Supporting Information

Notes S1

Trait expectations and covariances are conditional on individual 'type'. We must distinguish individuals of the reference line (P_0), individuals of the random line (P_x), the F1 hybrids from the cross of random line x to the reference line (F_{1x}), and the corresponding F2s (F_{2x}). We assume diploid, autosomal inheritance for all loci influencing the trait. The relevant moments for **g*** are derived by first considering a single locus and then summing across QTL. For a particular trait, let α_i denote the additive effect of allele A_i and δ_{ij} as the dominance deviation associated with genotype A_iA_j. Here, we are using the standard least squares partitioning of the genotypic values to define α_i and δ_{ij} (see Falconer & Mackay, 1996, ch 7). Let q_i be the population frequency of allele A_i and define the allele that is homozygous in the Reference Line as A_0.

At this locus, the mean genotypic values (g) for each cross-type are:

$$E[g_{P_0}] = 2\alpha_0 + \delta_{00} \qquad \text{Eqn S1}$$

$$E[g_{P_x}] = \sum_i q_i(2\alpha_i + \delta_{ii}) = h \qquad \text{Eqn S2}$$

$$E[g_{F_{1x}}] = \sum_i q_i(\alpha_0 + \alpha_i + \delta_{0i}) = \alpha_0 \qquad \text{Eqn S3}$$

$$E[g_{F_{2x}}] = \sum_i q_i[(2\alpha_0 + \delta_{00})/4 + (\alpha_0 + \alpha_i + \delta_{0i})/2 + (2\alpha_i + \delta_{ii})/4]$$

$$= \alpha_0 + \delta_{00}/4 + h/4 \qquad \text{Eqn S4}$$

where h is the inbreeding depression at this locus and the subscript x is for a random Line Cross Family.

Table S1 Key to variance components

Single locus: Summation over alleles (i)	Entire genome (g*): Summation over loci (j)
$h = \sum_i q_i \delta_{ii}$	$A_0 = \sum_j \alpha_{0j}$
$v_a = 2\sum_i q_i \alpha_i^2$	$\Delta_{00} = \sum_j \delta_{00j}$
$v_d = \sum_i \sum_j q_i q_j \delta_{ij}^2$	$H = \sum_j h_j$
$v'_d = \sum_i q_i \delta_{0i}^2$	$C_{11} = \sum_j v_{aj}/2 + 2c'_{adj} + v'_{dj}$
$c_{ad} = \sum_i q_i \alpha_i \delta_{ii}$	$C_{12} = \sum_j v_{aj} + 2c'_{adj} + c_{adj} + v'_{dij}$
$c'_{ad} = \sum_i q_i \alpha_i \delta_{0i}$	$C_{22} = \sum_j 2v_{aj} + 4c_{adj} + v_{dij}$
$v_{di} = \sum_i q_i \delta_{ii}^2$	$V_s = \sum_j v_{S_j}$
$v'_{di} = \sum_i q_i \delta_{0i} \delta_{ii}$	$V_A = \sum_j v_{a_j}$

$$v_S = \frac{1}{16}[3h^2 + 8\alpha_0^2 + 8\alpha_0\delta_{00} + 3\delta_{00}^2 - 8h\alpha_0 - 2h\delta_{00}]$$

The variances of genotypic values for (random) parental lines and F1s at this locus are:

$$Var[g_{P_x}] = 2v_a + 4c_{ad} + v_{di} \quad = \quad c_{22} \qquad \text{Eqn S5}$$

$$Var[g_{F_{1x}}] = v_a/2 + 2c'_{ad} + v'_d \quad = \quad c_{11} \qquad \text{Eqn S6}$$

The genetic covariance is:

$$Cov[g_{P_x}, g_{F_{1x}}] = v_a + 2c'_{ad} + c_{ad} + v'_{di} \quad = \quad c_{12} \qquad \text{Eqn S7}$$

