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 23Â°C with 65% relative humidity, and with the light at a fluence rate of 125 to 175 Î¼mol mâ^'2 sâ^'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 23Â°C with 65% relative humidity, and with the light at a fluence rate of 125 to 175 Î¼mol mâ¯2 sâ¯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 23Â°C with 65% relative humidity, and with the light at a fluence rate of 125 to 175 Î¼mol mâ¯2 sâ¯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

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 21æŽ³C) 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 10ç¢Œl RiboLock RNase inhibitor (40U/ç¢Œl) (ThermoFisher, #EO0381) was added to 2g of stem. Samples were chopped manually on ice for 10 min. Nuclei were collected by centrifuge (1000g, 10min, 4æŽ³C) and gently washed by cold resuspension buffer (same formula as isolation buffer but without Triton X-100) for two times. 300ç¢Œl of resuspension buffer supplemented with 10ç¢Œg/ml Hoechst 33342 at final concentration and 5ç¢Œl 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 ç¢Œm sort nozzle according to GFP signal level, except for LTP1_GFP+_S21 which was 10,800 nuclei. RNA was extracted into 15 ç¢Œl water according to manufacture's protocol.", '1 ç¢Œl 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 é˚¥æ¼enomeSAindexNbases 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/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 21æŽ³C) 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 10ç¢Œl RiboLock RNase inhibitor (40U/ç¢Œl) (ThermoFisher, #EO0381) was added to 2g of stem. Samples were chopped manually on ice for 10 min. Nuclei were collected by centrifuge (1000g, 10min, 4æŽ³C) and gently washed by cold resuspension buffer (same formula as isolation buffer but without Triton X-100) for two times. 300ç¢Œl of resuspension buffer supplemented with 10ç¢Œg/ml Hoechst 33342 at final concentration and 5ç¢Œl 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 ç¢Œm sort nozzle according to GFP signal level, except for LTP1_GFP+_S21 which was 10,800 nuclei. RNA was extracted into 15 ç¢Œl water according to manufacture's protocol.", '1 ç¢Œl 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 é^¥æ¼enomeSAindexNbases 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']

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: {'DESIGN_DESCRIPTION': None, 'SAMPLE_DESCRIPTOR': {'@accession': 'SRS605129', 'IDENTIFIERS': {'PRIMARY_ID': 'SRS605129'}}}

LIBRARY_DESCRIPTOR: {'LIBRARY_NAME': None, 'LIBRARY_STRATEGY': 'RNA-Seq', 'LIBRARY_SOURCE': 'OTHER', 'LIBRARY_SELECTION': 'other', 'LIBRARY_LAYOUT': {'SINGLE': None}}

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': {'SINGLE': None}}

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

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 4æŽ³C and germinated on half-strength Murashige and Skoog medium (1% sucrose) in long-day conditions (16 h light/8 h darkness; 21æŽ³C). 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: ["Kæžshler'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']

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 22æŽ³C/18æŽ³C. Light intensity during day hours was approximately 100 ç¢ŒE 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']

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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']

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 21æŽ³C) 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 10ç¢Œl RiboLock RNase inhibitor (40U/ç¢Œl) (ThermoFisher, #EO0381) was added to 2g of stem. Samples were chopped manually on ice for 10 min. Nuclei were collected by centrifuge (1000g, 10min, 4æŽ³C) and gently washed by cold resuspension buffer (same formula as isolation buffer but without Triton X-100) for two times. 300ç¢Œl of resuspension buffer supplemented with 10ç¢Œg/ml Hoechst 33342 at final concentration and 5ç¢Œl 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 ç¢Œm sort nozzle according to GFP signal level, except for LTP1_GFP+_S21 which was 10,800 nuclei. RNA was extracted into 15 ç¢Œl water according to manufacture's protocol.", '1 ç¢Œl 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 é^¥æ¼enomeSAindexNbases 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']

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 22æŽ³C/18æŽ³C. Light intensity during day hours was approximately 100 ç¢ŒE 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']

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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']

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']

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 21æŽ³C) 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 10ç¢Œl RiboLock RNase inhibitor (40U/ç¢Œl) (ThermoFisher, #EO0381) was added to 2g of stem. Samples were chopped manually on ice for 10 min. Nuclei were collected by centrifuge (1000g, 10min, 4æŽ³C) and gently washed by cold resuspension buffer (same formula as isolation buffer but without Triton X-100) for two times. 300ç¢Œl of resuspension buffer supplemented with 10ç¢Œg/ml Hoechst 33342 at final concentration and 5ç¢Œl 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 ç¢Œm sort nozzle according to GFP signal level, except for LTP1_GFP+_S21 which was 10,800 nuclei. RNA was extracted into 15 ç¢Œl water according to manufacture's protocol.", '1 ç¢Œl 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 é^¥æ¼enomeSAindexNbases 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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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']

