Table Data to PDF

ERX2067749

IR	1.0
type	ERX
database	SRA

Info

TITLE: Illumina HiSeq 2000 paired end sequencing; Transcriptomes and differential gene expression in the Arabidopsis shoot phloem companion cells during flowering
SRA_ID: ERX2067749
STUDY_REF: ERP023520
BioProject: PRJEB21286
DESIGN:
DESIGN_DESCRIPTION: Transcriptomes and differential gene expression in the Arabidopsis shoot phloem companion cells during flowering
SAMPLE_DESCRIPTOR:
@accession: ERS1788394
IDENTIFIERS:
PRIMARY_ID: ERS1788394
EXTERNAL_ID:
@namespace: BioSample
#text: SAMEA104124501
LIBRARY_DESCRIPTOR:
LIBRARY_NAME: Sample 6_p
LIBRARY_STRATEGY: RNA-Seq
LIBRARY_SOURCE: TRANSCRIPTOMIC
LIBRARY_SELECTION: RANDOM
LIBRARY_LAYOUT:
PAIRED:
@NOMINAL_LENGTH: 300
@NOMINAL_SDEV: 30
LIBRARY_CONSTRUCTION_PROTOCOL: For each biological replicate, approximately 500 INTACT reporter plants were grown in SDs for 21 days before shifting to LDs. The 0LD, 1LD, 2LD and 3LD samples were collected on the 21st day in SDs and 1, 2, and 3 days after the shift to LD. For each sample, the whole shoot material was collected from approximately 120 seedlings and frozen immediately in Eppendorf tubes suspended in liquid nitrogen. Plants of the shoot-phloem-companion-cell-tagged INTACT reporter line (Transgenic SUC2::redNTF and UBQ10::BirA in Col-0 background) were cultivated in growth chambers, in short-day (SD) conditions (8 h light/16 h dark) for 21 days and then shifted to long-day (LD) conditions (16 h light/8 h dark) to induce flowering. The growth-chamber condition was at 23°C with 65% relative humidity, and with the light at a fluence rate of 125 to 175 $\mu mol\ m^{-2}\ s^{-1}$. Total nuclear RNA was extracted from approximately 10,000 nuclei of each sample using the RNeasy Micro Kit (Qiagen). Genomic DNA was removed by DNase I treatment (Thermo Scientific). Double-strand cDNA was synthesized and linearly amplified (Clontech SMARTer Ultra Low Input RNA for Illumina Sequencing-HV kit). Low Input Library Prep Kit (Clontech) was used for preparation of sequencing libraries
PLATFORM:
ILLUMINA:
INSTRUMENT_MODEL: Illumina HiSeq 2000
SUBMISSION_lab_name: European Nucleotide Archive
DESCRIPTOR:
STUDY_TITLE: Transcriptomes and differential gene expression in the Arabidopsis shoot phloem companion cells during flowering
STUDY_TYPE:
@existing_study_type: Transcriptome Analysis
STUDY_ABSTRACT: We investigated the transcriptomes and differential gene expression at the Arabidopsis shoot phloem companion cells during flowering using INTACT reporter lines. Samples were collected in three biological replications.
STUDY_DESCRIPTION: We investigated the transcriptomes and differential gene expression at the Arabidopsis shoot phloem companion cells during flowering using INTACT reporter lines. Samples were collected in three biological replications.
Biosample_ID: SAMEA104124501

ERX2067750

IR	1.0
type	ERX

database SRA

Info

TITLE: Illumina HiSeq 2000 paired end sequencing; Transcriptomes and differential gene expression in the Arabidopsis shoot phloem companion cells during flowering
SRA_ID: ERX2067750
STUDY_REF: ERP023520
BioProject: PRJEB21286
DESIGN:
DESIGN_DESCRIPTION: Transcriptomes and differential gene expression in the Arabidopsis shoot phloem companion cells during flowering
SAMPLE_DESCRIPTOR:
@accession: ERS1788395
IDENTIFIERS:
PRIMARY_ID: ERS1788395
EXTERNAL_ID:
@namespace: BioSample
#text: SAMEA104124502
LIBRARY_DESCRIPTOR:
LIBRARY_NAME: Sample 7_p
LIBRARY_STRATEGY: RNA-Seq
LIBRARY_SOURCE: TRANSCRIPTOMIC
LIBRARY_SELECTION: RANDOM
LIBRARY_LAYOUT:
PAIRED:
@NOMINAL_LENGTH: 300
@NOMINAL_SDEV: 30
LIBRARY_CONSTRUCTION_PROTOCOL: For each biological replicate, approximately 500 INTACT reporter plants were grown in SDs for 21 days before shifting to LDs. The 0LD, 1LD, 2LD and 3LD samples were collected on the 21st day in SDs and 1, 2, and 3 days after the shift to LD. For each sample, the whole shoot material was collected from approximately 120 seedlings and frozen immediately in Eppendorf tubes suspended in liquid nitrogen. Plants of the shoot-phloem-companion-cell-tagged INTACT reporter line (Transgenic SUC2::redNTF and UBQ10::BirA in Col-0 background) were cultivated in growth chambers, in short-day (SD) conditions (8 h light/16 h dark) for 21 days and then shifted to long-day (LD) conditions (16 h light/8 h dark) to induce flowering. The growth-chamber condition was at 23°C with 65% relative humidity, and with the light at a fluence rate of 125 to 175 µmol m^{-2} s^{-1}. Total nuclear RNA was extracted from approximately 10,000 nuclei of each sample using the RNeasy Micro Kit (Qiagen). Genomic DNA was removed by DNase I treatment (Thermo Scientific). Double-strand cDNA was synthesized and linearly amplified (Clontech SMARTer Ultra Low Input RNA for Illumina Sequencing-HV kit). Low Input Library Prep Kit (Clontech) was used for preparation of sequencing libraries
PLATFORM:
ILLUMINA:
INSTRUMENT_MODEL: Illumina HiSeq 2000
SUBMISSION_lab_name: European Nucleotide Archive
DESCRIPTOR:
STUDY_TITLE: Transcriptomes and differential gene expression in the Arabidopsis shoot phloem companion cells during flowering
STUDY_TYPE:
@existing_study_type: Transcriptome Analysis
STUDY_ABSTRACT: We investigated the transcriptomes and differential gene expression at the Arabidopsis shoot phloem companion cells during flowering using INTACT reporter lines. Samples were collected in three biological replications.
STUDY_DESCRIPTION: We investigated the transcriptomes and differential gene expression at the Arabidopsis shoot phloem companion cells during flowering using INTACT reporter lines. Samples were collected in three biological replications.
Biosample_ID: SAMEA104124502

ERX2067754

IR	1.0
type	ERX
database	SRA

Info

TITLE: Illumina HiSeq 2000 paired end sequencing; Transcriptomes and differential gene expression in the Arabidopsis shoot phloem companion cells during flowering
SRA_ID: ERX2067754

STUDY_REF: ERP023520
BioProject: PRJEB21286
DESIGN:
DESIGN_DESCRIPTION: Transcriptomes and differential gene expression in the Arabidopsis shoot phloem companion cells during flowering
SAMPLE_DESCRIPTOR:
@accession: ERS1788399
IDENTIFIERS:
PRIMARY_ID: ERS1788399
EXTERNAL_ID:
@namespace: BioSample
#text: SAMEA104124506
LIBRARY_DESCRIPTOR:
LIBRARY_NAME: Sample 11_p
LIBRARY_STRATEGY: RNA-Seq
LIBRARY_SOURCE: TRANSCRIPTOMIC
LIBRARY_SELECTION: RANDOM
LIBRARY_LAYOUT:
PAIRED:
@NOMINAL_LENGTH: 300
@NOMINAL_SDEV: 30
LIBRARY_CONSTRUCTION_PROTOCOL: For each biological replicate, approximately 500 INTACT reporter plants were grown in SDs for 21 days before shifting to LDs. The 0LD, 1LD, 2LD and 3LD samples were collected on the 21st day in SDs and 1, 2, and 3 days after the shift to LD. For each sample, the whole shoot material was collected from approximately 120 seedlings and frozen immediately in Eppendorf tubes suspended in liquid nitrogen. Plants of the shoot-phloem-companion-cell-tagged INTACT reporter line (Transgenic SUC2::redNTF and UBQ10::BirA in Col-0 background) were cultivated in growth chambers, in short-day (SD) conditions (8 h light/16 h dark) for 21 days and then shifted to long-day (LD) conditions (16 h light/8 h dark) to induce flowering. The growth-chamber condition was at 23°C with 65% relative humidity, and with the light at a fluence rate of 125 to 175 $\mu mol\ m^{-2}\ s^{-1}$. Total nuclear RNA was extracted from approximately 10,000 nuclei of each sample using the RNeasy Micro Kit (Qiagen). Genomic DNA was removed by DNase I treatment (Thermo Scientific). Double-strand cDNA was synthesized and linearly amplified (Clontech SMARTer Ultra Low Input RNA for Illumina Sequencing-HV kit). Low Input Library Prep Kit (Clontech) was used for preparation of sequencing libraries
PLATFORM:
ILLUMINA:
INSTRUMENT_MODEL: Illumina HiSeq 2000
SUBMISSION_lab_name: European Nucleotide Archive
DESCRIPTOR:
STUDY_TITLE: Transcriptomes and differential gene expression in the Arabidopsis shoot phloem companion cells during flowering
STUDY_TYPE:
@existing_study_type: Transcriptome Analysis
STUDY_ABSTRACT: We investigated the transcriptomes and differential gene expression at the Arabidopsis shoot phloem companion cells during flowering using INTACT reporter lines. Samples were collected in three biological replications.
STUDY_DESCRIPTION: We investigated the transcriptomes and differential gene expression at the Arabidopsis shoot phloem companion cells during flowering using INTACT reporter lines. Samples were collected in three biological replications.
Biosample_ID: SAMEA104124506

ERX3438324

IR	0.667
type	ERX
database	SRA

Info

TITLE: Illumina HiSeq 2500 sequencing; Single-end sequencing of Arabidopsis thaliana leaf before and during heat or cold or salt stress in four mediator mutants and WT plants
SRA_ID: ERX3438324
STUDY_REF: ERP116123
BioProject: PRJEB33339
DESIGN:
DESIGN_DESCRIPTION: Standard Illumina SE rnaseq protocol.
SAMPLE_DESCRIPTOR:
@accession: ERS3558383
IDENTIFIERS:

PRIMARY_ID: ERS3558383
EXTERNAL_ID:
@namespace: BioSample
#text: SAMEA5754927
LIBRARY_DESCRIPTOR:
LIBRARY_NAME: P6960_225
LIBRARY_STRATEGY: RNA-Seq
LIBRARY_SOURCE: TRANSCRIPTOMIC
LIBRARY_SELECTION: RANDOM
LIBRARY_LAYOUT:
LIBRARY_CONSTRUCTION_PROTOCOL: Standard Illumina SE protocol
PLATFORM:
ILLUMINA:
INSTRUMENT_MODEL: Illumina HiSeq 2500
SUBMISSION_lab_name: European Nucleotide Archive
DESCRIPTOR:
STUDY_TITLE: Specific functions for Mediator complex subunits from different modules in the transcriptional response of Arabidopsis thaliana to abiotic stress
STUDY_TYPE:
@existing_study_type: Transcriptome Analysis
STUDY_ABSTRACT: Adverse environmental conditions, including heat, cold, high salinity and drought, are detrimental to plant growth and development. Acclimation to these abiotic stress conditions involves activation of signaling pathways which often results in changes in gene expression via networks of transcription factors (TFs). Mediator is a highly conserved co-regulator complex and an essential component of the transcriptional machinery in eukaryotes. Some Mediator subunits have been implicated in stress-responsive signaling pathways; however, much remains unknown regarding the role of plant Mediator in abiotic stress responses. Here, we use RNA-seq to analyze the transcriptional response of Arabidopsis thaliana to heat, cold and salt stress conditions. We identify a set of common abiotic stress regulons and describe the sequential and combinatorial nature of TFs involved in their transcriptional regulation. Furthermore, we identify stress-specific roles for the Mediator subunits MED9, MED16, MED18 and CDK8, and putative TFs connecting them to different stress signaling pathways. Our data also indicate different modes of action for subunits or modules of Mediator at the same gene loci, including a co-repressor function for MED16 prior to stress. These results illuminate a poorly understood but important player in the transcriptional response of plants to abiotic stress and identify target genes and mechanisms as a prelude to further biochemical characterization
Biosample_ID: SAMEA5754927

