

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](#).

Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. 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
- ☐ ☒ An indication of 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 statistics 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
- ☐ ☒ Clearly defined error bars
State explicitly what error bars represent (e.g. SD, SE, CI)

Our web collection on [statistics for biologists](#) may be useful.

Software and code

Policy information about [availability of computer code](#)

Data collection

Plots were generated using Jmp pro version 13.1.0 (SAS, NC, USA) and Microsoft Excel for PC v. 14.0 (Microsoft Corporation, USA)
Photosynthesis data was collected using the Li-6400 and Li-6400XT gas exchange systems (LICOR biosciences, Lincoln, NE, USA)

Data analysis

Data was analyzed using Jmp pro version 13.1.0 (SAS, NC, USA) and Microsoft Excel for PC v. 14.0 (Microsoft Corporation, USA)

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 upon request. 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

The data generated and analyzed during this study are available from the corresponding author on reasonable request.

Field-specific reporting

Please select 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/authors/policies/ReportingSummary-flat.pdf](https://www.nature.com/authors/policies/ReportingSummary-flat.pdf)

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	Sample size was based on previous literature and experimental set up (for example: the availability of plant growth space in growth chambers or number of available Li-6400 machines). Sample size was determined to be adequate based on consistent differences between experimental groups. No statistical methods were used to predetermine sample size.
Data exclusions	No data were excluded
Replication	All attempts at replication were successful. All experiments were carried out at two or more times; replication numbers are given in the manuscript.
Randomization	Plants of the same genotype were distributed randomly in the growth chambers or greenhouse.
Blinding	Blinding was not possible or relevant for most of the experiments because the process of sample collection and analysis was carried out by the same person.

Reporting for specific materials, systems and methods

Materials & experimental systems

n/a	Involved in the study
☐	☒ Unique biological materials
☐	☒ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology
☒	☐ Animals and other organisms
☒	☐ Human research participants

Methods

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

Unique biological materials

Policy information about [availability of materials](#)

Obtaining unique materials	There are no restrictions on material availability, although an MTA will be required prior to dissemination, and permits may be required for movement of transgenic lines.
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Antibodies

Antibodies used	Antibodies used were: polyclonal anti-LS (Agrisera AS030307), 1:10000 polyclonal anti-Flag (Agrisera AS153037), 1:10000 polyclonal anti-RCA (Agrisera AS10700), 1:10000 polyclonal anti-ME (a kind gift of Dr. Timothy Nelson, formerly of Yale University), 1:10000 polyclonal anti-PEPC (Agrisera AS09458), 1:10000 polyclonal anti-BSD2 (details of antibody production in reference 15), 1:2000 polyclonal anti-RAF1 (details of antibody production in reference 14), 1:10000
Validation	Antibodies were validated by Agrisera as stated on their website or as described in the respective original articles and also when received by immunoblot in maize.