

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
<i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i> |
| ☒ | ☐ 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
<i>Give P values as exact values whenever suitable.</i> |
| ☒ | ☐ 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 TF DAP-seq libraries were sequenced with Illumina NovaSeq 6000 system.

Data analysis fastp (version 0.20.0); Trim Galore (version 0.4.4); Burrows–Wheeler Aligner (version 0.7.17-r1188); HISAT2 (version 2.2.1); MACS (version 2.2.6); featureCount program of the Subread package (version 2.0.0); HiC-Pro (version 2.11.1); Homer (version 4.11); Juicer (version 1.21.01); Juicerbox (version 1.11.08); MEME software toolkit (version 5.1.1); R package motifStack (version 1.34.0); R package universalmotif (version 1.4.0); mummer (version 4.0.0beta2); ROAST (version 3) from multiz; PHAST (version 1.4); R package WGCNA (version 1.70.3); Cytoscape (version 3.8.2); BLASTN (version 2.9.0); Circos (version 0.69-8); MAFFT (version v7.149b); EMBOSS (version 6.6.0.0); FastTree (version 2.1.10); R package ggtree (version 2.4.1); Orthofinder (version 2.3.12); Jalview (version 2.11.1.3); Integrative Genomics Viewer (version 2.8.10)

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](#)

The DAP-sequencing data generated in this study have been submitted to the NCBI Gene Expression Omnibus (GEO; <https://www.ncbi.nlm.nih.gov/geo/>) under

accession number GSE192815 (<https://www.ncbi.nlm.nih.gov/geo/GSE192815>). Tracks for all sequencing data can be visualized through our local genome browser (http://bioinfo.sibs.ac.cn/dap-seq_CS_jbrowse/). histone ChIP-seq data of 7 typical tissues and 8 external stimuli, RNA-seq and DNase-seq data of Chinese Spring (CS) seedling are under accession numbers GSE139019 and GSE121903 in NCBI GEO database. Hi-C data of CS is under accession number GSE133885 deposited in NCBI GEO database. The hexaploid wheat transcriptomic data of 536 samples were downloaded from Wheat Expression Browser (<http://www.wheat-expression.com/>). The OsHOX24 ChIP-seq data of *Oryza sativa* is under accession number GSE144419 deposited in NCBI GEO database. The TFBS of *Arabidopsis thaliana* were downloaded from Plant Cistrome Database (http://neomorph.salk.edu/dap_web/pages/index.php). Scripts are available at https://github.com/yuyun-zhang/hexa_dap.

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	No statistics method is used to predetermine sample size for TF DAP-seq. We cloned 189 TFs from 30 families, of which 107 were highly expressed TFs and 82 were functionally annotated TFs or hub TFs in the co-expression network. The 30 TF families (63% of all large TF families with the number of TFs > 100 in CS) is the sufficient sample size to analyze the regulatory pattern of subgenomes.
Data exclusions	The TF data were classified according to the de novo identification or enrichment of canonical representative motifs, resulting in 45 high-, 48 median-, and 97 low-confidence TF datasets (HC, MC and LC) (Fig. 1a and Fig. S1). The HC and MC were used for the main analysis.
Replication	Replicated assays were performed and reproduced the main results in this study (Fig. S9 and Fig. S13).
Randomization	Because we did not have group allocation and perform different treatments in this study, the randomization was not used.
Blinding	Because we did not have group allocation in this study, the blinding was not used.

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
☒	☐ Human research participants
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

n/a	Involved in the study
☐	☒ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Antibodies

Antibodies used	Halo: Promega, cat # G7281, lot # 0000384548
Validation	The Halo antibody has been validated by the supplier. The reports could be found on the the supplier website.

ChIP-seq

Data deposition

- ☒ Confirm that both raw and final processed data have been deposited in a public database such as [GEO](https://www.ncbi.nlm.nih.gov/geo/).
- ☒ Confirm that you have deposited or provided access to graph files (e.g. BED files) for the called peaks.

Data access links <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE192815>
May remain private before publication.

