Data accession

- Go to http://www.ncbi.nlm.nih.gov/gds/?term=arabidopsis, choose "Arabidopsis thaliana" for Organism and "Expression profiling by high throughput sequencing" for study type, I'll have 186 experiments.
- choose experiments that have biological replicates for each treatment (4 - 200) . 160 remained
- filter by "libraryStrategy = RNA-Seq", "LibrarySource=transcriptome", "librarySelection=cDNA" and "LibraryLayout=Single" and # of total reads >= 5 million
- If measurements are taken over time, we choose samples collected at the same time point.

Timeline of Arabidopsis Growth Stages https://www.arabidopsis.org/portals/education/growth.jsp and https://www.arabidopsis.org/info/ontologies/boyes2001.pdf
Ecotype https://www.arabidopsis.org/i/arabidopsis_ecotype_map.jpg
More information https://www.arabidopsis.org/portals/education/aboutarabidopsis.jsp

GEO	Tissue cluster	# rep	Ecotype	Genotype	growth protocol	extracted molecule	Age	Platform	Ave.Length
GSE35288	flower	6	Col-0	WT, hae-3/hsl2-3	Stratified seeds were irradiated with WL at 21C for 3 h to induce germination, followed by a FR pulse for 15 min to suppress pseudo dark effects, and grown in darkness at 21C for 2 d before harvest	total RNA	stage 15	Illumina HiSeq 2000	100
GSE37159	seedling	8	Col-0	bzr1-1D, pifq and pifq;bzr1-1D	Seedlings were grown on MS medium containing BRZ (brassinosteroid biosynthesis inhibitor) in the dark for 5 days before harvesting	total RNA	5 days	Illumina HiSeq 2000	36
GSE38400	seedling	12	Col-0	**Col-0 strain nrpe1, swi3b, idn2**	Strains were grown under long day conditions for 2-3 weeks	total RNA	2-3 week	Illumina HiSeq 2000	48-55
GSE38879	seedling	12		rve8-1 RVE8::RVE8:GR	Arabidopiss rve8-1 RVE8::RVE8:GR and rve8-1 seeds (30 seeds/ per sample) were sterilized and stratified on fine nylon mesh on MS +3% sucrose at 4 degree in the dark for 2 days. Seedlings were grown in 12 hours light (50 micro Ei white light)/ 12 hours dark for 7 days.	total RNA	7 days	Illumina HiSeq 2000	44
GSE39214	seedling	12		WT/pif3/ pif145/pifq	Stratified seeds were irradiated with WL at 21C for 3 h to induce germination, followed by a FR pulse for 15 min to suppress pseudo dark effects, and grown in darkness at 21C for 2 d before harvest.	poly RNA	2 days	Illumina Genome Analyzer IIx, Illumina HiSeq 2000	36 or 50
GSE39463	leaves	48	Col-0	Col-0 pen2-1 pad4-1 sag101-2 mutant	Growth of plants and pathogens was performed as described in V. Lipka, et al., Science 310, 1180 (2005) (PMID 16293760).	total RNA	6, 12, 18, 24 hours post inoculation (hpi) of Bgh	Illumina HiSeq 2000	97 or 101
GSE42957	seed	14	ColA9 X Col-0	Hybrid/Control	All plants were grown under long day conditions (16hrs light at 21C and 8hrs dark at 18C) in a controlled environment facility at Davis, CA.	total RNA	3 days after pollination	Illumina Genome Analyzer IIx, Illumina HiSeq 2000.	34 or 84
GSE43865	seedling	6	Col-0	WT/link1link2 double mutants	Seeds were sown onto MS and grown at 22C in continuous light or long day conditions, depending on the experiment.	total RNA	9 days	Illumina Genome Analyzer IIx	

Table 0.1: Organism= Arabidopsis Thaliana. LibraryStrategy = RNA-Seq, LibrarySource = transcriptomic, LibrarySelection= cDNA, LibraryLayout=Single

