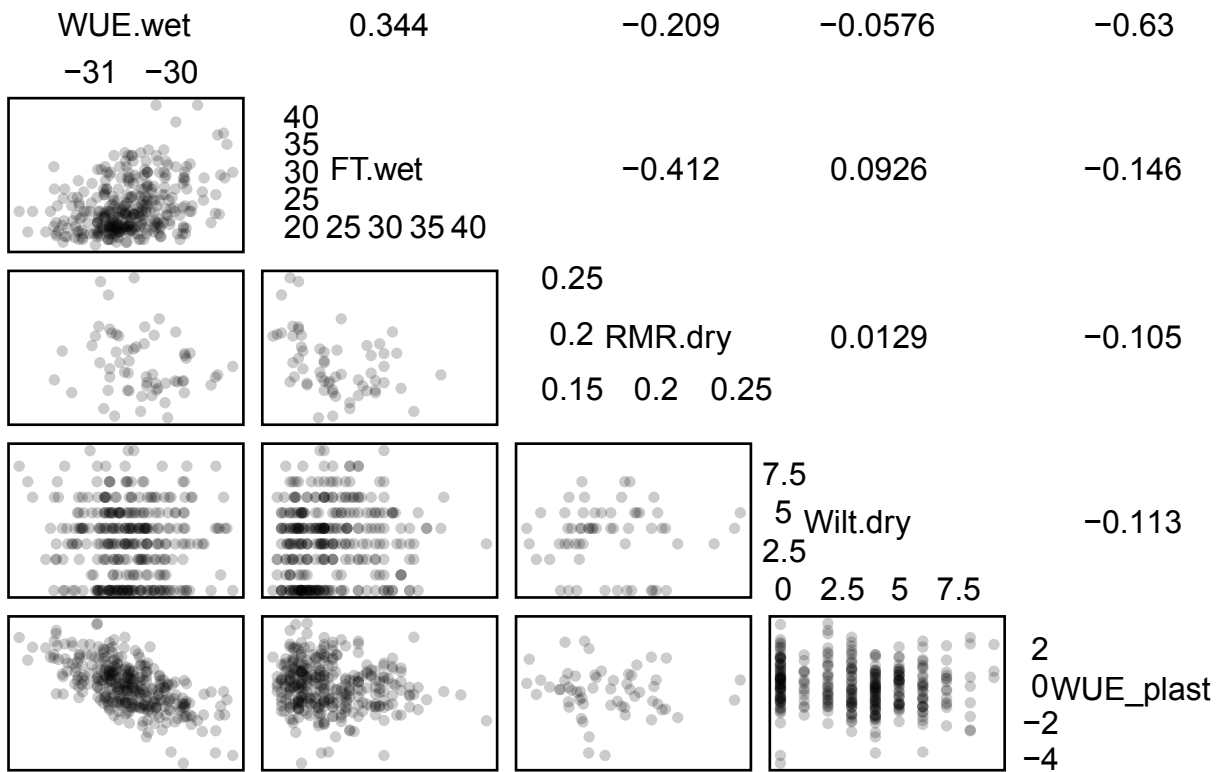
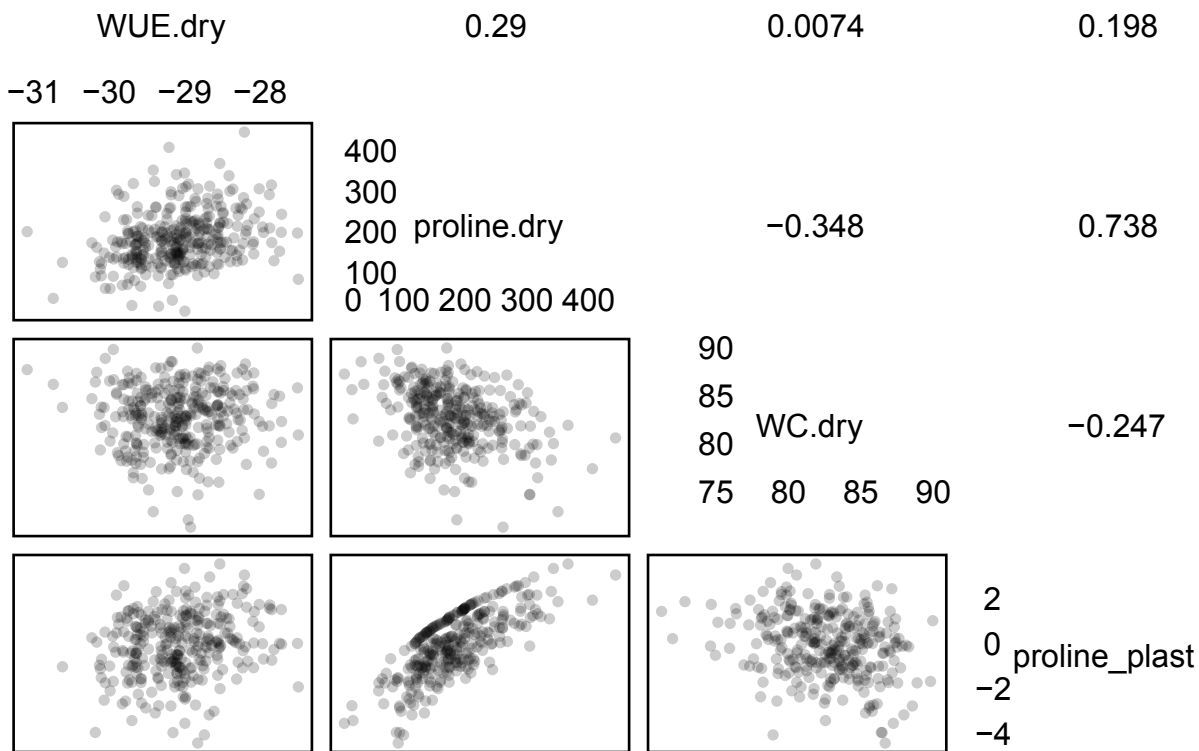


Supplemental Figure 1. Visualization of the concept of the covariate scan approach. A phenotype was simulated within a simulated map so that a QTL with an effect size of 1 would be found at 45cM on Chr 1. A one-QTL scan was performed using no covariates (green line) and several simulated covariates. The covariates were generated so that the normal distribution, sample size, mean and standard deviation of the simulated phenotype data were maintained. The random covariates (grey lines) were 100 sets of permuted vectors of the simulated phenotype data. A correlated covariate (red line) value was generated for each RIL by making a draw from a distribution around the RIL phenotype value with a standard deviation of the entire RIL population. The residual covariate (blue line) was generated in an identical manner to the correlated covariate, except that the RIL phenotypic value was replaced with its residual from the original QTL model.

