1 Genotyping

1.1 Array hybridization

We used SNP-tiling arrays (Affymetrix 250K SNP-tiling array, AtSNPtile1) containing probe sets for 248,584 SNPs[6] for genotyping. Each SNP has four probes (two alleles on sense and anti-sense strand, respectively). Genomic DNA was extracted using Wizard Magnetic 96 DNA Plant System (Promega). For each sample, approximately 250 ng genomic DNA (in 48 uL distilled water) was labeled using BioPrime DNA labeling system (Invitrogen), at conditions modified as previously described[29]. 16 ug of labeled product was hybridized to each array using standard Affymetrix array washing and staining protocols. Samples were processed at the microarray core facilities at the University of Chicago and the Children's Hospital of Los Angeles (USC).

1.2 Data processing

1.2.1 Overview

SNPs were called using a modified version of the Oligo package[30] (as described in Section 1.2.2). The resulting calls were then filtered in several steps to remove substandard arrays and SNPs. Following these procedures, missing SNPs were imputed using NPUTE[31].

1.2.2 Modifications to the Oligo SNP-calling algorithm

The Oligo[30] package was designed to call genotypes with the Affymetrix Human Mapping array sets. The calling algorithm summarizes each strand across arrays and SNPs to estimate the cluster centers or spread for each SNP based on a training data set. Our modifications were as follows: (1) the readcel.R file in the package was modified such that it could read in the intensities of the 250k array's custom probe sets (*i.e.*, four perfect match probes for each SNP); (2) only homozygotes were called (*A. thaliana* lines are almost completely inbred); (3) the *A. thaliana* Perlegen data set[32], comprising 20 lines (with some duplicate arrays) was used as the training set. (4) Using a "leave-one-out" approach, the cluster parameters were estimated and logistic regression was applied to predicted calls to determine the confidence intervals for the two homozygous clusters.

1.2.3 Data sets used for quality control

We leveraged four *A. thaliana* data sets from previous projects to help achieve high quality genotype calls:

2010 The **2010** data[4], which consists of approximately 1500 fragment loci sequenced in 96 inbred lines using PCR-based direct Sanger sequencing.

Perlegen The **Perlegen** data[32], which consists of whole genome tiling arrays used to resequence 20 diverse accessions selected from the 96 used to generate the **2010** data. The SNPs for the 250k SNP chip were chosen from these data.

384 SNP An Illumina BeadStation was used to genotype 384 SNPs from the **2010** data in 96 inbred lines, most of which were used in the present study.

149 SNP Over 6,000 lines (including the accessions used in this study) have been genotyped using 149 SNPs from the **2010** data, and Sequenom iPLEX assay technology.

The latter two data sets are less reliable (and smaller) than the former two and were mostly used to identify substandard arrays and to guard against sample contamination. The **2010** data were used for the same purpose, and also (due to its high quality) to estimate error rates. The **Perlegen** data were used to identify unreliable SNPs.

1.2.4 Pipeline

1. *Run Oligo.* Oligo was applied to all arrays with training parameters. After running Oligo, we retained calls whose posterior probability was above or equal to 0.85 and marked the rest as missing. We then applied the following steps in sequential order.

2. *Filter out bad arrays and contaminated samples using the mismatch rate.* Arrays with a mismatch rate above 10% following comparison with the combined **2010 / 384 SNP / 149 SNP** data were discarded. The mismatch rate was set to a permissive 10%, as lines in our study that were not genotyped in the **2010** data, could only be compared to 60 - 150 SNPs available to use from the **149 SNP** and **384 SNP** data, which were found to have error rates as high as 5%. The purpose of this step was to remove failed arrays and contaminants (the SNP mismatch rate between non-identical individuals was almost always above 30%).

3. *Filter out bad SNPs using the mismatch rate.* Any SNP whose mismatch rate from a comparison with the **Perlegen** dataset was above 10% was discarded. The permissive criterion of 10% was chosen because the **Perlegen** data includes only 20 lines and the confidence interval is wide. 19,441 SNPs (7.82%) were removed.

4. *Substitute missing SNPs with corresponding calls from the **Perlegen** data.* Due to the high-quality and whole-genome coverage of the **Perlegen** data, we decided to substitute any missing SNP calls in our data for equivalent calls from the 20 accessions available in the **Perlegen** data. On average, 1,021 missing calls were substituted per accession and 123 non-missing calls were replaced per accession.

5. *Filter out substandard SNPs using the rate of missing calls.* 13,132 SNPs (5.28%) with a missing call rate of more than 25% were discarded. This filter was required because the imputation algorithm used in the last step imputes every missing call without assigning confidence and hence basing imputation on SNPs with low call rates is not ideal.

6. *Remove monomorphic SNPs.* These SNPs are of no interest in association mapping, and could furthermore cause difficulties during the imputation step. However, no monomorphic SNPs were present.

7. *Impute all remaining missing calls.* On average, 8,248 calls per accession (3.32%) were imputed with NPUTE[31], a sliding-window nearest-neighbor searching algorithm, which was chosen based on accuracy (comparable to fastPHASE[33]) and performance (considerably faster than fastPHASE). The disadvantage in using NPUTE is that it does not assign probability to the imputed calls, but this issue was addressed in the previous step by removing SNPs with missing call rates above 25%. The only parameter of this algorithm is window size (defined as the number of SNPs within the sliding window). We investigated using window sizes of up 90 SNPs with increments of 10 and resolved upon 30 SNPs as there was almost no effect on the quality of the imputed calls once the window size exceeded 10 SNPs.

8. *Remove redundant arrays and contaminated lines.* Duplicate arrays were removed. In addition 3 lines (Uod-2, Blh-1, Santa Clara), which were suspected contaminants, either because the genotype data did not agree with the **2010**, **384** or **149** datasets or because the phenotype result for the particular accession did not agree with earlier scores. This step essentially removes contaminants which can easily occur in these types of study.

9. *Insert polymorphisms from the* FRI *and* CLF *regions.* Based on earlier studies, *FRI* was known and *CLF* suspected to be involved in flowering time variation[5,9] and these genes surrounding regions were fully sequenced in the **2010** data. For *FRI*, we incorporated the two known functional deletions and another newly discovered deletion in the 3'UTR region into the 250k data. 166 SNPs around *CLF* were incorporated into the 250k data. Alleles were imputed from accessions in our study that were not sequenced in the **2010** dataset.

10. *Substitute SNPs with corresponding calls from the combined **2010 / 384 SNP / 149 SNP** data.* A very small fraction of calls (12 per accession, on average) were changed based on the **2010 / 384 SNP / 149 SNP** data. This step had almost no effect on the final data.

11. *Remove non-binary SNPs.* 50 SNPs were found to harbor more than two alleles after calls were substituted by **2010** dataset. As our association methods do not consider SNPs with more than two alleles these 50 SNPs were removed.

Supplementary Figure 1 – Distribution of error estimates across 75 lines before (top panel) and after (bottom panel) imputation.

1.2.5 Error Estimates

The manually curated **2010** sequencing data[4] are of very high quality, and appropriate for quality-control purposes[32]. Of the 95 lines that overlap between these data and the 250k SNP data, 20 were used in SNP detection (and had their 250k SNP calls substituted by the **Perlegen** data). They are thus not representative of the quality of the 250k data. For the remaining 75, the average mismatch rate before imputation is 1.396% with a standard deviation (across lines) of 0.00772 (Supplementary Fig. 1). After imputation, the mismatch rate increases slightly, to 1.595%, with a standard deviation of 0.00834. Across lines, the increase in mismatch rate due to imputation is below 0.5%, except for one line, Mr-0, whose error estimate is increased by 0.96% (Supplementary Fig. 2).

2 Association mapping methods

Three types of association mapping methods were used, two non-parametric and one parametric. The non-parametric methods were a Wilcoxon rank-sum test for ordered categorical and quantitative phenotypes, and Fisher's Exact Test

Supplementary Figure 2 – Error estimates before vs. after imputation. The red line denotes equality.

for binary phenotypes. To handle confounding by population structure, a parametric mixed model was also used.

2.1 Mixed model (EMMA)

2.1.1 Introduction

EMMA (Efficient Mixed-Model Association)[13] is an implementation of a linear mixed model which accounts for population structure by adding a genetic random effect with a fixed covariance structure. Specifically,

$$\mathbf{Y} = \beta X + \mathbf{u} + \epsilon,$$

where Y denotes the vector of phenotypes, X the vector of genotypes at the locus being tested, β the fixed phenotypic effects attributable to this locus, and $\mathbf{u} \sim N_n(0, \sigma_g^2 K)$ and $\epsilon \sim N_n(0, \sigma_e^2 I_n)$ are random effects meant to capture the variance due to background genetic factors and the environment, respectively.

The kinship matrix K accounts for genome-wide patterns of relatedness between the individuals and is estimated only once. The parameters of the model β, σ_g^2, and σ_e^2 are estimated using REML (restricted maximum likelihood) for each marker (SNP). A general t-statistic testing the null hypothesis $\beta = 0$ is calculated to get the p-value. The percentage of phenotypic variation explained by each SNP is calculated as

$$\frac{\sum_i (x_i\hat{\beta} - \bar{x_i}\hat{\beta})^2}{\sum_i (y_i - \bar{y})^2}.$$

2.1.2 Minor allele frequency dependence

For several phenotypes, EMMA demonstrated enrichment in low p-values among rare allele SNPs (Supplementary Figure 3). The same trend is not seen for the Wilcoxon test, and most of these low-frequency associations are therefore probably spurious, reflecting either poor model choice, or a poor fit to a reasonable model (see further below). Following Kang *et al.*[13], we therefore discard all results with MAF < 0.1 for EMMA.

Supplementary Figure 3 – The dependence of p-values distributions on MAF (here number of alleles out of 192) for EMMA (top panel) and Wilcoxon (bottom panel).

2.1.3 Kinship matrix estimation

The kinship matrix was estimated using identity-in-state, which was shown to work well in previous studies[9,13]. UPGMA clustering of the genotypes using the resulting kinship matrix as a distance matrix (Supplementary Fig. 4) consistently placed Col-0 as an outlier (together with H55 which is closely related to the Col-0 accession). This contradicts clustering using sequencing data, which identifies Col-0 as a Central European accession[4]. This discrepancy presumably reflects SNP ascertainment bias. To assess the effect of this bias on GWA, the performance of EMMA was evaluated using kinship matrices estimated from four different sets of data:

- the full 250k data;
- reduced 250k data, using only the SNPs that overlap with the 2010 sequence data (approximately 1600 SNPs);
- the 2010 data, complemented with 250k data for overlapping SNPs for lines missing from the 2010 data, and;
- reduced 2010 data, using only SNPs that overlap 250k data, again complemented with 250k data to handle missing lines.

Supplementary Figure 4 – UPGMA clustering of the genotypes in the 250k data, based on the kinship matrix.

The full 250k data resulted in the most uniform p-value distribution for most confounded phenotypes and was therefore used to estimate the final kinship matrix.

2.1.4 Transformation of quantitative phenotypes

Deciding which transformation was appropriate was not trivial. Three types of transformations were considered:

- no transformation;
- log transformation (for phenotypes with negative values, a constant was added before transforming), and;
- ranks (to compare with the non-parametric Wilcoxon test).

EMMA produced a reasonably uniform p-value distribution regardless of which transformation was used, even for binary phenotypes. This property is thus of little use in picking a transformation. It is clear that the choice matters as different transformations often resulted in different SNPs being declared significant. Since the mixed-model is fit independently for each SNP, it is not feasible to check the distribution of the residuals for all the SNPs. Instead we focused on properties like the MAF-dependence of the p-values, and the enrichment of *a priori* candidates. Generally, these criteria weakly favored the log transformation and unless evidence suggested otherwise phenotypes were transformed (see Supplementary Tables 2–5).

2.1.5 Assessment of robustness

Observations of the dependence of p-values on allele frequency and sensitivity to the choice of transformation suggested that the EMMA results were not robust. To investigate this, jackknife estimates of the standard deviation of the p-values were calculated. For each phenotype, an accession was removed, one at a time, and the analysis re-run. The standard deviation of the estimated $\log$(p-values) (from EMMA and Wilcoxon) was then reported for each SNP and phenotype. Since EMMA is computationally intensive, a random subset of 1% of the SNPs were used instead of the full data. As shown in Supplementary Fig. 5, p-values from EMMA have a much higher standard deviation than those from Wilcoxon's test. Furthermore, with EMMA smaller p-values have decreased robustness, whereas smaller p-values for Wilcoxon's test have increased robustness. We note that these conclusions are likely to depend sensitively on both sample size and the underlying distribution of the data.

2.1.6 Quantifying population structure

The confounding effects of population structure were evident in the bias toward significance in the genome-wide p-value distributions resulting from applying Wilcoxon's test (Fisher's Exact Test for binary phenotypes). Four different statistics were used to quantify this phenomenon:

Supplementary Figure 5 – The standard deviation of $\log$(p-values) across all phenotypes, plotted against the observed $-\log$(p-value). The lines denote binned averages, using 20 bins and requiring at least 5 observations in each.

- *Kolmogorov-Smirnov statistic*, $D = \max_p\{|F_{obs}(p) - F_{exp}(p)|\}$, where p denotes the p-values, and F_{obs} the observed distribution function, and F_{exp} the expected distribution function.
- *Median p-value bias*, defined as $M = E(\text{median(p)}) - \text{median(p)}$.
- *Area between the expected and observed distribution functions*, i.e. $A = \int_0^1 |F_{obs}(p) - F_{exp}(p)|dp$.
- *The mean logarithmic ratio*, $S = \int_0^1 \frac{\log(F_{obs}(p))}{\log(F_{exp}(p))} dp$.

Since some of the phenotypes are binary or essentially ordered categorical, the p-value distribution was discontinuous and non-uniform. The expected p-value distribution was therefore estimated using a permutation test, where the individuals were permuted 1000 times for Wilcoxon and 100 times for Fisher's exact test, and a random 1% of the p-values used to estimate the distribution function. The integrals and the expectations were estimated using the estimated distribution function, and permutation p-values of the observed statistics were estimated for all the statistics and phenotypes. The permutation test lessens the effect of the observed phenotypic values on the statistics, and enables comparison between different phenotypes (and methods). The Q-Q plots in Supplementary Figs. 12–118 were also plotted using the estimated p-value distributions.

EMMA greatly improves the fit of the p-value distribution to the expected compared to the Wilcoxon or Fisher's Exact Test (see Supplementary Figs. 6 and 7). This is even the case for the binary phenotypes, where mixed-model assumptions of normally distributed residuals generally fail. For the corresponding permutation p-values for the observed statistics (see

Supplementary Figure 6 – Summaries of the degree of confounding for quantitative phenotypes. The blue and the green bars are for Wilcoxon's test; red and yellow bars are for EMMA.

Supplementary Fig. 8), phenotypes generally show significant over-representation of small p-values, and the flowering-related phenotypes stand out as having a highly significant over-representation of small p-values.

3 Enrichment for *a priori* candidates

3.1 Candidate gene lists

The flowering gene list was initially constructed to enable the candidate enrichment ratio analysis. In addition gene lists were made for each phenotype (except the life cycle phenotypes FT duration GH-RP GH) to enable faster assignation of genes to suitable candidates that have been previously identified as connected to the phenotype. Gene lists were constructed by searching The Arabidopsis Information Resource (http://www.arabidopsis.org/), for genes with suitable annotation and literature searches, however, literature searches were not extensive. All gene lists were constructed without looking at the association plots. Whilst a proportion of these genes have not yet directly been shown to be functionally responsible for the traits described, they would be selected for further analysis in any mapping experiment. Some phenotypes were checked with several appropriate gene lists, for example all early development phenotypes (germination, dormancy etc) were checked against the dormancy, germination and hypocotyl elongation gene lists. Any genes that were selected post gene list construction are marked with an asterisk in the gene tables (Supplementary Figs. 12–118). Candidate gene lists can be found on our website: http://arabidopsis.usc.edu.

3.2 Bounding the false-discovery rate

We know that there must be true positives because a higher proportion of candidate SNPs than non-candidate SNPs are significant at a given threshold. If we assume that all non-candidates are false, then we can get an estimate of the fraction of true ones for the candidates by simply subtracting the fraction of non-candidates that are declared significant, y, from the fraction of candidates that are declared significant, x. An upper bound for the false-discovery rate *among candidate SNPs* can be obtained as $1 - (x - y)/x = y/x$.

3.3 Testing the significance of enrichment

The statistical significance of the observed enrichment was assessed using a permutation scheme that preserves the linkage-disequilibrium structure in the data[4]. Briefly, the association results were randomized with respect to the SNP positions without disrupting the order of either. The enrichment was then re-calculated, and the p-value calculated in the standard fashion. Note that, although the magnitude of the enrichment generally increased with more stringent cut-offs, the significance of the enrichment was usually higher for less stringent cut-offs, simply as a consequence of the larger number of observation in the latter case (Supplementary Fig. 11).

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Supplementary Figure 7 – Summaries of the degree of confounding for binary phenotypes. The blue and the green bars are for Fisher's Exact Test; red and yellow bars are for EMMA.

Supplementary Figure 8 – Significance of the deviation from expectation of summaries of the degree of confounding. Bar heights indicate negative log p-values for the deviations shown in Supplementary Figs. 6–7, estimated using permutation. The dotted horizontal line denotes the 95% significance level.

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Name	Origin	Stock ID	Name	Origin	Stock ID	Name	Origin	Stock ID
Aa-0	GER	CS6600	Hov2-1	SWE		Pna-10	USA	CS22571
Ag-0	FRA	CS22630	Hov4-1	SWE		Pna-17	USA	CS22570
Alc-0	ESP	CS1656	HR-10	UK	CS22597	Pog-0	CAN	CS6842
Algutsrum	SWE		HR-5	UK	CS22596	Pro-0	ESP	CS22649
An-1	BEL	CS22626	Hs-0	GER	CS1237	Pu2-23	CZE	CS22593
Ang-0	BEL	CS949	HSm	CZE		Pu2-7	CZE	CS22592
Ba-1	UK	CS6607	In-0	AUT	CS1239	Pu2-8	CZE	CS22449
Bå1-2	SWE		Is-0	GER	CS1241	Ra-0	FRA	CS22632
Bå4-1	SWE		Jl-3	CZE	CS6745	Rak-2	CZE	CS1485
Bå5-1	SWE		Jm-0	CZE	CS1259	Rd-0	GER	CS1482
Bay-0	GER	CS22633	Ka-0	AUT	CS1267	Rd-0	GER	CS1483
Bg-2	USA	CS22342	Kas-2	IND	CS6751	Ren-1	FRA	CS22610
Bil-5	SWE	CS22578	Kävlinge-1	SWE		Ren-11	FRA	CS22611
Bil-7	SWE	CS22579	Kelsterbach-4	GER	CS6041	Rev-1	SWE	
Bla-1	ESP	CS971	Kin-0	USA	CS22654	Rmx-A02	USA	CS22568
Blh-1	CZE	CS1031	Kni-1	SWE		Rmx-A180	USA	CS22569
Boo2-1	SWE		Kno-10	USA	CS22566	RRS-10	USA	CS22565
Bor-1	CZE	CS22590	Kno-18	USA	CS22567	RRS-7	USA	CS22564
Bor-4	CZE	CS22591	Köln	GER	CS6003	Rsch-4	RUS	CS1494
Br-0	CZE	CS22628	Kondara	TJK	CS22651	Rubezhnoe-1	UKR	CS927
Brö1-6	SWE		Kulturen-1	SWE		San-2	SWE	
Bs-1	SUI	CS997	Kz-1	KAZ	CS22606	Sanna-2	SWE	
Bu-0	GER	CS1007	Kz-9	KAZ	CS22607	Sap-0	CZE	CS1507
Buckhorn Pass	USA	CS8067	Lc-0	UK	CS1307	Sav-0	CZE	CS1515
Bur-0	IRL	CS22656	Ler-1	GER	CS22618	Se-0	ESP	CS22646
C24	POR	CS22620	Li-7	GER	CS6778	Seattle-0	USA	CS6187
Ca-0	GER	CS6658	Liarum	SWE		Sha	TJK	CS22652
Can-0	ESP	CS1065	Lillö-1	SWE		Sorbo	TJK	CS22653
Cen-0	FRA	CS1067	Lip-0	POL	CS1337	Spr1-2	SWE	CS22582
CIBC-17	UK	CS22603	Lis-1	SWE		Spr1-6	SWE	CS22583
CIBC-5	UK	CS22602	Lis-2	SWE		Sq-1	UK	CS22600
Cnt-1	UK	CS6921	Lisse	NED	CS6033	Sq-8	UK	CS22601
Co	POR	CS3180	LL-0	ESP	CS22650	St-0	SWE	CS1535
Col-0	USA	CS22625	Lm-2	FRA	CS1345	Ste-0	GER	CS6864
Ct-1	ITA	CS22639	Lom1-1	SWE		Stw-0	RUS	CS1539
Cvi-0	CPV	CS22614	Löv-1	SWE	CS22574	Ta-0	CZE	CS1549
Da-0	GER	CS6676	Löv-5	SWE	CS22575	Tamm-2	FIN	CS22604
Da(1)-12	CZE	CS917	Lp2-2	CZE	CS22594	Tamm-27	FIN	CS22605
Dem-4	USA		Lp2-6	CZE	CS22595	Tottarp-2	SWE	
Dra3-1	SWE		Lu-1	SWE	CS1353	Ts-1	ESP	CS22647
DraII-1	CZE		Lund	SWE		Ts-5	ESP	CS22648
DraIII-1	CZE		Lz-0	FRA	CS22615	Tsu-1	JPN	CS22641
Duk	CZE		Mh-0	POL	CS6792	Tu-0	ITA	CS1567
Eden-1	SWE	CS22572	Mir-0	ITA	CS1379	Ull1-1	SWE	
Eden-2	SWE	CS22573	Mr-0	ITA	CS22640	Ull2-3	SWE	CS22587
Edi-0	UK	CS22657	Mrk-0	GER	CS22635	Ull2-5	SWE	CS22586
Eds-1	SWE		Mt-0	LIB	CS22642	Uod-1	AUT	CS22612
Ei-2	GER	CS22616	Mz-0	GER	CS22636	Uod-7	AUT	CS22613
En-1	GER	CS1137	N13	RUS	CS22491	Van-0	CAN	CS22627
Ep-0	GER	CS6697	Na-1	FRA	CS1385	Vår2-1	SWE	CS22580
Est-1	RUS	CS22629	Nd-1	SUI	CS22619	Vår2-6	SWE	CS22581
Fäb-2	SWE	CS22576	NFA-10	UK	CS22599	Västervik	SWE	
Fäb-4	SWE	CS22577	NFA-8	UK	CS22598	Vimmerby	SWE	
Fei-0	POR	CS22645	No-0	GER	CS3081	Vinslöv	SWE	
Fjä1-1	SWE		Nok-3	NED	CS22643	Wa-1	POL	CS22644
Ga-0	GER	CS22634	Nyl-2	SWE		WAR	USA	CS8143
Gd-1	GER	CS1185	ÖMö2-1	SWE	CS22584	Wei-0	SUI	CS22622
Ge-0	SUI	CS1187	ÖMö2-3	SWE	CS22585	Wil-1-Dean-Lab	LTU	
Gie-0	GER	CS6720	Or-0	GER	CS6822	Ws-0	RUS	CS22623
Got-22	GER	CS22609	Ör-1	SWE		Ws-2	RUS	CS22659
Got-7	GER	CS22608	Ost-0	SWE	CS1431	Wt-5	GER	CS22637
Gr-1	AUT	CS1199	Oy-0	NOR	CS22658	Yo-0	USA	CS22624
Gu-0	GER	CS22617	Pa-1	ITA	CS1439	Zdr-1	CZE	CS22588
Gy-0	FRA	CS22631	Per-1	RUS	CS1445	Zdr-6	CZE	CS22589
H55	CZE	CS923	Petergof	RUS	CS926	Zu-1	SUI	CS6903
Ha-0	GER	CS6733	PHW-2	ITA	CS6002			

Supplementary Table 1 – Genotyped lines.