ERX3438328

IR	0.714
type	ERX
database	SRA

Info

TITLE: Illumina HiSeq 2500 sequencing; Single-end sequencing of Arabidopsis thaliana leaf before and during heat or cold or salt stress in four mediator mutants and WT plants
SRA_ID: ERX3438328
STUDY_REF: ERP116123
BioProject: PRJEB33339
DESIGN:
DESIGN_DESCRIPTION: Standard Illumina SE rnaseq protocol.
SAMPLE_DESCRIPTOR:
@accession: ERS3558387
IDENTIFIERS:
PRIMARY_ID: ERS3558387
EXTERNAL_ID:
@namespace: BioSample
#text: SAMEA5754931
LIBRARY_DESCRIPTOR:
LIBRARY_NAME: P6960_229
LIBRARY_STRATEGY: RNA-Seq
LIBRARY_SOURCE: TRANSCRIPTOMIC
LIBRARY_SELECTION: RANDOM
LIBRARY_LAYOUT:
LIBRARY_CONSTRUCTION_PROTOCOL: Standard Illumina SE protocol
PLATFORM:

ILLUMINA:
INSTRUMENT_MODEL: Illumina HiSeq 2500
SUBMISSION_lab_name: European Nucleotide Archive
DESCRIPTOR:
STUDY_TITLE: Specific functions for Mediator complex subunits from different modules in the transcriptional response of Arabidopsis thaliana to abiotic stress
STUDY_TYPE:
@existing_study_type: Transcriptome Analysis
STUDY_ABSTRACT: Adverse environmental conditions, including heat, cold, high salinity and drought, are detrimental to plant growth and development. Acclimation to these abiotic stress conditions involves activation of signaling pathways which often results in changes in gene expression via networks of transcription factors (TFs). Mediator is a highly conserved co-regulator complex and an essential component of the transcriptional machinery in eukaryotes. Some Mediator subunits have been implicated in stress-responsive signaling pathways; however, much remains unknown regarding the role of plant Mediator in abiotic stress responses. Here, we use RNA-seq to analyze the transcriptional response of Arabidopsis thaliana to heat, cold and salt stress conditions. We identify a set of common abiotic stress regulons and describe the sequential and combinatorial nature of TFs involved in their transcriptional regulation. Furthermore, we identify stress-specific roles for the Mediator subunits MED9, MED16, MED18 and CDK8, and putative TFs connecting them to different stress signaling pathways. Our data also indicate different modes of action for subunits or modules of Mediator at the same gene loci, including a co-repressor function for MED16 prior to stress. These results illuminate a poorly understood but important player in the transcriptional response of plants to abiotic stress and identify target genes and mechanisms as a prelude to further biochemical characterization
Biosample_ID: SAMEA5754931

ERX2067745

IR	0.778
type	ERX
database	SRA

Info

TITLE: Illumina HiSeq 2000 paired end sequencing; Transcriptomes and differential gene expression in the Arabidopsis shoot phloem companion cells during flowering
SRA_ID: ERX2067745
STUDY_REF: ERP023520
BioProject: PRJEB21286
DESIGN:
DESIGN_DESCRIPTION: Transcriptomes and differential gene expression in the Arabidopsis shoot phloem companion cells during flowering
SAMPLE_DESCRIPTOR:
@accession: ERS1788390
IDENTIFIERS:
PRIMARY_ID: ERS1788390
EXTERNAL_ID:
@namespace: BioSample
#text: SAMEA104124497
LIBRARY_DESCRIPTOR:
LIBRARY_NAME: Sample 2_p
LIBRARY_STRATEGY: RNA-Seq
LIBRARY_SOURCE: TRANSCRIPTOMIC
LIBRARY_SELECTION: RANDOM
LIBRARY_LAYOUT:
PAIRED:
@NOMINAL_LENGTH: 300
@NOMINAL_SDEV: 30
LIBRARY_CONSTRUCTION_PROTOCOL: For each biological replicate, approximately 500 INTACT reporter plants were grown in SDs for 21 days before shifting to LDs. The 0LD, 1LD, 2LD and 3LD samples were collected on the 21st day in SDs and 1, 2, and 3 days after the shift to LD. For each sample, the whole shoot material was collected from approximately 120 seedlings and frozen immediately in Eppendorf tubes suspended in liquid nitrogen. Plants of the shoot-phloem-companion-cell-tagged INTACT reporter line (Transgenic SUC2::redNTF and UBQ10::BirA in Col-0 background) were cultivated in growth chambers, in short-day (SD) conditions (8 h light/16 h dark) for 21 days and then shifted to long-day (LD) conditions (16 h light/8 h dark) to induce flowering. The growth-chamber condition was at 23°C with 65% relative humidity, and with the light at a fluence rate of 125 to 175 µmol m^{-2} s^{-1}. Total nuclear RNA was extracted from approximately 10,000 nuclei of each sample using the RNeasy Micro Kit (Qiagen). Genomic DNA was removed by DNase I treatment (Thermo Scientific). Double-strand cDNA was synthesized and linearly amplified (Clontech SMARTer Ultra Low Input RNA for Illumina Sequencing-HV kit). Low Input Library Prep Kit (Clontech) was used for preparation of sequencing libraries

PLATFORM:
ILLUMINA:
INSTRUMENT_MODEL: Illumina HiSeq 2000
SUBMISSION_lab_name: European Nucleotide Archive
DESCRIPTOR:
STUDY_TITLE: Transcriptomes and differential gene expression in the Arabidopsis shoot phloem companion cells during flowering
STUDY_TYPE:
@existing_study_type: Transcriptome Analysis
STUDY_ABSTRACT: We investigated the transcriptomes and differential gene expression at the Arabidopsis shoot phloem companion cells during flowering using INTACT reporter lines. Samples were collected in three biological replications.
STUDY_DESCRIPTION: We investigated the transcriptomes and differential gene expression at the Arabidopsis shoot phloem companion cells during flowering using INTACT reporter lines. Samples were collected in three biological replications.
Biosample_ID: SAMEA104124497

ERX1767706

IR	0.793
type	ERX
database	SRA

Info

TITLE: Illumina HiSeq 2000 paired end sequencing; Transcriptomes and differential gene expression at the Arabidopsis shoot meristem during flowering
SRA_ID: ERX1767706
STUDY_REF: ERP018177
BioProject: PRJEB16325
DESIGN:
DESIGN_DESCRIPTION: Transcriptomes and differential gene expression at the Arabidopsis shoot meristem during flowering
SAMPLE_DESCRIPTOR:
@accession: ERS1417352
IDENTIFIERS:
PRIMARY_ID: ERS1417352
EXTERNAL_ID:
@namespace: BioSample
#text: SAMEA4518173
LIBRARY_DESCRIPTOR:
LIBRARY_NAME: Sample 13_p
LIBRARY_STRATEGY: RNA-Seq
LIBRARY_SOURCE: TRANSCRIPTOMIC
LIBRARY_SELECTION: RANDOM
LIBRARY_LAYOUT:
PAIRED:
@NOMINAL_SDEV: 30
@NOMINAL_LENGTH: 300
LIBRARY_CONSTRUCTION_PROTOCOL: For each biological replicate, approximately 6,000 INTACT reporter plants were grown in SDs for 21 days before shifting to LDs. The 0LD, 1LD, 2LD and 3LD samples were collected on the 21st day in SDs and 1, 2, and 3 days after the shift to LD. For each sample, the shoot apical region was manually dissected from approximately 1,300 INTACT reporter plants and frozen immediately in Eppendorf tubes suspended in liquid nitrogen. Plants of the meristem-specific INTACT reporter line were cultivated in growth chambers, in short-day (SD) conditions (8 h light/16 h dark) for 21 days and then shifted to long-day (LD) conditions (16 h light/8 h dark) to induce flowering. The growth-chamber condition was at 23°C with 65% relative humidity, and with the light at a fluence rate of 125 to 175 µmol m^{-2} s^{-1}. Total nuclear RNA was extracted from approximately 10,000 nuclei of each sample using the RNeasy Micro Kit (Qiagen). Genomic DNA was removed by DNase I treatment (Thermo Scientific). Double-strand cDNA was synthesized and linearly amplified (Clontech SMARTer Ultra Low Input RNA for Illumina Sequencing-HV kit). Low Input Library Prep Kit (Clontech) was used for preparation of sequencing libraries
PLATFORM:
ILLUMINA:
INSTRUMENT_MODEL: Illumina HiSeq 2000
SUBMISSION_lab_name: European Nucleotide Archive
DESCRIPTOR:
STUDY_TITLE: Transcriptomes and differential gene expression at the Arabidopsis shoot meristem during flowering
STUDY_TYPE:
@existing_study_type: Transcriptome Analysis

STUDY_ABSTRACT: We investigated the transcriptomes and differential gene expression at the Arabidopsis shoot meristem during flowering using INTACT reporter lines. Samples were collected in four biological replications.
STUDY_DESCRIPTION: We investigated the transcriptomes and differential gene expression at the Arabidopsis shoot meristem during flowering using INTACT reporter lines. Samples were collected in four biological replications.
Biosample_ID: SAMEA4518173

GSM4217881

IR	0.684
type	GSM
database	GEO

Info

title:
NST3_GFP-_S48
geo_accession:
GSM4217881
status:
Public on Feb 10 2020
submission_date:
Dec 13 2019
last_update_date:
Feb 10 2020
type:
SRA
channel_count:
1
source_name_ch1:
Inflorescence stem nuclei
organism_ch1:
Arabidopsis thaliana
taxid_ch1:
3702
characteristics_ch1:
strain: Col-0
genotype: NST3pro:H4-GFP
sample type: GFP negative
growth_protocol_ch1:
Arabidopsis were grown on soil for three weeks in short days (8h light 16h dark, constant 21°C) and then transfered to long days (16h light 8h dark) to stimulate flowering.
molecule_ch1:
total RNA
extract_protocol_ch1:
2nd internode of Arabidopsis inflorescence stem were collected in a petri dish on ice. 2ml cold isolation buffer (20mM Tris (pH=7.5), 40mM NaCl, 90mM KCl, 2mM EDTA (pH=8.0), 0.5mM EGTA, 0.05% Triton X-100, 0.5mM Spermidine, 0.2mM Spermine, 15mM 2-Mercaptoethanol, 0.5mM PMSF, cOmplete Protease Inhibitor Cocktail (Roche, #11697498001)) supplemented with 10µl RiboLock RNase inhibitor (40U/µL) (ThermoFisher, #EO0381) was added to 2g of stem. Samples were chopped manually on ice for 10 min. Nuclei were collected by centrifuge (1000g, 10min, 4°C) and gently washed by cold resuspension buffer (same formula as isolation buffer but without Triton X-100) for two times. 300µl of resuspension buffer supplemented with 10µg/ml Hoechst 33342 at final concentration and 5µl RiboLock RNase inhibitor were added to the centrifuged nuclei. 15,000 nuclei were sorted into TRIzol solution as a replicate sample by BD FACSAriaTM IIIu cell sorter using a 70 µm sort nozzle according to GFP signal level, except for LTP1_GFP+_S21 which was 10,800 nuclei. RNA was extracted into 15 µl water according to manufacture's protocol.
1 µl was used for mRNA-seq library construction by Smart-seq2 protocol (Picelli et al., Nature Methods, 2013; Hofmann et al., Plant Reprod., 2019). NEBNext Ultra II gDNA prep kit with the NEBNext Multiplex Oligos for Illumina was used for library preparation
description:
nuclear RNA
data_processing:
Araport11 gene annotation file was taken (Araport11_GFF3_genes_transposons.201606.gtf).
FASTQ files were trimmed by Cutadapt (v2.3) using following options -g AAGCAGTGGTATCAACGCAGAGTACGGG -a CCCGTACTCTGCGTTGATACCACTGCTT -g AAGCAGTGGTATCAACGCAGAGTAC -a GTACTCTGCGTTGATACCACTGCTT -b "A 30" -b "T 30 " -n 2 -g AGATCGGAAGAGC -l 50 -m 23 --overlap 5. By these options, oligo sequence used in Smart-seq2 amplification, poly A or T sequence, Illumina adaptor sequence were removed from the reads.

