

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
<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. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P 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 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

SensorTrace Suite v3.1.100, Genevestigator, Image Lab Software for Chemidoc

Data analysis

LAS X life science software, Blast algorithm, Muscle algorithm, Weblogo 3, Mega 7, Image J, Microsoft Excel 2016

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

Accession numbers of all the Arabidopsis genes analysed in this study are listed in the text or figure legends. All numerical Source Data used to generate the graphs displayed in this report are provided as a supplementary excel file. Seeds of transgenic lines used in this study are available from the corresponding authors upon request.

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](https://www.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 sample size calculation was performed. The sample size was chosen based on the funding availability, the possibility of simultaneous processing by the experimenter and taking into consideration the sample size commonly chosen by similar studies by other research groups.
Data exclusions	No data were excluded from the analyses.
Replication	The conclusions and hypothesis drawn in this study are based on results that could be successfully reproduced at least two times, as indicated in the figure legends. The effect of inducible ZPR2 on pTAA1 reporter could only be performed once due to limited F1 seed pools.
Randomization	Randomisation of plant growth was applied when possible. Randomisation was not used for western blot, biochemical and qPCR assays.
Blinding	Investigators were only blinded to group allocation in the following cases: GUS staining assessment, leaf number count.

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	monoclonal anti-GFP distributed by Sigma Aldrich clones 7.1 and 13.1, catalog number 11814460001, lot number unavailable at the time of manuscript submission. Working dilution: 1:1000.
Validation	Validation of the antibody for western blotting of <i>A. thaliana</i> extracts has been performed independently by several groups (, including the authors as reported by the supplier (10.1186/gb-2014-15-4-r62, 10.3389/fpls.2017.00163, 10.1093/nar/gkw156). A band corresponding to the expected size of GFP or GFP-tagged proteins was observed in transgenic Arabidopsis plants but not in the wild type. Antibody profile: https://www.labome.com/product/Roche-Applied-Science/11814460001.html