Phenotype	Accessions	Phenotype Description	Growth conditions	Phenotype scoring
LD*	167	Days to flowering time (FT) under Long Day (LD) and Short Day (SD) + / - vernalization.	18°C, 16 hrs daylight[1].	Number of days following stratification to opening of first flower. The experiment was stopped at 200 d, and accessions that had not flowered at that point were assigned a value of 200. Data previously published in[9].
LDV*	168		18°C, 16 hrs daylight, vernalized (5 wks, 4 °C)[1].	
SD*	162		18°C, 8 hrs daylight[1].	
SDV*	159		18°C, 8 hrs daylight, vernalized (5 wks, 4 °C)[1].	
0W*	137	Days to FT under LD with varying vernalization.	23°C, 16hrs daylight. Not vernalized.[6].	Number of days required for the bolt height to reach 5cm. Data previously published in[9].
2W*	152		23°C, 16hrs daylight. Vernalized for 2 wks at 5 °C, 8hrs daylight.[5].	
4W*	119		23°C, 16hrs daylight. Vernalized for 4 wks at 5 °C, 8hrs daylight.[5].	
8W*	155		23°C, 16hrs daylight. Vernalized for 8 wks at 5 °C, 8hrs daylight.[5].	
FLC*	167	FLC and FRI gene expression.	Growth in greenhouse, ~20-22°C, 16hrs daylight[6].	RNA was extracted from leaves after 4 wks of growth. FLC and FRI gene expression levels were determined by Northern hybridization quantified relative to β-TUBULIN expression. Data previously published[5].
FRI*	164			
FT10*	194	Flowering time (FT) and leaf number at flowering time (LN).	10°C, 16 hrs daylight[1].	Plants were checked bi-weekly for presence of first buds, and the average flowering time and average leaf number of 4 plants of the same accession at each temperature were collected.
FT16*	193		16°C, 16 hrs daylight[1].	
FT22*	193		22°C, 16 hrs daylight[1].	
LN10*	177		10°C, 16 hrs daylight[1].	
LN16*	176		16°C, 16 hrs daylight[1].	
LN22*	176		22°C, 16 hrs daylight[1].	
8W GH FT*	162	Days to FT and LN at FT.	20-22°C, natural light from the middle of October 2002 till March 2003, vernalized for 8wks at 4 °C, 8hrs daylight[6].	Flowering time was scored as the number of days for the bolt to reach 5cm and leaf number counted as the number of rosette leaves and the number of cauline leaves. Data previously published[5].
8W GH LN*	163			
0W GH FT*	153		20-22°C, natural light from the middle of October 2002 till March 2003[5].	
0W GH LN*	135			

Phenotype	Accessions	Phenotype Description	Growth conditions	Phenotype scoring
FT Field	180	Days to flowering of plants grown in the field.	Growth in field or greenhouse (20°C, 16h daylight), started in October[4].	Flowering time was scored as the number of days between germination date and appearance of the first flower. The diameter at flowering date was the longest diameter of the plant measured on the day the first flower was observed.
FT Diameter Field	180	Plant diameter at flowering (field).		
FT GH*	166	Days to flowering (greenhouse).		

Supplementary Table 2 – Flowering phenotypes. Phenotypes labeled with an asterisk were analyzed after log-transformation. Superscript numbers after growth conditions refer to the group that collected the phenotypic data and correspond to the author affiliations on the front page.

Phenotype	Accessions	Phenotype Description	Growth conditions	Phenotype scoring
AvrPphB	90	Hypersensitive Response.	20°C, 12 hrs daylight[2].	Following inoculation of two leaves per plant with 0.1 ml of 10^{-8} cfu/ml bacteria in 10 mM MgSO4 buffer using a blunt-tipped syringe, leaf collapse was scored at 20 hrs and again at 24 hrs after inoculation. A positive score at either time point was deemed a hypersensitive response. Data previously published[8].
AvrRpm1	84			
AvrB	87			
AvrRpt2	89			
Emco5	86	Disease presence or absence following inoculation with each isolate.	20-22°C, 10 hrs daylight, 70% humidity[8].	Propagation, inoculum preparation, infection and incubation were conducted as described previously[34]. All interactions were scored specifically on first true leaves as compatible, incompatible or intermediate depending on the consistency of presence / absence of sporangiophores determined on 5-10 seedlings of each genotype with three independent replications.
Emwa1	85			
Emoy2	76			
Hiks1	84			
Noco2	87			
LP23.1a*	175	Disease presence or absence following inoculation with each isolate.	20°C, 12 hrs daylight[2].	Each of the 5 *Pseudomonas viridiflava* strains was tested in a separate experiment with 6 replicates / accession. Four days after inoculation, inoculated leaves were scored by eye for disease symptom using a scale from 0 (no visible symptom) to 10 (leaves collapse and turn yellow), with an increment of 1.
RMX23.1a*	175			
RMX3.1b*	175			
PNA3.3a*	175			
ME3.1b*	175			
LP23.1a CFU2	175	*In planta* bacterial growth following inoculation with each isolate.	20°C, 12 hrs daylight[2].	*In planta* bacterial growth (number of CFU / leaf area) of the 5 *P. viridiflava* strains were individually measured as described previously[35].
RMX23.1a CFU2	175			
RMX3.1b CFU2	175			
PNA3.3a CFU2	175			
ME3.1b CFU2	175			
Trichome number C*	94	Trichome density.	20°C, 12 hrs daylight[2].	Measurements were collected from leaf disks removed from the 11th leaf of plants that had been treated with either 0.6 ml of a 0.45mM solution of jasmonic acid (Sigma J-2500) in water (JA) or 0.6ml of a water control (C). Trichome density was calculated as the trichome number per disk divided by the disk area.
Trichome number JA*	94			

Phenotype	Accessions	Phenotype Description	Growth conditions	Phenotype scoring
DC3000	95	Bacterial titers of *Pseudomonas syringae pv. tomato* DC3000.	20°C, 12 hrs daylight[2].	Following inoculation into leaf tissues, the titers of bacteria were measured from hole-punched leaf disks ground in 200μL of 10 mM MgSO4 at 0 and 4 days post inoculation. Measurements were expressed as colony forming units per unit area and replicated in triplicate.
Aphid number	95	Aphid offspring.	20°C, 12 hrs daylight[2].	On day 25 of growth, two alate females of the common peach aphid, *Myzus persicae*, were placed on each of four plants of each of the 96 genotypes. Nine days later, the number of offspring produced by these aphids on each plant were recorded.

Supplementary Table 3 – Defense-related phenotypes. Phenotypes labeled with an asterisk were analyzed after log-transformation. Superscript numbers after growth conditions refer to the group that collected the phenotypic data and correspond to the author affiliations on the front page.

Phenotype	Accessions	Phenotype Description	Growth conditions	Phenotype scoring
Lithium (Li7)	93	*In planta* ion concentration.	20°C, 16 hrs daylight[3,9].	Elemental analysis was performed with an ICP-MS (PerkinElmer). All samples were normalized to calculated weights as previously described[20].
Boron (B11)	93			
Sodium (Na23)*	93			
Magnesium (Mg25)	93			
Phosphorus (P31)	93			
Sulfur (S34)	93			
Potassium (K39)	93			
Calcium (Ca43)	93			
Manganese (Mn55)*	93			
Iron (Fe56)	93			
Colbolt (Co59)*	93			
Nickel (Ni60)	93			
Copper (Cu65)	93			
Zinc (Zn66)	93			
Arsenic (As75)*	93			
Selenium (Se82)	93			
Molybdenum (Mo98)*	93			
Cadmium (Cd114)*	93			

Supplementary Table 4 – Ionomics phenotypes. Phenotypes labeled with an asterisk were analyzed after log-transformation. Superscript numbers after growth conditions refer to the group that collected the phenotypic data and correspond to the author affiliations on the front page.

Phenotype	Accessions	Phenotype Description	Growth conditions	Phenotype scoring
LES	95	Presence or absence of lesioning.	Plants were grown for 7 weeks at 23°C[10].	Plants were scored for presence or absence of lesioning and yellowing. (Lesioning is the presence in older leaves of necrotic spots, that spread to the whole leaf. Yellowing is a precocious, more diffused leaf chlorosis).The results are the average of 4 plants / accession.
YEL	95	Presence or absence of yellowing.		
LY	95	Presence or absence of either lesioning or yellowing.		
FW*	95	Fresh weight of plants.	Plants were grown for 7 weeks at 23°C[10].	Six fully-expanded, non-lesioned leaves were collected from each of four plants for each accession, and weighed to obtain the fresh weight measurements. Leaves were then dried overnight at 85°C, and weighed again to obtain the dry weight measurements. The results are the average of 4 plants / accession.
DW*	95	Dry weight of plants.		
Chlorosis 10	177	Visual chlorosis presence.	10°C, 16 hrs daylight[1].	Results expressed as binary data, determined by the presence (1) or absence (0) of chlorosis in all 4 plants / accession at each temperature after 5wks of growth for 16°C, and 22°C, and 8wks for 10°C.
Chlorosis 16	176		16°C, 16 hrs daylight[1].	
Chlorosis 22	176		22°C, 16 hrs daylight[1].	
Anthocyanin 10	177	Visual anthocyanin presence.	10°C, 16 hrs daylight[1].	Results expressed as binary data, determined by the presence (1) or absence (0) of anthocyanin in all 4 plants / accession at each temperature after 5wks of growth for 16°C, and 22°C, and 8wks for 10°C.
Anthocyanin 16	176		16°C, 16 hrs daylight[1].	
Anthocyanin 22	177		22°C, 16 hrs daylight[1].	
Seed Dormancy	83	Seed dormancy level.	Seeds stored in cellulose paper bags and kept in a dark incubator at 20°C, 40% relative humidity[1].	Number of days of seed dry storage required to reach 50% germination, or DSDS50 value[36]. The measurement for each genotype was calculated as the average value across all available replicates.
Germ 10	177	Days to germination.	Stratified for 3 days at 4°C in the dark, followed by growth at 10°C, 16°C or 22°C with 16 hrs daylight[1].	Days from removal from stratification until emergence of first cotyledon at each of the 3 growth temperatures.
Germ 16	176			
Germ 22*	177			
Seedling Growth	101	Seedling growth rate.	Seeds were grown for one week in the greenhouse under long day (16 hours light)[7].	Seedling growth rate was given by leaf area at the beginning of the cold treatment and divided by the number of days of growth since sowing (in cm^2/day).

Phenotype	Accessions	Phenotype Description	Growth conditions	Phenotype scoring
Vern Growth	111	Vegetative growth rate during vernalization.	Seeds were grown for one week in the greenhouse under long day (16 hours light), vernalized for 4 weeks (4°C, 16h light, 50% relative humidity)[7].	Vegetative growth rate during vernalization was estimated as the increment of cm^2 leaf area per day between first day and last day of vernalization.
After Vern Growth	111	Vegetative growth rate after vernalization.	Seeds were grown for one week in the greenhouse under long day (16 hours light), vernalized for 4 weeks (4°C, 16h light, 50% relative humidity)and then returned to greenhouse[7].	Vegetative growth rate after vernalization was estimated as the increment of cm^2 leaf area per day between last day of vermalization and the seventh day after vernalization in greenhouse.
Secondary Dorm*	94	Decrease in germination rate after prolonged exposure to cold temperature.	Fully after-ripened seeds were treated with a 1 and 6-week long exposure to 4°C[7].	Secondary dormancy was given by the slope between the germination percentages of non-dormant seeds after one and six weeks of cold treatment. Viability of non germinating seeds after cold treatment was confirmed as described[37].
Germ in dark	94	Germination in the dark.	4°C, in the dark[7].	The ability to germinate in the dark at 4°C was measured as the percentage of non dormant seeds that can germinate during 1-week long cold exposure, in the absence of light.
DSDS50*	110	Duration of seed dry storage required for 50% of the seeds to germinate.	Dry storage, followed by 25°C, 12h day, 20°C, 12h night for 1 week[7].	Number of days of seed dry storage required to reach 50% germination, or DSDS50 value[36].
Seed bank 133-91	111	Non-monotonous dynamic of dormancy release.	Between 91 and 133 days of dry storage[7].	Genotypes consistently decreased their percentage of germination between 91 and 133 days of dry storage. The time point for this sudden reduction in germination rate was scored by the slope between germination percentages at these two time points.
Storage 7 days*	111	Primary dormancy.	7 days dry storage as described[367].	Primary dormancy was measured as the progressive increase of germination rate measured after 7 days of dry storage.
Storage 28 days*	111	Primary dormancy.	28 days dry storage as described[367].	Primary dormancy was measured as the progressive increase of germination rate measured after 28 days of dry storage.
Storage 56 days	111	Primary dormancy.	56 days dry storage as described[367].	Primary dormancy was measured as the progressive increase of germination rate measured after 56 days of dry storage.

Phenotype	Accessions	Phenotype Description	Growth conditions	Phenotype scoring
Hypocotyl length*	89	Hypocotyl length.	Seeds were vapour sterilized, plated in a random design on 1/2 MS agar plates (-sucrose), stratified for 4 days at 4° C in the dark, before transferring to photocycles (12 h 100 μ E/m^{2}s cool white light / 12 hours dark) and thermocycles (12 h 22° C / 12 h 12° C)[5].	After 7 days growth under the photocycle and thermocycle treatment, plants were flattened directly on the agar and imaged on a flatbed scanner. Hypocotyl lengths were determined using NIH Image.
Width 10*	176	Plant diameter.	Plants were grown at 10°C, 16°C or 22°C with 16 hrs daylight[1].	The diameters of 4 plants of each accession were measured at each temperature and the results were expressed as an average value across all available replicates.Plants were scored 5 weeks post germination for plants grown at 16 and 22°C and 8 weeks post germination for plants grown at 10°C (when the plants were mature).
Width 16	175			
Width 22	175			
Leaf serr 10	174	Level of leaf serration.	Plants were grown at 10°C, 16°C or 22°C with 16 hrs daylight[1].	Results expressed as level of serration ranging from 0 (entire lamina) to 1.5 (sharp/ jagged serration) across in all 4 plants / accession at 5 weeks post germination for plants grown at 16 and 22°C and 8 weeks post germination for plants grown at 10°C.
Leaf serr 16	176			
Leaf serr 22	176			
Leaf roll 10	177	Leaf roll presence.	Plants were grown at 10°C, 16°C or 22°C with 16 hrs daylight[1].	Results expressed as binary data, determined by the presence (1) or absence (0) of rolled leaves in all 4 plants / accession at 5 weeks post germination for plants grown at 16 and 22°C and 8 weeks post germination for plants grown at 10°C.
Leaf Roll 16	176			
Leaf Roll 22	176			
Rosette Erect 22	176	Presence of rosette errectness.	Plants were grown at 22°C, with 16 hrs daylight[1].	22°C was the only temperature at which this phenotype was frequently observed. Results were expressed as binary data, determined by the central rosette being erect (1) or not (0) in all 4 plants / accession phenotyped at 5 weeks post germination.
Silique Length 16	95	Silique length.	Plants were grown at 16°C or 22°C with 16 hrs daylight[1].	The average length of 4 siliques was measured for each accession after growth had concluded.
Silique Length 22	95			

Phenotype	Accessions	Phenotype Description	Growth conditions	Phenotype scoring
FT Duration GH*	147	Flowering period duration.	Growth in greenhouse, 20°C, 16hrs daylight[4].	Number of days between appearance of the first flower and the senescence of the last flower.
LC Duration GH*	147	Life cycle period.		Number of days between germination and plant complete senescence.
LFS GH*	148	Last flower senescence.		Number of days between germination and senescence of the last flower.
MT GH	147	Maturation period.		Number of days between last flower senescence and complete plant senescence.
RP GH	147	Reproduction period.		Number of days between the appearance of the first flower and the plant complete senescence.

Supplementary Table 5 – Developmental phenotypes. Phenotypes labeled with an asterisk were analyzed after log-transformation. Superscript numbers after growth conditions refer to the group that collected the phenotypic data and correspond to the author affiliations on the front page.

Gene name	Number of phenotypes			Nature of phenotype(s)	Suppl. Fig(s)
	Wilc.	EMMA	Both		
ARABIDOPSIS THALIANA HOMEOBOX 1 (*ATH1*)	18	12	9	Flowering	120
SHORT VEGETATIVE PHASE (*SVP*)	16	18	16	Flowering	121
FRIGIDA (*FRI*)	13	21	13	Flowering, life cycle and seedling dev.	122, 127
FLOWERING PROMOTING FACTOR 1 (*FPF1*)	6	7	4	Flowering	123
GIBBERELLIN 20-OXIDASE 3 (*YAP169*)	11	10	6	Flowering	124
RELATED TO AB13/VP1 (*RAV-1*)	11	6	5	Flowering	125
SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 4 (*SPL4*)	9	10	7	Flowering	126
CRYPTIC PRECOCIOUS (*CRP*)	8	14	6	Flowering	127
SPA1-RELATED 2 (*SPA2*)	16	7	6	Flowering	128
SPA1-RELATED 4 (*SPA4*)	10	10	7	Flowering	129
SIMILAR TO REDUCED VERNALIZATION RESPONSE (*sim to VRN1*)	18	13	11	Flowering	130
DELAY OF GERMINATION 1 (*DOG1*)	25	24	21	Flowering, life cycle, seedling dev.	131
DWARF IN LIGHT 2 (*DFL2*)	25	18	15	Flowering and seedling dev.	132
FLOWERING LOCUS C (*FLC*)	15	18	12	Flowering, life cycle, seedling dev.	133
ENHANCER OF TRY AND CPC 3 (*ETC3*)	16	18	14	Flowering	127
FLOWERING LOCUS T (*FT*)	2	11	1	Flowering, life cycle and seedling dev.	134
ENHANCER OF AG-4 2 (*HUA2*)	2	1	0	Flowering	135
HUA ENHANCER 2 (*HEN2*)	9	9	6	Flowering	136
VERNALIZATION INSENSITIVE 3 (*VIN3*)	7	5	3	Flowering	137
RESISTANCE TO P. SYRINGAE PV MACULICOLA 1 (*RPM1*)	3	4	3	Bacterial and fungal resistance	
CONSTITUTIVE TRIPLE RESPONSE (*CTR1*)	5	5	5	Bacterial and fungal resistance	138
RESISTANT TO P. SYRINGAE 2 (*RPS2*)	1	1	1	*AvrRpt2*	139
RESISTANT TO P. SYRINGAE 5 (*RPS5*)	2	2	1	Bacterial resistance	140
TRICHOMELESS 1 and *2* (*TCL1*, *TCL2*) and *ENHANCER OF TRY AND CPC 2* (*ETC2*)	2	2	2	Trichomes	141
HIGH-AFFINITY K+ TRANSPORTER 1 (*HKT1*)	1	1	1	Sodium	143
MOLYBDATE TRANSPORTER 1 (*MOT1*)	1	0	0	Molybdenum	144
SULFATE TRANSPORTER 1;2 (*SULTR1;2*)	1	2	1	Sulfur and Selenium	145
COMATOSE (*CTS*)	6	4	4	Seedling development and flowering	146
LIGHT-DEPENDENT SHORT HYPOCOTYLS 1 (*LSH1*)	1	1	1	Seedling development	147
LONG HYPOCOTYL IN FAR-RED (*HFR1*)	3	1	0	Seedling development and rosette erect	148
ACCELERATED CELL DEATH 6 (*ACD6*)	12	14	11	Bacterial and fungal resistance, aphid number, trichomes, weight, lesioning and chlorosis	149
SUPPRESSOR OF G2 ALLELE OF SKP1 (*SGT1A*)	9	8	6	Bacterial and fungal resistance, trichomes, weight, lesioning	150
ARABIDOPSIS THALIANA HOMOLOG OF YEAST AUTOPHAGY 18 (*AtATG18h*)	3	4	3	weight, aphid number and lesioning	151
FLAVANOL SYNTHASE (*FLS*)	1	1	1	Anthocyanin presence at 22°C	152

Supplementary Table 6 – Selected candidates and phenotypic associations.