Trimmed files were then mapped to the genome by STAR (v2.5.0a) using --outFilterMultimapNmax 1 --alignIntronMax 10000 --alignMatesGapMax 10000 --outFilterScoreMinOverLread 0.9 options.
For GFP reads, GFP sequence was indexed by STAR using --enomeSAindexNbases 4 option, and then reads were mapped using STAR with --alignIntronMax 1 --alignMatesGapMax 1 --outFilterScoreMinOverLread 0.90 options.
Further analysis was carried out in R (v3.5.0). GTF file was imported using makeTxDbFromGRanges in GenomicFeatures library (v1.32.3) with drop.stop.codons option. Position of each gene was extracted by genes function, which also includes the intron region. Reads counts per gene were obtained using summarizeOverlaps in GenomicAlignments library (v1.16.0) with mode = "Union", ignore.strand = TRUE options. Only genes of Arabidopsis was kept, and GFP reads were added in the last line in rawCounts table for selected samples. bigWig files were generated by bamCoverage in deepTools from bam files.
Genome_build: Arabidopsis Tair 10
Supplementary_files_format_and_content: Csv files include raw counts values for each Sample. bigWig files are generated from bam files for coverage tracks.
platform_id:
GPL17639
contact_name:
Thomas,,Greb
contact_email:
thomas.greb@cos.uni-heidelberg.de
contact_laboratory:
Greb
contact_department:
Centre for Organismal Studies
contact_institute:
Heidelberg University
contact_address:
Im Neuenheimer Feld 360
contact_city:
Heidelberg
contact_zip/postal_code:
69120
contact_country:
Germany
instrument_model:
Illumina HiSeq 2500
library_selection:
cDNA
library_source:
transcriptomic
library_strategy:
RNA-Seq
relation:
BioSample: https://www.ncbi.nlm.nih.gov/biosample/SAMN13561654
SRA: https://www.ncbi.nlm.nih.gov/sra?term=SRX7368459
supplementary_file_1:
ftp://ftp.ncbi.nlm.nih.gov/geo/samples/GSM4217nnn/GSM4217881/suppl/GSM4217881_NST3n-S48.bw
series_id:
GSE142032
GSE142034
data_row_count:
0

GSM4231551

IR	0.714
type	GSM
database	GEO

Info

title:
p-T3R1
geo_accession:
GSM4231551

status:
Public on Dec 24 2019
submission_date:
Dec 23 2019
last_update_date:
Dec 24 2019
type:
SRA
channel_count:
1
source_name_ch1:
seedling leaf tissue
organism_ch1:
Arabidopsis thaliana
taxid_ch1:
3702
characteristics_ch1:
time point: T3
cultivar: Col-0
tissue: leaf
sampling temperature: 45°C
treatment_protocol_ch1:
We collected samples of 11 time-points. 11 plates each containing about 80 germinated Arabidopsis seedlings were divided into the acclimated and non-acclimated group. At each sampling time-point from the experimental design (Figure 2.2 A), all leaf tissue from the designated plate was harvested and divided into two separate Eppendorf tubes, snap-frozen in liquid nitrogen and stored at -80°C. At day 12 after seed germination, T1 samples were taken right after the start of the photoperiod and before acclimation treatment starts. Plates from acclimated group were exposed to the heat acclimation treatment and samples were taken after 3 h (T2), 6 h (T3) and 7.5 h (T4), while other plates were returned to normal growth conditions and samples were collected two days (T5) and four days (T6) after at 1:30 pm. At day 16, the remaining acclimated and all the non-acclimated plants were exposed to heat shock treatment (45°C for 90 min), and samples were taken before the heat treatment (T7 for acclimated seedlings, T9 for non-acclimated seedlings), at the end of the heat shock (T8 for acclimated seedlings, T10 for non-acclimated seedlings) and two days after the application of heat stress at 1:30pm (T9 for the acclimated seedlings, T11 for non-acclimated seedlings).
growth_protocol_ch1:
Plates each containing about 80 Arabidopsis Col-0 seedlings were grown inside growth chamber (Percival) with 22°C under 16h / 8h of light / dark cycle (~100 µmol m^{-2} s^{-1}) with 60% relative humidity. The acclimation treatment was applied by subjecting plates with Arabidopsis seedlings into the growth chamber (Percival) with the temperature gradually rising from 22°C to 45°C over the course of 6 hours (starting at the beginning of the photoperiod) in the light and keep at 45°C for 90 mins. Subsequently, the plates were transferred back to a growth chamber with standard (22°C) temperature. For the heat shock application, the growth chamber (Percival) was pre-heated to 45°C with lighting (~100 µmol m^{-2} s^{-1}) and 60% relative humidity. Each plate containing 80 acclimated or non-acclimated seedlings was transferred from the control growth condition (22°C) chamber to a heated growth chamber (45°C) for 90 mins from 1:30 pm to 3:00 pm (7.5 - 9h after the beginning of the photoperiod).
molecule_ch1:
total RNA
extract_protocol_ch1:
RNA extraction was performed for each sample using RNeasy Plant Mini Kit (Qiagen)
2æ¸g of RNA for each sample was used to construct mRNA library following the protocol of Illuminaé¯¥æªš TruSeq Stranded mRNA Library Prep Kit.
description:
replicate 1
batch1
data_processing:
bcl2fastq v1.8.4 for raw data processing
Sequenced reads were trimmed for adaptor sequence, and masked for low-complexity or low-quality sequence, then mapped to TAIR genome by Tophat, and quantified in samtools htseq-count
Reads were mapped to TAIR10 genome by TopHat (v2.0.14), with Bowtie (2.1.0.0)
Transcripts were quantified using Samtools ht-seq-count
Counts per million (cpm) were calculated and normalized by the size of the library.
Genome_build: Arabidopsis TAIR10
Supplementary_files_format_and_content: Expression values of cpm (log2 transformed) for each sample.
platform_id:
GPL17639
contact_name:
Magdalena,,Julkowska
contact_email:
magdalena.julkowska@kaust.edu.sa
contact_department:
BESE

contact_institute:
King Abdullah University of Science and Technology
contact_address:
KAUST
contact_city:
Thuwal
contact_state:
Makkah
contact_zip/postal_code:
23955-6900
contact_country:
Saudi Arabia
instrument_model:
Illumina HiSeq 2500
library_selection:
cDNA
library_source:
transcriptomic
library_strategy:
RNA-Seq
relation:
BioSample: https://www.ncbi.nlm.nih.gov/biosample/SAMN13673067
SRA: https://www.ncbi.nlm.nih.gov/sra?term=SRX7434655
supplementary_file_1:
ftp://ftp.ncbi.nlm.nih.gov/geo/samples/GSM4231nnn/GSM4231551/suppl/GSM4231551_p-T3R1.sam.count.txt.gz
series_id:
GSE142537
data_row_count:
0

GSM4217865

IR	0.714
type	GSM
database	GEO

Info

title:
APL_GFP+_S14
geo_accession:
GSM4217865
status:
Public on Feb 10 2020
submission_date:
Dec 13 2019
last_update_date:
Feb 10 2020
type:
SRA
channel_count:
1
source_name_ch1:
Inflorescence stem nuclei
organism_ch1:
Arabidopsis thaliana
taxid_ch1:
3702
characteristics_ch1:
strain: Col-0
genotype: APLpro:H4-GFP
sample type: GFP positive
growth_protocol_ch1:

Arabidopsis were grown on soil for three weeks in short days (8h light 16h dark, constant 21°C) and then transfered to long days (16h light 8h dark) to stimulate flowering.
molecule_ch1:
total RNA
extract_protocol_ch1:
2nd internode of Arabidopsis inflorescence stem were collected in a petri dish on ice. 2ml cold isolation buffer (20mM Tris (pH=7.5), 40mM NaCl, 90mM KCl, 2mM EDTA (pH=8.0), 0.5mM EGTA, 0.05% Triton X-100, 0.5mM Spermidine, 0.2mM Spermine, 15mM 2-Mercaptoethanol, 0.5mM PMSF, cOmplete Protease Inhibitor Cocktail (Roche, #11697498001)) supplemented with 10µl RiboLock RNase inhibitor (40U/µL) (ThermoFisher, #EO0381) was added to 2g of stem. Samples were chopped manually on ice for 10 min. Nuclei were collected by centrifuge (1000g, 10min, 4°C) and gently washed by cold resuspension buffer (same formula as isolation buffer but without Triton X-100) for two times. 300µl of resuspension buffer supplemented with 10µg/ml Hoechst 33342 at final concentration and 5µl RiboLock RNase inhibitor were added to the centrifuged nuclei. 15,000 nuclei were sorted into TRIzol solution as a replicate sample by BD FACSAriaTM IIIu cell sorter using a 70 µm sort nozzle according to GFP signal level, except for LTP1_GFP+_S21 which was 10,800 nuclei. RNA was extracted into 15 µl water according to manufacture's protocol.
1 µl was used for mRNA-seq library construction by Smart-seq2 protocol (Picelli et al., Nature Methods, 2013; Hofmann et al., Plant Reprod., 2019). NEBNext Ultra II gDNA prep kit with the NEBNext Multiplex Oligos for Illumina was used for library preparation
description:
nuclear RNA
data_processing:
Araport11 gene annotation file was taken (Araport11_GFF3_genes_transposons.201606.gtf).
FASTQ files were trimmed by Cutadapt (v2.3) using following options -g AAGCAGTGGTATCAACGCAGAGTACGGG -a CCCGTACTCTGCGTTGATACCACTGCTT -g AAGCAGTGGTATCAACGCAGAGTAC -a GTACTCTGCGTTGATACCACTGCTT -b "A 30" -b "T 30 " -n 2 -g AGATCGGAAGAGC -l 50 -m 23 --overlap 5. By these options, oligo sequence used in Smart-seq2 amplification, poly A or T sequence, Illumina adaptor sequence were removed from the reads.
Trimmed files were then mapped to the genome by STAR (v2.5.0a) using --outFilterMultimapNmax 1 --alignIntronMax 10000 --alignMatesGapMax 10000 --outFilterScoreMinOverLread 0.9 options.
For GFP reads, GFP sequence was indexed by STAR using --enomeSAindexNbases 4 option, and then reads were mapped using STAR with --alignIntronMax 1 --alignMatesGapMax 1 --outFilterScoreMinOverLread 0.90 options.
Further analysis was carried out in R (v3.5.0). GTF file was imported using makeTxDbFromGRanges in GenomicFeatures library (v1.32.3) with drop.stop.codons option. Position of each gene was extracted by genes function, which also includes the intron region. Reads counts per gene were obtained using summarizeOverlaps in GenomicAlignments library (v1.16.0) with mode = "Union", ignore.strand = TRUE options. Only genes of Arabidopsis was kept, and GFP reads were added in the last line in rawCounts table for selected samples. bigWig files were generated by bamCoverage in deepTools from bam files.
Genome_build: Arabidopsis Tair 10
Supplementary_files_format_and_content: Csv files include raw counts values for each Sample. bigWig files are generated from bam files for coverage tracks.
platform_id:
GPL17639
contact_name:
Thomas,,Greb
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thomas.greb@cos.uni-heidelberg.de
contact_laboratory:
Greb
contact_department:
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contact_institute:
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contact_address:
Im Neuenheimer Feld 360
contact_city:
Heidelberg
contact_zip/postal_code:
69120
contact_country:
Germany
instrument_model:
Illumina HiSeq 2500
library_selection:
cDNA
library_source:
transcriptomic
library_strategy:
RNA-Seq
relation:

