File S1: confidence intervals for broad-sense heritability

Confidence intervals for the broad-sense heritability estimates obtain from the ANOVA mean sums of squares are traditionally obtained from the ratio $F = MS(G)/MS(E)$ and the quantiles of the F-distribution with the corresponding degrees of freedom. Given n genotypes with $r_1, \ldots, r_n$ replicates, the intervals are given by

$$\frac{F/F_{\mathrm{df1,df2},0.95} - 1}{F/F_{\mathrm{df1,df2},0.95} + \bar{r} - 1} < H^2 < \frac{F/F_{\mathrm{df1,df2},0.05} - 1}{F/F_{\mathrm{df1,df2},0.05} + \bar{r} - 1},$$

where $\mathrm{df1} = n - 1$, $\mathrm{df2} = \sum(r_i - 1)$ and $\bar{r} = (n-1)^{-1}(\sum r_i - (\sum r_i^2)/(\sum r_i))$. In case of a balanced design with $r_i = r$ replicates, this reduces to $\bar{r} = r$ and $\mathrm{df2} = n(r-1)$. See [1] (p.563) or [2].

File S2: analysis of flowering traits of [3]

Our broad-sense heritability estimates differ from those reported in Supplementary table 7 of [3], for the following three reasons. First, the broad-sense heritability estimates in [3] were calculated using the formula

$$\frac{MS(G)}{MS(G) + MS(E)}. \tag{1}$$

Although this quantity may be an adequate criterion to compare heritabilities of traits within the same experiment (as long as they have the same number of replicates), this is a biased estimator of broad-sense-heritability. Since the expectation of $MS(G)$ is $r\sigma^2_G + \sigma^2_E$, $MS(G)/(MS(G) + MS(E))$ will tend to overestimate heritability. The usual estimator defined in the materials and methods section is also biased, but this bias is usually small, and (in contrast to (1)) tends to zero when the number of genotypes increases ([4], [2]).

Second, broad-sense heritability estimates in [3] were based on more accessions: 189 for LDV and 186 for LD. To allow a direct comparison with mixed model analysis we restricted our analysis to genotyped accessions, excluding 21 accessions for LDV and for 19 LD. This had little impact on heritability estimates.

Third, the analysis of variance in [3] did not include a replicate effect. In our analysis, the mean sums of squares for replicates removes some environmental variance, therefore giving higher estimates than in an analysis without a replicate effect. This however did not compensate for the use of (1); hence our heritability estimates are lower than those reported in [3].

File S3: the likelihood is constant for a kinship matrix with compound symmetry structure

Mixed model based estimation of heritability using genotypic means may become problematic when the sample size is small and the kinship matrix is close to compound symmetry, i.e. the structure where all off-diagonal elements are equal. Here we show that in the case the kinship matrix is exactly compound symmetry, the likelihood is constant in $\eta = \sigma_E^2/\sigma_A^2$. We use the notation η to avoid confusion with $\delta = \sigma_A^2/\sigma_E^2$, used in our results on genomic prediction. We write 1_n for the $n \times 1$ column vector of ones, and I_n for the n-dimensional identity matrix. Finally, let J_n be the $n \times n$ matrix of ones.

Suppose that $K = I_n + aJ_n$, for some $a > 0$. The key observation is that the covariance matrix of the data can be written as

$$\Sigma = \sigma_A^2 K + \sigma_E^2 I_n = \tilde{\sigma}_A^2 \tilde{K} + \tilde{\sigma}_E^2 I_n = \tilde{\sigma}_A^2 (\tilde{K} + \tilde{\eta} I_n),$$

where $\tilde{\sigma}_A^2 = \sigma_A^2$, $\tilde{\sigma}_E^2 = \sigma_A^2 + \sigma_E^2$, $\tilde{K} = aJ_n = a1_n 1_n^t$ and $\tilde{\eta} = (\sigma_A^2 + \sigma_E^2)/\sigma_A^2 > 0$. We can then directly apply the results in section 3 of [5], with (in their notation) $k = 1$, $d = 1$ and $X = 1_n$ (we only include an intercept, and no marker effect), and replacing σ_A^2, σ_E^2, η and K by respectively $\tilde{\sigma}_A^2$, $\tilde{\sigma}_E^2$, $\tilde{\eta}$ and $\tilde{K}$. In particular, we have the spectral decomposition

$$\begin{aligned}\tilde{K} = USU^t &= [U_1, U_2] \begin{bmatrix} S_1 & 0 \\ 0 & S_2 \end{bmatrix} [U_1, U_2]^t \\ &= \begin{pmatrix} n^{-\frac{1}{2}} & 0 & \dots & 0 \\ \vdots & \vdots & & \vdots \\ n^{-\frac{1}{2}} & 0 & \dots & 0 \end{pmatrix} \begin{pmatrix} na & 0 & \dots & 0 \\ 0 & 0 & \dots & 0 \\ \vdots & & \ddots & \vdots \\ 0 & \dots & \dots & 0 \end{pmatrix} \begin{pmatrix} n^{-\frac{1}{2}} & \dots & n^{-\frac{1}{2}} \\ 0 & \dots & 0 \\ 0 & \dots & 0 \end{pmatrix},\end{aligned}$$

i.e. the only non-zero eigenvalue of $\tilde{K}$ is an, with eigenvector $(n^{-\frac{1}{2}}, \dots, n^{-\frac{1}{2}})$.

For this choice of X and $\tilde{K}$, the expressions for the (RE)ML estimates of β and $\tilde{\sigma}_A^2$ given in sections 3.2 and 4 of [5] greatly simplify: $\hat{\beta} = \bar{y}$ and the REML-estimate of $\tilde{\sigma}_A^2$ is $\sum_{i=1}^n (y_i - \bar{y})^2/(\tilde{\eta}(n-1))$. The extra terms

$$\frac{1}{2}\left(d \log(2\pi\tilde{\sigma}_A^2) + \log|X^t X| - \log|X^t(\tilde{K} + \tilde{\eta} I_n)^{-1} X|\right)$$

in the REML-log-likelihood (see the first equation in section 4 of [5]), now equal

$$\frac{1}{2}\left(d \log(2\pi\tilde{\sigma}_A^2) + \log n - \log\left(\frac{n}{na + \tilde{\eta}}\right)\right).$$

Combining this with their equation (3.7), it follows that the REML-log-likelihood is constant in $\tilde{\eta} = (\sigma_A^2 + \sigma_E^2)/\sigma_A^2 > 0$, and hence also constant in $\eta = \tilde{\eta} - 1 = \sigma_E^2/\sigma_A^2$.

File S4: Simulation results for a different genetic architecture.

Table 1: **Comparison of the marker-based estimators heritability estimators h_r^2 and h_m^2 for simulated data.** We simulated 5000 traits, for random samples of 200 accessions drawn from the Structured regmap and Hapmap. A single QTL was simulated, which explained 90 percent of the genetic variance. The simulated heritability was 0.2, 0.5 and 0.8. Standard errors are given relative to those of the broad sense heritability estimator (H^2).

	bias	standard error	relative standard error
Structured regmap			
$h^2 = 0.2$			
broad-sense (H^2)	-0.00127	0.04787	1.00000
replicates (h_r^2)	-0.00066	0.05102	1.06585
means (h_m^2)	0.00782	0.08626	1.80191
$h^2 = 0.5$			
broad-sense (H^2)	-0.00279	0.04500	1.00000
replicates (h_r^2)	-0.00571	0.07001	1.55569
means (h_m^2)	0.01295	0.16461	3.65791
$h^2 = 0.8$			
broad-sense (H^2)	-0.00257	0.02458	1.00000
replicates (h_r^2)	-0.01163	0.05404	2.19850
means (h_m^2)	0.00337	0.20855	8.48496
Hapmap			
$h^2 = 0.2$			
broad-sense (H^2)	-0.00110	0.04344	1.00000
replicates (h_r^2)	-0.00098	0.04320	0.99453
means (h_m^2)	0.06629	0.26168	6.02448
$h^2 = 0.5$			
broad-sense (H^2)	-0.00123	0.03437	1.00000
replicates (h_r^2)	-0.00187	0.03736	1.08695
means (h_m^2)	0.03062	0.33527	9.75477
$h^2 = 0.8$			
broad-sense (H^2)	-0.00027	0.01633	1.00000
replicates (h_r^2)	-0.00106	0.02029	1.24235
means (h_m^2)	-0.07852	0.33486	20.50621

Table 2: **Marker-based estimation of heritability: width and coverage confidence intervals obtained from the individual plant data and the genotypic means.** Results for broad sense heritability intervals are reported for comparison. We simulated 5000 traits, for random samples of 200 accessions drawn from the structured regmap (top) and Hapmap (bottom). A single QTL was simulated, which explained 90 percent of the genetic variance. The simulated heritability was 0.2, 0.5 and 0.8.

	coverage	interval width
Structured regmap		
$h^2 = 0.2$		
broad-sense	0.940	0.178
replicates (standard)	0.945	0.201
replicates (log-transformed)	0.962	0.202
means (standard)	0.911	0.315
means (log-transformed)	0.960	0.321
$h^2 = 0.5$		
broad-sense	0.926	0.160
replicates (standard)	0.837	0.194
replicates (log-transformed)	0.847	0.192
means (standard)	0.814	0.446
means (log-transformed)	0.886	0.427
$h^2 = 0.8$		
broad-sense	0.914	0.084
replicates (standard)	0.674	0.097
replicates (log-transformed)	0.666	0.097
means (standard)	0.714	0.437
means (log-transformed)	0.840	0.547
Hapmap		
$h^2 = 0.2$		
broad-sense	0.961	0.178
replicates (standard)	0.961	0.181
replicates (log-transformed)	0.972	0.182
means (standard)	0.807	0.537
means (log-transformed)	0.899	0.675
$h^2 = 0.5$		
broad-sense	0.979	0.160
replicates (standard)	0.971	0.164
replicates (log-transformed)	0.975	0.163
means (standard)	0.800	0.766
means (log-transformed)	0.967	0.819
$h^2 = 0.8$		
broad-sense	0.990	0.084
replicates (standard)	0.963	0.085
replicates (log-transformed)	0.964	0.085
means (standard)	0.820	0.840
means (log-transformed)	0.849	0.903

