Theoretical and Applied Genetics

Identifying QTLs involved in hybrid performance and heterotic group complementarity: new GWAS models applied to factorial and admixed diallel maize hybrid panels

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APPENDIX

S1 Appendix: Spatial correction model for Het2 by environment

Local spatial effects were corrected in each Het2 environment using the following model:

$$\begin{aligned} Y_{htrc} &= \mu + \lambda_t + R_r + C_c + G_h + E_{htrc} \\ R &\sim N(0, I\sigma_R^2) \\ C &\sim N(0, I\sigma_C^2) \\ G &\sim N(0, I\sigma_G^2) \\ E &\sim N(0, I\sigma_\varepsilon^2) \\ & R \perp C \perp G \perp E \end{aligned}$$

where Y_{htrc} is the phenotype of hybrid h with check status t, at row r, column c, μ is the intercept, λ_t is the effect of check t (including 5 levels, one for each of the 4 checks and 1 for experimental hybrids), R_R is the random effect of row r with σ_R^2 the row variance and C_c is the random effect of column c with σ_C^2 the column variance, G_h is the random effect of genotype h with σ_G^2 the genotypic variance and E is a vector for the error with σ_ε^2 the error variance.

S2 Appendix: Broad Sense Heritability

Broad sense heritability was calculated based on a single environment genetic model on corrected phenotypes:

$$Y_{hk} = \mu + G_h + E_{hk}$$

$$G \sim N(0, I\sigma_G^2), E \sim N(0, I\sigma_\varepsilon^2), G \perp E$$

where Y_{hk} is the k^{th} phenotype measure of hybrid h, μ is the intercept, G_h is the random effect of genotype h with σ_G^2 the genotypic variance and E is a vector for the error with σ_ε^2 the error variance. Single environment heritability is given by the following formula:

$$H_S^2 = \frac{{\sigma_G}^2}{\sigma_G^2 + \frac{\sigma_\varepsilon^2}{n_{rep}}}$$

where σ_G^2 and ${\sigma_\varepsilon}^2$ are described above and n_{rep} is the mean number of repeated values.

In addition, broad sense heritability was calculated based on multi-environment genetic model:

$$Y_{hek} = \mu + \theta_e + G_h + GE_{he} + E_{hek}$$

$$G \sim N(0, I\sigma_G^2), GE \sim N(0, I\sigma_{GE}^2), E \sim N(0, I\sigma_\varepsilon^2), G \perp GE \perp E$$

where Y_{hek} is the k^{th} phenotype measure of hybrid h in the environment e, μ is the intercept, θ_e is the effect of the environment e, G_h is the random effect of genotype h with σ_G^2 the genotypic variance, GE_h is the random effect of genotype-by-environment interactions with variance σ_{GE}^2 and E is the vector for the error with σ_ε^2 is error variance.

Multi environment heritability was defined as follows:

$$H^2 = \frac{{\sigma_G}^2}{\sigma_G^2 + \frac{\sigma_{GE}^2}{n_{env}} + \frac{\sigma_\varepsilon^2}{n_{rep} * n_{env}}}$$

where σ_G^2, σ_{GE}^2 and ${\sigma_\varepsilon}^2$ are described above, n_{env} is the number of environment and n_{rep} is the mean number of replicates per trial.

S3 Appendix: Variance estimation procedure in GWAS

GWAS models requires the inference of numerous variance parameters. Fitting such models for each marker would require a prohibitive computation time. A 2-step procedure has been suggested to reduce this issue. In a first step, variance parameters were estimated in a H_0 model including no marker effect, corresponding to the MONO model of "Variance partition" section:

$$Y = 1\mu + Z^A A + Z^D D + Z^{I^{aa}} I^{aa} + Z^{I^{ad}} I^{ad} + Z^{I^{dd}} I^{dd} + E$$

$$A \sim N(0, K_a\sigma_a^2), D \sim N(0, K_d\sigma_d^2),$$

$$I^{aa} \sim N(0, K_{aa}\sigma_{aa}^2), I^{ad} \sim N(0, K_{ad}\sigma_{ad}^2), I^{dd} \sim N(0, K_{dd}\sigma_{dd}^2)$$

$$E \sim N(0, I\sigma_\varepsilon^2)$$

where Y is the vector of phenotypic values, μ is the intercept, A, D, I^{aa}, I^{ad} and I^{dd} are vectors of random effects for additivity, dominance and epistasis with incidence matrices Z^A, Z^D, $Z^{I^{aa}}$, $Z^{I^{ad}}$ and $Z^{I^{dd}}$ and variance σ_a^2, σ_d^2, σ_{aa}^2, σ_{ad}^2 and σ_{dd}^2 respectively, K_a, K_d, K_{aa}, K_{ad} and K_{dd} are kinship matrices of those effects and E is a vector for the error of variance σ_ε^2. The phenotypic covariance matrix $\mathrm{V(Y)}_{SE}$ can be expressed as:

$$\mathrm{V(Y)}_{SE} = \sigma_a^2 Z^A K_a {Z^A}^T + \sigma_d^2 Z^D K_d {Z^D}^T + \sigma_{aa}^2 Z^{I^{aa}} K_{aa} {Z^{I^{aa}}}^T + \sigma_{ad}^2 Z^{I^{ad}} K_{ad} {Z^{I^{ad}}}^T + \sigma_{dd}^2 Z^{I^{dd}} K_{dd} {Z^{I^{dd}}}^T + \sigma_\varepsilon^2 I$$

In a second step, the phenotypic covariance was considered as known in the marker-by-marker GWAS model. A "all-in-one" model was at marker m:

$$Y = 1\mu + X\beta + E$$

$$E \sim N(0, \mathrm{V(Y)}_{SE})$$

where Y is the vector of phenotypic values, μ is the intercept, X is the incidence matrix of SO genotypes at marker m and β is the vector of parameters for SO genotypes, E is a vector of effects accounting for polygenic and environment effects with covariance matrix $\mathrm{V(Y)}_{SE}$.

This simplification reduced drastically the number of estimated variances but decreased the detection power of the GWAS. We applied an adapted version of this procedure to give more flexibility for fitting the model during the marker-by-marker analysis. We decomposed the

phenotypic covariance matrix into three terms (additive, non-additive and residual effects) and considered it as partially known.

Then, the phenotypic covariance matrix was:

$$\mathrm{V(Y)}_{SE} = \lambda_A \left[\sigma_a^2 Z^A K_a Z^{A^T}\right] + \lambda_{DI}\left[\sigma_d^2 Z^D K_d Z^{D^T} + \sigma_{aa}^2 Z^{I^{aa}} K_{aa} Z^{I^{aa}T} + \sigma_{ad}^2 Z^{I^{ad}} K_{ad} Z^{I^{ad}T} + \sigma_{dd}^2 Z^{I^{dd}} K_{dd} Z^{I^{dd}T}\right] + \lambda_E[\sigma_\varepsilon^2 I]$$

or in a simpler way:

$$\mathrm{V(Y)}_{SE} = \lambda_A[\mathrm{V(Y)}_{SE}^A] + \lambda_{DI}[\mathrm{V(Y)}_{SE}^{DI}] + \lambda_E[\mathrm{V(Y)}_{SE}^E].$$

where λ_A, λ_{DI} and λ_E are fitting parameters for additive, non-additive and residual terms.

We performed a GWAS using the following model:

At marker *m*: $Y = 1\mu + X\beta + I^n A + I^n DI + I^n E$

$$A \sim N(0, \lambda_A \mathrm{V(Y)}_{SE}^A),\ DI \sim N(0, \lambda_{DI}\ \mathrm{V(Y)}_{SE}^{DI}),\ E \sim N(0, \lambda_E \mathrm{V(Y)}_{SE}^E)$$

where X is the incidence matrix of SO genotypes at marker *m*, β is the vector of parameter for SO genotypes, I^n is an identity matrix of dimension n-by-n, n being the number of observations, A and DI is a random effect accounting for additive and non-additive polygenic effect, E is a vector of effects accounting for covariance due to environment effects, λ_A, λ_{DI} and λ_E are estimated for each marker which results in a better fitting of the model than the "all-in-one" procedure.

Splitting phenotypic covariance into three terms is a reasonable trade-off between full GWAS model (Gso-MONO model) and the "all-in-one" procedure. A gain in detection power were shown in comparison with the "all-in-one" procedure, leading to the identification of new candidate QTL whereas strongly decrease the computational times of the full model (result not shown). This strategy was applied with success as well in previous article (Rio S 2019).