Flowering phenotypes		Defense-related phenotypes		Ionomics phenotypes		Developmental phenotypes	
Phenotype	H^2	Phenotype	H^2	Phenotype	H^2	Phenotype	H^2
LD	0.99	*AvrPphB*	NA	Lithium	0.74	LES	NA
LDV	0.94	*AvrRpm1*	NA	Boron	0.89	YEL	NA
SD	1.00	*AvrB*	NA	Sodium	0.96	LY	NA
SDV	0.94	*AvrRpt2*	NA	Magnesium	0.93	FW	0.97
0W	0.99	Emco5	NA	Phosphorus	0.90	DW	0.92
2W	0.99	Emoy2	NA	Sulfur	0.86	Chlorosis 10	NA
4W	0.99	Hiks1	NA	Potassium	0.88	Chlorosis 16	NA
8W	0.96	Noco2	NA	Calcium	0.86	Chlorosis 22	NA
FLC	NA	At1	0.69	Manganese	0.82	Anthocyanin 10	NA
FRI	NA	As	0.66	Iron	0.69	Anthocyanin 16	NA
FT10	1.00	Bs	0.64	Colbolt	0.81	Anthocyanin 22	NA
FT16	0.99	At2	0.69	Nickel	0.60	Seed dormancy	0.99
FT22	0.99	As2	0.68	Copper	0.63	Germ 10	NA
LN10	0.98	At1 CFU2	0.54	Zinc	0.91	Germ 16	NA
LN16	0.98	As CFU2	0.60	Arsenic	0.59	Germ 22	NA
LN22	0.99	Bs CFU2	0.51	Selenium	0.77	Seedling growth	0.74
8W GH FT	1.00	At2 CFU2	0.62	Molybdenum	0.89	Vern growth	0.86
8W GH LN	1.00	As2 CFU2	0.66	Cadmium	0.84	After vern growth	0.78
0W GH FT	1.00	Trichome avg C	0.88			Secondary dorm	0.91
0W GH LN	1.00	Trichome avg JA	0.88			Germ in dark	0.91
FT Field	0.91	Bacterial titer	0.66			DSDS50	0.95
Diameter field	0.60	Aphid number	0.42			Seed bank 133-91	0.79
FT GH	0.99					Storage 7 days	0.95
						Storage 28 days	0.92
						Storage 56 days	0.94
						Hypocotyl length	0.97
						Width 10	NA
						Width 16	NA
						Width 22	NA
						Leaf serr 10	NA
						Leaf serr 16	NA
						Leaf serr 22	NA
						Leaf roll 10	NA
						Leaf roll 16	NA
						Leaf roll 22	NA
						Rosette erect 22	NA
						Silique length 16	0.97
						Silique length 22	0.99
						FT duration GH	0.89
						LC duration GH	0.96
						LFS GH	0.97
						MT GH	0.84
						RP GH	0.89

Supplementary Table 7 – Heritability estimates. Broad-sense heritabilities were estimated by dividing the genetic variance by the total phenotypic variance, using the mean-square values from standard analysis of variance. Estimation was not possible for some phenotypes, either because of the way measurements were taken, or because measurements for individuals are no longer available.

Supplementary Figure 9 – The pattern of correlations between phenotypes. Phenotypes are grouped into the four categories described in the text (blue = flowering, red = developmental, green = defense, purple = ionomics).

Supplementary Figure 10 – Candidate SNPs are over-represented among strong associations. Enrichment ratios across all flowering-related phenotypes, using the same significance-thresholds as in Fig. 3. Stars mark values significantly different from 1 at the 0.05 level (Supplementary Section 3.3). More stringent thresholds typically yield stronger enrichment, but the variance also increases because the number of significant genes decreases, and there is thus no simple relationship between degree of enrichment and its statistical significance (Supplementary Fig. 11).

Supplementary Figure 11 – The enrichment for candidate SNPs as a function of the nominal p-value cut-off across all flowering related phenotypes (*cf.* Fig 3). **a**, Wilcoxon's test, **b**, EMMA (**b**. Each line represents a single phenotype. Note that enrichment cannot always be calculated for high cut-offs as the number of SNP significant at this level could be zero.

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
2	11.7406	ETC3	AT4G01060	4	454542	-5930
3	11.298	SVP	AT2G22540	2	9588685	0
5	10.4959	ATARP4	AT1G18450	1	6369765	17797
8	10.0205	DFL2	AT4G03400	4	1516895	-17031
13	9.95211	ATH1	AT4G32980	4	15930436	-12389
15	9.84147	AGL17	AT2G22630	2	9611587	-13865
30	9.35821	PAT1	AT5G48150	5	19525511	13970
47	8.90731	DOG1*	AT5G45830	5	18625634	-17007
52	8.90358	sim to VRN1	AT4G33280	4	16034947	12411
105	8.3998	ATGA2OX7	AT1G50960	1	18887008	-6209

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
1	8.57121	SVP	AT2G22540	2	9588685	0
2	6.24143	FLC	AT5G10140	5	3188328	-8879
4	6.12352	AGL17	AT2G22630	2	9611587	-13865
10	5.54344	GI	AT1G22770	1	8051936	-9897
11	5.47408	ETC3	AT4G01060	4	454542	-5930
17	5.30428	SPA4	AT1G53090	1	19802665	12095
17	5.30428	SPL4	AT1G53160	1	19802665	-7422
21	5.09294	PAT1	AT5G48150	5	19525511	13970
24	4.88787	AT2G30810	AT2G30810	2	13151174	-15431
37	4.6557	GA1	AT4G02780	4	1260796	-15983

Supplementary Figure 12 – Summary of GWA results for Days to Flowering under Long Days (LD)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
1	11.4763	ATH1	AT4G32980	4	15930436	-12389
8	10.8829	sim to VRN1	AT4G33280	4	16034947	12411
28	10.1255	SVP	AT2G22540	2	9588685	0
31	10.0175	DOG1*	AT5G45830	5	18599929	6780
34	9.87989	DFL2	AT4G03400	4	1517051	-17187
56	9.52242	AGL17	AT2G22630	2	9606045	-19407
63	9.36984	AGL16	AT3G57230	3	21198120	6209
65	9.353	PHYA	AT1G09570	1	3104296	-3937
69	9.32824	SPA2	AT4G11110	4	6776344	0
70	9.30387	CO	AT5G15840	5	5186340	-13579

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
3	6.63436	DOG1*	AT5G45830	5	18599929	6780
5	5.91773	SVP	AT2G22540	2	9588685	0
31	4.57224	CRY1	AT4G08920	4	5742291	15041
35	4.54373	AGL17	AT2G22630	2	9606045	-19407
39	4.52727	sim to VRN1	AT4G33280	4	16034947	12411
59	4.36158	ATH1	AT4G32980	4	15930436	-12389
68	4.25248	CO	AT5G15840	5	5186340	-13579
68	4.25248	COL1	AT5G15850	5	5186340	-8440
69	4.22293	FD	AT4G35900	4	17025163	18873
82	4.0457	HEN2*	AT2G06990	2	2896755	0

Supplementary Figure 13 – Summary of GWA results for Days to Flowering under Long Days with vernalization (LDV)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
6	10.8001	ATGA2OX7	AT1G50960	1	18903090	7703
9	10.7614	sim to VRN1	AT4G33280	4	16068468	-19109
17	10.1598	ATH1	AT4G32980	4	15930436	-12389
23	9.38477	DOG1*	AT5G45830	5	18627646	-19019
44	8.96423	RAV1	AT1G13260	1	4553530	9791
53	8.84692	DFL2	AT4G03400	4	1517051	-17187
108	8.15704	PAT1	AT5G48150	5	19525511	13970
115	8.02712	ATARP4	AT1G18450	1	6369609	17641
133	7.88967	SPA2	AT4G11110	4	6776344	0
138	7.83315	DDF1	AT1G12610	1	4283872	6070

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
3	5.7025	ETC3	AT4G01060	4	458226	-2246
4	5.13541	HEN2*	AT2G06990	2	2916675	15600
5	5.12315	ATGA2OX7	AT1G50960	1	18903090	7703
17	4.6684	SVP	AT2G22540	2	9588685	0
20	4.53821	DOG1*	AT5G45830	5	18627646	-19019
30	4.25684	PAT1	AT5G48150	5	19525511	13970
34	4.19098	ATH1	AT4G32980	4	15930436	-12389
51	4.06349	SPA2	AT4G11110	4	6793109	15888
61	4.00216	sim to VRN1	AT4G33280	4	16068468	-19109
84	3.85566	LKP2	AT2G18915	2	8221164	-16599

Supplementary Figure 14 – Summary of GWA results for Days to Flowering under Short Days (SD)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
4	9.15154	ATGA2OX7	AT1G50960	1	18903090	7703
17	8.32555	sim to VRN1	AT4G33280	4	16068468	-19109
43	7.88579	DOG1*	AT5G45830	5	18617347	-8720
44	7.87713	DFL2	AT4G03400	4	1517051	-17187
59	7.59222	ATH1	AT4G32980	4	15930436	-12389
93	7.21393	FD	AT4G35900	4	17023128	16838
105	7.11653	DDF1	AT1G12610	1	4285007	4935
107	7.10616	HOS1	AT2G39810	2	16634891	9756
122	6.9728	SPA2	AT4G11110	4	6776344	0
149	6.81923	RAV1	AT1G13260	1	4540454	-1711

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
5	6.87858	ICU2	AT5G67100	5	26794176	-44
84	4.21087	AT3G10185	AT3G10185	3	3129928	-15656
102	4.0192	AGL15	AT5G13790	5	4430178	18839
117	3.91362	AGL20	AT2G45660	2	18803692	10920
117	3.91362	AGL6	AT2G45650	2	18803692	-7732
120	3.89624	ELF6	AT5G04240	5	1164843	-4702
121	3.89149	ATGID1B/GID1B	AT3G63010	3	23320329	17868
143	3.80016	VIN3	AT5G57380	5	23249199	14422
143	3.80016	ZTL	AT5G57360	5	23249199	-9454
153	3.75152	AGL19	AT4G22950	4	12031221	-3789

Supplementary Figure 15 – Summary of GWA results for Days to Flowering under Short Days with vernalization (SDV)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
5	8.64406	DOG1*	AT5G45830	5	18599929	6780
11	7.63685	AGL17	AT2G22630	2	9606045	-19407
11	7.63685	SVP	AT2G22540	2	9606045	15072
16	7.42352	ATARP4	AT1G18450	1	6369765	17797
30	7.00318	ETC3	AT4G01060	4	454542	-5930
34	6.85811	GA1	AT4G02780	4	1228186	9581
46	6.6054	ATGA2OX7	AT1G50960	1	18903090	7703
51	6.5377	DFL2	AT4G03400	4	1516895	-17031
63	6.38646	PAT1	AT5G48150	5	19525511	13970
91	6.13445	RAV1	AT1G13260	1	4559545	15806

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
5	5.51136	DOG1*	AT5G45830	5	18592535	14174
23	4.50434	ETC3	AT4G01060	4	454542	-5930
26	4.46126	GA1	AT4G02780	4	1248265	-3452
27	4.42836	ATARP4	AT1G18450	1	6369765	17797
55	4.00266	SVP	AT2G22540	2	9588685	1731
57	3.9937	LD	AT4G02560	4	1115702	7788
94	3.69007	CRP	AT4G00450	4	205170	0
108	3.60569	AGL17	AT2G22630	2	9606657	-18795
129	3.48307	sim to EDS4	AT4G00690	4	268809	-12836
129	3.48307	FRI	AT4G00650	4	268809	-217

Supplementary Figure 16 – Summary of GWA results for No vernalization, grown at JIC (0W)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
3	6.08452	ETC3	AT4G01060	4	454542	-5930
8	5.55105	SVP	AT2G22540	2	9588685	0
18	5.1009	ATARP4	AT1G18450	1	6369765	17797
21	5.037	FLC	AT5G10140	5	3188328	-8879
37	4.66299	ATGA2OX7	AT1G50960	1	18887008	-6209
46	4.49465	PAT1	AT5G48150	5	19525511	13970
52	4.34154	FHL	AT5G02200	5	441370	2478
57	4.26302	DOG1*	AT5G45830	5	18614346	-5719
85	4.01878	sim to FCA	AT2G47310	2	19424011	-6743
89	3.98623	AGL17	AT2G22630	2	9611587	-13865

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
3	6.08452	ETC3	AT4G01060	4	454542	-5930
8	5.55105	SVP	AT2G22540	2	9588685	0
18	5.1009	ATARP4	AT1G18450	1	6369765	17797
21	5.037	FLC	AT5G10140	5	3188328	-8879
37	4.66299	ATGA2OX7	AT1G50960	1	18887008	-6209
45	4.49465	PAT1	AT5G48150	5	19525511	13970
50	4.34154	FHL	AT5G02200	5	441370	2478
54	4.26302	DOG1*	AT5G45830	5	18614346	-5719
83	3.98623	AGL17	AT2G22630	2	9611587	-13865
114	3.73038	PIF4	AT2G43010	2	17914822	18695

Supplementary Figure 17 – Summary of GWA results for 2 weeks vernalization, grown at JIC (2W)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
18	8.10388	DOG1*	AT5G45830	5	18607728	0
21	7.99396	ATH1	AT4G32980	4	15930436	-12389
33	7.89219	ATARP4	AT1G18450	1	6369765	17797
52	7.59895	sim to VRN1	AT4G33280	4	16034947	12411
60	7.59393	DFL2	AT4G03400	4	1516895	-17031
98	7.20296	SVP	AT2G22540	2	9588685	0
100	7.19271	RAV1	AT1G13260	1	4559545	15806
112	7.14885	ATGA2OX7	AT1G50960	1	18887008	-6209
136	7.04275	ELF4	AT2G40080	2	16729405	11967
139	7.00863	PAT1	AT5G48150	5	19525511	13970

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
1	7.83035	SVP	AT2G22540	2	9588685	0
5	5.89822	DOG1*	AT5G45830	5	18607728	0
8	5.66563	PAT1	AT5G48150	5	19525511	13970
12	5.1676	ETC3	AT4G01060	4	454542	-5930
14	5.16114	AGL17	AT2G22630	2	9606045	-19407
40	4.47289	PIL2	AT3G62090	3	23019510	-17826
41	4.47006	ATARP4	AT1G18450	1	6369765	17797
42	4.46738	VIN3	AT5G57380	5	23249199	14422
42	4.46738	ZTL	AT5G57360	5	23249199	-9454
82	3.9455	DFL2	AT4G03400	4	1516895	-17031

Supplementary Figure 18 – Summary of GWA results for 4 weeks vernalization, grown at JIC (4W)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
1	10.3023	RAV1	AT1G13260	1	4559545	15806
7	9.20954	ATH1	AT4G32980	4	15930436	-12389
10	9.09475	ATGA2OX7	AT1G50960	1	18903090	7703
15	8.80655	DOG1*	AT5G45830	5	18618012	-9385
30	8.3178	CUL4	AT5G46210	5	18773872	-19835
39	8.25028	sim to VRN1	AT4G33280	4	16034947	12411
48	8.18372	HEN2*	AT2G06990	2	2896755	0
67	7.95567	GASA5	AT3G02885	3	633650	4378
84	7.66337	sim to FCA	AT2G47310	2	19441616	7269
107	7.55465	FLC	AT5G10140	5	3188328	-8879

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
21	4.46966	FLC	AT5G10140	5	3188328	-8879
27	4.30108	ATH1	AT4G32980	4	15930436	-12389
29	4.28395	TFL2	AT5G17690	5	5812299	14874
31	4.19141	CO	AT5G15840	5	5186340	-13579
31	4.19141	COL1	AT5G15850	5	5186340	-8440
42	3.94036	PHYB	AT2G18790	2	8159983	8471
57	3.81037	HEN2*	AT2G06990	2	2896755	0
58	3.80001	RAV1	AT1G13260	1	4559545	15806
61	3.77858	sim to FCA	AT2G47310	2	19436533	2186
130	3.43423	sim to VRN1	AT4G33280	4	16040939	6419

Supplementary Figure 19 – Summary of GWA results for 8 weeks vernalization, grown at JIC (8W)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
3	8.9246	SVP	AT2G22540	2	9578960	-7994
5	8.59608	AGL17	AT2G22630	2	9611587	-13865
7	8.49959	SPA4	AT1G53090	1	19790829	259
7	8.49959	SPL4	AT1G53160	1	19790829	-19258
12	8.18367	ETC3	AT4G01060	4	454542	-5930
17	7.96135	DFL2	AT4G03400	4	1507838	-7974
20	7.81214	DOG1*	AT5G45830	5	18625726	-17099
25	7.74903	CRP	AT4G00450	4	200026	-3445
40	7.37903	EMF1	AT5G11530	5	3677099	-18764
47	7.24378	sim to VRN1	AT4G33280	4	16056698	-7339

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
16	4.84345	ETC3	AT4G01060	4	454542	-5930
35	4.56274	SPA4	AT1G53090	1	19790829	259
35	4.56274	SPL4	AT1G53160	1	19790829	-19258
39	4.49707	CRP	AT4G00450	4	205170	0
41	4.42654	DFL2	AT4G03400	4	1487946	9589
71	3.90626	sim to EDS4	AT4G00690	4	268809	-12836
71	3.90626	FRI	AT4G00650	4	268809	-217
72	3.9053	SVP	AT2G22540	2	9578960	-7994
101	3.62535	RGA1	AT2G01570	2	243650	11598
113	3.56265	DOG1*	AT5G45830	5	18623805	-15178

Supplementary Figure 20 – Summary of GWA results for FLC gene expression (FLC)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
1	14.291	FRI	AT4G00650	4	268809	-217
1	14.291	sim to ESD4	AT4G00690	4	268809	-12836
11	8.32062	CRP	AT4G00450	4	219919	8916
36	6.04476	ETC3	AT4G01060	4	478305	17220
93	4.9258	YAP169	AT5G07200	5	2229186	14368
114	4.75766	ESD4	AT4G15880	4	9034861	18730
120	4.70695	SPA1	AT2G46340	2	19048218	-13732
136	4.64302	CUL4	AT5G46210	5	18762327	-8290
189	4.42435	SKB1	AT4G31120	4	15124553	7464
201	4.3737	ATARP4	AT1G18450	1	6338795	-9305

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
1	23.4027	FRI	AT4G00650	4	268809	-217
1	23.4027	sim to ESD4	AT4G00690	4	268809	-12836
11	11.1729	CRP	AT4G00450	4	219919	8916
38	6.28005	ETC3	AT4G01060	4	479773	18688
88	4.291	SKB1	AT4G31120	4	15124553	7464
99	4.15739	CUL4	AT5G46210	5	18762327	-8290
141	3.76624	AGL18	AT3G57390	3	21261205	14317
170	3.52783	ATGID1B	AT3G63010	3	23290623	-9777
233	3.27626	sim to REF6	AT5G46910	5	19047981	-17026
234	3.27625	AGL8	AT5G60910	5	24505973	13735

Supplementary Figure 21 – Summary of GWA results for FRI gene expression (FRI)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
1	11.3864	ATH1	AT4G32980	4	15930436	-12389
2	11.3786	SVP	AT2G22540	2	9588685	0
5	10.8544	AGL17	AT2G22630	2	9611587	-13865
25	9.92236	sim to VRN1	AT4G33280	4	16040939	6419
36	9.7753	FES1	AT2G33835	2	14332703	-10927
36	9.7753	SPL3	AT2G33810	2	14332703	19555
40	9.62578	DOG1*	AT5G45830	5	18607728	0
58	9.19259	DFL2	AT4G03400	4	1517051	-17187
59	9.17769	GASA5	AT3G02885	3	633891	4137
76	8.92443	ATARP4	AT1G18450	1	6369765	17797

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
4	5.83594	FLC	AT5G10140	5	3188328	-8879
21	5.14093	sim to ESD4	AT4G00690	4	288749	5620
21	5.14093	FRI	AT4G00650	4	288749	17246
30	4.73222	DOG1*	AT5G45830	5	18614346	-5719
32	4.65948	FT	AT1G65480	1	24345319	7722
52	4.10145	BAS1	AT2G26710	2	11408353	17663
53	4.09725	NUA	AT1G79280	1	29817176	6893
61	3.98117	SVP	AT2G22540	2	9588685	0
80	3.83659	LD	AT4G02560	4	1114351	9139
135	3.42989	CRP	AT4G00450	4	226062	15059

Supplementary Figure 22 – Summary of GWA results for Days to flowering at 10°C (FT10)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
2	11.69	ETC3	AT4G01060	4	454542	-5930
4	11.4261	AGL17	AT2G22630	2	9611587	-13865
5	11.3772	ATH1	AT4G32980	4	15930436	-12389
7	11.0602	ATARP4	AT1G18450	1	6369609	17641
8	11.0553	SVP	AT2G22540	2	9588685	0
10	11.0289	sim to VRN1	AT4G33280	4	16056698	-7339
20	10.7701	DFL2	AT4G03400	4	1516895	-17031
54	10.1493	FPF1	AT5G24860	5	8545284	2832
71	10.0034	FLC	AT5G10140	5	3188328	-8879
147	9.16419	GASA5	AT3G02885	3	633213	4815