GEO	Tissue cluster	Sample size	Ecotype	Genotype	Growth protocol	Overall Design	extracted molecule	Age	Platform	Average length
GSE48767	seedling	6	Ler	WT and phyA-1	grown in the dark for 4 d and irradiated with 3 hour of Far red light	The wild-type seedlings and the phyA-1 mutant (both of the Landsberger ecta [Ler] ecotype) were grown in the same conditions used for the phyA ChIP-seq analysis (D4d+FR3h) prior to RNA isolation. Three independent biological replicates were subjected to RNA-seq analysis.	polyA RNA	4 days	Illumina HiSeq 2000	76
GSE51119	seedling	10	Col-0	IBH1OE/IBH1dn	Arabidopsis thaliana plants (ecotype Col-0) were grown at 22ÂřC and a 16-h photoperiod (65 ÎijE mâĹŠ2 sâĹŠ1) on half-strength MS medium and 0.7 % plant tissue culture agar. Entire seedlings were collected at 10 days after sawing.	For loss-of-function mutant, homozygous ibh1(SALK 049177) and ibl1(SALK 119457) were compared to wild type (Col). For gain-of-function mutant, homozygous 35Spro:IBH1-GFP and 35Spro:IBL1-GFP were compared to wild type (Col). Total RNAs were extactced from seedling of each genotypes. For each genotype two biological replicates were sequenced.	polyA RNA	10 days	Illumina HiSeq 2000	50
GSE51772	seedling	8	Col-0	WT and iaa3	Seedlings were grown on medium containing 2 ÂţM propiconazole (PPZ) in the dark for 5 days and treated with mock or 100 nM BL for 4 hr before harvesting.	Seedlings (Col-0 and iaa3) were grown on medium containing 2 ÂţM propiconazole (PPZ) in the dark for 5 days and treated with mock or 100 nM BL for 4 hr before harvesting for total RNA extraction.	total RNA	5 days	Illumina HiSeq 2000	101
GSE53078	seedling	4	Col-0	Col-0 and 35S::HBI1-YFP	Wild type Arabidopsis, 35S::HBI1-YFP and Col were grown on half-strength MS medium for 5 days under constant light.	Compare the transcriptome of HBI1-Ox and wild type.	total RNA	5 days	Illumina Genome Analyzer	36
GSE57806	seedling	6		WT/hid1		Total RNA was isolated from 5-day-old cR-grown WT and hid1(hidden treasure 1)seedlings using RNeasy Plant Mini Kits (Qiagen). Three biological replicates for each sample were subjected to RNA-seq.	total RNA	5 days	Illumina HiSeq 2000	100
GSE58082	seedling	6		GFP-FHY1 fhy1-1 transgenic, fhy1-1 mutant		The 35S: GFP-FHY1 fhy1-1 transgenic line and the fhy1-1 mutant were grown under the same light conditions used (D4d+FR3h) for RNA preparation and sequencing. Three biologically replicates were subjected to high-throughput Solexa (Illumina) sequencing.	total RNA	4 days	Illumina HiSeq 2000	76

