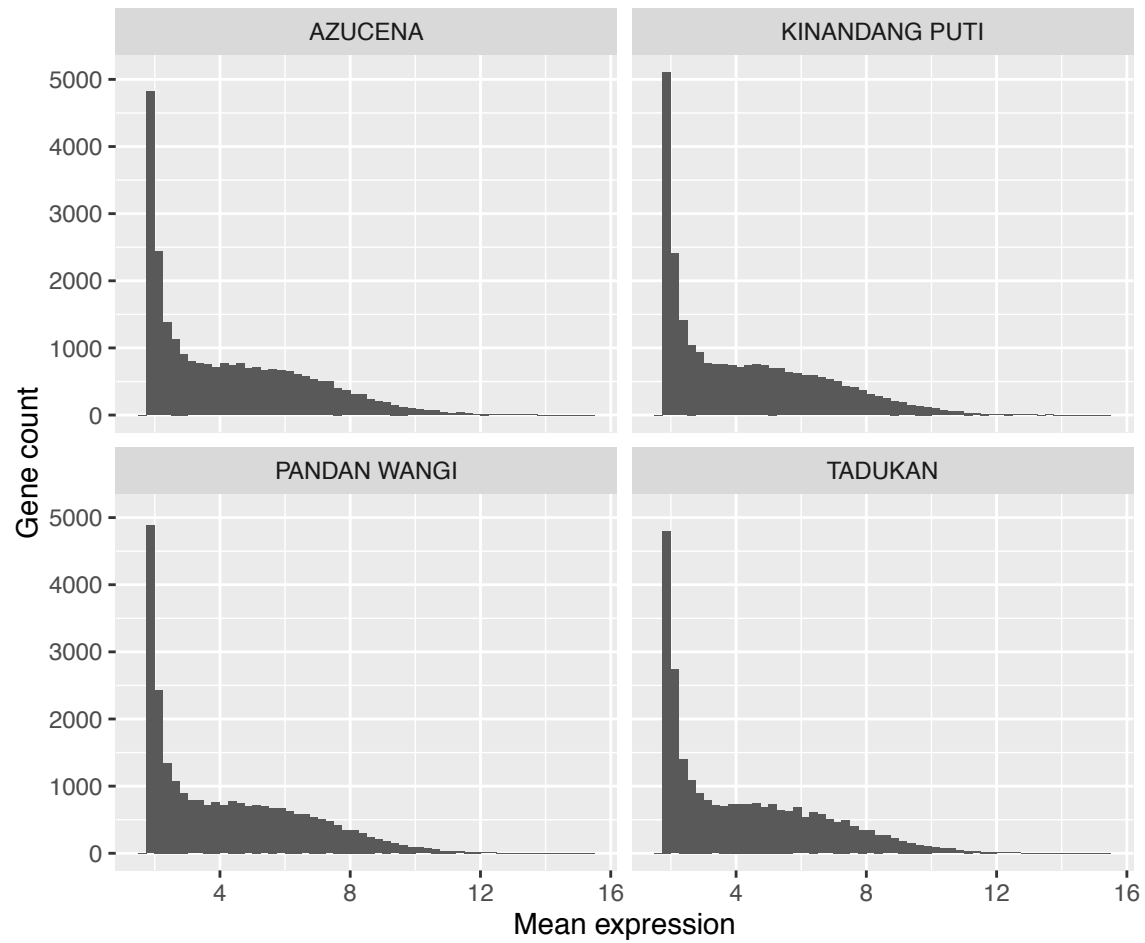
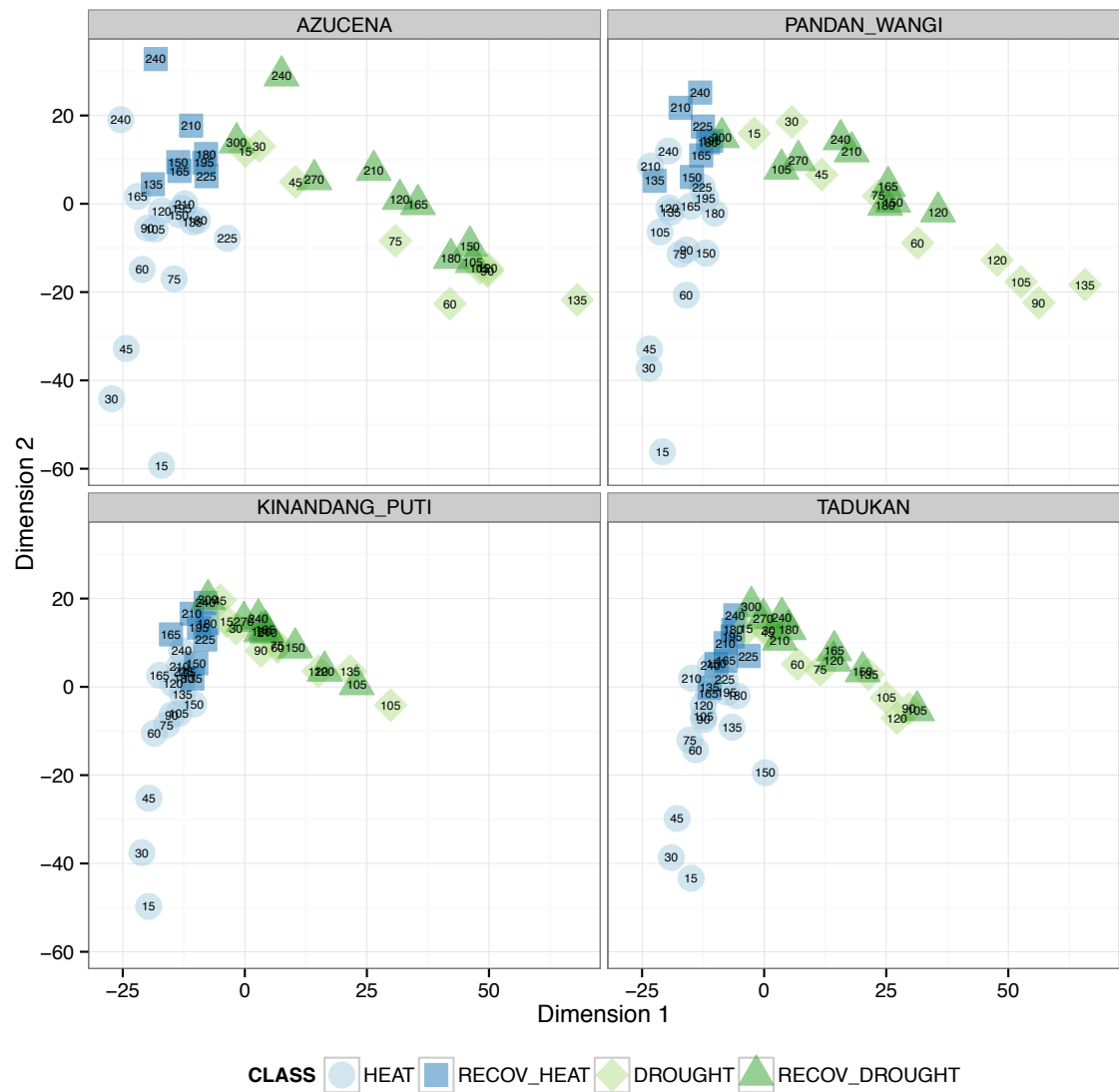