Raw data: Alfin-4D-1_1.fq.gz;Alfin-4D-1_2.fq.gz;AP2-B_1.fq.gz;AP2-B_2.fq.gz;AP2-D_1.fq.gz;AP2-D_2.fq.gz;AP2-DREB-1A-1_1.fq.gz;AP2-DREB-1A-1_2.fq.gz;AP2-DREB-1B-1_1.fq.gz;AP2-DREB-1B-1_2.fq.gz;AP2-DREB-1D-1_1.fq.gz;AP2-DREB-1D-1_2.fq.gz;AP2-DREB-2D-1_1.fq.gz;AP2-DREB-2D-1_2.fq.gz;AP2-DREB-5B-3_1.fq.gz;AP2-DREB-5B-3_2.fq.gz;AP2-ERF-3A-1_1.fq.gz;AP2-ERF-3A-1_2.fq.gz;AP2-ERF-4B-2_1.fq.gz;AP2-ERF-4B-2_2.fq.gz;AP2-ERF-5B-1_1.fq.gz;AP2-ERF-5B-1_2.fq.gz;AP2-ERF-5B-2_1.fq.gz;AP2-ERF-5B-2_2.fq.gz;AP2-ERF-5D-1_1.fq.gz;AP2-ERF-5D-1_2.fq.gz;AP2-ERF-6A-1_1.fq.gz;AP2-ERF-6A-1_2.fq.gz;AP2-ERF-6A-2_1.fq.gz;AP2-ERF-6A-2_2.fq.gz;AP2-ERF-6D-1_1.fq.gz;AP2-ERF-6D-1_2.fq.gz;AP2-RAV-4B-1_1.fq.gz;AP2-RAV-4B-1_2.fq.gz;B3-2A-1_1.fq.gz;B3-2A-1_2.fq.gz;B3-2B-2_1.fq.gz;B3-2B-2_2.fq.gz;B3-4A-1_1.fq.gz;B3-4A-1_2.fq.gz;B3-4B-1_1.fq.gz;B3-4B-1_2.fq.gz;B3-4B-2_1.fq.gz;B3-4B-2_2.fq.gz;B3-5A-1_1.fq.gz;B3-5A-1_2.fq.gz;B3-5B-1_1.fq.gz;B3-5B-1_2.fq.gz;B3-5D-2_1.fq.gz;B3-5D-2_2.fq.gz;B3-6D-1_1.fq.gz;B3-6D-1_2.fq.gz;B3-6D-2_1.fq.gz;B3-6D-2_2.fq.gz;B3-7B-1_1.fq.gz;B3-7B-1_2.fq.gz;B3-7D-1_1.fq.gz;B3-7D-1_2.fq.gz;B3-ARF-2D-1_1.fq.gz;B3-ARF-2D-1_2.fq.gz;B3-ARF-3A-1_1.fq.gz;B3-ARF-3A-1_2.fq.gz;BES1-B_1.fq.gz;BES1-B_2.fq.gz;BES1-D_1.fq.gz;BES1-D_2.fq.gz;BES1-B_1.fq.gz;BES1-B_2.fq.gz;BES1-D_1.fq.gz;BES1-D_2.fq.gz;BHLH-1A-1_1.fq.gz;BHLH-1A-1_2.fq.gz;BHLH-3A-2_1.fq.gz;BHLH-3A-2_2.fq.gz;BHLH-4B-1_1.fq.gz;BHLH-4B-1_2.fq.gz;BHLH-5A-1_1.fq.gz;BHLH-5A-1_2.fq.gz;BHLH-5A-4_1.fq.gz;BHLH-5A-4_2.fq.gz;BHLH-6A-1_1.fq.gz;BHLH-6A-1_2.fq.gz;BHLH-7A-2_1.fq.gz;BHLH-7A-2_2.fq.gz;BHLH-7A-3_1.fq.gz;BHLH-7A-3_2.fq.gz;BHLH-7D-2_1.fq.gz;BHLH-7D-2_2.fq.gz;BHLH-U_1.fq.gz;BHLH-U_2.fq.gz;BZIP-2A-2_1.fq.gz;BZIP-2A-2_2.fq.gz;BZIP-2A-3_1.fq.gz;BZIP-2A-3_2.fq.gz;BZIP-3A-1_1.fq.gz;BZIP-3A-1_2.fq.gz;BZIP-3A-2_1.fq.gz;BZIP-3A-2_2.fq.gz;BZIP-5A-1_1.fq.gz;BZIP-5A-1_2.fq.gz;BZIP-5B-3_1.fq.gz;BZIP-5B-3_2.fq.gz;BZIP-6A-1_1.fq.gz;BZIP-6A-1_2.fq.gz;BZIP-7A-1_1.fq.gz;BZIP-7A-1_2.fq.gz;BZIP-A_1.fq.gz;BZIP-A_2.fq.gz;BZIP-B_1.fq.gz;BZIP-B_2.fq.gz;BZIP-D_1.fq.gz;BZIP-D_2.fq.gz;C2-A_1.fq.gz;C2-A_2.fq.gz;C2-B_1.fq.gz;C2-B_2.fq.gz;C2C2-Dof-2A-1_1.fq.gz;C2C2-Dof-2A-1_2.fq.gz;C2C2-Dof-2D-1_1.fq.gz;C2C2-Dof-2D-1_2.fq.gz;C2C2-Dof-4A-1_1.fq.gz;C2C2-Dof-4A-1_2.fq.gz;C2C2-Dof-4D-1_1.fq.gz;C2C2-Dof-4D-1_2.fq.gz;C2-D_1.fq.gz;C2-D_2.fq.gz;C2H2-2A-1_1.fq.gz;C2H2-2A-1_2.fq.gz;C2H2-3A-1_1.fq.gz;C2H2-3A-1_2.fq.gz;C2H2-3D-2_1.fq.gz;C2H2-3D-2_2.fq.gz;C2H2-4A-1_1.fq.gz;C2H2-4A-1_2.fq.gz;C2H2-5B-1_1.fq.gz;C2H2-5B-1_2.fq.gz;C2H2-6A-1_1.fq.gz;C2H2-6A-1_2.fq.gz;C2H2-6B-1_1.fq.gz;C2H2-6B-1_2.fq.gz;C2H2-6D-2_1.fq.gz;C2H2-6D-2_2.fq.gz;C3H-1A-1_1.fq.gz;C3H-1A-1_2.fq.gz;C3H-1B-1_1.fq.gz;C3H-1B-1_2.fq.gz;C3H-1D-2_1.fq.gz;