A similar partition of the phenotypic covariance was applied for **MULTI** model:

$$Y = 1\mu + W\theta + Z^A A + Z^D D + Z^{I^{aa}} I^{aa} + Z^{I^{ad}} I^{ad} + Z^{I^{dd}} I^{dd} + \sum_e [Z_e^{AE} AE_e + Z_e^{DE} DE_e + Z_e^E E_e]$$

$$A \sim N(0, K_a \sigma_a^2)\ , D \sim N(0, K_d \sigma_d^2)\ ,$$

$$I^{aa} \sim N(0, K_{aa}\sigma_{aa}^2), I^{ad} \sim N(0, K_{ad}\sigma_{ad}^2)\ , I^{dd} \sim N(0, K_{dd}\sigma_{dd}^2)$$

$$AE_e \sim N\left(0, K_a \sigma_{a(e)}^2\right) IND, DE_e \sim N\left(0, K_d \sigma_{d(e)}^2\right) IND$$

$$E_e \sim N(0, I\sigma_{\varepsilon(e)}^2)$$

where W is the incidence matrix of environmental effects and θ is the vector of environmental parameters, AE_e, DE_e and E_e are vectors of random effects for environment specific additivity, dominance and error effects respectively, with environment specific variances $\sigma_{a(e)}^2$, $\sigma_{d(e)}^2$ and $\sigma_{\varepsilon(e)}^2$. E_e is a vector for environment specific error with variance $\sigma_{\varepsilon(e)}^2$. Other terms were equivalent to the MONO decomposition. The phenotypic covariance matrix can be expressed as:

$$\mathrm{V(Y)}_{ME} = \lambda_A \left[Z^A K_a \sigma_a^2 Z^{A^T} + \sum_e \left[Z_e^{AE} K_a \sigma_{a(e)}^2 Z_e^{AE^T} \right] \right] + \lambda_{DI} \left[Z^D K_d \sigma_d^2 Z^{D^T} + Z^{I^{aa}} K_{aa} \sigma_{aa}^2 Z^{I^{aa}T} + Z^{I^{ad}} K_{ad} \sigma_{ad}^2 Z^{I^{ad}T} + Z^{I^{dd}} K_{dd} \sigma_{dd}^2 Z^{I^{dd}T} + \sum_e \left[Z_e^{DI} K_d \sigma_{d(e)}^2 Z_e^{DI^T} \right] \right] + \lambda_E \left[\sum_e \left[Z_e^E \sigma_{\varepsilon(e)}^2 Z_e^{E^T} \right] \right]$$

or:

$$\mathrm{V(Y)}_{ME} = \lambda_A [\mathrm{V(Y)}_{ME}^A] + \lambda_{DI} [\mathrm{V(Y)}_{ME}^{DI}] + \lambda_E [\mathrm{V(Y)}_{ME}^E].$$

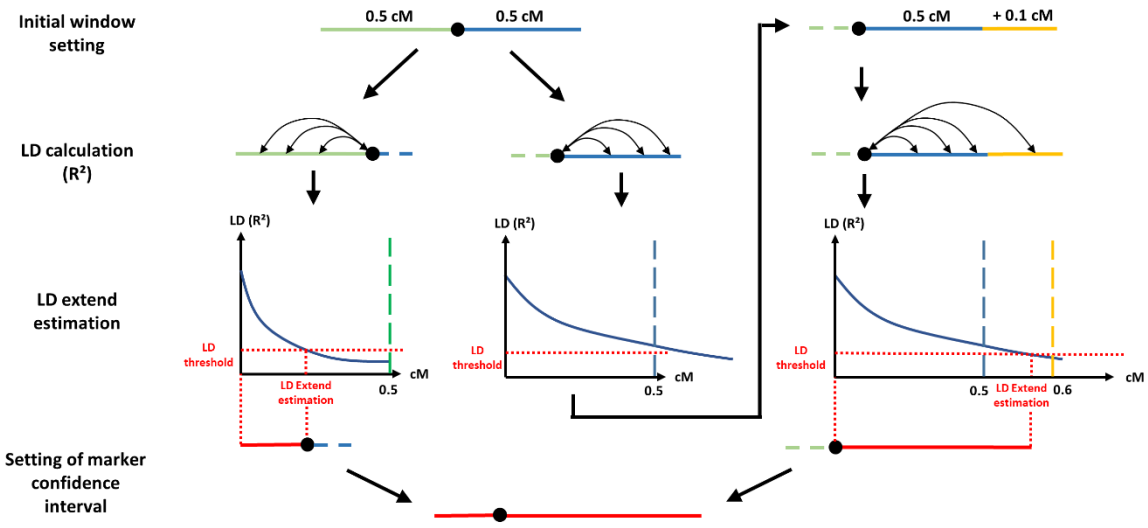
The GWAS model was:

At marker m: $Y = 1\mu + W\alpha + X\beta + I^n A + I^n DI + I^n E$

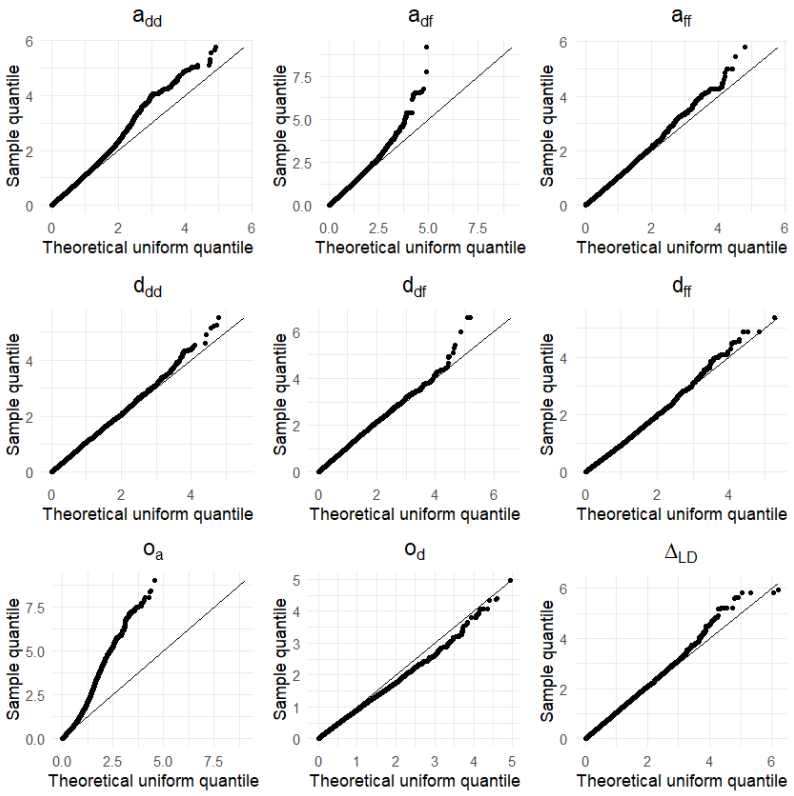
$$A \sim N(0, \lambda_A \mathrm{V(Y)}_{SE}^A),\ DI \sim N(0, \lambda_{DI} \mathrm{V(Y)}_{SE}^{DI}),\ E \sim N(0, \lambda_E \mathrm{V(Y)}_{SE}^E),$$

where X is the incidence matrix of SO genotypes at marker m, β is the vector of parameter for SO genotypes, I^n is an identity matrix of dimension n-by-n, n being the number of observations, A and DI are a random effect accounting for additive and non-additive residual polygenic effect. E is a vector of effects accounting for covariance due to environment effects, λ_A, λ_{DI} and λ_E are fitting parameters for additive, non-additive and residual terms.