BioSample: https://www.ncbi.nlm.nih.gov/biosample/SAMN13561639
SRA: https://www.ncbi.nlm.nih.gov/sra?term=SRX7368443
supplementary_file_1:
ftp://ftp.ncbi.nlm.nih.gov/geo/samples/GSM4217nnn/GSM4217865/suppl/GSM4217865_APL-S14.bw
series_id:
GSE142032
GSE142034
data_row_count:
0

GSM3475790

IR	0.739
type	GSM
database	GEO

Info

title:
Col-0 TSA RNA-Seq1
geo_accession:
GSM3475790
status:
Public on Nov 11 2019
submission_date:
Nov 15 2018
last_update_date:
Nov 11 2019
type:
SRA
channel_count:
1
source_name_ch1:
whole seedling
organism_ch1:
Arabidopsis thaliana
taxid_ch1:
3702
characteristics_ch1:
developmental stage: 5 days after germination
genotype/variation: Col-0
treatment: 2h 25uM dexamethasone,1uM trichostatin
treatment_protocol_ch1:
0.015% Silwet, 25µM dexamethasone, with or without 1µM trichostatin, in 0.5xMS for 2h
growth_protocol_ch1:
23°C; 65% humidity; 16h light/8h dark; LED lights 200µE
molecule_ch1:
total RNA
extract_protocol_ch1:
RNAeasy plant mini kit according to manufacturer instructions (Qiagen, Hilden, Germany)
The RNA were poly A selected using the NEB Poly (A) Magnetic isolation module (7490), then the NEBnext Ultra Direction RNA Prep Kit (E7420) for Illumina with the NEBnext Multiplex Oligo's for Illumina (E7335). For RNA 1 µg input was used.
description:
RNA-Seq control
data_processing:
Quality control: FastQC
Raw sequence concatenation
Read alignment: HISAT2
Read counting: featureCounts
DEG calling: DESeq2
Genome_build: TAIR10
Supplementary_files_format_and_content: raw count matrix in .txt format
platform_id:

GPL13222
contact_name:
Jan,U,Lohmann
contact_email:
jan.lohmann@cos.uni-heidelberg.de
contact_department:
Stem Cell Biology
contact_institute:
Centre for Organismal Studies
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Im Neuenheimer Feld 230
contact_city:
Heidelberg
contact_zip/postal_code:
69120
contact_country:
Germany
instrument_model:
Illumina HiSeq 2000
library_selection:
cDNA
library_source:
transcriptomic
library_strategy:
RNA-Seq
relation:
BioSample: https://www.ncbi.nlm.nih.gov/biosample/SAMN10433680
SRA: https://www.ncbi.nlm.nih.gov/sra?term=SRX5015033
supplementary_file_1:
NONE
series_id:
GSE122610
GSE122611
data_row_count:
0

GSM3590024

IR	0.765
type	GSM
database	GEO

Info

title:
Chomatin RNAseq rep1
geo_accession:
GSM3590024
status:
Public on Nov 25 2019
submission_date:
Feb 04 2019
last_update_date:
Nov 25 2019
type:
SRA
channel_count:
1
source_name_ch1:
unopened flower buds
organism_ch1:
Arabidopsis thaliana
taxid_ch1:

3702
characteristics_ch1:
molecule: rRNA-depleted Chromatin RNA
growth_protocol_ch1:
Plants were grown with 16hr of light at 22 °C
molecule_ch1:
total RNA
extract_protocol_ch1:
The total RNA was extracted with trizol, and treated with Dnase I to clean up the genomic DNA contamination
All the libraries were built using directional RNA libraries preparation kit s(NEB) using different RNA input including rRNA-depleted tota RNA, rRNA-depleted chromatin RNA, mRNA
data_processing:
All sequenced reads were collapsed to non-redudant reads and mapped back to Araport 11 genome using STAR with maximum 8 mismatches.
Genome_build: Araport 11
Supplementary_files_format_and_content: Wiggle format files with normalized read densities for each nucleotide. The normalized reads were calculated as RPM(reads per million)
platform_id:
GPL23157
contact_name:
shaofang,,Li
contact_department:
Institute of Plant Protection
contact_institute:
Chinese Academy of Agricultural Sciences
contact_address:
No 2, Yuanmingyuanxilu, HAIDIAN
contact_city:
Beijing
contact_state:
Beijing
contact_zip/postal_code:
100193
contact_country:
China
instrument_model:
HiSeq X Ten
library_selection:
cDNA
library_source:
transcriptomic
library_strategy:
RNA-Seq
relation:
BioSample: https://www.ncbi.nlm.nih.gov/biosample/SAMN10869604
SRA: https://www.ncbi.nlm.nih.gov/sra?term=SRX5330800
supplementary_file_1:
ftp://ftp.ncbi.nlm.nih.gov/geo/samples/GSM3590nnn/GSM3590024/suppl/GSM3590024_chromatin_R1U.WIG.gz
series_id:
GSE126064
data_row_count:
0

GSM2834599

IR	0.765
type	GSM
database	GEO

Info

title:
sw-cbf2 24hr-cold rep2
geo_accession:

GSM2834599
status:
Public on Jul 30 2018
submission_date:
Oct 27 2017
last_update_date:
May 15 2019
type:
SRA
channel_count:
1
source_name_ch1:
aerial part
organism_ch1:
Arabidopsis thaliana
taxid_ch1:
3702
characteristics_ch1:
tissue: entire aerial part
age: 23 days after germination
genotype: Swedish ecotype
treatment_protocol_ch1:
Cold treatment was for 24 hour or 2 weeks at 4é^¦ç™^ under a 12 h photoperiod of ~35 µmol m-2 sec-1
Cold treated and control samples (all samples) were collected at ZT4
growth_protocol_ch1:
Plants were grown on soil at 22é^¦ç™^ under a 12 h photoperiod with 100-120 µmol m-2 s-1 light intensity
molecule_ch1:
total RNA
extract_protocol_ch1:
RNA was extracted using the RNeasy plant mini kit (Qiagen)
RNA libraries were prepared for sequencing using standard Illumina protocols
description:
Plants grown at 22é^¦ç™^ on soil under a photoperiod of 12 h for 23 days, sampled at ZT4
data_processing:
Illumina Real Time Analysis (RTA) v1.18.64 software used for basecalling.
Reads were mapped to the Arabidopsis reference genome (TAIR10) using Tophat version 2.1.0 in default mode with minimum and maxmum intron lengths being set to 10 and 15,000 bp, respectively. The transcript abundance (FPKM) was estimated using Cufflinks (version 2.1.1). Cuffdiff was run using default parameters with inputs of the TAIR10 genome and transcript annotations.
Genome_build: TAIR v10
Supplementary_files_format_and_content: comma-delimited text files include FPKM values for each Sample
platform_id:
GPL17639
contact_name:
Sunchung,,Park
contact_email:
Sunchung.park@usda.gov
contact_laboratory:
SPCL
contact_department:
ARS-NEA
contact_institute:
USDA -ARS
contact_address:
10300 Baltimore ave, Bldg001
contact_city:
Beltsville
contact_state:
MD
contact_zip/postal_code:
20705
contact_country:
USA
instrument_model:
Illumina HiSeq 2500
library_selection:

cDNA
library_source:
transcriptomic
library_strategy:
RNA-Seq
relation:
BioSample: https://www.ncbi.nlm.nih.gov/biosample/SAMN07842328
SRA: https://www.ncbi.nlm.nih.gov/sra?term=SRX3339024
supplementary_file_1:
NONE
series_id:
GSE106284
data_row_count:
0

GSM2932482

IR	0.818
type	GSM
database	GEO

Info

title:
rna_dark_rep2
geo_accession:
GSM2932482
status:
Public on Jul 27 2018
submission_date:
Jan 12 2018
last_update_date:
Jul 27 2018
type:
SRA
channel_count:
1
source_name_ch1:
rna_dark_rep2
organism_ch1:
Arabidopsis thaliana
taxid_ch1:
3702
characteristics_ch1:
treatment: dark condition
molecule_ch1:
total RNA
extract_protocol_ch1:
RNA extraction, preadenylated linker ligation, rRNA depeletion, reverse transcription, cDNA circularization, PCR amplification (for ribosome profiling) or TruSeq (illumina) (for mRNA-seq)
data_processing:
Basecalling with Illumina Casava 1.8 software
3' adapter trimming with FastX-toolkit
Library sorting based on sample barcode sequence with custom script
random barcode triming with custom script
rRNA and other non-coding RNA alignment with bowtie2 v2.1.0
Alignment with TopHat v2.0.9
Read quantitation using custom scripts
Genome_build: tair10
Supplementary_files_format_and_content: text files contain three columns: 1. transcript name;2. CDS region (nt) used for read counting;3. read counts
platform_id:
GPL21785

contact_name:
tomoya,,fujita
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tomoya.fujita.at.riken@gmail.com
contact_laboratory:
RNA Systems Biochemistry Laboratory
contact_department:
Cluster for Pioneering Research
contact_institute:
RIKEN
contact_address:
2-1, Hirosawa
contact_city:
Wako
contact_state:
Saitama
contact_zip/postal_code:
3510198
contact_country:
Japan
instrument_model:
Illumina HiSeq 4000
library_selection:
cDNA
library_source:
transcriptomic
library_strategy:
RNA-Seq
relation:
BioSample: https://www.ncbi.nlm.nih.gov/biosample/SAMN08358233
SRA: https://www.ncbi.nlm.nih.gov/sra?term=SRX3556787
supplementary_file_1:
ftp://ftp.ncbi.nlm.nih.gov/geo/samples/GSM2932nnn/GSM2932482/suppl/GSM2932482_RNA_dark2.k.txt.gz
series_id:
GSE109122
data_row_count:
0

GSM4217864

IR	0.871
type	GSM
database	GEO

Info

title:
APL_GFP+_S13
geo_accession:
GSM4217864
status:
Public on Feb 10 2020
submission_date:
Dec 13 2019
last_update_date:
Feb 10 2020
type:
SRA
channel_count:
1
source_name_ch1:
Inflorescence stem nuclei
organism_ch1:

