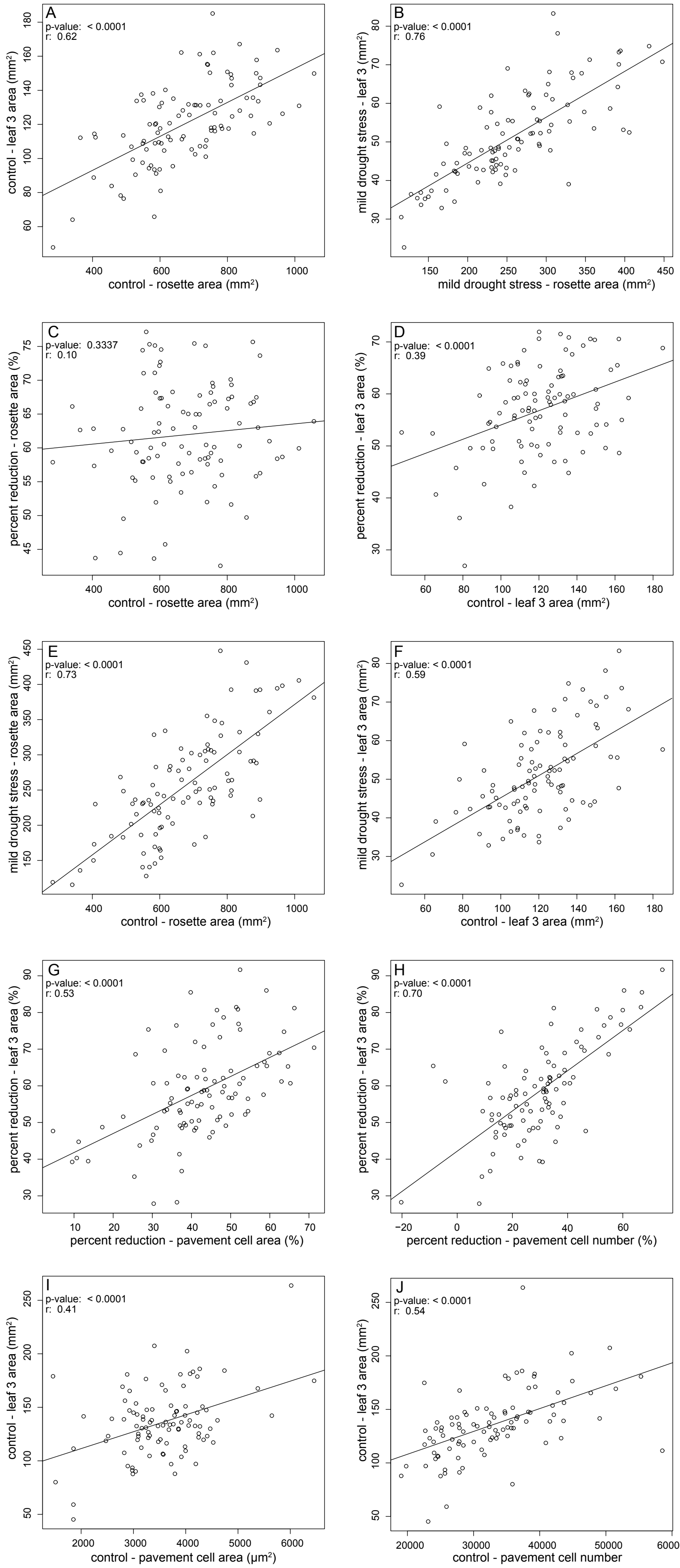

A
p-value: < 0.0001
r: 0.62
control - leaf 3 area (mm²)
60 80 100 120 140 160 180
control - rosette area (mm²)
400 600 800 1000
B
p-value: < 0.0001
r: 0.76
mild drought stress - leaf 3 (mm²)
30 40 50 60 70 80
mild drought stress - rosette area (mm²)
150 200 250 300 350 400 450
C
p-value: 0.3337
r: 0.10
percent reduction - rosette area (%)
45 50 55 60 65 70 75
control - rosette area (mm²)
400 600 800 1000
D
p-value: < 0.0001
r: 0.39
percent reduction - leaf 3 area (%)
30 40 50 60 70
control - leaf 3 area (mm²)
60 80 100 120 140 160 180
E
p-value: < 0.0001
r: 0.73
mild drought stress - rosette area (mm²)
150 200 250 300 350 400 450
control - rosette area (mm²)
400 600 800 1000
F
p-value: < 0.0001
r: 0.59
mild drought stress - leaf 3 area (mm²)
30 40 50 60 70 80
control - leaf 3 area (mm²)
60 80 100 120 140 160 180
G
p-value: < 0.0001
r: 0.53
percent reduction - leaf 3 area (%)
30 40 50 60 70 80 90
percent reduction - pavement cell area (%)
10 20 30 40 50 60 70
H
p-value: < 0.0001
r: 0.70
percent reduction - leaf 3 area (%)
30 40 50 60 70 80 90
percent reduction - pavement cell number (%)
−20 0 20 40 60
I
p-value: < 0.0001
r: 0.41
control - leaf 3 area (mm²)
50 100 150 200 250
control - pavement cell area (µm²)
2000 3000 4000 5000 6000
J
p-value: < 0.0001
r: 0.54
control - leaf 3 area (mm²)
50 100 150 200 250
control - pavement cell number
20000 30000 40000 50000 60000

Supplemental Figure 1. **Correlations between different phenotypic measurements in 98 accessions.**

(A) Rosette area vs. third leaf area, in control conditions.

