nature research

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Last updated by author(s): Jan 14, 2020

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.

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	Sequencing data was generated and collected on the Illumina HiSeq 2500, HiSeq 4000 and MiSeq Sequencing systems. Proteomics data was collected on a Fusion Lumos mass spectrometer (Thermo Fisher Scientific). Root length was measured using ImageJ.
Data analysis	Genomics: TopHat 2.1.1, HTSeq, EdgeR 3.6.2, EdgeR 3.18.1, PlantTFDB 4.0, Bowtie 2 v.2-2.0.5, MACS2 v.2.1, PhantomPeakQualTools v.2.0, BEDtools v.2.17.0, ChIPpeakAnno v.2.2.0, SICER, BEDtools, clusterProfiler, Salmon v0.8.1, TSIS R package, SAMtools and Thalemine Proteomics: MaxQuant version 1.6.3.3, PoissonSeq Gene regulatory network (GRN) inference: RTP-STAR (https://github.com/nmclark2/RTP-STAR), Dynamic Time Warping (DTW)

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. 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

All described lines can be requested from the corresponding author. Sequence data can be downloaded from GEO (GSE133408, reviewer password 'efinoygcdbanzgh'). Proteomics data are deposited at Proteome Exchange under the accession ID PXD013592 (Reviewer Access: Username: "reviewer72788@ebi.ac.uk" and password: "Dwq1vRej"). Visualized sequencing data can be found under http://neomorph.salk.edu/MYC2.

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 sizes in our study were chosen based on accepted sample sizes in relevant published reports within this field. (2-3 biological replicates for genomics and proteomic analyses were used).
Data exclusions	No data was excluded.
Replication	All of the experiments were repeated more than two times, and were reproduced successfully. A completely independent pool of side-by-side grown plants is considered as a biological replicate.
Randomization	Different genotypes were grown on individual plates and were allocated randomly in the growth and treatment chamber.
Blinding	Not applicable since no group allocation was conducted in this study.

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
☒	☐ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data

Methods

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

Antibodies

Antibodies used	Htz1 / Histone H2A.Z antibody (pAb), Rabbit polyclonal (Active Motif Cat# 39647, RRID:AB_2793289), Lot 29018003, 10µl per reaction Anti-trimethyl-Histone H3 (Lys4), clone 15-10C-E4, Recombinant antibody, Rabbit monoclonal (Millipore Cat# 05-745R, RRID:AB_1587134), Lot 2420405, 4µl per reaction Anti-GFP antibody, Clones 7.1 and 13.1, Mouse monoclonal, (Sigma-Aldrich Cat# 11814460001, RRID:AB_390913), 5µl per reaction ChromPure Mouse IgG, whole molecule, Jackson ImmunoResearch, (Jackson ImmunoResearch Labs Cat# 015-000-003, RRID:AB_2337188), Lot 99413, 2µl per reaction goat anti-GFP supplied by David Dreschel, Max Planck Institute of Molecular Cell Biology and Genetics
Validation	All used antibodies were previously published in plant science-related studies (Htz1 / Histone H2A.Z antibody PMID:31418686), (Anti-trimethyl-Histone H3 (Lys4) PMID:31418686, PMID:30657772), anti-GFP PMID:28943086). Specificity of the Htz1 / Histone H2A.Z antibody was tested in Arabidopsis thaliana (PMID:31418686). The Anti-trimethyl-Histone H3 (Lys4) antibody has a broad species cross-reactivity expected and is used in various organism (PMID:30955888, PMID:24341414, PMID:22763441). Detailed antibody information can be found on the Antibody registry website (https://antibodyregistry.org) (Htz1 / Histone H2A.Z antibody, AB_2793289), (Anti-trimethyl-Histone H3 (Lys4), RRID:AB_1587134), (Anti-GFP antibody, RRID:AB_390913), (ChromPure Mouse IgG, RRID:AB_2337188).