GEO	Tissue cluster	Sample size	Ecotype	Genotype	Growth protocol	Overall Design	extracted molecule	Age	Platform	Average length
GSE35288	flower	6	Col-0	WT, hae-3/hsl2-3	Plants were grown in 16h light 8h dark at 22C	6 samples were sequenced, 3 biological replicates of Col-0 wild type and 3 biological replicates of the hae-3 hsl2-3 double mutant. Samples were barcoded and all 6 samples multiplexed and sequenced on 3 lanes, each lane on a separate flow cell, of an Illumina HiSeq 2000.	total RNA	stage 15	Illumina HiSeq 2000	100
GSE35408	hypocotyl	6	Columbia	bzr1-1D and WT	Wild type Arabidopsis and bzr1-1D were grown in media containing 1 ÎijM PAC and 0 or 2 ÎijM PPZ for 4.5 days in dark	Wild type Arabidopsis and bzr1-1D were grown in media containing 1 ÎijM PAC and 0 or 2 ÎijM PPZ for 4.5 days in dark, then treated with 10 ÎijM GA3 or mock solution for 12 hr. Total RNA was extracted with Spectrum Plant Total RNA Kit (Sigma) and the mRNA sequencing libraries were constructed with barcodes using TruSeqTM RNA Sample Preparation Kit (Illumina). Six barcoded libraries were pooled together and sequenced by Illumina HiSeq2000.	total RNA	4.5 days	Illumina HiSeq 2000	36
GSE48235	rosettle leaves	6	Columbia	col-0	Arabidopsis thaliana (Col-0) plants were grown in potting soil in growth rooms at 22 ÂřC with a 12-h light photoperiod and light intensity of 180 Îijmol mâĹŠ 2 sâĹŠ1.	For each condition (water, S1, and S3) the transcriptome was sequenced for two replicates. The watered condition is considered the control.	total RNA	9 days	Illumina Genome Analyzer II	75 or 101
GSE53952	seed	27		fae1/CL37/PDAT	All plant lines were grown randomized across a growth chamber under constant 100-170 ÎijE light, 22Âř C and 60% humidity.	Transcript profiles of Arabidopsis developing seeds of three lines, at three stages of development were generated by deep sequencing, in triplicate, using Illumina	total RNA	7-12 days	Illumina Genome Analyzer Iix and Illumina HiSeq 2000	50 or 55
GSE56326	carpels (15 developing inflorescences) growth protocol	8	Columbia	wt, nga mutant and , NGA overexpression	seed were sow on soil, and plant were grown under long day condition	Expression profile comparation of wild type, nga mutant and NGA overexpression	total RNA	stage 8-13	Illumina HiSeq 2000	50

GEO	Tissue cluster	# rep	Ecotype	Genotype	growth protocol	extracted molecule	Age	Platform	Ave.Length
GSE36626	leaves	4	Columbia	HTR13-GFP/HTR5-GFP	Plants were grown in short day conditions (8h light -16h dark, 20 to 22C) for 4 weeks after stratification at 4C and in dark for 5 days. For harvesting the tissues, we dissected the plants with scalpels under a binocular scope.	polyA RNA	4 weeks	Illumina Genome Analyzer IIx	76
GSE39463	leaves	12	Columbia-0	pen2-1 pad4-1 sag101-2 mutant expressing MLA1-HA	Growth of plants and pathogens was performed as described in V. Lipka, et al., Science 310, 1180 (2005) (PMID 16293760)	total RNA	6, 12, 18, 24 hours post inoculation (hpi) of Bgh	Illumina HiSeq 2000	97 or 101
GSE48235	rosette leaves	6	Columbia	Col-0	Arabidopsis thaliana (Col-0) plants were grown in potting soil in growth rooms at 22 C with a 12-h light photoperiod and light intensity of 180 mumol mâĹŠ 2 sâĹŠ1.	total RNA	9 days	Illumina Genome Analyzer II	75 or 101
GSE51304	leaves	18	Col0	WT,drm12, drm12cmt2 etc.,	Plants were grown under continuous light	polyA RNA	3 weeks	Illumina HiSeq 2000	50 or 51
GSE54677	leaves	20	Col	WT, morc1 morc2 morc6 etc	All plants were grown at 22 degrees celsius in constant light.	total RNA	adult	Illumina HiSeq 2000	50 or 51