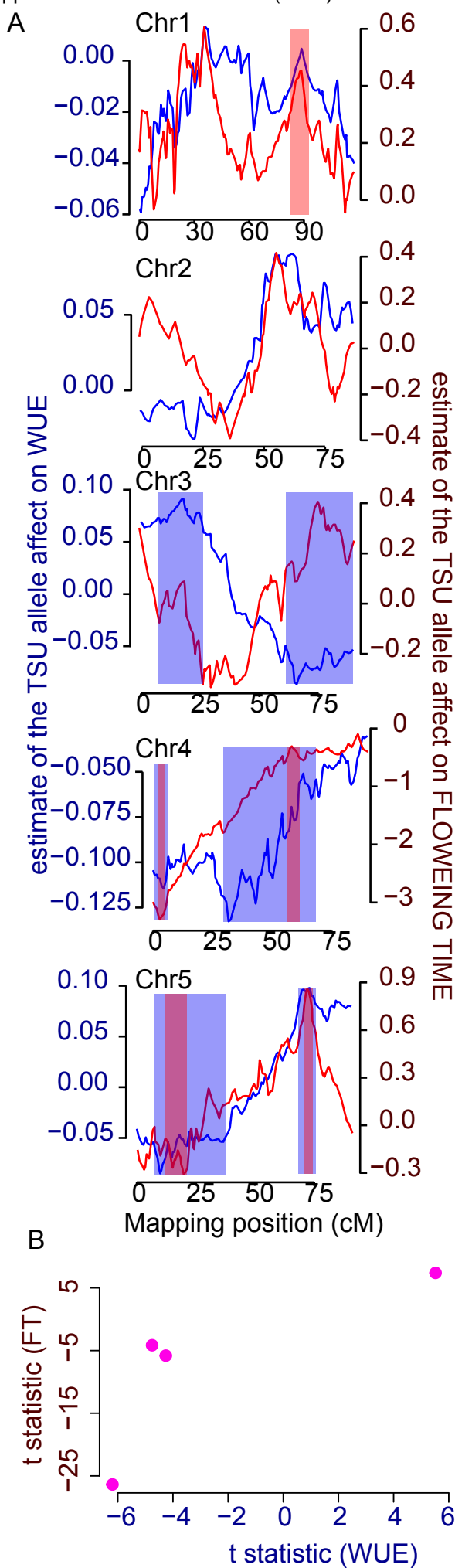
A correlation of phenotypes with QTL near 4@4



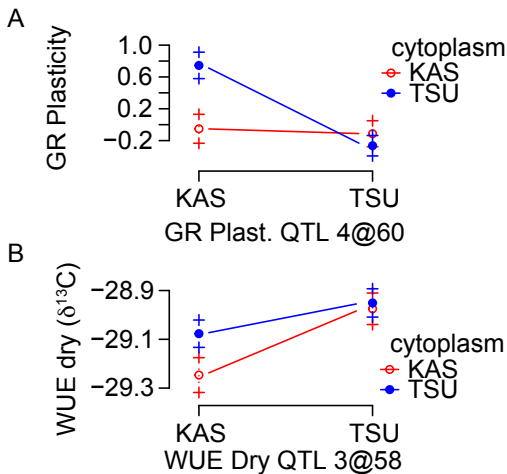
B correlation of phenotypes with QTL near 2@74



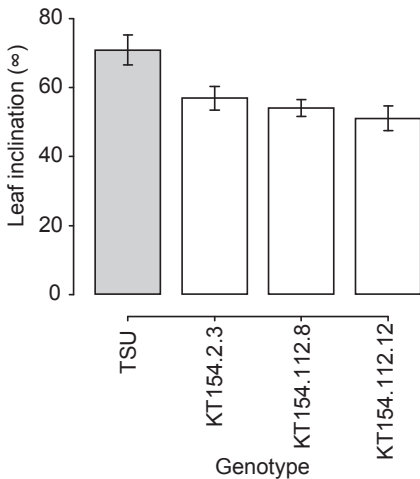
Supplemental Figure 2. Correlation of phenotypes with colocalized QTL on proximate Chr4 (A) and distal Chr2 (B). Pearson's correlation coefficients (r) are printed in the upper diagonal of each matrix.