C3H-1D-2_2.fq.gz;C3H-3A-1_1.fq.gz;C3H-3A-1_2.fq.gz;C3H-3A-2_1.fq.gz;C3H-3A-2_2.fq.gz;C3H-4B-1_1.fq.gz;C3H-4B-1_2.fq.gz;C3H-7B-1_1.fq.gz;C3H-7B-1_2.fq.gz;DBB-7A-1_1.fq.gz;DBB-7A-1_2.fq.gz;DBP-1B-1_1.fq.gz;DBP-1B-1_2.fq.gz;DBP-1D-1_1.fq.gz;DBP-1D-1_2.fq.gz;EIL-4D-1_1.fq.gz;EIL-4D-1_2.fq.gz;GARP-ARR-6A-1_1.fq.gz;GARP-ARR-6A-1_2.fq.gz;GARP-ARR-7A-1_1.fq.gz;GARP-ARR-7A-1_2.fq.gz;GARP-ARR-7A-3_1.fq.gz;GARP-ARR-7A-3_2.fq.gz;GARP-G2-2A-1_1.fq.gz;GARP-G2-2A-1_2.fq.gz;GARP-G2-2B-1_1.fq.gz;GARP-G2-2B-1_2.fq.gz;GARP-G2-3B-1_1.fq.gz;GARP-G2-3B-1_2.fq.gz;GARP-G2-4A-1_1.fq.gz;GARP-G2-4A-1_2.fq.gz;GARP-G2-4D-2_1.fq.gz;GARP-G2-4D-2_2.fq.gz;GARP-G2-5B-3_1.fq.gz;GARP-G2-5B-3_2.fq.gz;GRAS-2A-1_1.fq.gz;GRAS-2A-1_2.fq.gz;GRAS-4B-1_1.fq.gz;GRAS-4B-1_2.fq.gz;GRAS-4B-2_1.fq.gz;GRAS-4B-2_2.fq.gz;GRF4-2A-1_1.fq.gz;GRF4-2A-1_2.fq.gz;GRF4-2B-1_1.fq.gz;GRF4-2B-1_2.fq.gz;GRF4-2D-1_1.fq.gz;GRF4-2D-1_2.fq.gz;GRF-6A-1_1.fq.gz;GRF-6A-1_2.fq.gz;HB-BELL-4B-1_1.fq.gz;HB-BELL-4B-1_2.fq.gz;HB-BELL-5D-1_1.fq.gz;HB-BELL-5D-1_2.fq.gz;HB-HD-ZIP-2A-1_1.fq.gz;HB-HD-ZIP-2A-1_2.fq.gz;HB-HD-ZIP-2A-2_1.fq.gz;HB-HD-ZIP-2A-2_2.fq.gz;HB-HD-ZIP-2B-1_1.fq.gz;HB-HD-ZIP-2B-1_2.fq.gz;HB-HD-ZIP-6A-1_1.fq.gz;HB-HD-ZIP-6A-1_2.fq.gz;HB-HD-ZIP-6A-2_1.fq.gz;HB-HD-ZIP-6A-2_2.fq.gz;HB-HD-ZIP-6B-2_1.fq.gz;HB-HD-ZIP-6B-2_2.fq.gz;HB-PHD-6A-1_1.fq.gz;HB-PHD-6A-1_2.fq.gz;HB-WOX-A_1.fq.gz;HB-WOX-A_2.fq.gz;HB-WOX-B_1.fq.gz;HB-WOX-B_2.fq.gz;HB-WOX-D_1.fq.gz;HB-WOX-D_2.fq.gz;HSF-U_1.fq.gz;HSF-U_2.fq.gz;IPA1-7B-1_1.fq.gz;IPA1-7B-1_2.fq.gz;LIM-7B-1_1.fq.gz;LIM-7B-1_2.fq.gz;LIM-7D-1_1.fq.gz;LIM-7D-1_2.fq.gz;LOB-1A-1_1.fq.gz;LOB-1A-1_2.fq.gz;LOB-3A-1_1.fq.gz;LOB-3A-1_2.fq.gz;LOB-3B-1_1.fq.gz;LOB-3B-1_2.fq.gz;LOB-3D-1_1.fq.gz;LOB-3D-1_2.fq.gz;LOB-3D-2_1.fq.gz;LOB-3D-2_2.fq.gz;MADS1-lgy3-4A-1_1.fq.gz;MADS1-lgy3-4A-1_2.fq.gz;MADS1-lgy3-4B-1_1.fq.gz;MADS1-lgy3-4B-1_2.fq.gz;MADS1-lgy3-4D-1_1.fq.gz;MADS1-lgy3-4D-1_2.fq.gz;MADS-M-4D-1_1.fq.gz;MADS-M-4D-1_2.fq.gz;MADS-MIKK-5A-1_1.fq.gz;MADS-MIKK-5A-1_2.fq.gz;MADS-MIKK-7A-1_1.fq.gz;MADS-MIKK-7A-1_2.fq.gz;MYB-1A-1_1.fq.gz;MYB-1A-1_2.fq.gz;MYB-1A-2_1.fq.gz;MYB-1A-2_2.fq.gz;MYB-2A-1_1.fq.gz;MYB-2A-1_2.fq.gz;MYB-2A-2_1.fq.gz;MYB-2A-2_2.fq.gz;MYB-3A-1_1.fq.gz;MYB-3A-1_2.fq.gz;MYB-3D-1_1.fq.gz;MYB-3D-1_2.fq.gz;MYB-4A-1_1.fq.gz;MYB-4A-1_2.fq.gz;MYB-4A-2_1.fq.gz;MYB-4A-2_2.fq.gz;MYB-5A-1_1.fq.gz;MYB-5A-1_2.fq.gz;MYB-5B-1_1.fq.gz;MYB-5B-1_2.fq.gz;MYB-6D-1_1.fq.gz;MYB-6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Peak files: Alfin-4D-1_PE_peaks.filter.p10.bed;AP2-B_PE_peaks.filter.p10.bed;AP2-D_PE_peaks.filter.p10.bed;AP2-DREB-1A-1_PE_peaks.filter.p10.bed;AP2-DREB-1B-1_PE_peaks.filter.p10.bed;AP2-DREB-1D-1_PE_peaks.filter.p10.bed;AP2-