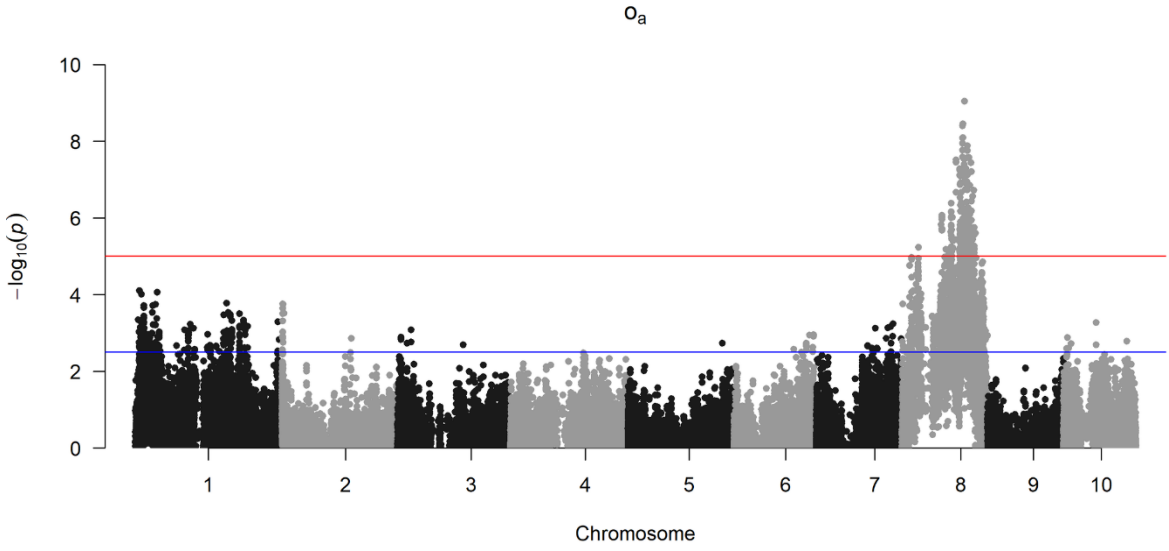
FIGURES



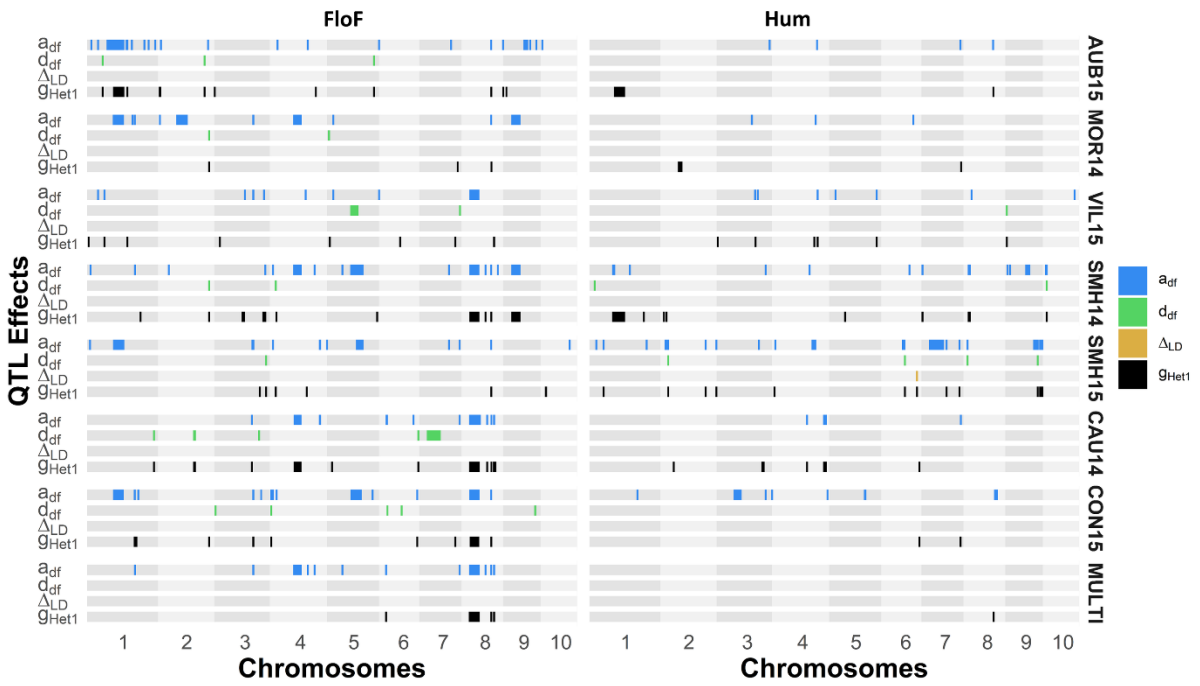
S1 Fig. Estimation of the confidence interval around significant marker. The confidence interval estimation starts with the definition of an arbitrary interval of 1 cM on both sides of the significant marker. LD (Linkage Disequilibrium) is calculated as a R^2 between the significant marker and the other markers within each interval using genotypic information. Then, LD is used to estimated LD extend with a threshold of 0.1. If the LD extend value is superior to the size of the interval, the interval size is increased by 0.1 cM. The procedure is repeated from the LD calculation until the LD extend reach a value inferior to the interval size. Lastly, the LD extend value is used to defined the limits of the confidence interval around the significant marker.



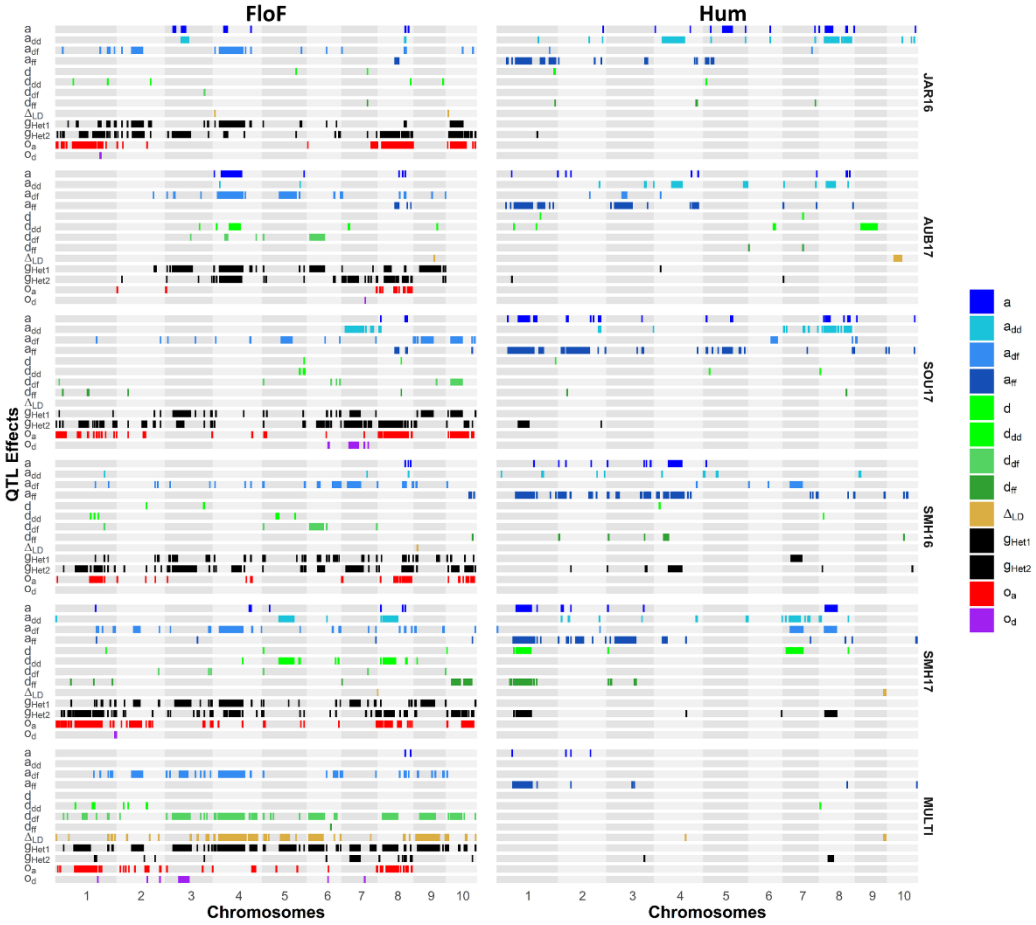
S2 Fig. Quantile-by-Quantile diagram of Pvalues for the Male Flowering time (FloM) in JAR16 (Het2). Black line represents the ideal distribution of the Pvalue according a uniform law.



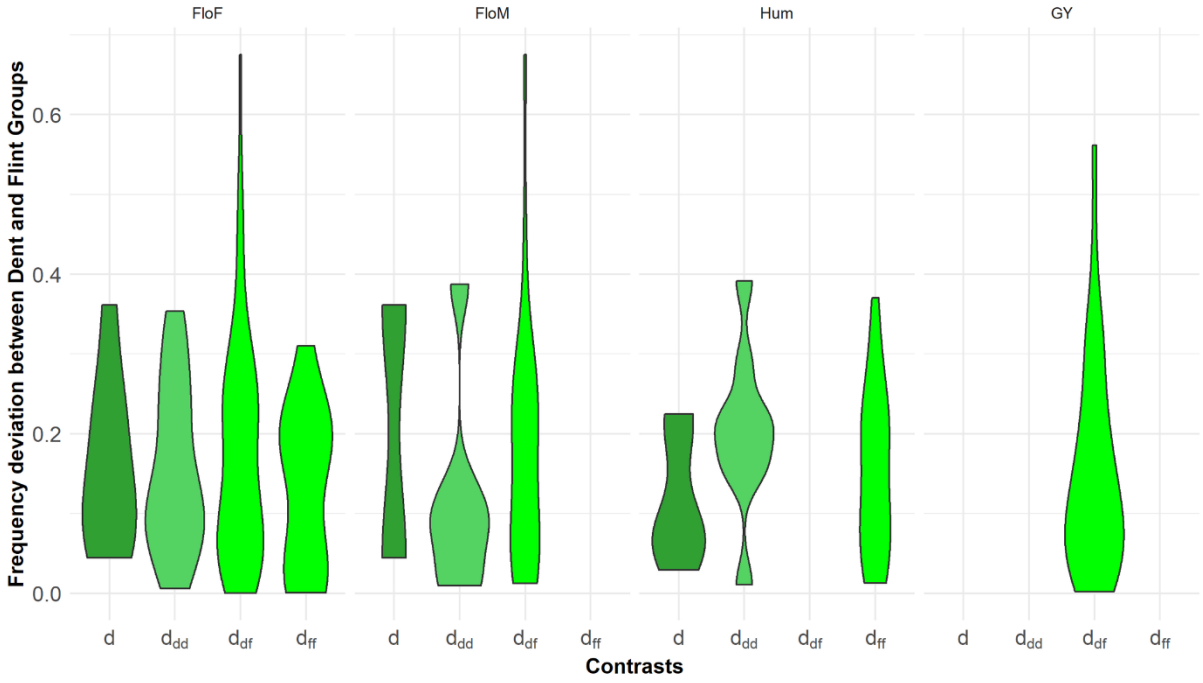
S3 Fig. Manhattan plot for the Male flowering time (FloM) in JAR16 (Het2) for the additive effect of the origin (o_a). Blue and red lines represent the Pvalue threshold for FDR levels of 0.2 and 0.05.



