

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 |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> The statistical test(s) used AND whether they are one- or two-sided
<i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i> |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> A description of all covariates tested |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> 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) |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> For null hypothesis testing, the test statistic (e.g. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted
<i>Give P values as exact values whenever suitable.</i> |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> 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

SRA Toolkit (version 2.5.1)

Data analysis

Trim Galore program (version 0.4.1)
 FastQC (version 0.11.8)
 Bowtie2 (version 2.2.6)
 Picard tools (version 2.60; <http://broadinstitute.github.io/picard/>)
 SAMtools (version 0.1.19)
 MACS2 (version 2.1.0)
 phantompeakqualtools package (<https://code.google.com/p/phantompeakqualtools/>)
 BEDTools (version 2.25.0)
 DeepTools (version 3.5.0)
 WashU Epigenome Browser (version 46.2)
 BLAST (version 2.9.0)
 FIMO (version 5.4.1)
 ChromHMM (version 1.19)
 LastZ (version 1.04.03)
 Basset (<https://github.com/davek44/Basset>)
 Shiny (version 1.5.12.933)
 ggplot2 (version 3.3.3)
 R (version 3.4.1)
 Hotspot (HotSpot5)

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](#)

Raw data and related annotation information were obtained from NCBI SRA (<https://www.ncbi.nlm.nih.gov/sra>), GEO (<https://www.ncbi.nlm.nih.gov/geo>), European Nucleotide Archive (ENA, <https://www.ebi.ac.uk/ena>), PlantTFDB (http://planttfdb.gao-lab.org/quick_search_result.php), JASPAR (<https://jaspar.genereg.net/>) and CIS-BP (<http://cisbp.cabr.utoronto.ca/>). ChIP-Hub is available at <https://biobigdata.nju.edu.cn/ChIPHub/>. Users can view the processed data through the Epigenome Browser <https://biobigdata.nju.edu.cn/browser/>. All the analysis results (including peak files in the BED format, signal files in the bigwig format, comparative genomics data, predicted promoters/enhancers and gene regulatory networks) can be downloaded through the link https://biobigdata.nju.edu.cn/ChIPHub_download/. Metadata and peak files (in the BED format) for all curated experiments in the current version of ChIP-Hub are also deposited at Zenodo (doi: <https://doi.org/10.5281/zenodo.5912234>). Source Data are provided with this paper.

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	This study collected >10000 publicly available datasets for >40 plant species from ~540 original publications.
Data exclusions	All downloaded data were included in the analysis.
Replication	All the data analysis are provided the related codes to ensure its reproducibility. All attempts to repeat bioinformatic analyses were successful.
Randomization	This research does not involve randomization or grouping of samples.
Blinding	None of analysis could be influenced at any stage nor did they have known a priori outcomes. No additional blinding measures were required.

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 | Involvement in the study |
|-------------------------------------|--|
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Antibodies |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Eukaryotic cell lines |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Palaeontology and archaeology |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Animals and other organisms |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Human research participants |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Clinical data |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Dual use research of concern |

Methods

- | n/a | Involvement in the study |
|-------------------------------------|---|
| <input checked="" type="checkbox"/> | <input type="checkbox"/> ChIP-seq |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Flow cytometry |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> MRI-based neuroimaging |