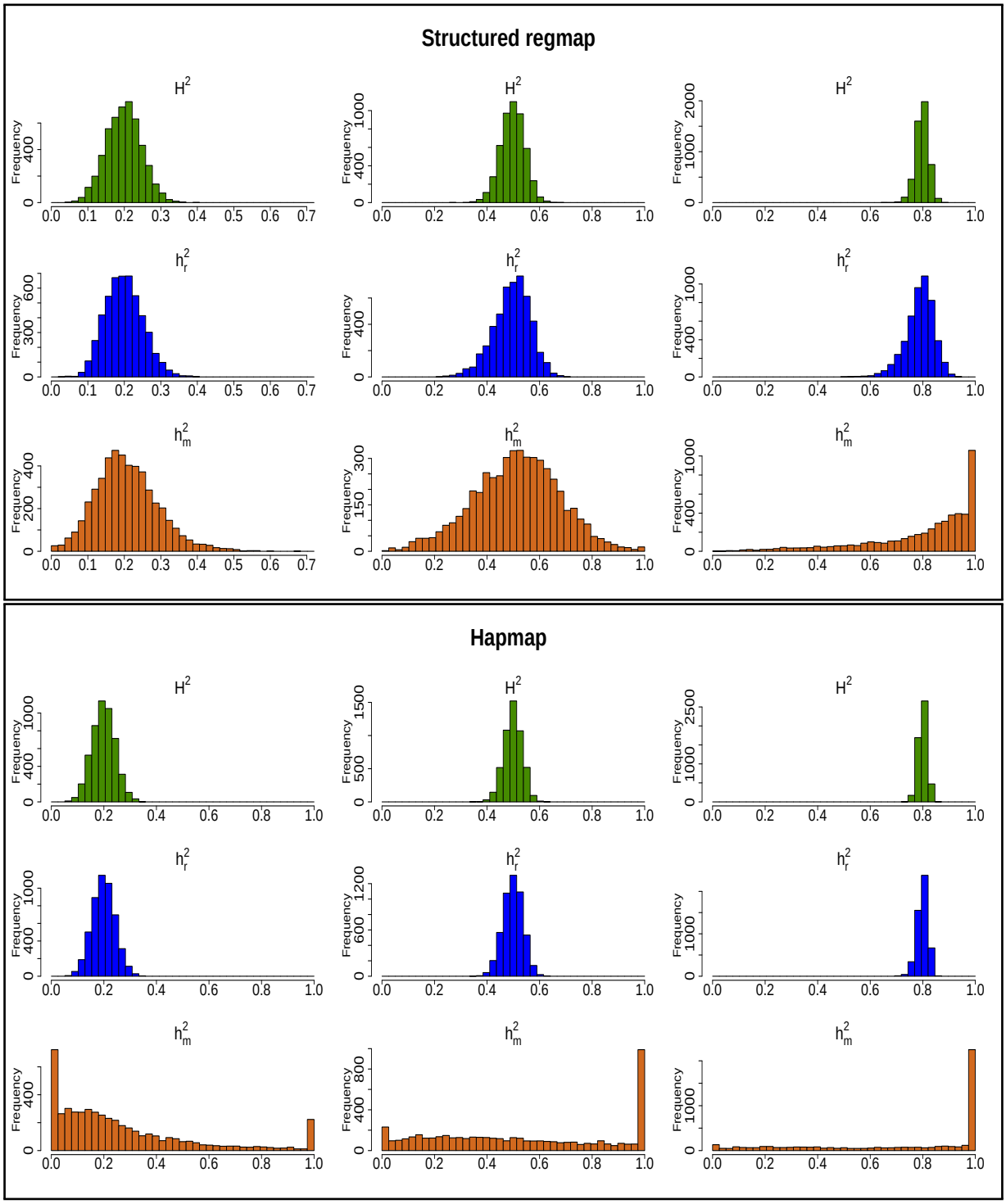

Figure 1: **Heritability estimates for 5000 simulated traits for random samples of 200 accessions drawn from the Structured regmap (top panel) and the Hapmap (bottom panel).** 1 QTL was simulated, which explained 90% of the genetic variance. The simulated heritability was 0.2 (left column), 0.5 (middle column) and 0.8 (right column). Within each panel, the first row shows the ANOVA-based estimates of broad-sense heritability, the second row the mixed model based estimates based on the individual data, and the third row the mixed model based estimates based on genotypic means.

File S5: prediction error variance in the training- and validation set.

We assume a balanced and completely random design, with n genotypes and r replicates. Given the model $y_{i,j} = \mu + G_i + E_{i,j}$, the best linear unbiased predictor (BLUP) of $G = (G_1, \ldots, G_n)^t$ and the best linear unbiased estimator (BLUE) of μ are given by

$$\hat{G} = \delta K Z^t (\delta Z K Z^t + I_N)^{-1}(y - \hat{\mu} 1_N), \quad \hat{\mu} = \frac{1_N^t (\delta Z K Z^t + I_N)^{-1} y}{1_N^t (\delta Z K Z^t + I_N)^{-1} 1_N}, \tag{2}$$

where $\delta = \sigma_A^2/\sigma_E^2$ is the shrinkage parameter, N is the total number of individuals and Z is the $N \times n$ incidence matrix assigning individuals to genotypes. See e.g. [6] or [7], or equation (23) in the present work (Appendix C). The parameter $\delta = h^2/(1-h^2)$ is a function of the heritability, and determines the extent to which the phenotypic data y are 'shrunk' towards zero. When the heritability is high, δ is large, and there is little shrinkage, i.e. $\hat{G}$ will be close to the observed phenotypic observations y. For low heritability, δ is small, and y will be shrunk towards the vector of zeros. When BLUPs are based on the genotypic means the same expressions hold, with $N = n$ and $Z = I_n$, and $\hat{G} = \delta_r K (\delta_r K + I_n)^{-1}((\bar{y}_1, \ldots, \bar{y}_n)^t - \hat{\mu} 1_n)$. Since the noise level is reduced from σ_E^2 to $r^{-1}\sigma_E^2$, the shrinkage parameter δ becomes $\sigma_A^2/(r^{-1}\sigma_E^2)$.

The preceding expressions assume the shrinkage parameter to be known, while it is usually estimated from the data. As a consequence, the standard error of $\hat{\mu}$ and prediction error variance of $\hat{G}$ obtained by setting $\delta = \hat{\delta} = \hat{h}^2/(1-\hat{h}^2)$ in (2) are larger than what would be obtained when δ is known ([8], [9]). Before we give examples of too much or too little shrinkage (section), we first give expressions for the prediction error variance for the training and validation set, for the case when heritability is known ($\hat{\delta} = \delta$). These can be derived as a special case of the more general expressions in e.g. [6] or [7].

Prediction error variance when $\delta = \hat{\delta}$

First we consider the genetic effects $G = (G_1, \ldots, G_n)^t$ of the genotypes in the training sample. If we assume that $G \sim N(0, \sigma_A^2 K)$ (i.e. in equation (21) in the main text (Appendix B), γ and the QTL-effects α_m are zero), the prediction error variance is given by the diagonal elements of

$$E(\hat{G} - G)(\hat{G} - G)^t = (Z^t Z + \delta^{-1} K^{-1} - J_n)^{-1}, \tag{3}$$

where Z is the $N \times n$ incidence matrix assigning plants to genotypes, and J_n is the $n \times n$ matrix with identical elements $1/n$. In case the phenotypic data consists of genotypic means, $N = n$. For efficient computation, see [10] [11].

The genetic effects $G_{\text{pred}} = (G_{n+1}, \ldots, G_{n+m})^t$ of m unobserved (but genotyped) genotypes can be predicted with the conditional mean

$$\hat{G}_{\text{pred}} := E[G_{\text{pred}}|y] = \hat{\delta} K_{\text{pred.obs}} Z^t (\hat{\delta} Z K Z^t + I_N)^{-1}(y - \hat{\mu} 1_N), \tag{4}$$

where $K_{\text{pred.obs}}$ is the $m \times n$ matrix of kinship coefficients for the unobserved versus observed genotypes. To give expressions for the prediction error variance $E(\hat{G}_{\text{pred}} - G_{\text{pred}})_{i'}^2$ $(i' = 1, \ldots, m)$ we assume again that $\gamma = 0$, all genetic signal being polygenic. Writing $K_{\text{pred.pred}}$ for the $m \times m$ kinship matrix of the unobserved genotypes, it is assumed that the kinship matrix is the $(n+m) \times (n+m)$ block matrix with K and $K_{\text{pred.pred}}$ on the diagonal and off-diagonal blocks $K_{\text{pred.obs}}$ and $K_{\text{pred.obs}}^t$. Then the conditional distribution of $G_{\text{pred}}|G$ is

$$G_{\text{pred}}|G \sim N\left(K_{\text{pred.obs}} K^{-1} G, \sigma_A^2 \left(K_{\text{pred.pred}} - K_{\text{pred.obs}} K^{-1} K_{\text{pred.obs}}^t\right)\right).$$

Since $\hat{G}_{\text{pred}} = K_{\text{pred.obs}} K^{-1} \hat{G}$ (by comparing (2) and (4)), it follows that

$$\begin{aligned} (\hat{G}_{\text{pred}} - G_{\text{pred}})|(\hat{G} - G) &= K_{\text{pred.obs}} K^{-1}(\hat{G} - G) - Y, \\ \text{where} \quad Y &\sim N\left(0, \sigma_A^2 (K_{\text{pred.pred}} - K_{\text{pred.obs}} K^{-1} K_{\text{pred.obs}}^t)\right). \end{aligned}$$

Consequently, the prediction error variances $E(\hat{G}_{\text{pred}} - G_{\text{pred}})_i^2$ are the diagonal elements of

$$\begin{aligned} &E(\hat{G}_{\text{pred}} - G_{\text{pred}})(\hat{G}_{\text{pred}} - G_{\text{pred}})^t = E\left[E(\hat{G}_{\text{pred}} - G_{\text{pred}})(\hat{G}_{\text{pred}} - G_{\text{pred}})^t \mid (\hat{G} - G)\right] \\ &= (K_{\text{pred.obs}} K^{-1}) \left[E(\hat{G} - G)(\hat{G} - G)^t\right] K^{-1} K_{\text{pred.obs}}^t \\ &\quad + \sigma_A^2 (K_{\text{pred.pred}} - K_{\text{pred.obs}} K^{-1} K_{\text{pred.obs}}^t). \end{aligned} \tag{5}$$

Hence, the prediction error variance for the validation set contains a term depending on $\delta^{-1} = \sigma_E^2/\sigma_A^2$ (see (3)), as well as a term which depends only on the genetic variance σ_A.