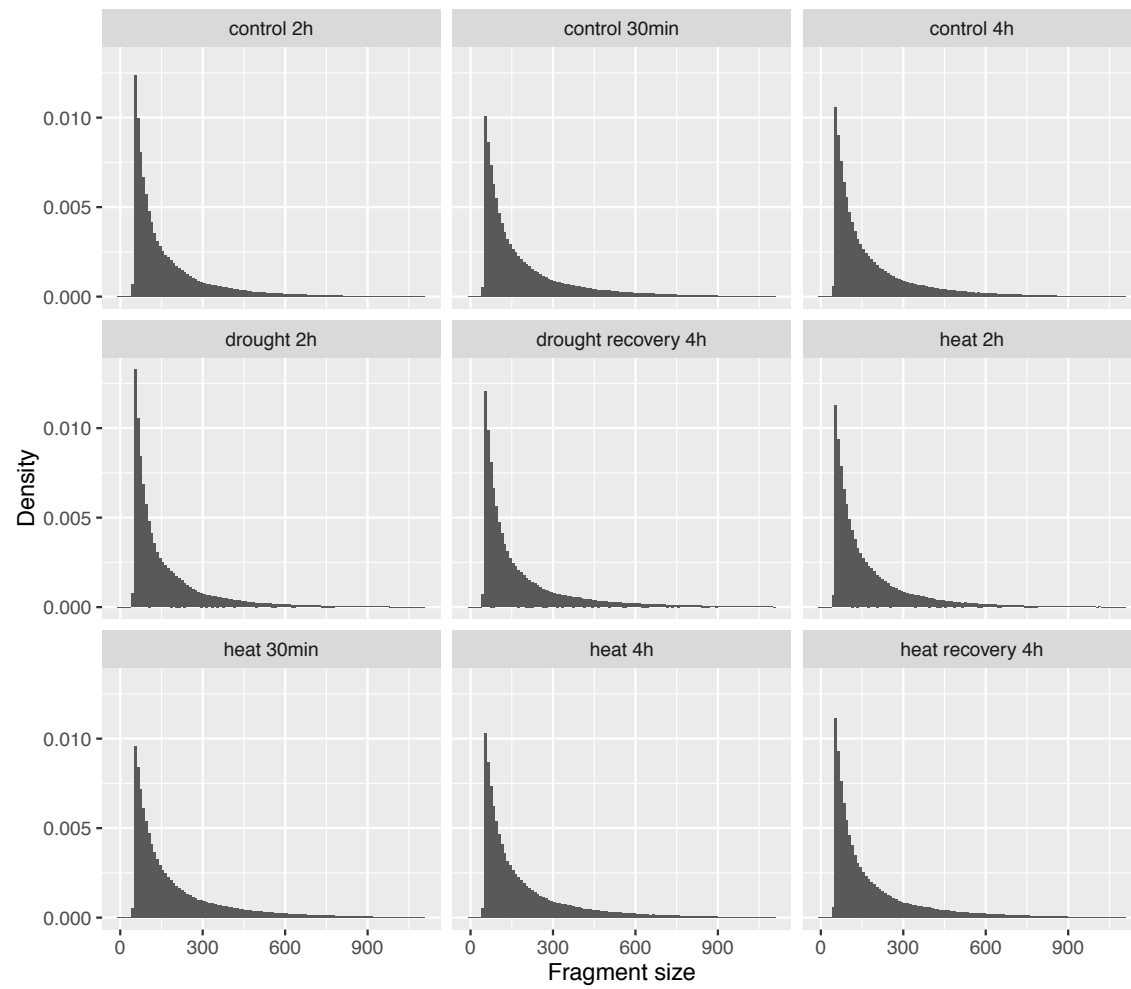
Supplemental Figure 1: Plant functional responses. The relative photosynthetic (A, C, E, G) and gas exchange rates (B, D, F, H) of stress treated plants are presented ($n=3$ for each treatment). The vertical dashed lines indicate the end of stress treatments and the start of the recovery treatments. Water deficit measurements are noted in green; heat stress measurements are noted in blue. A, B Azucena; C, D Kinandang puti; E, F Pandan wangi; G, H Tadukan.