GEO	Tissue cluster	Sample size	Ecotype	Genotype	Growth protocol	Overall Design	extracted molecule	Age	Platform	Average length
GSE32202	seedling	6	Col-0	WT	Surface-sterilized seeds were sown on respective medium and imbibed at 4ÃĆÂřC for 3d. Plates were kept under light for 3 4h after imbibition to promote seed germination, wrapped with aluminum foil, and incubated in the dark at 22ÃĆÂřC for 3d.	RNA seq of 3 samples: Col-0 on MS medium, Col-0 on MS+Kyn medium, wei8 tar2(+/-) on MS medium.	total RNA	3 days	Illumina HiSeq 2000	100
GSE41766	seedling	6	Col-0	WT,35S:IBH1-myc and 35S:IBH1-myc/35S:PRE1-YFP	Wild type Arabidopsis, 35S:IBH1-myc and 35S:IBH1-myc/35S:PRE1-YFP were grown on half-strength MS medium for 5 days under constant light.	Compare the transcriptome of IBH1 and PRE1	total RNA	5 days	Illumina HiSeq 2000	
GSE43983	roots, leaves, flowers, and siliques	8	Col-0	WT and clf-28 mutant	Arabidopsis plant (Col-0 and clf-28) materials were grown under long day conditions at 22âĎČ. Aerial part and roots were collected from two-week old plants that grew on MS plate. Flowers and siliques were collected from five-week old plants that grew in soil.	Transcriptom profiling in roots, leaves, flowers and siliques of clf-28 plants.	total RNA	2 weeks	Illumina HiSeq 2000	
GSE55884	leaves	6	Col-0	pad4-1 and smg7 pad4	Plants were germinated on soil and grown for 3 weeks at 21ÂřC, 16 h	Total RNA (ribosomal RNA depleted) illumina sequencing of three single end libraries respectively of adult pad4 leaves (control) vs adult smg7 pad4 mutant leaves (mutant)	total RNA	3 weeks	Illumina HiSeq 2000	
GSE57215	flower buds	36		dcl234, WT etc.	Plants were grown with 16hr of light	To detect siRNA precursors transcribed by RNA polymerase IV, the genome wide profiling of RNA were carried out at dcl234 and dcl234 nrpd1. Different types of RNA (including Total RNA, polyA+ RNA, polyA- RNA, double stranded RNA) libraries were built to detect different transcripts. RDR2 is a RNA-dependent RNA polymerase in Pol IV complex, so the RNA-seq libraries with the mutation of RDR2 were also built. In addition, smRNA libraries with mutations blocking siRNA biogenesis were also built	total RNA		Illumina HiSeq 2000	

GEO	Tissue cluster	Sample size	Ecotype	Genotype	Growth protocol	Overall Design	extracted molecule	Age	Platform	Average length
GSE58029	leaves	4	Col-0	WT and suvr5-1 etc.	All plants were grown under long day conditions.	Investigation of gene expression profiles of suvr5-1, ldl1 ldl2 and suvr5 ldl1 ldl2 mutants. For more information on this study contact Dr. Elena Caro at ecarobernat-at-gmail.com	total RNA	5 days	Illumina HiSeq 2000	50
GSE58662	seedling	4		wbc19 mutant	Control (SALK_064816C) and wbc19 mutant (SALK_107731) lines were used. SALK_064816C mutants served as controls as they carry a T-DNA insertion that does not disrupt a gene. The T-DNA insertion is located in the vicinity of the TRANSPARENT TESTA 4 gene, 260 bp upstream of the start codon and the mutants have no visible phenotype. After stratification (3 days at 4ÂřC), plates were transferred to a controlled-environment cabinet (23ÂřC, 16 h light; 18ÂřC, 8 h dark) and plant material was harvested and flash frozen 5 days later.	Examination of transcriptome in control and wbc19 mutant seedlings with or without exposure to kanamycin.	total RNA	5 days	Illumina Genome Analyzer II	36 or 40
GSE58856	FACS-sorted protoplasts from aerial tissue	11		marker line: ML1p::YFP-RCI2A in Col	Seedlings were grown for 10 days on 1/2 strength Murashige and Skoog (MS) medium under long day (16-hours light, 8-hours dark) conditions at 25C.	Total RNA was extracted from purified protoplasts (4,000 to 20,000 cells/replicate; 2 replicates/marker line; 3 replicates/SSY marker line) and transcript abundance measured using RNA sequencing.	total RNA	10 days	Illumina HiSeq 2000	50 - 59
GSE58974	seedling	10	Col-0	UBQ10:NTF/ACT2p:BirA	Affinity-purified nuclei used in this study were extracted from 10-day-old seedlings of UBQ10:NTF/ACT2p:BirA Columbia-0 (Col-0) ecotype of Arabidopsis thaliana using the INTACT methodology. All plants were grown at 20ÂřC, in a 16 h light/8 h dark cycle	Protein interaction profile sequencing (PIP-seq) in Arabidopsis seedling nuclei. These are crosslinked with formaldehyde and treated with two RNases (ssRNase and dsRNase) with two replicates	total RNA		Illumina HiSeq 2000	50
GSE59154	whole plant	8	Can-0, Hen-16		Seedlings were germinated in controlled-environment growth chambers at the University of Chicago greenhouses on a 16-hour light, 8-hour dark cycle.	m6A-seq in two accessions of Arabidopsis, two replicates for each sample	polyA RNA	5-7 days	Illumina HiSeq 2000	101