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
1	6.76866	FLC	AT5G10140	5	3188328	-8879
6	5.15681	sim to EDS4	AT4G00690	4	268809	-12836
6	5.15681	FRI	AT4G00650	4	268809	-217
20	4.5821	DOG1*	AT5G45830	5	18598041	8668
54	4.33335	FT	AT1G65480	1	24341923	4326
59	4.25287	CRP	AT4G00450	4	219312	8309
68	4.205	ATARP4	AT1G18450	1	6369765	17797
82	4.02845	LD	AT4G02560	4	1113916	9574
85	4.02267	BAS1	AT2G26710	2	11408353	17663
87	4.01148	AGL17	AT2G22630	2	9611587	-13865

Supplementary Figure 23 – Summary of GWA results for Days to flowering at 16°C (FT16)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
4	11.6112	ATARP4	AT1G18450	1	6369609	17641
16	10.824	DFL2	AT4G03400	4	1516895	-17031
19	10.6444	AGL17	AT2G22630	2	9611587	-13865
43	9.88639	SVP	AT2G22540	2	9606045	15072
52	9.74982	ATH1	AT4G32980	4	15930436	-12389
97	9.14786	sim to VRN1	AT4G33280	4	16040939	6419
103	9.14404	ATGA2OX7	AT1G50960	1	18903090	7703
138	8.93617	RAV1	AT1G13260	1	4541173	-992
139	8.90838	ETC3	AT4G01060	4	454542	-5930
153	8.79855	FLC	AT5G10140	5	3188328	-8879

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
1	7.35652	FLC	AT5G10140	5	3188328	-8879
21	6.02586	sim to ESD4	AT4G00690	4	268809	-12836
21	6.02586	FRI	AT4G00650	4	268809	-217
39	4.95198	DOG1*	AT5G45830	5	18590971	15738
80	4.31728	CDF1	AT5G62430	5	25084106	2213
98	4.18876	ATARP4	AT1G18450	1	6369765	17797
180	3.62105	CRP	AT4G00450	4	206784	0
188	3.58201	SPA4	AT1G53090	1	19790829	259
188	3.58201	SPL4	AT1G53160	1	19790829	-19258
199	3.54707	RGA1	AT2G01570	2	260329	-2780

Supplementary Figure 24 – Summary of GWA results for Days to flowering at 22°C (FT22)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
1	10.7383	ATH1	AT4G32980	4	15930436	-12389
5	9.96091	AGL17	AT2G22630	2	9611587	-13865
6	9.86254	DOG1*	AT5G45830	5	18607728	0
8	9.73402	SVP	AT2G22540	2	9606045	15072
15	9.52932	sim to VRN1	AT4G33280	4	16034947	12411
41	8.60168	DFL2	AT4G03400	4	1517051	-17187
70	7.9712	ATARP4	AT1G18450	1	6369765	17797
88	7.80368	GASA5	AT3G02885	3	633891	4137
108	7.61248	ATGID1B	AT3G63010	3	23294580	-5820
117	7.54299	SPA4	AT1G53090	1	19802665	12095

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
7	4.96507	DOG1*	AT5G45830	5	18600041	6668
10	4.75953	DFL1	AT5G54510	5	22166178	-15274
11	4.72347	sim to VRN1	AT4G33280	4	16056494	-7135
23	4.37626	ATH1	AT4G32980	4	15930436	-12389
24	4.27912	SPA4	AT1G53090	1	19802665	12095
24	4.27912	SPL4	AT1G53160	1	19802665	-7422
36	4.16855	FT	AT1G65480	1	24341937	4340
94	3.75715	CIP7	AT4G27430	4	13743010	19680
102	3.72526	SVP	AT2G22540	2	9588685	0
110	3.68391	AGL17	AT2G22630	2	9606045	-19407

Supplementary Figure 25 – Summary of GWA results for Leaf Number at 10°C (LN10)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
9	10.8254	ATARP4	AT1G18450	1	6369609	17641
25	10.0518	sim to VRN1	AT4G33280	4	16034947	12411
34	9.90458	ETC3	AT4G01060	4	454542	-5930
35	9.8285	AGL17	AT2G22630	2	9611587	-13865
42	9.81923	ATH1	AT4G32980	4	15930436	-12389
88	9.12519	SVP	AT2G22540	2	9588685	0
94	8.99851	DFL2	AT4G03400	4	1517051	-17187
154	8.28101	FLC	AT5G10140	5	3188328	-8879
162	8.23112	YAP169	AT5G07200	5	2264248	-18908
199	8.04169	SPA2	AT4G11110	4	6793109	15888

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
2	5.5663	ETC3	AT4G01060	4	454542	-5930
29	4.27582	sim to ESD4	AT4G00690	4	280774	-871
29	4.27582	FRI	AT4G00650	4	280774	9271
41	4.05769	DFL2	AT4G03400	4	1500178	-314
92	3.65582	sim to PCL1	AT5G59570	5	24008772	-12342
92	3.65582	SRR1	AT5G59560	5	24008772	9010
100	3.61767	GA1	AT4G02780	4	1248265	-3452
118	3.52327	YAP169	AT5G07200	5	2264248	-18908
137	3.45341	sim to VRN1	AT4G33280	4	16040939	6419
182	3.26357	FPF1	AT5G24860	5	8545330	2878

Supplementary Figure 26 – Summary of GWA results for Leaf Number at 16°C (LN16)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
5	10.2239	ATARP4	AT1G18450	1	6369609	17641
10	9.78994	AGL17	AT2G22630	2	9611587	-13865
13	9.67532	DFL2	AT4G03400	4	1516895	-17031
24	9.38415	ETC3	AT4G01060	4	454542	-5930
25	9.36401	ATGA2OX7	AT1G50960	1	18903090	7703
54	8.97539	SVP	AT2G22540	2	9606045	15072
56	8.96646	ATH1	AT4G32980	4	15930436	-12389
97	8.54422	sim to VRN1	AT4G33280	4	16034947	12411
137	8.26798	FRI	AT4G00650	4	254137	-14889
179	7.91885	DOG1*	AT5G45830	5	18599929	6780

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
4	5.30509	ETC3	AT4G01060	4	454542	-5930
18	4.70901	ATGA2OX7	AT1G50960	1	18903090	7703
29	4.37363	DOG1*	AT5G45830	5	18599929	6780
37	4.19623	DFL2	AT4G03400	4	1498770	0
38	4.18079	GA1	AT4G02780	4	1261211	-16398
47	4.0692	sim to ESD4	AT4G00690	4	268809	-12836
47	4.0692	FRI	AT4G00650	4	268809	-217
52	3.96494	FLC	AT5G10140	5	3188328	-8879
67	3.86083	CRY1	AT4G08920	4	5742291	15041
69	3.8371	ATHB51	AT5G03790	5	987681	-17301

Supplementary Figure 27 – Summary of GWA results for Leaf Number at 22°C (LN22)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
13	9.45204	DOG1*	AT5G45830	5	18618012	-9385
27	8.78487	sim to VRN1	AT4G33280	4	16068468	-19109
48	8.41001	HEN2*	AT2G06990	2	2896755	0
58	8.23991	ATGA2OX7	AT1G50960	1	18903090	7703
60	8.21011	GASA5	AT3G02885	3	633213	4815
63	8.08653	ATH1	AT4G32980	4	15930436	-12389
87	7.84994	RAV1	AT1G13260	1	4559545	15806
100	7.55871	sim to FCA	AT2G47310	2	19441616	7269
158	7.09915	SHP2	AT2G42830	2	17813490	-13842
216	6.78661	AGL17	AT2G22630	2	9623626	-1826

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
3	5.68175	DOG1*	AT5G45830	5	18599929	6780
10	4.92142	FLC	AT5G10140	5	3188328	-8879
37	4.30737	ELF8	AT2G06210	2	2445300	-8616
62	3.96084	LDL1	AT1G62830	1	23262633	5522
71	3.89735	PAT1	AT5G48150	5	19525511	13970
92	3.83531	SVP	AT2G22540	2	9588685	0
95	3.82346	GASA5	AT3G02885	3	633213	4815
124	3.61616	VIP5	AT1G61040	1	22484552	-2320
133	3.58601	FES1	AT2G33835	2	14332703	-10927
133	3.58601	SPL3	AT2G33810	2	14332703	19555

Supplementary Figure 28 – Summary of GWA results for Days to Flowering, 8wks vernalization, greenhouse (8W GH FT)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
2	9.12376	DOG1*	AT5G45830	5	18617347	-8720
6	8.80264	ATGA2OX7	AT1G50960	1	18903090	7703
7	8.75653	CRY1	AT4G08920	4	5735788	8538
8	8.72322	ATH1	AT4G32980	4	15930436	-12389
12	8.65723	sim to VRN1	AT4G33280	4	16068468	-19109
22	8.33749	HEN2*	AT2G06990	2	2886573	-8364
65	7.19898	PHYB	AT2G18790	2	8159983	8471
78	7.04572	ETC3	AT4G01060	4	475865	14780
87	7.02188	CO	AT5G15840	5	5186340	-13579
87	7.02188	COL1	AT5G15850	5	5186340	-8440

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
2	6.8722	FRI	AT4G00650	4	269962	0
2	6.8722	sim to ESD4	AT4G00690	4	269962	-11683
7	5.55414	AGL15	AT5G13790	5	4429786	19231
9	5.02585	DOG1*	AT5G45830	5	18599929	6780
13	4.75819	HEN2*	AT2G06990	2	2886573	-8364
31	4.37153	CRY1	AT4G08920	4	5735788	8538
32	4.35096	ATH1	AT4G32980	4	15933766	-15719
36	4.19578	CO	AT5G15840	5	5181027	-8266
36	4.19578	COL1	AT5G15850	5	5181027	-3127
39	4.13468	FRL1	AT5G16320	5	5332862	-11643

Supplementary Figure 29 – Summary of GWA results for Leaf Number at Flowering with 8 wks vernalization, greenhouse (8W GH LN)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
6	9.51193	ETC3	AT4G01060	4	454542	-5930
13	9.25378	AGL17	AT2G22630	2	9606045	-19407
13	9.25378	SVP	AT2G22540	2	9606045	15072
17	9.24797	DFL2	AT4G03400	4	1516895	-17031
30	8.85728	ATARP4	AT1G18450	1	6369609	17641
48	8.58298	RAV1	AT1G13260	1	4559545	15806
77	8.27901	ATH1	AT4G32980	4	15930436	-12389
86	8.21846	FRI	AT4G00650	4	257795	-11231
110	8.07613	GASA5	AT3G02885	3	633213	4815
123	7.96829	PAT1	AT5G48150	5	19525511	13970

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
10	5.81731	SVP	AT2G22540	2	9606045	15072
10	5.81731	AGL17	AT2G22630	2	9606045	-19407
24	5.26745	FRI	AT4G00650	4	269962	0
24	5.26745	sim to ESD4	AT4G00690	4	269962	-11683
35	4.98061	AT2G30810	AT2G30810	2	13151174	-15431
39	4.85632	SPA4	AT1G53090	1	19802665	12095
39	4.85632	SPL4	AT1G53160	1	19802665	-7422
49	4.68024	SMZ	AT3G54990	3	20405700	-18201
54	4.56776	ETC3	AT4G01060	4	454542	-5930
60	4.48035	ATARP4	AT1G18450	1	6371569	19601

Supplementary Figure 30 – Summary of GWA results for Days to Flowering, no vernalization, greenhouse (0W GH FT)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
1	7.21016	ETC3	AT4G01060	4	454542	-5930
5	6.74401	DOG1*	AT5G45830	5	18625726	-17099
47	5.27161	FRI	AT4G00650	4	269962	0
47	5.27161	sim to ESD4	AT4G00690	4	269962	-11683
61	5.13955	CO	AT5G15840	5	5181027	-8266
61	5.13955	COL1	AT5G15850	5	5181027	-3127
100	4.74291	ATH1	AT4G32980	4	15930436	-12389
106	4.70271	VIM1	AT1G57820	1	21416526	1309
198	4.3151	sim to VRN1	AT4G33280	4	16034947	12411
207	4.30446	FHL	AT5G02200	5	441370	2478

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
8	4.40313	FRI	AT4G00650	4	269962	0
8	4.40313	sim to ESD4	AT4G00690	4	269962	-11683
107	3.29776	FCA	AT4G16280	4	9203105	3508
107	3.29776	PHYD	AT4G16250	4	9203105	-3604
119	3.24721	ETC3	AT4G01060	4	458226	-2246
151	3.1231	AGL24	AT4G24540	4	12687473	-13391
156	3.09849	AGL14	AT4G11880	4	7123531	-19578
189	3.00315	SEPALLATA2	AT3G02310	3	468101	-1020
189	3.00315	COL2	AT3G02380	3	468101	19142
204	2.97328	FD	AT4G35900	4	17024734	18444

Supplementary Figure 31 – Summary of GWA results for Leaf Number at Flowering, no vernalization, greenhouse (0W GH LN)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
19	10.1569	ATH1	AT4G32980	4	15930436	-12389
21	10.0736	AGL16	AT3G57230	3	21198120	6209
29	9.76096	sim to VRN1	AT4G33280	4	16034947	12411
35	9.5235	DOG1*	AT5G45830	5	18617347	-8720
39	9.24223	AGL18	AT3G57390	3	21250463	3575
68	8.73049	ETC3	AT4G01060	4	473140	12055
90	8.33638	MMP	AT1G70170	1	26417569	-9968
94	8.25415	LKP2	AT2G18915	2	8195445	6209
100	8.16873	FY	AT5G13480	5	4333359	-1657
117	7.96492	ATGA2OX7	AT1G50960	1	18903090	7703

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
3	5.7133	TSF	AT4G20370	4	10989741	11041
8	4.99778	APRR5	AT5G24470	5	8361420	-2544
12	4.57815	ATHAP2B	AT3G05690	3	1683884	-4946
17	4.41825	HEN2*	AT2G06990	2	2916675	15600
31	4.10872	DOG1*	AT5G45830	5	18618012	-9385
33	4.04498	ELF5	AT5G62640	5	25175269	-5502
50	3.92096	LD	AT4G02560	4	1135406	-6985
100	3.485	GI	AT1G22770	1	8084983	17278
102	3.47798	DDF2	AT1G63030	1	23372416	-341
121	3.41989	sim to VRN1	AT4G33280	4	16068010	-18651

Supplementary Figure 32 – Summary of GWA results for Days to flowering, field (FT Field)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
1	9.74548	SVP	AT2G22540	2	9588685	0
3	9.4309	ICU2	AT5G67100	5	26809133	6803
82	7.30149	FHL	AT5G02200	5	432812	-4646
143	6.80907	FPF1	AT5G24860	5	8545284	2832
187	6.5702	GA4H	AT1G80340	1	30221280	-14188
237	6.40908	DDF1	AT1G12610	1	4272546	17396
253	6.35884	ELF5	AT5G62640	5	25152024	14635
257	6.35111	FES1	AT2G33835	2	14307001	11862
257	6.35111	SPL3	AT2G33810	2	14307001	-5076
316	6.11017	FWA	AT4G25530	4	13019314	-19055

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
16	8.70176	ETC3	AT4G01060	4	454542	-5930
17	8.53689	DOG1*	AT5G45830	5	18625726	-17099
31	7.98428	ATARP4	AT1G18450	1	6369765	17797
40	7.789	CO	AT5G15840	5	5174905	-2144
40	7.789	COL1	AT5G15850	5	5174905	1189
45	7.72477	SVP	AT2G22540	2	9588685	0
46	7.68272	ATH1	AT4G32980	4	15930436	-12389
47	7.64895	FRI	AT4G00650	4	257795	-11231
54	7.52425	AGL17	AT2G22630	2	9611587	-13865
58	7.47533	YAP169	AT5G07200	5	2264248	-18908

Supplementary Figure 33 – Summary of GWA results for Diameter of plants at flowering, field (FT Diameter Field)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
5	4.99591	ICU2	AT5G67100	5	26809133	6803
19	4.21499	SVP	AT2G22540	2	9588685	0
33	3.95209	FHL	AT5G02200	5	432812	-4646
59	3.6236	DDF2	AT1G63030	1	23373075	-1000
143	3.26417	FLP1	AT4G31380	4	15220167	-9624
215	3.07062	SAR3	AT1G80680	1	30342756	9095
245	3.01107	PHYD	AT4G16250	4	9176721	18896
278	2.96784	LIP1	AT5G64813	5	25919411	-8094
304	2.91061	DDF1	AT1G12610	1	4275223	14719
321	2.88968	VIM1	AT1G57820	1	21440729	-19118

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
1	7.02089	ATARP4	AT1G18450	1	6371569	19601
15	5.14164	AGL17	AT2G22630	2	9611587	-13865
17	5.1299	SVP	AT2G22540	2	9606045	15072
19	5.11259	YAP169	AT5G07200	5	2264248	-18908
30	4.73865	ETC3	AT4G01060	4	458226	-2246
31	4.7336	DOG1*	AT5G45830	5	18625726	-17099
36	4.47972	FRI	AT4G00650	4	257795	-11231
37	4.47586	DFL2	AT4G03400	4	1513980	-14116
58	3.9579	PAT1	AT5G48150	5	19525511	13970
66	3.9173	SPA4	AT1G53090	1	19790829	259

Supplementary Figure 34 – Summary of GWA results for Days to flowering, greenhouse (FT GH)

Phenotype histogram and quantile-quantile plots of p-values

Fisher's exact test results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
1	16.2034	RPS5	AT1G12220	1	4146712	0
1	16.2034	RFL1	AT1G12210	1	4143161	0
20	6.27622	FRK1	AT2G19190	2	8345276	-8250
29	5.99331	AT4G23690	AT4G23690	4	12348175	-8418
30	5.93593	AT5G11250	AT5G11250	5	3581255	6724
32	5.82899	AT3G44400	AT3G44400	3	16060932	-244
35	5.71193	AT1G12280	AT1G12280	1	4163167	11706
41	5.63875	AT4G19060	AT4G19060	4	10464658	-18347
46	5.53084	AT1G77920	AT1G77920	1	29318528	12771
57	5.29313	ATPP2-A7	AT5G45090	5	18240316	-18089

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
1	21.2529	RPS5	AT1G12220	1	4146712	0
1	21.2529	RFL1	AT1G12210	1	4143161	0
12	5.65013	HSP81-1	AT5G52640	5	21357089	-12536
17	5.17814	AT1G12280	AT1G12280	1	4163167	11706
18	5.10236	AT4G23690	AT4G23690	4	12348175	-8418
23	4.70469	AT4G19060	AT4G19060	4	10464658	-18347
25	4.6634	ATTRX5	AT1G45145	1	17071777	5605
44	4.36367	GcpE	AT5G60600	5	24387864	7153
47	4.23399	AT3G26470	AT3G26470	3	9700429	11550
50	4.18452	AT4G14610	AT4G14610	4	8382017	1474

Supplementary Figure 35 – Summary of GWA results for *AvrPphB*

Phenotype histogram and quantile-quantile plots of p-values

Fisher's exact test results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
1	11.6797	RPM1	AT3G07040	3	2227823	0
38	5.37362	CTR1*	AT5G03730	5	980341	493
57	4.9404	AT5G58120	AT5G58120	5	23528056	-6662
104	4.36207	AT1G58170	AT1G58170	1	21544828	4327
164	3.94676	AT3G28890	AT3G28890	3	10907617	-7539
170	3.89614	AT5G47250	AT5G47250	5	19203727	0
183	3.83911	AT4G09360	AT4G09360	4	5927294	-12889
183	3.83911	ATMKK3	AT5G40440	5	16216269	14414

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
1	16.0583	RPM1	AT3G07040	3	2227823	0
67	4.71172	CTR1*	AT5G03730	5	980341	493
36	5.49555	AT5G58120	AT5G58120	5	23528056	-6662
40	5.42319	AT1G31540	AT1G31540	1	11273835	14598
71	4.62411	RBK1	AT5G10520	5	3328044	-5133
75	4.60962	AT2G03200	AT2G03200	2	976276	-8361
76	4.58902	ATMKK3	AT5G40440	5	16216269	14414
103	4.06069	AT1G61300	AT1G61300	1	22595752	15379
124	3.94977	AT4G19470	AT4G19470	4	10610171	2833

Supplementary Figure 36 – Summary of GWA results for *AvrRpm1*

Phenotype histogram and quantile-quantile plots of p-values

Fisher's exact test results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
1	9.46995	RPS2	AT4G26090	4	13225030	0
10	4.71137	AT4G23515	AT4G23515	4	12271968	0
27	3.99291	ACD2	AT4G37000	4	17446741	2892
36	3.95202	AT4G23440	AT4G23440	4	12220072	-17703
36	3.95202	SGT1A	AT4G23570	4	12280847	-18986
61	3.69793	AT4G11180	AT4G11180	4	6820562	0
84	3.61859	AT4G23690	AT4G23690	4	12354385	-14628
86	3.59883	ATMKK4	AT1G51660	1	19167275	7660

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
1	18.1429	RPS2	AT4G26090	4	13225030	0
12	5.52885	KELP	AT4G10920	4	6682980	13728
36	4.44658	AT4G13880	AT4G13880	4	8019670	-6130
39	4.39734	MLO6	AT1G61560	1	22718242	-2533
42	4.36038	AT4G16990	AT4G16990	4	9561902	0
43	4.33277	AT4G19925	AT4G19925	4	10800512	0
88	3.96664	SHM1	AT4G37930	4	17826798	4927
97	3.92061	SGT1A	AT4G23570	4	12280847	-18986
127	3.76846	ACD2	AT4G37000	4	17446741	2892
150	3.66746	RIN4	AT3G25070	3	9123833	-8484