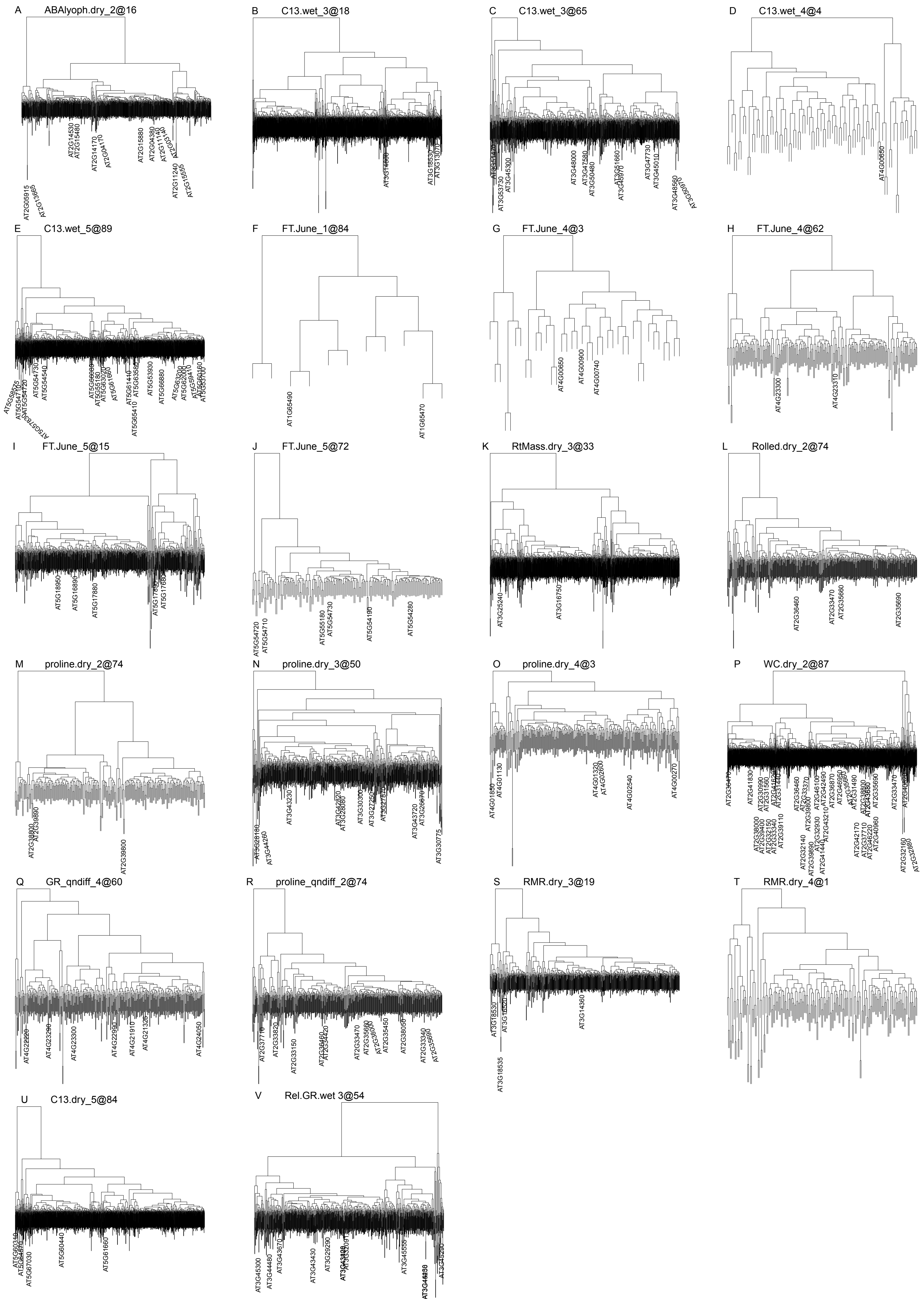
Supplemental Figure 3. Effect of allelic variation on the correlation between WUE and FT. Allelic effects at each marker for WUE (blue) and FT (red) are plotted as solid lines and are standardized by the maximum values for each trait and chromosome (A). The QTL confidence intervals are shaded with the respective colors. The four pleiotropic QTLs (for both WUE and FT) promoted a positive correlation between WUE and FT (B).



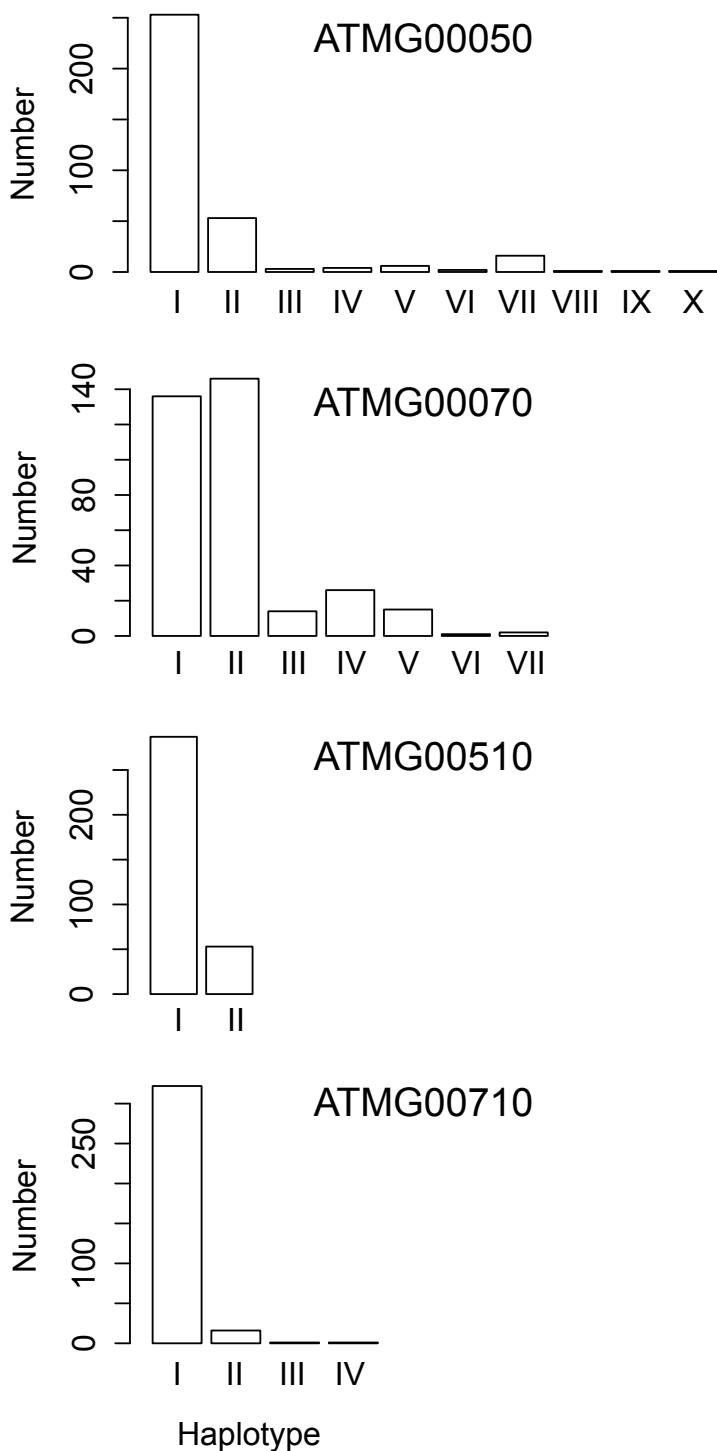
Supplemental Figure 4. Cytoplasmic interactions with genomic QTLs. Data are presented for two significant QTLs for growth rate plasticity (A) and WUE in the dry environment (B). Allelic means \pm SE are reported.



Supplemental Figure 5. Validation of the allelic effect of *CSA1* using NILs. Leaf inclination of four genotypes- the NILs have KAS alleles at FT QTL 5@15, but TSU alleles elsewhere. Leaf inclination was measured in ImageJ. Means +/- SE are reported.