(B) Rosette area vs. third leaf area, under mild drought stress.

(C) Rosette area in control conditions vs. percent reduction under mild drought stress of rosette area

(D) Third leaf area in control conditions vs. percent reduction under mild drought stress of third leaf area vs..

(E) Rosette area in control conditions vs. mild drought.

(F) Third leaf area in control conditions vs. mild drought.

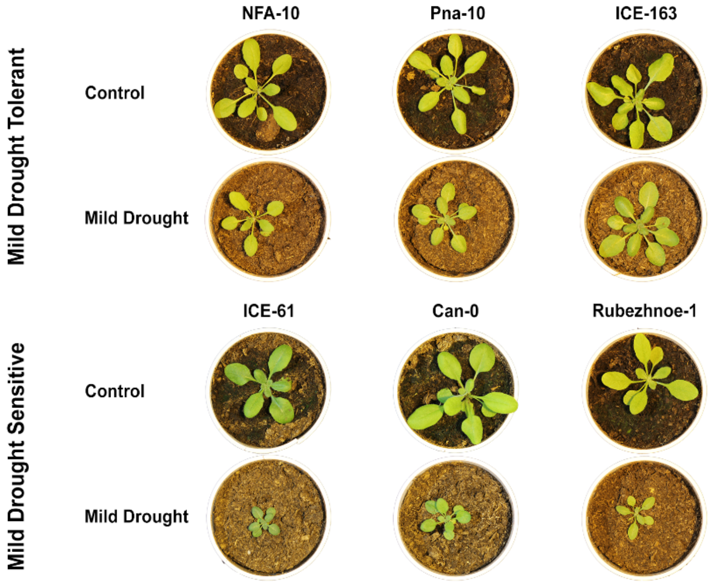
(G) Percent reduction of pavement cell area vs. percent reduction of third leaf area.

(H) Percent reduction of pavement cell number vs. percent reduction of third leaf area.

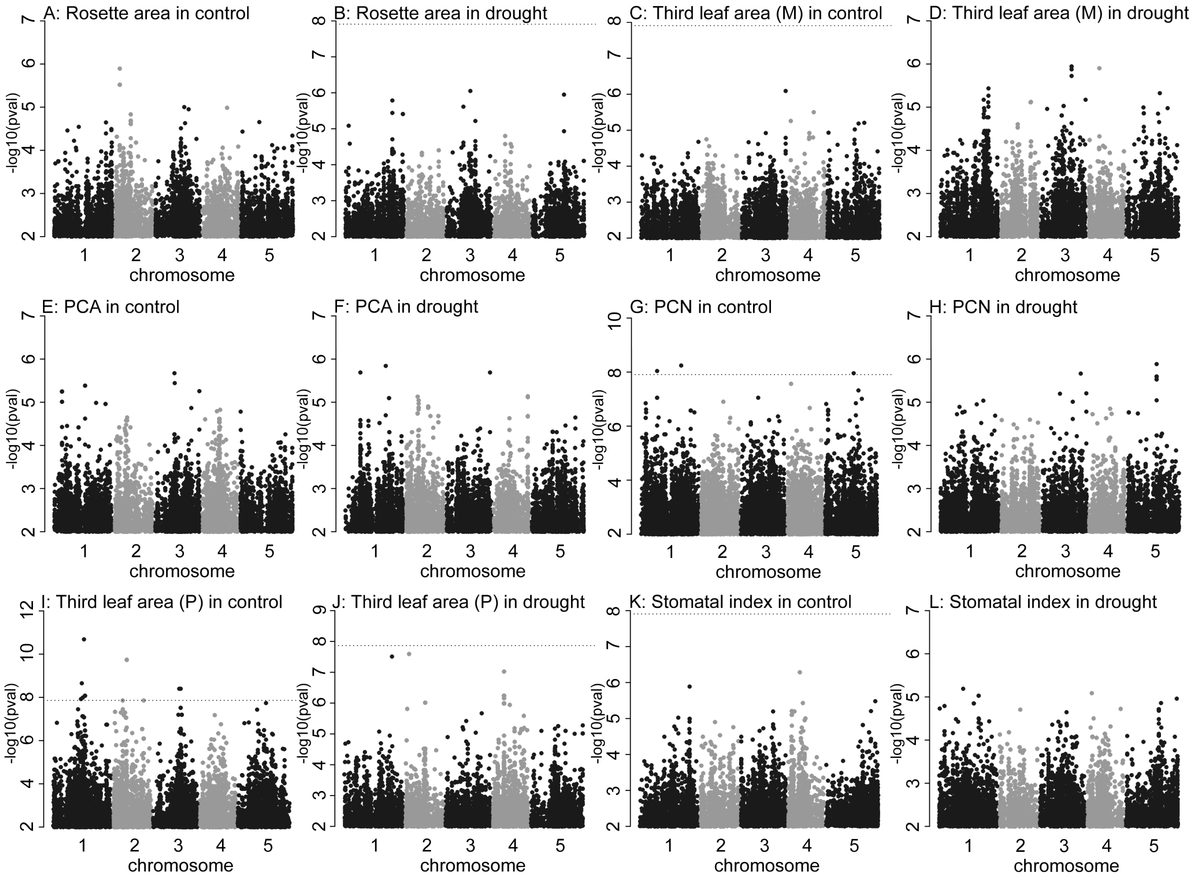
(I) Pavement cell area vs. third leaf area, both in control conditions.