Supplementary Figure 37 – Summary of GWA results for *AvrRpt2*

Phenotype histogram and quantile-quantile plots of p-values

Fisher's exact test results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
1	12.5471	RPM1	AT3G07040	3	2227823	0
28	5.53339	CTR1*	AT5G03730	5	980341	493
79	4.51827	MLO3	AT3G45290	3	16626151	2378
84	4.5062	AT5G58120	AT5G58120	5	23528056	-6662
100	4.38287	AT3G13650	AT3G13650	3	4461932	-967
103	4.35815	AT5G47250	AT5G47250	5	19203727	0
115	4.26213	AT5G48620	AT5G48620	5	19745431	6753
129	4.18301	AT4G09360	AT4G09360	4	5952496	9219
142	4.08758	AT3G28890	AT3G28890	3	10907617	-7539
149	4.03732	PAD4	AT3G52430	3	19444164	0

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
1	16.1107	RPM1	AT3G07040	3	2227823	0
21	6.00182	AT2G03200	AT2G03200	2	976276	-8361
33	5.4264	AT1G31540	AT1G31540	1	11273835	14598
36	5.06718	CTR1*	AT5G03730	5	980341	493
93	4.13182	AT5G45490	AT5G45490	5	18451281	1657
99	4.06284	AT3G26470	AT3G26470	3	9694773	5894
114	3.98485	AT3G28890	AT3G28890	3	10905693	-5615
120	3.88845	AT3G13650	AT3G13650	3	4461932	-967
134	3.73195	AT5G47250	AT5G47250	5	19204823	0
134	3.73195	AT5G47260	AT5G47260	5	19204823	-1815

Supplementary Figure 38 – Summary of GWA results for *AvrB*

Phenotype histogram and quantile-quantile plots of p-values

Fisher's exact test results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
3	4.9251	CTR1*	AT5G03730	5	977815	0
35	3.83538	AT1G63360	AT1G63360	1	23520531	-14697
65	3.46948	ACD6*	AT4G14400	4	8300284	1686
74	3.43479	JAR1	AT2G46370	2	19024496	-16359
81	3.39491	AT4G16990	AT4G16990	4	9567659	2085
84	3.37242	MLO6	AT1G61560	1	22724187	-8478
116	3.24189	AT4G14610	AT4G14610	4	8380912	0
116	3.24189	NHL8	AT1G32340	1	11674163	-8125
116	3.24189	OPR3	AT2G06050	2	2345749	13362
116	3.24189	RPP13	AT3G46530	3	17126475	14877

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
14	5.33818	AT4G12010	AT4G12010	4	7185491	11714
24	4.79918	CTR1*	AT5G03730	5	977815	0
26	4.76628	AT3G23120	AT3G23120	3	8228676	0
27	4.72475	ACD6*	AT4G14400	4	8300284	1686
66	4.01373	AT1G29715	AT1G29715	1	10397063	-5121
69	3.99478	AT3G23010	AT3G23010	3	8189706	13054
87	3.75697	AT2G33210	AT2G33210	2	14070312	11672
143	3.54386	NPR1	AT1G64280	1	23837754	18657
149	3.52388	ACD2	AT4G37000	4	17432696	-9910

Supplementary Figure 39 – Summary of GWA results for Emco5

Phenotype histogram and quantile-quantile plots of p-values

Fisher's exact test results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
19	4.75301	AT1G63860	AT1G63860	1	23700530	5371
32	4.30891	WRKY17	AT2G24570	2	10439419	5058
47	4.1245	AT5G64120	AT5G64120	5	25669710	6822
48	4.06415	AT4G12470	AT4G12470	4	7399613	1493
49	4.06118	AT1G29715	AT1G29715	1	10395782	-3840
51	4.04429	AT2G02660	AT2G02660	2	751077	11309
55	4.03782	AT5G43310	AT5G43310	5	17397338	0
57	4.0081	AT1G63750	AT1G63750	1	23657699	0
77	3.908	NPR1	AT1G64280	1	23858618	0
85	3.84292	ACD6*	AT4G14400	4	8318370	19772

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
1	9.25392	MOS4	AT3G18165	3	6217133	-6061
8	6.45851	AT1G63860	AT1G63860	1	23700530	5371
30	4.97336	WRKY17	AT2G24570	2	10439419	5058
59	4.08789	AT1G56510	AT1G56510	1	21155531	-15723
77	3.87545	NHL8	AT1G32340	1	11644061	18989
78	3.8648	ACD6*	AT4G14400	4	8318370	19772
88	3.84954	AT2G16870	AT2G16870	2	7305997	9162
92	3.81027	AT5G47250	AT5G47250	5	19204376	0
118	3.50406	NPR1	AT1G64280	1	23858618	0
137	3.37826	AT5G64120	AT5G64120	5	25669710	6822

Supplementary Figure 40 – Summary of GWA results for Emwa1

Phenotype histogram and quantile-quantile plots of p-values

Fisher's exact test results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
2	5.62674	AT2G21030	AT2G21030	2	9027176	4809
4	5.34437	AT1G52660	AT1G52660	1	19622094	3740
5	5.15086	AT1G57650	AT1G57650	1	21355394	0
32	4.13757	ACD1	AT3G44880	3	16408376	11079
32	4.13757	AT5G40910	AT5G40910	5	16400733	-12002
38	4.04396	AT5G48620	AT5G48620	5	19720028	-13674
41	3.95093	AT1G57830	AT1G57830	1	21421505	-2469
41	3.95093	AT1G57850	AT1G57850	1	21421505	-8850
58	3.83565	AT4G13920	AT4G13920	4	8050211	3657
63	3.77891	AT3G13650	AT3G13650	3	4453154	-9745

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
2	6.174	AT1G52660	AT1G52660	1	19622094	3740
3	6.00048	AT2G21030	AT2G21030	2	9027176	4809
14	4.81571	AT1G57650	AT1G57650	1	21355394	0
15	4.77592	AIG1	AT1G33960	1	12344937	1275
23	4.53766	AT1G57840	AT1G57840	1	21426870	-1594
32	4.08443	AT3G13650	AT3G13650	3	4453154	-9745
35	4.02003	AT1G47370	AT1G47370	1	17355738	12600
36	3.9819	AT4G13920	AT4G13920	4	8050211	3657
43	3.83847	WRKY53	AT4G23810	4	12391750	630
47	3.77757	AT1G63750	AT1G63750	1	23658828	0

Supplementary Figure 41 – Summary of GWA results for Emoy2

Phenotype histogram and quantile-quantile plots of p-values

Fisher's exact test results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
1	6.65524	ATTRX3	AT5G42980	5	17257411	-2424
4	4.98215	AT1G61190	AT1G61190	1	22583408	19056
8	4.71618	RPP8	AT5G43470	5	17477817	1958
19	4.43448	AT5G35180	AT5G35180	5	13440961	-687
33	4.03951	AT2G34315	AT2G34315	2	14488257	0
64	3.73778	AT1G60320	AT1G60320	1	22245244	5973
78	3.59124	AT1G47880	AT1G47880	1	17624318	-19397
83	3.5905	AT1G57830	AT1G57830	1	21413989	-9985
87	3.58293	EDS1	AT3G48090	3	17765010	1349
103	3.55875	RPM1	AT3G07040	3	2234435	-5405

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
5	5.74055	ATTRX3	AT5G42980	5	17257411	-2424
28	4.15055	AT1G61190	AT1G61190	1	22583408	19056
33	4.01613	AT1G58602	AT1G58602	1	21744588	-5431
44	3.92746	NHL22	AT4G09590	4	6061419	-4706
59	3.84102	RPP8	AT5G43470	5	17477817	1958
83	3.59955	RPM1	AT3G07040	3	2234435	-5405
103	3.52147	AT2G34315	AT2G34315	2	14488257	0
114	3.47425	DND1	AT5G15410	5	5026197	-19294
168	3.30221	AT5G66640	AT5G66640	5	26619920	745
176	3.25442	AT4G13810	AT4G13810	4	7988152	16906

Supplementary Figure 42 – Summary of GWA results for Hiks1

Phenotype histogram and quantile-quantile plots of p-values

Fisher's exact test results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
5	4.986	RIN3	AT5G51450	5	20918636	3819
13	4.65661	AT1G31540	AT1G31540	1	11303441	-9707
21	4.24979	AT1G58602	AT1G58602	1	21764047	0
22	4.20946	AT5G47250	AT5G47250	5	19202541	480
50	3.8631	PR5	AT1G75040	1	28176156	-5208
65	3.78642	DND1	AT5G15410	5	4983482	19828
75	3.76147	AT5G23400	AT5G23400	5	7880828	0
80	3.71809	AT5G27060	AT5G27060	5	9513154	9383
85	3.71085	EDR3	AT3G60190	3	22255824	0
112	3.57179	CESA3	AT5G05170	5	1554149	-18734

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
10	4.9987	RIN3	AT5G51450	5	20918636	3819
16	4.66752	AT1G58602	AT1G58602	1	21764047	0
24	4.43965	AT1G31540	AT1G31540	1	11303441	-9707
27	4.3031	AT5G47250	AT5G47250	5	19202541	480
46	4.03565	EDR3	AT3G60190	3	22255824	0
71	3.82374	NSL1	AT1G28380	1	9977437	11131
111	3.65488	DND1	AT5G15410	5	4983482	19828
114	3.64574	CESA3	AT5G05170	5	1554149	-18734
136	3.59281	AT5G23400	AT5G23400	5	7880828	0
158	3.55083	PR5	AT1G75040	1	28176156	-5208

Supplementary Figure 43 – Summary of GWA results for Noco2

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
10	4.57388	AT5G49140	AT5G49140	5	19958648	-18007
12	4.49561	ATMKK5	AT3G21220	3	7453506	6149
24	4.25497	WRKY33	AT2G38470	2	16127475	9631
39	4.04157	AT4G16990	AT4G16990	4	9568272	2698
63	3.81092	RIN4	AT3G25070	3	9130225	-2092
67	3.78492	AT5G45000	AT5G45000	5	18174372	-8238
75	3.75061	LEJ1	AT4G34120	4	16360327	17205
109	3.60025	DND1	AT5G15410	5	5007511	-608
114	3.58772	AT1G52900	AT1G52900	1	19719069	-12485
287	3.18746	CDR1	AT5G33340	5	12607640	-4057

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
4	5.15682	AT5G49140	AT5G49140	5	19958648	-18007
23	4.02577	AT1G43180	AT1G43180	1	16278313	-3075
43	3.83221	AT5G66640	AT5G66640	5	26629887	10712
51	3.73997	ATMKK5	AT3G21220	3	7453506	6149
56	3.65164	AT4G19530	AT4G19530	4	10652410	0
58	3.63487	AT1G52900	AT1G52900	1	19719069	-12485
59	3.62881	WRKY33	AT2G38470	2	16127475	9631
70	3.53952	AT5G45000	AT5G45000	5	18174372	-8238
79	3.45365	PLDBETA1	AT2G42010	2	17556474	-10996
93	3.36124	ACD6*	AT4G14400	4	8291057	-3385

Supplementary Figure 44 – Summary of GWA results for LP23.1a

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
1	4.79892	AT1G19160	AT1G19160	1	6629169	-13964
24	3.64585	AT5G66910	AT5G66910	5	26750588	-12106
34	3.58447	AT5G27060	AT5G27060	5	9518942	3595
45	3.45712	MOS4	AT3G18165	3	6230765	5387
62	3.39473	AT5G46270	AT5G46270	5	18793608	-7540
64	3.37843	NPR4	AT4G19660	4	10710196	-11943
68	3.36308	WRKY11	AT4G31550	4	15280478	9475
69	3.35516	RLM1	AT1G64070	1	23789180	2068
80	3.30235	ER	AT2G26330	2	11225413	-4364
83	3.29355	AT3G26470	AT3G26470	3	9695263	6384

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
1	5.17929	JAZ1	AT1G19180	1	6629169	5558
1	5.17929	AT1G19230	AT1G19230	1	6629169	-15011
16	4.05476	AT5G66910	AT5G66910	5	26750588	-12106
18	4.02563	RLM1	AT1G64070	1	23789180	2068
29	3.77273	AT5G27060	AT5G27060	5	9518942	3595
44	3.69117	MOS4	AT3G18165	3	6230765	5387
54	3.57418	RPP13	AT3G46530	3	17129110	12242
56	3.56642	AT1G77920	AT1G77920	1	29316517	10760
94	3.36662	AT4G11210	AT4G11210	4	6831714	-973
98	3.35	ER	AT2G26330	2	11225413	-4364

Supplementary Figure 45 – Summary of GWA results for LP23.1a CFU2

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
12	4.07289	AT5G66640	AT5G66640	5	26629887	10712
14	4.03954	AT2G17060	AT2G17060	2	7450383	16424
29	3.86687	AT3G50950	AT3G50950	3	18947425	0
45	3.71526	AT3G23270	AT3G23270	3	8303309	-13134
47	3.66962	AT4G16095	AT4G16095	4	9101433	-3125
51	3.59917	AT4G19050	AT4G19050	4	10452305	-8508
51	3.59917	AT4G19060	AT4G19060	4	10452305	-5994
51	3.59917	EDR2	AT4G19040	4	10452305	-14863
63	3.56624	HR4	AT3G50480	3	18745135	0
99	3.40708	ATMKK3	AT5G40440	5	16200633	0

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
2	5.82719	AT5G66640	AT5G66640	5	26629887	10712
14	4.3661	AT4G16095	AT4G16095	4	9101433	-3125
40	3.85508	AT4G11340	AT4G11340	4	6882545	11658
61	3.6394	JAZ7	AT2G34600	2	14581562	627
62	3.63546	AT2G17060	AT2G17060	2	7450383	16424
79	3.51266	AT1G63730	AT1G63730	1	23634044	-11389
85	3.46815	AT4G08450	AT4G08450	4	5370710	0
88	3.44879	AT1G63750	AT1G63750	1	23634947	-19564
94	3.41773	AT3G50950	AT3G50950	3	18947425	0
106	3.3816	AT3G24020	AT3G24020	3	8672298	-6447

Supplementary Figure 46 – Summary of GWA results for RMX23.1a

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
3	4.44123	AT4G13580	AT4G13580	4	7913416	12092
14	4.00032	RLM1	AT1G64070	1	23803289	16177
19	3.9191	ATPP2-A5	AT1G65390	1	24291458	-4683
21	3.90579	LACS2	AT1G49430	1	18314866	15373
25	3.86091	SOBER1	AT4G22300	4	11795769	-4702
30	3.78648	AT1G72520	AT1G72520	1	27315513	0
31	3.77779	AT5G27060	AT5G27060	5	9520423	2114
59	3.53862	RDR6	AT3G49500	3	18381078	-16888
71	3.47602	AT4G12010	AT4G12010	4	7196568	637
76	3.44469	AT1G69545	AT1G69545	1	26140379	12120

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
5	4.09743	SOBER1	AT4G22300	4	11795769	-4702
8	4.0383	LACS2	AT1G49430	1	18290565	-4146
23	3.78357	AT5G27060	AT5G27060	5	9520423	2114
29	3.70066	ATPP2-A5	AT1G65390	1	24291458	-4683
39	3.56872	AT1G72520	AT1G72520	1	27315513	0
44	3.53052	AT5G43730	AT5G43730	5	17579329	0
47	3.487	ATTRX3	AT5G42980	5	17253042	-6793
49	3.47673	OCP3	AT5G11270	5	3616878	-19779
55	3.40595	AT1G69545	AT1G69545	1	26140379	12120
78	3.29824	AT5G11250	AT5G11250	5	3599671	-7710

Supplementary Figure 47 – Summary of GWA results for RMX23.1a CFU2

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
10	4.41328	AT4G16095	AT4G16095	4	9101344	-3214
27	4.09883	AT4G23440	AT4G23440	4	12246301	5465
30	4.07674	AT1G19160	AT1G19160	1	6621981	-6776
30	4.07674	JAZ1	AT1G19180	1	6621981	-104
36	4.01612	MLO6	AT1G61560	1	22731789	-16080
38	3.94515	AT1G53350	AT1G53350	1	19913412	2832
45	3.93928	ATRBOHB	AT1G09090	1	2955709	19121
58	3.79667	AT5G43310	AT5G43310	5	17388717	8102
67	3.74302	AT4G16095	AT4G16095	4	9101764	-2794
68	3.72825	AT1G63880	AT1G63880	1	23728414	-8627

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
13	4.41998	AT4G16095	AT4G16095	4	9101344	-3214
28	4.09252	AT1G19160	AT1G19160	1	6621981	-6776
37	3.96331	AT1G53350	AT1G53350	1	19912220	1640
43	3.8499	ATRBOHB	AT1G09090	1	2955709	19121
45	3.84659	AT3G05370	AT3G05370	3	1546178	-7453
53	3.75531	AT4G23440	AT4G23440	4	12246301	5465
54	3.75196	AT5G43310	AT5G43310	5	17388717	8102
61	3.66655	AT5G66630	AT5G66630	5	26614251	1103
82	3.47834	EFR	AT5G20480	5	6910162	-12320
83	3.44776	MLO6	AT1G61560	1	22731789	-16080

Supplementary Figure 48 – Summary of GWA results for RMX3.1b

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
9	5.07903	ATRBOHB	AT1G09090	1	2941600	5012
21	4.62539	AT3G45860	AT3G45860	3	16886048	-9022
26	4.4954	IQD1	AT3G09710	3	2981271	-1997
31	4.4307	AT2G21030	AT2G21030	2	9034975	-2316
33	4.41642	ATMKK4	AT1G51660	1	19178488	18873
54	4.33938	AT2G34930	AT2G34930	2	14745855	0
57	4.32595	AT5G35180	AT5G35180	5	13440861	-787
85	4.22319	AT1G69545	AT1G69545	1	26140020	12479
101	4.14919	AT4G36150	AT4G36150	4	17113915	5201
104	4.13855	AT5G44870	AT5G44870	5	18117135	-14758

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
9	4.28973	ATRBOHB	AT1G09090	1	2924614	-8127
13	4.20684	AT2G34930	AT2G34930	2	14745855	0
22	4.10379	HSP81-1	AT5G52640	5	21374001	1414
27	3.99455	AT2G28670	AT2G28670	2	12302606	4730
28	3.99212	AT1G69545	AT1G69545	1	26140020	12479
29	3.9514	AT5G46270	AT5G46270	5	18796716	-10648
87	3.46148	AT5G17890	AT5G17890	5	5901094	-15878
102	3.37514	RPP13	AT3G46530	3	17143074	0
174	3.11228	IAR3	AT1G51760	1	19201724	-1364
184	3.08855	PDF1.2c	AT5G44430	5	17936640	-9906

Supplementary Figure 49 – Summary of GWA results for RMX3.1b CFU2

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
11	4.85613	AT1G72950	AT1G72950	1	27448156	-90
17	4.7289	NHL3	AT5G06320	5	1945775	-14006
38	4.39514	AT5G66640	AT5G66640	5	26629887	10712
53	4.20204	SGT1A	AT4G23570	4	12304480	1751
88	3.96357	CDR1	AT5G33340	5	12614724	1542
112	3.83425	AT2G38870	AT2G38870	2	16262833	-18475
125	3.7961	NPR4	AT4G19660	4	10715699	-17446
130	3.77479	AT5G49040	AT5G49040	5	19884973	14929
148	3.71499	AGB1	AT4G34460	4	16481252	-1720
156	3.68745	AT1G52660	AT1G52660	1	19601291	-15852

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
1	6.60309	AT5G63020	AT5G63020	5	25316566	-13338
7	5.32394	AT5G66640	AT5G66640	5	26629887	10712
10	5.07307	AGB1	AT4G34460	4	16481252	-1720
12	4.98988	NPR4	AT4G19660	4	10703622	-5369
29	4.45171	BAP1	AT3G61190	3	22660767	735
52	4.0498	ATNFXL1	AT1G10170	1	3331125	2472
54	4.04479	AT2G33020	AT2G33020	2	14011267	9684
81	3.91437	BON1	AT5G61900	5	24865652	7235
85	3.89682	AT4G13820	AT4G13820	4	8015396	-4655
90	3.85755	RPS4	AT5G45250	5	18336285	2856

Supplementary Figure 50 – Summary of GWA results for PNA3.3a

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
55	3.64309	AT5G66640	AT5G66640	5	26629887	10712
58	3.61456	AT4G19050	AT4G19050	4	10440963	0
58	3.61456	EDR2	AT4G19040	4	10440963	-3521
78	3.45104	AT2G34930	AT2G34930	2	14730743	13402
96	3.34982	AT1G61100	AT1G61100	1	22495691	16512
101	3.32215	OCP3	AT5G11270	5	3598795	-1696
115	3.2633	AT2G15010	AT2G15010	2	6478194	-13267
119	3.25328	AT5G36930	AT5G36930	5	14577563	7289
127	3.22717	PROPEP2	AT5G64890	5	25949382	-2412
138	3.19277	AT3G50950	AT3G50950	3	18958631	8851

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
21	4.11656	EDR2	AT4G19040	4	10440963	-3521
54	3.64005	AOC4	AT1G13280	1	4539653	-7798
57	3.62269	AT5G66640	AT5G66640	5	26629887	10712
59	3.61226	AT1G61100	AT1G61100	1	22495691	16512
70	3.53168	OCP3	AT5G11270	5	3598795	-1696
81	3.44641	AT5G44870	AT5G44870	5	18134974	0
83	3.44054	RRS1	AT5G45260	5	18363740	13904
96	3.36687	AT1G69550	AT1G69550	1	26162385	-5167
108	3.32689	AT2G39430	AT2G39430	2	16482084	10475
140	3.19907	AT5G36930	AT5G36930	5	14577563	7289