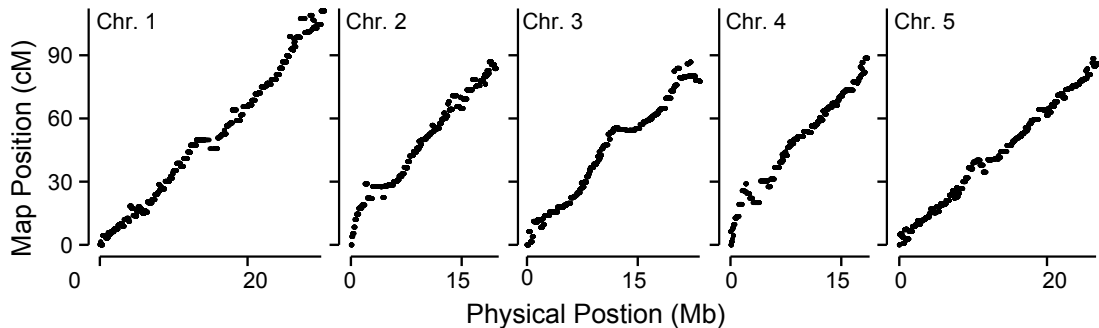


Supplemental Figure 6. Hierarchical clustering of the covariance of all genes within each narrow QTL interval. Tip labels indicate the names of significant candidate genes. Empty tips signify genes that were not significant candidates. Gene labels that overlapped are distinguished by the positioning of the right-most overlapping gene at an angle to the left label.



Supplemental Figure 7. Haplotype diversity of the four genes that contained SNPs in the mitochondrial genome. The total membership of each haplotype is represented by vertical bars, $n = 340$. The 340 mitochondrial gene sequences for each of the four genes were downloaded from the 1001 genomes project.

Supplemental Data. Lovell et al. (2015). Plant Cell 10.1105/tpc.15.00122



Supplemental Figure 8. Comparison of the physical position (bp) for all TAIR10 gene models with the mapping position in cM.

Supplemental Data. Lovell et al. (2015). Plant Cell 10.1105/tpc.15.00122

Supplemental Table 1. Phenotypic correlations between plasticity and mean breeding values for all measured phenotypic traits. Correlation coefficients are reported; * indicates significant correlations at $\alpha = 0.05$.

	LA	SFM	SDM	RDM	RMR	WUE	proline	SR	GR	WC
LA										
SFM	0.89*									
SDM	0.77*	0.84*								
RDM	0.65*	0.69*	0.60*							
RMR	-0.03	-0.08	-0.06	0.35*						
WUE	-0.02	0	-0.02	0.09	0.07					
proline	0.12*	0.1	0.06	0.11	0.06	-0.21*				
SR	-0.01	0.02	0.14	-0.31*	-0.73*	-0.1	0.04			
GR	0.51*	0.41*	0.29*	0.16	-0.25	0.03	0.12*	0.2		
WC	0.21*	0.20*	-0.09	-0.03	0.14	-0.01	0.33*	0	0.25*	
ABA	0.04	0	0.02	0.05	0.14	-0.02	0.02	-0.05	-0.02	-0.01

Supplemental Table 2. Summary statistics for all terms in each QTL models. ANOVA statistics (LOD, % variance explained, F-statistic and P-value of the F statistic) are derived by calculating the difference between a full ANOVA model and one where terms are iteratively removed. Effect estimates (Effect) are calculated through a t-test of the effect of alleles at the QTL position on the respective phenotype. The associated standard error and t statistic are reported.

