nature research

Corresponding author(s): Jiří Friml

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	The TipTracker script that was used to collect data was described previously (von Wangenheim et al., 2017; https://doi.org/10.7554/eLife.26792.022)
Data analysis	Following software was used to analyze data: FIJI / ImageJ v 1.51w; Microsoft Excel 2010 and 2016; BoxPlotR (http://shiny.chemgrid.org/boxplotr/); RStudio 1.1.383. Figures were assembled using Adobe Photoshop CS5, Adobe Illustrator CS5 and CC, and LibreOffice Draw 6.1.0.3.

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 datasets generated during and/or analysed during the current 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

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 size; sample size was determined empirically throughout experiments as an optimal trade-off between sample size, image quality and feasibility in each particular epxeriment. The sample sizes were considered sufficient sice all observed trends were consistent between samples within an experiment as well as between independent experimental replicates.
Data exclusions	No data was excluded from the analysis
Replication	Each experiment was repeated 2-4 times and all attempts at replication were successful
Randomization	Selecting seedlings for mock/experimental treatments and/or imaging from a plate containing at least one order of magnitude more individuals than needed for the experiment was inherently random; no other randomization method was used.
Blinding	Blinding was not possible due to the effects of each mutation/treatment on the growth and/or morphology of the plants that were obvious at first sight.

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	All unique biological materials (Arabidopsis transgenic lines and DNA constructs) are available from the corresponding author with the exception of the KN::PIN2-GFP x XVE>>DRP1a-mRFP line, since F1 seeds were used in this case and their amount is thus very limited. Upon request, KN::PIN2-GFP seeds and XVE>>DRP1a-mRFP expression clone (also available from Yunpei Takano, corresponding author of Yoshinari et al., 2016, where the construct was described) can be provided instead so that the line can be re-created as described in Materials and Methods.