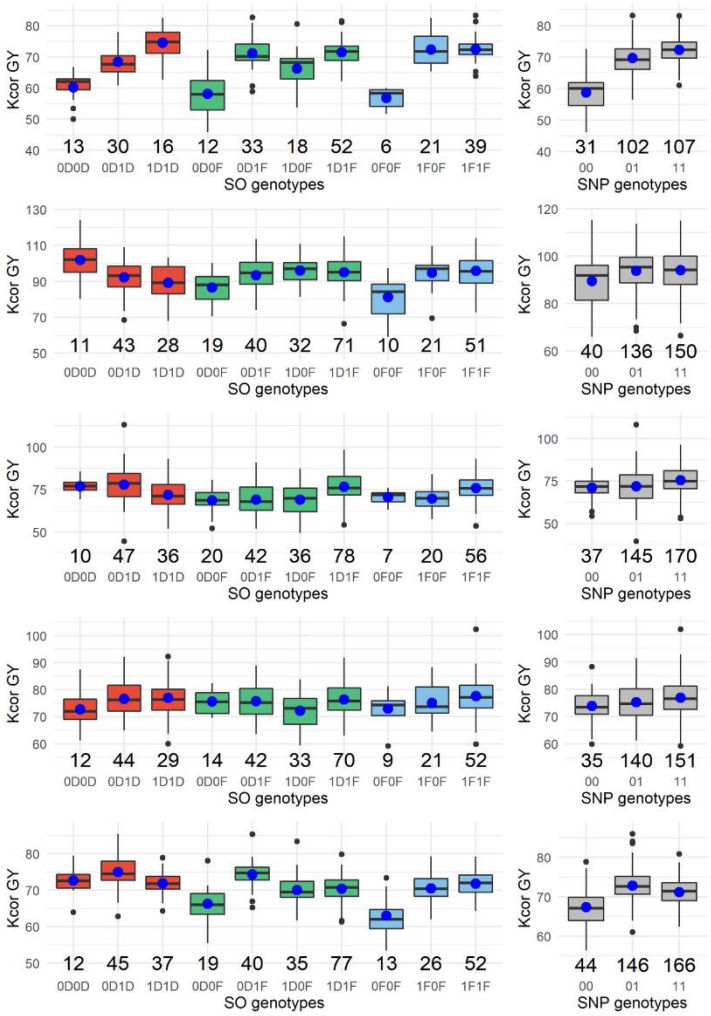
S4 Fig. Representation of QTLs for the Female flowering (FloF) and the grain moisture (Hum) in Het1. Rectangles represent the confidence interval of QTLs. AUB14, MOR14, VIL15, SMH14, SMH15, CAU14 and CON15 indicate environments analysed with Gso-MONO model. Gso-MULTI indicates Gso-MULTI model. The FDR level is 0.2.



S5 Fig. Representation of QTLs identified for the Female flowering (FloF) and the grain moisture (Hum) in Het2. Rectangles represent the confidence interval of QTLs. JAR16, AUB17, SOU17, SMH16 and SMH17 indicate environments analysed with Gso-MONO model. Gso-MULTI indicates for Gso-MULTI model. The FDR level is 0.2.



S6 Fig. Differences between Dent and Flint allelic frequencies for dominance QTLs in Het2. Violin plot of the difference of SNP allelic frequencies between the Dent and the Flint group calculated as $Diff = |p_D - p_F|$ with p_D and p_F the Dent and Flint frequencies.



S7 Fig. Illustration of the variation of additive effect in the dent genetic background across environments. Boxplot of phenotype corrected by the kinship according to the Gso genotypes of marker AX-91203539 on chromosome 1 for the grain yield (GY) in all Het2 environment (Coloured boxplot; red, green and blue are for DD, DF and FF genetic backgrounds) and Gad model (Grey boxplot). The number at the bottom indicates the number of observations for each SO genotype.

TABLES

S1 Table: Contrast matrix for g_{Het1} effect (global QTL based on Het1 SO genotypes)

	β_{1D1D}	β_{0D0D}	β_{1F1F}	β_{0F0F}	β_{1D1F}	β_{0D0F}	β_{0D1D}	β_{1F0F}	β_{0D1F}	β_{1D0F}
$\beta_{1D1F} - \beta_{0D0F} = 0$					1	-1				
$\beta_{1D1F} - \beta_{0D1F} = 0$					1				-1	
$\beta_{1D1F} - \beta_{1D0F} = 0$					1					-1

Contrast matrix defined to test a global effect of a QTL based on SO genotypes present in Het1 panel. Empty spaces indicate a weight of 0. With C the matrix (defined above) associating weights to the fixed parameters of the model, one can test: H_0: $\{C\beta = 0\}$ vs H_1: $\{C\beta \neq 0\}$.

S2 Table: Contrast matrix for g_{Het2} effect (global QTL based on Het2 SO genotypes)

	β_{1D1D}	β_{0D0D}	β_{1F1F}	β_{0F0F}	β_{1D1F}	β_{0D0F}	β_{0D1D}	β_{1F0F}	β_{0D1F}	β_{1D0F}
$\beta_{1D1D} - \beta_{0D0D} = 0$	1	-1								
$\beta_{1D1D} - \beta_{1F1F} = 0$	1		-1							
$\beta_{1D1D} - \beta_{0F0F} = 0$	1			-1						
$\beta_{1D1D} - \beta_{1D1F} = 0$	1				-1					
$\beta_{1D1D} - \beta_{0D0F} = 0$	1					-1				
$\beta_{1D1D} - \beta_{0D1D} = 0$	1						-1			
$\beta_{1D1D} - \beta_{1F0F} = 0$	1							-1		
$\beta_{1D1D} - \beta_{0D1F} = 0$	1								-1	
$\beta_{1D1D} - \beta_{1D0F} = 0$	1									-1

Contrast matrix defined to test a global effect of a QTL based on SO genotypes present in Het2 panel. Empty spaces indicate a weight of 0. With C the matrix (defined above) associating weights to the fixed parameters of the model, one can test: $H_0: \{C\beta = 0\}$ vs $H_1: \{C\beta \neq 0\}$.

S3 Table: Summary of agronomic traits with single environment models (MONO models)

Panel	Trait	Env	Mean	Min	Max	Std. Dev.	σ_G^2	σ_ε^2	H_s^2
Het1	FloF	CAU14	196	184	209	5,11	25,4	0,399	0,987
		AUB15	194	186	208	3,81	13,3	1,53	0,915
		RHO15	197	186	211	4,21	18,3	0,479	0,98
		MOR14	204	197	215	3,45	11,3	0,493	0,965
		VIL15	199	189	209	3,7	13,7	0,516	0,971
		SMH14	199	192	209	3,61	12,7	0,458	0,971
		SMH15	198	189	210	3,7	13,4	0,46	0,975
	FloM	CAU14	193	182	207	4,64	20,8	0,224	0,991
		AUB15	191	183	205	3,57	11,7	1,51	0,905
		RHO15	198	188	213	4,7	23,1	0,42	0,986
		MOR14	203	200	214	2,56	6,1	0,44	0,944
		VIL15	197	188	208	3,51	12,4	0,398	0,975
		SMH14	198	189	210	3,14	9,64	0,387	0,968
		SMH15	195	186	205	3,7	12,6	0,821	0,954
	Hum	CAU14	25,7	15,5	39,5	3,76	12,4	1,64	0,902
		AUB15	30,6	18,4	40,4	3,76	13,1	1,55	0,912
		RHO15	33,5	17	42	4,11	16,3	0,666	0,969
		MOR14	29,6	19,3	38,7	2,89	6,23	2,17	0,778
		VIL15	29,9	19,4	41,1	3,44	11,3	0,543	0,963
		SMH14	25,5	17,4	38,9	3,28	9,78	0,991	0,923
		SMH15	28,4	21,2	42,5	3,12	8,72	1,26	0,903
	GY	CAU14	83,2	24,2	139	19,7	301	101	0,784
		AUB15	112	30,7	164	22,2	362	144	0,756
		RHO15	87,9	26,3	130	18,4	253	97,2	0,77
		MOR14	73,2	34,2	123	16,6	190	87,5	0,726
		VIL15	86,5	45,7	116	13,9	126	67,8	0,699
		SMH14	100	39,1	161	20	290	93,8	0,79
		SMH15	85,6	31,5	132	16,6	129	144	0,548

Het2	FloF	JAR16	206	197	218	4,43	18,1	0,651	0,972
		AUB17	195	188	209	3,93	14,8	0,662	0,967
		SOU17	187	178	197	3,19	8,53	1,81	0,861
		SMH16	197	190	208	3,01	8,57	0,907	0,924
		SMH17	194	187	204	3,47	10,5	0,83	0,941
	FloM	JAR16	204	195	218	3,71	12,6	0,507	0,969
		AUB17	193	186	207	3,35	10,1	1,13	0,921
		SOU17	185	177	195	2,91	6,3	2,27	0,785
		SMH16	196	190	207	2,83	7,29	1,01	0,903
		SMH17	192	186	200	2,9	7,6	0,561	0,945
	Hum	JAR16	30,4	21,7	41,4	3,63	11,3	1,8	0,888
		AUB17	28,5	19,5	39,6	4,2	16,3	1,86	0,919
		SOU17	29,8	12,5	38,6	3,59	10,9	2,58	0,848
		SMH16	21,1	16,5	31,5	2,1	2,47	1,98	0,614
		SMH17	19,9	16	28,4	2,21	4,62	0,296	0,952
	GY	JAR16	69,8	37,1	102	13,1	115	48,6	0,745
		AUB17	93,9	31,2	139	19,6	234	152	0,668
		SOU17	73,6	14,1	130	23,2	391	159	0,764
		SMH16	76,1	38,7	119	14	110	88,1	0,615
		SMH17	71,4	37,3	116	13,3	141	38,1	0,823

Min, Max, Mean, Std.Dev are the minimum, maximum, mean and standard deviation of corrected phenotypic values. The variances σ_G^2 and σ_ε^2 are respectively for genetic and error effects. H_S^2 is the single environment heritability.