Phenotype	Treatment	Chr.	Pos. (cM)	LOD	% Var	F	P-value	Effect	SE	t-statistic
LA	dry	1	31.651	2.7	3.49	12.55	0.0005	-0.6144	0.1734	-3.5433
LA	dry	3	89.501	2.56	3.3	11.89	0.0006	0.5843	0.1694	3.4486
RMR	dry	3	18.982	3.58	19.79	18	0.0001	0.0122	0.0029	4.2424
RMR	dry	4	1.473	2.96	15.98	14.53	0.0003	0.011	0.0029	3.8115
RGR	dry	1	12.321	2.4	3.31	11.15	0.0009	-0.0098	0.0029	-3.3399
RGR	dry	3	29.815	2.77	3.81	12.87	0.0004	-0.0102	0.0028	-3.5875
Wilt	dry	4	2.132	2.85	4.01	70.95	0.0003	-0.4779	0.1309	-3.651
WUE	dry	2	74.357	2.81	3.6	13.02	0.0004	0.117	0.0324	3.6079
WUE	dry	3	58.473	2.93	3.77	13.61	0.0003	-0.115	0.0312	-3.6888
WUE	dry	5	84.177	2.75	3.53	12.77	0.0004	0.113	0.0316	3.5728
ABA	dry	2	15.5013	3.64	5.16	270.04	<0.0001	-0.9857	0.2385	-4.1333
RGR	wet	cytoplasm		0.06	0.08	0.28	0.5938	-0.0029	0.0055	-0.5339
RGR	wet	3	53.591	4.77	6.7	22.54	<0.0001	-0.0132	0.0028	-4.7481
WUE	wet	cytoplasm		2.36	2.35	10.78	0.0011	-0.1427	0.0435	-3.2826
WUE	wet	3	17.916	3.12	3.13	14.33	0.0002	0.0866	0.0229	3.785
WUE	wet	3	64.783	5.06	5.15	23.57	<0.0001	-0.1147	0.0236	-4.8549
WUE	wet	4	4.408	6.89	7.1	32.49	<0.0001	-0.1281	0.0225	-5.7001
WUE	wet	4	42.395	2.59	2.59	11.87	0.0006	-0.0777	0.0225	-3.4453
WUE	wet	5	37.2105	3.47	3.49	15.98	0.0001	-0.0923	0.0231	-3.9976
WUE	wet	5	89.2057	6.18	6.33	29	<0.0001	0.1261	0.0234	5.385
FT	wet	cytoplasm		0.26	0.12	1.15	0.2837	0.3242	0.3019	1.0737
FT	wet	1	83.846	7.9	3.95	37.48	<0.0001	0.9542	0.1559	6.122
FT	wet	4	2.791	72.94	59.12	280.3	<0.0001	-3.6757	0.1553	-23.6752
FT	wet	4	62.073	10.21	5.19	24.62	<0.0001	-0.8558	0.1553	-5.51
FT	wet	5	15.25	3.78	1.84	17.42	<0.0001	-0.6427	0.154	-4.1743
FT	wet	5	71.677	8.44	4.24	40.22	<0.0001	0.9833	0.1551	6.3416
FT	wet	4*4	2.8*62.1	4.85	2.38	22.54	<0.0001	0.747	0.1573	4.748
RDM	dry	cytoplasm		0	0.01	0.01	0.9197	-0.0001	0.0008	-0.1013
RDM	dry	3	32.992	2.83	19.23	13.81	0.0005	0.0014	0.0004	3.7161
GR	dry	cytoplasm		0.01	0.02	0.05	0.8235	-0.073	0.3272	-0.2233
GR	dry	3	3.905	3.23	4.57	15.08	0.0001	-0.6342	0.1633	-3.8833
roll	dry	cytoplasm		3.45	4.55	16.11	0.0001	-0.9839	0.2451	-4.0141
roll	dry	2	73.572	4.68	6.24	22.08	<0.0001	-0.5878	0.1251	-4.6992
proline	dry	cytoplasm		11.68	10.63	57.41	<0.0001	42.8159	5.6506	7.5773
proline	dry	2	74.357	24.81	24.9	67.25	<0.0001	34.0946	3.0141	11.3118
proline	dry	3	50.173	5.64	4.91	13.27	<0.0001	-10.5931	2.8986	-3.6546
proline	dry	4	2.791	4.02	3.46	18.72	<0.0001	-12.1285	2.8036	-4.3261
proline	dry	2*3	74.4*50.2	2.68	2.29	12.35	0.0005	-10.8614	3.0909	-3.514
WC	dry	cytoplasm		3.06	4.07	14.25	0.0002	-1.279	0.3388	-3.7755
WC	dry	2	86.92	2.53	3.35	11.73	0.0007	-0.6043	0.1764	-3.4254
LA	plast	cytoplasm		1.48	1.88	6.82	0.0094	-0.3405	0.1303	-2.6121
LA	plast	1	3.304	2.46	3.14	11.38	0.0008	-0.2239	0.0664	-3.3732
LA	plast	3	27.474	3.26	4.18	15.18	0.0001	-0.2573	0.0661	-3.8956
GR	plast	cytoplasm		0.43	0.61	1.97	0.1615	0.2197	0.1565	1.4035
GR	plast	3	3.905	3.06	4.39	14.26	0.0002	-0.2944	0.078	-3.7756
GR	plast	4	59.798	3.36	4.83	15.68	0.0001	-0.3221	0.0813	-3.96
WUE	plast	cytoplasm		1.9	2.6	8.81	0.0032	0.4016	0.1353	2.9674
WUE	plast	4	4.408	2.53	3.47	11.77	0.0007	0.2336	0.0681	3.4309
proline	plast	cytoplasm		1.79	2.29	8.26	0.0043	0.4286	0.1491	2.8744
proline	plast	2	73.572	10.01	13.66	49.25	<0.0001	0.5289	0.0754	7.0179

Supplemental Table 3. T statistics for the additive effect of cytoplasm. Significance is measured by a Bonferroni threshold.

phenotype	<i>t</i>	<i>df</i>	<i>P</i>	significance
LA.wet	-1.4	327.17	1.64E-01	
LA.dry	1.65	314.44	9.94E-02	
SFM.wet	-1.47	313.36	1.41E-01	
SFM.dry	1.49	307.21	1.37E-01	
SDM.wet	-2.2	324.58	2.88E-02	
SDM.dry	-2.03	310.15	4.36E-02	
RDM.wet	-2.06	27.69	4.88E-02	
RDM.dry	0.03	31.91	9.78E-01	
RMR.wet	1.03	36.91	3.08E-01	
RMR.dry	2.17	45.03	3.55E-02	
SR.wet	-0.6	15.61	5.57E-01	
SR.dry	-2.22	14.03	4.38E-02	
GR.wet	2.2	277.71	2.85E-02	
GR.dry	0.08	268.85	9.36E-01	
RGR.wet	0.11	297.42	9.14E-01	
RGR.dry	-0.38	281.68	7.03E-01	
Wilt.dry	0.03	305.15	9.79E-01	
Roll.dry	3.58	282.09	4.10E-04	**
WUE.wet	3.23	308.45	1.39E-03	**
WUE.dry	-1.26	267.93	2.08E-01	
ABA.wet	-4.74	305.91	3.32E-06	**
ABA.dry	-6.85	290.67	4.29E-11	**
proline.wet	-0.12	201.55	9.05E-01	
proline.dry	-5.59	302.63	5.04E-08	**
FT.wet	-0.77	313.88	4.45E-01	
WC.dry	3.44	287.6	6.60E-04	**
WC.wet	0.75	315.75	4.57E-01	

Supplemental Table 4. Significance of cytoplasm epistasis on each QTL. Statistics were derived from iterative post-hoc ANOVAs comparing a complete model to one without the cytoplasm epistas