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: {'DESIGN_DESCRIPTION': None, 'SAMPLE_DESCRIPTOR': {'@accession': 'SRS605129', 'IDENTIFIERS': {'PRIMARY_ID': 'SRS605129'}}}

LIBRARY_DESCRIPTOR: {'LIBRARY_NAME': None, 'LIBRARY_STRATEGY': 'RNA-Seq', 'LIBRARY_SOURCE': 'OTHER', 'LIBRARY_SELECTION': 'other', 'LIBRARY_LAYOUT': {'SINGLE': None}}

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

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': {'SINGLE': None}}

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

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']

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/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']

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': {'SINGLE': None}}

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

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': {'SINGLE': None}}

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

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': {'SINGLE': None}}

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

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 23Â°C with 65% relative humidity, and with the light at a fluence rate of 125 to 175 Î¼mol mâ^'2 sâ^'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

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 23Â°C with 65% relative humidity, and with the light at a fluence rate of 125 to 175 Î¼mol mâ¯2 sâ¯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

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 ç¢Œmol 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 æ¸mol 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']

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 æŽ³C']

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']

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, 25ç¢ŒM dexamethasone, with or without 1ç¢ŒM trichostatin, in 0.5xMS for 2h']

growth_protocol_ch1: ['23æŽ³C; 65% humidity; 16h light/8h dark; LED lights 200ç¢ŒE']

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 ç¢Œg 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']

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contact_department: ['Stem Cell Biology']

contact_institute: ['Centre for Organismal Studies']

contact_address: ['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']

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': {'SINGLE': None}, '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

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 21æŽ³C) 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 10ç¢Œl RiboLock RNase inhibitor (40U/ç¢Œl) (ThermoFisher, #EO0381) was added to 2g of stem. Samples were chopped manually on ice for 10 min. Nuclei were collected by centrifuge (1000g, 10min, 4æŽ³C) and gently washed by cold resuspension buffer (same formula as isolation buffer but without Triton X-100) for two times. 300ç¢Œl of resuspension buffer supplemented with 10ç¢Œg/ml Hoechst 33342 at final concentration and 5ç¢Œl 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 ç¢Œm sort nozzle according to GFP signal level, except for LTP1_GFP+_S21 which was 10,800 nuclei. RNA was extracted into 15 ç¢Œl water according to manufacture's protocol.", '1 ç¢Œl 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 é^¥æ¼enomeSAindexNbases 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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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/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']

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: 45æŽ³C']

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 -80æŽ³C. 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 (45æŽ³C 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 22æŽ³C under 16h / 8h of light / dark cycle (~100 æ¸mol mé^2 sé^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 22é£©ç™^ to 45é£©ç™^ over the course of 6 hours (starting at the beginning of the photoperiod) in the light and keep at 45é£©ç™^ for 90 mins. Subsequently, the plates were transferred back to a growth chamber with standard (22é£©ç™^) temperature. For the heat shock application, the growth chamber (Percival) was pre-heated to 45é£©ç™^ with lighting (~100 æ¸mol mé^2 sé^1) and 60% relative humidity. Each plate containing 80 acclimated or non-acclimated seedlings was transferred from the control growth condition (22é£©ç™^) chamber to a heated growth chamber (45é£©ç™^) 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']

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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']

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 21æŽ³C) 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 10ç¢Œl RiboLock RNase inhibitor (40U/ç¢Œl) (ThermoFisher, #EO0381) was added to 2g of stem. Samples were chopped manually on ice for 10 min. Nuclei were collected by centrifuge (1000g, 10min, 4æŽ³C) and gently washed by cold resuspension buffer (same formula as isolation buffer but without Triton X-100) for two times. 300ç¢Œl of resuspension buffer supplemented with 10ç¢Œg/ml Hoechst 33342 at final concentration and 5ç¢Œl 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 ç¢Œm sort nozzle according to GFP signal level, except for LTP1_GFP+_S21 which was 10,800 nuclei. RNA was extracted into 15 ç¢Œl water according to manufacture's protocol.", '1 ç¢Œl 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 é^¥æ¼enomeSAindexNbases 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']

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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/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']

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': {'SINGLE': None}, '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

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: {'DESIGN_DESCRIPTION': None, 'SAMPLE_DESCRIPTOR': {'@accession': 'SRS605129', 'IDENTIFIERS': {'PRIMARY_ID': 'SRS605129'}}}

LIBRARY_DESCRIPTOR: {'LIBRARY_NAME': None, 'LIBRARY_STRATEGY': 'RNA-Seq', 'LIBRARY_SOURCE': 'OTHER', 'LIBRARY_SELECTION': 'other', 'LIBRARY_LAYOUT': {'SINGLE': None}}

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

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': {'SINGLE': None}}

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

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': {'SINGLE': None}}

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