Arabidopsis thaliana
taxid_ch1:
3702
characteristics_ch1:
strain: Col-0
genotype: APLpro:H4-GFP
sample type: GFP positive
growth_protocol_ch1:
Arabidopsis were grown on soil for three weeks in short days (8h light 16h dark, constant 21°C) and then transfered to long days (16h light 8h dark) to stimulate flowering.
molecule_ch1:
total RNA
extract_protocol_ch1:
2nd internode of Arabidopsis inflorescence stem were collected in a petri dish on ice. 2ml cold isolation buffer (20mM Tris (pH=7.5), 40mM NaCl, 90mM KCl, 2mM EDTA (pH=8.0), 0.5mM EGTA, 0.05% Triton X-100, 0.5mM Spermidine, 0.2mM Spermine, 15mM 2-Mercaptoethanol, 0.5mM PMSF, cOmplete Protease Inhibitor Cocktail (Roche, #11697498001)) supplemented with 10µl RiboLock RNase inhibitor (40U/µL) (ThermoFisher, #EO0381) was added to 2g of stem. Samples were chopped manually on ice for 10 min. Nuclei were collected by centrifuge (1000g, 10min, 4°C) and gently washed by cold resuspension buffer (same formula as isolation buffer but without Triton X-100) for two times. 300µl of resuspension buffer supplemented with 10µg/ml Hoechst 33342 at final concentration and 5µl RiboLock RNase inhibitor were added to the centrifuged nuclei. 15,000 nuclei were sorted into TRIzol solution as a replicate sample by BD FACSAriaTM IIIu cell sorter using a 70 µm sort nozzle according to GFP signal level, except for LTP1_GFP+_S21 which was 10,800 nuclei. RNA was extracted into 15 µl water according to manufacture's protocol.
1 µl was used for mRNA-seq library construction by Smart-seq2 protocol (Picelli et al., Nature Methods, 2013; Hofmann et al., Plant Reprod., 2019). NEBNext Ultra II gDNA prep kit with the NEBNext Multiplex Oligos for Illumina was used for library preparation
description:
nuclear RNA
data_processing:
Araport11 gene annotation file was taken (Araport11_GFF3_genes_transposons.201606.gtf).
FASTQ files were trimmed by Cutadapt (v2.3) using following options -g AAGCAGTGGTATCAACGCAGAGTACGGG -a CCCGTACTCTGCGTTGATACCACTGCTT -g AAGCAGTGGTATCAACGCAGAGTAC -a GTACTCTGCGTTGATACCACTGCTT -b "A 30" -b "T 30 " -n 2 -g AGATCGGAAGAGC -l 50 -m 23 --overlap 5. By these options, oligo sequence used in Smart-seq2 amplification, poly A or T sequence, Illumina adaptor sequence were removed from the reads.
Trimmed files were then mapped to the genome by STAR (v2.5.0a) using --outFilterMultimapNmax 1 --alignIntronMax 10000 --alignMatesGapMax 10000 --outFilterScoreMinOverLread 0.9 options.
For GFP reads, GFP sequence was indexed by STAR using --enomeSAindexNbases 4 option, and then reads were mapped using STAR with --alignIntronMax 1 --alignMatesGapMax 1 --outFilterScoreMinOverLread 0.90 options.
Further analysis was carried out in R (v3.5.0). GTF file was imported using makeTxDbFromGRanges in GenomicFeatures library (v1.32.3) with drop.stop.codons option. Position of each gene was extracted by genes function, which also includes the intron region. Reads counts per gene were obtained using summarizeOverlaps in GenomicAlignments library (v1.16.0) with mode = "Union", ignore.strand = TRUE options. Only genes of Arabidopsis was kept, and GFP reads were added in the last line in rawCounts table for selected samples. bigWig files were generated by bamCoverage in deepTools from bam files.
Genome_build: Arabidopsis Tair 10
Supplementary_files_format_and_content: Csv files include raw counts values for each Sample. bigWig files are generated from bam files for coverage tracks.
platform_id:
GPL17639
contact_name:
Thomas,,Greb
contact_email:
thomas.greb@cos.uni-heidelberg.de
contact_laboratory:
Greb
contact_department:
Centre for Organismal Studies
contact_institute:
Heidelberg University
contact_address:
Im Neuenheimer Feld 360
contact_city:
Heidelberg
contact_zip/postal_code:
69120
contact_country:
Germany
instrument_model:

Illumina HiSeq 2500
library_selection:
cDNA
library_source:
transcriptomic
library_strategy:
RNA-Seq
relation:
BioSample: https://www.ncbi.nlm.nih.gov/biosample/SAMN13561640
SRA: https://www.ncbi.nlm.nih.gov/sra?term=SRX7368442
supplementary_file_1:
ftp://ftp.ncbi.nlm.nih.gov/geo/samples/GSM4217nnn/GSM4217864/suppl/GSM4217864_APL-S13.bw
series_id:
GSE142032
GSE142034
data_row_count:
0

GSM4217863

IR	1.0
type	GSM
database	GEO

Info

title:
SMXL5_GFP+_S12
geo_accession:
GSM4217863
status:
Public on Feb 10 2020
submission_date:
Dec 13 2019
last_update_date:
Feb 10 2020
type:
SRA
channel_count:
1
source_name_ch1:
Inflorescence stem nuclei
organism_ch1:
Arabidopsis thaliana
taxid_ch1:
3702
characteristics_ch1:
strain: Col-0
genotype: SMXL5pro:H4-GFP
sample type: GFP positive
growth_protocol_ch1:
Arabidopsis were grown on soil for three weeks in short days (8h light 16h dark, constant 21°C) and then transfered to long days (16h light 8h dark) to stimulate flowering.
molecule_ch1:
total RNA
extract_protocol_ch1:
2nd internode of Arabidopsis inflorescence stem were collected in a petri dish on ice. 2ml cold isolation buffer (20mM Tris (pH=7.5), 40mM NaCl, 90mM KCl, 2mM EDTA (pH=8.0), 0.5mM EGTA, 0.05% Triton X-100, 0.5mM Spermidine, 0.2mM Spermine, 15mM 2-Mercaptoethanol, 0.5mM PMSF, cOmplete Protease Inhibitor Cocktail (Roche, #11697498001)) supplemented with 10µl RiboLock RNase inhibitor (40U/µL) (ThermoFisher, #EO0381) was added to 2g of stem. Samples were chopped manually on ice for 10 min. Nuclei were collected by centrifuge (1000g, 10min, 4°C) and gently washed by cold resuspension buffer (same formula as isolation buffer but without Triton X-100) for two times. 300µl of resuspension buffer supplemented with 10µg/ml Hoechst 33342 at final concentration and 5µl RiboLock RNase inhibitor were added to the centrifuged nuclei. 15,000 nuclei were sorted into TRIzol solution as a replicate sample by BD FACSAriaTM IIIu cell sorter using a

70 µm sort nozzle according to GFP signal level, except for LTP1_GFP+_S21 which was 10,800 nuclei. RNA was extracted into 15 µl water according to manufacture's protocol.
1 µl was used for mRNA-seq library construction by Smart-seq2 protocol (Picelli et al., Nature Methods, 2013; Hofmann et al., Plant Reprod., 2019). NEBNext Ultra II gDNA prep kit with the NEBNext Multiplex Oligos for Illumina was used for library preparation
description:
nuclear RNA
data_processing:
Araport11 gene annotation file was taken (Araport11_GFF3_genes_transposons.201606.gtf).
FASTQ files were trimmed by Cutadapt (v2.3) using following options -g AAGCAGTGGTATCAACGCAGAGTACGGG -a CCCGTACTCTGCGTTGATACCACTGCTT -g AAGCAGTGGTATCAACGCAGAGTAC -a GTACTCTGCGTTGATACCACTGCTT -b "A 30" -b "T 30 " -n 2 -g AGATCGGAAGAGC -l 50 -m 23 --overlap 5. By these options, oligo sequence used in Smart-seq2 amplification, poly A or T sequence, Illumina adaptor sequence were removed from the reads.
Trimmed files were then mapped to the genome by STAR (v2.5.0a) using --outFilterMultimapNmax 1 --alignIntronMax 10000 --alignMatesGapMax 10000 --outFilterScoreMinOverLread 0.9 options.
For GFP reads, GFP sequence was indexed by STAR using --enomeSAindexNbases 4 option, and then reads were mapped using STAR with --alignIntronMax 1 --alignMatesGapMax 1 --outFilterScoreMinOverLread 0.90 options.
Further analysis was carried out in R (v3.5.0). GTF file was imported using makeTxDbFromGRanges in GenomicFeatures library (v1.32.3) with drop.stop.codons option. Position of each gene was extracted by genes function, which also includes the intron region. Reads counts per gene were obtained using summarizeOverlaps in GenomicAlignments library (v1.16.0) with mode = "Union", ignore.strand = TRUE options. Only genes of Arabidopsis was kept, and GFP reads were added in the last line in rawCounts table for selected samples. bigWig files were generated by bamCoverage in deepTools from bam files.
Genome_build: Arabidopsis Tair 10
Supplementary_files_format_and_content: Csv files include raw counts values for each Sample. bigWig files are generated from bam files for coverage tracks.
platform_id:
GPL17639
contact_name:
Thomas,,Greb
contact_email:
thomas.greb@cos.uni-heidelberg.de
contact_laboratory:
Greb
contact_department:
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Heidelberg University
contact_address:
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contact_city:
Heidelberg
contact_zip/postal_code:
69120
contact_country:
Germany
instrument_model:
Illumina HiSeq 2500
library_selection:
cDNA
library_source:
transcriptomic
library_strategy:
RNA-Seq
relation:
BioSample: https://www.ncbi.nlm.nih.gov/biosample/SAMN13561641
SRA: https://www.ncbi.nlm.nih.gov/sra?term=SRX7368441
supplementary_file_1:
ftp://ftp.ncbi.nlm.nih.gov/geo/samples/GSM4217nnn/GSM4217863/suppl/GSM4217863_SMXL5-S12.bw
series_id:
GSE142032
GSE142034
data_row_count:
0

GSM4217871

IR	1.0
type	GSM
database	GEO

Info

title:
PXY_GFP+_S8
geo_accession:
GSM4217871
status:
Public on Feb 10 2020
submission_date:
Dec 13 2019
last_update_date:
Feb 10 2020
type:
SRA
channel_count:
1
source_name_ch1:
Inflorescence stem nuclei
organism_ch1:
Arabidopsis thaliana
taxid_ch1:
3702
characteristics_ch1:
strain: Col-0
genotype: PXYpro:H4-GFP
sample type: GFP positive
growth_protocol_ch1:
Arabidopsis were grown on soil for three weeks in short days (8h light 16h dark, constant 21°C) and then transfered to long days (16h light 8h dark) to stimulate flowering.
molecule_ch1:
total RNA
extract_protocol_ch1:
2nd internode of Arabidopsis inflorescence stem were collected in a petri dish on ice. 2ml cold isolation buffer (20mM Tris (pH=7.5), 40mM NaCl, 90mM KCl, 2mM EDTA (pH=8.0), 0.5mM EGTA, 0.05% Triton X-100, 0.5mM Spermidine, 0.2mM Spermine, 15mM 2-Mercaptoethanol, 0.5mM PMSF, cOmplete Protease Inhibitor Cocktail (Roche, #11697498001)) supplemented with 10µl RiboLock RNase inhibitor (40U/µL) (ThermoFisher, #EO0381) was added to 2g of stem. Samples were chopped manually on ice for 10 min. Nuclei were collected by centrifuge (1000g, 10min, 4°C) and gently washed by cold resuspension buffer (same formula as isolation buffer but without Triton X-100) for two times. 300µl of resuspension buffer supplemented with 10µg/ml Hoechst 33342 at final concentration and 5µl RiboLock RNase inhibitor were added to the centrifuged nuclei. 15,000 nuclei were sorted into TRIzol solution as a replicate sample by BD FACSAriaTM IIIu cell sorter using a 70 µm sort nozzle according to GFP signal level, except for LTP1_GFP+_S21 which was 10,800 nuclei. RNA was extracted into 15 µl water according to manufacture's protocol.
1 µl was used for mRNA-seq library construction by Smart-seq2 protocol (Picelli et al., Nature Methods, 2013; Hofmann et al., Plant Reprod., 2019). NEBNext Ultra II gDNA prep kit with the NEBNext Multiplex Oligos for Illumina was used for library preparation
description:
nuclear RNA
data_processing:
Araport11 gene annotation file was taken (Araport11_GFF3_genes_transposons.201606.gtf).
FASTQ files were trimmed by Cutadapt (v2.3) using following options -g AAGCAGTGGTATCAACGCAGAGTACGGG -a CCCGTACTCTGCGTTGATACCACTGCTT -g AAGCAGTGGTATCAACGCAGAGTAC -a GTACTCTGCGTTGATACCACTGCTT -b "A 30" -b "T 30 " -n 2 -g AGATCGGAAGAGC -l 50 -m 23 --overlap 5. By these options, oligo sequence used in Smart-seq2 amplification, poly A or T sequence, Illumina adaptor sequence were removed from the reads.
Trimmed files were then mapped to the genome by STAR (v2.5.0a) using --outFilterMultimapNmax 1 --alignIntronMax 10000 --alignMatesGapMax 10000 --outFilterScoreMinOverLread 0.9 options.
For GFP reads, GFP sequence was indexed by STAR using --enomeSAindexNbases 4 option, and then reads were mapped using STAR with --alignIntronMax 1 --alignMatesGapMax 1 --outFilterScoreMinOverLread 0.90 options.
Further analysis was carried out in R (v3.5.0). GTF file was imported using makeTxDbFromGRanges in GenomicFeatures library (v1.32.3) with drop.stop.codons option. Position of each gene was extracted by genes function, which also includes the intron region. Reads counts per gene were obtained using summarizeOverlaps in GenomicAlignments library (v1.16.0) with mode = "Union", ignore.strand = TRUE options. Only genes

of Arabidopsis was kept, and GFP reads were added in the last line in rawCounts table for selected samples. bigWig files were generated by bamCoverage in deepTools from bam files.
Genome_build: Arabidopsis Tair 10
Supplementary_files_format_and_content: Csv files include raw counts values for each Sample. bigWig files are generated from bam files for coverage tracks.
platform_id:
GPL17639
contact_name:
Thomas,,Greb
contact_email:
thomas.greb@cos.uni-heidelberg.de
contact_laboratory:
Greb
contact_department:
Centre for Organismal Studies
contact_institute:
Heidelberg University
contact_address:
Im Neuenheimer Feld 360
contact_city:
Heidelberg
contact_zip/postal_code:
69120
contact_country:
Germany
instrument_model:
Illumina HiSeq 2500
library_selection:
cDNA
library_source:
transcriptomic
library_strategy:
RNA-Seq
relation:
BioSample: https://www.ncbi.nlm.nih.gov/biosample/SAMN13561672
SRA: https://www.ncbi.nlm.nih.gov/sra?term=SRX7368449
supplementary_file_1:
ftp://ftp.ncbi.nlm.nih.gov/geo/samples/GSM4217nnn/GSM4217871/suppl/GSM4217871_PXY-S8.bw
series_id:
GSE142032
GSE142034
data_row_count:
0