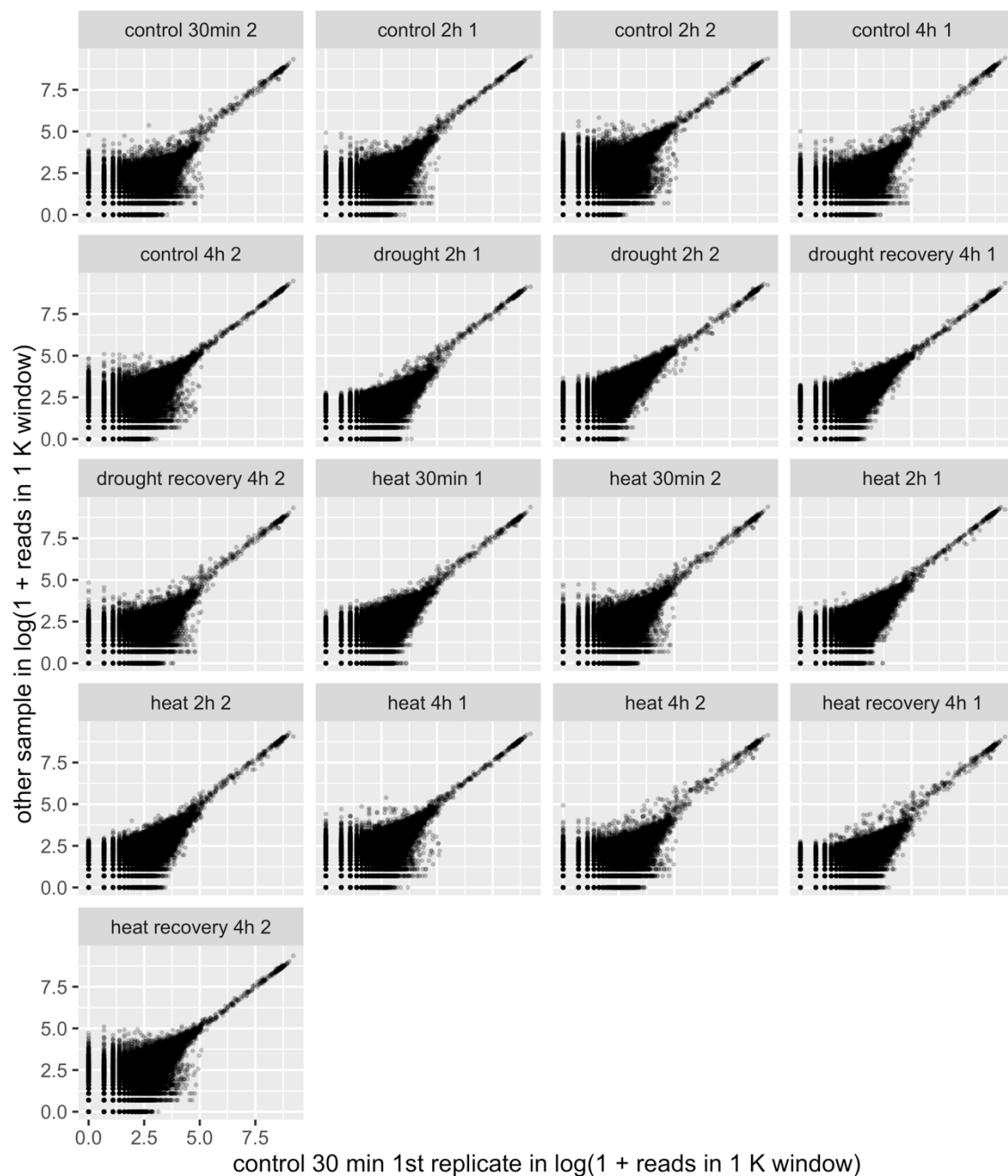
Supplemental Figure 2: Histogram of averaged expression across control conditions.