DREB-2D-1_PE_peaks.filter.p10.bed;AP2-DREB-5B-3_PE_peaks.filter.p10.bed;AP2-ERF-3A-1_PE_peaks.filter.p10.bed;AP2-ERF-4B-2_PE_peaks.filter.p10.bed;AP2-ERF-5B-1_PE_peaks.filter.p10.bed;AP2-ERF-5B-2_PE_peaks.filter.p10.bed;AP2-ERF-5D-1_PE_peaks.filter.p10.bed;AP2-ERF-6A-1_PE_peaks.filter.p10.bed;AP2-ERF-6A-2_PE_peaks.filter.p10.bed;AP2-ERF-6D-1_PE_peaks.filter.p10.bed;AP2-RAV-4B-1_PE_peaks.filter.p10.bed;B3-2A-1_PE_peaks.filter.p10.bed;B3-2B-2_PE_peaks.filter.p10.bed;B3-4A-1_PE_peaks.filter.p10.bed;B3-4B-1_PE_peaks.filter.p10.bed;B3-4B-2_PE_peaks.filter.p10.bed;B3-5A-1_PE_peaks.filter.p10.bed;B3-5B-1_PE_peaks.filter.p10.bed;B3-5D-2_PE_peaks.filter.p10.bed;B3-6D-1_PE_peaks.filter.p10.bed;B3-6D-2_PE_peaks.filter.p10.bed;B3-7B-1_PE_peaks.filter.p10.bed;B3-7D-1_PE_peaks.filter.p10.bed;B3-ARF-2D-1_PE_peaks.filter.p10.bed;B3-ARF-3A-1_PE_peaks.filter.p10.bed;B3-ARF-3B-2_PE_peaks.filter.p10.bed;BES1-6A-1_PE_peaks.filter.p10.bed;BES1-A_PE_peaks.filter.p10.bed;BES1-B_PE_peaks.filter.p10.bed;BES1-D_PE_peaks.filter.p10.bed;bHLH-1A-1_PE_peaks.filter.p10.bed;bHLH-3A-2_PE_peaks.filter.p10.bed;bHLH-4B-1_PE_peaks.filter.p10.bed;bHLH-5A-1_PE_peaks.filter.p10.bed;bHLH-5A-4_PE_peaks.filter.p10.bed;bHLH-6A-1_PE_peaks.filter.p10.bed;bHLH-7A-2_PE_peaks.filter.p10.bed;bHLH-7A-3_PE_peaks.filter.p10.bed;bHLH-7D-2_PE_peaks.filter.p10.bed;bHLH-U_PE_peaks.filter.p10.bed;bZIP-2A-2_PE_peaks.filter.p10.bed;bZIP-2A-3_PE_peaks.filter.p10.bed;bZIP-3A-1_PE_peaks.filter.p10.bed;bZIP-3A-2_PE_peaks.filter.p10.bed;bZIP-5A-1_PE_peaks.filter.p10.bed;bZIP-5B-3_PE_peaks.filter.p10.bed;bZIP-6A-1_PE_peaks.filter.p10.bed;bZIP-7A-1_PE_peaks.filter.p10.bed;bZIP-A_PE_peaks.filter.p10.bed;bZIP-B_PE_peaks.filter.p10.bed;bZIP-D_PE_peaks.filter.p10.bed;C2-A_PE_peaks.filter.p10.bed;C2-B_PE_peaks.filter.p10.bed;C2C2-Dof-2A-1_PE_peaks.filter.p10.bed;C2C2-Dof-2D-1_PE_peaks.filter.p10.bed;C2C2-Dof-4A-1_PE_peaks.filter.p10.bed;C2C2-Dof-4D-1_PE_peaks.filter.p10.bed;C2-D_PE_peaks.filter.p10.bed;C2H2-2A-1_PE_peaks.filter.p10.bed;C2H2-3A-1_PE_peaks.filter.p10.bed;C2H2-3D-2_PE_peaks.filter.p10.bed;C2H2-4A-1_PE_peaks.filter.p10.bed;C2H2-5B-1_PE_peaks.filter.p10.bed;C2H2-6A-1_PE_peaks.filter.p10.bed;C2H2-6B-1_PE_peaks.filter.p10.bed;C2H2-6D-2_PE_peaks.filter.p10.bed;C3H-1A-1_PE_peaks.filter.p10.bed;C3H-1B-1_PE_peaks.filter.p10.bed;C3H-1D-2_PE_peaks.filter.p10.bed;C3H-3A-1_PE_peaks.filter.p10.bed;C3H-3A-2_PE_peaks.filter.p10.bed;C3H-4B-1_PE_peaks.filter.p10.bed;C3H-7B-1_PE_peaks.filter.p10.bed;DBB-7A-1_PE_peaks.filter.p10.bed;DBP-1B-1_PE_peaks.filter.p10.bed;DBP-1D-1_PE_peaks.filter.p10.bed;EIL-4D-1_PE_peaks.filter.p10.bed;GARP-ARR-6A-1_PE_peaks.filter.p10.bed;GARP-ARR-7A-1_PE_peaks.filter.p10.bed;GARP-ARR-7A-3_PE_peaks.filter.p10.bed;GARP-G2-2A-1_PE_peaks.filter.p10.bed;GARP-G2-2B-1_PE_peaks.filter.p10.bed;GARP-G2-3B-1_PE_peaks.filter.p10.bed;GARP-G2-4A-1_PE_peaks.filter.p10.bed;GARP-G2-4D-2_PE_peaks.filter.p10.bed;GARP-G2-5B-3_PE_peaks.filter.p10.bed;GRAS-2A-1_PE_peaks.filter.p10.bed;GRAS-4B-1_PE_peaks.filter.p10.bed;GRF4-2A-1_PE_peaks.filter.p10.bed;GRF4-2B-1_PE_peaks.filter.p10.bed;GRF4-2D-1_PE_peaks.filter.p10.bed;GRF-6A-1_PE_peaks.filter.p10.bed;HB-BELL-4B-1_PE_peaks.filter.p10.bed;HB-BELL-5D-1_PE_peaks.filter.p10.bed;HB-HD-ZIP-2A-1_PE_peaks.filter.p10.bed;HB-HD-ZIP-2A-2_PE_peaks.filter.p10.bed;HB-HD-ZIP-2B-1_PE_peaks.filter.p10.bed;HB-HD-ZIP-6A-1_PE_peaks.filter.p10.bed;HB-HD-ZIP-6A-2_PE_peaks.filter.p10.bed;HB-HD-ZIP-6B-2_PE_peaks.filter.p10.bed;HB-PHD-6A-1_PE_peaks.filter.p10.bed;HB-WOX-A_PE_peaks.filter.p10.bed;HB-WOX-B_PE_peaks.filter.p10.bed;HB-WOX-D_PE_peaks.filter.p10.bed;HSF-U_PE_peaks.filter.p10.bed;IPA1-7B-1_PE_peaks.filter.p10.bed;LIM-7B-1_PE_peaks.filter.p10.bed;LIM-7D-1_PE_peaks.filter.p10.bed;LOB-1A-1_PE_peaks.filter.p10.bed;LOB-3A-1_PE_peaks.filter.p10.bed;LOB-3B-1_PE_peaks.filter.p10.bed;LOB-3D-1_PE_peaks.filter.p10.bed;LOB-3D-2_PE_peaks.filter.p10.bed;MADS1-lgy3-4A-1_PE_peaks.filter.p10.bed;MADS1-lgy3-4B-1_PE_peaks.filter.p10.bed;MADS1-lgy3-4D-1_PE_peaks.filter.p10.bed;MADS-M-4D-1_PE_peaks.filter.p10.bed;MADS-MIKC-5A-1_PE_peaks.filter.p10.bed;MADS-MIKC-7A-1_PE_peaks.filter.p10.bed;MYB-1A-1_PE_peaks.filter.p10.bed;MYB-1A-2_PE_peaks.filter.p10.bed;MYB-2A-1_PE_peaks.filter.p10.bed;MYB-2A-2_PE_peaks.filter.p10.bed;MYB-3A-1_PE_peaks.filter.p10.bed;MYB-3D-1_PE_peaks.filter.p10.bed;MYB-4A-1_PE_peaks.filter.p10.bed;MYB-4A-2_PE_peaks.filter.p10.bed;MYB-5A-1_PE_peaks.filter.p10.bed;MYB-5B-1_PE_peaks.filter.p10.bed;MYB-6D-1_PE_peaks.filter.p10.bed;MYB-7A-3_PE_peaks.filter.p10.bed;MYB-7A-5_PE_peaks.filter.p10.bed;NAC-1D-1_PE_peaks.filter.p10.bed;NAC-2A-1_PE_peaks.filter.p10.bed;NAC-2A-3_PE_peaks.filter.p10.bed;NAC-2A-4_PE_peaks.filter.p10.bed;NAC-2D-6_PE_peaks.filter.p10.bed;NAC-3A-1_PE_peaks.filter.p10.bed;NAC-3D-1_PE_peaks.filter.p10.bed;NAC-6A-1_PE_peaks.filter.p10.bed;NAC-6B-1_PE_peaks.filter.p10.bed;NAC-6D-1_PE_peaks.filter.p10.bed;NAC-7A-1_PE_peaks.filter.p10.bed;NAC-7A-2_PE_peaks.filter.p10.bed;NAC-7B-2_PE_peaks.filter.p10.bed;NAC-7D-2_PE_peaks.filter.p10.be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bw files: Alfin-4D-1.sort.q20.rmdup.rpm.bw;AP2-B.sort.q20.rmdup.rpm.bw;AP2-D.sort.q20.rmdup.rpm.bw;AP2-DREB-1A-1.sort.q20.rmdup.rpm.bw;AP2-DREB-1B-1.sort.q20.rmdup.rpm.bw;AP2-DREB-1D-1.sort.q20.rmdup.rpm.bw;AP2-DREB-2D-1.sort.q20.rmdup.rpm.bw;AP2-DREB-5B-3.sort.q20.rmdup.rpm.bw;AP2-ERF-3A-1.sort.q20.rmdup.rpm.bw;AP2-ERF-4B-2.sort.q20.rmdup.rpm.bw;AP2-ERF-5B-1.sort.q20.rmdup.rpm.bw;AP2-ERF-5B-2.sort.q20.rmdup.rpm.bw;AP2-ERF-5D-1.sort.q20.rmdup.rpm.bw;AP2-ERF-6A-1.sort.q20.rmdup.rpm.bw;AP2-ERF-6A-2.sort.q20.rmdup.rpm.bw;AP2-ERF-6D-1.sort.q20.rmdup.rpm.bw;AP2-RAV-4B-1.sort.q20.rmdup.rpm.bw;B3-2A-1.sort.q20.rmdup.rpm.bw;B3-2B-2.sort.q20.rmdup.rpm.bw;B3-4A-1.sort.q20.rmdup.rpm.bw;B3-4B-1.sort.q20.rmdup.rpm.bw;B3-4B-2.sort.q20.rmdup.rpm.bw;B3-5A-1.sort.q20.rmdup.rpm.bw;B3-5B-1.sort.q20.rmdup.rpm.bw;B3-5D-2.sort.q20.rmdup.rpm.bw;B3-6D-1.sort.q20.rmdup.rpm.bw;B3-6D-2.sort.q20.rmdup.rpm.bw;B3-7B-1.sort.q20.rmdup.rpm.bw;B3-7D-1.sort.q20.rmdup.rpm.bw;B3-ARF-2D-1.sort.q20.rmdup.rpm.bw;B3-ARF-3A-1.sort.q20.rmdup.rpm.bw;B3-ARF-3B-2.sort.q20.rmdup.rpm.bw;BES1-6A-1.sort.q20.rmdup.rpm.bw;BES1-A.sort.q20.rmdup.rpm.bw;BES1-B.sort.q20.rmdup.rpm.bw;BES1-D.sort.q20.rmdup.rpm.bw;bHLH-1A-1.sort.q20.rmdup.rpm.bw;bHLH-3A-2.sort.q20.rmdup.rpm.bw;bHLH-4B-1.sort.q20.rmdup.rpm.bw