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.

reviewer password 'efinoygcdbanzgh' for GEO deposition GSE133408

Files in database submission

ChIP-seq_Col-0_IgG.fastq.gz
ChIP-seq_Col-0_air_H3K4me3.fastq.gz
ChIP-seq_Col-0_4hJA_H3K4me3.fastq.gz
ChIP-seq_myc2_air_H3K4me3.fastq.gz
ChIP-seq_myc2_4hJA_H3K4me3.fastq.gz
ChIP-seq_Col-0_air_H2A.Z.fastq.gz
ChIP-seq_Col-0_4hJA_H2A.Z.fastq.gz
ChIP-seq_myc2_air_H2A.Z.fastq.gz
ChIP-seq_myc2_4hJA_H2A.Z.fastq.gz
110915_2-W200-G600-FDR0.01-islandfiltered-normalized.wig
110915_6-W200-G600-FDR0.01-islandfiltered-normalized.wig
110915_9-W200-G600-FDR0.01-islandfiltered-normalized.wig
110915_12-W200-G600-FDR0.01-islandfiltered-normalized.wig
110915_1-W200-G600-FDR0.01-islandfiltered-normalized.wig
110915_5-W200-G600-FDR0.01-islandfiltered-normalized.wig
110915_8-W200-G600-FDR0.01-islandfiltered-normalized.wig
110915_11-W200-G600-FDR0.01-islandfiltered-normalized.wig
ANAC055_JA_2hr_ChIP_rep1.fastq.gz
ANAC055_JA_2hr_ChIP_rep2.fastq.gz
ANAC055_JA_2hr_ChIP_rep3.fastq.gz
MYC2_JA_2hr_ChIP_rep1.fastq.gz
MYC2_JA_2hr_ChIP_rep2.fastq.gz
MYC2_JA_2hr_ChIP_rep3.fastq.gz
MYC2_JA_2hr_ChIP_rep4.fastq.gz
MYC3_JA_2hr_ChIP_rep1.fastq.gz
MYC3_JA_2hr_ChIP_rep2.fastq.gz
MYC3_JA_2hr_ChIP_rep3.fastq.gz
STZ_AIR_2hr_ChIP_rep1.fastq.gz
STZ_AIR_2hr_ChIP_rep2.fastq.gz
STZ_AIR_2hr_ChIP_rep3.fastq.gz
STZ_JA_2hr_ChIP_rep1.fastq.gz
STZ_JA_2hr_ChIP_rep2.fastq.gz
HAL_1205_controlreads.fastq.gz
JONAS_2093_controlreads.fastq.gz
MISEQ_5018_controlreads.fastq.gz
JONAS_2096_controlreads_1.fastq.gz
JONAS_2096_controlreads_2.fastq.gz
HAL_1389_AT1G32640_JA_MGLCHIP16_3_150521_peaks.bed
JONAS_2273_AT1G32640_JA_MGLCHIP34_151214_summits.bed
JONAS_2273_AT1G32640_JA_MGLCHIP35_151214_summits.bed
JONAS_2206_AT1G32640_JA_JS_ChIP_8_2014_04_16_summits.bed
JONAS_2206_AT5G46760_JA_JS_ChIP_8_2014_04_16_summits.bed
JONAS_2273_AT5G46760_JA_MGLCHIP34_151214_summits.bed
JONAS_2273_AT5G46760_JA_MGLCHIP35_151214_summits.bed
HAL_1422_AT1G27730_AIR_MGLCHIP38_160125_summits.bed
HAL_1424_AT1G27730_AIR_MGLCHIP39_160315_summits.bed
HAL_1424_AT1G27730_AIR_MGLCHIP41_160315_summits.bed
HAL_1422_AT1G27730_JA_MGLCHIP38_160125_summits.bed
HAL_1424_AT1G27730_JA_MGLCHIP39_160315_summits.bed
JONAS_2257_AT3G15500_JA_MGLCHIP18_150608_summits.bed
HAL_1422_AT3G15500_JA_MGLCHIP38_160125_summits.bed
HAL_1424_AT3G15500_JA_MGLCHIP39_160315_summits.bed

Genome browser session
(e.g. UCSC)

http://neomorph.salk.edu/MYC2

Methodology

Replicates

MYC2 ChIP-seq - 4 biological replicates
MYC3 ChIP-seq - 3 biological replicates
ANAC055 ChIP-seq - 3 biological replicates
ZAT10 air ChIP-seq - 3 biological replicates

ZAT10 JA ChIP-seq - 2 biological replicates
H3K4me3 and H2A.Z ChIP-seq - 1 biological replicate

Sequencing depth

Listed by file below - total reads, uniquely mapped reads. All TF ChIP-seq samples were 100 bp single-read sequencing. Histone ChIP-seq samples were 130bp single-read sequencing.