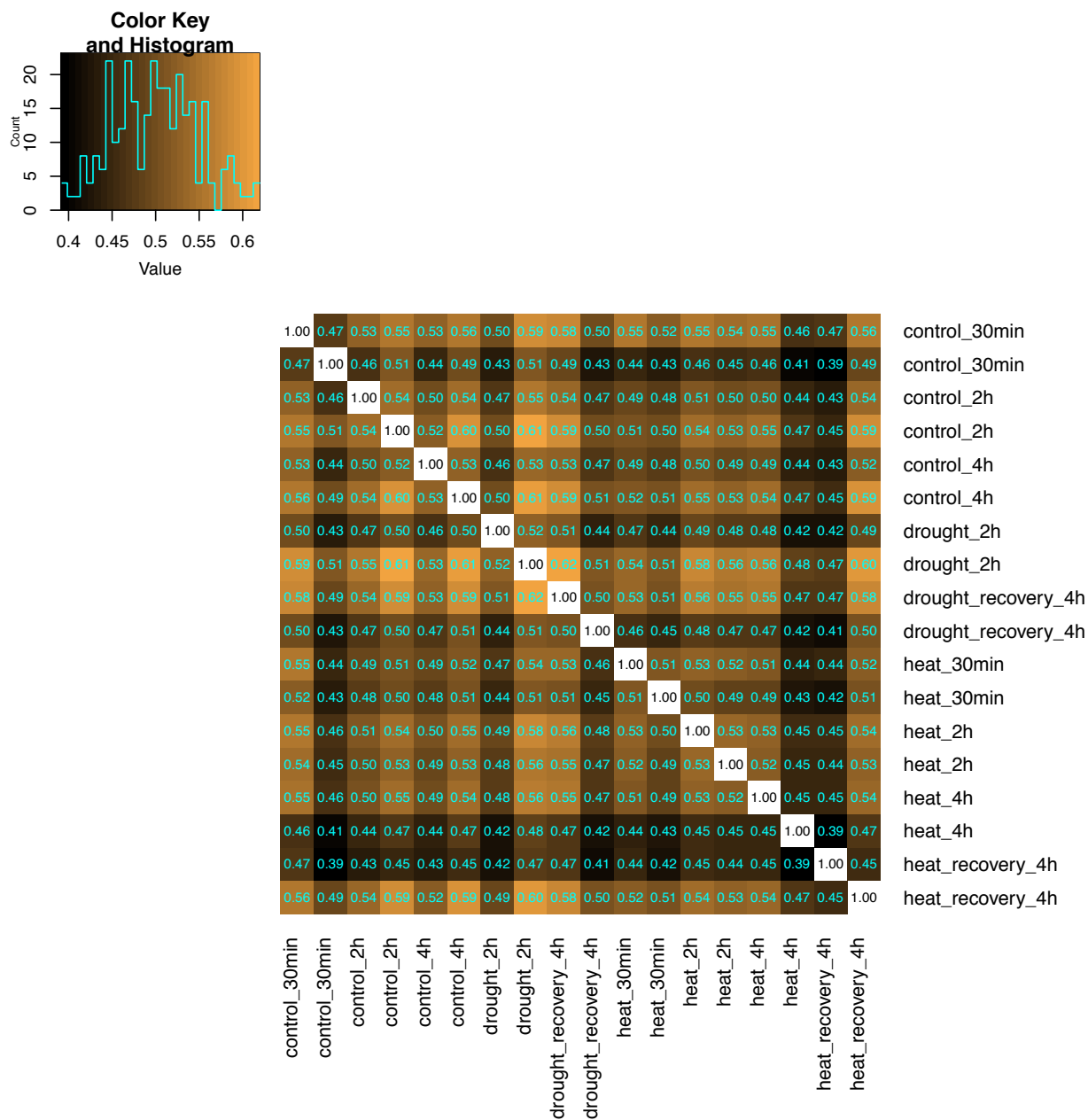
Supplemental Figure 3: Multi-dimensional scaling plot based on Euclidean distance of log-fold-change of 2097 differentially expressed genes are presented. The number inside each data point indicates the time in minutes since the onset of the treatment at which the sample was collected.