p.rpm.bw;bHLH-5A-1.sort.q20.rmdup.rpm.bw;bHLH-5A-4.sort.q20.rmdup.rpm.bw;bHLH-6A-1.sort.q20.rmdup.rpm.bw;bHLH-7A-2.sort.q20.rmdup.rpm.bw;bHLH-7A-3.sort.q20.rmdup.rpm.bw;bHLH-7D-2.sort.q20.rmdup.rpm.bw;bHLH-U.sort.q20.rmdup.rpm.bw;bZIP-2A-2.sort.q20.rmdup.rpm.bw;bZIP-2A-3.sort.q20.rmdup.rpm.bw;bZIP-3A-1.sort.q20.rmdup.rpm.bw;bZIP-3A-2.sort.q20.rmdup.rpm.bw;bZIP-5A-1.sort.q20.rmdup.rpm.bw;bZIP-5B-3.sort.q20.rmdup.rpm.bw;bZIP-6A-1.sort.q20.rmdup.rpm.bw;bZIP-7A-1.sort.q20.rmdup.rpm.bw;bZIP-A.sort.q20.rmdup.rpm.bw;bZIP-B.sort.q20.rmdup.rpm.bw;bZIP-D.sort.q20.rmdup.rpm.bw;C2-A.sort.q20.rmdup.rpm.bw;C2-B.sort.q20.rmdup.rpm.bw;C2C2-Dof-2A-1.sort.q20.rmdup.rpm.bw;C2C2-Dof-2D-1.sort.q20.rmdup.rpm.bw;C2C2-Dof-4A-1.sort.q20.rmdup.rpm.bw;C2C2-Dof-4D-1.sort.q20.rmdup.rpm.bw;C2-D.sort.q20.rmdup.rpm.bw;C2H2-2A-1.sort.q20.rmdup.rpm.bw;C2H2-3A-1.sort.q20.rmdup.rpm.bw;C2H2-3D-2.sort.q20.rmdup.rpm.bw;C2H2-4A-1.sort.q20.rmdup.rpm.bw;C2H2-5B-1.sort.q20.rmdup.rpm.bw;C2H2-6A-1.sort.q20.rmdup.rpm.bw;C2H2-6B-1.sort.q20.rmdup.rpm.bw;C2H2-6D-2.sort.q20.rmdup.rpm.bw;C3H-1A-1.sort.q20.rmdup.rpm.bw;C3H-1B-1.sort.q20.rmdup.rpm.bw;C3H-1D-2.sort.q20.rmdup.rpm.bw;C3H-3A-1.sort.q20.rmdup.rpm.bw;C3H-3A-2.sort.q20.rmdup.rpm.bw;C3H-4B-1.sort.q20.rmdup.rpm.bw;C3H-7B-1.sort.q20.rmdup.rpm.bw;DBB-7A-1.sort.q20.rmdup.rpm.bw;DBP-1B-1.sort.q20.rmdup.rpm.bw;DBP-1D-1.sort.q20.rmdup.rpm.bw;EIL-4D-1.sort.q20.rmdup.rpm.bw;GARP-ARR-6A-1.sort.q20.rmdup.rpm.bw;GARP-ARR-7A-1.sort.q20.rmdup.rpm.bw;GARP-ARR-7A-3.sort.q20.rmdup.rpm.bw;GARP-G2-2A-1.sort.q20.rmdup.rpm.bw;GARP-G2-2B-1.sort.q20.rmdup.rpm.bw;GARP-G2-3B-1.sort.q20.rmdup.rpm.bw;GARP-G2-4A-1.sort.q20.rmdup.rpm.bw;GARP-G2-4D-2.sort.q20.rmdup.rpm.bw;GARP-G2-5B-3.sort.q20.rmdup.rpm.bw;GRAS-2A-1.sort.q20.rmdup.rpm.bw;GRAS-4B-1.sort.q20.rmdup.rpm.bw;GRAS-4B-2.sort.q20.rmdup.rpm.bw;GRF4-2A-1.sort.q20.rmdup.rpm.bw;GRF4-2B-1.sort.q20.rmdup.rpm.bw;GRF4-2D-1.sort.q20.rmdup.rpm.bw;GRF-6A-1.sort.q20.rmdup.rpm.bw;Halo-merge.rpm.bw;HB-BELL-4B-1.sort.q20.rmdup.rpm.bw;HB-BELL-5D-1.sort.q20.rmdup.rpm.bw;HB-HD-ZIP-2A-1.sort.q20.rmdup.rpm.bw;HB-HD-ZIP-2A-2.sort.q20.rmdup.rpm.bw;HB-HD-ZIP-2B-1.sort.q20.rmdup.rpm.bw;HB-HD-ZIP-6A-1.sort.q20.rmdup.rpm.bw;HB-HD-ZIP-6A-2.sort.q20.rmdup.rpm.bw;HB-HD-ZIP-6B-2.sort.q20.rmdup.rpm.bw;HB-PHD-6A-1.sort.q20.rmdup.rpm.bw;HB-WOX-A.sort.q20.rmdup.rpm.bw;HB-WOX-B.sort.q20.rmdup.rpm.bw;HB-WOX-D.sort.q20.rmdup.rpm.bw;HSF-IP-1A-1.sort.q20.rmdup.rpm.bw;IPA1-7B-1.sort.q20.rmdup.rpm.bw;LIM-7B-1.sort.q20.rmdup.rpm.bw;LIM-7D-1.sort.q20.rmdup.rpm.bw;LOB-1A-1.sort.q20.rmdup.rpm.bw;LOB-3A-1.sort.q20.rmdup.rpm.bw;LOB-3B-1.sort.q20.rmdup.rpm.bw;LOB-3D-1.sort.q20.rmdup.rpm.bw;LOB-3D-2.sort.q20.rmdup.rpm.bw;MADS1-lgy3-4A-1.sort.q20.rmdup.rpm.bw;MADS1-lgy3-4B-1.sort.q20.rmdup.rpm.bw;MADS1-lgy3-4D-1.sort.q20.rmdup.rpm.bw;MADS-M-4D-1.sort.q20.rmdup.rpm.bw;MADS-MIKC-5A-1.sort.q20.rmdup.rpm.bw;MADS-MIKC-7A-1.sort.q20.rmdup.rpm.bw;MYB-1A-1.sort.q20.rmdup.rpm.bw;MYB-1A-2.sort.q20.rmdup.rpm.bw;MYB-2A-1.sort.q20.rmdup.rpm.bw;MYB-2A-2.sort.q20.rmdup.rpm.bw;MYB-3A-1.sort.q20.rmdup.rpm.bw;MYB-3D-1.sort.q20.rmdup.rpm.bw;MYB-4A-1.sort.q20.rmdup.rpm.bw;MYB-4A-2.sort.q20.rmdup.rpm.bw;MYB-5A-1.sort.q20.rmdup.rpm.bw;MYB-5B-1.sort.q20.rmdup.rpm.bw;MYB-6D-1.sort.q20.rmdup.rpm.bw;MYB-7A-3.sort.q20.rmdup.rpm.bw;MYB-7A-5.sort.q20.rmdup.rpm.bw;NAC-1D-1.sort.q20.rmdup.rpm.bw;NAC-2A-1.sort.q20.rmdup.rpm.bw;NAC-2A-3.sort.q20.rmdup.rpm.bw;NAC-2A-4.sort.q20.rmdup.rpm.bw;NAC-2D-6.sort.q20.rmdup.rpm.bw;NAC-3A-1.sort.q20.rmdup.rpm.bw;NAC-3D-1.sort.q20.rmdup.rpm.bw;NAC-6A-1.sort.q20.rmdup.rpm.bw;NAC-6B-1.sort.q20.rmdup.rpm.bw;NAC-6D-1.sort.q20.rmdup.rpm.bw;NAC-7A-1.sort.q20.rmdup.rpm.bw;NAC-7A-2.sort.q20.rmdup.rpm.bw;NAC-7B-2.sort.q20.rmdup.rpm.bw;NAC-7D-2.sort.q20.rmdup.rpm.bw;NAM-B1-6A-1.sort.q20.rmdup.rpm.bw;NAM-B1-6D-1.sort.q20.rmdup.rpm.bw;NF-YB-1B-1.sort.q20.rmdup.rpm.bw;PIF-5B-1.sort.q20.rmdup.rpm.bw;PIF-5D-1.sort.q20.rmdup.rpm.bw;PLATZ-YA.sort.q20.rmdup.rpm.bw;PLATZ-B.sort.q20.rmdup.rpm.bw;PLATZ-D.sort.q20.rmdup.rpm.bw;Q-5A-1.sort.q20.rmdup.rpm.bw;Q-5B-1.sort.q20.rmdup.rpm.bw;REF6-3D-1_ampDAP.sort.q20.rmdup.rpm.bw;REF6-3D-1.sort.q20.rmdup.rpm.bw;Rht-4B-1.sort.q20.rmdup.rpm.bw;Rht-4D-1.sort.q20.rmdup.rpm.bw;RWP-RK-2D-1.sort.q20.rmdup.rpm.bw;SBP-7B-2.sort.q20.rmdup.rpm.bw;SPL16-gw8-7B-1.sort.q20.rmdup.rpm.bw;SPL16-gw8-7D-1.sort.q20.rmdup.rpm.bw;Tify-5A-1.sort.q20.rmdup.rpm.bw;Tify-5B-1.sort.q20.rmdup.rpm.bw;Tify-6B-1.sort.q20.rmdup.rpm.bw;Trihelix-2A-1.sort.q20.rmdup.rpm.bw;Trihelix-2B-1.sort.q20.rmdup.rpm.bw;TUB-1B-1.sort.q20.rmdup.rpm.bw;TUB-3A-1.sort.q20.rmdup.rpm.bw;Vrn1-5D-1.sort.q20.rmdup.rpm.bw;WRKY-1D-1.sort.q20.rmdup.rpm.bw;WRKY-1D-2.sort.q20.rmdup.rpm.bw;WRKY-6A-1.sort.q20.rmdup.rpm.bw;GNI-2D.sort.q20.rmdup.rpm.bw;GNI-U.sort.q20.rmdup.rpm.bw;TaMOR-4B.sort.q20.rmdup.rpm.bw;TaMOR-4D.sort.q20.rmdup.rpm.bw;Tamyb10-3B.sort.q20.rmdup.rpm.bw;Tamyb10-3D.sort.q20.rmdup.rpm.bw;TaSEP3-7A.sort.q20.rmdup.rpm.bw;TaSEP3-7B.sort.q20.rmdup.rpm.bw;TaSEP3-7D.sort.q20.rmdup.rpm.bw;TaVRT2-7D.sort.q20.rmdup.rpm.bw;TdDof-3A.sort.q20.rmdup.rpm.bw