Prediction error variance with incorrect shrinkage ($\delta \neq \hat{\delta}$)

For the case that the amount of shrinkage is not chosen correctly ($\hat{\delta} \neq \delta = \sigma_A^2/(r^{-1}\sigma_E^2)$), we now give an expression for the prediction error variance for the training set based on genotypic means, under the additional assumption that μ is known to be zero. The BLUP for G then simplifies to

$$\hat{G} = \hat{\delta}K(\hat{\delta}K + I_n)^{-1}\bar{y}, \tag{6}$$

where we recall that we still assume a balanced and completely random design. Hence $\bar{y}_i = G_i + \bar{E}_i$, with $\bar{E}_i \sim N(0, r^{-1}\sigma_E^2)$ and $G = (G_1, \ldots, G_n)^t \sim N(0, \sigma_A^2 K)$. Since $\bar{y} = (\bar{y}_1, \ldots, \bar{y}_n)^t \sim N(0, \sigma_A^2 K + r^{-1}\sigma_E^2 I_n) = N(0, \sigma_E^2(\delta K + r^{-1} I_n)$, the variance-covariance matrix of $\hat{G} - G$ equals

$$\mathrm{Var}(\hat{G} - G) = \sigma_A^2 K - 2\hat{\delta}K(\hat{\delta}K + I_n)^{-1}\sigma_A^2 K + \hat{\delta}K(\hat{\delta}K + I_n)^{-1}(\delta K + r^{-1} I_n)(\hat{\delta}K + I_n)^{-1}\hat{\delta}K\sigma_E^2,$$

where we used that (by the independence of G and E)

$$\mathrm{Cov}(G, \hat{G}) = \mathrm{Cov}(G, \hat{\delta}K(\hat{\delta}K + I_n)^{-1}G) = \hat{\delta}K(\hat{\delta}K + I_n)^{-1}\sigma_A^2 K$$

and that (using $\bar{y} \sim N(0, \sigma_E^2(\delta K + r^{-1} I_n)$ and the symmetry of K and I_n)

$$\hat{G} = \hat{\delta}K(\hat{\delta}K + I_n)^{-1}\bar{y} \sim N(0, \hat{\delta}K(\hat{\delta}K + I_n)^{-1}(\delta K + r^{-1} I_n)(\hat{\delta}K + I_n)^{-1}\hat{\delta}K\sigma_E^2).$$

In particular, when $\hat{\delta} = \infty$ (i.e. $\hat{h}^2 = 1$), there is no shrinkage, and $\hat{G} = \bar{y}$. The prediction error variance is then completely determined by the residual variance, since $\hat{G} - G = \bar{y} - G = \bar{E}$, and

$$E(\hat{G} - G)(\hat{G} - G)^t = r^{-1}\sigma_E^2 I_n.$$

On the other hand, when $\hat{\delta} = 0$ (i.e. $\hat{h}^2 = 0$), there is 'total' shrinkage towards zero, i.e. $\hat{G} = 0$, and

$$E(\hat{G} - G)(\hat{G} - G)^t = E(GG^t) = \sigma_A^2 K.$$

This explains the asymmetry in the observed accuracy in our simulations, in particular when $h^2 = 0.5$: when the number of replicates r is sufficiently large, overestimating the heritability will have less impact on the prediction error variance (and hence accuracy) than underestimating it.

Figure S1: histograms of the off-diagonal kinship coefficients, for 4 sub-populations of the regmap.

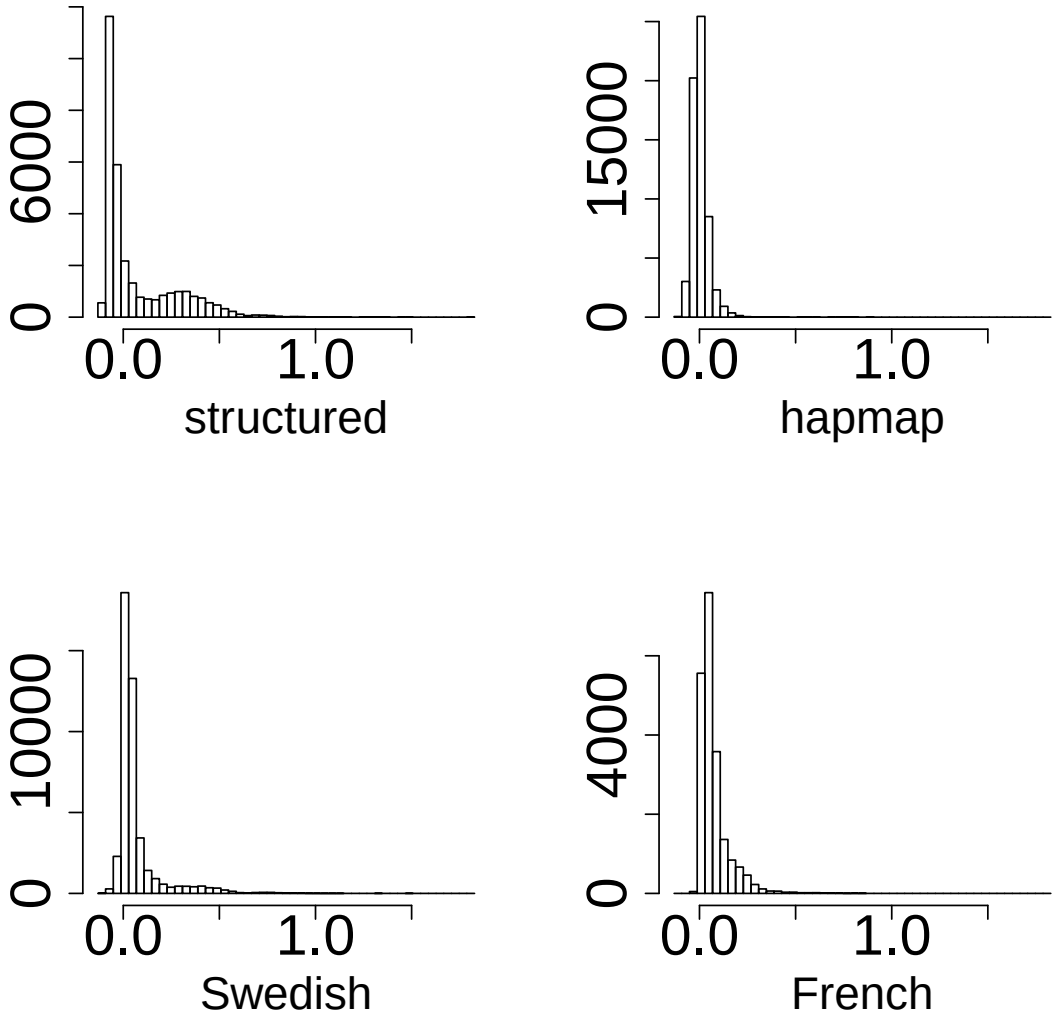

Figure S1 : **Off-diagonal coefficients of the genetic relatedness matrix (equation (1) in the main text), for 4 sub-populations of the regmap.**

Figure S2: histograms of the off-diagonal identity-by-state coefficients, for 4 sub-populations of the regmap.

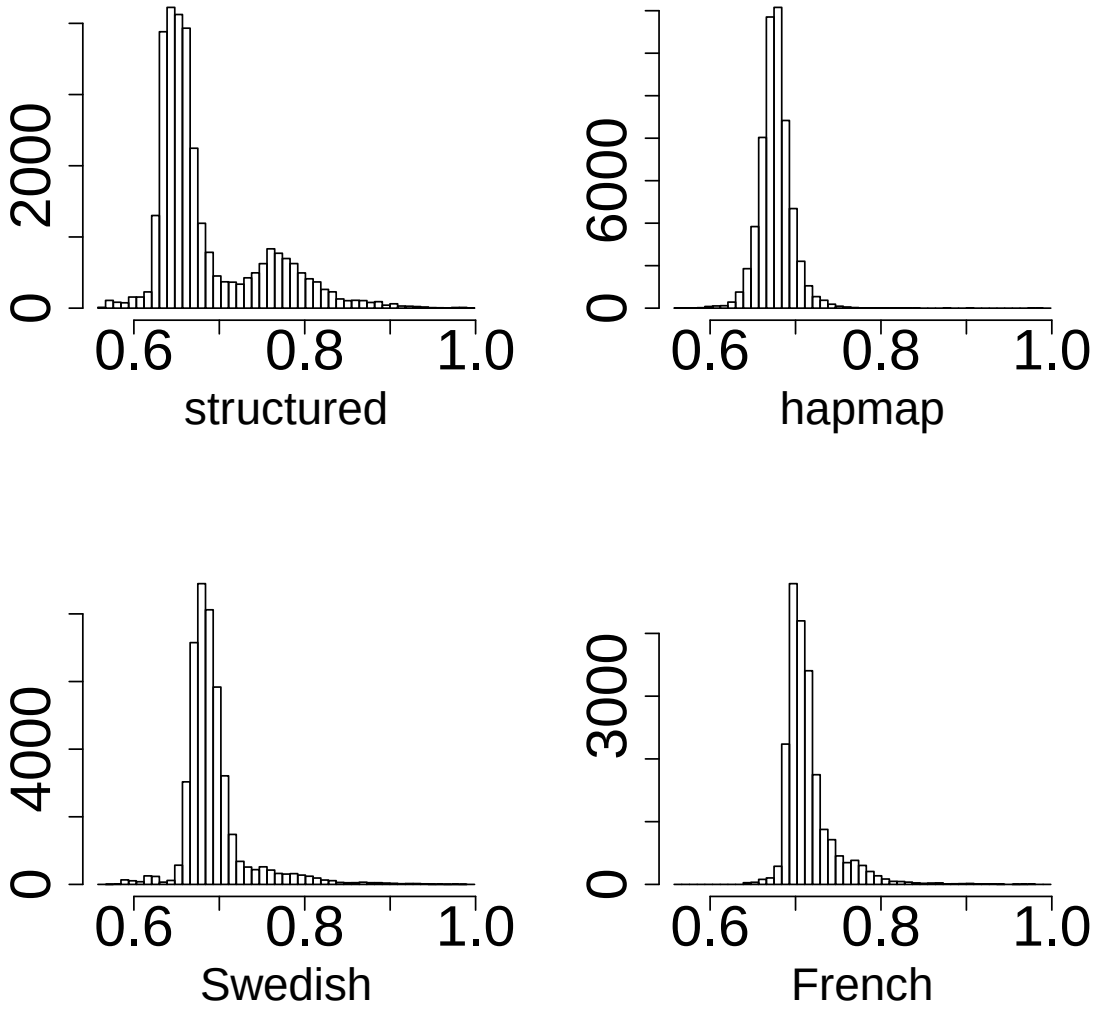

Figure S2 : **Off-diagonal identity-by-state kinship coefficients, for 4 sub-populations of the regmap.**

