Supplementary Table S5. Parameters used for bioinformatic analyses.

Analysis step	Software		Parameters
Read trimming and filtering	Trimmomatic		\-phred 33 LEADING:3 TRAILING:3 SLIDINGWINDOW:4:15 MINLEN:25
Read alignment	HISAT2		default parameters and mate inner distance according to the replicate
Read count	R 4.0.0	GenomicFeatures	makeTxDbFromBiomart(biomart = "plants_mart", dataset = "athaliana_eg_gene", id_prefix = "ensembl_", host = "plants.ensembl.org", taxonomyId = 3702) %>% transcriptsBy("gene")
		GenomicAlignments	summarizeOverlaps with mode = Union, singleEnd = F, ignore.strand = FALSE, fragments = T
Filtering out weakly expressed genes		CustomSeletion	mean(TPM) < mean(DAFS cutoff)
Variation between replicates and samples		DESeq2	plotPCA with ntop = All Arabidopsis genes expressed in samples
Differential expression analysis			estimateSizeFactors with controlGenes; DESeq(betaPrior = T), |log2(Fold change)| ≥ 2 and adjusted pValue ≤ 0.01
GO enrichment		clusterProfiler	enrichGO with universe = All Arabidopsis genes expressed in samples, OrgDb = org.At.tair.db, ont = "BP", keyType = "TAIR", pAdjustMethod = "BH", pvalueCutoff = 0.01, qvalueCutoff = 0.05. readable = TRUE) %>% simplify()
KEGG enrichment		KEGGprofile	find_enriched_pathway with species = "ath" and download_latest = TRUE
Co-expression network analysis		WGCNA	blockwiseModules with log2-transformed TPM values of deregulated genes, power = 14, TOMType = "unsigned", minModuleSize = 30, reassignThreshold = 0, mergeCutHeight = 0.3, numericLabels = TRUE, pamRespectsDendro = FALSE