

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

Software used for data collection in this study are as follows: qRT-PCR, StepOne Software ver. 2.3 (Applied Biosystems); RNA-seq analysis, HiSeq Control Software ver. 2.2.58 (HiSeq 2500, illumina); protein phosphatase 2C assay, SF6 ver. 4.7.11 (CORONA ELECTRIC); soil water potential and contents, ECH2O ver. 1.82 (METER); gas-exchange measurements, OPEN ver. 6.1 (LI-6400, Li-Cor) and Bluestem ver. 1.2.2 (LI-6800, Li-Cor); $\delta^{13}\text{C}$ analysis, Isodat Acquisition ver. 3.0 (Thermo); Size exclusion chromatography analysis, LabSolutions ver. 5.81 (Shimadzu); ABA measurement, Analyst ver. 1.6.2 (AB Sciex); NMR analysis, TopSpin ver. 3.0 (Bruker BioSpin).

Data analysis

Software used for data analysis in this study are as follows: phylogenetic analysis, MEGA ver. 6.06 (Build#: 6140226); $\delta^{13}\text{C}$ analysis, Isodat Workspace ver. 3.0 (Thermo); measurement of stomatal area and seedling length, ImageJ ver. 1.48 (<https://imagej.nih.gov/ij/>); measurement of seed area, SmartGRAIN ver. 1.2 (<http://www.naro.affrc.go.jp/archive/nias/ql/SmartGrain/>); statistical analysis, Microsoft Excel 2016 MSO (ver. 16.0.10730.20127) and R statistical software (ver. 3.4.4; <https://www.r-project.org/>); quality trimming of the NGS (mRNA-seq) resultant sequence reads, Trim Galore (ver. 0.5.0; https://www.bioinformatics.babraham.ac.uk/projects/trim_galore/); read mapping, Kallisto-Sleuth (ver. 0.44.0; <https://pachterlab.github.io/kallisto/about>); transcriptional analysis and drawing heatmap and ternary plot, gplots (ver. 3.0.1; <https://cran.r-project.org/web/packages/gplots/index.html>) and ade4 (ver. 1.7-4; <https://pbil.univ-lyon1.fr/ade4/ade4-html/00Index.html>); ABA measurement, MultiQuant ver. 3.01 (AB Sciex); principal component analysis, R statistical software with package library prcomp (ver. 3.4.4).

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

Newly identified wheat ABA receptors (TaPYLs) were deposited in NCBI databases: TaPYL1, MG273651; TaPYL3, MG273653; TaPYL6, MG273656; TaPYL7, MG273657; TaPYL8, MG273658; and TaPYL9, MG273659. To update TaPYL2, TaPYL4 and TaPYL5 information, MG273652, MG273654 and MG273655 were also deposited. The wheat reference gene annotation and sequence (IWGSC v1.1) are available at <https://wheat-urgi.versailles.inra.fr/Seq-Repository/Annotations>. The raw sequence and processed data for our RNA-seq analysis were deposited in the NCBI Gene Expression Omnibus (GEO) database under the specific accession number GSE79522.

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](https://www.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	Sample size was chosen based on previous studies and experience. We analyzed three transgenic wheat lines, which were isolated from independent callus. For the gene expression, seed component (limited water condition) and protein phosphatase analyses, a minimum number of three independent replicates was used. For soil water content analysis using soil moisture sensor and movie analysis using video camera, the experiments were repeated twice with similar results. Data other than those were obtained from at least more than four independent samples, and the detail information are described in our manuscript.
Data exclusions	No data were excluded from analyses.
Replication	All experiments were repeated at least twice with similar results. The number of biological replicates is noted in each figure legend.
Randomization	We sometimes changed the positions of planters under well watered condition in plant water use efficiency assay. In limited watered condition assay, plants were moved constantly on automatic turntable. In other analyses, samples were collected randomly.
Blinding	RNA-seq and seed component analyses were performed without material information. In other analyses, we did not apply blinding because the process of sample collection and analysis was carried out by the same person.

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