S4 Table: Summary of agronomic traits with multiple environment models (MULTI model)

Panel	Trait	Mean	Min	Max	Std. Dev.	Mean with correction by the checks	σ_G^2	σ_{GE}^2	σ_ε^2	H_M^2
Het1	FloF	198	184	215	4,95	197,5	14,3	1,5	0,613	0,98
	FloM	197	182	214	5,27	195,8	12,3	1,46	0,622	0,977
	Hum	29	15,5	42,5	4,36	28,97	8,63	2,34	1,29	0,945
	GY	89,8	24,2	164	21,9	89,03	173	65,4	109	0,881
Het2	FloF	195	178	218	7,2	196,2	10,3	1,76	1,03	0,951
	FloM	194	177	218	6,99	194,6	7,75	0,965	1,16	0,951
	Hum	25,8	12,5	41,4	5,57	25,08	6,56	2,37	1,75	0,894
	GY	77,2	14,1	139	19,4	79,11	126	76	102	0,789

Min, Max, Mean, Std.Dev are the minimum, maximum, mean and standard deviation of corrected phenotypic values. "Mean with correction by the checks" is the phenotypic mean of all environments corrected by the value of the checks. The variances σ_G^2, σ_{GE}^2 and σ_ε^2 are respectively for genetic, genetic-by-environment interaction and error effects. H_M^2 is the multi environment heritability.

S5 Table: Single environment variance partition with MONO model

Panel	Trait	Env	σ_a^2	σ_d^2	σ_{aa}^2	σ_{ad}^2	σ_{dd}^2	σ_ε^2	$\sigma_a^2/V(G)$	$\sigma_d^2/V(G)$	$(\sigma_I^2)/V(G)$

Het1	FloF	CAU14	17,34	0,00	0,00	0,97	0,48	0,40	0,92	0,00	0,08
		AUB15	8,86	0,01	0,00	0,08	0,73	1,45	0,92	0,00	0,08
		RHO15	11,80	0,13	0,02	0,99	0,83	0,47	0,86	0,01	0,13
		MOR14	8,03	0,14	0,17	0,16	0,13	0,49	0,93	0,02	0,05
		VIL15	9,74	0,08	0,04	0,39	0,37	0,54	0,92	0,01	0,08
		SMH14	9,07	0,01	0,01	0,65	0,37	0,47	0,90	0,00	0,10
		SMH15	9,64	0,11	0,08	0,20	0,20	0,46	0,94	0,01	0,05
	FloM	CAU14	13,40	0,01	0,01	0,98	0,59	0,23	0,89	0,00	0,11
		AUB15	8,27	0,01	0,01	0,12	0,32	1,43	0,95	0,00	0,05
		RHO15	16,24	0,08	0,00	0,89	0,62	0,41	0,91	0,00	0,08
		MOR14	3,90	0,10	0,17	0,28	0,21	0,43	0,84	0,02	0,14
		VIL15	8,01	0,03	0,01	0,66	0,60	0,42	0,86	0,00	0,14
		SMH14	6,34	0,01	0,01	0,44	0,31	0,39	0,89	0,00	0,11
		SMH15	8,50	0,04	0,02	0,13	0,15	0,82	0,96	0,00	0,03
	Hum	CAU14	8,59	0,00	0,00	0,44	1,86	1,66	0,79	0,00	0,21
		AUB15	9,90	0,00	0,01	0,00	0,01	1,49	1,00	0,00	0,00
		RHO15	11,24	0,01	0,00	0,54	2,26	0,67	0,80	0,00	0,20
		MOR14	5,54	0,00	0,00	0,00	0,00	1,93	1,00	0,00	0,00
		VIL15	8,19	0,00	0,36	0,62	0,75	0,51	0,83	0,00	0,17
		SMH14	8,35	0,00	0,37	0,15	0,13	0,99	0,93	0,00	0,07
		SMH15	5,97	0,51	0,97	0,33	0,22	1,26	0,75	0,06	0,19
	GY	CAU14	200,03	64,73	0,00	0,12	0,56	98,92	0,75	0,24	0,00
		AUB15	272,10	5,90	0,05	8,44	40,04	139,59	0,83	0,02	0,15
		RHO15	192,16	1,64	0,32	16,24	12,62	94,51	0,86	0,01	0,13
		MOR14	140,42	2,37	1,02	11,84	12,96	86,29	0,83	0,01	0,15
		VIL15	106,25	0,00	0,00	0,01	0,01	67,03	1,00	0,00	0,00
		SMH14	212,97	0,00	0,00	8,29	32,08	93,09	0,84	0,00	0,16
		SMH15	111,15	0,00	0,00	0,31	17,43	143,53	0,86	0,00	0,14
Het2	FloF	JAR16	13,64	0,06	0,22	0,78	0,65	0,65	0,89	0,00	0,11
		AUB17	12,39	0,57	0,03	0,11	0,11	0,65	0,94	0,04	0,02
		SOU17	5,75	0,21	1,79	0,14	0,15	1,78	0,71	0,03	0,26
		SMH16	7,13	0,12	0,38	0,12	0,13	0,91	0,90	0,02	0,08
		SMH17	6,69	0,39	0,75	1,10	0,74	0,84	0,69	0,04	0,27
	FloM	JAR16	9,74	0,03	0,05	0,48	0,56	0,51	0,90	0,00	0,10
		AUB17	8,46	0,18	0,01	0,04	0,04	1,12	0,97	0,02	0,01
		SOU17	4,27	0,14	1,34	0,07	0,08	2,20	0,72	0,02	0,25
		SMH16	5,97	0,01	0,01	0,38	0,43	1,01	0,88	0,00	0,12
		SMH17	5,80	0,35	0,07	0,28	0,26	0,55	0,86	0,05	0,09
	Hum	JAR16	7,06	0,45	0,02	1,37	0,39	1,81	0,76	0,05	0,19
		AUB17	12,23	0,80	0,10	0,60	0,24	1,87	0,88	0,06	0,07
		SOU17	8,02	0,00	0,98	0,22	0,29	2,51	0,84	0,00	0,16
		SMH16	2,20	0,03	0,01	0,03	0,03	1,97	0,96	0,01	0,03
		SMH17	3,47	0,36	0,36	0,07	0,05	0,30	0,81	0,08	0,11
	GY	JAR16	82,07	4,52	19,39	2,86	2,75	48,02	0,74	0,04	0,22
		AUB17	167,46	31,85	18,96	4,88	3,76	149,76	0,74	0,14	0,12
		SOU17	292,57	40,63	23,47	16,90	17,91	158,31	0,75	0,10	0,15
		SMH16	75,43	35,07	0,60	0,76	0,68	81,76	0,67	0,31	0,02
		SMH17	110,50	35,18	0,01	0,00	0,00	37,28	0,76	0,24	0,00

The variances σ_a^2 , σ_d^2 , σ_{aa}^2 , σ_{ad}^2 , σ_{dd}^2 and σ_ε^2 are respectively for additivity, dominance, additive-by-additive epistasis, additive-by-dominance epistasis, dominance-by-dominance epistasis and error effects. The epistatic variance σ_I^2 is the sum of σ_{aa}^2 , σ_{ad}^2 and σ_{dd}^2 variances. V(G) is the global genetic variance defined as: $V(G) = \sigma_a^2 + \sigma_d^2 + \sigma_{aa}^2 + \sigma_{ad}^2 + \sigma_{dd}^2$.

S6 Table: Multi environment variance partition (MULTI model) in Het1

	FloF	FloM	Hum	GY

σ^2_a	8,56	7,08	6,45	112,18
$\sigma^2_{a(CAU14)}$	2,34	1,51	0,57	25,00
$\sigma^2_{a(AUB15)}$	0,87	1,27	0,72	19,70
$\sigma^2_{a(RHO15)}$	0,72	0,46	0,64	75,48
$\sigma^2_{a(MOR14)}$	0,44	0,01	2,62	94,66
$\sigma^2_{a(VIL15)}$	1,26	2,42	1,90	22,39
$\sigma^2_{a(SMH14)}$	0,23	0,20	1,16	3,54
$\sigma^2_{a(SMH15)}$	0,08	0,08	0,18	49,36
σ^2_d	0,03	0,02	0,00	0,00
$\sigma^2_{d(CAU14)}$	1,00	0,71	1,81	52,37
$\sigma^2_{d(AUB15)}$	0,07	0,00	0,00	23,48
$\sigma^2_{d(RHO15)}$	0,06	0,02	0,73	0,05
$\sigma^2_{d(MOR14)}$	0,04	0,00	0,38	54,13
$\sigma^2_{d(VIL15)}$	2,01	2,20	2,81	32,39
$\sigma^2_{d(SMH14)}$	0,57	0,69	1,23	2,07
$\sigma^2_{d(SMH15)}$	0,76	0,51	2,04	0,00
σ^2_{aa}	0,01	0,01	0,04	0,00
σ^2_{ad}	0,41	0,31	0,03	3,82
σ^2_{dd}	0,58	0,38	0,11	18,71
$\sigma^2_{\varepsilon(CAU14)}$	0,40	0,23	1,90	94,31
$\sigma^2_{\varepsilon(AUB15)}$	1,37	1,46	1,58	145,34
$\sigma^2_{\varepsilon(RHO15)}$	0,49	0,41	0,68	94,69
$\sigma^2_{\varepsilon(MOR14)}$	0,47	0,41	1,77	78,50
$\sigma^2_{\varepsilon(VIL15)}$	0,57	0,45	0,54	69,95
$\sigma^2_{\varepsilon(SMH14)}$	0,48	0,41	1,05	91,05
$\sigma^2_{\varepsilon(SMH15)}$	0,45	0,79	1,43	159,02

The variances σ^2_a , σ^2_d , σ^2_{aa} , σ^2_{ad} , σ^2_{dd} and σ^2_ε are respectively for additivity, dominance, additive-by-additive epistasis, additive-by-dominance epistasis, dominance-by-dominance epistasis and error effects. The variances $\sigma^2_{a(e)}$, $\sigma^2_{d(e)}$ and $\sigma^2_{\varepsilon(e)}$ are environment specific variance for the environment *e*.