Figure S3

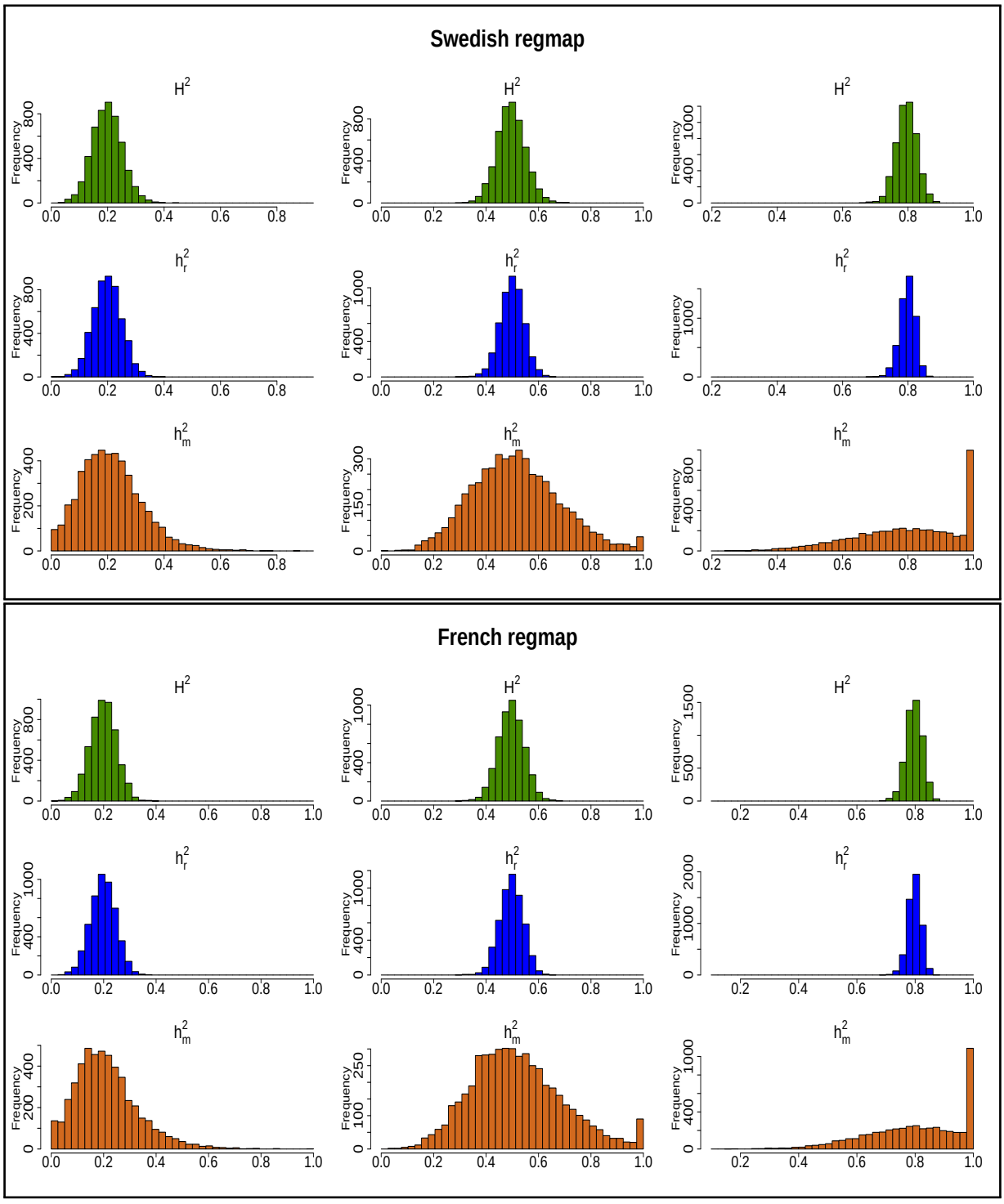

Figure S3 : **Heritability estimates for 5000 simulated traits for random samples of 200 accessions drawn from the Swedish regmap (top panel) and the French regmap (bottom panel).** 20 QTLs were simulated, which explained half of the genetic variance. The simulated heritability was 0.2 (left column), 0.5 (middle column) and 0.8 (right column). Within each panel, the first row shows the ANOVA-based estimates of broad-sense heritability, the second row the mixed model based estimates based on the individual data, and the third row the mixed model based estimates based on genotypic means.

Figure S4: Monotone likelihood

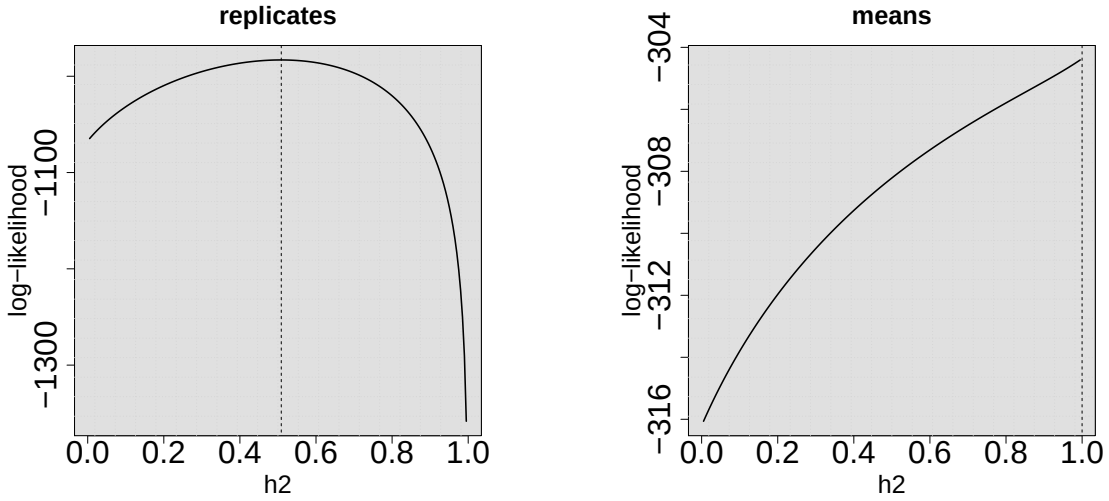

Figure S4 : **Log-likelihood as function of the heritability, for one of the 5000 simulated traits from Figure 1 (in the main text), for accessions drawn from the HapMap and a simulated heritability of 0.5** Here we choose one of the 882 traits (17.6%) for which the heritability estimate based on means ($\hat{h}^2_m$) was larger than 0.99. For these traits, the heritability estimate based on replicates ($\hat{h}^2_r$) was on average 0.502. For the trait shown here, $\hat{h}^2_m = 0.5087$ (left) and $\hat{h}^2_m = 0.9999$ (right).