(J) Pavement cell number vs. third leaf area, both in control conditions.

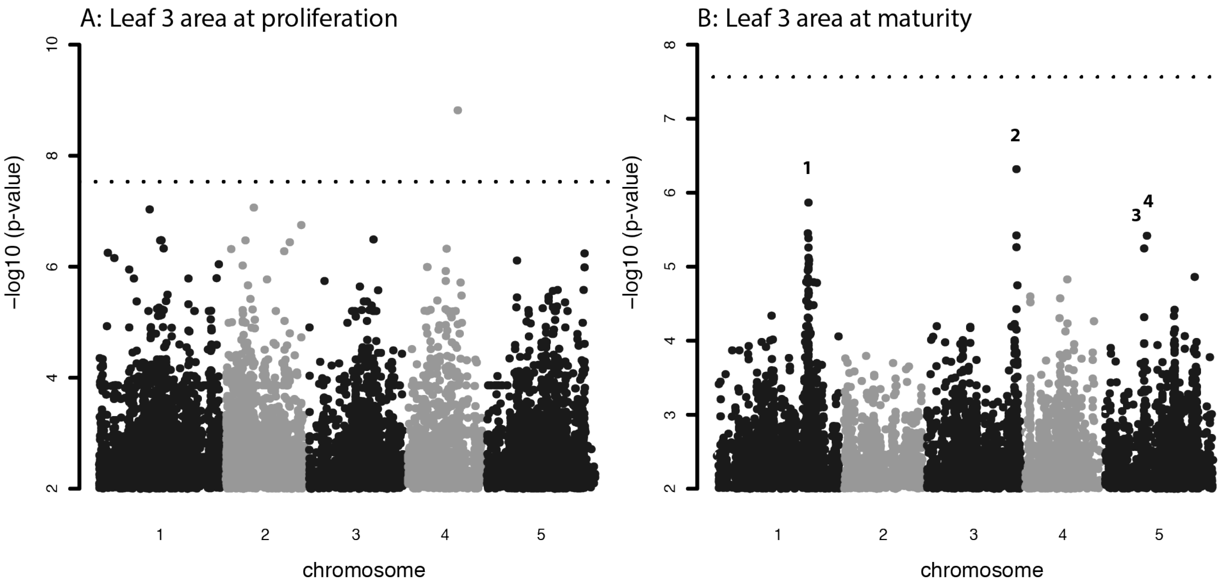
Percent reductions correspond to the reductions under mild drought stress, relative to the control conditions. *P*-values (*t*-test) give the significance of the correlations, r is the Pearson correlation coefficient.



Supplemental Figure 2. Rosette Images of Mild Drought Tolerant and Sensitive Accessions. Photographs from the WIWAMxy platform showing the rosettes of the most tolerant (NFA-10, Pna-10 and ICE-163) and the most sensitive (ICE-61, Can-0 and Rubezhnoe-1) accessions, both in control and mild drought conditions RRat 22 DAS.



Supplemental Figure 3. Manhattan Plots for Each of the Single-Trait GWAS. Rosette area in control (A), rosette area in drought (B), third leaf area at maturity in control (C), third leaf area at maturity in drought (D), pavement cell area in control (E), pavement cell area in drought (F), pavement cell number in control (G), pavement cell number in drought (H), third leaf area at proliferation in control (I), third leaf area at proliferation in drought (J), stomatal index in control (K), stomatal index in drought (L). M: Maturity; PCA:Pavement cell area; PCN: Pavement cell number; P: Proliferation.