GSM4217866

IR	0.833
type	GSM
database	GEO

Info

title:
APL_GFP+_S15
geo_accession:
GSM4217866
status:
Public on Feb 10 2020
submission_date:
Dec 13 2019
last_update_date:
Feb 10 2020
type:

SRA
channel_count:
1
source_name_ch1:
Inflorescence stem nuclei
organism_ch1:
Arabidopsis thaliana
taxid_ch1:
3702
characteristics_ch1:
strain: Col-0
genotype: APLpro:H4-GFP
sample type: GFP positive
growth_protocol_ch1:
Arabidopsis were grown on soil for three weeks in short days (8h light 16h dark, constant 21°C) and then transfered to long days (16h light 8h dark) to stimulate flowering.
molecule_ch1:
total RNA
extract_protocol_ch1:
2nd internode of Arabidopsis inflorescence stem were collected in a petri dish on ice. 2ml cold isolation buffer (20mM Tris (pH=7.5), 40mM NaCl, 90mM KCl, 2mM EDTA (pH=8.0), 0.5mM EGTA, 0.05% Triton X-100, 0.5mM Spermidine, 0.2mM Spermine, 15mM 2-Mercaptoethanol, 0.5mM PMSF, cOmplete Protease Inhibitor Cocktail (Roche, #11697498001)) supplemented with 10µl RiboLock RNase inhibitor (40U/µL) (ThermoFisher, #EO0381) was added to 2g of stem. Samples were chopped manually on ice for 10 min. Nuclei were collected by centrifuge (1000g, 10min, 4°C) and gently washed by cold resuspension buffer (same formula as isolation buffer but without Triton X-100) for two times. 300µl of resuspension buffer supplemented with 10µg/ml Hoechst 33342 at final concentration and 5µl RiboLock RNase inhibitor were added to the centrifuged nuclei. 15,000 nuclei were sorted into TRIzol solution as a replicate sample by BD FACSAriaTM IIIu cell sorter using a 70 µm sort nozzle according to GFP signal level, except for LTP1_GFP+_S21 which was 10,800 nuclei. RNA was extracted into 15 µl water according to manufacture's protocol.
1 µl was used for mRNA-seq library construction by Smart-seq2 protocol (Picelli et al., Nature Methods, 2013; Hofmann et al., Plant Reprod., 2019). NEBNext Ultra II gDNA prep kit with the NEBNext Multiplex Oligos for Illumina was used for library preparation
description:
nuclear RNA
data_processing:
Araport11 gene annotation file was taken (Araport11_GFF3_genes_transposons.201606.gtf).
FASTQ files were trimmed by Cutadapt (v2.3) using following options -g AAGCAGTGGTATCAACGCAGAGTACGGG -a CCCGTACTCTGCGTTGATACCACTGCTT -g AAGCAGTGGTATCAACGCAGAGTAC -a GTACTCTGCGTTGATACCACTGCTT -b "A 30" -b "T 30 " -n 2 -g AGATCGGAAGAGC -l 50 -m 23 --overlap 5. By these options, oligo sequence used in Smart-seq2 amplification, poly A or T sequence, Illumina adaptor sequence were removed from the reads.
Trimmed files were then mapped to the genome by STAR (v2.5.0a) using --outFilterMultimapNmax 1 --alignIntronMax 10000 --alignMatesGapMax 10000 --outFilterScoreMinOverLread 0.9 options.
For GFP reads, GFP sequence was indexed by STAR using --enomeSAindexNbases 4 option, and then reads were mapped using STAR with --alignIntronMax 1 --alignMatesGapMax 1 --outFilterScoreMinOverLread 0.90 options.
Further analysis was carried out in R (v3.5.0). GTF file was imported using makeTxDbFromGRanges in GenomicFeatures library (v1.32.3) with drop.stop.codons option. Position of each gene was extracted by genes function, which also includes the intron region. Reads counts per gene were obtained using summarizeOverlaps in GenomicAlignments library (v1.16.0) with mode = "Union", ignore.strand = TRUE options. Only genes of Arabidopsis was kept, and GFP reads were added in the last line in rawCounts table for selected samples. bigWig files were generated by bamCoverage in deepTools from bam files.
Genome_build: Arabidopsis Tair 10
Supplementary_files_format_and_content: Csv files include raw counts values for each Sample. bigWig files are generated from bam files for coverage tracks.
platform_id:
GPL17639
contact_name:
Thomas,,Greb
contact_email:
thomas.greb@cos.uni-heidelberg.de
contact_laboratory:
Greb
contact_department:
Centre for Organismal Studies
contact_institute:
Heidelberg University
contact_address:
Im Neuenheimer Feld 360
contact_city:

Heidelberg
contact_zip/postal_code:
69120
contact_country:
Germany
instrument_model:
Illumina HiSeq 2500
library_selection:
cDNA
library_source:
transcriptomic
library_strategy:
RNA-Seq
relation:
BioSample: https://www.ncbi.nlm.nih.gov/biosample/SAMN13561638
SRA: https://www.ncbi.nlm.nih.gov/sra?term=SRX7368444
supplementary_file_1:
ftp://ftp.ncbi.nlm.nih.gov/geo/samples/GSM4217nnn/GSM4217866/suppl/GSM4217866_APL-S15.bw
series_id:
GSE142032
GSE142034
data_row_count:
0

GSM2932483

IR	0.833
type	GSM
database	GEO

Info

title:
rna_blue_rep1
geo_accession:
GSM2932483
status:
Public on Jul 27 2018
submission_date:
Jan 12 2018
last_update_date:
Jul 27 2018
type:
SRA
channel_count:
1
source_name_ch1:
rna_blue_rep1
organism_ch1:
Arabidopsis thaliana
taxid_ch1:
3702
characteristics_ch1:
treatment: blue light condition
molecule_ch1:
total RNA
extract_protocol_ch1:
RNA extraction, preadenylated linker ligation, rRNA depeletion, reverse transcription, cDNA circularization, PCR amplification (for ribosome profiling) or TruSeq (illumina) (for mRNA-seq)
data_processing:
Basecalling with Illumina Casava 1.8 software
3' adapter trimming with FastX-toolkit
Library sorting based on sample barcode sequence with custom script

random barcode triming with custom script
rRNA and other non-coding RNA alignment with bowtie2 v2.1.0
Alignment with TopHat v2.0.9
Read quantitation using custom scripts
Genome_build: tair10
Supplementary_files_format_and_content: text files contain three columns: 1. transcript name;2. CDS region (nt) used for read counting;3. read counts
platform_id:
GPL21785
contact_name:
tomoya,,fujita
contact_email:
tomoya.fujita.at.riken@gmail.com
contact_laboratory:
RNA Systems Biochemistry Laboratory
contact_department:
Cluster for Pioneering Research
contact_institute:
RIKEN
contact_address:
2-1, Hirosawa
contact_city:
Wako
contact_state:
Saitama
contact_zip/postal_code:
3510198
contact_country:
Japan
instrument_model:
Illumina HiSeq 4000
library_selection:
cDNA
library_source:
transcriptomic
library_strategy:
RNA-Seq
relation:
BioSample: https://www.ncbi.nlm.nih.gov/biosample/SAMN08358232
SRA: https://www.ncbi.nlm.nih.gov/sra?term=SRX3556788
supplementary_file_1:
ftp://ftp.ncbi.nlm.nih.gov/geo/samples/GSM2932nnn/GSM2932483/suppl/GSM2932483_RNA_blue1.k.txt.gz
series_id:
GSE109122
data_row_count:
0

GSM3900880

IR	0.837
type	GSM
database	GEO

Info

title:
s02_WT_plaNETseq_biorep2
geo_accession:
GSM3900880
status:
Public on Feb 14 2020
submission_date:
Jun 21 2019

last_update_date:
Feb 14 2020
type:
SRA
channel_count:
1
source_name_ch1:
Whole seedlings
organism_ch1:
Arabidopsis thaliana
taxid_ch1:
3702
characteristics_ch1:
tissue: Whole seedlings
ecotype: Columbia (Col-0)
genotype: Wild type
age: 10 day
growth_protocol_ch1:
Arabidopsis seedlings were grown on plates (1/2 Murashige and Skoog medium, 1% sucrose) with a 16h light/8h dark cycle at 22°C/18°C. Light intensity during day hours was approximately 100 µE m-2 s-1.
molecule_ch1:
total RNA
extract_protocol_ch1:
PlaNET-Seq: Nuclei were isolated from 3 grams of seedlings. Chromatin was solubilized by DNase I treatment. Nascent RNA fraction was enriched by immunoprecipitation of FLAG-tagged RNAPII elongation complexes using anti-FLAG antibody (F3165, Sigma-Aldrich) coupled to Dynabeads Protein G. Finally, RNAPII complexes were eluted from Dynabeads by 3xFLAG peptide, and the nascent RNA was purified using miRNeasy kit (QIAgen). RNA-Seq: total RNA was isolated from seedlings using QIAgen Plant RNeasy kit.
PlaNET-Seq: NGS libraries were constructed from nascent RNA using Small RNA-Seq Kit v3 (Bioo Scientific). The original protocol was modified to incorporate alkaline RNA fragmentation step after 3' adapter ligation. RNA-Seq: polyA-enriched libraries were constructed using Illumina TruSeq RNA Sample Prep Kit v2.
description:
library strategy: PlaNET-Seq
Nascent RNA
PlaNET-Seq of wild type seedlings (replicate 2)
data_processing:
Illumina Casava v1.7 software was used for basecalling.
PlaNET-Seq: 1) Trim 4bp UMI barcodes from 5' ends of both R1 and R2 reads (UMI-Tools extract v0.5.3); 2) Align R2 reads to TAIR10 (STAR v2.5.2b; --outSAMmultNmax 1 --alignEndsType Extend5pOfRead1 --clip3pAdapterSeq GATCGTCGGACT); 3) Sort BAM files (Samtools v1.3.1); 4) Remove PCR duplicates (UMI-Tools dedup); 5) Remove reads aligned to rRNA, tRNA, snRNA or snoRNA loci from Araport11 (BEDTools v2.17.0); 6) Remove reads with MAPQ < 10 (Samtools v1.3.1); 7) Import BAM files into R environment v3.5.1 (GenomicAlignments_1.18.1, GenomicRanges_1.34.0); 8) Flip the strand orientation; 9) Skip all split reads; 10) Skip reads with 3' end overlapping known splice sites (combined from TxDb.Athaliana.BioMart.plantsmart28_3.2.2 and Araport11); 11) Convert reads to genomic coverage (separately for + and - strands); 12) Export as BigWig files (rtracklayer_1.42.2). RNA-Seq: 1) Trim adapters using Trim Galore v0.4.3 (--paired --illumina); 2) Align to TAIR10 using STAR v2.5.2b (--outSAMmultNmax 1 --alignEndsType Local --outSAMtype BAM Unsorted); 3) Sort BAM files and remove reads with MAPQ < 10 using Samtools v1.3.1; 4) Convert BAM files to Bedgraph using BEDtools genomecov v2.26.0 (-bg -split); 5) Convert Bedgraph files to BigWig using kentUtils bedGraphToBigWig v4.
Genome_build: TAIR10
Supplementary_files_format_and_content: BigWig files show sequencing coverage with single base resolution (no signal smoothing, transformation or normalization were applied). PlaNET-Seq BigWigs are strand-specific, RNA-Seq BigWigs are unstranded.
platform_id:
GPL21785
contact_name:
Maxim,,Ivanov
contact_email:
maxim.ivanov@plen.ku.dk
contact_department:
Dept. of Plant and Environmental Sciences
contact_institute:
University of Copenhagen
contact_address:
Thorvaldsensvej 40
contact_city:
Frederiksberg C
contact_zip/postal_code:
1871