S7 Table: Multi environment variance partition (MULTI model) in Het2

	FloF	FloM	Hum	GY
σ^2_a	7,24	5,68	3,21	85,63
$\sigma^2_{a(JAR16)}$	2,02	0,95	4,75	45,70
$\sigma^2_{a(AUB17)}$	0,60	0,03	2,83	116,35
$\sigma^2_{a(SOU17)}$	0,25	0,16	0,01	0,26
$\sigma^2_{a(SMH16)}$	0,07	0,39	0,01	22,67
$\sigma^2_{a(SMH17)}$	2,59	1,95	2,77	69,70
σ^2_d	0,23	0,15	0,03	11,25
$\sigma^2_{d(JAR16)}$	0,29	0,00	1,32	37,72
$\sigma^2_{d(AUB17)}$	0,07	0,24	0,48	70,29

$\sigma^2_{d(SOU17)}$	0,30	0,26	0,00	34,62
$\sigma^2_{d(SMH16)}$	1,37	0,47	3,11	23,08
$\sigma^2_{d(SMH17)}$	1,03	0,58	1,66	6,33
σ^2_{aa}	0,62	0,01	0,14	0,35
σ^2_{ad}	0,10	0,19	0,13	0,14
σ^2_{dd}	0,08	0,21	0,17	0,08
$\sigma^2_{\varepsilon(JAR16)}$	0,67	0,52	1,83	48,26
$\sigma^2_{\varepsilon(AUB17)}$	0,66	1,04	1,89	154,47
$\sigma^2_{\varepsilon(SOU17)}$	2,17	2,45	2,86	162,30
$\sigma^2_{\varepsilon(SMH16)}$	1,01	1,10	1,71	81,10
$\sigma^2_{\varepsilon(SMH17)}$	0,93	0,60	0,30	38,25

The variances σ^2_a , σ^2_d , σ^2_{aa} , σ^2_{ad} , σ^2_{dd} and σ^2_ε are respectively for additivity, dominance, additive-by-additive epistasis, additive-by-dominance epistasis, dominance-by-dominance epistasis and error effects. The variances $\sigma^2_{a(e)}$, $\sigma^2_{d(e)}$ and $\sigma^2_{\varepsilon(e)}$ are environment specific variance for the environment *e*.

S8 Table: Synthetic table of multiple environment variance partition (MULTI model)

Panel	Trait	σ^2_a	$V(AxE)$	σ^2_d	$V(DxE)$	σ^2_{aa}	σ^2_{ad}	σ^2_{dd}	$V(\varepsilon xE)$	$\frac{\sigma^2_a}{V(G)}$	$\frac{\sigma^2_d}{V(G)}$	$\frac{V(AxE)}{V(G)}$	$\frac{V(DxE)}{V(G)}$
Het1	FloF	8,56	0,85	0,03	0,64	0,01	0,41	0,58	0,60	0,89	0,00	0,09	0,07
	FloM	7,08	0,85	0,02	0,59	0,01	0,31	0,38	0,59	0,91	0,00	0,11	0,08
	Hum	6,45	1,11	0,00	1,28	0,04	0,03	0,11	1,28	0,97	0,00	0,17	0,19
	GY	112,18	41,44	0,00	23,50	0,00	3,82	18,71	104,69	0,83	0,00	0,31	0,17
Het2	FloF	7,24	1,10	0,23	0,61	0,62	0,10	0,08	1,09	0,88	0,03	0,13	0,07
	FloM	5,68	0,70	0,15	0,31	0,01	0,19	0,21	1,14	0,91	0,02	0,11	0,05
	Hum	3,21	2,07	0,03	1,31	0,14	0,13	0,17	1,72	0,87	0,01	0,56	0,36
	GY	85,63	50,93	11,25	34,41	0,35	0,14	0,08	96,88	0,88	0,12	0,52	0,35

The variances σ^2_a , σ^2_d , σ^2_{aa} , σ^2_{ad} , σ^2_{dd} and σ^2_ε are respectively for additivity, dominance, additive-by-additive epistasis, additive-by-dominance epistasis, dominance-by-dominance epistasis and error effects. The variances $\sigma^2_{a(e)}$, $\sigma^2_{d(e)}$ and $\sigma^2_{\varepsilon(e)}$ are environment specific variance for the environment *e*. V(AxE) is the average additive-by-environment interaction variance (calculated as $\frac{\sum_e \sigma^2_{a(e)}}{n_e}$). V(DxE) is the average dominance-by-environment interaction variance (calculated as $\frac{\sum_e \sigma^2_{d(e)}}{n_e}$). $V(\varepsilon xE)$ is the average environment specific error variance (calculated as $\frac{\sum_e \sigma^2_{d(e)}}{n_e}$). The term n_e refers to the number of environments. V(G) is the global genetic variance of main effects defined as: $V(G) = \sigma^2_a + \sigma^2_d + \sigma^2_{aa} + \sigma^2_{ad} + \sigma^2_{dd}$.

S9 Table. Number of candidate markers in Het1 for model Gad.

Trait	Env	α	δ
FloF	AUB15	345860	345860
	MOR14	348579	348579
	VIL15	329092	329092
	SMH14	347024	347024
	SMH15	349883	349883
	CAU14	351133	351133
	CON15	346542	346542
	MULTI	433854	433854
FloM	AUB15	345860	345860
	MOR14	349307	349307
	VIL15	329092	329092
	SMH14	347024	347024
	SMH15	350601	350601
	CAU14	351847	351847
	CON15	346542	346542
	MULTI	433854	433854
Hum	AUB15	346337	346337
	MOR14	349307	349307
	VIL15	329092	329092
	SMH14	347639	347639
	SMH15	350601	350601
	CAU14	351847	351847
	CON15	346542	346542
	MULTI	433986	433986
GY	AUB15	346337	346337
	MOR14	349307	349307
	VIL15	329092	329092
	SMH14	347639	347639
	SMH15	350601	350601
	CAU14	351847	351847
	CON15	346542	346542
	MULTI	433986	433986

Number of candidate markers according to the environments, the traits and the contrast tests after filter on the minor allele frequency (MAF) and the number of individuals in each genotypic class. AUB14, MOR14, VIL15, SMH14, SMH15, CAU14 and CON15 indicate for Gso-MONO models. MULTI indicates for the Gso-MULTI model.

S10 Table. Number of candidate markers in Het2 for model Gad.

Trait	Env	α	δ
FloF	JAR16	365725	365725
	SOU17	377282	377282
	AUB17	370975	370975

	SMH16	372279	372279
	SMH17	378696	378696
	MULTI	451578	451578
FloM	JAR16	366009	366009
	SOU17	377282	377282
	AUB17	370975	370975
	SMH16	372279	372279
	SMH17	378696	378696
	MULTI	451361	451361
Hum	JAR16	365364	365364
	SOU17	377282	377282
	AUB17	370975	370975
	SMH16	373073	373073
	SMH17	378696	378696
	MULTI	450583	450583
GY	JAR16	343449	343449
	SOU17	377282	377282
	AUB17	370975	370975
	SMH16	373073	373073
	SMH17	378696	378696
	MULTI	449104	449104

Number of candidate markers according to the environments, the traits and the contrast tests after filter on the minor allele frequency (MAF) and the number of individuals in each genotypic class. JAR16, AUB17, SOU17, SMH16 and SMH17 indicate for Gso-MONO models. MULTI indicates for the Gso-MULTI model.

S11 Table. Number of candidate markers in Het1 for model Gso.

Trait	Env	a_{DF}	d_{DF}	Δ_{LD}	g_{Het1}
FloF	AUB15	345860	344253	428623	344253
	MOR14	348579	346223	429835	346223
	VIL15	327046	324343	416506	324343
	SMH14	347024	345455	430084	345455
	SMH15	349883	348330	431656	348330
	CAU14	351133	349213	431250	349213
	CON15	346542	344630	429036	344630
	MULTI	433854	432675	471123	432675
FloM	AUB15	345860	344253	428623	344253
	MOR14	349307	346951	430743	346951
	VIL15	329092	326376	419050	326376
	SMH14	347024	345455	430084	345455
	SMH15	350601	349046	432530	349046
	CAU14	351847	349927	432142	349927
	CON15	346542	344630	429036	344630

	MULTI	433854	432675	471123	432675
Hum	AUB15	346337	344484	428809	344484
	MOR14	349307	346951	430743	346951
	VIL15	329092	326376	419050	326376
	SMH14	347639	346090	430381	346090
	SMH15	350601	349046	432530	349046
	CAU14	351847	349927	432142	349927
	CON15	346542	344630	429036	344630
	MULTI	433986	432808	471147	432808
GY	AUB15	346337	344484	428809	344484
	MOR14	349307	346951	430743	346951
	VIL15	329092	326376	419050	326376
	SMH14	347639	346090	430381	346090
	SMH15	350601	349046	432530	349046
	CAU14	351847	349927	432142	349927
	CON15	346542	344630	429036	344630
	MULTI	433986	432808	471147	432808

Number of candidate markers according to the environments, the traits and the contrast tests after filter on the minor allele frequency (MAF) and the number of individuals in each genotypic class. AUB14, MOR14, VIL15, SMH14, SMH15, CAU14 and CON15 indicate for Gso-MONO models. MULTI indicates for the Gso-MULTI model.

S12 Table: Number of candidate markers in Het2 for model Gso.