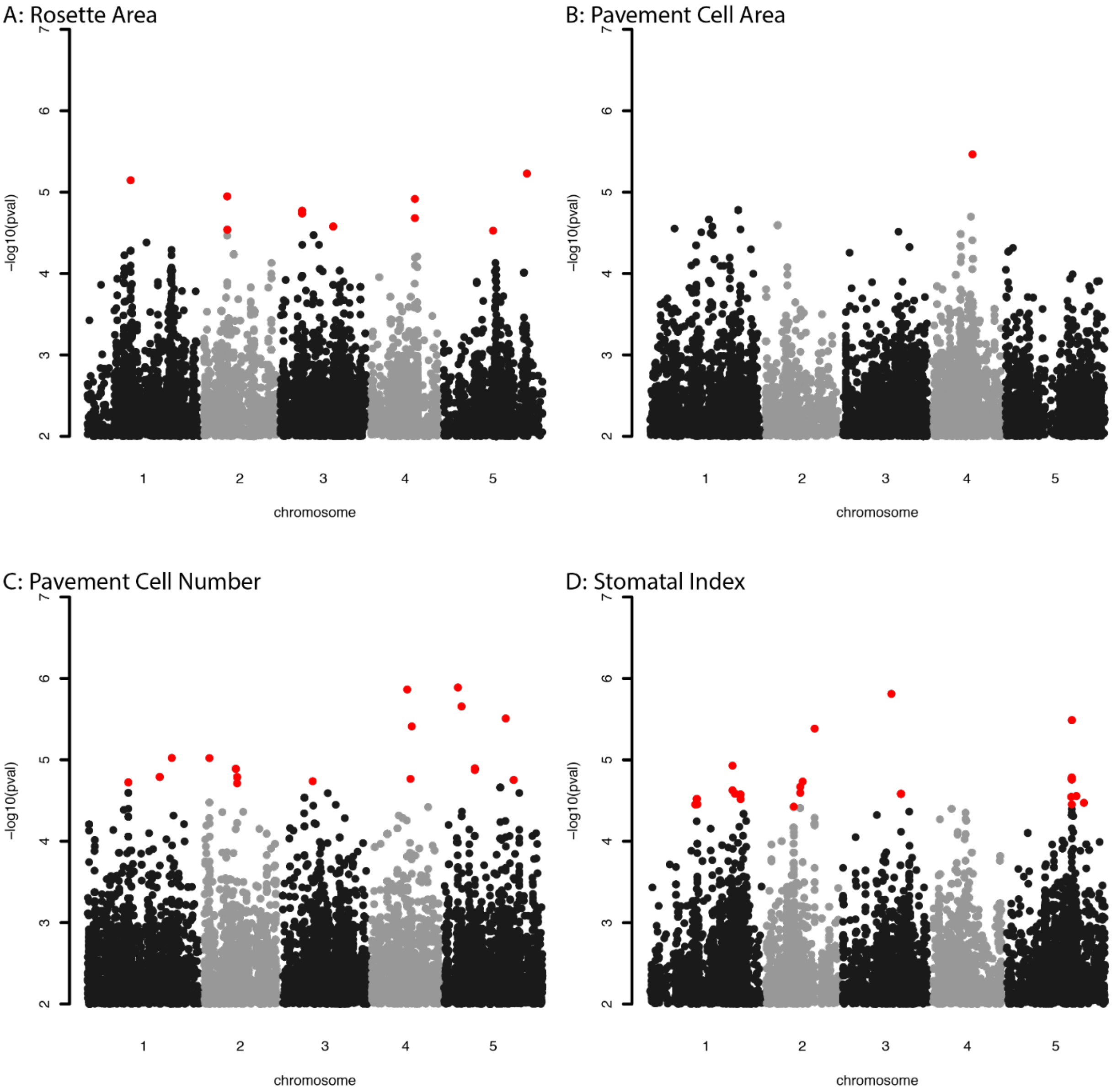


Supplemental Figure 4. Manhattan Plots Showing Significance of the Association of Each SNP with the Studied Phenotype.

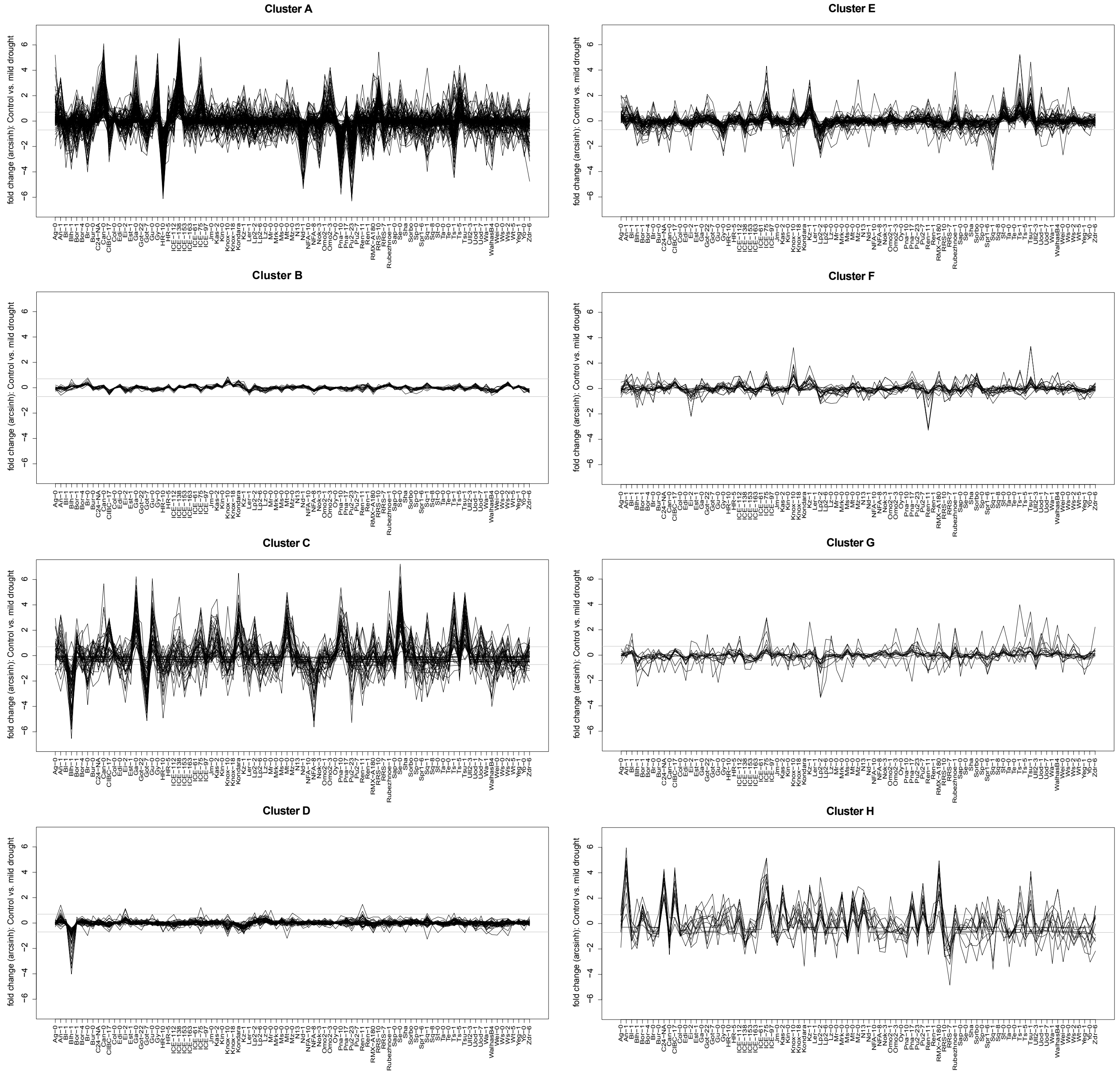
(A) Association of SNPs with the differential response of the third leaf area at proliferation to mild drought stress.