Figure S5

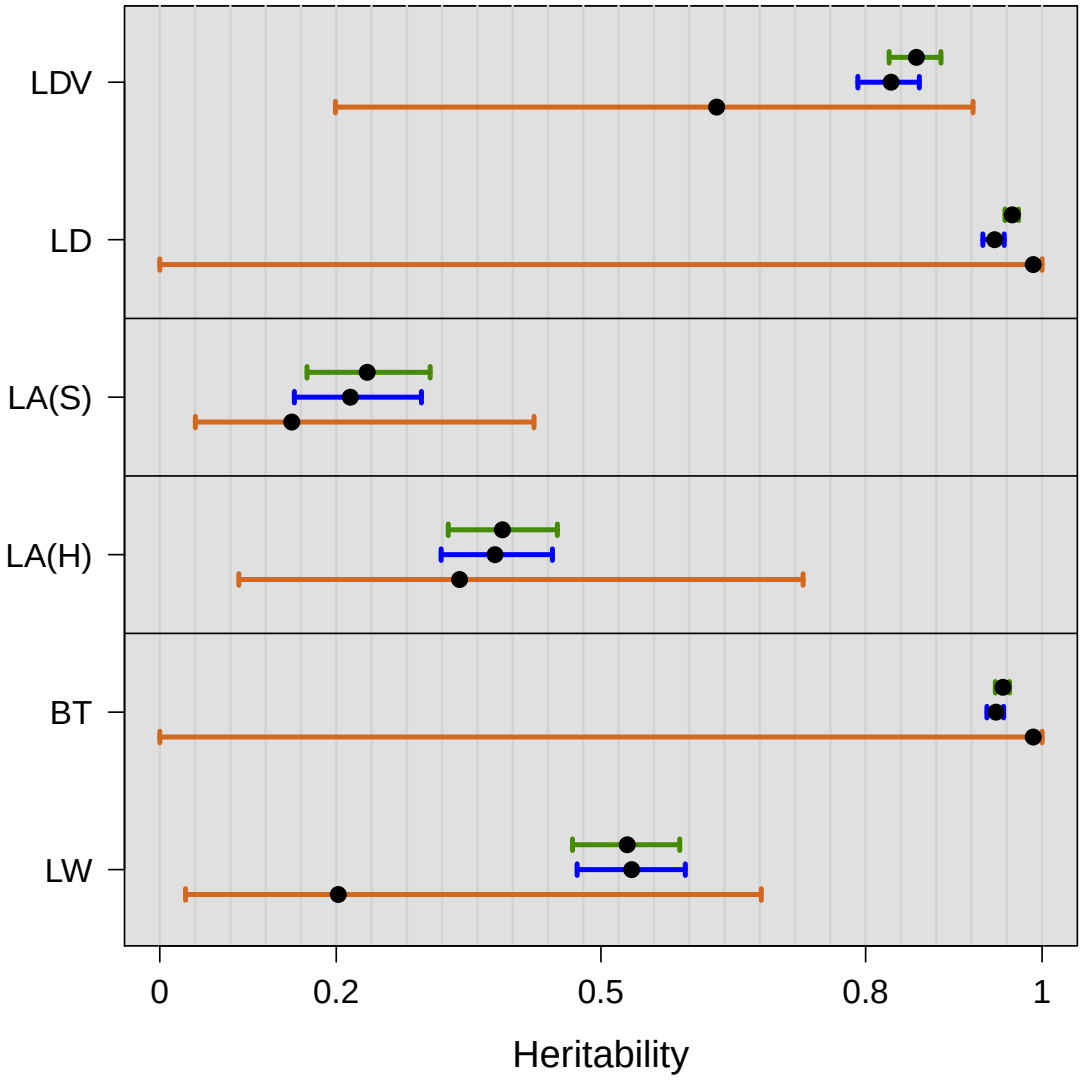

Figure S5 : **Heritability estimates and confidence intervals for two flowering traits from [3] (LDV and LD), and 4 traits from new experiments.** Three estimators were used: the ANOVA-based estimator of broad-sense heritability ($\hat{H}^2$, green), the marker-based estimator using individual plant data ($\hat{h}^2_r$, blue) and the marker-based estimator using genotypic means ($\hat{h}^2_m$, brown). Traits from different experiments are separated by the black horizontal lines. Trait abbreviations are given in Table 1 of the main text. The LD-adjusted kinship matrix was computed using version 2.0 of the LDAK-software [12].We used sections of 1000 SNPs, with a buffer of 200. The maximum distance considered for LD was 250kb; the 'halflife' parameter (modeling LD-decay) was set to 20kb.

Figure S6

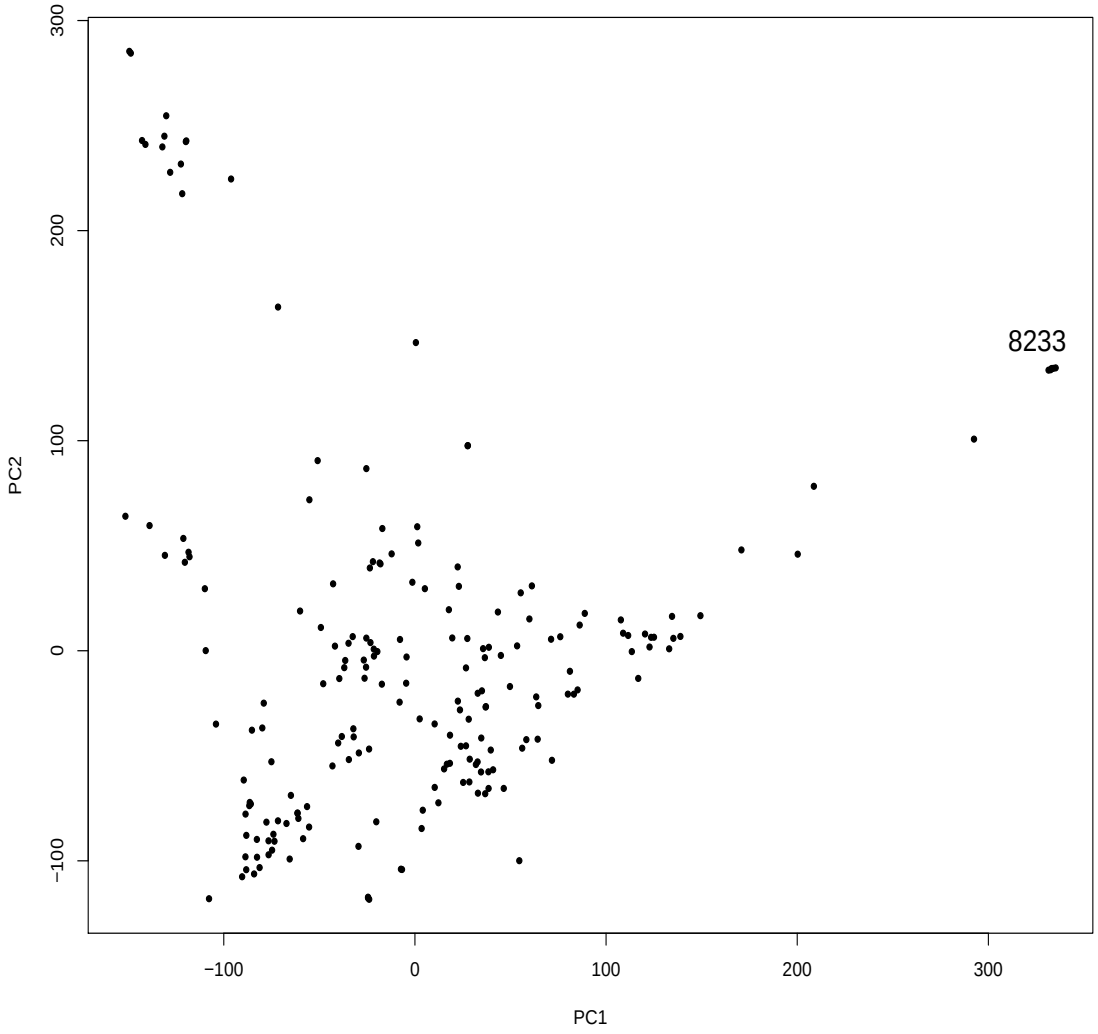

Figure S6 : **The first two principal component of the genetic markers for the panel of [3], restricted for the** 168 **accessions for which the trait LDV was measured.** On the very right are the accessions with ecotype ID's 8233, 7526 and 7515.

Figure S7

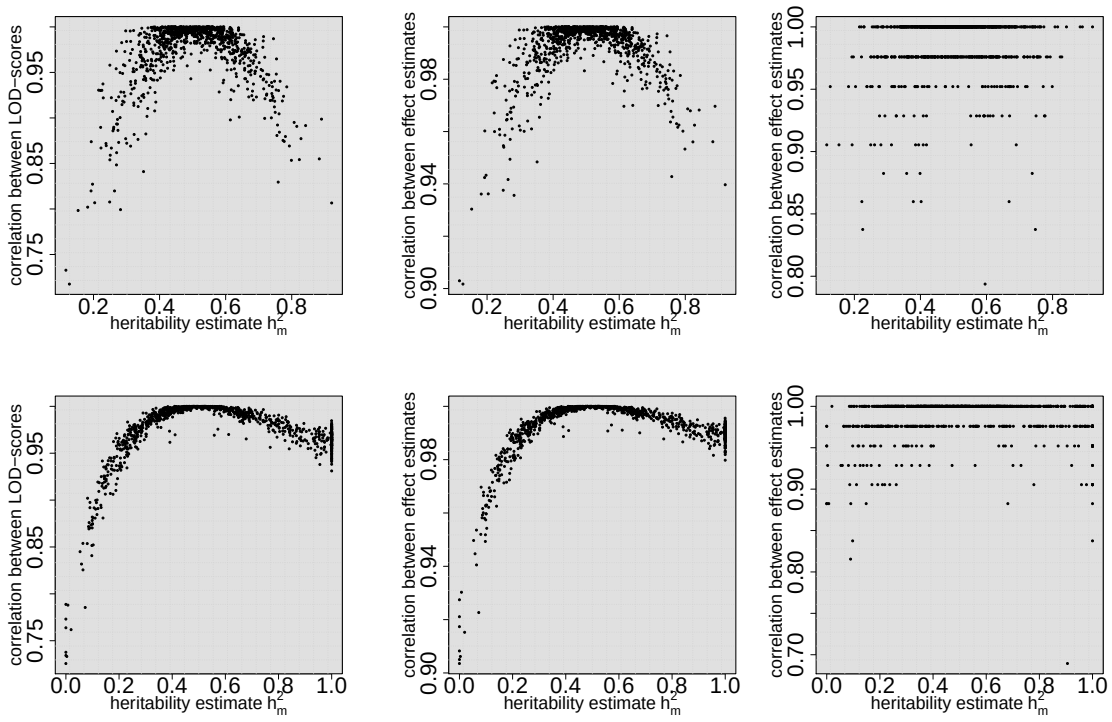

Figure S7 : **Rank correlation (Spearman ρ^2) between effect-size estimates obtained with a one- and two-stage approach, versus the heritability estimates obtained in the two-stage approach ($\hat{h}^2_m$).** 1000 traits were simulated for the Structured RegMap (first row) and the HapMap (second row), with a simulated heritability of 0.5. 10 QTLs were simulated, which explained 75% of the genetic variance. Left column: rank correlation between LOD-scores of all SNPs. Middle column: rank correlation between effect-size estimates for all SNPs. Right column: rank correlation between effect-size estimates for the 10 simulated QTLs.

Table S1: ecotype-IDs of the structured regmap.