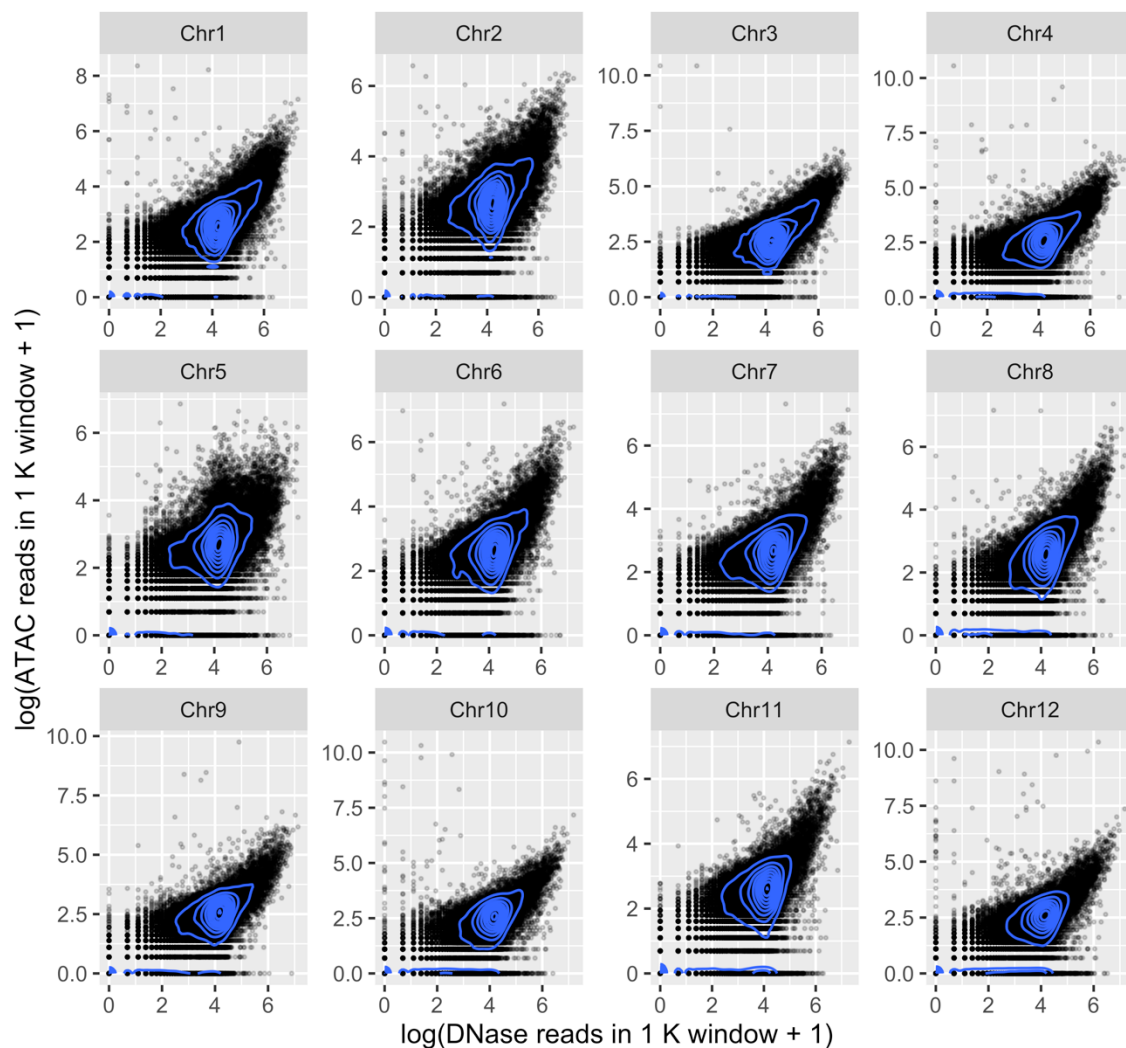
Supplemental Figure 4: Histograms of fragment size of the aligned paired-end ATAC-seq reads. Replicates are combined for the different conditions.