contact_country:
Denmark
instrument_model:
Illumina HiSeq 4000
library_selection:
cDNA
library_source:
transcriptomic
library_strategy:
RNA-Seq
relation:
BioSample: https://www.ncbi.nlm.nih.gov/biosample/SAMN12107341
SRA: https://www.ncbi.nlm.nih.gov/sra?term=SRX6102430
supplementary_file_1:
ftp://ftp.ncbi.nlm.nih.gov/geo/samples/GSM3900nnn/GSM3900880/suppl/GSM3900880_s02_WT_plaNETseq_biorep2_Minus.bw
supplementary_file_2:
ftp://ftp.ncbi.nlm.nih.gov/geo/samples/GSM3900nnn/GSM3900880/suppl/GSM3900880_s02_WT_plaNETseq_biorep2_Plus.bw
series_id:
GSE133143
data_row_count:
0

GSM3900881

IR	0.915
type	GSM
database	GEO

Info

title:
s03_nrpb2-Y732F_plaNETseq_biorep1
geo_accession:
GSM3900881
status:
Public on Feb 14 2020
submission_date:
Jun 21 2019
last_update_date:
Feb 14 2020
type:
SRA
channel_count:
1
source_name_ch1:
Whole seedlings
organism_ch1:
Arabidopsis thaliana
taxid_ch1:
3702
characteristics_ch1:
tissue: Whole seedlings
ecotype: Columbia (Col-0)
genotype: nrpb2-Y732F
age: 10 day
growth_protocol_ch1:
Arabidopsis seedlings were grown on plates (1/2 Murashige and Skoog medium, 1% sucrose) with a 16h light/8h dark cycle at 22°C/18°C. Light intensity during day hours was approximately 100 µE m-2 s-1.
molecule_ch1:
total RNA
extract_protocol_ch1:
PlaNET-Seq: Nuclei were isolated from 3 grams of seedlings. Chromatin was solubilized by DNase I treatment. Nascent RNA fraction was enriched by immunoprecipitation of FLAG-tagged RNAPII elongation complexes using anti-FLAG antibody (F3165, Sigma-Aldrich) coupled to

Dynabeads Protein G. Finally, RNAPII complexes were eluted from Dynabeads by 3xFLAG peptide, and the nascent RNA was purified using miRNeasy kit (QIAgen). RNA-Seq: total RNA was isolated from seedlings using QIAgen Plant RNeasy kit.
PlaNET-Seq: NGS libraries were constructed from nascent RNA using Small RNA-Seq Kit v3 (Bioo Scientific). The original protocol was modified to incorporate alkaline RNA fragmentation step after 3' adapter ligation. RNA-Seq: polyA-enriched libraries were constructed using Illumina TruSeq RNA Sample Prep Kit v2.
description:
library strategy: PlaNET-Seq
Nascent RNA
PlaNET-Seq of mutant seedlings with accelerated transcription speed (replicate 1)
data_processing:
Illumina Casava v1.7 software was used for basecalling.
PlaNET-Seq: 1) Trim 4bp UMI barcodes from 5' ends of both R1 and R2 reads (UMI-Tools extract v0.5.3); 2) Align R2 reads to TAIR10 (STAR v2.5.2b; --outSAMmultNmax 1 --alignEndsType Extend5pOfRead1 --clip3pAdapterSeq GATCGTCGGACT); 3) Sort BAM files (Samtools v1.3.1); 4) Remove PCR duplicates (UMI-Tools dedup); 5) Remove reads aligned to rRNA, tRNA, snRNA or snoRNA loci from Araport11 (BEDTools v2.17.0); 6) Remove reads with MAPQ < 10 (Samtools v1.3.1); 7) Import BAM files into R environment v3.5.1 (GenomicAlignments_1.18.1, GenomicRanges_1.34.0); 8) Flip the strand orientation; 9) Skip all split reads; 10) Skip reads with 3' end overlapping known splice sites (combined from TxDb.Athaliana.BioMart.plantsmart28_3.2.2 and Araport11); 11) Convert reads to genomic coverage (separately for + and - strands); 12) Export as BigWig files (rtracklayer_1.42.2). RNA-Seq: 1) Trim adapters using Trim Galore v0.4.3 (--paired --illumina); 2) Align to TAIR10 using STAR v2.5.2b (--outSAMmultNmax 1 --alignEndsType Local --outSAMtype BAM Unsorted); 3) Sort BAM files and remove reads with MAPQ < 10 using Samtools v1.3.1; 4) Convert BAM files to Bedgraph using BEDtools genomecov v2.26.0 (-bg -split); 5) Convert Bedgraph files to BigWig using kentUtils bedGraphToBigWig v4.
Genome_build: TAIR10
Supplementary_files_format_and_content: BigWig files show sequencing coverage with single base resolution (no signal smoothing, transformation or normalization were applied). PlaNET-Seq BigWigs are strand-specific, RNA-Seq BigWigs are unstranded.
platform_id:
GPL21785
contact_name:
Maxim,,Ivanov
contact_email:
maxim.ivanov@plen.ku.dk
contact_department:
Dept. of Plant and Environmental Sciences
contact_institute:
University of Copenhagen
contact_address:
Thorvaldsensvej 40
contact_city:
Frederiksberg C
contact_zip/postal_code:
1871
contact_country:
Denmark
instrument_model:
Illumina HiSeq 4000
library_selection:
cDNA
library_source:
transcriptomic
library_strategy:
RNA-Seq
relation:
BioSample: https://www.ncbi.nlm.nih.gov/biosample/SAMN12107340
SRA: https://www.ncbi.nlm.nih.gov/sra?term=SRX6102431
supplementary_file_1:
ftp://ftp.ncbi.nlm.nih.gov/geo/samples/GSM3900nnn/GSM3900881/suppl/GSM3900881_s03_nrpb2-Y732F_plaNETseq_biorep1_Minus.bw
supplementary_file_2:
ftp://ftp.ncbi.nlm.nih.gov/geo/samples/GSM3900nnn/GSM3900881/suppl/GSM3900881_s03_nrpb2-Y732F_plaNETseq_biorep1_Plus.bw
series_id:
GSE133143
data_row_count:
0

GSM3387232

IR	0.929
type	GSM
database	GEO

Info

title:
at-endosperm-RNAseq_replicate1_Landsberg_wt_x_Columbia_wt
geo_accession:
GSM3387232
status:
Public on Feb 07 2019
submission_date:
Sep 13 2018
last_update_date:
Feb 07 2019
type:
SRA
channel_count:
1
source_name_ch1:
AT F1-Endosperm Landsberg x Columbia
organism_ch1:
Arabidopsis thaliana
taxid_ch1:
3702
characteristics_ch1:
tissue: endosperm
genotype: Ler x Col
treatment_protocol_ch1:
Material was generated by manually crossing of pistillata (Ler) mutants with pollen of INT line (Col) and the INT line in dde2 background pollinated with Ler.
growth_protocol_ch1:
All seeds were surface sterilized (70%, 30% ethanol 10min), stratified for 2 days at 4°C and germinated on half-strength Murashige and Skoog medium (1% sucrose) in long-day conditions (16 h light/8 h darkness; 21°C). Plants were transferred to soil after 10 to 12 days and grown under long day conditions.
molecule_ch1:
total RNA
extract_protocol_ch1:
For RNA sequencing, endosperm nuclei from seeds derived from indicated crosses were isolated using the INTACT protocol using replicates as indicated. RNA was extracted following a mirVana kit (Ambion). mRNA extraction was performed using NEBNext Poly(A) mRNA Magnetic Isolation kit.
Samples were sequenced at the National Genomic Infrastructure (NGI) from SciLife Laboratory (Uppsala, Sweden) on an Illumina HiSeq2500 in paired-end 125bp read length.
description:
Arabidopsis thaliana F1-endosperm of Landsberg-0 (female) crossed with Columbia-0 (male)
ler_x_col_rep1
data_processing:
Reads were trimmed by removing the 15 bp from the 5é¯¥ end and mapped in a single-end mode to the Arabidopsis (TAIR10) genome previously masked for rRNA genes and for the SNP positions between the TAIR10(Col) and the Landsberg (Ler) genome, using using TopHat v2.1. (Trapnell et al, 2009) (parameters adjusted as -g 1 -a 10 -i 40 -I 5000 -F 0 -r 130).
Genome_build: TAIR10
Supplementary_files_format_and_content: RNA-seq: expression levels (RPKM) are shown for genes in TAIR10 for each condition and replicate.
platform_id:
GPL17639
contact_name:
Juan,C,Santos-Gonzè°©lez
contact_email:
juan.santos@slu.se
contact_laboratory:
Kæžhler's lab
contact_department:
Department of Plant Biology and Forest Genetics
contact_institute:

SLU
contact_address:
Almas AllèŒ… 5
contact_city:
Uppsala
contact_state:
Uppsala
contact_zip/postal_code:
75007
contact_country:
Sweden
instrument_model:
Illumina HiSeq 2500
library_selection:
cDNA
library_source:
transcriptomic
library_strategy:
RNA-Seq
relation:
BioSample: https://www.ncbi.nlm.nih.gov/biosample/SAMN10055949
SRA: https://www.ncbi.nlm.nih.gov/sra?term=SRX4676986
supplementary_file_1:
NONE
series_id:
GSE119915
data_row_count:
0

SRX1066974

IR	0.667
type	SRX
database	SRA

Info

TITLE: Genome-wide RNA immuno-precipitation of SR45-Associated transcripts
SRA_ID: SRX1066974
STUDY_REF: SRP041864
BioProject: PRJNA246656
DESIGN:
SAMPLE_DESCRIPTOR:
@accession: SRS605129
IDENTIFIERS:
PRIMARY_ID: SRS605129
LIBRARY_DESCRIPTOR:
LIBRARY_STRATEGY: RNA-Seq
LIBRARY_SOURCE: OTHER
LIBRARY_SELECTION: other
LIBRARY_LAYOUT:
PLATFORM:
ILLUMINA:
INSTRUMENT_MODEL: NextSeq 500
SUBMISSION_lab_name: Reddy lab
DESCRIPTOR:
STUDY_TITLE: Arabidopsis thaliana strain:Col Transcriptome or Gene expression
STUDY_TYPE:
@existing_study_type: Transcriptome Analysis
STUDY_ABSTRACT: This study aims to identify in planta transcripts physically associated with alternative splicing regulator SR45
CENTER_PROJECT_NAME: Arabidopsis thaliana strain:Col
Biosample_ID: SAMN02769469