Genome browser session
(e.g. [UCSC](http://ucsc))

http://bioinfo.sibs.ac.cn/dap-seq_CS_jbrowse/

Methodology

Replicates

AP2-DREB-1A-1, AP2-DREB-1B-1, AP2-DREB-1D-1, AP2-ERF-6A-1 with two biological replicates (Fig. S9 and Fig. S13).

Sequencing depth

All DAP-seq reads were paired-end 150bp. The number of raw reads and mapped reads ($q > 20$ and PCR duplicates removed) were show below:

TF raw_reads mapped_reads
Alfin-4D-1 55,009,100 19,689,151
AP2-B 70,829,430 12,971,559
AP2-D 118,943,322 30,049,193
AP2-DREB-1A-1 123,122,794 46,388,339
AP2-DREB-1B-1 160,151,212 51,840,155
AP2-DREB-1D-1 166,769,898 53,758,258
AP2-DREB-2D-1 138,967,776 71,018,771
AP2-DREB-5B-3 62,945,094 26,997,903
AP2-ERF-3A-1 155,541,720 10,279,445
AP2-ERF-4B-2 90,995,392 22,182,956
AP2-ERF-5B-1 51,626,096 27,662,222
AP2-ERF-5B-2 80,049,018 38,960,090
AP2-ERF-5D-1 21,859,116 9,165,569

AP2-ERF-6A-1 90,533,246 15,683,919
 AP2-ERF-6A-2 44,479,564 15,478,423
 AP2-ERF-6D-1 91,120,804 13,797,802
 AP2-RAV-4B-1 85,839,768 54,655,218
 B3-2A-1 95,680,130 13,468,080
 B3-2B-2 43,393,962 9,389,401
 B3-4A-1 77,311,956 10,827,336
 B3-4B-1 65,755,304 10,900,078
 B3-4B-2 21,319,906 2,885,777
 B3-5A-1 60,256,972 7,084,077
 B3-5B-1 68,370,206 9,036,174
 B3-5D-2 36,026,250 5,348,336
 B3-6D-1 12,722,186 2,257,540
 B3-6D-2 77,502,176 9,453,211
 B3-7B-1 96,640,536 13,620,553
 B3-7D-1 109,964,842 14,851,470
 B3-ARF-2D-1 41,541,530 13,175,965
 B3-ARF-3A-1 81,368,118 11,958,287
 B3-ARF-3B-2 41,796,286 11,168,249
 BES1-6A-1 55,760,022 19,940,467
 BES1-A 63,161,308 24,112,754
 BES1-B 77,264,522 27,482,981
 BES1-D 67,965,750 23,834,253
 bHLH-1A-1 37,524,668 18,053,634
 bHLH-3A-2 54,346,954 5,839,845
 bHLH-4B-1 42,696,912 16,996,941
 bHLH-5A-1 50,441,536 8,378,814
 bHLH-5A-4 21,555,530 3,668,223
 bHLH-6A-1 44,877,492 7,169,096
 bHLH-7A-2 21,468,076 5,544,651
 bHLH-7A-3 29,859,530 6,703,328
 bHLH-7D-2 31,487,904 8,866,724
 bHLH-U 39,570,572 6,730,247
 bZIP-2A-2 38,644,394 13,411,524
 bZIP-2A-3 51,931,212 22,177,905
 bZIP-3A-1 90,971,558 55,697,499
 bZIP-3A-2 163,403,766 104,336,039
 bZIP-5A-1 61,359,848 17,524,656
 bZIP-5B-3 110,357,470 64,110,141
 bZIP-6A-1 26,633,698 6,747,306
 bZIP-7A-1 65,040,060 42,425,714
 bZIP-A 86,922,542 14,963,020
 bZIP-B 117,318,182 16,121,077
 bZIP-D 81,336,132 11,306,481
 C2-A 12,479,536 4,808,854
 C2-B 6,790,040 2,578,201
 C2C2-Dof-2A-1 80,659,996 14,024,563
 C2C2-Dof-2D-1 69,815,316 11,920,330
 C2C2-Dof-4A-1 78,514,658 35,468,366
 C2C2-Dof-4D-1 86,827,478 35,211,048
 C2-D 9,423,056 3,971,008
 C2H2-2A-1 137,936,616 60,281,599
 C2H2-3A-1 107,733,744 37,262,136
 C2H2-3D-2 51,222,352 17,471,085
 C2H2-4A-1 43,410,668 18,371,682
 C2H2-5B-1 17,069,050 3,415,589
 C2H2-6A-1 42,264,124 9,713,026
 C2H2-6B-1 20,833,098 7,004,265
 C2H2-6D-2 82,709,502 8,233,337
 C3H-1A-1 53,548,242 8,413,518
 C3H-1D-2 37,601,504 7,673,397
 C3H-3A-1 30,715,470 15,291,443
 C3H-3A-2 55,463,244 15,484,599
 C3H-7B-1 22,160,948 4,521,051
 DBB-7A-1 35,884,136 4,550,475
 DBP-1B-1 50,864,722 6,548,695
 DBP-1D-1 43,270,114 5,657,622
 EIL-4D-1 52,580,906 11,861,565