Accession information was taken from the Bergelson lab (`http://bergelson.uchicago.edu/Members/mhorton/resources/snps/accession_coordinates.xls`). The following table contains geographic information for 242 of the 250 accessions from our structured regmap. Geographic information was not available for eight accessions: 6909, 8428, 5712, 6143, 5708, 5730, 5829 and 8254. Accessions were selected based on the variance of the off-diagonal kinship coefficients of each row: the accessions corresponding to the rows with the 250 highest variances were chosen.

country	number of accessions
Czech Republic	7
Finland	2
France	2
Ireland	2
Sweden	83
Tajikistan	3
United Kingdom	40
United States of America	103
unknown	8

ecotype-id	country	latitude	longitude	population	native-name
1716	United States of America	42.405	-85.398	Americas	KBS-Mac-8
1718	United States of America	42.405	-85.398	Americas	KBS-Mac-15
1719	United States of America	42.405	-85.398	Americas	KBS-Mac-16
1722	United States of America	42.405	-85.398	Americas	KBS-Mac-23
1724	United States of America	42.405	-85.398	Americas	KBS-Mac-28
1726	United States of America	42.405	-85.398	Americas	KBS-Mac-33
1729	United States of America	42.405	-85.398	Americas	KBS-Mac-41
1730	United States of America	42.405	-85.398	Americas	KBS-Mac-43
1733	United States of America	42.405	-85.398	Americas	KBS-Mac-53
1736	United States of America	42.405	-85.398	Americas	KBS-Mac-58
1738	United States of America	42.405	-85.398	Americas	KBS-Mac-64
1740	United States of America	42.405	-85.398	Americas	KBS-Mac-72
1743	United States of America	42.405	-85.398	Americas	KBS-Mac-75
1744	United States of America	42.405	-85.398	Americas	KBS-Mac-76
1745	United States of America	42.405	-85.398	Americas	KBS-Mac-78
1749	United States of America	42.405	-85.398	Americas	KBS-Mac-88
1750	United States of America	42.405	-85.398	Americas	KBS-Mac-89
1751	United States of America	42.405	-85.398	Americas	KBS-Mac-91
1752	United States of America	42.405	-85.398	Americas	KBS-Mac-95
1753	United States of America	42.405	-85.398	Americas	KBS-Mac-96
1782	United States of America	42.184	-86.358	Americas	Ker-38
1829	United States of America	42.051	-86.509	Americas	Mdn-1
1850	United States of America	43.595	-86.2657	Americas	MNF-Pot-8
1853	United States of America	43.595	-86.2657	Americas	MNF-Pot-21
1858	United States of America	43.595	-86.2657	Americas	MNF-Pot-47
1864	United States of America	43.595	-86.2657	Americas	MNF-Pot-60
1871	United States of America	43.595	-86.2657	Americas	MNF-Pot-76
1872	United States of America	43.595	-86.2657	Americas	MNF-Pot-75
1873	United States of America	43.595	-86.2657	Americas	MNF-Pot-79
1874	United States of America	43.595	-86.2657	Americas	MNF-Pot-80
1938	United States of America	43.5251	-86.1843	Americas	MNF-Che-41
1941	United States of America	43.5251	-86.1843	Americas	MNF-Che-45
1948	United States of America	43.5251	-86.1843	Americas	MNF-Che-58

1960	United States of America	43.5187	-86.1739	Americas	MNF-Jac-22
1963	United States of America	43.5187	-86.1739	Americas	MNF-Jac-26
2057	United States of America	42.166	-86.412	Americas	Map-42
2148	United States of America	42.148	-86.431	Americas	Paw-1
2150	United States of America	42.148	-86.431	Americas	Paw-3
2157	United States of America	42.148	-86.431	Americas	Paw-11
2160	United States of America	42.148	-86.431	Americas	Paw-14
2180	United States of America	42.148	-86.431	Americas	Paw-40
2201	United States of America	43.7623	-86.3929	Americas	Pent-22
2204	United States of America	43.7623	-86.3929	Americas	Pent-30
2214	United States of America	43.7623	-86.3929	Americas	Pent-49
2274	United States of America	43.665	-86.496	Americas	SLSP-30
2280	United States of America	43.665	-86.496	Americas	SLSP-58
2294	United States of America	42.03	-86.514	Americas	Ste-9
2300	United States of America	42.03	-86.514	Americas	Ste-15
6927	United States of America	41.2816	-86.621	Americas	Kno-10
6983	United States of America	37.45	-119.35	Americas	Yo-0
7033	United States of America	41.3599	-122.755	Americas	Buckhorn Pass
7515	United States of America	41.5609	-86.4251	Americas	RRS-10
7523	United States of America	42.0945	-86.3253	Americas	Pna-17
7524	United States of America	42.036	-86.511	Americas	Rmx-A02
7525	United States of America	42.036	-86.511	Americas	Rmx-A180
7526	United States of America	42.0945	-86.3253	Americas	Pna-10
7566	United States of America	42.093	-86.359	Americas	627ME-13Y1
7578	United States of America	42.0945	-86.3253	Americas	627PNA-1Y1
7580	United States of America	42.0945	-86.3253	Americas	627PNA-2B3
7584	United States of America	42.0945	-86.3253	Americas	627PNA-3M4
7787	United States of America	41.273	-86.625	Americas	KNO2.77
7837	United States of America	42.093	-86.359	Americas	ME3.41
7847	United States of America	42.093	-86.359	Americas	ME3.51
7867	United States of America	42.093	-86.359	Americas	ME4.20
8122	United States of America	42.036	-86.511	Americas	RMX3.11
8233	United States of America	41.1876	-87.1923	Americas	Dem-4
8557	United States of America	42.093	-86.359	Americas	328ME032
8612	United States of America	42.093	-86.359	Americas	11ME1.34
8616	United States of America	42.093	-86.359	Americas	11ME1.41
8619	United States of America	42.093	-86.359	Americas	11ME1.44
8629	United States of America	42.093	-86.359	Americas	11ME2.10
8673	United States of America	42.0945	-86.3253	Americas	328PNA032
8724	United States of America	42.0945	-86.3253	Americas	11PNA1.15
8725	United States of America	42.0945	-86.3253	Americas	11PNA1.4
8727	United States of America	42.0945	-86.3253	Americas	11PNA1.6
8730	United States of America	42.0945	-86.3253	Americas	11PNA1.9
8760	United States of America	42.0945	-86.3253	Americas	11PNA3.19
8770	United States of America	42.0945	-86.3253	Americas	11PNA3.65
8777	United States of America	42.0945	-86.3253	Americas	11PNA3.75
8787	United States of America	42.0945	-86.3253	Americas	11PNA3.86
8796	United States of America	42.0945	-86.3253	Americas	11PNA4.101
8824	United States of America	42.0945	-86.3253	Americas	11PNA4.129
8954	United States of America	42.036	-86.511	Americas	RMX413.1
8961	United States of America	42.036	-86.511	Americas	RMX413.16
8965	United States of America	42.036	-86.511	Americas	RMX413.2
8966	United States of America	42.036	-86.511	Americas	RMX413.20
8967	United States of America	42.036	-86.511	Americas	RMX413.21
8969	United States of America	42.036	-86.511	Americas	RMX413.24
8970	United States of America	42.036	-86.511	Americas	RMX413.25
8973	United States of America	42.036	-86.511	Americas	RMX413.29

8975	United States of America	42.036	-86.511	Americas	RMX413.30
8976	United States of America	42.036	-86.511	Americas	RMX413.31
8977	United States of America	42.036	-86.511	Americas	RMX413.32
8992	United States of America	42.036	-86.511	Americas	RMX413.48
8996	United States of America	42.036	-86.511	Americas	RMX413.51
9001	United States of America	42.036	-86.511	Americas	RMX413.57
9004	United States of America	42.036	-86.511	Americas	RMX413.6
9006	United States of America	42.036	-86.511	Americas	RMX413.62
9007	United States of America	42.036	-86.511	Americas	RMX413.63
9012	United States of America	42.036	-86.511	Americas	RMX413.7
9041	United States of America	42.039	-86.5154	Americas	RMXF413.10
9045	United States of America	42.039	-86.5154	Americas	RMXF413.15
9053	United States of America	42.039	-86.5154	Americas	RMXF413.6
5991	Czech Republic	49.4112	16.2815	Austria-Hungary	DraIV 6-20
5997	Czech Republic	49.4112	16.2815	Austria-Hungary	DraIV 6-27
6427	Czech Republic	49.3853	16.2544	Austria-Hungary	ZdrI 2-1
6435	Czech Republic	49.3853	16.2544	Austria-Hungary	ZdrI 2-10
6444	Czech Republic	49.3853	16.2544	Austria-Hungary	ZdrI 2-20
6903	Czech Republic	49.4013	16.2326	Austria-Hungary	Bor-4
7461	Czech Republic	49	15	Austria-Hungary	H55
4632	United Kingdom	50.4	-4.7	British-Isles	UKSW06-025
4675	United Kingdom	50.4	-4.7	British-Isles	UKSW06-070
4862	United Kingdom	50.3	-4.9	British-Isles	UKSW06-262
5106	United Kingdom	51.3	0.5	British-Isles	UKSE06-254
5133	United Kingdom	52.2	-1.7	British-Isles	UKSE06-302
5207	United Kingdom	51.3	0.4	British-Isles	UKSE06-429
5232	United Kingdom	51.2	0.4	British-Isles	UKSE06-466
5292	United Kingdom	51.3	1.1	British-Isles	UKSE06-556
5331	United Kingdom	51.1	0.4	British-Isles	UKSE06-618
5341	United Kingdom	51.1	0.4	British-Isles	UKSE06-628
5380	United Kingdom	54.4	-3	British-Isles	UKNW06-059
5381	United Kingdom	54.4	-3	British-Isles	UKNW06-060
5385	United Kingdom	54.4	-3	British-Isles	UKNW06-078
5469	United Kingdom	54.4	-3	British-Isles	UKNW06-210
5582	United Kingdom	54.7	-3.4	British-Isles	UKNW06-410
5678	United Kingdom	54.6	-3.1	British-Isles	UKNW99-025
5709	United Kingdom	54.6	-2.6	British-Isles	UKID2
5719	Ireland	54.1335	-6.1667	British-Isles	Bur-0
5720	United Kingdom	53.3	-1.6	British-Isles	Cal-2
5723	United Kingdom	51.3	1	British-Isles	Chr-1
5724	United Kingdom	51.4	0.1	British-Isles	UKID17
5731	United Kingdom	54.9	-2.9	British-Isles	Crl-1
5732	United Kingdom	54.9	-2.9	British-Isles	UKID25
5737	United Kingdom	51.3	0.1	British-Isles	UKID32
5758	United Kingdom	50.3	-5.2	British-Isles	UKID53
5774	United Kingdom	51.1	0.6	British-Isles	Sis-1
5780	United Kingdom	53.1	-1	British-Isles	UKID75
5788	United Kingdom	50.8	-2	British-Isles	UKID83
5792	United Kingdom	50.8	-0.7	British-Isles	UKID87
5793	United Kingdom	51.3	0.6	British-Isles	UKID88
5798	United Kingdom	53.1	-3.3	British-Isles	UKID93
5804	United Kingdom	50.8	-1.1	British-Isles	UKID100
5807	United Kingdom	51.8	-0.5	British-Isles	UKID103
6905	Ireland	54.1	-6.2	British-Isles	Bur-0
6923	United Kingdom	51.4083	-0.6383	British-Isles	HR-10
6924	United Kingdom	51.4083	-0.6383	British-Isles	HR-5
6944	United Kingdom	51.4083	-0.6383	British-Isles	NFA-8