ANAC055_JA_2hr_ChIP_rep1.fastq.gz 21579630 15584500
ANAC055_JA_2hr_ChIP_rep2.fastq.gz 10130742 7224047
ANAC055_JA_2hr_ChIP_rep3.fastq.gz 49536769 32819761
MYC2_JA_2hr_ChIP_rep1.fastq.gz 34003716 25391190
MYC2_JA_2hr_ChIP_rep2.fastq.gz 20608966 15047692
MYC2_JA_2hr_ChIP_rep3.fastq.gz 51803765 38110692
MYC2_JA_2hr_ChIP_rep4.fastq.gz 38302426 32517237
MYC3_JA_2hr_ChIP_rep1.fastq.gz 30218545 22198075
MYC3_JA_2hr_ChIP_rep2.fastq.gz 50956817 38186708
MYC3_JA_2hr_ChIP_rep3.fastq.gz 30155159 21448372
ZAT10_AIR_2hr_ChIP_rep1.fastq.gz 42120531 31505002
ZAT10_AIR_2hr_ChIP_rep2.fastq.gz 38712323 27326200
ZAT10_AIR_2hr_ChIP_rep3.fastq.gz 37810305 22967198
ZAT10_JA_2hr_ChIP_rep1.fastq.gz 55361855 39415920
ZAT10_JA_2hr_ChIP_rep2.fastq.gz 48383504 34173250
HAL_1205_controlreads.fastq.gz 40354104 27796842
JONAS_2093_controlreads.fastq.gz 9011923 4912769
MISEQ_5018_controlreads.fastq.gz 3767246 2642492
JONAS_2096_controlreads_1.fastq.gz 4000000 2699412
JONAS_2096_controlreads_2.fastq.gz 3011044 2033072
ChIP-seq_Col-0_IgG.fastq.gz 13651415
ChIP-seq_Col-0_air_H3K4me3.fastq.gz 18808057
ChIP-seq_Col-0_4hJA_H3K4me3.fastq.gz 24758457
ChIP-seq_myc2_air_H3K4me3.fastq.gz 17103736
ChIP-seq_myc2_4hJA_H3K4me3.fastq.gz 18261319
ChIP-seq_Col-0_air_H2A.Z.fastq.gz 20268643
ChIP-seq_Col-0_4hJA_H2A.Z.fastq.gz 19722520
ChIP-seq_myc2_air_H2A.Z.fastq.gz 26945152

Antibodies

Htz1 / Histone H2A.Z antibody (pAb), Rabbit polyclonal (Active Motif Cat# 39647, RRID:AB_2793289), Lot 29018003, 10µl per reaction
Anti-trimethyl-Histone H3 (Lys4), clone 15-10C-E4, Recombinant antibody, Rabbit monoclonal (Millipore Cat# 05-745R, RRID:AB_1587134), Lot 2420405, 4µl per reaction
Anti-GFP antibody, Clones 7.1 and 13.1, Mouse monoclonal, (Sigma-Aldrich Cat# 11814460001, RRID:AB_390913), 5µl per reaction
ChromPure Mouse IgG, whole molecule, Jackson ImmunoResearch, (Jackson ImmunoResearch Labs Cat# 015-000-003, RRID:AB_2337188), Lot 99413, 2µl per reaction
goat anti-GFP supplied by David Dreschel, Max Planck Institute of Molecular Cell Biology and Genetics

Peak calling parameters

For TF ChIP-seq, enriched binding sites were identified using MACS2 v.2.1 (options -p 99e-2 --nomodel –shiftsize --down-sample --call-summits) against sequence reads from whole IgG control samples (Zhang et al., 2008). The shift size was calculated using PhantomPeakQualTools v.2.0 (Kharchenko et al., 2008). Significant enrichments of histone modifications and histone variants were identified with the SICER software (Zang et al., 2009) using the TAIR10 genome assembly.

Data quality

Transcription factor summit lists were filtered with a lower cut-off of -log10(25) and remaining summits expanded from single nucleotides to 150 nt. Only summits with at least 10% nt overlap between at least two biological replicates were retained. These overlapping summits were merged between replicates using BEDtools v.2.17.0 to give the final set of high-stringency summits, which were then annotated using ChIPpeakAnno v.2.2.0 to any gene within 500 nt of the center of the summit or, alternatively, the nearest neighbor if there was no gene within 500 nt.

Software

Bowtie 2 v.2-2.0.5, MACS2 v.2.1, PhantomPeakQualTools v.2.0, BEDtools v.2.17.0, ChIPpeakAnno v.2.2.0, SICER