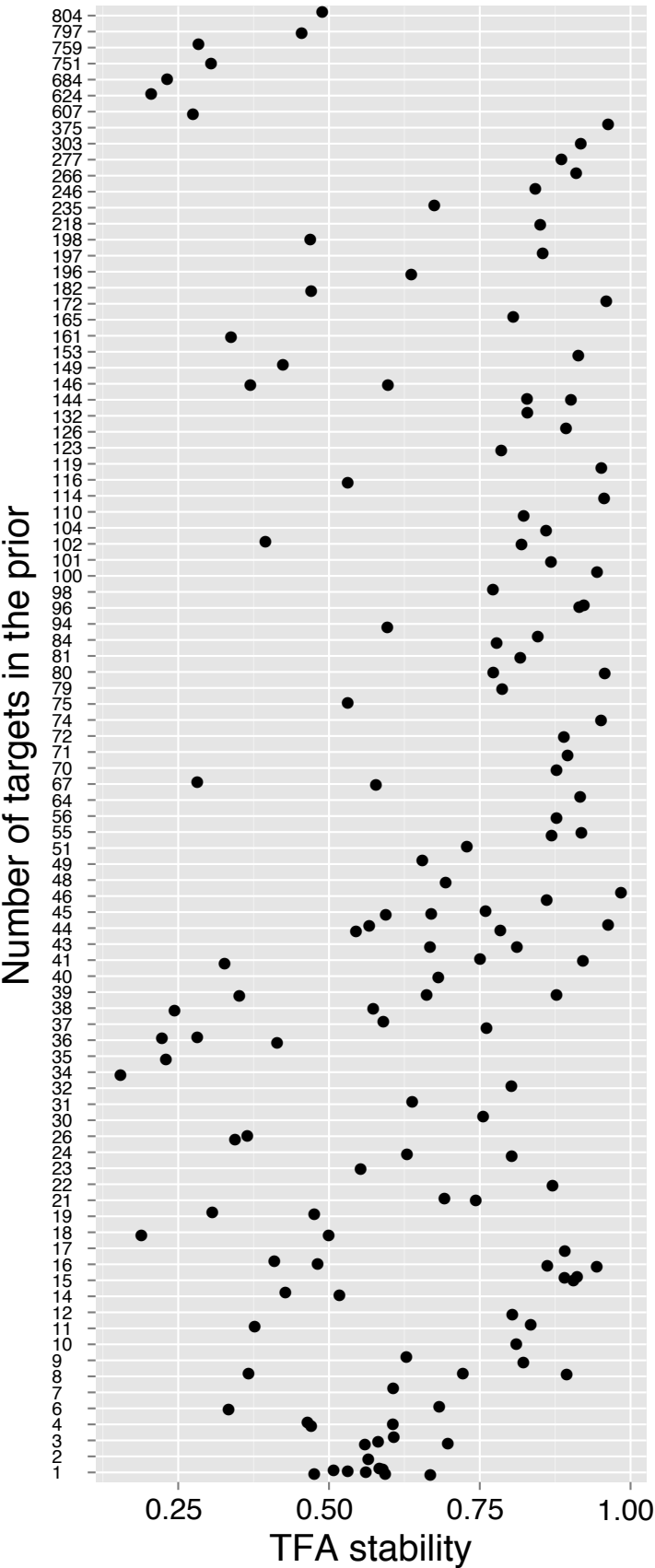
Supplemental Figure 5: ATAC-seq reproducibility across samples. Each point represents a 1K bp window of the genome. Plotted is the log of the number of ATAC-seq reads starting in that window in the first 30 minute control sample (x-axis) and the number of ATAC-seq reads starting in that window in all other samples (y-axis, each sample is one panel).



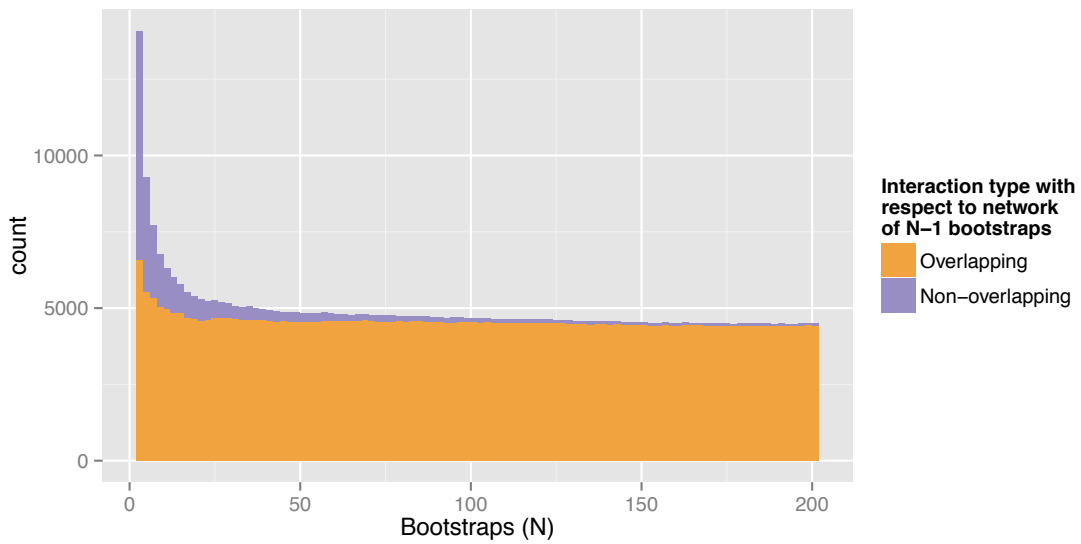
Supplemental Figure 6: Summary of ATAC-seq reproducibility. Heatmap showing the Pearson correlation between all ATAC samples (based on the log of the read counts in non-overlapping 1K windows, see Supplemental Figure 5). This shows that overall replicates are not more alike than any other two samples.