Each (co)variance is a function of the 'causal' variance components defined in Table S1. v_a is the standard additive genetic or genic variance for a single locus. c_{ad} and v_{di} are the covariance of additive effects with homozygous dominance effects and the variance of homozygous dominance effects, respectively. These components routinely appear when considering the resemblance of inbred relatives (Cockerham & Weir, 1984). The terms c'_{ad}, v'_d and v'_{di} are specific to the Replicated F2 design and emerge from the dominance deviations when the specific Reference Line allele is combined with random alleles from other lines. The terms c_{11}, c_{12}, and c_{22} refer to the sums of components in Eqns S5–S7. These aggregations are useful because all of the phenotypic (co)variances are linear combinations of c_{11}, c_{12}, and c_{22}.

Since the Random Line and F1 types are internally homogenous, the genetic covariance of distinct individuals is the same as the genetic variance. The F2 family is genetically heterogeneous and the covariances involving F2s are:

$$Var[g_{F_{2x}}] \quad = \quad c_{11}/2 + c_{22}/4 + v_S \qquad \text{Eqn S8}$$

$$Cov[g_{P_x}, g_{F_{2x}}] \quad = \quad c_{12}/2 + c_{22}/4 \qquad \text{Eqn S9}$$

$$Cov[g_{F_{1x}}, g_{F_{2x}}] \quad = \quad c_{11}/2 + c_{12}/4 \qquad \text{Eqn S10}$$

where v_S is the segregational variance for this locus (Table S1). The covariance between two different F2 individuals from the same family is

$$Cov[g_{F_{2.1x}}, g_{F_{2.2x}}] = c_{11}/4 + c_{12}/4 + c_{22}/16 \quad \text{Eqn S11}$$

Under the assumptions that the loci determine **g*** are unlinked, and that we can ignore linkage disequilibria and epistasis, the variances and covariances for **g*** are simple sums of per-locus components. Each of the quantities in Eqns S1–S11 has a multi-locus analog and the moments for **g*** are functions of these quantities. For example,

$$E[g^*_{P_0}] = 2\mathrm{A}_0 + \Delta_{00} \quad \text{Eqn S12}$$

$$E[g^*_{P_x}] = H \quad \text{Eqn S13}$$

$$E[g^*_{F_{1x}}] = \mathrm{A}_0 \quad \text{Eqn S14}$$

$$E[g^*_{F_{2x}}] = \mathrm{A}_0 + \Delta_{00}/4 + H/4 \quad \text{Eqn S15}$$

The (co)variances for **g*** are given by Eqns S5–S11 with multi-locus (Upper Case) variance components replacing single locus components (see Table S1). When fitting this model to single trait data, we actually estimate V_S, C_{11}, C_{12}, and C_{22}. We cannot isolate the causal components with dominance in the Replicated F2 Design. With additive inheritance, $C_{11} = V_A/2$, $C_{12} = V_A$, and $C_{22} = 2\ V_A$.

Notes S2

The maximum likelihood parameter set was determined for each trait individually for all combinations of four models of the genetic background and four QTL models. There are two variance components (V_E and V_A) for GBM2, three for GBM3 and GBM3a (V_E, V_A, and V_S), and five for GBM5 (V_E, C_{11}, C_{12}, C_{22}, and V_S). GBM3a assumes an additive model for type means (fixed effects) while all other models use Eqn 2. We calculate the standardized AIC value across models for each trait (Table S2). AIC is $-2l+2K$, where *K* is the number of parameters and *l* is the maximum log-likelihood (Burnham & Anderson, 2002, p. 61). The 'selected model', which represents the best compromise between model fit and model complexity has the lowest AIC. We standardize the values in Table S2 by subtracting the minimum AIC from all models for a trait. As a consequence, the best model has value 0.0.