SRX1066971

IR	1.0
type	SRX
database	SRA

Info

TITLE: Genome-wide RNA immune-precipitation of SR45 Associated Trancripts
SRA_ID: SRX1066971
STUDY_REF: SRP041864
BioProject: PRJNA246656
DESIGN:
SAMPLE_DESCRIPTOR:
@accession: SRS605129
IDENTIFIERS:
PRIMARY_ID: SRS605129
LIBRARY_DESCRIPTOR:
LIBRARY_STRATEGY: RNA-Seq
LIBRARY_SOURCE: OTHER
LIBRARY_SELECTION: other
LIBRARY_LAYOUT:
PLATFORM:
ILLUMINA:
INSTRUMENT_MODEL: NextSeq 500
SUBMISSION_lab_name: Reddy lab
DESCRIPTOR:
STUDY_TITLE: Arabidopsis thaliana strain:Col Transcriptome or Gene expression
STUDY_TYPE:
@existing_study_type: Transcriptome Analysis
STUDY_ABSTRACT: This study aims to identify in planta transcripts physically associated with alternative splicing regulator SR45
CENTER_PROJECT_NAME: Arabidopsis thaliana strain:Col
Biosample_ID: SAMN02769469

SRX5187327

IR	1.0
type	SRX
database	SRA

Info

TITLE: RNA-seq of Arabidopsis thaliana: apical part of 14 days old plants with 49 (h) after low R/FR treatment
SRA_ID: SRX5187327
STUDY_REF: SRP174647
BioProject: PRJNA512107
DESIGN:
DESIGN_DESCRIPTION: Full Transcript RNA sequencing with YourSeq Dual Kit (Amaryllis Nucleics, CA)
SAMPLE_DESCRIPTOR:
@accession: SRS4193716
IDENTIFIERS:
PRIMARY_ID: SRS4193716
LIBRARY_DESCRIPTOR:
LIBRARY_NAME: myc234_49h_L_R3
LIBRARY_STRATEGY: RNA-Seq
LIBRARY_SOURCE: TRANSCRIPTOMIC
LIBRARY_SELECTION: cDNA
LIBRARY_LAYOUT:
PLATFORM:
ILLUMINA:
INSTRUMENT_MODEL: Illumina HiSeq 4000

SUBMISSION_lab_name: Plant Biology
DESCRIPTOR:
STUDY_TITLE: Shade responsive genes in Col, myc234, npr1, and sid2/eds16
STUDY_TYPE:
@existing_study_type: Other
STUDY_ABSTRACT: 14 days old plants grown in simulated sun condition were transferred to simulated shade condition. Given hours after transfer young leaf/primordia were collected and two or three plants were pooled for one biological replicate.
Biosample_ID: SAMN10660713

SRX1977908

IR	0.833
type	SRX
database	SRA

Info

TITLE: novel P mutants: Sample pfs2_P_limited
SRA_ID: SRX1977908
STUDY_REF: SRP079906
BioProject: PRJNA330878
DESIGN:
DESIGN_DESCRIPTION: TruSeq Stranded Total RNA with Ribo-Zero Plant
SAMPLE_DESCRIPTOR:
@accession: SRS1585616
IDENTIFIERS:
PRIMARY_ID: SRS1585616
EXTERNAL_ID:
@namespace: BioSample
#text: SAMN05429019
LIBRARY_DESCRIPTOR:
LIBRARY_NAME: pfs2-R1
LIBRARY_STRATEGY: RNA-Seq
LIBRARY_SOURCE: TRANSCRIPTOMIC
LIBRARY_SELECTION: RANDOM
LIBRARY_LAYOUT:
PLATFORM:
ILLUMINA:
INSTRUMENT_MODEL: Illumina HiSeq 1500
SUBMISSION_lab_name: Whelan lab
DESCRIPTOR:
STUDY_TITLE: Arabidopsis thaliana cultivar:Col-0 Transcriptome or Gene expression
STUDY_TYPE:
@existing_study_type: Other
STUDY_ABSTRACT: Identification of novel, cell-type enriched genes involved in P homeostasis
CENTER_PROJECT_NAME: Arabidopsis thaliana cultivar:Col-0
Biosample_ID: SAMN05429019

SRX5187276

IR	0.818
type	SRX
database	SRA

Info

TITLE: RNA-seq of Arabidopsis thaliana: apical part of 14 days old plants with 1 (h) after high R/FR treatment
SRA_ID: SRX5187276
STUDY_REF: SRP174647
BioProject: PRJNA512107

DESIGN:
DESIGN_DESCRIPTION: Full Transcript RNA sequencing with YourSeq Dual Kit (Amaryllis Nucleics, CA)
SAMPLE_DESCRIPTOR:
@accession: SRS4193665
IDENTIFIERS:
PRIMARY_ID: SRS4193665
LIBRARY_DESCRIPTOR:
LIBRARY_NAME: myc234_1h_H_R2
LIBRARY_STRATEGY: RNA-Seq
LIBRARY_SOURCE: TRANSCRIPTOMIC
LIBRARY_SELECTION: cDNA
LIBRARY_LAYOUT:
PLATFORM:
ILLUMINA:
INSTRUMENT_MODEL: Illumina HiSeq 4000
SUBMISSION_lab_name: Plant Biology
DESCRIPTOR:
STUDY_TITLE: Shade responsive genes in Col, myc234, npr1, and sid2/eds16
STUDY_TYPE:
@existing_study_type: Other
STUDY_ABSTRACT: 14 days old plants grown in simulated sun condition were transferred to simulated shade condition. Given hours after transfer young leaf/primordia were collected and two or three plants were pooled for one biological replicate.
Biosample_ID: SAMN10660700

SRX5187275

IR	0.818
type	SRX
database	SRA

Info

TITLE: RNA-seq of Arabidopsis thaliana: apical part of 14 days old plants with 1 (h) after high R/FR treatment
SRA_ID: SRX5187275
STUDY_REF: SRP174647
BioProject: PRJNA512107
DESIGN:
DESIGN_DESCRIPTION: Full Transcript RNA sequencing with YourSeq Dual Kit (Amaryllis Nucleics, CA)
SAMPLE_DESCRIPTOR:
@accession: SRS4193664
IDENTIFIERS:
PRIMARY_ID: SRS4193664
LIBRARY_DESCRIPTOR:
LIBRARY_NAME: myc234_1h_H_R1
LIBRARY_STRATEGY: RNA-Seq
LIBRARY_SOURCE: TRANSCRIPTOMIC
LIBRARY_SELECTION: cDNA
LIBRARY_LAYOUT:
PLATFORM:
ILLUMINA:
INSTRUMENT_MODEL: Illumina HiSeq 4000
SUBMISSION_lab_name: Plant Biology
DESCRIPTOR:
STUDY_TITLE: Shade responsive genes in Col, myc234, npr1, and sid2/eds16
STUDY_TYPE:
@existing_study_type: Other
STUDY_ABSTRACT: 14 days old plants grown in simulated sun condition were transferred to simulated shade condition. Given hours after transfer young leaf/primordia were collected and two or three plants were pooled for one biological replicate.
Biosample_ID: SAMN10660699

SRX1977897

IR	0.818
type	SRX
database	SRA

Info

TITLE: novel P mutants: Sample Col2_P_limited
SRA_ID: SRX1977897
STUDY_REF: SRP079906
BioProject: PRJNA330878
DESIGN:
DESIGN_DESCRIPTION: TruSeq Stranded Total RNA with Ribo-Zero Plant
SAMPLE_DESCRIPTOR:
@accession: SRS1585612
IDENTIFIERS:
PRIMARY_ID: SRS1585612
EXTERNAL_ID:
@namespace: BioSample
#text: SAMN05429015
LIBRARY_DESCRIPTOR:
LIBRARY_NAME: Col2-R2
LIBRARY_STRATEGY: RNA-Seq
LIBRARY_SOURCE: TRANSCRIPTOMIC
LIBRARY_SELECTION: RANDOM
LIBRARY_LAYOUT:
PLATFORM:
ILLUMINA:
INSTRUMENT_MODEL: Illumina HiSeq 1500
SUBMISSION_lab_name: Whelan lab
DESCRIPTOR:
STUDY_TITLE: Arabidopsis thaliana cultivar:Col-0 Transcriptome or Gene expression
STUDY_TYPE:
@existing_study_type: Other
STUDY_ABSTRACT: Identification of novel, cell-type enriched genes involved in P homeostasis
CENTER_PROJECT_NAME: Arabidopsis thaliana cultivar:Col-0
Biosample_ID: SAMN05429015

SRX5187329

IR	0.667
type	SRX
database	SRA

Info

TITLE: RNA-seq of Arabidopsis thaliana: apical part of 14 days old plants with 1 (h) after high R/FR treatment
SRA_ID: SRX5187329
STUDY_REF: SRP218372
BioProject: PRJNA560257
DESIGN:
DESIGN_DESCRIPTION: Full Transcript RNA sequencing with YourSeq Dual Kit (Amaryllis Nucleics, CA)
SAMPLE_DESCRIPTOR:
@accession: SRS4193718
IDENTIFIERS:
PRIMARY_ID: SRS4193718
LIBRARY_DESCRIPTOR:
LIBRARY_NAME: npr1_1h_H_R1
LIBRARY_STRATEGY: RNA-Seq
LIBRARY_SOURCE: TRANSCRIPTOMIC
LIBRARY_SELECTION: cDNA
LIBRARY_LAYOUT:
PLATFORM:

ILLUMINA:
INSTRUMENT_MODEL: Illumina HiSeq 4000
SUBMISSION_lab_name: Plant Biology
DESCRIPTOR:
STUDY_TITLE: Arabidopsis thaliana cultivar:Col Transcriptome or Gene expression
STUDY_TYPE:
@existing_study_type: Other
STUDY_ABSTRACT: Shade responsive genes in npr1, and sid2/eds16
CENTER_PROJECT_NAME: Arabidopsis thaliana cultivar:Col
Biosample_ID: SAMN10660715

SRX1066977

IR	0.833
type	SRX
database	SRA

Info

TITLE: Genome-wide RNA immune-precipitation of SR45-Associated transcripts
SRA_ID: SRX1066977
STUDY_REF: SRP041864
BioProject: PRJNA246656
DESIGN:
SAMPLE_DESCRIPTOR:
@accession: SRS605129
IDENTIFIERS:
PRIMARY_ID: SRS605129
LIBRARY_DESCRIPTOR:
LIBRARY_STRATEGY: RNA-Seq
LIBRARY_SOURCE: OTHER
LIBRARY_SELECTION: other
LIBRARY_LAYOUT:
PLATFORM:
ILLUMINA:
INSTRUMENT_MODEL: NextSeq 500
SUBMISSION_lab_name: Reddy lab
DESCRIPTOR:
STUDY_TITLE: Arabidopsis thaliana strain:Col Transcriptome or Gene expression
STUDY_TYPE:
@existing_study_type: Transcriptome Analysis
STUDY_ABSTRACT: This study aims to identify in planta transcripts physically associated with alternative splicing regulator SR45
CENTER_PROJECT_NAME: Arabidopsis thaliana strain:Col
Biosample_ID: SAMN02769469

SRX5187334

IR	0.667
type	SRX
database	SRA

Info

TITLE: RNA-seq of Arabidopsis thaliana: apical part of 14 days old plants with 1 (h) after low R/FR treatment
SRA_ID: SRX5187334
STUDY_REF: SRP218372
BioProject: PRJNA560257
DESIGN:
DESIGN_DESCRIPTION: Full Transcript RNA sequencing with YourSeq Dual Kit (Amaryllis Nucleics, CA)
SAMPLE_DESCRIPTOR:

@accession: SRS4193723
IDENTIFIERS:
PRIMARY_ID: SRS4193723
LIBRARY_DESCRIPTOR:
LIBRARY_NAME: npr1_1h_L_R2
LIBRARY_STRATEGY: RNA-Seq
LIBRARY_SOURCE: TRANSCRIPTOMIC
LIBRARY_SELECTION: cDNA
LIBRARY_LAYOUT:
PLATFORM:
ILLUMINA:
INSTRUMENT_MODEL: Illumina HiSeq 4000
SUBMISSION_lab_name: Plant Biology
DESCRIPTOR:
STUDY_TITLE: Arabidopsis thaliana cultivar:Col Transcriptome or Gene expression
STUDY_TYPE:
@existing_study_type: Other
STUDY_ABSTRACT: Shade responsive genes in npr1, and sid2/eds16
CENTER_PROJECT_NAME: Arabidopsis thaliana cultivar:Col
Biosample_ID: SAMN10660720