Trait	Env	a	a_{DD}	a_{DF}	a_{FF}	s_a	t_a	d	d_{DD}	d_{DF}	d_{FF}	s_d	t_d	Δ_{LD}	o_a	o_d	g_{Het2}	g_{Het1}
FloF	JAR16	91622	202061	260774	183863	92357	91622	91396	202060	248892	183862	92355	91396	356715	92357	91622	91396	248892
	SOU17	106529	219019	278583	199993	107238	106529	106353	219019	268850	199986	107238	106353	370451	107238	106529	106353	268850
	AUB17	66935	148659	191596	133191	67418	66935	66789	148658	182739	133191	67417	66789	257959	67418	66935	66789	182739
	SMH16	99561	216040	265965	191216	100388	99561	99377	216040	255006	191216	100388	99377	360979	100388	99561	99377	255006
	SMH17	108462	220663	278234	203149	109112	108462	108321	220663	268827	203148	109111	108321	373471	109112	108462	108321	268827
	MULTI	257011	353402	394626	344940	260251	257011	256734	353385	390239	344857	260160	256734	446459	260251	257011	256734	390239
FloM	JAR16	92097	202367	261091	184348	92818	92097	91870	202366	249249	184347	92816	91870	357049	92818	92097	91870	249249
	SOU17	106529	219019	278583	199993	107238	106529	106353	219019	268850	199986	107238	106353	370451	107238	106529	106353	268850
	AUB17	94496	205538	269028	190784	95162	94496	94329	205537	257333	190784	95161	94329	360220	95162	94496	94329	257333
	SMH16	99561	216040	265965	191216	100388	99561	99377	216040	255006	191216	100388	99377	360979	100388	99561	99377	255006
	SMH17	108462	220663	278234	203149	109112	108462	108321	220663	268827	203148	109111	108321	373471	109112	108462	108321	268827
	MULTI	257319	353607	394718	345141	260546	257319	257041	353593	390329	345058	260455	257041	446478	260546	257319	257041	390329
Hum	JAR16	90999	201111	260259	183333	91681	90999	90772	201110	247924	183332	91679	90772	355677	91681	90999	90772	247924
	SOU17	106529	219019	278583	199993	107238	106529	106353	219019	268850	199986	107238	106353	370451	107238	106529	106353	268850
	AUB17	94496	205538	269028	190784	95162	94496	94329	205537	257333	190784	95161	94329	360220	95162	94496	94329	257333
	SMH16	101365	217806	266829	192799	102195	101365	101172	217806	256279	192799	102195	101172	362605	102195	101365	101172	256279
	SMH17	108462	220663	278234	203149	109112	108462	108321	220663	268827	203148	109111	108321	373471	109112	108462	108321	268827
	MULTI	257171	353481	394423	345048	260409	257171	256893	353457	390034	344965	260320	256893	446418	260409	257171	256893	390034
GY	JAR16	63294	166041	234267	150303	64066	63294	62955	166040	216824	150302	64065	62955	328388	64066	63294	62955	216824
	SOU17	106529	219019	278583	199993	107238	106529	106353	219019	268850	199986	107238	106353	370451	107238	106529	106353	268850
	AUB17	94496	205538	269028	190784	95162	94496	94329	205537	257333	190784	95161	94329	360220	95162	94496	94329	257333
	SMH16	101365	217806	266829	192799	102195	101365	101172	217806	256279	192799	102195	101172	362605	102195	101365	101172	256279
	SMH17	108462	220663	278234	203149	109112	108462	108321	220663	268827	203148	109111	108321	373471	109112	108462	108321	268827
	MULTI	249305	346812	390188	340013	252539	249305	249062	346776	385529	339926	252441	249062	444713	252539	249305	249062	385529

Number of candidate markers according to the environments, the traits and the contrast tests after filter on the minor allele frequency (MAF) and the number of individuals in each genotypic class. JAR16, AUB17, SOU17, SMH16 and SMH17 indicate for Gso-MONO models. MULTI indicates for the Gso-MULTI model.

S13 Table: Number of significant markers in Het1

Trait	Env	a_{DF}	d_{DF}	Δ_{LD}	g_{Het1}
FloF	AUB15	54 | 0	5 | 0	0 | 0	25 | 0
	MOR14	41 | 4	2 | 0	0 | 0	9 | 4
	VIL15	27 | 1	21 | 0	0 | 0	11 | 0
	SMH14	48 | 0	2 | 0	0 | 0	33 | 0
	SMH15	20 | 0	1 | 0	0 | 0	11 | 0
	CAU14	48 | 3	13 | 0	0 | 0	31 | 4
	CON15	51 | 1	5 | 1	0 | 0	13 | 1
	MULTI	68 | 4	0 | 0	0 | 0	16 | 4
FloM	AUB15	10 | 2	0 | 0	0 | 0	4 | 0
	MOR14	39 | 7	3 | 0	4 | 0	24 | 2
	VIL15	5 | 1	0 | 0	1 | 0	1 | 0
	SMH14	14 | 1	1 | 0	1 | 0	7 | 0
	SMH15	11 | 3	0 | 0	1 | 0	5 | 0
	CAU14	10 | 3	13 | 0	0 | 0	10 | 1
	CON15	20 | 5	0 | 0	2 | 0	11 | 0
	MULTI	13 | 7	0 | 0	0 | 0	4 | 1
Hum	AUB15	6 | 1	0 | 0	0 | 0	4 | 0
	MOR14	5 | 1	0 | 0	0 | 0	2 | 0
	VIL15	17 | 3	1 | 0	0 | 0	23 | 0
	SMH14	27 | 11	3 | 0	0 | 0	19 | 0
	SMH15	53 | 19	6 | 1	1 | 0	22 | 3
	CAU14	3 | 0	0 | 0	0 | 0	15 | 0
	CON15	22 | 0	0 | 0	0 | 0	2 | 0
	MULTI	0 | 0	0 | 0	0 | 0	18 | 0
GY	AUB15	21 | 1	12 | 0	12 | 1	16 | 0
	MOR14	22 | 2	0 | 0	0 | 0	7 | 0
	VIL15	9 | 5	3 | 0	6 | 0	11 | 0
	SMH14	2 | 0	13 | 0	0 | 0	8 | 0
	SMH15	3 | 1	2 | 0	0 | 0	5 | 0
	CAU14	1 | 0	0 | 0	0 | 0	0 | 0
	CON15	3 | 0	1 | 0	1 | 0	1 | 0
	MULTI	0 | 0	0 | 0	0 | 0	0 | 0

Number of significant markers identified for each trait and each environment in Het1. The first and second value are respectively for an FDR levels of 0.2 and 0.05. CAU14, AUB14, CON15, MOR14, VIL15, SMH14 and SMH15 indicate for Gso-MONO models. MULTI indicates for Gso-MULTI model.