(B) Association of SNPs with the differential response of the third leaf area at maturity to mild drought stress.

Numbers indicate the peaks for which the genes were selected for identification (Supplemental Table 1). The dotted lines indicate the significance threshold (0.05) after Bonferroni correction.

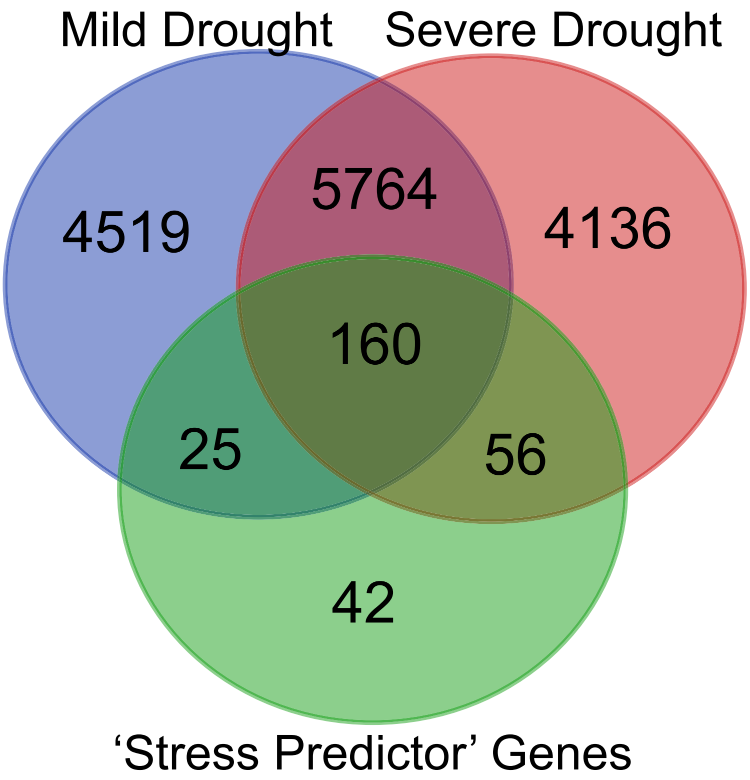


Supplemental Figure 5. Manhattan Plots Showing Chosen SNPs (Red) for Gene Selection. Association of SNPs with differential response to mild drought of rosette area **(A)**, pavement cell area **(B)**, pavement cell number **(C)** and stomatal index **(D)**. Genes underlying the SNPs indicated in red can be found in Supplemental Table 2. Significance thresholds were outside the range of the plots.