QTL Interact phenotype	Type.III.SS	LOD	%var	F.value	Pvalue.Chi2.
3@53.6:cyto\$ RGR.wet	0	0.05	0.06	0.21	0.64
3@17.9:cyto\$ WUE.wet	0.03	0.04	0.04	0.18	0.67
3@64.8:cyto\$ WUE.wet	0.16	0.24	0.23	1.07	0.29
4@4.4:cyto\$c WUE.wet	0.21	0.31	0.31	1.41	0.23
4@42.4:cyto\$ WUE.wet	0.01	0.01	0.01	0.06	0.81
5@37.2:cyto\$ WUE.wet	0	0	0	0	0.97
5@89.2:cyto\$ WUE.wet	0.08	0.12	0.12	0.54	0.46
1@83.8:cyto\$ FT.wet	2.73	0.08	0.04	0.36	0.54
4@2.8:cyto\$c FT.wet	8.25	0.25	0.12	1.1	0.29
4@62.1:cyto\$ FT.wet	18.04	0.54	0.25	2.43	0.12
5@15.2:cyto\$ FT.wet	3.02	0.09	0.04	0.4	0.52
5@71.7:cyto\$ FT.wet	8.2	0.24	0.12	1.1	0.29
1@31.7:cyto\$ LA.dry	6.73	0.16	0.2	0.74	0.39
3@89.5:cyto\$ LA.dry	10.6	0.26	0.32	1.16	0.28
3@33.0:cyto\$ RDM.dry	0	0.07	0.45	0.32	0.56
3@19.0:cyto\$ RMR.dry	0	0.01	0.03	0.02	0.88
4@1.5:cyto\$c RMR.dry	0	0.71	3.3	3.08	0.07
3@3.9:cyto\$c GR.dry	7.1	0.19	0.26	0.86	0.35
1@12.3:cyto\$ RGR.dry	0	0.16	0.22	0.75	0.38
3@29.8:cyto\$ RGR.dry	0	0.08	0.1	0.35	0.55
4@2.1:cyto\$c Wilt.dry	0.54	0.02	0.03	0.1	0.75
2@73.6:cyto\$ Roll.dry	0.12	0.01	0.01	0.03	0.87
2@74.4:cyto\$ WUE.dry	1.13	0.87	1.09	3.97	0.04*
3@58.5:cyto\$ WUE.dry	0.36	0.28	0.35	1.27	0.26
5@84.2:cyto\$ WUE.dry	0.02	0.01	0.01	0.05	0.82
2@15.5:cyto\$ ABA.dry	62.79	0.98	1.2	4.47	0.03*
2@74.4:cyto\$ proline.dry	5904.98	0.54	0.45	2.42	0.12
3@50.2:cyto\$ proline.dry	233.73	0.02	0.02	0.1	0.76
4@2.8:cyto\$c proline.dry	674.45	0.06	0.05	0.28	0.6
2@86.9:cyto\$ WC.dry	19.72	0.47	0.61	2.15	0.14
1@3.3:cyto\$c LA.plast	0.63	0.1	0.13	0.46	0.49
3@27.5:cyto\$ LA.plast	0.65	0.1	0.13	0.48	0.49
3@3.9:cyto\$c GR.plast	0.34	0.04	0.06	0.19	0.66
4@59.8:cyto\$ GR.plast	12.41	1.58	2.18	7.23	<0.01*
4@4.4:cyto\$c WUE.plast	0.08	0.01	0.02	0.06	0.81
2@73.6:cyto\$ proline.plast	1.03	0.14	0.17	0.63	0.43

AT3G23600	RDM.dry_3_33	RDM.dry	3	32.992 C3_8206469	dry	YES	0.9586	-1.705797659	1	0.002795359	0	0
AT3G15180	RDM.dry_3_33	RDM.dry	3	32.992 C3_8206469	dry	YES	0.9623	-1.91384703	1	0	0	0
AT3G18540	RDM.dry_3_33	RDM.dry	3	32.992 C3_8206469	dry	YES	0.9659	-1.994829098	1	0.009913259	0.026119403	0
AT3G16400	RDM.dry_3_33	RDM.dry	3	32.992 C3_8206469	dry	YES	0.9791	-2.477153748	1	0.006369427	0.006382979	0
AT3G18830	RDM.dry_3_33	RDM.dry	3	32.992 C3_8206469	dry	YES	0.9787	-2.540293764	1	0.014197531	0.001855288	0
AT3G18535	RDM.dry_3_33	RDM.dry	3	32.992 C3_8206469	dry	YES	0.9847	-2.975762663	1 NA	NA	NA	NA
AT3G16770	RDM.dry_3_33	RDM.dry	3	32.992 C3_8206469	dry	YES	0.9908	-3.616791051	1	0.033467202	0.036290323	0
AT3G25470	RDM.dry_3_33	RDM.dry	3	32.992 C3_8206469	dry	YES	0.9996	-11.63941622	1	0.007726269	0.003322259	0
AT2G33340	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0	0.999560187	0	0.001319585	0.003966618	0
AT2G43530	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0	0.983653322	0	0.019379845	0.023529412	0
AT2G43210	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0	0.948187435	0	0.001253133	0.001883239	0
AT2G46220	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0	0.941620866	0	0.00137741	0.004149378	0
AT2G43680	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0	0.852994539	0	0.001493653	0.004487661	0
AT2G46100	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0	0.841243532	0	0	0	0
AT2G38800	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0	0.815860209	0	0.002175095	0.004901961	0
AT2G32150	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0	0.807382898	0	0.007575758	0.003802281	0
AT2G42490	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0	0.751402301	0	0.002145002	0.00128866	0
AT2G32160	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	1.00E-04	0.732812577	0.001328571	0.010034589	0.020389912	0
AT2G35690	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0	0.691399333	0	0.002145002	0.00128866	0
AT2G35660	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	2.00E-04	0.574318474	0.002367273	0.020073434	0.019481339	0
AT2G41440	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	3.00E-04	0.5650256	0.003367241	0	0	0
AT2G41620	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	3.00E-04	0.561852137	0.003367241	0.000773395	0	0
AT2G31560	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	4.00E-04	0.552065936	0.00434	0.01642036	0.004950495	0
AT2G46950	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	7.00E-04	0.544019642	0.006801493	0.000581734	0.001748252	0
AT2G39800	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	8.00E-04	0.535503993	0.007547826	0.001006258	0.001511682	0
AT2G30990	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0.0012	0.47657037	0.009888608	0.000576092	0	0
AT2G31440	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0.0011	0.464856607	0.009548	0	0	0
AT2G36870	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0.0012	0.434137125	0.009888608	0	0	0
AT2G40820	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0.0024	0.411686186	0.017555056	0.000676133	0.00203252	0
AT2G42170	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0.0021	0.394719689	0.015535227	0.017171717	0.03343465	0
AT2G39400	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0.0038	0.375403271	0.02576875	0.009615385	0.003215434	0
AT2G32880	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0.0053	0.360040633	0.033826471	0.00522466	0.006289308	0
AT2G32930	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0.0055	0.359533821	0.034427885	0	0	0
AT2G39110	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0.0055	0.357195407	0.034427885	0.003058104	0.002298851	0
AT2G37710	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0.0085	0.314288685	0.045731405	0.024654832	0.017777778	0
AT2G38000	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0.009	0.301209057	0.04725	0.000793651	0.002386635	0
AT2G36470	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0.0119	0.299862952	0.058688636	0.00203252	0	0
AT2G31490	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0.0102	0.291869998	0.051474419	0.00462963	0	0
AT2G39890	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0.0095	0.287548833	0.049083333	0.005267118	0	0
AT2G32140	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0.0136	0.285731082	0.064156522	0.015065913	0.025495751	0
AT2G41830	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0.0146	0.270242274	0.066004167	0.001949318	0	0
AT2G36460	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0.0146	0.259707728	0.066004167	0.001550396	0.003269307	0
AT2G40960	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0.0167	0.248995812	0.07296443	0.002840999	0.005698006	0
AT2G33370	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0.0224	0.23311418	0.090014815	0	0	0
AT2G33470	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0.0221	0.227741208	0.08936087	0.006568144	0	0
AT2G32040	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0.0401	0.191078798	0.135964063	0.001188354	0	0
AT2G40750	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0.0941	0.11865877	0.261791026	0.00192123	0	0
AT2G45960	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0.0931	0.114405312	0.260120601	0.002318209	0	0
AT2G31320	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0.1161	0.099399413	0.307240244	0.00203252	0.002034588	0
AT2G41410	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0.1181	0.09825996	0.3108	0.004608295	0.00462963	0
AT2G47210	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0.2078	0.054990201	0.466475172	0	0	0
AT2G44180	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0.2625	0.037201976	0.548581529	0.001508296	0.004535147	0
AT2G33150	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0.2635	0.034669414	0.548581529	0	0	0
AT2G40060	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0.3122	0.025355777	0.60844209	0.027027027	0.011627907	0
AT2G36305	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0.3426	0.018646465	0.652138776	0.003205128	0.006430868	0
AT2G34760	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0.3529	0.016655071	0.66398237 NA	NA	NA	NA
AT2G44290	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0.4804	0.001337139	0.830586207	0.01618123	0.024390244	0
AT2G47140	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0.6619	-0.019356551	1	0.00129199	0.003891051	0
AT2G45660	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0.7266	-0.031973185	1	0	0	0
AT2G45340	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0.8298	-0.07284471	1	0.001926782	0.001447178	0
AT2G38860	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0.9363	-0.160214149	1	0.001920399	0	0
AT2G46450	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0.9431	-0.172020219	1	0.002051282	0.003081664	0
AT2G43620	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0.9951	-0.453053182	1	0.005868545	0	0
AT2G45510	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0.9973	-0.471591324	1	0.001302083	0.001956947	0
AT2G43980	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0.9994	-0.657539829	1	0.000681663	0	0
AT2G47400	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0.9997	-0.836164862	1	0.013333333	0.016129032	0
AT2G38530	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	0.9998	-0.923894493	1	0	0	0
AT2G45910	WC.dry_2_87	WC.dry	2	86.92 2-18752604	dry	YES	1	-1.036397392	1	0.000798403	0.001199041	0