Supplementary Figure 51 – Summary of GWA results for PNA3.3a CFU2

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
30	4.41049	AT4G38700	AT4G38700	4	18066682	9771
60	3.99506	AT4G13820	AT4G13820	4	8014932	-4191
76	3.82345	AT1G69710	AT1G69710	1	26232197	1882
77	3.82323	AT1G22900	AT1G22900	1	8111705	-7211
87	3.75712	SGT1A	AT4G23570	4	12304531	1802
106	3.63602	AT1G72950	AT1G72950	1	27448156	-90
107	3.61739	AT3G23270	AT3G23270	3	8330090	9746
112	3.60145	ACD6*	AT4G14400	4	8298599	1
121	3.55917	AT5G42140	AT5G42140	5	16873318	-14450
135	3.49843	AT1G12280	AT1G12280	1	4176840	0

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
1	7.36257	AT5G66640	AT5G66640	5	26629887	10712
27	5.00279	NPR4	AT4G19660	4	10703622	-5369
29	4.95259	BAP1	AT3G61190	3	22661519	0
42	4.67348	AT5G41550	AT5G41550	5	16636778	0
66	4.34368	AOC4	AT1G13280	1	4548797	0
70	4.33315	AT1G72520	AT1G72520	1	27313560	0
74	4.31233	AT5G36930	AT5G36930	5	14583189	1663
75	4.30719	AT3G28890	AT3G28890	3	10896717	497
163	3.78358	AT4G13820	AT4G13820	4	8014932	-4191
175	3.75097	AT1G58390	AT1G58390	1	21695550	2562

Supplementary Figure 52 – Summary of GWA results for ME3.1b

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
5	4.67751	EFR	AT5G20480	5	6921697	-785
20	3.92728	CYT1	AT2G39770	2	16582228	-13552
27	3.82944	AT4G14610	AT4G14610	4	8375463	5380
63	3.55016	AT5G23400	AT5G23400	5	7868852	-11486
68	3.51042	AT3G14460	AT3G14460	3	4856563	-292
103	3.36218	AT2G32660	AT2G32660	2	13844841	15994
126	3.2606	LSD1	AT4G20380	4	11024655	17856
134	3.22429	AT3G23270	AT3G23270	3	8312964	-3479
143	3.20083	AT5G46260	AT5G46260	5	18779109	0
202	3.02868	EDR3	AT3G60190	3	22240051	15093

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
8	4.512	YSL7	AT1G65730	1	24450590	636
14	4.20155	CYT1	AT2G39770	2	16588913	-6867
31	3.77221	AT3G13650	AT3G13650	3	4452910	-9989
44	3.67826	AT5G23400	AT5G23400	5	7868681	-11657
47	3.65842	OCP3	AT5G11270	5	3605026	-7927
51	3.63768	EFR	AT5G20480	5	6923761	0
64	3.54676	AT2G32660	AT2G32660	2	13844841	15994
66	3.51751	AT1G57830	AT1G57830	1	21422295	-1679
68	3.49712	AT3G23270	AT3G23270	3	8312964	-3479
71	3.48929	AT5G49040	AT5G49040	5	19892774	7128

Supplementary Figure 53 – Summary of GWA results for ME3.1b CFU2

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
1	6.03849	TCL2	AT2G30424	2	12974047	0
1	6.03849	TCL1	AT2G30432	2	12974047	1645
1	6.03849	ETC2	AT2G30420	2	12974047	-4808
66	4.63223	ACD6	AT4G14400	4	8297531	0
107	4.45996	TTG1	AT5G24520	5	8373389	-539
133	4.3383	HDG9	AT5G17320	5	5723888	-16249
284	4.0376	CPC	AT2G46410	2	19062326	-4912
402	3.87148	ELC	AT3G12400	3	3961979	-16121

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
6	4.75326	TCL2	AT2G30424	2	12974047	-1502
6	4.75326	TCL1	AT2G30432	2	12974047	1645
6	4.75326	ETC2	AT2G30420	2	12974047	-4808
103	3.24969	RHL2	AT5G02820	5	634363	-8193
123	3.19616	ACD6	AT4G14400	4	8282280	-12162
219	2.92683	HDG1	AT3G61150	3	22654091	7993
253	2.86963	STI	AT2G02480	2	682528	16894
259	2.85844	GL1	AT3G27920	3	10361989	1193
469	2.59518	TTG1	AT5G24520	5	8371200	1650

Supplementary Figure 54 – Summary of GWA results for Trichome number C

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
3	6.44673	TCL2	AT2G30424	2	12968950	2633
3	6.44673	TCL1	AT2G30432	2	12968950	6742
3	6.44673	ETC2	AT2G30420	2	12968950	0
5	6.28312	ETC3	AT4G01060	4	460561	0
120	4.52655	HDG9	AT5G17320	5	5723888	-16249
174	4.40995	ACD6	AT4G14400	4	8297531	0
187	4.35215	TTG1	AT5G24520	5	8391566	-18716
359	4.00356	ELC	AT3G12400	3	3955811	-9953
450	3.87782	KINESIN	AT3G16630	3	5659495	2895

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
1	7.28113	TCL2	AT2G30424	2	12974047	-1502
1	7.28113	TCL1	AT2G30432	2	12974047	1645
1	7.28113	ETC2	AT2G30420	2	12974047	-4808
30	4.16251	ETC3	AT4G01060	4	460561	0
55	3.70109	KINESIN	AT3G16630	3	5656571	5819
154	3.17772	TTG1	AT5G24520	5	8391566	-18716
213	3.02522	GL1	AT3G27920	3	10362095	1087
220	3.01372	RHL2	AT5G02820	5	634363	-8193
239	2.97729	HDG9	AT5G17320	5	5723888	-16249
277	2.90741	KLK	AT5G18410	5	6093154	4119

Supplementary Figure 55 – Summary of GWA results for Trichome number JA

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
35	5.11922	ATMPK6	AT2G43790	2	18167365	19300
105	4.57335	AT5G44870	AT5G44870	5	18126979	-4914
109	4.55281	SSI2	AT2G43710	2	18143907	13941
119	4.5348	AT5G67160	AT5G67160	5	26830714	-14447
181	4.50298	PEN2	AT2G44490	2	18358237	-13595
192	4.45531	AT1G31540	AT1G31540	1	11296082	-2348
223	4.37942	AT4G19530	AT4G19530	4	10658683	1391
259	4.30514	AT4G13880	AT4G13880	4	8025880	0
264	4.29739	AT2G17050	AT2G17050	2	7404976	12941
266	4.2833	AT2G17055	AT2G17055	2	7420240	4894

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
25	4.04952	AT4G19530	AT4G19530	4	10658683	1391
54	3.64599	AT5G46270	AT5G46270	5	18797191	-11123
84	3.49207	AT1G31540	AT1G31540	1	11296082	-2348
91	3.47703	AT5G44870	AT5G44870	5	18126979	-4914
97	3.44027	AT5G35450	AT5G35450	5	13669740	-15176
104	3.38666	AT4G38700	AT4G38700	4	18069802	6651
121	3.34218	AT4G13880	AT4G13880	4	8025880	0
122	3.32311	ST	AT2G03760	2	1137847	11487
123	3.31858	AT5G27060	AT5G27060	5	9506959	15578

Supplementary Figure 56 – Summary of GWA results for *Pseudomonas syringae pv. tomato* DC3000

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
1	4.15926	IMS1	AT1G74040	1	27854680	5243
3	4.02606	MOS2	AT1G33520	1	12165444	-6511
10	3.77507	AT4G16990	AT4G16990	4	9576637	11063
47	3.25185	MAM3	AT5G23020	5	7736079	14237
167	2.85258	NPR1	AT1G64280	1	23852414	3997
402	2.53541	NIMIN-2	AT3G25882	3	9482610	-10423
439	2.5144	MAM1	AT5G23010	5	7722281	15382

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
7	4.17368	MOS2	AT1G33520	1	12165444	-6511
9	4.11427	IMS1	AT1G74040	1	27854680	5243
20	3.84907	AT4G16990	AT4G16990	4	9576637	11063
62	3.307	MAM3	AT5G23020	5	7736079	14237
132	3.05833	NIMIN-2	AT3G25882	3	9482610	-10423
308	2.71974	ATMYC2	AT1G32640	1	11786799	11991
327	2.70766	CYP83A1	AT4G13770	4	7975934	14547
345	2.68785	ATTPS03	AT4G16740	4	9423595	12696
410	2.61498	AT5G51630	AT5G51630	5	20977443	-9404
500	2.54324	AT3G28740	AT3G28740	3	10782763	7172

Supplementary Figure 57 – Summary of GWA results for Aphid number

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

	Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
No known candidate genes identified	.						

EMMA results

	Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
No known candidate genes identified	.						

Supplementary Figure 58 – Summary of GWA results for Lithium concentration (Li)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

	Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
No known candidate genes identified	.						

EMMA results

	Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
No known candidate genes identified	.						

Supplementary Figure 59 – Summary of GWA results for Boron concentration (B)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
1	6.24769	HKT1	AT4G10310	4	6391200	780

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
1	8.3708	HKT1	AT4G10310	4	6391200	780

Supplementary Figure 60 – Summary of GWA results for Sodium concentration (Na)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

	Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
No known candidate genes identified	.						

EMMA results

	Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
No known candidate genes identified	.						

Supplementary Figure 61 – Summary of GWA results for Magnesium concentration (Mg)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

	Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
No known candidate genes identified	.						

EMMA results

	Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
No known candidate genes identified	.						

Supplementary Figure 62 – Summary of GWA results for Phosphorus concentration (P)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
44	3.69288	SULTR1;1	AT4G08620	4	5510830	4568
140	3.17072	SULTR1;2	AT1G78000	1	29331886	2743

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
157	3.33987	SULTR1;2	AT1G78000	1	29331886	2743

Supplementary Figure 63 – Summary of GWA results for Sulfur concentration (S)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
No known candidate genes identified	.					

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
No known candidate genes identified	.					

Supplementary Figure 64 – Summary of GWA results for Potassium concentration (K)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

	Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
No known candidate genes identified	.						

EMMA results

	Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
No known candidate genes identified	.						

Supplementary Figure 65 – Summary of GWA results for Calcium concentration (Ca)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

	Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
No known candidate genes identified	.						

EMMA results

	Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
No known candidate genes identified	.						

Supplementary Figure 66 – Summary of GWA results for Manganese concentration (Mn)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

	Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
No known candidate genes identified	.						

EMMA results

	Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
No known candidate genes identified	.						

Supplementary Figure 67 – Summary of GWA results for Iron concentration (Fe)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
No known candidate genes identified	.					

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
No known candidate genes identified	.					

Supplementary Figure 68 – Summary of GWA results for Cobolt concentration (Co)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

	Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
No known candidate genes identified	.						

EMMA results

	Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
No known candidate genes identified	.						

Supplementary Figure 69 – Summary of GWA results for Nickel concentration (Ni)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

	Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
No known candidate genes identified	.						

EMMA results

	Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
No known candidate genes identified	.						

Supplementary Figure 70 – Summary of GWA results for Copper concentration (Cu)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

	Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
No known candidate genes identified	.						

EMMA results

	Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
No known candidate genes identified	.						

Supplementary Figure 71 – Summary of GWA results for Zinc concentration (Zn)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

	Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
No known candidate genes identified	.						

EMMA results

	Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
No known candidate genes identified	.						

Supplementary Figure 72 – Summary of GWA results for Arsenic concentration (As)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
74	3.6625	SULTR3;4	AT3G15990	3	5431251	365

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
154	3.15122	SULTR1;2	AT1G78000	1	29331886	2743

Supplementary Figure 73 – Summary of GWA results for Selenium concentration (Se)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
31	4.3145	MOT1	AT2G25680	2	10941413	0

EMMA results

	Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
No known candidate genes identified	.						

Supplementary Figure 74 – Summary of GWA results for Molybdenum concentration (Mo)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
13	4.86761	HMA3	AT4G30120	4	14749887	-16371
17	4.77198	HMA2	AT4G30110	4	14735923	-11333

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
131	3.29429	HMA3	AT4G30120	4	14732262	0
131	3.29429	HMA2	AT4G30110	4	14732262	-7672

Supplementary Figure 75 – Summary of GWA results for Cadmium concentration (Cd)

Phenotype histogram and quantile-quantile plots of p-values

Fisher's exact test results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
1	12.8478	ACD6	AT4G14400	4	8297888	3446
1	12.8478	AT4G14420	AT4G14420	4	8297888	4054
11	6.60179	SGT1A	AT4G23570	4	12298370	-1463
28	5.74684	AtATG18h	AT1G54710	1	20425136	-434
28	5.74684	AtATG18b	AT4G30510	4	14920770	-13172

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
1	17.3608	ACD6	AT4G14400	4	8297888	0
1	17.3608	AT4G14420	AT4G14420	4	8297888	4054
35	4.75288	PEN2	AT2G44490	2	18353672	-18160
41	4.6208	AtATG18h	AT1G54710	1	20425136	-434
73	3.95505	ATHCHIB	AT3G12500	3	3971103	-7132
148	3.56372	CPN60B	AT1G55490	1	20702900	16329
201	3.40747	EDR2	AT4G19040	4	10429098	2433

Supplementary Figure 76 – Summary of GWA results for Lesioning (LES)

Phenotype histogram and quantile-quantile plots of p-values

Fisher's exact test results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
23	6.4437	BAP1	AT3G61190	3	22652796	8706
32	6.2637	ATRBOHA	AT5G07390	5	2319345	16551
52	6.06173	AHG2/ATPARN	AT1G55870	1	20909655	7568
52	6.06173	BIK1	AT2G39660	2	16556812	15803
95	5.63606	PBS3	AT5G13320	5	4278080	7026
164	5.36772	EDR2	AT4G19040	4	10416226	15305
225	5.20398	AT4G25020	AT4G25020	4	12865864	-3879
275	5.12256	ALPHA-DOX1	AT3G01420	3	170811	-7967

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
26	6.81113	ATRBOHA	AT5G07390	5	2319345	16551
40	6.12453	BAP1	AT3G61190	3	22652796	8706
120	4.93016	VSP2	AT5G24770	5	8492569	7910
133	4.77627	RRS1	AT5G45260	5	18356959	7123
221	4.18227	PMR6	AT3G54920	3	20357099	0
229	4.11913	ACD6	AT4G14400	4	8302699	4101

Supplementary Figure 77 – Summary of GWA results for Yellowing (YEL)

Phenotype histogram and quantile-quantile plots of p-values

Fisher's exact test results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
2	8.57487	ACD6	AT4G14400	4	8297888	0
2	8.57487	AT4G14420	AT4G14420	4	8297888	4054
59	6.35352	EDR2	AT4G19040	4	10434370	3072
208	5.30592	ATGSTU7	AT2G29420	2	12626797	-821
280	5.20954	CPK31	AT4G04695	4	2368557	13075
293	5.06938	SGT1A	AT4G23570	4	12298370	1463
468	4.66652	MOS6	AT4G02150	4	939826	10785

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
1	10.7964	ACD6	AT4G14400	4	8297888	0
1	10.7964	AT4G14420	AT4G14420	4	8297888	4054
4	6.18193	EDR2	AT4G19040	4	10429098	2433
197	3.4665	CPK31	AT4G04695	4	2373192	8440

Supplementary Figure 78 – Summary of GWA results for Lesioning and Yellowing (LY)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
No known candidate genes identified	.					

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
108	3.67151	ACD6	AT4G14400	4	8278786	-15656

Supplementary Figure 79 – Summary of GWA results for Fresh weight (FW)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
163	4.07261	ACD6	AT4G14400	4	8306678	8080

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
21	4.71524	ACD6	AT4G14400	4	8274503	-19939

Supplementary Figure 80 – Summary of GWA results for Dry weight (DW)

Phenotype histogram and quantile-quantile plots of p-values

Fisher's exact test results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
158	2.73658	MOD1	AT2G05990	2	2314673	-7546
211	2.6227	ST	AT2G03760	2	1138186	11148
268	2.51071	ACD6	AT4G14400	4	8280060	-14382
283	2.48069	MOS2	AT1G33520	1	12165002	-6069

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
128	3.05059	BSMT1	AT3G11480	3	3612746	-1697
152	2.96909	ST	AT2G03760	2	1138186	11148
198	2.85131	AT4G19500	AT4G19500	4	10608893	-16905
312	2.6325	MOD1	AT2G05990	2	2314004	-8215

Supplementary Figure 81 – Summary of GWA results for Presence or absense of chlorosis at 10°C

Phenotype histogram and quantile-quantile plots of p-values

Fisher's exact test results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
76	3.09187	ACD6	AT4G14400	4	8296951	2509
76	3.09187	AT4G14420	AT4G14420	4	8296951	4991
85	3.05292	ATGSTU7	AT2G29420	2	12626942	-966
94	3.01091	CAD1	AT1G29690	1	10400102	-17993

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
74	3.2565	CAD1	AT1G29690	1	10400102	-17993
80	3.21103	ACD6	AT4G14400	4	8296951	0
80	3.21103	AT4G14420	AT4G14420	4	8296951	4991
84	3.18981	AT4G19500	AT4G19500	4	10617786	-8012
91	3.14313	ATGSTU7	AT2G29420	2	12626942	-966

Supplementary Figure 82 – Summary of GWA results for Presence or absense of chlorosis at 16°C

Phenotype histogram and quantile-quantile plots of p-values

Fisher's exact test results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
23	4.97874	MOS3	AT1G80680	1	30319799	-9101
46	4.56789	AT4G16960	AT4G16960	4	9554907	-3881
131	4.07291	AHG2	AT1G55870	1	20888464	-10787
232	3.76328	CAD1	AT1G29690	1	10359684	19322
313	3.61149	EDR2	AT4G19040	4	10452345	-14903
342	3.5703	CRK13	AT4G23210	4	12140530	8195

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
62	3.66512	AT4G16960	AT4G16960	4	9554907	-3881
94	3.47017	MOS3	AT1G80680	1	30319799	-9101
140	3.30837	MOS2	AT1G33520	1	12156536	600
146	3.28079	AHG2	AT1G55870	1	20881326	-17925
161	3.23167	ACD6	AT4G14400	4	8286430	-8012
161	3.23167	AT4G14420	AT4G14420	4	8286430	15512
295	2.88201	EDR2	AT4G19040	4	10454058	-16616

Supplementary Figure 83 – Summary of GWA results for Presence or absense of chlorosis at 22°C

Phenotype histogram and quantile-quantile plots of p-values

Fisher's exact test results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
54	4.40411	SCPL1	AT5G36180	5	14239024	-17234
187	3.76057	EGL3	AT1G63650	1	23606078	0
233	3.62774	AT1G03940	AT1G03940	1	1003329	6212
239	3.59545	ABI3	AT3G24650	3	9001147	77
307	3.44247	ATAN11	AT1G12910	1	4413142	-16853
333	3.38054	AT4G00350	AT4G00350	4	144124	-7795

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
72	3.81914	ATAN11	AT1G12910	1	4413142	-16853
79	3.75789	SCPL1	AT5G36180	5	14239024	-17234
175	3.35343	ABI3	AT3G24650	3	9001147	77
176	3.35332	SCPL6	AT1G73270	1	27555710	0
176	3.35332	SCPL3	AT1G73280	1	27555710	921
176	3.35332	SCPL5	AT1G73290	1	27555710	4348
176	3.35332	SCPL2	AT1G73300	1	27555710	7624
176	3.35332	SCPL4	AT1G73310	1	27555710	10766
378	2.86765	EMS1	AT5G07280	5	2293787	5100

Supplementary Figure 84 – Summary of GWA results for Presence or absense of anthocyanin at 10°C

Phenotype histogram and quantile-quantile plots of p-values

Fisher's exact test results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
149	3.70902	TTG1	AT5G24520	5	8356944	13646
211	3.53629	AT5G17050	AT5G17050	5	5591041	16750

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
173	3.08801	TTG1	AT5G24520	5	8356944	13646

Supplementary Figure 85 – Summary of GWA results for Presence or absense of anthocyanin at 16°C

Phenotype histogram and quantile-quantile plots of p-values

Fisher's exact test results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
3	6.11483	FLS*	AT5G08640	5	2804243	0
62	4.62719	TT7*	AT5G07990	5	2563370	260
397	3.4418	ANL2	AT4G00730	4	320630	-16122
454	3.37899	HY5	AT5G11260	5	3589521	3860

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
139	3.24477	TT7*	AT5G07990	5	2545425	-14970
145	3.21998	AT5G17050	AT5G17050	5	5608356	0
350	2.771	RNS1	AT2G02990	2	864545	-8960

Supplementary Figure 86 – Summary of GWA results for Presence or absense of anthocyanin at 22°C

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
7	5.84953	ATMYB65	AT3G11440	3	3621028	15918
12	5.65225	ATCUL1	AT4G02570	4	1135235	1539
12	5.65225	LD	AT4G02560	4	1135235	-6814
18	5.58598	CYCD4;1	AT5G65420	5	26163842	-2623
19	5.54763	AGL15	AT5G13790	5	4441129	7888
27	5.35615	SPA4	AT1G53090	1	19780965	-6055
34	5.2128	PIL5	AT2G20180	2	8716537	-2564
73	4.92847	WER1	AT5G14750	5	4767923	-3182
99	4.79737	HBT	AT2G20000	2	8642534	0
106	4.7611	SDP1	AT5G04040	5	1108259	15081

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
3	5.58007	BME3	AT3G54810	3	20315875	6206
19	5.16262	PSD	AT1G72560	1	27346777	-13648
23	5.02769	FRS2*	AT2G32250	2	13694310	-5872
29	4.68931	PIL6	AT3G59060	3	21845262	-3778
29	4.68931	TT12	AT3G59030	3	21845262	12845
30	4.6591	PIN8	AT5G15100	5	4873406	18756
35	4.4622	HOS1	AT2G39810	2	16637428	12293
39	4.41261	HUA2*	AT5G23150	5	7812212	19720
54	4.23509	SMZ*	AT3G54990	3	20392223	-4724
56	4.21585	OLEO1	AT4G25140	4	12911865	10278