GARP-ARR-6A-1 72,836,418 16,861,457
 GARP-ARR-7A-1 46,385,926 5,522,207
 GARP-ARR-7A-3 49,942,646 6,022,140
 GARP-G2-2A-1 128,563,374 66,079,363
 GARP-G2-2B-1 116,315,468 32,402,132
 GARP-G2-3B-1 50,751,050 7,958,844
 GARP-G2-4A-1 96,368,650 22,757,854
 GARP-G2-4D-2 70,031,588 37,244,870
 GARP-G2-5B-3 160,127,610 39,608,807
 GNI-2D 45,999,758 22,514,143
 GNI-U 53,919,062 22,541,915
 GRAS-2A-1 21,998,140 9,883,083
 GRAS-4B-2 65,429,870 6,485,100
 GRF4-2A-1 52,860,800 14,419,128
 GRF4-2B-1 63,830,928 19,809,060
 GRF4-2D-1 44,699,428 16,632,855
 GRF-6A-1 92,825,442 16,052,200
 HB-BELL-4B-1 71,353,844 14,351,300
 HB-BELL-5D-1 67,235,040 10,779,044
 HB-HD-ZIP-2A-1 24,586,010 12,158,542
 HB-HD-ZIP-2A-2 59,190,696 23,294,154
 HB-HD-ZIP-2B-1 35,132,180 9,122,619
 HB-HD-ZIP-6A-1 53,793,388 31,374,482
 HB-HD-ZIP-6A-2 60,728,028 14,986,024
 HB-HD-ZIP-6B-2 59,949,072 15,204,030
 HB-PHD-6A-1 86,870,186 31,686,694
 HB-WOX-A 3,134,048 1,309,940
 HB-WOX-B 4,612,136 1,566,386
 HB-WOX-D 2,833,386 1,263,046
 HSF-U 30,208,124 12,793,545
 IPA1-7B-1 57,540,476 19,639,449
 LIM-7B-1 59,620,982 23,772,393
 LIM-7D-1 62,426,170 19,506,992
 LOB-1A-1 25,877,258 10,246,768
 LOB-3A-1 40,391,124 8,911,961
 LOB-3B-1 26,984,848 7,108,793
 LOB-3D-1 45,258,494 9,454,122
 LOB-3D-2 47,184,314 8,515,444
 MADS1-lgy3-4A-1 92,699,698 21,721,010
 MADS1-lgy3-4B-1 23,524,664 7,636,929
 MADS1-lgy3-4D-1 46,510,940 11,539,835
 MADS-M-4D-1 64,031,630 7,620,777
 MADS-MIKC-5A-1 49,216,104 23,183,259
 MADS-MIKC-7A-1 59,255,066 7,608,336
 MYB-1A-1 55,393,490 5,703,732
 MYB-1A-2 75,142,620 7,855,907
 MYB-2A-1 74,602,568 8,979,639
 MYB-2A-2 87,494,586 10,255,650
 MYB-3A-1 26,598,050 12,676,840
 MYB-3D-1 58,027,346 7,771,393
 MYB-4A-1 77,285,006 7,925,038
 MYB-4A-2 60,080,772 5,767,530
 MYB-5A-1 154,255,784 15,407,933
 MYB-5B-1 90,658,504 8,200,771
 MYB-6D-1 162,781,464 49,461,208
 MYB-7A-3 100,118,238 63,345,793
 MYB-7A-5 40,704,660 7,604,570
 NAC-1D-1 37,179,260 4,944,215
 NAC-2A-1 48,705,844 23,474,274
 NAC-2A-3 110,230,986 17,308,375
 NAC-2A-4 146,410,732 18,429,403
 NAC-2D-6 49,905,060 6,235,623
 NAC-3A-1 169,423,432 56,466,856
 NAC-3D-1 126,989,858 30,368,126
 NAC-6A-1 146,620,102 42,829,632
 NAC-6B-1 180,218,562 42,379,353
 NAC-6D-1 120,707,436 29,103,419
 NAC-7A-1 76,424,528 8,302,185

NAC-7A-2 52,247,296 11,168,524
 NAC-7B-2 68,506,578 11,746,421
 NAC-7D-2 87,454,148 15,556,111
 NAM-B1-6A-1 74,131,190 34,515,759
 NAM-B1-6D-1 66,949,012 39,152,598
 NF-YB-1B-1 28,823,556 3,902,526
 PIF-5B-1 65,754,164 24,982,431
 PIF-5D-1 68,345,658 24,625,944
 PLATZ-A 76,759,158 22,794,684
 PLATZ-B 85,546,406 22,901,495
 PLATZ-D 71,006,516 20,923,779
 Q-5A-1 70,132,144 27,405,111
 Q-5B-1 50,809,016 5,667,335
 REF6-3D-1 108,122,454 40,632,219
 REF6-3D-1_ampDAP 68,236,362 7,794,211
 Rht-4B-1 73,947,030 11,707,690
 Rht-4D-1 86,263,286 10,856,621
 RWP-RK-2D-1 68,020,216 9,612,135
 SBP-7B-2 92,861,456 11,896,682
 SPL16-gw8-7B-1 85,198,998 37,154,176
 SPL16-gw8-7D-1 89,686,500 25,387,552
 TaMOR-4B 54,948,490 23,542,528
 TaMOR-4D 41,410,958 18,297,595
 Tamyb10-3B 38,604,326 18,996,085
 Tamyb10-3D 36,497,072 17,264,955
 TaSEP3-7A 106,775,486 35,649,127
 TaSEP3-7B 16,886 2,756
 TaSEP3-7D 2,436 185
 TaVRT2-7D 43,741,480 18,882,545
 TdDof-3A 45,935,788 20,778,765
 Tify-5A-1 55,446,618 26,460,902
 Tify-5B-1 67,757,274 16,629,259
 Tify-6B-1 66,982,266 15,111,212
 Trihelix-2A-1 79,676,848 23,483,438
 Trihelix-2B-1 49,642,780 9,375,668
 TUB-1B-1 61,032,540 7,429,468
 TUB-3A-1 52,739,064 17,779,513
 Vrn1-5D-1 76,937,672 7,556,115
 WRKY-1D-1 39,472,466 17,429,727
 WRKY-1D-2 77,893,180 18,628,939
 WRKY-6A-1 23,901,952 10,604,028

Antibodies

Halo: Promega, cat # G7281, lot # 0000384548

Peak calling parameters

MACS2 was used with parameters: "-c \${Halo} -f BAMPE -g 14271578887 --nomodel --nolambda", FDR < 0.05 and P value < 1e-10.

