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Reporting Summary

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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	MassLynxTM software (vers. 4.1, Waters), Leica LAS AF (LEICA Microsystems GmbH), analySIS^D (Olympus Soft Imaging Solutions GmbH), Axiovision 4.4 software (Carl Zeiss Imaging solutions GmbH), ZEN software (vers. 2.3, blue edition, Carl Zeiss Microscopy GmbH), ZEN 2012 SP1 software (vers. 8.1, black edition, 64 bits, LSM 710, Carl Zeiss Microscopy GmbH), ZEN (vers. 2.1, black edition, 64 bits, LSM 780, Carl Zeiss Microscopy GmbH)
Data analysis	GraphPad Prism (vers. 6.05), AxioVisionLE (vers. 4.7.1.0 Carl Zeiss Imaging Solutions GmbH), LEICA LAS AF lite (LEICA Microsystems GmbH). GraphPad InStat 3.1 software. R version 3.4.3 (The R foundation for Statistical Computing)

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 that support the findings of this study are available from the corresponding authors upon request. Correspondence and requests for material should be sent to Hélène S. Robert (helene.robert.boisivon@ceitec.muni.cz), Jiri Friml (jiri.friml@ist.ac.at), Thomas Laux (laux@biologie.uni-freiburg.de).

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

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	Auxin measurement: number of ovules were optimized using independent experiment and 750 ovules were collected for each biological replicate for each sample, in five biological replicates. Maize: The samples are technically difficult to prepare, as different stages are analysed. The goal was to determine at least 5 samples per stage. The exact number of analysed ovule per stage is indicated in the figure legend (Supplementary Fig. 3) and range from 8 to 10. Phenotyping: because of reduced penetration of the phenotypes, at least 400 embryos were observed with wei8 mutants. In other cases, more than 100 embryos were observed, from at least 3 plants. Fluorescent signal quantification: The experiment used more than 100 embryos were observed.
Data exclusions	No data were excluded from the analysis, except for the auxin measurement: one outlier in Supplementary Table 1.
Replication	Auxin measurement: the experiment was repeated twice with similar output. Phenotyping: The experiment was independently repeated more than three times, by three different labs. Fluorescent signal quantification: The experiment was independently repeated twice
Randomization	Auxin measurement, Maize, Phenotyping, Fluorescent signal quantification: no randomization was used.
Blinding	Auxin measurement, Maize, Phenotyping, Fluorescent signal quantification: no blinding was used.

Materials & experimental systems

Policy information about availability of materials

n/a	Involved in the study
☐	☒ Unique materials
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Research animals
☒	☐ Human research participants

Unique materials

Obtaining unique materials	pWOX2::iaaM wei8 tar1 line, pBAN:iaaL DR5:GFP line, pBAN:bdl DR5:GFP Arabidopsis lines. These materials are readily available from the authors.

Method-specific reporting

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ Magnetic resonance imaging