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

The data from MS/MS were processed by MaxQuant search engine (v.1.6.15.0)
Sequences of transcriptome were generated by Illumina DNBSEQ-T7 sequencer
The fluorescence signal was detected using a confocal microscopy (Carl Zeiss, LSM710)
The LCI images were captured using a plant-living imaging system (Berthold, Night Shade LB 985)
The F. pg fungals were observed with a scanning electron microscope (TEM, Hitachi, HT7700)
The stained basial stem segments were observed and photographed by a stereomicroscope (Olympus, Tokyo, Japan)

Data analysis	Motif analysis: Motif-X software Protein-protein interaction analysis: Cytoscape Predicted subcellular localization analysis: WoLFPSORT Protein domain functional analysis: InterPro Kinase-substrate regulation analysis: GPS (version 5.0) Hub genes for each module analysis: WGCNA R package The differential expression analysis in transcriptome: DESeq2 Prediction of Transcription factors: PlantTFDB Gene regulatory network analysis: GRNboost2 (version 0.1.6) DRRG prediction: RGA prediction pipeline GO functional enrichment: R Bioconductor package cluster profiler (version 4.4.4)

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 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

Data supporting the findings of this work are available within the article and Supplementary Information files. The RNA-seq data have been deposited in the NCBI database under accession PRJNA1037187. The mass spectrometry proteomics data were deposited in the ProteomeXchange Consortium [http://proteomecentral.proteomexchange.org] via the iProX partner repository, under the accession numbers PXD041703 and PXD042492. The raw data of identified proteins, phosphorylation sites, and lysine acetylation sites in 20 wheat tissues (Fig. 1b) were deposited at repository Zenodo [https://zenodo.org/records/14822020]. The raw GRN data were deposited at repository Zenodo [https://zenodo.org/records/14625876]. The Chinese Spring wheat reference genome (IWGSC RefSeq v2.1) is publicly available at IWGSC data repository hosted by URGI-INRAE [http://wheat-urgi.versailles.inra.fr/Seq-Repository/Assemblies] and in the NCBI database under accession PRJNA669381. Source data are provided in this paper.

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	NA
Reporting on race, ethnicity, or other socially relevant groupings	NA
Population characteristics	NA
Recruitment	NA
Ethics oversight	NA

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	The sample size is described in the relevant figure legends and supplementary information.
Data exclusions	No data were excluded from the analyses.
Replication	For the qRT-PCR, subcellular localization, SEM, histological analysis, Y2H, LCI, Co-IP, pull down, immunoblots, and F.pg Inhibition experiment, the results are generated from 3-4 biologically independent experiments. For the DI, the results are generated from 5 biologically independent experiments. Three independent transgenic lines were generated for TaHDA9 and TaP5CS1, respectively. All of these experiments were successfully repeated.

Randomization	All samples were randomly collected for the experiment in this study.
Blinding	For molecular biology experiments, bias could not be introduced since samples were treated identically and collected randomly. The investigation of agronomic traits was performed without prior knowledge of the results.

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

Antibodies

Antibodies used	The anti-acetyl-lysine antibody agarose conjugated antibody beads (PTM Biolabs, Cat#PTM104), anti-acetylated lysine antibody (Cell Signaling Technology, Catalog No.9681), anti-Flag antibody (Abmart, M20008), anti-actin antibody (Abbkine, Lot number ABM40122), anti-His antibody (Abmart, M20001), anti-GST (Abmart ,M20007), goat anti-rabbit IgG antibody (Abmart, Cat#M21002), goat anti-mouse IgG antibody (Abmart, Cat#M21001), and goat anti-mouse IgG antibody (Abmart, Cat#M21004) were used in this study.
Validation	The validation statements and experiments can be obtained from the following websites: The anti-acetyl-lysine antibody agarose conjugated antibody beads (http://www.ptm-biolab.com.cn/search.html?keyword=104) anti-acetylated lysine antibody (https://www.cellsignal.cn/products/primary-antibodies/acetylated-lysine-ac-k-103-mouse-mab/9681) anti-Flag antibody (https://www.ab-mart.com.cn/page.aspx?node=%2059%20&id=%20968) anti-actin antibody (https://www.abbkine.cn/w/product/detail/ABM40122/CN/s) anti-His antibody (Abmart, M20001, https://www.ab-mart.com.cn/page.aspx?node=%2059%20&id=%20959) anti-GST (https://www.ab-mart.com.cn/page.aspx?node=%2059%20&id=%20967), goat anti-rabbit IgG antibody (https://www.ab-mart.com.cn/page.aspx?node=%2062%20&id=%20980) goat anti-mouse IgG antibody (https://www.ab-mart.com.cn/page.aspx?node=%2062%20&id=%20960) goat anti-mouse IgG antibody (https://www.ab-mart.com.cn/page.aspx?node=%2062%20&id=%2017686)

Plants

Seed stocks	Yunong 268 was released in 2023 as a middle-strong gluten wheat cultivar. EMS mutants and overexpressed lines of Kronos and Fielder were stored in Henan Agricultural University.
Novel plant genotypes	EMS mutants and overexpressed plants of TaP5CS1 and TaHDA9.
Authentication	EMS mutants and overexpressed plants of TaP5CS1 and TaHDA9 were verified by gene sequencing, RT-qPCR and PCR amplification.