GEO	Tissue cluster	Sample size	Ecotype	Genotype	Growth protocol	Overall Design	extracted molecule	Age	Platform	Average length
GSE59167	root tip tissue	11	Col-0	WT, clavata2-gabi	Seeds were grown on plant agar containing germination medium consisting of Murashige and Skoog (2.2 g/l) salts with Gamborgs no. 5 vitamins , 2-(N-morpholino) ethanesulfonic acid (0.5 g/l) and sucrose (10 g/l) and grown in a vertical position at 21ÂřC under constant light conditions.	m6A-seq in two accessions of Arabidopsis, two replicates for each sample	total RNA		Illumina HiSeq 2000	101
GSE59637	inflorescences and siliques	4	Columbia	stk-/- and WT	Arabidopsis thaliana wild-type (ecotype Columbia) and stk mutant plants were grown at 22ÂřC under short-day (8 h light/16 h dark) or long-day (16 h light/8 h dark) conditions.	mRNA profiles from both Arabidopsis wild-type and stk mutant inflorescences and siliques until 5 DAP were generated by deep sequencing, in duplicate according to the manufacturerâĂŹs instructions by TruSeq RNA Sample Prep kit (Illumina Inc.) and sequenced on Illumina HiSeq2000 in one lane single-read 50bp..	total RNA	inflorescences and siliques until 5 DAP	Illumina HiSeq 2000	51
GSE60183	Epidermis including guard cells	6	gl1	phot1 phot2 double mutant		phot1-5 phot2-1 in gl1 background (phot1 phot2) and pGC1::SOC1-GFP/phot1 phot2 were grown under 16 h light / 8h dark, constant 22ËŽC conditions for 4 to 5 weeks. Epidermis including guard cells were isolated from leaves of these plants. Three biological replicates were used	total RNA	3 weeks after germination	Ion Torrent PGM	73-124
GSE60835	seedling	12		wild type, det1-1	Seeds were vernalized for 3 d at 4 ÂřC after surface sterilization. Then seeds were exposed to light for 12 h and grown in darkness for 4 days.	Total of twelve samples, two treatments and three genotypes, and each have three replicates.	total RNA	4 days	Illumina Genome Analyzer	36
GSE61542	whole rosette	24		Col-0, C24, Te, CT101	eight plants per genotype. All plants were randomly placed, grown in controlled chamber (Weiss Bio1300; Weiss Gallenkamp), at 22ÂřC/19ÂřC, and relative humidity of 70%/90%, under a 12-h light/12-h dark cycle for two weeks.	Transcriptome profiling of ozone response using two arabidopsis accessions C24 and Te with different ozone sensitivity	total RNA	3 weeks old plants	Illumina HiSeq 2500	51
GSE62799	aerial tissue	6		frg1/2 and Col-0 WT	Plants were grown on 1x MS medium at 21 ÂžC and continuous light for 14 days after germination.	mRNA profiles of 14 days old seedlings of Columbia 0 wild type and frg1-1 frg2-1 double mutants, 3 biological replicates each.	total RNA	14 days	Illumina HiSeq 2000	51

