nature portfolio

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Reporting Summary

Nature Portfolio 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 Portfolio policies, see our Editorial Policies 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	Data were collected using a Leica binocular and a Leica SP8 confocal microscope.
Data analysis	Image analyses were done using MorphoGraphX (MGX), MorphoMechanX, ImageJ ver. 2.9.0. Data analyses (sepal curving and sepal morphological parameters) were done using Microsoft Excel 2019.

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 and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio 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 description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our policy

There are raw images used for analysis and generation of graphs in Fig 4. There is no restriction on data availability. All data generated in this study are included within the main text and supplementary information. Raw images are available from the corresponding author upon request. All experimental materials generated in this work are available from the corresponding author upon request.

Research involving human participants, their data, or biological material

Policy information about studies with [human participants or human data](). See also policy information about [sex, gender (identity/presentation), and sexual orientation]() and [race, ethnicity and racism]().

Reporting on sex and gender	Not applicable to our study.
Reporting on race, ethnicity, or other socially relevant groupings	Not applicable to our study.
Population characteristics	Not applicable to our study.
Recruitment	Not applicable to our study.
Ethics oversight	Not applicable to our study.

Note that full information on the approval of the study protocol must also be provided in the manuscript.

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	Sample size was chosen based on standards and previous experience in the field. Minimum of three biological samples were used for each genotype.
Data exclusions	No data was excluded in the analysis.
Replication	Similar dynamics of sepal curving in the WT were observed in 2 independent plants by a binocular. The dynamics of sepal curving in early development of WT sepals were further confirmed in 3 independent samples using a confocal microscope. The observation was similar in 2 different studies. Similar dynamics of sepal curving in the pWOX1::sYFP2-PHS1ΔP mutant were observed in 4 different plants. The overall sepal phenotype of the transgenic plants was confirmed in several independent lines and in different generations.
Randomization	Not applicable to the study. All imaging to compare WT and mutant happened at a specific time of the day and follow the order of the first time point. The samples should not be influenced by the observer.
Blinding	Blinding was not relevant for the study. Moreover, each genotype analyzed here had distinct phenotype that could be easily recognized.

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 and archaeology
☒	☐ Animals and other organisms
☒	☐ Clinical data
☒	☐ Dual use research of concern
☐	☒ Plants

Methods

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

Dual use research of concern

Policy information about dual use research of concern

Hazards

Could the accidental, deliberate or reckless misuse of agents or technologies generated in the work, or the application of information presented in the manuscript, pose a threat to:

No	Yes	
☒	☐	Public health
☒	☐	National security
☒	☐	Crops and/or livestock
☒	☐	Ecosystems
☒	☐	Any other significant area

Experiments of concern

Does the work involve any of these experiments of concern:

No	Yes	
☒	☐	Demonstrate how to render a vaccine ineffective
☒	☐	Confer resistance to therapeutically useful antibiotics or antiviral agents
☒	☐	Enhance the virulence of a pathogen or render a nonpathogen virulent
☒	☐	Increase transmissibility of a pathogen
☒	☐	Alter the host range of a pathogen
☒	☐	Enable evasion of diagnostic/detection modalities
☒	☐	Enable the weaponization of a biological agent or toxin
☒	☐	Any other potentially harmful combination of experiments and agents

Plants

Seed stocks	WT Col-0 plants are widely available. Mutants (spr2-2, mad5, xxt1 xxt2) can be obtained from The Nottingham Arabidopsis Stock Centre (NASC) or from the authors of the original studies.
Novel plant genotypes	pWOX1::sYFP2-PHS1ΔP transgenic lines. 10 independent lines were obtained by Agrobacterium transformation, and displayed similar flower phenotype. The data included in the study were from T3 plants.
Authentication	The transgenic lines were selected by antibiotics, correct expression pattern of the transgene, and the expected phenotype. The transgenic construct was confirmed by sequencing.