Supplementary Figure 87 – Summary of GWA results for Seed dormancy

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
4	5.46674	FCA*	AT4G16280	4	9205673	940
4	5.46674	PHYD*	AT4G16250	4	9205673	-6172
15	4.5843	ATEPR1	AT2G27380	2	11724708	1934
22	4.48423	ELF8	AT2G06210	2	2445040	-8356
27	4.37523	AGL24*	AT4G24540	4	12671203	0
29	4.36181	EFE	AT1G05010	1	1429372	1817
32	4.29033	sim to VRN1*	AT4G33280	4	16028697	18661
50	4.07098	ABI1	AT4G26080	4	13221445	848
67	3.98489	OLEO1	AT4G25140	4	12918081	16494
68	3.9507	SRD2	AT1G28560	1	10036110	1914

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
5	5.24705	FCA*	AT4G16280	4	9205673	940
16	4.34004	PHYD*	AT4G16250	4	9206304	-6803
18	4.33389	sim to VRN1*	AT4G33280	4	16028697	18661
22	4.14269	AGL24*	AT4G24540	4	12671203	0
23	4.13082	ATEPR1	AT2G27380	2	11724708	1934
35	3.98813	EFE	AT1G05010	1	1429372	1817
38	3.96287	ELF8	AT2G06210	2	2445040	-8356
48	3.82599	RTV1	AT1G49480	1	18328484	-8171
50	3.81723	SRD2	AT1G28560	1	10036110	1914
63	3.69169	ABI1	AT4G26080	4	13221445	0

Supplementary Figure 88 – Summary of GWA results for Days to germination at 10°C

Phenotype histogram and quantile-quantile plots of p-values

Fisher's exact test results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
2	5.02045	TSD2*	AT1G78240	1	29444417	3040
19	4.29967	ARF2	AT5G62000	5	24915861	-11723
23	4.23412	NPH3	AT5G64330	5	25726177	-18386
39	3.98839	BIN4	AT5G24630	5	8422255	10271
48	3.90119	AOX2	AT5G64210	5	25721325	-18435
81	3.66654	ATTOP6B	AT3G20780	3	7271727	-3149
81	3.66654	TOC1*	AT5G61380	5	24702886	7110
106	3.55365	LFY	AT5G61850	5	24845945	-15576
119	3.47071	FWA*	AT4G25530	4	13041699	0

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
1	6.76904	TSD2*	AT1G78240	1	29444417	-3040
17	4.15443	ATTOP6B	AT3G20780	3	7271727	-3149
20	4.08442	TOC1	AT5G61380	5	24704840	9064
33	3.84419	HOS1*	AT2G39810	2	16601283	-18595
40	3.80913	VIP2*	AT5G59710	5	24098411	19267
46	3.72953	GA1*	AT4G02780	4	1260311	-15498
49	3.69955	BME3	AT3G54810	3	20304676	-2534
52	3.67896	FWA*	AT4G25530	4	13041699	0
58	3.6311	FRL1*	AT5G16320	5	5360422	14400
83	3.42385	similar to DOG1	AT4G18660	4	10267167	-6324

Supplementary Figure 89 – Summary of GWA results for Days to germination at 16°C

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
1	6.89057	EER5	AT2G19560	2	8473322	0
9	4.85116	SCD1*	AT1G49040	1	18143730	0
22	4.17583	FT*	AT1G65480	1	24342848	5251
24	4.15532	SEPALLATA3	AT1G24260	1	8584281	9350
37	4.00096	SPA2*	AT4G11110	4	6786084	8863
39	3.99895	RGL1	AT1G66350	1	24755730	2024
48	3.82397	EZA1	AT4G02020	4	868050	-18550
68	3.73996	sim to DOG1	AT4G18660	4	10268561	-4930
74	3.70853	LHY	AT1G01060	1	53901	-16061

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
1	5.5983	EER5	AT2G19560	2	8455368	17482
4	4.95534	SCD1*	AT1G49040	1	0	8919
5	4.77771	SEPALLATA3	AT1G24260	1	8584281	9350
12	4.36052	SPA2*	AT4G11110	4	6786084	8863
27	4.01556	FHY1	AT2G37678	2	15828728	-18857
29	3.99637	TIC*	AT3G22380	3	7934502	14985
34	3.975	HLS1	AT4G37580	4	17640138	-18468
45	3.82084	EZA1	AT4G02020	4	868050	-18550
76	3.57447	LHY	AT1G01060	1	53901	-16061
85	3.50848	FRS1	AT4G19990	4	10818263	-14595

Supplementary Figure 90 – Summary of GWA results for Days to germination at 22°C

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
7	4.49477	TWD1	AT3G21640	3	7634734	-13250
56	3.47779	ABH1	AT2G13540	2	5625884	-18082
61	3.4256	IAA7	AT3G23050	3	8198919	1759
62	3.41825	SHD	AT4G24190	4	12549174	2553
62	3.41825	SLY1	AT4G24210	4	12549174	-14389
79	3.3408	ABA2	AT1G52340	1	19498608	-3291
95	3.25878	BIN4	AT5G24630	5	8419676	12850
146	3.0556	SPT	AT4G36930	4	17413399	-725
173	3.00128	CIP1	AT5G41790	5	16738374	-6384
194	2.93296	DAG1	AT3G61850	3	22904359	-1884

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
17	4.10221	IAA7	AT3G23050	3	8198919	1759
19	4.0981	CAND1*	AT2G02560	2	669884	-19903
25	4.01706	AGL31*	AT5G65050	5	25992654	-6826
46	3.61854	NUA	AT1G79280	1	29839534	-1663
56	3.54362	similar to LSH1	AT3G04510	3	1212312	3330
58	3.52199	LIP1	AT5G64813	5	25949715	19593
62	3.4735	BIN4	AT5G24630	5	8419676	12850
64	3.47115	ABA2	AT1G52340	1	19498608	-3291
66	3.46134	ABH1	AT2G13540	2	5625884	-18082
69	3.45162	SLY1	AT4G24210	4	12549174	-14389

Supplementary Figure 91 – Summary of GWA results for Seedling growth

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
2	4.55017	SPT	AT4G36930	4	17416904	613
23	3.51761	similar to DRM1	AT2G33830	2	14311215	5345
96	3.0418	IMB1	AT2G34900	2	14736609	-3880
132	2.93044	AT1G54070	AT1G54070	1	20183306	-3001
140	2.89996	ABI1	AT4G26080	4	13215741	4229
153	2.8754	EMS1	AT5G07280	5	2277218	-7823

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
1	6.87733	SPT	AT4G36930	4	17416904	613
9	4.12721	ELF8	AT2G06210	2	2426982	1918
19	3.80692	EER5	AT2G19560	2	8460380	12470
37	3.64544	TWD1	AT3G21640	3	7606169	12768
42	3.59043	EIR1	AT5G57090	5	23108371	-9548
50	3.50462	YAP169*	AT5G07200	5	2235834	7720
50	3.50462	ATS3*	AT5G07190	5	2235834	1674
60	3.4876	AT1G54070	AT1G54070	1	20183306	-3001
64	3.47149	MSI1	AT5G58230	5	23572897	-341
80	3.4151	ZFP1	AT1G80730	1	30355812	-10673

Supplementary Figure 92 – Summary of GWA results for Vegetative growth rate during vernalization (Vern growth)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
7	4.11622	ATS3*	AT5G07190	5	2235834	-1674
23	3.53972	VIN3*	AT5G57380	5	23263587	34
29	3.44251	CLV2	AT1G65380	1	24306481	13569
30	3.44061	GA4H	AT1G80340	1	30195155	10430
36	3.36984	FUS6	AT3G61140	3	22631510	-5727
42	3.34915	SPT	AT4G36930	4	17416904	613
60	3.19901	AHG2	AT1G55870	1	20879615	-19636
64	3.18473	ABA2	AT1G52340	1	19491510	1953
74	3.11408	FUS3	AT3G26790	3	9856956	0
114	2.93266	CIP1	AT5G41790	5	16769529	19454

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
2	5.10822	ATS3*	AT5G07190	5	2235834	-1674
4	4.77153	SPT	AT4G36930	4	17416904	613
15	3.88694	AP1	AT1G69120	1	25983643	2350
21	3.7115	ELF8	AT2G06210	2	2426982	1918
26	3.65243	ABA2	AT1G52340	1	19491510	1953
35	3.58327	AHG2	AT1G55870	1	20879615	-19636
40	3.54669	FUS3	AT3G26790	3	9856956	0
48	3.45903	APRR5	AT5G24470	5	8377696	-18820
53	3.35717	SPA3*	AT3G15354	3	5156199	12903
53	3.35717	SPL5*	AT3G15270	3	5156199	-14844

Supplementary Figure 93 – Summary of GWA results for Vegetative growth rate after vernalization (After vern growth)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
1	6.84223	CUL4	AT5G46210	5	18737357	11288
7	5.80704	PIN5	AT5G16530	5	5381631	-19107
17	5.32313	AT3G29970	AT3G29970	3	11764053	15004
50	4.91147	SMZ	AT3G54990	3	20368973	15722
68	4.79768	RGA1	AT2G01570	2	260584	-3035
74	4.73996	VRN5*	AT3G24440	3	8862085	13949
113	4.5054	MAF5*	AT5G65080	5	26015363	0
163	4.33035	EMS1	AT5G07280	5	2298420	9733
195	4.24459	GA1	AT4G02780	4	1225277	12490
210	4.21064	CIPK3	AT2G26980	2	11526552	-969

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
6	4.42936	GA4	AT1G15550	1	5361649	-15488
15	3.95779	CUL4*	AT5G46210	5	18737357	11288
40	3.62182	CIPK3	AT2G26980	2	11526552	-969
58	3.47661	similar to FRL2*	AT5G27230	5	9582938	-1157
78	3.37052	AT1G56220	AT1G56220	1	21055754	7351
89	3.32306	SEPALLATA3	AT1G24260	1	8579221	14410
93	3.30501	HY5	AT5G11260	5	3588592	4789
96	3.29316	VRN5*	AT3G24440	3	8859072	16962
101	3.26845	SPA1*	AT2G46340	2	19039722	-5236
110	3.2306	AT3G29970	AT3G29970	3	11764053	15004

Supplementary Figure 94 – Summary of GWA results for Secondary dormancy

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
18	5.25646	RCI2B	AT3G05890	3	1764835	-6337
42	4.80407	VRN5*	AT3G24440	3	8862085	13949
43	4.79027	ELF8	AT2G06210	2	2416665	12235
49	4.70829	GA1	AT4G02780	4	1260361	-15548
52	4.67725	SHP2*	AT2G42830	2	17808221	-19111
60	4.62212	DFL2	AT4G03400	4	1495176	2359
81	4.45089	TEL1	AT3G26120	3	9527950	-19685
95	4.34536	PIN3	AT1G70940	1	26758582	8525
121	4.19497	HAB1	AT1G72770	1	27398919	1976
121	4.19497	HAP2C	AT1G72830	1	27398919	10199

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
30	4.65885	DWF1*	AT3G19820	3	6874323	5300
42	4.01552	SHP2*	AT2G42830	2	17808221	-19111
47	3.89569	VRN5*	AT3G24440	3	8862517	13517
49	3.87479	ELF4	AT2G40080	2	16747199	-5209
55	3.82547	DFL2	AT4G03400	4	1494311	3224
57	3.80704	VIN3*	AT5G57380	5	23244201	19420
93	3.52172	TEL1	AT3G26120	3	9527950	-19685
159	3.20315	PIF3	AT1G09530	1	3091677	12136
162	3.1966	AT2G33830	AT2G33830	2	14326088	-8661
172	3.1607	DOG1	AT5G45830	5	18625091	-16464

Supplementary Figure 95 – Summary of GWA results for Germination in the dark (Germ 4C 7d)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
32	6.31068	COMATOSE	AT4G39850	4	18491140	0
53	6.00096	ELF4	AT2G40080	2	16729405	11967
62	5.92629	HBT*	AT2G20000	2	8642534	0
71	5.88552	CYCD4;1	AT5G65420	5	26167140	-5921
107	5.65344	DFL2	AT4G03400	4	1517051	-17187
111	5.62377	ATS3*	AT5G07190	5	2241523	2851
151	5.46186	EMS1	AT5G07280	5	2297704	9017
156	5.46076	ATMYB65	AT3G11440	3	3621028	15918
170	5.37576	ATRAB28	AT1G03120	1	770282	17142
190	5.2813	FLC*	AT5G10140	5	3188328	-8879

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
18	4.35971	ELF4	AT2G40080	2	16729405	11967
91	3.54974	IAA6	AT1G52830	1	19690968	-13656
98	3.50137	PKL	AT2G25170	2	10749896	18831
111	3.39456	HY2	AT3G09150	3	2797374	-6159
129	3.27598	FRS1*	AT4G19990	4	10830760	-2098
158	3.15411	COMATOSE	AT4G39850	4	18491434	0
173	3.12085	DFL1	AT5G54510	5	22135025	13294
188	3.07406	UVI4	AT2G42260	2	17626506	-15795
197	3.04985	DOG1	AT5G45830	5	18599415	7294

Supplementary Figure 96 – Summary of GWA results for Seed dormancy level (DSDS50)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
9	5.24948	ARR3	AT1G59940	1	22081068	-10430
15	4.92119	GRV2	AT2G26890	2	11474181	0
16	4.91378	COL9	AT3G07650	3	2453015	8477
21	4.81076	GASA4	AT5G15230	5	4943957	-946
26	4.74926	EPR1	AT1G18330	1	6323583	-15580
48	4.50613	ATGA2OX8	AT4G21200	4	11308052	1441
58	4.37476	EER5	AT2G19560	2	8494072	-17874
60	4.34696	SPK-2-2	AT3G50500	3	18756113	-1059
69	4.30587	HY1	AT2G26670	2	11350817	167
96	4.15025	ELF5	AT5G62640	5	25184222	-14455

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
1	4.87018	AP1	AT1G69120	1	26005435	-15459
42	3.69464	PHYD	AT4G16250	4	9176873	18744
63	3.55835	RGL3	AT5G17490	5	5749371	14694
76	3.48837	FVE*	AT2G19520	2	8455985	-7033
89	3.42541	VRN2*	AT4G16845	4	9477005	0
146	3.21059	similar to NPH4	AT2G03070	2	924679	15610
149	3.20396	ABI5	AT2G36270	2	15227928	-13321
155	3.19319	EER5	AT2G19560	2	8466290	6560
160	3.1833	AT4G21540	AT4G21540	4	11475239	12621
161	3.18163	DFL2	AT4G03400	4	1495901	1634

Supplementary Figure 97 – Summary of GWA results for Reduction in germination rate (Seed bank 133-91)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
41	5.87448	NCED9	AT1G78390	1	29479269	16519
54	5.73754	PHYB	AT2G18790	2	8165576	14064
132	5.47282	SHY2	AT1G04240	1	1145606	-16056
137	5.46925	EMS1	AT5G07280	5	2297704	9017
142	5.4688	COMATOSE	AT4G39850	4	18491140	0
154	5.40765	LKP2	AT2G18915	2	8185020	16634
155	5.40389	ZFP1	AT1G80730	1	30338768	5447
157	5.39549	DFL2	AT4G03400	4	1517051	-17187
164	5.35569	ATS3*	AT5G07190	5	2222946	-14562
173	5.31955	ABA1	AT5G67030	5	26793918	-19456

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
32	4.66173	NCED9	AT1G78390	1	29479269	16519
33	4.65738	EMF1	AT5G11530	5	3719911	18362
34	4.60894	VRN5*	AT3G24440	3	8866118	9916
61	4.21009	FY	AT5G13480	5	4308421	18110
63	4.18653	HYL1	AT1G09700	1	3138580	0
66	4.15523	FLC*	AT5G10140	5	3178232	0
134	3.73271	TFL1	AT5G03840	5	1027938	-2127
177	3.55875	COMATOSE	AT4G39850	4	18516649	19519
232	3.39237	AT5G44300	AT5G44300	5	17862574	850
367	3.07196	DOG1	AT5G45830	5	18599101	7608

Supplementary Figure 98 – Summary of GWA results for Primary Dormancy with 7 days dry storage (Storage 7 days)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
21	6.20501	COMATOSE	AT4G39850	4	18491140	0
23	6.17584	ATMYB65	AT3G11440	3	3621028	15918
26	6.10511	SPA4*	AT1G53090	1	19780965	-6055
37	6.01469	ELF4	AT2G40080	2	16729405	11967
38	6.00612	ATGID1B	AT3G63010	3	23290445	-9955
41	5.9587	AGL15	AT5G13790	5	4429786	19231
56	5.82535	IMB1	AT2G34900	2	14735537	-2808
70	5.7262	DFL2	AT4G03400	4	1517051	-17187
75	5.69726	PGI1	AT4G24620	4	12723011	-10176
100	5.62778	EMS1	AT5G07280	5	2297704	9017

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
2	5.89834	FLC*	AT5G10140	5	3171211	2287
15	4.46862	ACT7	AT5G09810	5	3050873	-1225
17	4.37073	ZFP1	AT1G80730	1	30338768	5447
50	3.80453	IMB1	AT2G34900	2	14735537	-2808
52	3.78542	AT5G01560	AT5G01560	5	219459	0
79	3.52273	NCED9	AT1G78390	1	29479269	16519
87	3.47038	GIL1	AT5G58960	5	23804153	-18790
109	3.36139	ELF5	AT5G62640	5	25154213	12446
149	3.20885	PKS2	AT1G14280	1	4873342	-4280
153	3.20207	PSD	AT1G72560	1	27348820	-15691

Supplementary Figure 99 – Summary of GWA results for Primary Dormancy with 28 days dry storage (Storage 28 days)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
31	6.39096	HBT	AT2G20000	2	8642534	0
33	6.29298	FLC*	AT5G10140	5	3188328	-8879
46	5.95613	AGL15*	AT5G13790	5	4429786	19231
60	5.76202	ATGID1B	AT3G63010	3	23290445	-9955
62	5.73333	COMATOSE	AT4G39850	4	18491140	0
67	5.69039	ATMYB65	AT3G11440	3	3621028	15918
77	5.57797	IMB1	AT2G34900	2	14735537	-2808
86	5.56102	ELF4	AT2G40080	2	16729405	11967
94	5.50112	AGL20*	AT2G45660	2	18826719	-8598
95	5.49346	ATS3*	AT5G07190	5	2241523	2851

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
8	4.37042	FLC*	AT5G10140	5	3171211	2287
16	4.15566	LBA1	AT5G47010	5	19083198	-6038
22	4.05406	ZFP1	AT1G80730	1	30338768	5447
29	3.95268	DDF1*	AT1G12610	1	4304481	-13466
37	3.84108	KNAT3	AT5G25220	5	8757437	18850
41	3.80086	PKL	AT2G25170	2	10749896	18831
67	3.51887	GA1	AT4G02780	4	1227355	10412
76	3.42835	IAA6	AT1G52830	1	19660176	15988
79	3.40602	HBT*	AT2G20000	2	8642534	0
88	3.36822	COL9	AT3G07650	3	2453015	8477

Supplementary Figure 100 – Summary of GWA results for Primary Dormancy with 56 days dry storage (Storage 56 days)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
28	5.12859	LSH1	AT5G28490	5	10471897	-16697
29	5.0957	HFR1	AT1G02340	1	472498	-4654
96	4.55502	CYCD1;1	AT1G70210	1	26430501	-13026
112	4.46003	ATPSK4	AT3G49780	3	18474121	-2543
120	4.4513	DFL1	AT5G54510	5	22136514	11805
148	4.32914	HLS1	AT4G37580	4	17658439	-167
167	4.23165	DOG1	AT5G45830	5	18586904	19805
178	4.21388	PKL	AT2G25170	2	10739197	8132
191	4.16765	GA20OX2	AT5G51810	5	21070315	2099

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
5	5.35688	DFL1	AT5G54510	5	22136514	11805
31	4.31065	DDF1*	AT1G12610	1	4275030	14912
62	3.88562	VIP5*	AT1G61040	1	22497068	7434
74	3.873	VRN2*	AT4G16845	4	9479034	0
93	3.71775	DFL2	AT4G03400	4	1479219	18316
103	3.65649	EMF1	AT5G11530	5	3679325	-16538
109	3.60681	AGL15*	AT5G13790	5	4463263	-12417
109	3.60681	LEP	AT5G13910	5	4463263	19189
124	3.55111	LIP1	AT5G64813	5	25940347	10225
125	3.54923	GIL1	AT5G58960	5	23834050	8346

Supplementary Figure 101 – Summary of GWA results for Hypocotyl length

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
2	7.83245	TET3*	AT3G45600	3	16750136	3200
10	6.09059	SAB*	AT1G58250	1	21600056	0
106	4.17852	BIN4	AT5G24630	5	8442179	-6006
282	3.60952	CCH	AT3G56240	3	20879331	-3808
424	3.3769	TIP1	AT5G20350	5	6893657	12385
493	3.28949	REM1	AT4G31610	4	15305349	-12156

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
5	6.99357	TET3*	AT3G45600	3	16750136	3200
38	4.13247	SAB*	AT1G58250	1	21600056	0

Supplementary Figure 102 – Summary of GWA results for Plant diameter at 10°C (Width 10)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
13	4.63002	WUS	AT2G17950	2	7813172	2781
63	4.00711	CCH	AT3G56240	3	20882629	-7106
133	3.65904	CPC	AT2G46410	2	19048218	8027
164	3.51707	BAM1	AT5G65700	5	26285796	-13187
202	3.43691	BIN4	AT5G24630	5	8442179	-6006
245	3.35871	BAM2	AT3G49670	3	18438149	6058
251	3.35373	TWD1	AT3G21640	3	7610441	8496