Data quality

The peaks detected from samples introduced with Halo tag only were considered as non-specific bindings, and TF peaks overlapping with peaks detected from Halo samples were removed for subsequent analysis. Peak numbers are listed below:

AP2-DREB-1A-1 244,870
 AP2-DREB-1B-1 228,748
 AP2-DREB-1D-1 244,122
 AP2-DREB-2D-1 239,133
 AP2-RAV-4B-1 424,412
 AP2-ERF-4B-2 5,098
 AP2-ERF-5B-2 96,729
 AP2-DREB-5B-3 135,566
 AP2-ERF-6A-1 69,258
 AP2-ERF-6D-1 35,523
 bHLH-1A-1 11,892
 bHLH-7D-2 224
 bZIP-2A-3 129,202
 bZIP-3A-1 175,818
 bZIP-3A-2 113,502
 bZIP-5B-3 56,164
 bZIP-7A-1 1,495
 C2C2-Dof-4A-1 259,937
 C2C2-Dof-4D-1 243,497
 C2H2-2A-1 230,160
 C2H2-3A-1 125,633

EIL-4D-1 20,791
 GARP-G2-2A-1 672,630
 GARP-G2-2B-1 316,825
 GARP-G2-4A-1 43,303
 GARP-G2-4D-2 301,029
 GARP-G2-5B-3 315,378
 HB-HD-ZIP-2A-2 2,765
 HB-HD-ZIP-6A-1 77,918
 HB-HD-ZIP-6A-2 42,577
 HB-HD-ZIP-6B-2 54,786
 HB-PHD-6A-1 223,167
 HSF-U 33,065
 MYB-2A-2 2,863
 MYB-7A-3 200,700
 NAC-2D-6 1,567
 NAC-3A-1 1,849
 NAC-6A-1 263,558
 NAC-6B-1 248,604
 NAC-6D-1 158,055
 NAC-7A-1 2,532
 NAC-7D-2 611
 SBP-7B-2 4,112
 Trihelix-2A-1 187,258
 Trihelix-2B-1 9,419
 AP2-B 188
 AP2-D 526
 AP2-ERF-3A-1 304
 AP2-ERF-5B-1 79
 AP2-ERF-5D-1 27
 AP2-ERF-6A-2 3,073
 Q-5A-1 158
 Q-5B-1 208
 bHLH-3A-2 76
 bHLH-5A-1 68
 bHLH-6A-1 53
 bHLH-7A-2 47
 bHLH-7A-3 21
 bHLH-U 39
 PIF-5D-1 78
 bZIP-2A-2 24
 bZIP-5A-1 70
 bZIP-6A-1 10
 bZIP-A 255
 bZIP-B 579
 C2C2-Dof-2A-1 203
 C2C2-Dof-2D-1 91
 REF6-3D-1_ampDAP 24,509
 GARP-ARR-6A-1 510
 GNI-2D 354
 GNI-U 346
 MYB-1A-1 149
 MYB-1A-2 158
 MYB-2A-1 153
 MYB-3A-1 135
 MYB-3D-1 77
 MYB-4A-1 180
 MYB-4A-2 131
 MYB-5A-1 399
 MYB-5B-1 154
 MYB-6D-1 596
 MYB-7A-5 36
 Tamyb10-3B 232
 Tamyb10-3D 490
 NAC-1D-1 39
 NAC-2A-3 184
 NAC-2A-4 329
 NAC-3D-1 297
 NAC-7A-2 195

NAC-7B-2 194
NAM-B1-6A-1 292
NAM-B1-6D-1 416
WRKY-1D-2 7,900
Alfin-4D-1 104
B3-2A-1 214
B3-2B-2 41
B3-4A-1 133
B3-4B-1 102
B3-4B-2 74
B3-5A-1 95
B3-5B-1 112
B3-5D-2 31
B3-6D-1 26
B3-6D-2 117
B3-7B-1 124
B3-7D-1 161
B3-ARF-2D-1 8
B3-ARF-3A-1 87
B3-ARF-3B-2 180
BES1-6A-1 42
BES1-A 70
BES1-B 134
BES1-D 73
bHLH-4B-1 132
bHLH-5A-4 43
PIF-5B-1 70
bZIP-D 287
C2-A 19
C2-B 17
C2-D 4
TdDof-3A 585
C2H2-3D-2 21
C2H2-4A-1 933
C2H2-5B-1 41
C2H2-6A-1 49
C2H2-6B-1 39
C2H2-6D-2 856
REF6-3D-1 4,342
C3H-1A-1 88
C3H-1D-2 29
C3H-3A-1 153
C3H-3A-2 19
C3H-7B-1 15
DBB-7A-1 221
DBP-1B-1 67
DBP-1D-1 52
GARP-ARR-7A-1 58
GARP-ARR-7A-3 55
GARP-G2-3B-1 71
GRAS-2A-1 19
GRAS-4B-2 115
Rht-4B-1 90
Rht-4D-1 143
GRF4-2A-1 26
GRF4-2B-1 30
GRF4-2D-1 38
GRF-6A-1 62
HB-BELL-4B-1 36
HB-BELL-5D-1 34
HB-HD-ZIP-2A-1 123
HB-HD-ZIP-2B-1 46
HB-WOX-A 11
HB-WOX-B 31
HB-WOX-D 8
LIM-7B-1 80
LIM-7D-1 46
LOB-1A-1 19

LOB-3A-1 61
 LOB-3B-1 23
 LOB-3D-1 61
 LOB-3D-2 41
 TaMOR-4B 467
 TaMOR-4D 204
 MADS1-lgy3-4A-1 70
 MADS1-lgy3-4B-1 13
 MADS1-lgy3-4D-1 29
 MADS-M-4D-1 92
 MADS-MIKC-5A-1 189
 MADS-MIKC-7A-1 83
 TaSEP3-7A 841
 TaSEP3-7B 606
 TaSEP3-7D 44
 TaVRT2-7D 272
 Vrn1-5D-1 361
 NAC-2A-1 212
 NF-YB-1B-1 81
 PLATZ-A 75
 PLATZ-B 69
 PLATZ-D 49
 RWP-RK-2D-1 146
 IPA1-7B-1 113
 SPL16-gw8-7B-1 167
 SPL16-gw8-7D-1 319
 Tify-5A-1 89
 Tify-5B-1 52
 Tify-6B-1 229
 TUB-1B-1 74
 TUB-3A-1 30
 WRKY-1D-1 9
 WRKY-6A-1 19

Software

fastp (version 0.20.0); Trim Galore (version 0.4.4); Burrows–Wheeler Aligner (version 0.7.17-r1188); MACS (version 2.2.6); MEME software toolkit (version 5.1.1); R package motifStack (version 1.34.0); R package universalmotif (version 1.4.0); BLASTN (version 2.9.0); Circos(version 0.69-8); MAFFT (version v7.149b); R Jalview (version 2.11.1.3)