7064	United Kingdom	51.3	1.1	British-Isles	Cnt-1
7109	United Kingdom	51.3	0.5	British-Isles	Ema-1
7483	United Kingdom	51.2878	0.0565	British-Isles	PHW-14
9490	United Kingdom	55.9218	-3.17108	British-Isles	02B6
9504	United Kingdom	55.8877	-3.16377	British-Isles	12A1
6929	Tajikistan	38.48	68.49	Eastern-Range	Kondara
6962	Tajikistan	38.35	68.48	Eastern-Range	Shahdara
7168	Tajikistan	38.48	68.49	Eastern-Range	Hodja-Obi-Garm
1247	Sweden	59.4333	17.0167	Fennoscandia	Tos-31-374
1254	Sweden	59.4333	17.0167	Fennoscandia	Tos-82-387
1409	Sweden	62.8	18.2	Fennoscandia	Rd-38
1416	Sweden	62.8	18.2	Fennoscandia	Rd-45
1435	Sweden	62.8	18.2	Fennoscandia	Rd-17-319
1552	Sweden	63.0833	18.3667	Fennoscandia	Sku-30
5835	Sweden	63.324	18.484	Fennoscandia	Bil-3
5856	Sweden	63.0167	17.4914	Fennoscandia	Dr-10
5860	Sweden	62.6814	18.0165	Fennoscandia	Dra-3
6009	Sweden	62.877	18.177	Fennoscandia	Eden-1
6010	Sweden	62.877	18.177	Fennoscandia	Eden-5
6011	Sweden	62.877	18.177	Fennoscandia	Eden-6
6012	Sweden	62.877	18.177	Fennoscandia	Eden-7
6013	Sweden	62.877	18.177	Fennoscandia	Eden-9
6016	Sweden	62.9	18.4	Fennoscandia	Eds-1
6017	Sweden	62.9	18.4	Fennoscandia	Eds-9
6024	Sweden	55.7509	13.3712	Fennoscandia	Fly2-2
6025	Sweden	62.6437	17.7339	Fennoscandia	Gro-3
6030	Sweden	62.806	18.1896	Fennoscandia	Grn-5
6043	Sweden	62.801	18.079	Fennoscandia	Lv-1
6046	Sweden	62.801	18.079	Fennoscandia	Lv-5
6064	Sweden	62.9513	18.2763	Fennoscandia	Nyl-2
6069	Sweden	62.9513	18.2763	Fennoscandia	Nyl-7
6071	Sweden	62.9308	18.3448	Fennoscandia	Omn-5
6077	Sweden	55.6942	13.4504	Fennoscandia	Rev-3
6091	Sweden	55.6525	13.215	Fennoscandia	T1010
6104	Sweden	55.7	13.2	Fennoscandia	T1160
6118	Sweden	55.7	13.2	Fennoscandia	T610
6154	Sweden	62.6422	17.7406	Fennoscandia	TAA 04
6163	Sweden	62.6425	17.7356	Fennoscandia	TAA 14
6166	Sweden	62.6425	17.7372	Fennoscandia	TAA 17
6169	Sweden	62.8714	18.3447	Fennoscandia	TD 01
6170	Sweden	62.8717	18.3442	Fennoscandia	TD 02
6171	Sweden	62.8717	18.3444	Fennoscandia	TD 03
6172	Sweden	62.8717	18.3436	Fennoscandia	TD 04
6173	Sweden	62.8717	18.3419	Fennoscandia	TD 05
6174	Sweden	62.8719	18.3422	Fennoscandia	TD 06
6177	Sweden	62.6322	17.69	Fennoscandia	TL 03
6180	Sweden	62.6322	17.6906	Fennoscandia	TL 07
6184	Sweden	62.8892	18.4522	Fennoscandia	TB 01
6209	Sweden	62.8836	18.1842	Fennoscandia	TEDEN 02
6210	Sweden	62.8839	18.1836	Fennoscandia	TEDEN 03
6212	Sweden	63.0175	18.3239	Fennoscandia	TF 02
6214	Sweden	63.0175	18.3281	Fennoscandia	TF 04
6215	Sweden	63.0172	18.3281	Fennoscandia	TF 05
6216	Sweden	63.0167	18.3283	Fennoscandia	TF 06
6217	Sweden	63.0169	18.3283	Fennoscandia	TF 07
6218	Sweden	63.0172	18.3283	Fennoscandia	TF 08
6220	Sweden	62.806	18.1896	Fennoscandia	TGR 01

6221	Sweden	62.806	18.1896	Fennoscandia	TGR 02
6226	Sweden	62.7994	17.9033	Fennoscandia	TH 08
6231	Sweden	62.96	18.2844	Fennoscandia	TNY 04
6235	Sweden	62.9611	18.3589	Fennoscandia	TOM 01
6236	Sweden	62.9617	18.36	Fennoscandia	TOM 02
6237	Sweden	62.9619	18.35	Fennoscandia	TOM 03
6238	Sweden	62.9619	18.35	Fennoscandia	TOM 04
6240	Sweden	62.9622	18.35	Fennoscandia	TOM 06
6241	Sweden	62.9614	18.3608	Fennoscandia	TOM 07
6244	Sweden	62.9169	18.4728	Fennoscandia	TR 01
6900	Sweden	63.324	18.484	Fennoscandia	Bil-5
6901	Sweden	63.324	18.484	Fennoscandia	Bil-7
6913	Sweden	62.877	18.177	Fennoscandia	Eden-2
6917	Sweden	63.0165	18.3174	Fennoscandia	Fb-2
6918	Sweden	63.0165	18.3174	Fennoscandia	Fb-4
6968	Finland	60	23.5	Fennoscandia	Tamm-2
6969	Finland	60	23.5	Fennoscandia	Tamm-27
8218	Sweden	62.877	18.177	Fennoscandia	Eden-4
8227	Sweden	62.7989	17.9103	Fennoscandia	TH 03
8335	Sweden	55.71	13.2	Fennoscandia	Lund
8376	Sweden	62.69	18	Fennoscandia	Sanna-2
9321	Sweden	62.8622	18.336	Fennoscandia	dal 1
9323	Sweden	62.8622	18.336	Fennoscandia	dal 3
9332	Sweden	62.8698	18.381	Fennoscandia	Bar 1
9354	Sweden	62.8762	18.1746	Fennoscandia	Eden 15
9355	Sweden	62.8762	18.1746	Fennoscandia	Eden 16
9356	Sweden	62.8762	18.1746	Fennoscandia	Eden 17
9363	Sweden	62.9147	18.4045	Fennoscandia	EdJ 2
9371	Sweden	63.016	18.3175	Fennoscandia	FL 1
9378	Sweden	63.0165	18.3174	Fennoscandia	FU 4
9386	Sweden	62.806	18.1896	Fennoscandia	Grn 12
9388	Sweden	62.806	18.1896	Fennoscandia	Grn 14
9427	Sweden	62.8815	18.4055	Fennoscandia	Ns 2
9433	Sweden	62.9513	18.2763	Fennoscandia	Nyl 13
9434	Sweden	62.8959	18.3659	Fennoscandia	de 2
9471	Sweden	56.0648	13.9707	Fennoscandia	UllA 1
171	France	47.3833	5.31667	France	MIB-20
228	France	47.3833	5.31667	France	MIB-9

Table S2

Table S2 : **Comparison of the marker-based estimators heritability estimators h_r^2 and h_m^2 for simulated data.** We simulated 5000 traits, for random samples of 200 accessions drawn from Swedish and French regmap. 20 unlinked QTLs were simulated, which explained 50 percent of the genetic variance. The simulated heritability was 0.2, 0.5 and 0.8. Standard errors are given relative to those of the broad sense heritability estimator (H^2).

	bias	standard error	relative standard error
Swedish regmap			
$h^2 = 0.2$			
broad-sense (H^2)	-0.00162	0.05227	1.00000
replicates (h_r^2)	-0.00109	0.04991	0.95498
means (h_m^2)	0.01302	0.11018	2.10798
$h^2 = 0.5$			
broad-sense (H^2)	-0.00403	0.05373	1.00000
replicates (h_r^2)	-0.00173	0.04506	0.83860
means (h_m^2)	0.01494	0.16662	3.10123
$h^2 = 0.8$			
broad-sense (H^2)	-0.00458	0.03130	1.00000
replicates (h_r^2)	-0.00180	0.02319	0.74095
means (h_m^2)	-0.00104	0.16227	5.18435
French regmap			
$h^2 = 0.2$			
broad-sense (H^2)	-0.00183	0.04958	1.00000
replicates (h_r^2)	-0.00196	0.04780	0.96421
means (h_m^2)	0.01306	0.12049	2.43043
$h^2 = 0.5$			
broad-sense (H^2)	-0.00396	0.04930	1.00000
replicates (h_r^2)	-0.00396	0.04409	0.89431
means (h_m^2)	0.01952	0.17547	3.55941
$h^2 = 0.8$			
broad-sense (H^2)	-0.00341	0.02808	1.00000
replicates (h_r^2)	-0.00236	0.02246	0.79988
means (h_m^2)	0.00202	0.16461	5.86175

Table S3

Table S3: : **Marker-based estimation of heritability: width and coverage confidence intervals obtained from the individual plant data and the genotypic means.** Results for broad sense heritability intervals are reported for comparison. We simulated 5000 traits, for random samples of 200 accessions drawn from the Swedish regmap (top) and French (bottom). 20 unlinked QTLs were simulated, which explained 50 percent of the genetic variance. The simulated heritability was 0.2, 0.5 and 0.8.

	coverage	interval width
Swedish regmap		
$h^2 = 0.2$		
broad-sense	0.912	0.178
replicates (standard)	0.933	0.188
replicates (log-transformed)	0.961	0.189
means (standard)	0.899	0.381
means (log-transformed)	0.968	0.405
$h^2 = 0.5$		
broad-sense	0.864	0.160
replicates (standard)	0.946	0.176
replicates (log-transformed)	0.950	0.175
means (standard)	0.921	0.594
means (log-transformed)	0.970	0.560
$h^2 = 0.8$		
broad-sense	0.823	0.085
replicates (standard)	0.945	0.088
replicates (log-transformed)	0.947	0.088
means (standard)	0.960	0.635
means (log-transformed)	0.938	0.748
French regmap		
$h^2 = 0.2$		
broad-sense	0.929	0.178
replicates (standard)	0.941	0.184
replicates (log-transformed)	0.962	0.185
means (standard)	0.898	0.396
means (log-transformed)	0.960	0.431
$h^2 = 0.5$		
broad-sense	0.898	0.160
replicates (standard)	0.953	0.173
replicates (log-transformed)	0.956	0.171
means (standard)	0.927	0.619
means (log-transformed)	0.976	0.585
$h^2 = 0.8$		
broad-sense	0.866	0.084
replicates (standard)	0.947	0.088
replicates (log-transformed)	0.947	0.088
means (standard)	0.966	0.652
means (log-transformed)	0.948	0.767