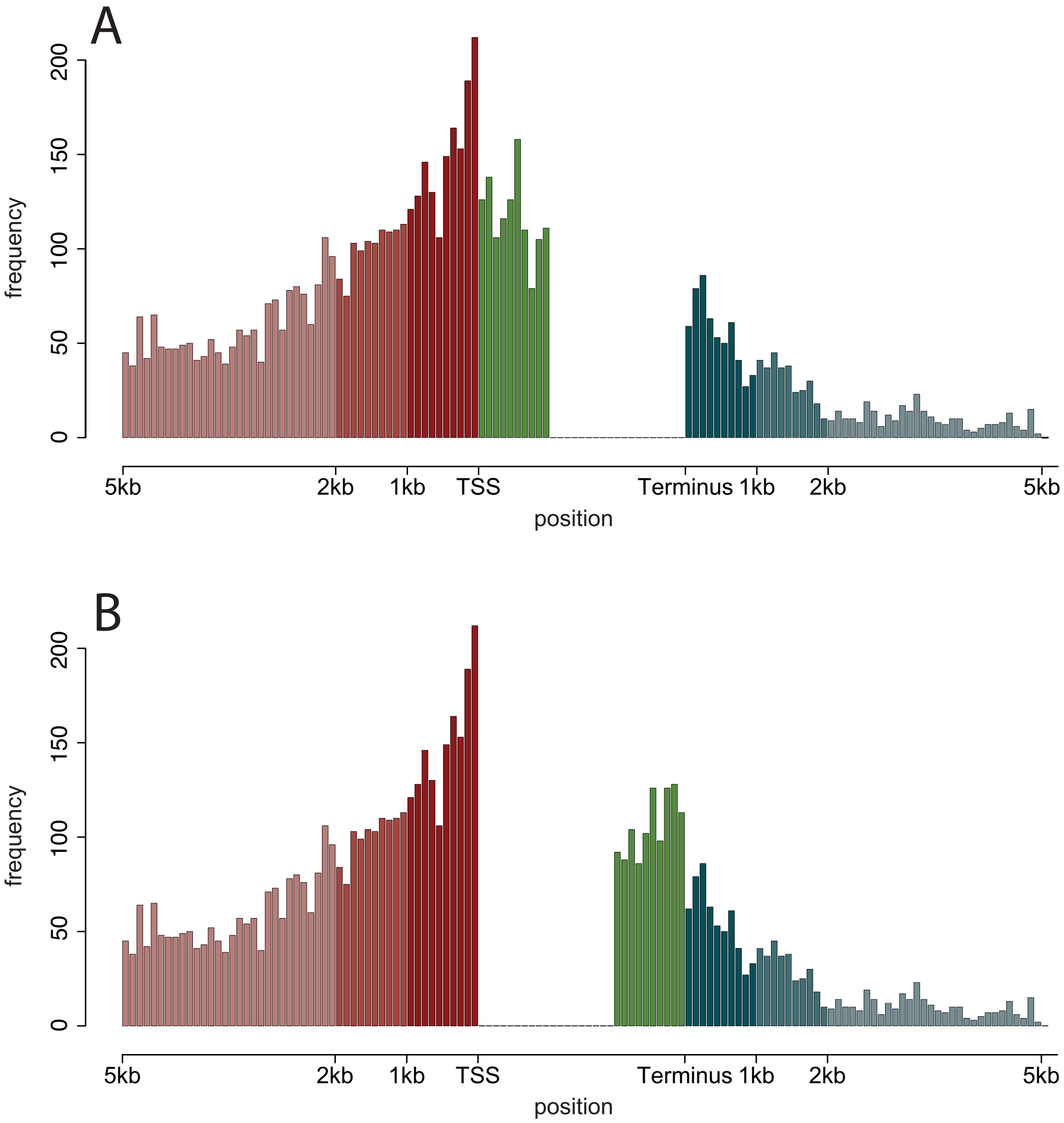


Supplemental Figure 6. Differential Expression Profile of Co-Expression Clusters A-H.

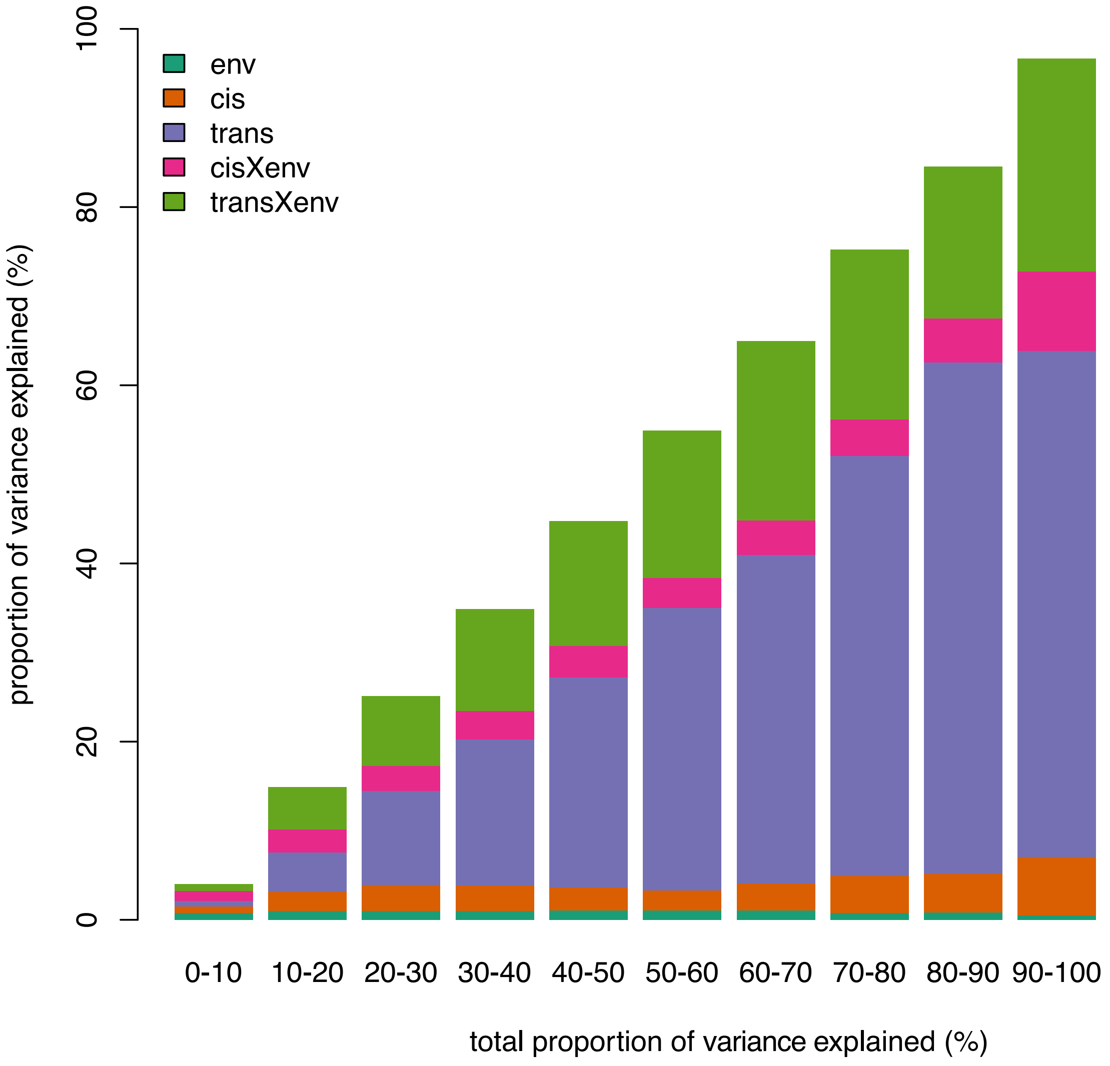
Each line represents the expression profile of a gene from the different co-expression clusters, visualizing the co-expression of the genes within each cluster over all accessions. Gray lines indicate a twofold expression difference (0.7 arcsinh-transformed difference).