GEO	Tissue cluster	Sample size	Ecotype	Genotype	Growth protocol	Overall Design	extracted molecule	Age	Platform	Average length
GSE63355	shoot apical meristem	16	Col-0		plants were grown for seven days on solid Â¡ MS media at 16 h light: 8 h dark at 21ÂřC.	Examination of transcriptional changes in response to mock, 24 h and 5 days 20 ÂţM zebularine and 24 h 10 ÂţM MMC treatment in Arabidopsis wild-type and/or atr-2.	total RNA	7 days	Illumina HiSeq 2500	94
GSE64381	Root	40	Col-0		WOX5:GFP (Col-0 background) plants were grown on plates (1xMS, 0.5% Sucrose, 0.8% Agar) and harvested at 5 DAS (Days after stratification)	40 cells from the QC	polyA RNA	5 DAS	Illumina HiSeq 2000	76
GSE64410	Root	48	Col-0		re stratified in the dark, at 4ÂřC for 2 days, and then transferred to 22ÂřC in continuous light (70 Îijmol mâĹŠ2 sâĹŠ1), for 6 days.	24 samples of polyribosome-associated mRNA (following 0, 3, and 8 hours of BR treatment, in two biological repetitions), were collected.	total RNA	6 days	Illumina HiSeq 2500	50 or 51
GSE64870	seedling	22	background: Ba-1, Got-7, Lip-0 ect.		plants were grown for 14 days on soil at long day conditions (day: 16 h, 6 am to 10 pm, light intensity 150 Âţmol m-2 s-1, 22Âř C; night: 8 h, no light, 18Âř C) and 50% relative humidity	Examination of transcriptional changes in response to UV treatment in Arabidopsis natural accessions	total RNA	14 days	Illumina HiSeq 2500	94
GSE65740	whole rosette	24	Col-0	triple mutants coi1-16 ein2 sid2 and tga2 tga5 tga6	Seeds were sown on 1:1 peat: vermiculite, stratified for three days, and then grown at 22ÂřC/19ÂřC for a week. All plants were randomly placed, grown in controlled chamber (Weiss Bio1300; Weiss Gallenkamp), at 22ÂřC/19ÂřC, and relative humidity of 70%/90%, under a 12-h light/12-h dark cycle for two weeks.	Transcriptome profiling of ozone response using two arabidopsis triple mutants coi1-16 ein2 sid2 and tga2 tga5 tga6 related to Jasmonic acid, salicylic acid and ethylene signaling to identify hormone-independant apoplastic ROS signaling	total RNA	3 weeks	Illumina HiSeq 2500	49 or 51
GSE66666	whole 4-day-old seedling (root, hypocotyl, cotyledon)	6	Columbia	WT and athb1-1 mutant	Wild-type and athb1-1 mutant seeds were plated in Petri dishes containing 0.5 % Murashige and Skoog basal medium supplemented with vitamins (PhytoTechnology LaboratoriesTM) and 0.9 % agar. Seeds were then stratified for 3 days at 4ÂžC in darkness, and then transferred to a growth chamber (120 umol/m2/s) during 4 days under short day conditions. Seedlings were harvested 1 h before the end of the night.	RNA-Seq data for 4-day-old wild-type (Col-0) and athb1-1 mutant seedlings grown under short-day conditions. Biological triplicates were performed for each genotype analyzed.	total RNA	4 days	Illumina HiSeq 2000	50