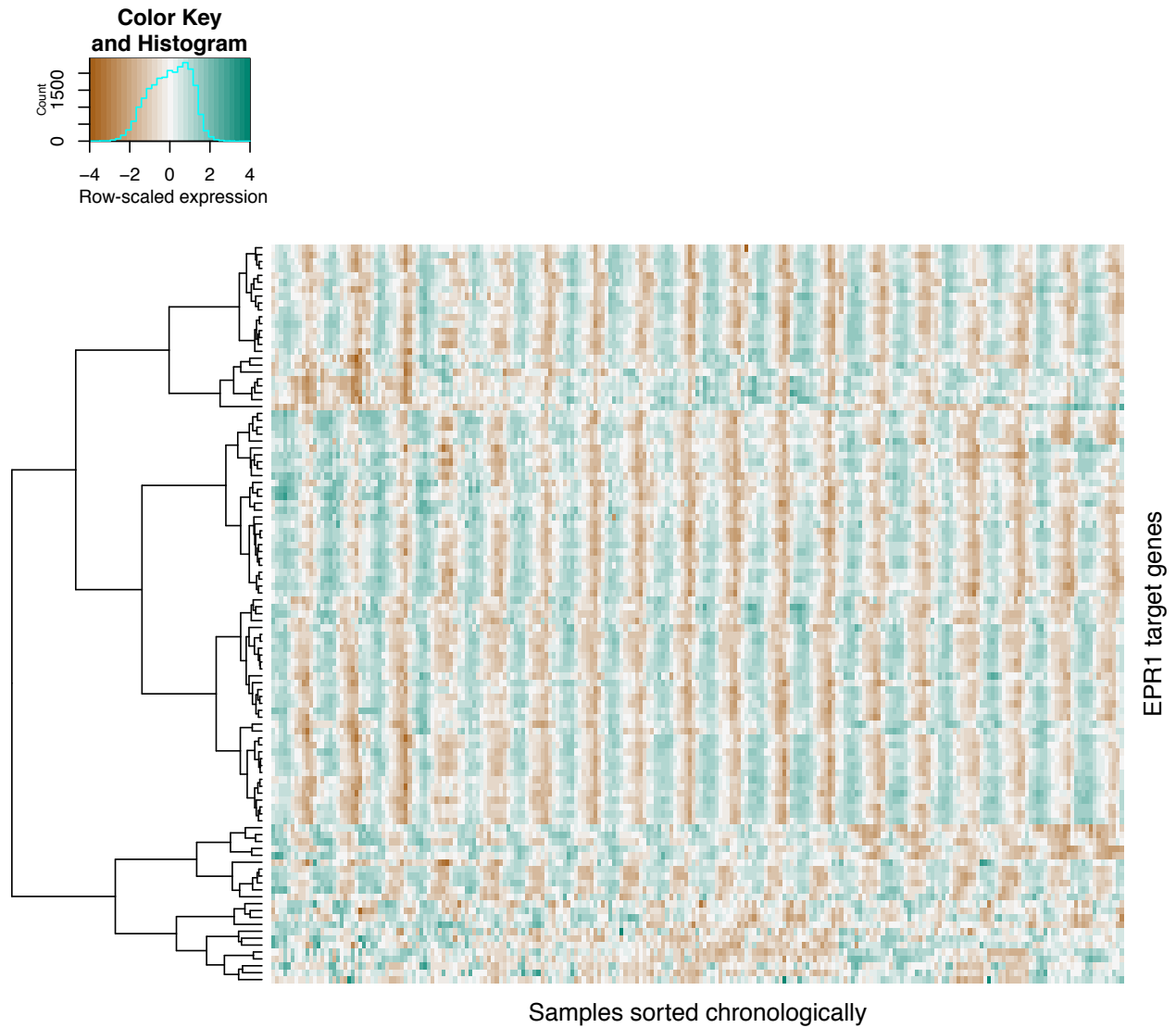
Supplemental Figure 7: Comparison of the chromosome-wide distribution of ATAC and DNase cut sites. Each point represents a 1K bp window of the genome. Plotted is the log of the number of DNase-seq reads starting in that window on the x-axis (GEO Sample GSM655033, union of all three samples) and the number of ATAC-seq reads starting in that window on the y-axis (union of all control samples).



Supplemental Figure 8: Mean TFA stability (quantified as correlation of TFA estimates between 201 bootstrap subsamples of the network prior) for the 143 TFs and TF groups with targets in the network prior.



Supplemental Figure 9: Convergence of network inference. As we do more bootstraps (subsampling from the expression data and also the prior interactions), the inferred network converges to a stable set of interactions. Only around 1% of interactions differ between the solutions obtained using 200 bootstraps and 201 bootstraps.



