The nextflow nf-core/chipseq v 2.1.0 pipeline was used to perform raw read QC, adapter trimming, read alignment, duplicate marking, read filtering, and peak calling1–3. R version 4.3.2 was used for downstream analysis4. Specifically, bwa v 0.7.18-r1243-dirty was used to align reads to the reference genome (Arabidopsis thaliana TAIR10 ensembl release 60)5, cutadapt v 3.4 was used to remove contaminating Illumina adaptor sequences and trim low quality bases from the ends of reads6, and the MarkDuplicates tool in picard-tools v 3.2.0-1-g3948afb6b was used to mark duplicate reads7.  Reads with the following criteria were removed:

* reads mapping to the mitochondria and chloroplast genomes
* reads mapping to the `TAIR10.Klasfeld.arabidopsis\_greenscreen\_20inputs.bed` exclusion list, accessed using the *excluderanges* v 0.99.8 R package4,8,9.
* reads that are marked as duplicates
* reads that are not marked as primary alignments
* reads that are unmapped
* reads that map to multiple locations
* reads containing > 4 mismatches
* reads that have an insert size > 2kb
* reads that map to different chromosomes
* reads that aren’t in FR orientation
* reads where only one read of the pair fails the above criteria

MACS3 v 3.0.1with the default parameters was used to call narrow peaks in each replicate of each condition10. Peaks with FDR < 0.05 were used in downstream analyses. The *consensusSeekeR* v 1.30.0 R package was used to identify consensus peaks shared in 2 of 3 replicates per condition with expandToFitPeakRegion = TRUE and

shrinkToFitPeakRegion = TRUE11. Non-overlapping peaks between the consensus peak sets in each condition (condition-specific peaks) were identified using BEDTools v 2.31.012.

*DiffBind* v3.8.4 R package with the default parameters was used to identify peaks differentially bound between each pair of conditions13,14. Specifically, for each pair of conditions, a union peak set was derived that includes peaks present in the consensus peak sets of both conditions. No exclusion list was used to filter out regions; however, a custom greylist built using the inputs for each sample using the *GreyListChIP* v 1.34.0 R package was used15. Differentially bound regions with FDR < .05 were considered for downstream analyses.

annotatePeaks.pl from HOMER v 5.1 was used along with the Arabidopsis thaliana TAIR10 ensembl release 60 annotation file to identify the nearest gene to each peak16.

*topGO* v 2.54.0 with Fisher’s exact test and the gene ontology annotations from the *org.At.tair.db* v 3.18.0 bioconductor annotation package was used to check for enrichment of genes related to specific biological processes, molecular functions, and cellular compartments among genes near ChIP peaks17. Only GO terms with 5 > n genes > 200 were included.

*MEME* and *SEA* from MEME v 5.5.4 were used to discover novel, de novo motifs and find enrichment for known motifs, respectively18,19. Known motifs came from DNA affinity purification sequencing results included with the MEME software package (ArabidopsisDAPv1.meme) and originally reported by O'Malley et al. 20.