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GSE48767	seedling	6	Ler	WT and phyA-1	polyA RNA	4 days	Illumina HiSeq 2000	76
	growth protocol	grown in the dark for 4 d and iradiated with 3 hour of Far red light						
	treatment protocol	The wild-type seedlings and the phyA-1 mutant (both of the Landsberger ecta [Ler] ecotype) were grown in the same conditions used for the phyA ChIP-seq analysis (D4d+FR3h) prior to RNA isolation. Three independent biological replicates were subjected to RNA-seq analysis.						
GSE51119	seedling	10	Col-0	IBH1OE/IBH1OE	polyA RNA	10 days	Illumina HiSeq 2000	50
	growth protocol	Arabidopsis thaliana plants (ecotype Col-0) were grown at 22C and a 16-h photoperiod (65 μEm-2-s-1) on half-strength MS medium and 0.7 % plant tissue culture agar. Entire seedlings were collected at 10 days after sawing.						
	treatment protocol	no treatment						
GSE51772	seedling	8	Col-0	WT and iaa3	total RNA	5 days	Illumina HiSeq 2000	101
	growth protocol	Seedlings were grown on medium containing 2 μM propiconazole (PPZ) in the dark for 5 days and treated with mock or 100 nM BL for 4 hr before harvesting.						
GSE53078	seedling	4	Columbia???	Col-0 and 35S::HBI1-YFP	total RNA	5 days	Illumina Genome Analyzer	36
	growth protocol	Wild type Arabidopsis, 35S::HBI1-YFP and Col were grown on half-strength MS medium for 5 days under constant light.						
GSE57086	seedling	6	Columbia?	WT/hid1	total RNA	5 days	Illumina HiSeq 2000	100
GSE58082	seedling	6	??	GFP-FHY1 fhy1-1 transgenic, fhy1-1 mutant	total RNA	4 days	Illumina HiSeq 2000	76
	growth protocol	The 35S: GFP-FHY1 fhy1-1 transgenic line and the fhy1-1 mutant were grown under the same light conditions used (D4d+FR3h) for RNA preparation and sequencing. Three biologically replicates were subjected to high-throughput Solexa (Illumina) sequencing						

Table 0.2: Organism= Arabidopsis Thaliana. LibraryStrategy = RNA-Seq, LibrarySource = transcriptomic, LibrarySelection= cDNA, LibraryLayout=Single

GEO	Tissue cluster	# rep	Ecotype	Genotype	extracted molecule	Age	Platform	Ave.Length
GSE35288	flower	6	Col-0	WT, hae-3/hsl2-3	total RNA	stage 15	Illumina HiSeq 2000	100
	growth protocol	Stratified seeds were irradiated with WL at 21C for 3 h to induce germination, followed by a FR pulse for 15 min to suppress pseudo dark effects, and grown in darkness at 21C for 2 d before harvest						
	treatment protocol	The wild-type seedlings and the phyA-1 mutant (both of the Landsberger ecta [Ler] ecotype) were grown in the same conditions used for the phyA ChIP-seq analysis (D4d+FR3h) prior to RNA isolation. Three independent biological replicates were subjected to RNA-seq analysis.						
GSE35408	Hypocotyl	10	Columbia	bzr1-1D and WT	total RNA	4.5 days in dark	Illumina HiSeq 2000	36
GSE48235	rosette leaves	6	Columbia	Col-0	total RNA	9 days	Illumina Genome Analyzer II	75 or 101
	growth protocol	Arabidopsis thaliana (Col-0) plants were grown in potting soil in growth rooms at 22 C with a 12-h light photoperiod and light intensity of 180 *mu*mol mâĹŠ 2 sâĹŠ1.						
	treatment protocol	Repeated dehydration stresses were performed by air-drying for 2 h followed by a 22 h period of full re-hydration recovery. S1 sample taken at first dehydration, S3 at third dehydration.						
GSE53952	seed	27		fae1/CL37/PDAT	total RNA	7-12 days	Illumina Genome Analyzer IIx and Illumina HiSeq 2000	50 or 55
	growth protocol	All plant lines were grown randomized across a growth chamber under constant 100-170 μE light, 22 C and 60% humidity.						
GSE56326	carpels (15 developing inflorescences)	8	Columbia	wt, nga mutant and NGA overexpression	total RNA	stage 8-13	Illumina HiSeq 2000	50
	growth protocol	seed were sow on soil, and plant were grown under long day condition						