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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	Custom code was used to perform enrichment test. Most quantitative score was got by the colorimeteric method with spectromether, fluorescence intensities from captured picture by Axiovision or, luminescence intensities by luminometer.
Data analysis	Custom code mentioned above is written by Perl. Microsoft Excel 2013, MEGA7 (7.0.14), ImageJ (1.51s) and "multcomp" package of R software (ver 3.3.3) were employed.

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 author upon 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	We did not predetermine sample size because we describe very distinct phenotypic differences between wild type, nst1 nst3 and ERF transgenic plants. Sample size for cell wall analysis (n = 4), qRT-PCR (n = 6), transient reporter-effector assay (n = 4 or 8), growth properties (n= 16 or 17), was determined according to our previous experience and realistic cost and space. Sample size of cell wall regeneration assay was in range from 29 to 64. The difference between samples in this experiment was large enough and confidence interval of each sample differs significantly.
Data exclusions	We did not exclude any particular data.
Replication	Most experiments were repeated twice or more and all replications gave similar data. Detail was described in figure legends.
Randomization	Place for cultivation in green house and location in a tray were different in each repeated experiment. All pictures and quantitative data were collected from all plants in one experimental batch and we confirmed most data showed similar results.
Blinding	Most quantitative analyses about cell wall were performed by technicians who don't know characteristics of each sample.

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 materials are available from the corresponding author upon reasonable request.

Antibodies

Antibodies used	Antibodies were purchased from CarboSource (CCRC-M1, CCRC-M87, and CCRC-M89) and PlantProbe (CBM3a, LM5, LM6, LM10, LM18, and JIM7), MBL (Anti-His-tag mAb AlexaFluor 488; Cat No: D291-A48, Lot No: 003 and 004), Thermo Fisher (Alexa Fluor 488 goat anti-body; Cat No:A-11001, lot No: 1787787, and Alexa Fluor 488 goat anti-rat IgG; Cat No:A-11006, lot No: 1689880)
Validation	The references for used anti-bodies and carbohydrate binding protein were cited in the manuscript. The specificity of them was shown in PlantProbe (http://www.plantprobes.net/index.php) or CarboSource (https://www.ccrc.uga.edu/~carbosource/CSS_mabs7-07.html) MBL (http://ruo.mbl.co.jp/bio/sch/?kw=D291-A48), and Thermo Fisher website.