Supplemental Figure 10: The expression of the targets of EPR1 (LOC_Os06g51260) in the network prior in a circadian data set¹.

1. Nagano, A. J. *et al.* Deciphering and prediction of transcriptome dynamics under fluctuating field conditions. *Cell* **151**, 1358–69 (2012).

Supplemental Data Set Legends:

Supplemental Data Set 1: Differentially expressed genes

All genes that are differentially expressed in at least one experimental condition have a non-zero value in this matrix. The numerical value indicates the number of conditions in which this gene was differentially expressed. For example, LOC_Os01g04360 has a value of 63 in the “Heat_UP” column. This means that this gene was more highly expressed in 63 of the 64 heat stress conditions than in the paired control treatments (64 heat stress conditions = 16 time points X 4 genotypes). Differential expression testing was done using DESeq2 as described in Materials & Methods section. A gene was called differentially expressed in a given condition if the reported adjusted p-value was below 0.0001 and absolute log-fold change larger than 2.

Supplemental Data Set 2: Open chromatin regions

This file in GFF format specifies all genomic regions that were called open using our method.

Supplemental Data Set 3: Sample order for heatmaps and TFA plots

This file lists the samples in the order in which they appear in all heatmaps and TFA plots in the paper.

Supplemental Data Set 4: The network prior

Each row in this matrix defines a regulatory interaction in the network prior. The first value in the row identifies the regulator, either a TF or a TF predictor group, and the second value identifies the target gene.

Supplemental Data Set 5: TF predictor groups

Members of each of the 62 TF predictor groups are described in this file. Each entry includes the TF predictor group name (group.name) and the gene identifiers of the TFs comprising the predictor group (members).

Supplemental Data Set 6: Mean of estimated TF activities

The mean estimated activity of each TF and TF predictor group for each experimental condition is reported in this matrix. Each row in the matrix is a TF or TF predictor group; each column is an experimental condition.

Supplemental Data Set 7: TFA plots

The activity of each TF and TF predictor group is plotted for each experimental condition. The TFA for each regulator was estimated 201 times by using bootstrap subsamples of the network prior. In these plots, the light band shows the region between the 5th and 95th percentile of bootstrap TFAs; the dark line shows the average TFA.

Supplemental Data Set 8: Inferred network

This matrix is the EGRIN. Each row is a regulatory interaction between a TF or TF predictor group and a target gene. The columns in this matrix contain the following data: “regulator” is the TF or TF predictor group, “target” is the regulatory target of the regulator, “variance.explained” is the fraction of target variance that is explained by this regulator, “partial.cor” is the partial correlation of regulator and target, “absolute.partial.cor” is the absolute value of the partial correlation, a value of 1 in the “prior” column indicates that a regulatory interaction was also in the network prior.

Supplemental Data Set 9: Network predictor statistics

This matrix is a summary of the regulatory statistics for all TFs and TF predictor groups in the EGRIN. For each regulator, this table includes the number of targets in the raw network prior (targets.raw.prior), the number of targets in the coherence filtered network prior (targets.prior), the number of targets predicted in the EGRIN (targets.predicted), the number of targets predicted by the EGRIN that were not in the network prior (targets.predicted.novel), the fraction of the targets predicted by the EGRIN that were not in the network prior (targets.predicted.novel.frac), the fraction of targets predicted by the EGRIN that were also in the network prior (targets.predicted.recov.frac), the fraction of the targets in the network prior that were

also predicted in the EGRIN (targets.prior.recov.frac) and, for TF predictor groups, the individual TFs comprising the TF predictor group (member.tfs).

Supplemental Data Set 10: Gene Ontology enrichment results

This table details the GO term enrichment results for each regulator, TF and TF predictor groups, with targets in the EGRIN. For each regulator, all enriched GO terms are reported. Each entry includes information on the Ontology to which the GO term belongs (Ont: BP for Biological Process, CC for Cellular Compartment, MF for Molecular Function), the numerical identifier for the enriched GO term (GOID), the P-value for the enrichment (Pvalue), the enrichment odds ratio (OddsRatio), the expected number of genes in this GO term, given the number of genes in this target group and the background frequency of this term, if this group of genes were not enriched for genes in this GO term (ExpCount), actual number of genes in this GO term (Count), the number of genes in this GO term in the background gene set (Size), and a description of the GO term (Terms).

Supplemental Data Set 11: RNA-seq summary statistics

This table summarizes the RNA-seq experimental data. For each sample, we report, the sample name (lib_ID), the cultivar (CULTIVAR), the type of treatment (CLASS), the number of minutes since the onset of the treatment (MINUTES), the season of the experiment (SEASON), the date of sampling in the field experiment (season.timepoint), the agricultural system in which the plants were grown (field), the number of reads in the library (Reads), the number of bases with a quality score of at least 30 (Q30bases), and the mean quality score of all bases called (MeanQS).