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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	Sequencing reads were undertaken with the BGISEQ-500 sequencer.
Data analysis	SigmaPlot v11, SPSS v18.0, GraphPad Prism, HISAT40, Bowtie2, RESM, SOAP aligner/soap2, Burrows-Wheeler Aligner and IGV2.3.91 statistical softwares were used for statistical analysis.

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

We have included a data availability statement in the revised version of the manuscript. The ChIP-seq data sets generated have been deposited in the Gene Expression Omnibus (GEO) under accession GSE114287.

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	Required experimental sample sizes were estimated based on our past experience performing similar experiments including field test.
Data exclusions	The results were excluded from the analysis if the positive control experiments were not successful.
Replication	All experiments were successfully repeated at least three times, and we have stated it in figure legends .
Randomization	Plants of equal initial sizes were randomly assigned to the treatment and control groups.
Blinding	Analysis were performed in a manner blinded to treatment assignment in all experiments.

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

Antibodies

Antibodies used	anti-Flag antibodies (Sigma, F1804, Lot No. # SLBN5629V, 1:5000), anti-OsGRF4 antibodies (Abmart, 1:2000), anti-SLR1 antibodies (ABclonal Technology, 1:2000), anti-OsLhca1 antibodies (Agrisera, AS01005, Lot No.1703, 1:5000), anti-OsLhca3 antibodies (Agrisera, AS01007, Lot No.1309, 1:5000), anti-OsLhca4 antibodies (Agrisera, AS01008, Lot No.1405 , 1:5000), anti-OsLhcb2 antibodies (Agrisera, AS01003, Lot No.1711, 1:5000), anti-OsPsaD antibodies (Agrisera, AS09461, Lot No.1309, 1:1000) , anti-OsPsaE antibodies (Agrisera, AS08324A, 1:1000), anti-HSP antibodies (BGI, AbM51099-31-PU, Lot No. 2017122801, 1:10000), anti-DDDDK-tag antibodies (MBL, M185-11, Lot No. 006, 1: 5000), and anti-HA antibodies (MBL, M180-7, Lot No. 004, 1: 5000).
Validation	anti-Flag antibodies (The ANTI-FLAG M2 mouse, affinity purified monoclonal antibody binds to fusion proteins containing a FLAG peptide sequence.The antibody recognizes the FLAG peptide sequence at the N-terminus, Met-N-terminus,C-terminus, and internal sites of the fusion protein.). anti-OsLhca1 antibodies, anti-OsLhca3 antibodies, anti-OsLhca4 antibodies and anti-OsLhcb2 antibodies (Reactivity: antibodies have been shown to be reactive in all dicots, monocots, and gymnosperms tested so far; some of them have even been found to be reactive against Lhc-proteins of Chlamydomonas reinhardtii). anti-OsPsaD antibodies (Confirmed reactivity: Arabidopsis thaliana, Chlamydomonas reinhardtii, Hordeum vulgare, Lactuca sativa, Oryza sativa, Physcomitrella patens, Spinacia oleracea, Synechocystis PCC 6803, Triticum aestivum, Zea mays; Predicted reactivity: plants (monocots, dicots and conifers), Bigelowiella natans, Cucumis melo, green algae). anti-OsPsaE antibodies (Confirmed reactivity: Arabidopsis thaliana; Predicted reactivity: dicots including Spinacia oleracea, monocots including: Hordeum vulgare, Oryza sativa, Zea mays, trees: Populus canadensis, algae: Chlamydomonas reinhardtii, Chlorella). anti-HSP antidodies (Reactivity: This antibody reacts with house-keeping gene HSP in rice). anti-DDDDK-tag antibodies (Reactivity: This antibody reacts with N-terminal, Internal and C-terminal DDDDK-tagged (DYKDDDDK) protein). anti-HA antibodies (Reactivity: This antibody reacts with N-terminal and C-terminal tagged protein). Loss-of-function mutants (e.g., osgrf4 mutant) were used to validate anti-OsGRF4 antibodies. Loss-of-function mutants (e.g., slr mutant) were used to validate anti-SLR1 antibodies.

ChIP-seq

Data deposition

☒ Confirm that both raw and final processed data have been deposited in a public database such as GEO.

☒ Confirm that you have deposited or provided access to graph files (e.g. BED files) for the called peaks.

Data access links *May remain private before publication.*	https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE114287 The following secure of record GSE114287 for reviewer while it remains in private status is yridcccmxbkjlcx.
Files in database submission	Input3.fastq, Flag3.fastg, Input4.fastq, Flag4.fastq, LH93-Input.fastq, LH93-Flag.fastq, LH93.bed, Flag3.bed, Flag4.bed
Genome browser session (e.g. UCSC)	http://ensembl.gramene.org/Oryza_sativa/Info/Index

Methodology

Replicates	Three biological repeat samples were mixed together
Sequencing depth	Average tag depth of Flag3 is 294. Average tag depth of Flag4 is 200. Average tag depth of LH93-Flag is 231.
Antibodies	anti-Flag antibodies (Sigma, F1804).
Peak calling parameters	Peak calling parameters ：-s 50 -g 380000000 -p 1e-5 -w --space 50 -m 10,30
Data quality	Clean Parameter: SOAPnuke filter -l 5 -q 0.5 -n 0.1 -Q 2 -c 25
Software	BGISEQ-500, SOAPaligner/SOAP2, Burrows-Wheeler Aligner, Model-based Analysis of ChIP -Seq, IGV2.3.91