Supplemental Data. Lovell et al. (2015). Plant Cell 10.1105/tpc.15.00122

Supplemental Table 6. List of cytoplasmic SNPs between TSU and KAS

Position	COL	TSU	KAS	Gene	Gene Start	Other names
4795	G	G	T	Intergenic		
7894	A	A	T	Intergenic		
16875	C	T	C	ATMG00050	16844	ORF131
18528	C	A	C	Intergenic		
24179	G	T	G	ATMG00070	23663	NAD9, NADH DEHYDROGENASE SUBUNIT 9
38291	C	C	T	Intergenic		
136960	C	G	C	ATMG00510	132071	NADH DEHYDROGENASE SUBUNIT 7
189636	A	A	T	Intergenic		
189637	A	A	T	Intergenic		
192055	T	T	C	Intergenic		
192056	C	C	A	Intergenic		
207568	T	G	T	ATMG00710	207553	ORF120
209160	G	G	T	Intergenic		
241974	C	C	T	Intergenic		
353877	C	A	C	Intergenic		
353878	C	A	C	Intergenic		

14 SUPPLEMENTAL MATERIALS

15 **Description of RILs and growth conditions.** The TSU-1 x KAS-1 mapping
16 population was generated and distributed by John K. McKay. A seed library of this
17 population is maintained at Colorado State University. These genotypes are made
18 publically available through the Arabidopsis Stock Center. The association of RIL
19 identifiers presented here, the R/qtl identification and the ARBC accession numbers can
20 be found Supplementary Table 8.

21

22 SUPPLEMENTAL METHODS

23 **Quantitative Genetic Model.** We calculated RIL-specific breeding values as the
24 least square mean from a mixed effect model with genotype as a fixed effect and growth
25 chamber as the random term. We calculated the simplest form of phenotypic plasticity-
26 the scale and center standardized difference in breeding values across experimental
27 conditions. This was implemented in R by quantile normalizing the wet and dry breeding
28 values, then taking the difference for each RIL. This was repeated for each phenotype.

29

30 **QTL Model Selection.** Breeding values for each RIL were generated as above-
31 these served as the RIL means used in QTL mapping. QTL mapping as implemented
32 here, due to the use of permutation test, is relatively robust to the distribution of the data.
33 However, to be conservative, we mapped QTL for both raw breeding values and quantile-
34 normalized values across the RIL population for each trait. The final models never
35 differed in the number, interaction type, or chromosome of the QTLs for any trait. The
36 QTL position moved slightly among models. Thus, the effect of normalization was very
37 subtle and did not impact the final models. As such, we opted to conduct QTL mapping
38 on the un-normalized phenotypes.

39 Prior to QTL mapping, we calculated genotype probabilities of any missing data
40 at each marker. Furthermore, we conducted identical calculations for a set of
41 pseudomarkers, placing these at intervals of 1cM within any gap >1cM. Pseudomarker
42 and missing data genotype probabilities were calculated using the Kosambi map function,
43 with an error probability of 0.01.

44 We generated QTL peak thresholds using permutations on the map with
45 calculated genotype probabilities via the Haley-Knott regression (Haley and Knott, 1992;
46 Broman 2003), assuming a normal phenotype distribution. The phenotype-covariate
47 structure was maintained and permuted relative to a fixed genotype matrix 10,000 times
48 for each phenotype. At each iteration, a two-way QTL scan was performed, and the peak
49 LOD score for a set of six model comparisons was output. The distribution of these
50 10,000 tests provided the significance threshold and P-values for each QTL and epistatic
51 interaction. Permutations were also performed without a covariate where the entire
52 phenotype matrix was sampled without replacement. From these distributions we
53 calculated three penalties, which were used to penalize the addition of a single QTL,
54 additional QTLs and epistatic interactions in the model selection protocol (Manichaikul
55 et al. 2009).