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
17	4.34187	ELO3	AT5G50320	5	20497728	124
23	4.18171	CCH	AT3G56240	3	20882629	-7106
50	3.72607	CPC	AT2G46410	2	19048218	8027
90	3.41288	BIN4	AT5G24630	5	8442179	-6006
260	2.89848	WUS	AT2G17950	2	7813172	2781

Supplementary Figure 103 – Summary of GWA results for Plant diameter at 16°C (Width 16)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
7	4.42509	ELO1*	AT3G11220	3	3504777	8760
234	3.13121	SHR	AT4G37650	4	17694359	605
352	2.94932	ZCW32	AT1G59640	1	21925712	-10846
356	2.93903	SMP2	AT4G37120	4	17477351	-9290
357	2.93893	BIN4	AT5G24630	5	8413716	18810
403	2.88857	SHD	AT4G24190	4	12558804	-2885

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
52	3.4997	ELO1*	AT3G11220	3	3504777	8760
291	2.79222	SHR	AT4G37650	4	17694359	605
363	2.70024	MSL3	AT1G58200	1	21539287	12565
375	2.68857	SHR	AT4G37650	4	17686280	-5500
382	2.67872	OLEO2	AT5G40420	5	16177787	12834

Supplementary Figure 104 – Summary of GWA results for Plant diameter at 22°C (Width 22)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
24	5.27395	AT4G18390	AT4G18390	4	10171238	-5665
39	5.05486	PAS1	AT3G54010	3	20034152	17991
91	4.56632	PTF1	AT3G02150	3	392114	0
196	4.17463	SE	AT2G27100	2	11596351	12615
197	4.17441	RPS15AD	AT3G46040	3	16910283	-15241
205	4.15439	ATS	AT5G42630	5	17106426	-13342
258	4.05334	MIR173	AT3G23125	3	8235844	-324
368	3.85108	ATL5	AT3G25520	3	9268740	1784
376	3.84515	CYC1	AT4G37490	4	17640138	-15859
395	3.81904	RIK	AT3G29390	3	11273009	-17841

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
14	4.07285	AT4G18390	AT4G18390	4	10171238	-5665
92	3.25956	RPS15AD	AT3G46040	3	16910283	-15241
204	2.95069	TAS1A	AT2G27400	2	11745344	-15798
208	2.94344	SE	AT2G27100	2	11596351	12615
221	2.92632	ATS	AT5G42630	5	17106426	-13342
235	2.90649	AXR1	AT1G05180	1	1505327	-3504
269	2.8609	AT1G33140	AT1G33140	1	12027655	2892
299	2.80461	AT1G29890	AT1G29890	1	10444133	-19254
314	2.79022	PAS1	AT3G54010	3	20034152	17991
371	2.71172	PTF1	AT3G02150	3	392114	0

Supplementary Figure 105 – Summary of GWA results for Presence of leaf serration at 10°C

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
84	3.95945	AGO1	AT1G48410	1	17879752	10014
129	3.78797	ANAC065	AT3G56560	3	20964531	-1852
274	3.40502	ANAC082	AT5G09330	5	2897805	-2382
280	3.39571	AT1G29890	AT1G29890	1	10452871	-10516
295	3.36742	TCP3	AT1G53230	1	19867229	-11836
402	3.20388	AT4G32700	AT4G32700	4	15788004	8302
481	3.11765	TCP4	AT3G15030	3	5079999	15877
498	3.10215	CYP72C1	AT1G17060	1	5841079	-5630

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
145	3.13165	RIK	AT3G29390	3	11272703	-18147
155	3.08794	ANAC013	AT1G32870	1	11922680	8753
204	2.94685	ANAC065	AT3G56560	3	20963308	-3075
205	2.93996	CYP72C1	AT1G17060	1	5841079	-5630
230	2.88852	AGO1	AT1G48410	1	17879752	10014
264	2.8361	ANAC079	AT5G07680	5	2419682	-16194
288	2.80952	ANAC074	AT4G28530	4	14072091	18404
306	2.78485	AT1G33140	AT1G33140	1	12042673	17910
340	2.75006	CAS1	AT2G07050	2	2933672	3003

Supplementary Figure 106 – Summary of GWA results for Presence of leaf serration at 16°C

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
62	4.30933	KNAT3	AT5G25220	5	8723472	-12605
76	4.15559	STV1	AT3G53020	3	19656679	14816
81	4.07561	MIR164	AT5G01747	5	301874	14143
82	4.05479	RIK	AT3G29390	3	11313868	17857
129	3.85693	ANAC074	AT4G28530	4	14073808	16687
375	3.35214	NPH4	AT5G20730	5	7001998	14449

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
4	5.0011	KNAT3	AT5G25220	5	8723472	-12605
11	4.36132	STV1	AT3G53020	3	19677624	-4621
66	3.42028	ANAC074	AT4G28530	4	14072091	18404
100	3.24533	ANAC103	AT5G64060	5	25667132	-14125
104	3.22861	MIR164	AT5G01747	5	301874	14143
281	2.79598	CUC1	AT3G15170	3	5100250	-9640
408	2.63898	MIR160	AT5G46845	5	19011264	15061
416	2.62825	AGO1	AT1G48410	1	17898848	-2594
436	2.60966	ANAC104/XND1	AT5G64530	5	25826789	12625
444	2.60077	AT1G29890	AT1G29890	1	10452871	-10516

Supplementary Figure 107 – Summary of GWA results for Presence of leaf serration at 22°C

Phenotype histogram and quantile-quantile plots of p-values

Fisher's exact test results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
131	4.56379	ICU2	AT5G67100	5	26786098	-8122
469	3.77949	REV	AT5G60690	5	24418262	0

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
25	4.54245	FKF1	AT1G68050	1	25507385	-4954
157	3.50838	TOR1	AT4G27060	4	13590138	-4977

Supplementary Figure 108 – Summary of GWA results for Presence of rolled leaves at 10°C

Phenotype histogram and quantile-quantile plots of p-values

Fisher's exact test results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
30	4.92698	PHV	AT1G30490	1	10805672	-4729
53	4.65782	YAB2	AT1G08465	1	2669712	-6098
143	4.19352	ROT4	AT2G36985	2	15529465	12393

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
29	4.37791	PHV	AT1G30490	1	10805672	-4729
64	3.82832	YAB2	AT1G08465	1	2669712	-6098
78	3.70678	FKF1	AT1G68050	1	25510841	-1498
428	2.80446	ICU2	AT5G67100	5	26812685	10355

Supplementary Figure 109 – Summary of GWA results for Presence of rolled leaves at 16°C

Phenotype histogram and quantile-quantile plots of p-values

Fisher's exact test results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
134	3.00117	KAN2	AT1G32240	1	11612456	13224
418	2.58211	ESR1	AT1G12980	1	4413142	-16574
497	2.49119	AFO	AT2G45190	2	18620754	14585

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
102	3.37775	KAN2	AT1G32240	1	11612456	13224
225	2.96991	AFO	AT2G45190	2	18620754	14585

Supplementary Figure 110 – Summary of GWA results for Presence of rolled leaves at 22°C

Phenotype histogram and quantile-quantile plots of p-values

Fisher's exact test results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
128	5.11262	ARF2	AT5G62000	5	24929565	0
445	4.1136	ERL2	AT5G07180	5	2225352	2220

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
49	3.83693	ARF2	AT5G62000	5	24929565	0
325	2.8857	ACS8	AT4G37770	4	17753006	0

Supplementary Figure 111 – Summary of GWA results for Presence of erect rosette at 22°C

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
28	4.0222	GA5*	AT4G25420	4	12986993	3901
34	3.95142	CUL4*	AT5G46210	5	18762116	-8079
54	3.73416	RGA1*	AT2G01570	2	271146	-13597
64	3.65914	ATMYB65*	AT3G11440	3	3612232	7122
64	3.65914	SPY*	AT3G11540	3	3612232	-19661
88	3.51928	AGL15*	AT5G13790	5	4455565	-4719
91	3.50155	AGL14*	AT4G11880	4	7158677	11461
94	3.49514	FUS3*	AT3G26790	3	9837239	17826
99	3.48472	LIP1*	AT5G64813	5	25932514	2392
109	3.45798	SNZ*	AT2G39250	2	16398244	-93

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
8	4.89322	FLK*	AT3G04610	3	1250422	137
11	4.86601	AGL15*	AT5G13790	5	4455565	-4719
19	4.24695	GA5*	AT4G25420	4	12986993	3901
35	3.96054	DFL1*	AT5G54510	5	22142549	5770
53	3.69279	AGL14*	AT4G11880	4	7158677	11461
57	3.65124	AT3G04510*	AT3G04510	3	1220072	-3108
63	3.56935	ATMYB65*	AT3G11440	3	3612232	7122
63	3.56935	SPY*	AT3G11540	3	3612232	-19661
64	3.56468	CUL4*	AT5G46210	5	18762116	-8079
91	3.44387	ATHXK1*	AT4G29130	4	14332437	19606

Supplementary Figure 112 – Summary of GWA results for Silique length at 16°C

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
15	5.9721	DDF1*	AT1G12610	1	4275009	14933
31	5.9721	CIP1*	AT5G41790	5	16769972	19897
41	5.39903	AP2*	AT4G36920	4	17382353	-18491
66	5.25912	FCA*	AT4G16280	4	9209491	0
66	5.25912	PHYD*	AT4G16250	4	9209491	-9990
206	4.62771	AMP1*	AT3G54720	3	20257523	8180
210	4.60944	HY5*	AT5G11260	5	3592609	772
222	4.58577	YAP169*	AT5G07200	5	2235056	8498
240	4.55483	HAP2A*	AT5G12840	5	4072138	-18529
376	4.30731	VIP1*	AT1G43700	1	16503722	15041

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
8	4.60044	GA1*	AT4G02780	4	1250359	-5546
23	4.09424	ICU2*	AT5G67100	5	26785000	-9220
33	3.89471	DFL1*	AT5G54510	5	22146360	1959
46	3.81935	TCH2*	AT5G37770	5	15010219	5865
51	3.74794	DDF1*	AT1G12610	1	4275009	14933
58	3.7192	SPL4*	AT1G53160	1	19829143	17867
77	3.68256	SEPALLATA4*	AT2G03710	2	1148414	16579
85	3.59299	AT3G21320*	AT3G21320	3	7482278	16781
153	3.19364	ELF4*	AT2G40080	2	16731019	10353
171	3.13874	CRY1*	AT4G08920	4	5716653	-7447

Supplementary Figure 113 – Summary of GWA results for Silique length at 22°C

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
3	6.06219	GASA4*	AT5G15230	5	4942411	-2492
12	5.36677	ICU2*	AT5G67100	5	26821993	19663
23	5.07589	ELF6*	AT5G04240	5	1190467	15588
40	4.82342	EMS1*	AT5G07280	5	2287470	0
44	4.73743	TFL1*	AT5G03840	5	1036127	-10316
99	4.4044	ATHB51*	AT5G03790	5	1010107	3735
116	4.31182	CO*	AT5G15840	5	5159928	11257
116	4.31182	COL1*	AT5G15850	5	5159928	16166
170	4.17324	ULT1*	AT4G28190	4	13996527	9260
175	4.14769	AT2G39540*	AT2G39540	2	16493075	-14869

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
2	7.72389	GASA4*	AT5G15230	5	4942411	-2492
30	4.89038	TFL1*	AT5G03840	5	1036127	-10316
31	4.85869	ICU2*	AT5G67100	5	26821993	19663
37	4.63856	ELF6*	AT5G04240	5	1190467	15588
48	4.34813	EMS1*	AT5G07280	5	2287470	0
65	4.05765	CO*	AT5G15840	5	5159928	11257
65	4.05765	COL1*	AT5G15850	5	5159928	16166
71	4.00853	GCR1*	AT1G48270	1	17827753	3868
83	3.89486	HUA2*	AT5G23150	5	7781354	-4484
125	3.67675	ETC3*	AT4G01060	4	460246	-226

Supplementary Figure 114 – Summary of GWA results for Duration of flowering time, greenhouse (FT duration GH)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
10	6.60842	ICU2*	AT5G67100	5	26807856	5526
37	5.91516	ETC3*	AT4G01060	4	458226	-2246
48	5.70703	AGL18*	AT3G57390	3	21239190	-5488
61	5.41654	SRR1*	AT5G59560	5	24005192	12590
90	5.18667	GASA4*	AT5G15230	5	4936803	-8100
98	5.11184	EZA1*	AT4G02020	4	911737	19782
100	5.10149	FAR1*	AT4G15090	4	8599640	-14423
107	5.0705	ATGA2OX7*	AT1G50960	1	18903090	7703
124	5.003	AGL14*	AT4G11880	4	7123531	-19578
133	4.94209	APRR3*	AT5G60100	5	24196322	18903

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
4	5.5404	AGL14*	AT4G11880	4	7123531	-19578
12	4.77407	ETC3*	AT4G01060	4	458226	-2246
40	4.00147	sim to VRN1*	AT4G33280	4	16056698	-7339
83	3.56067	FAR1*	AT4G15090	4	8604832	-9231
132	3.31958	FT*	AT1G65480	1	24341923	4326
158	3.23721	AGL18*	AT3G57390	3	21239190	-5488
171	3.19609	CUL4*	AT5G46210	5	18747783	862
174	3.19111	AT5G59570*	AT5G59570	5	24004227	-16887
174	3.19111	SRR1*	AT5G59560	5	24004227	13555
188	3.16607	SKB1*	AT4G31120	4	15126597	5420

Supplementary Figure 115 – Summary of GWA results for Life cycle duration, greenhouse (LC Duration GH)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
7	7.04614	ICU2*	AT5G67100	5	26807856	5526
41	5.85085	ETC3*	AT4G01060	4	458226	-2246
57	5.63531	GASA4*	AT5G15230	5	4936803	-8100
74	5.42484	ATGA2OX7*	AT1G50960	1	18903090	7703
92	5.31907	SRR1*	AT5G59560	5	24005192	12590
100	5.23133	EZA1*	AT4G02020	4	910200	18245
106	5.19726	FAR1*	AT4G15090	4	8599640	-14423
125	5.0691	AT5G59570*	AT5G59570	5	24005099	-16015
126	5.06899	AGL18*	AT3G57390	3	21239190	-5488
133	5.03744	APRR3*	AT5G60100	5	24195846	19379

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
20	4.33222	AGL15*	AT5G13790	5	4429786	19231
30	4.11271	ETC3*	AT4G01060	4	458226	-2246
32	4.10289	sim to VRN1*	AT4G33280	4	16056698	-7339
36	3.99126	AGL14*	AT4G11880	4	7123531	-19578
48	3.88101	FT*	AT1G65480	1	24341923	4326
57	3.83013	SKB1*	AT4G31120	4	15126597	5420
70	3.67151	FPF1*	AT5G24860	5	8540225	-1556
149	3.27233	YAP169*	AT5G07200	5	2264248	-18908
155	3.25513	FRI*	AT4G00650	4	266533	-2493
169	3.216	PHYB*	AT2G18790	2	8159983	8471

Supplementary Figure 116 – Summary of GWA results for Length till flower senescence, greenhouse (LFS GH)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
26	5.52847	INO*	AT1G23420	1	8317932	0
35	5.37416	ATHB-2*	AT4G16780	4	9450377	0
64	5.04365	MBD9*	AT3G01460	3	184954	2493
95	4.74992	VIM1*	AT1G57820	1	21412722	5113
108	4.66187	FRI*	AT4G00650	4	269962	0
129	4.5873	PHYB*	AT2G18790	2	8170415	18903
138	4.56465	CDF1*	AT5G62430	5	25096227	-8067
148	4.50558	ELIP2*	AT4G14690	4	8406484	-11794
185	4.35604	ATFYPP3*	AT3G19980	3	6980631	15517
193	4.33028	LD*	AT4G02560	4	1114498	8992

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
32	4.28567	ATFYPP3*	AT3G19980	3	6980631	15517
33	4.19755	ATHB-2*	AT4G16780	4	9450377	0
50	3.80929	TOC1*	AT5G61380	5	24695401	0
62	3.67719	PHYC*	AT5G35840	5	14011077	-13979
73	3.58915	PGI1*	AT4G24620	4	12721293	-8458
85	3.51907	GASA2*	AT4G09610	4	6075580	0
97	3.46113	FKF1*	AT1G68050	1	25531701	17149
107	3.43311	FRI*	AT4G00650	4	257828	-11198
149	3.21648	CIP1*	AT5G41790	5	16765589	15514
188	3.11331	VIM1*	AT1G57820	1	21412722	5113

Supplementary Figure 117 – Summary of GWA results for Time to maturation, greenhouse (MT GH)

Phenotype histogram and quantile-quantile plots of p-values

Wilcoxon results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
11	5.09769	DDF1*	AT1G12610	1	4278622	11320
29	4.70264	GASA4*	AT5G15230	5	4938181	-6722
49	4.49959	ELF6*	AT5G04240	5	1187736	12857
52	4.46503	ICU2*	AT5G67100	5	26821993	19663
58	4.38313	FY*	AT5G13480	5	4309970	16561
66	4.31713	YAP169*	AT5G07200	5	2238135	5419
75	4.23367	AGL18*	AT3G57390	3	21230854	-13824
84	4.21793	FLC*	AT5G10140	5	3163932	9566
85	4.21759	EMF1*	AT5G11530	5	3716414	14865
99	4.16041	ETC3*	AT4G01060	4	473140	12055

EMMA results

Rank	Score	Gene	Gene ID	Chr	SNP pos (bp)	Distance to gene (bp)
11	4.89777	ICU2*	AT5G67100	5	26821993	19663
24	4.36647	GA1*	AT4G02780	4	1262486	-17673
58	3.86547	ELF6*	AT5G04240	5	1187736	12857
69	3.76682	YAP169*	AT5G07200	5	2238135	5419
74	3.72861	TFL1*	AT5G03840	5	1036127	-10316
93	3.65705	TFL2*	AT5G17690	5	5821540	5633
238	3.1776	DDF1*	AT1G12610	1	4278622	11320
244	3.15998	AGL18*	AT3G57390	3	21239134	-5544
261	3.118	GASA2*	AT4G09610	4	6078158	-2516
302	3.05232	LCL1*	AT5G02840	5	651927	0

Supplementary Figure 118 – Summary of GWA results for Reproductive period, greenhouse (RP GH)

Supplementary Figure 119 – Clustered association peaks for flowering-related phenotypes. Blue dots indicate SNPs significant at the 10^{-8} level using the Wilcoxon test; red dots indicate SNPs significant at the 10^{-4} level using EMMA. At most the top 0.1% of SNPs for each phenotype are plotted. Deeper color indicates stronger association. The green lines indicate the positions of *a priori* candidates within 20 kb of one of the dots. The orange line marks *DOG1*, a strong *a posteriori* candidate.

Supplementary Figure 120 – Peak of association around *ATH1*[38] for LD.

Supplementary Figure 121 – Peak of association around *SVP*[39] for LD.

Supplementary Figure 122 – Peak of association around *FRI*[5], for FRI.

Supplementary Figure 123 – Peak of association around *FPF1*[40] for FT16.

Supplementary Figure 124 – Peak of association around *YAP169*[41] for FT16.

Supplementary Figure 125 – Peak of association around *RAV-1*[42] for SD.

Supplementary Figure 126 – Peak of association around *SPL4*[43] for FT16.

Supplementary Figure 127 – Peak of association around *CRP*[44], *ETC3*[45], and *FRI*[5] for FLC.

Supplementary Figure 128 – Peak of association around *SPA2*[46] for LDV.

Supplementary Figure 129 – Peak of association around *SPA4*[46] for FT16.

Supplementary Figure 130 – Peak of association around *SIM TO VRN1* for LDV.

Supplementary Figure 131 – Peak of association around *DOG1*[18] for LN10.

Supplementary Figure 132 – Peak of association around *DFL2*[47] for FT22.

Supplementary Figure 133 – Peak of association around *FLC*[17] for LN22.

Supplementary Figure 134 – Peak of association around *FT*[48] for LN 10.

Supplementary Figure 135 – Peak of association around *HUA2*[49] for FT DAYS GH.

Supplementary Figure 136 – Peak of association around *HEN2*[50] for 8W GH FT.

Supplementary Figure 137 – Peak of association around *VIN3*[51] for FT10.

Supplementary Figure 138 – Peak of association around *CTR1*[52] for *AvrRpm1*.

Supplementary Figure 139 – Peak of association around *RPS2*[53] for *AvrRpt2*.

Supplementary Figure 140 – Peak of association around *RPS5*[54] for *AvrPphB*.

Supplementary Figure 141 – Peak of association around *TCL1*[55], *TCL2*, and *ETC2*[56] for Trichome average JA.

Supplementary Figure 142 – Peak of association around *TTG1*[57] for Trichome average C.

Supplementary Figure 143 – Peak of association around *HKT1*[19] for Sodium.

Supplementary Figure 144 – Peak of association around *MOT1*[20] for Molybdenum.

Supplementary Figure 145 – Peak of association around *SULTR1;2*[58,59] for Selenium.

Supplementary Figure 146 – Peak of association around *CTS*[60] for Storage 28 days.

Supplementary Figure 147 – Peak of association around *LSH1*[61] for hypocotyl length.

Supplementary Figure 148 – Peak of association around *HFR1*[62] for hypocotyl length.

Supplementary Figure 149 – Peak of association around *ACD6*[22] for Lesioning.

Supplementary Figure 150 – Peak of association around *SGTA1*[63] for Lesioning.

Supplementary Figure 151 – Peak of association around *AtATG18h*[64] for Lesioning.

Supplementary Figure 152 – Peak of association around *FLS* for anthocyanin at 22°C.