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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	Adobe Photoshop CS6 (for lesion size determination); SpectraSuit MS Win v.64-bit (for spectraL scans); 7500 System SDS v.1.3 (for qPCR) .
Data analysis	SpectraSuite MS Win v.64-bit; Affymetrix Expression Console® software 2014; Significance Analysis of Microarrays v. 4.01; DNA-Chip Analyzer 2010; Araport 11; CLC Genomics Workbench 11.0.0; PANTHER v14.0; ClustalW v. 2.1; MrBayes v. 3.1.2; MEGA 5.01; INFOSTAT v. 2016; MassLynx 4.1 (includes application manager TargetLynx); GraphPad Prism v. 7.00

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

Raw reads from transcriptomic analyses were deposited in the NCBI Gene Expression Omnibus (GEO) (microarray, Series record GSE130255) or NCBI Sequence Read Archive (SRA) (RNAseq, PRJNA541199). Data will be automatically released by data banks after publication of this work.

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 specific statistical methods were used to determine sample size for the experiments reported in this manuscript. Instead, sample sizes were chosen based on our previous experience in the Arabidopsis system and its variability, availability of plants and space considerations. These sample sizes proved to be sufficient to detect significant differences between treatments/genotypes and to obtain reproducible results in independent runs of the same experiment.
Data exclusions	No exclusions
Replication	All experiments were performed at least twice (in most cases 3 times) using completely independent sets of plants and insects where applicable, with similar results. In each experiment, true biological replicates (i.e., independent plants and shelves/light sources) were used as replicates for statistical analyses (see Methods for details). For RNAseq, the experiment was performed only once, but with three true biological replicates (i.e., independent plants and shelves/light sources), and the results were validated by qPCR.
Randomization	Rosette-stage plants of similar age (3-4 weeks old) and size were selected for experiments and randomly assigned to treatments.
Blinding	In general, investigators were not blinded during data collection and analysis. The data on phytohormones, specialized metabolites and global transcriptomic data were acquired by personnel that only knew the sample numbers without access to treatment and genotype identityies

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	ChIP-qPCR: Antibody: HA-probe Antibody (F-7) X Supplier name: Santa Cruz Biotechnology Catalog number: #sc-7392 X, ChIP grade Clone name: not applicable Lot number: #E1517 Dilution: 10 ug/IP
Validation	Validated by manufacturer using Western blot analysis of HA-tagged fusion proteins and Immunofluorescence staining of methanol-fixed Cos cells transfected with HA fusion protein (see https://datasheets.scbt.com/sc-7392.pdf) Method paper describing a ChIP procedure in Arabidopsis using this antibody: Lee, J. H. et al. A fast, efficient chromatin immunoprecipitation method for studying protein-DNA binding in Arabidopsis mesophyll protoplasts. Plant Methods 13, 42, doi:10.1186/s13007-017-0192-4 (2017). A few citations using the same antibody for ChIP assays in Arabidopsis: Gan, E. S. et al. Jumonji demethylases moderate precocious flowering at elevated temperature via regulation of FLC in Arabidopsis. Nat Commun 5, 5098, doi:10.1038/ncomms6098 (2014). Xu, Y. et al. Arabidopsis MRG domain proteins bridge two histone modifications to elevate expression of flowering genes. Nucleic Acids Res 42, 10960-10974, doi:10.1093/nar/gku781 (2014).

Frank, A. et al. Circadian Entrainment in Arabidopsis by the Sugar-Responsive Transcription Factor bZIP63. Curr Biol 28, 2597-2606 e2596, doi:10.1016/j.cub.2018.05.092 (2018).
Fiorucci, A. S. et al. PHYTOCHROME INTERACTING FACTOR 7 is important for early responses to elevated temperature in Arabidopsis seedlings. New Phytol, doi:10.1111/nph.16316 (2019).