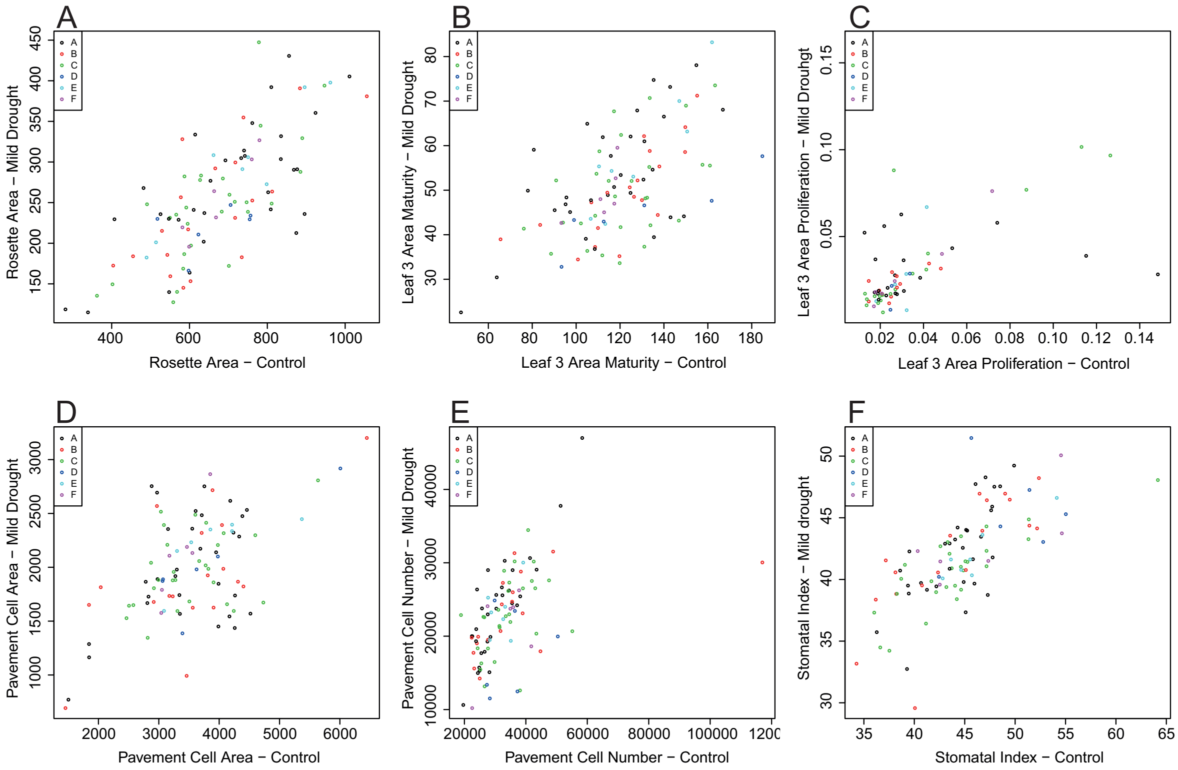
Supplemental Figure 7. Venn Diagram Showing the Overlap between 'Stress Predictor' Genes and Differentially Expressed Genes in Mature Leaf Tissue upon Mild Drought Treatments (Baerenfaller et al., 2012; Harb et al., 2010; Des Marais et al., 2012) and Severe Drought (Huang et al., 2008; Matsui et al., 2008; Harb et al., 2010).