56 We ran stepwise QTL model selection using two separate models, one with
57 cytoplasm as a covariate, and another without this term. Penalties were assigned based on
58 the model type and phenotype. Stepwise model selection was implemented in R/qtl using
59 a NULL starting model and screening for models with up to 12 QTL and an unlimited
60 number of epistatic interactions. At each step in the selection procedure, both interactive
61 and additive QTL were screened and the term that best improves the total penalized LOD
62 score of the model was retained. Additionally, at each step the position of each QTL was
63 refined to screen for improvements in model fit. The full, 12-QTL model was then
64 trimmed, one term at a time, and the whole-model penalized LOD score was recalculated.
65 The model with the highest penalized LOD score following this forwards-backwards
66 stepwise model selection was chosen. Finally, the two models, one with and the other
67 without a cytoplasm covariate were compared and the model with the highest penalized
68 LOD score was retained and fixed as the QTL model for that trait for all future analyses.

69 We calculated several statistics from each QTL model. First, we calculated the
70 1.5LOD drop confidence interval (Broman and Sen 2009) for the LOD profiles, which
71 resulted from the iterative scanning of positional effects used to refine QTL positions.
72 Second, we fit an ANOVA to the model and calculated several statistics. The whole-
73 model LOD, %variance, F-statistic and P-value were calculated from the full ANOVA fit
74 to the model. QTL-specific effects were calculated by comparing nested model fits,

75 where the LOD, % variance, F-statistic and P-value were derived from a test of models
 76 with and without the focal QTL term. Finally, estimated effects were generated by fitting
 77 t-tests to the genotype probabilities at each QTL.

78

79 **Candidate Gene Methodology.** QTL models and formulae were generated
 80 through automated stepwise model selection (described above). To isolate the effects of a
 81 specific QTL in a multiple QTL model, we fit a one-way QTL scan with all model terms,
 82 but the focal QTL, as covariates.

83 Take the simplest case, where a 1-QTL model without any experimental
 84 covariates provides the best model fit. For a single trait QTL scan for trait i , we obtained
 85 a LOD score by comparing the NULL model (without a QTL term, *model 1*) to a 1-QTL
 86 model (*model 2*) (Broman and Sen 2009) with a single QTL, g .

87

88 *model 1: NULL* $y_i = \mu + \varepsilon_i$

89 *model 2: 1-QTL* $y_i = \mu + \beta_g g_i + \varepsilon_i$

90

91 Following the framework of Li et al. (2006), who utilized structural equation modeling to
 92 define interactions among multiple phenotypic trait QTLs, we determined the
 93 significance of gene expression covariate as cases where using trait x as a covariate
 94 significantly reduces the LOD score of a QTL for trait i . In this case, x was associated
 95 with variance in trait i and may invoke causality. This test was accomplished by
 96 comparing the LOD score of a 1-QTL model (*model 2*) to a more complex model. In this
 97 case, we obtained the LOD score by comparing *model 1* with the fit of a model with trait
 98 x as a covariate (Broman and Sen 2009)

99

100 *model 3: 1 QTL, 1 Covariate* $y_i = \mu + \beta_x x_i + \beta_g g_i + \varepsilon_i$.

101

102 LOD scores for the QTL term for each model were extracted and compared. The effect of
 103 the difference in QTL-specific LOD scores was taken as

104

105 $covariate\ effect = (LOD_{model\ 2\ vs.\ model\ 1} - LOD_{model\ 3\ vs.\ model\ 1}) / LOD_{model\ 2\ vs.\ model\ 1}$.

106

107 Across all models, the position of QTL g was fixed as the QTL position best supported in
108 our multiple QTL modeling procedure.

109

110 The effects of random covariates were normally distributed around the LOD score for a
111 1-QTL model without covariates (Fig. S1, black lines). Positive effects were the result of
112 values that were un-correlated or orthogonal to the phenotypic trait values such that
113 residual variance in the model was absorbed by the covariate term, improving the effect
114 of the QTL term and thus the LOD score (Fig. S1, blue line). However, gene expression
115 values that were correlated with genotypes at the QTL, absorbed variance otherwise
116 attributed to the QTL, reducing the LOD score (Fig. S1, red line). As such, we expected
117 genes with expression polymorphism that drove phenotypic trait variation attributable to
118 the focal phenotype to be correlated, causing a decrease in LOD at the focal QTL.

119 Here, we implemented this approach for each candidate gene within the interval
120 surrounding the QTL. To determine significance, we sampled without replacement
121 (permuted) the gene expression vector 10,000 times. This generated a distribution around
122 the original QTL model that permitted a test for the significance of the observed effect
123 for each gene expression covariate. In the example presented in Figure S1, this would be
124 performed by comparing the red, correlated line to the distribution of black dotted lines
125 derived from permutations of the covariate data. Since we expected gene expression
126 variation to be responsible for QTL-specific trait variation when correlated with the
127 phenotypic trait values, and not the residuals, we defined candidate genes only as those
128 which, when incorporated as a covariate, significantly reduced the LOD score at a focal
129 QTL.

130 This approach is akin to partial correlation testing, in the framework of QTL
131 modeling. Furthermore, the original model, here the grey “no.covar” line, can be as
132 complex as the researcher chooses. To choose the least complex model that explains the
133 most variation, we implemented a penalized stepwise model search as described above.
134 Instead of rebuilding the model separately for each gene-expression covariate, we took
135 this selected model and added, then removed the covariate and examined the LOD effect

136 of this term. This procedure, and 10,000 permutations, was repeated for the gene
137 expression phenotypes of each candidate gene underneath each QTL.

138 It is important to note that our experimental design utilized gene expression on a
139 104 line subset of those RILs with phenotypic trait and genotype data. Since the
140 accompanying reduction in power limits our ability to detect QTL, we utilized the
141 original QTL models, but fit the covariates with the 104 line complete dataset. This
142 permitted comparisons among models without the discrepancies caused by differential
143 power among datasets.