization	Plants were randomly selected from the larger pools which were grown in identical conditions.
Blinding	No blinding was performed.

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	1) anti-NPR1 antibody (production protocol is provided in materials and methods; dilution 1:2,000) 2) anti-UGPase antibody (AS05 086; Agrisera; dilution 1:5,000) 3) anti-PR1 antibody (AS10 687; Agrisera; dilution 1: 5,000) 4) anti-HA antibody (12013819001; Roche; dilution 1:5,000) 5) anti-Myc antibody (sc-789; Santa Cruz Biotechnology; dilution 1:1,000) 6) anti-rabbit IgG, HRP-linked whole Ab donkey (NA934; GE healthcare; dilution 1:10,000)
Validation	Validation of the antibodies are shown in the provided links or descriptions: 1) a band size corresponding to the expected size of NPR1 protein was observed in wild-type Arabidopsis but not in npr1-6 mutant. 2) https://www.agrisera.com/en/artiklar/ugpase-udp-glucose-pyrophosphorylase-marker-of-cytoplasm.html 3) https://www.agrisera.com/en/artiklar/pr-1-pathogenesis-related-protein-1.html 4) https://www.sigmaaldrich.com/content/dam/sigma-aldrich/docs/Roche/Bulletin/1/12013819001bul.pdf 5) https://datasheets.scbt.com/sc-789.pdf