Supplemental Figure 8. Histogram of Locations of SNPs Associated with Treatment-Independent Expression. The transcription start site (TSS) and stop site (Terminus) are the UTR boundaries as determined by the Arabidopsis genome annotation (TAIR10; www.arabidopsis.org). Indicated in red are the associated SNPs located upstream of the TSS; the 1 kb, 2 kb and SNPs further upstream are colored in different shades of red. In blue are the associated SNPs downstream of the transcription stop site; different shades of blue indicate the different distances downstream of the transcription stop site (1 kb, 2 kb and further). In green are the associated SNPs located in the gene itself, with the distribution for the absolute SNP positions for the first 1000 bp (A) and the last 1000 bp (B) of each gene. Number of SNPs are raw SNP counts; bin size is 100 bp.



Supplemental Figure 9. Variance Component Analysis of Gene Expression. For each gene, a mixed model with environment, *cis*, *trans*, *cis* × environment and *trans* × environment was fitted. Genes were binned by the total variance explained by the model (x-axis).



Supplemental Figure 10. Phenotypic measurements with batches indicated. Control versus mild drought conditions for rosette area (A), third leaf area at maturity (B), third leaf area at proliferation (C), pavement cell area (D), pavement cell number (E) and stomatal index (F). Each dot represents the normalized estimate for one accession. Coloring indicates the batch in which each of the accessions was grown, showing no visual clustering.

Supplemental Table 1. Heritability Estimates for Single-Trait GWAS. Overview of the heritability estimates from the single-trait mixed model, for the different phenotypes in control and mild drought conditions. M: at maturity, P: at proliferation.

Phenotype	Heritability - Control	Heritability - Mild Drought
Rosette Area	0.45	0.99
Third Leaf Area M	0.76	0.39
Third Leaf Area P	0.13	0.59
Pavement Cell Area	0.86	0.99
Pavement Cell Number	0.99	0.75
Stomatal Index	0.47	0.72

Supplemental Table 2. Variance Explained by Single SNPs. Overview of the estimated phenotypic variance that is explained by the most significant SNP of each phenotype. MAF indicates the minor allele frequency. P-values indicate significance of association from the multi-trait mixed model.

Treatment	Phenotype	SNP	MAF	*P*-value	Variance Explained
Control	Rosette Area	2-2262889	0.11	1.28E-06	0.235
	Third Leaf Area M	3-22790470	0.16	8.19E-07	0.243
	Third Leaf Area P	1-16121421	0.06	2.06E-11	0.496
	Pavement Cell Area	3-9987904	0.19	2.11E-06	0.229
	Pavement Cell Number	1-21152058	0.06	5.56E-09	0.325
	Stomatal Index	4-6076495	0.26	5.21E-07	0.253
Mild Drought	Rosette Area	3-12336063	0.05	8.88E-07	0.241
	Third Leaf Area M	3-15896623	0.12	1.13E-06	0.237
	Third Leaf Area P	2-1930182	0.06	2.50E-08	0.373
	Pavement Cell Area	1-20926477	0.27	1.43E-06	0.238
	Pavement Cell Number	5-15245301	0.07	1.31E-06	0.240
	Stomatal Index	1-12570340	0.12	6.51E-06	0.212

Supplemental Table 3. Genes Underlying the Peaks (1-4) of SNPs Associated with the Response to Mild Drought of the Third Leaf Area at Maturity.

Peak	Gene	Gene Function
1	AT1G61260	Unknown
1	AT1G61270	Transmembrane amino acid transporter family protein
1	AT1G61275	U12 small nucleolar RNA (U12)
1	AT1G61280	Phosphatidylinositol N-acetylglucosaminyltransferase,
1	AT1G61290	SYNTAXIN OF PLANTS 124 (SYP124)
1	AT1G61300	LRR and NB-ARC domains-containing disease resistance protein
1	AT1G61667	Unknown
1	AT1G61670	Lung seven transmembrane receptor family protein
1	AT1G61680	TERPENE SYNTHASE 14 (TPS14)
1	AT1G61688	Defensin-like (DEFL) family protein
1	AT1G61690	Phosphoinositide binding
1	AT1G61700	RNA polymerases N / 8 kDa subunit
1	AT1G62020	Coatomer, alpha subunit
1	AT1G62030	Cysteine/Histidine-rich C1 domain family protein
1	AT1G62035	MicroRNA171C (MIR171c)
1	AT1G62040	Autophagy 8c (ATG8C)
1	AT1G62045	BEST Arabidopsis thaliana protein match is: ankyrin repeat family protein
1	AT1G62050	Ankyrin repeat family protein
2	AT3G60150	Unknown
2	AT3G60160	ATP-binding cassette C9 (ABCC9), multidrug resistance-associated protein 9 (MRP9)
2	AT3G60176	Other RNA
2	AT3G60180	P-loop containing nucleoside triphosphate hydrolases superfamily protein

Peak	Gene	Gene Function
2	AT3G60190	ARABIDOPSIS DYNAMIN-LIKE 4 (ADL4), ENHANCED DISEASE RESISTANCE 3 (EDR3)
2	AT3G60200	Unknown
2	AT3G60210	GroES-like family protein
3	AT5G27600	LONG-CHAIN ACYL-COA SYNTHETASE 7 (LACS7)
3	AT5G27606	Unknown
3	AT5G27610	ALWAYS EARLY 1 (ALY1)
4	AT5G28500	Unknown
4	AT5G28510	BETA GLUCOSIDASE 24 (BGLU24)