Table S2 The standardized AIC values (top) and likelihood ratio tests (bottom) are given for each trait. For AIC, we consider four different models for the genetic background combined with each of four models for QTL effects. NP is the total number of estimated parameters for that model. Bold type indicates the selected QTL model within GBM2, GBM3 and GBM5. Likelihood ratio tests are applied to each trait for each of two null hypotheses (H_0). No directional dominance compares GBM3 to GBM3a while ($V_S = V_A/4$) contrasts GBM3 to GBM3a. For both likelihood ratio tests, no QTLs are considered. However, similar results obtain regardless of the QTL model.

		NP	**CorWid**	**CorLen**	**Anther**	**Pistil**	**SA**	**PV**	**Pollen**	**DTB**	**Bud**
Standardized AIC values:											
GBM2	both QTL	13	57.63	38.65	47.74	17.36	15.81	**66.64**	**34.15**	**14.17**	3.08
	D/d	11	57.44	35.21	45.95	17.76	**13.57**	84.69	39.03	19.18	6.81
	C/c	11	53.72	36.54	44.66	**17.20**	25.08	94.71	35.82	16.90	**0.00**
	no QTL	9	**53.50**	**32.95**	**42.73**	17.53	22.95	111.05	40.33	21.48	3.47
GBM3	both QTL	14	55.94	34.37	35.46	19.15	11.75	**68.59**	**31.59**	**11.23**	4.81
	D/d	12	55.40	30.83	33.13	19.32	**9.58**	86.33	35.72	15.85	8.22
	C/c	12	51.99	32.14	31.78	**18.87**	20.38	96.29	32.83	13.77	**1.46**
	no QTL	10	**51.48**	**28.50**	**29.50**	19.14	18.39	112.53	36.78	18.13	4.88
GBM3a	both QTL	13	220.00	254.15	257.81	130.01	23.87	282.48	364.72	123.91	17.57
	D/d	11	225.10	253.61	259.73	133.66	21.07	296.61	366.39	122.30	22.50
	C/c	11	245.30	277.32	293.46	139.37	41.77	331.40	438.60	122.14	16.03
	no QTL	9	254.38	281.14	301.35	145.96	39.50	348.17	445.65	120.87	21.31
GBM5	both QTL	15	5.12	6.16	4.98	0.94	2.34	**0.00**	**0.00**	**0.00**	5.38
	D/d	13	3.94	3.28	3.46	1.21	**0.00**	17.15	4.48	1.62	9.15
	C/c	13	1.19	2.82	1.53	**0.00**	11.20	29.37	1.52	1.21	**2.20**
	no QTL	11	**0.00**	**0.00**	**0.00**	0.35	9.03	44.67	5.63	2.56	5.68
Likelihood ratio test values:											
H_0: No directional dominance			204.90	254.64	273.85	128.83	23.12	237.63	410.86	104.74	18.43
H_0: $V_S = V_A / 4$			4.02	6.44	15.23	0.39	6.56	0.52	5.54	5.35	0.59

For the first eight traits, the selected model has the most elaborate genetic background (GBM5). For Bud duration, GBM2 is selected. Within genetic background models, the same QTL model is routinely selected across genetic backgrounds (see bold entries in Table S2). For succinctness, we present QTL estimates only for the GBM3 background (Table 2). However, QTL effect estimates with the GBM5 background are very similar.

Specific hypotheses can also be tested using likelihood ratios (bottom of Table S2). For example, we can test for directional dominance by comparing GMB3 to GBM3a. All Likelihood Ratio values greatly exceed the critical value (3.84 from the chi-square distribution with 1 df) indicating significant directional dominance. A second null hypothesis concerns the segregational variance, V_S . If the genetic background is determined by a large number of additive loci (each making a small contribution) then V_S should be approximately equal to V_A /4 (Kelly 2009). Comparing GMB3 to GBM2, this simplification can be rejected for over the half the traits. While this might indicate that major factors segregate for the genetic background, it might also result from non-additive contributions of background loci. The latter explanation is certainly plausible given the strong general support for GBM5.