Table S4

Table S4: : **Heritability estimates and confidence intervals, for two flowering traits from [3] and four traits measured in new experiments (trait abbreviations given in Table 1 of the main text).**

trait	replicates	means	broad-sense
LDV	0.829 (0.791,0.861)	0.631 (0.199,0.922)	0.858 (0.827,0.885)
LD	0.946 (0.933,0.957)	1.000 (0.000,1.000)	0.966 (0.958,0.973)
LA(S)	0.216 (0.153,0.297)	0.150 (0.040,0.424)	0.235 (0.167,0.306)
LA(H)	0.380 (0.319,0.445)	0.340 (0.090,0.729)	0.388 (0.327,0.451)
BT	0.948 (0.937,0.956)	1.000 (0.000,1.000)	0.956 (0.947,0.963)
LW	0.535 (0.473,0.596)	0.202 (0.029,0.682)	0.530 (0.468,0.589)

Three estimators were used: mixed model based on replicates ($\hat{h}^2_r$), mixed model based on genotypic means ($\hat{h}^2_m$), and the usual ANOVA-based broad-sense heritability estimator ($\hat{H}^2$). An LD-adjusted kinship matrix was used in the mixed model for $\hat{h}^2_r$ and $\hat{h}^2_m$.

The LD-adjusted kinship matrix was computed using version 2.0 of the LDAK-software [12], available at `http://dougspeed.com/ldak/`. We used sections of 1000 SNPs, with a buffer of 200. The maximum distance considered for LD was 250kb; the 'halflife' parameter (modeling LD-decay) was set to 20kb.

Table S5

In the following tables, the second and third column contain the percentage of the 5000 traits for which the corresponding heritability estimates ($\hat{h}^2_r$ and $\hat{h}^2_m$) were contained in the intervals in the first column. The remaining columns show the correlation (r) between simulated and predicted genetic effects, averaged over these traits. 20 QTLs were simulated, which explained 50 percent of the genetic variance. Each trait was simulated for a randomly drawn training (200 accessions) and validation set (50 accessions). Genetic effects were predicted using G-BLUP, based on either a mixed model for the individual plants (replicates) or for the genotypic means.

Table S5(a) : **Prediction accuracy (r) of G-BLUP for** 5000 **simulated traits, for the structured regmap population, and a simulated heritability of** 0.2**.**

interval	$\hat{h}^2_r$	$\hat{h}^2_m$	r (replicates) Training set	r (means) Training set	r (replicates) Validation set	r (means) Validation set
$[0, 0.1)$	3.08 %	9.88 %	0.637	0.654	0.216	0.218
$[0.1, 0.3)$	93.96 %	76.38 %	0.770	0.770	0.280	0.279
$[0.3, 0.5)$	2.96 %	13.52 %	0.816	0.803	0.325	0.313
$[0.5, 0.7)$	0 %	0.22 %		0.782		0.287
$[0.7, 0.9)$	0 %	0 %				
$[0.9, 1]$	0 %	0 %				
$[0, 1]$	100 %	100 %	0.767	0.763	0.279	0.278

Table S5(b) : **Prediction accuracy (r) of G-BLUP for** 5000 **simulated traits, for the structured regmap population and a simulated heritability of** 0.5**.**

interval	$\hat{h}^2_r$	$\hat{h}^2_m$	r (replicates) Training set	r (means) Training set	r (replicates) Validation set	r (means) Validation set
$[0, 0.1)$	0 %	0.04 %		0.709		0.328
$[0.1, 0.3)$	0 %	5.24 %		0.836		0.269
$[0.3, 0.5)$	51.42 %	46.54 %	0.886	0.887	0.302	0.300
$[0.5, 0.7)$	48.58 %	42.12 %	0.905	0.903	0.333	0.337
$[0.7, 0.9)$	0 %	5.84 %		0.905		0.343
$[0.9, 1]$	0 %	0.22 %		0.888		0.386
$[0, 1]$	100 %	100 %	0.895	0.892	0.317	0.317

Table S5(c) : **Prediction accuracy (r) of G-BLUP for** 5000 **simulated traits, for the structured regmap population and a simulated heritability of** 0.8**.**

interval	$\hat{h}^2_r$	$\hat{h}^2_m$	r (replicates) Training set	r (means) Training set	r (replicates) Validation set	r (means) Validation set
$[0, 0.1)$	0 %	0 %				
$[0.1, 0.3)$	0 %	0.02 %		0.877		0.299
$[0.3, 0.5)$	0 %	1.42 %		0.930		0.283
$[0.5, 0.7)$	0.04 %	19.26 %	0.953	0.955	0.400	0.318
$[0.7, 0.9)$	99.96 %	59.26 %	0.964	0.964	0.343	0.344
$[0.9, 1]$	0 %	20.04 %		0.965		0.365
$[0, 1]$	100 %	100 %	0.964	0.962	0.343	0.343

Table S5(d) : **Prediction accuracy (r) of G-BLUP for** 5000 **simulated traits, for the HapMap population and a simulated heritability of** 0.2**.**

interval	$\hat{h}^2_r$	$\hat{h}^2_m$	r (replicates) Training set	r (means) Training set	r (replicates) Validation set	r (means) Validation set
$[0, 0.1)$	1.74 %	28.64 %	0.616	0.632	0.259	0.273
$[0.1, 0.3)$	96.7 %	40.7 %	0.673	0.674	0.341	0.348
$[0.3, 0.5)$	1.56 %	17.8 %	0.711	0.684	0.364	0.382
$[0.5, 0.7)$	0 %	5.8 %		0.681		0.366
$[0.7, 0.9)$	0 %	2.84 %		0.675		0.370
$[0.9, 1]$	0 %	4.22 %		0.669		0.357
$[0, 1]$	100 %	100 %	0.672	0.664	0.340	0.335

Table S5(e) : **Prediction accuracy (r) of G-BLUP for** 5000 **simulated traits, for the HapMap population and a simulated heritability of** 0.5**.**

interval	$\hat{h}^2_r$	$\hat{h}^2_m$	r (replicates) Training set	r (means) Training set	r (replicates) Validation set	r (means) Validation set
$[0, 0.1)$	0 %	6 %		0.811		0.285
$[0.1, 0.3)$	0 %	21.02 %		0.851		0.366
$[0.3, 0.5)$	51.78 %	22.56 %	0.862	0.867	0.395	0.413
$[0.5, 0.7)$	48.22 %	17.5 %	0.877	0.871	0.416	0.428
$[0.7, 0.9)$	0 %	10.86 %		0.873		0.426
$[0.9, 1]$	0 %	22.06 %		0.871		0.422
$[0, 1]$	100 %	100 %	0.869	0.863	0.405	0.401

Table S5(f) (given as Table 6 in the main text) : **Prediction accuracy (r) of G-BLUP for** 5000 **simulated traits, for the HapMap population and a simulated heritability of** 0.8**.**

interval	$\hat{h}^2_r$	$\hat{h}^2_m$	r (replicates) Training set	r (means) Training set	r (replicates) Validation set	r (means) Validation set
$[0, 0.1)$	0 %	2.58 %		0.890		0.289
$[0.1, 0.3)$	0 %	8.34 %		0.937		0.373
$[0.3, 0.5)$	0 %	12.34 %		0.954		0.409
$[0.5, 0.7)$	0.04 %	15.9 %	0.942	0.959	0.208	0.423
$[0.7, 0.9)$	99.96 %	15.62 %	0.961	0.961	0.431	0.443
$[0.9, 1]$	0 %	45.22 %		0.961		0.448
$[0, 1]$	100 %	100 %	0.961	0.956	0.431	0.428

References

[1] Lynch M, Walsh B (1998) Genetics and Analysis of Quantitative Traits. Sinauer Associates, 1 edition. URL `http://www.amazon.com/exec/obidos/redirect?tag=citeulike07-20&path=ASIN/0878934812`.

[2] Singh M, Ceccarelli S, Hamblin J (1993) Estimation of heritability from varietal trials data. Theoretical and Applied Genetics 86: 437-441.

[3] Atwell S, Huang YS, Vilhjalmsson BJ, Willems G, Horton M, et al. (2010) Genome-wide association study of 107 phenotypes in Arabidopsis thaliana inbred lines. Nature 465: 627–631.

[4] Nyquist WE, Baker R (1991) Estimation of heritability and prediction of selection response in plant populations. Critical Reviews in Plant Sciences 10: 235-322.

[5] Lippert C, Listgarten J, Liu Y, Kadie C, Davidson R, et al. (2011) FaST linear mixed models for genome-wide association studies: supplement. Nature Genetics 42: 833835.

[6] Henderson CR (1975) Best Linear Unbiased Estimation and Prediction under a Selection Model. Biometrics 31.

[7] Robinson GK (1991) That blup is a good thing: The estimation of random effects. Statistical Science 6: pp. 15-32.

[8] Kackar RN, Harville DA (1984) Approximations for standard errors of estimators of fixed and random effect in mixed linear models. Journal of the American Statistical Association 79: pp. 853-862.

[9] Kenward MG, Roger JH (1997) Small sample inference for fixed effects from restricted maximum likelihood. Biometrics 53: pp. 983-997.

[10] Gilmour A, Cullis B, Welham S, Gogel B, Thompson R (2004) An efficient computing strategy for prediction in mixed linear models. Computational Statistics & Data Analysis 44: 571 - 586.

[11] Welham S, Cullis B, Gogel B, Gilmour A, Thompson R (2004) Prediction in linear mixed models. Australian & New Zealand Journal of Statistics : 325–347.

[12] Speed D, Hemani G, Johnson MR, Balding DJ (2012) Improved Heritability Estimation from Genome-wide SNPs. The American Journal of Human Genetics 91: 1011–1021.