

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 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 (<i>n</i>) 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 <i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i>
☒	☐ 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. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted <i>Give P values as exact values whenever suitable.</i>
☒	☐ 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 <i>d</i> , Pearson's <i>r</i>), 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 Luminescence Recordings: ICE 1.0.6.0 (Berthold Technologies); qPCR: MxPro - Mx3000P v4.10 (Stratagene), Western blotting: ImageQuant LAS 4000 1.2.0.101 (GE Healthcare); DLS experiment: Zetasizer v6.20 (Malvern Pananalytical)

Data analysis Microsoft Excel 2013, RStudio 1.1.456, Tophat2 v2.1.131 (<http://ccb.jhu.edu/software/tophat>), HTseq v0.6.132 (<https://htseq.readthedocs.io/>), EdgeR package 3.24.3 (Bioinformatics 26, 139–140 (2010)), HISAT v2.1.0 (<https://ccb.jhu.edu/software/hisat2/index.shtml>), MUSCLE alignment (Nucleic Acids Res. 32, 1792–1797 (2004)), RAXML (Bioinformatics 30, 1312–1313 (2014)), CLC Main Workbench 7.9.1 (Qiagen), ImageJ 1.52, Leica Application Suite 2.7.3.9723, Zetasizer v6.20 (Malvern Pananalytical), Prism 8 v8.3.0 (GraphPad), ORIGIN software v7.0 (OriginLab, USA), BoxplotR (Nature Methods 11, 121–122 (2014))

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 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

All data in this study are available in the Article. Source data for Figs. 1–4 and Extended Data Figs. 1–4, 6–9 have been provided, along the supplementary informations (SI video 1–6 and SI data 1). RNA-seq data from this study have been deposited in NCBI's Gene Expression Omnibus and are accessible through GEO series accession number GSE128510. 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 previously obtained preliminary data and by similar studies by other research groups. Results were reproducible and thus, the sample sizes should be sufficient.
Data exclusions	Seedlings, which were poorly grown and confirmed not to be genetically related to the genotype and/or possibly due to sterilisation method used, were omitted from study. Plants which did not expressed sufficient amount of aequorin or R-GECO1, possibly due to silencing, were omitted from the study. This criteria has been pre-established in the research field that routinely employ reporter-expressing plants for research.
Replication	All experiments were replicated independently and showed similar results. Number of repeats is provided in the text and figure legends where appropriate. The main findings can be reliably reproduced by other member 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 position in the growth chambers/shelves. No randomization for Western blotting, biochemical and qPCR assays.
Blinding	For screening and RNAseq experiments, they were carried out without prior knowledge of the experimental outcome and thus, blinding was not applied. For other experiments, blinding was not possible since the author who performed the experiments also analysed the data. However, key results have been verified by other authors in the manuscripts as well as by other members of the research team.

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-phospho-p42/p44 MAPK (Erk1/2; Thr202/Tyr204; D13.14.4E) monoclonal antibody (Cat. Number 4370; Lot 17; dilution 1:2000; Supplier, Cell Signaling Technology, USA). 2) ECL Anti-rabbit IgG, HRP-linked whole antibody from donkey (Cat. number NA934; Lot 16677077; dilution 1:5000; Supplier, GE Healthcare) 3) anti-CARD1 antibody from rabbit (production protocol is provided in materials and methods; dilution 1:5000) 4) anti-AHA1 antibody from rabbit (Cat. number AS07 260; Lot 1201; dilution 1:5000; Supplier, Agrisera, Sweden) 5) anti-SMT1 antibody from rabbit (Cat. number AS07 266; Lot 1011; dilution 1:5000; Supplier, Agrisera, Sweden) 6) anti-rbcL antibody from rabbit (Cat. number AS03 037; Lot 1209; dilution 1:20000; Supplier, Agrisera, Sweden)
Validation	Validation of the antibodies are shown in the provided links or descriptions: 1) please see the link (https://en.cellsignal.jp/products/primary-antibodies/phospho-p44-42-mapk-erk1-2-thr202-tyr204-d13-14-4e-xp-rabbit-mab/4370) 2) please see the link (https://www.gelifesciences.com/en/us/shop/protein-analysis/blotting-and-detection/blotting-standards-and-reagents/amersham-ecl-hrp-conjugated-antibodies-p-06260) 3) a band size corresponding to the expected size of CARD1 protein was observed in wild-type Arabidopsis but not in card1-2 mutant (STOP codon mutant).

- 4) please see the link (<https://www.agrisera.com/en/artiklar/hatpase-plasma-membrane-hatpase.html>)
- 5) please see the link (<https://www.agrisera.com/en/artiklar/smt1-sterol-methyltransferase-1.html>)
- 6) please see the link (https://www.agrisera.com/en/artiklar/plant_algal-cell-biology/compartment-markers/plant-cytoplasm-marker-/rbcl-rubisco-large-subunit-form-i-and-form-iiplastid-stroma-global-antibody.html)