S14 Table: Number of significant markers in Het2

Trait	Env	a	a_{DD}	a_{DF}	a_{FF}	s_a	t_a	d	d_{DD}	d_{DF}	d_{FF}	s_d	t_d	Δ_{LD}	o_a	o_d	g_{Het2}	g_{Het1}
FloF	JAR16	21 | 6	8 | 0	217 | 0	25 | 0	0 | 0	0 | 0	2 | 0	14 | 0	1 | 0	1 | 0	0 | 0	2 | 0	5 | 0	1275 | 0	9 | 1	652 | 89	271 | 0
	AUB17	31 | 2	6 | 1	252 | 0	24 | 0	0 | 0	1 | 0	1 | 0	82 | 0	28 | 1	2 | 0	0 | 0	0 | 0	0 | 0	161 | 0	4 | 0	207 | 3	395 | 1
	SOU17	5 | 0	18 | 10	64 | 0	26 | 0	0 | 0	0 | 0	11 | 0	30 | 0	14 | 0	8 | 2	0 | 0	0 | 0	0 | 0	705 | 0	18 | 7	366 | 28	83 | 0
	SMH16	9 | 0	5 | 3	172 | 0	4 | 0	0 | 0	5 | 0	1 | 0	34 | 0	5 | 0	2 | 0	0 | 0	12 | 0	1 | 0	557 | 0	0 | 0	332 | 42	206 | 0
	SMH17	13 | 0	65 | 0	132 | 0	8 | 0	0 | 0	2 | 0	3 | 0	130 | 0	14 | 1	21 | 6	0 | 0	0 | 0	1 | 0	647 | 0	5 | 1	490 | 22	215 | 0
	MULTI	6 | 4	0 | 0	373 | 52	0 | 0	2 | 0	38 | 0	0 | 0	30 | 0	225 | 122	1 | 0	0 | 0	0 | 0	375 | 129	13 | 0	61 | 0	132 | 0	439 | 178
FloM	JAR16	28 | 16	41 | 0	51 | 26	10 | 0	0 | 0	0 | 0	0 | 0	0 | 0	9 | 0	0 | 0	0 | 0	9 | 1	7 | 0	3602 | 1406	0 | 0	2449 | 702	56 | 1
	AUB17	35 | 8	80 | 1	14 | 3	33 | 0	0 | 0	0 | 0	7 | 7	1 | 0	67 | 0	0 | 0	0 | 0	88 | 71	2 | 1	828 | 43	0 | 0	561 | 43	17 | 1
	SOU17	12 | 1	25 | 0	16 | 3	64 | 14	0 | 0	0 | 0	0 | 0	0 | 0	11 | 0	2 | 2	0 | 0	1 | 0	1 | 0	1204 | 172	0 | 0	376 | 26	25 | 0
	SMH16	6 | 0	11 | 0	10 | 0	11 | 1	0 | 0	3 | 0	1 | 1	4 | 0	6 | 0	0 | 0	0 | 0	15 | 14	1 | 0	1551 | 233	0 | 0	585 | 63	5 | 0
	SMH17	8 | 0	2 | 0	23 | 1	5 | 0	0 | 0	0 | 0	0 | 0	2 | 0	0 | 0	0 | 0	0 | 0	13 | 11	12 | 0	720 | 67	0 | 0	299 | 37	13 | 0
	MULTI	15 | 6	0 | 0	168 | 0	0 | 0	29 | 0	0 | 0	0 | 0	9 | 0	122 | 3	0 | 0	0 | 0	0 | 0	145 | 0	2807 | 245	0 | 0	1694 | 244	23 | 4
Hum	JAR16	49 | 9	221 | 0	3 | 0	93 | 1	0 | 0	0 | 0	8 | 0	1 | 0	0 | 0	25 | 1	0 | 0	0 | 0	0 | 0	0 | 0	0 | 0	5 | 0	0 | 0
	AUB17	38 | 0	98 | 0	4 | 0	265 | 0	0 | 0	0 | 0	2 | 0	29 | 14	0 | 0	2 | 0	0 | 0	0 | 0	1 | 0	0 | 0	0 | 0	4 | 0	2 | 2
	SOU17	102 | 2	203 | 5	6 | 1	721 | 107	0 | 0	0 | 0	1 | 0	2 | 0	0 | 0	2 | 0	0 | 0	0 | 0	0 | 0	0 | 0	0 | 0	7 | 0	0 | 0
	SMH16	13 | 1	34 | 0	48 | 3	273 | 56	0 | 0	0 | 0	1 | 0	1 | 0	0 | 0	6 | 0	0 | 0	0 | 0	0 | 0	0 | 0	0 | 0	9 | 0	3 | 3
	SMH17	44 | 0	50 | 0	16 | 0	137 | 5	0 | 0	0 | 0	22 | 0	0 | 0	0 | 0	72 | 3	0 | 0	0 | 0	2 | 1	0 | 0	0 | 0	12 | 1	0 | 0
	MULTI	8 | 0	0 | 0	0 | 0	49 | 5	0 | 0	0 | 0	0 | 0	8 | 0	0 | 0	0 | 0	0 | 0	0 | 0	4 | 0	0 | 0	0 | 0	4 | 0	0 | 0
GY	JAR16	2 | 0	0 | 0	0 | 0	0 | 0	0 | 0	0 | 0	0 | 0	0 | 0	1 | 0	0 | 0	0 | 0	0 | 0	1 | 0	19 | 0	20 | 4	88 | 0	18 | 1
	AUB17	1 | 0	0 | 0	0 | 0	0 | 0	0 | 0	6 | 1	0 | 0	0 | 0	80 | 53	0 | 0	0 | 0	0 | 0	0 | 0	67 | 0	23 | 2	131 | 0	59 | 51
	SOU17	0 | 0	0 | 0	0 | 0	0 | 0	0 | 0	13 | 6	1 | 0	0 | 0	9 | 2	0 | 0	0 | 0	0 | 0	0 | 0	576 | 0	68 | 18	1110 | 0	6 | 1
	SMH16	0 | 0	0 | 0	0 | 0	0 | 0	0 | 0	117 | 111	0 | 0	0 | 0	20 | 4	0 | 0	0 | 0	0 | 0	0 | 0	43 | 0	277 | 125	400 | 0	27 | 0
	SMH17	12 | 0	0 | 0	0 | 0	0 | 0	1 | 0	13 | 2	0 | 0	0 | 0	8 | 0	0 | 0	0 | 0	0 | 0	0 | 0	19 | 0	431 | 163	1012 | 0	7 | 2
	MULTI	13 | 0	0 | 0	0 | 0	0 | 0	0 | 0	0 | 0	0 | 0	0 | 0	16 | 14	0 | 0	0 | 0	5 | 0	1 | 0	0 | 0	70 | 1	0 | 0	22 | 0

Number of significant markers identified for each trait and each environment in Het1. The first and second value are respectively for an FDR levels of 0.2 and 0.05. JAR16, AUB17, SOU17, SMH16 and SMH17 indicate for Gso-MONO models. MULTI indicates for Gso-MULTI model

S15 Table: Description of highlighted markers

	Markers	A		B		C		D		E		F	
		AX-91769326		AX-90974317		AX-91747122		AX-90921960		AX-90654883		AX-91003160	
	Chromosome	8		5		8		5		1		6	
	Physical position (Mbp)	130		205		9,3		5,1		18,2		102	
	p_D	0,31		0,28		0,38		0,54		0,56		0,37	
	p_F	0,38		0,53		0,53		0,31		0,39		0,45	
		-log(Pvalue)	**Effect**	**-log(Pvalue)**	**Effect**	**-log(Pvalue)**	**Effect**	**-log(Pvalue)**	**Effect**	**-log(Pvalue)**	**Effect**	**-log(Pvalue)**	**Effect**
Gso	g_{Het2}	3,435	-	3,453	-	4,204	-	2,994	-	1,626	-	5,201	-
	g_{Het1}	1,883	-	2,004	-	0,548	-	4,72	-	0,278	-	0,472	-
	a	5,467	-1,466	0,692	-0,395	1,632	0,728	0,566	-0,39	0,668	-0,369	0,8	-0,44
	a_{DD}	2,178	-1,618	0,556	-0,593	5,516	2,617	0,22	0,263	0,009	-0,013	2,114	-1,391
	a_{DF}	2,905	-1,401	0,614	-0,464	0,253	0,195	0,436	-0,364	0,625	-0,444	0,001	-0,001
	a_{FF}	2,113	-1,379	0,093	-0,128	0,496	-0,626	0,798	-1,069	0,67	-0,649	0,045	0,073
	s_a	0,115	-0,239	0,266	-0,465	4,013	3,243	0,827	1,332	0,432	0,636	1,185	-1,464
	t_a	0,068	0,097	0,082	-0,104	0,972	-0,801	0,026	0,039	0,099	-0,113	0,769	0,658
	d	0,987	0,582	6,055	1,663	0,262	-0,217	2,213	1,056	0,339	0,255	3,502	1,228
	d_{DD}	0,506	0,677	3,607	2,376	0,52	-0,758	0,194	-0,281	0,866	-0,886	1,775	1,518
	d_{DF}	0,426	-0,458	2,482	-1,436	0,496	0,403	5,946	-2,51	0,127	-0,155	0,282	0,27
	d_{FF}	0,491	0,612	1,281	1,176	0,318	0,51	0,612	0,939	1,614	1,497	3,49	2,435
	s_d	0,026	0,065	0,755	1,201	0,644	-1,268	0,663	-1,22	2,142	-2,383	0,496	-0,916
	t_d	0,106	-0,187	0,217	-0,34	0,174	-0,279	2,637	2,181	0,089	-0,151	3,396	-2,247
	Δ_{LD}	0,086	0,084	0,348	0,286	0,762	-0,463	0,753	0,585	0,286	-0,243	1,02	0,559
	o_a	0,883	0,58	0,229	-0,196	3,613	1,498	1,037	0,74	4,271	1,386	0,276	0,238
	o_d	0,02	0,03	0,041	0,053	0,284	-0,303	1,131	-0,969	0,11	0,127	6,607	2,48
Gad	α	6,2	-1,517	0,744	-0,368	0,656	0,35	0,104	-0,081	0,557	-0,323	1,444	-0,62
	δ	1,027	0,568	6,861	1,58	0,292	-0,207	2,434	0,955	0,13	0,109	1,555	0,705

Markers A and B represent QTLs identified with both Gad and Gso models, respectively for additivity and dominance. Markers C and D represent background specific effects in Gso model with no effect in Gad model. Markers E and F represent the origin effect on Gso model. Markers A, C and E represent additive effect. Markers B, D and F represent dominance effect. The frequencies p_D and p_F are respectively the SNP allelic frequencies in the Dent and the Flint group. Effect indicates the estimated value of the contrast tests.

S16 Table. Repartition of partial and overdominance markers.

Panel	Trait	Env	Contrast	Nb of significant dominance QTLs	% of overdominance QTLs	Ratio |d/a|			
						Min	Max	Mean	Sd
Het2	FloF	JAR16	d	2	100	2,06	3,93	3	1,32
		JAR16	d_{DD}	11	100	1,71	12,3	4,32	4,19
		JAR16	d_{DF}	1	100	2,87	2,87	2,87	-
		JAR16	d_{FF}	1	100	2,08	2,08	2,08	-
		AUB17	d_{DD}	29	100	1,17	18,5	3,54	3,01
		AUB17	d_{DF}	27	100	1,08	63	18,4	15,3
		SOU17	d	11	100	2,29	5,92	3,63	1,29
		SOU17	d_{DD}	24	100	1,69	10,6	4,91	2,66
		SOU17	d_{DF}	15	100	1,5	50,1	6,95	12,1
		SOU17	d_{FF}	13	100	2,08	8,83	5,09	2,94
		SMH16	d	2	100	14,9	47,6	31,2	23,1
		SMH16	d_{DD}	32	100	1,55	46,3	27,9	13,6
		SMH16	d_{DF}	5	100	1,96	349	73,6	154
		SMH16	d_{FF}	2	100	8,07	49,5	28,8	29,3
		SMH17	d	4	100	2,18	3,06	2,52	0,38
		SMH17	d_{DD}	119	100	1,04	147	6,6	23
		SMH17	d_{DF}	14	100	1,59	261	34,5	73,7
		SMH17	d_{FF}	39	100	1,28	123	10,7	19,8
		MULTI	d_{DD}	31	100	1,35	7,54	1,94	1,23
		MULTI	d_{DF}	236	100	0,95	1040	10,6	67,4
		MULTI	d_{FF}	1	100	2,62	2,62	2,62	-
	FloM	JAR16	d_{DF}	9	100	1,98	10,1	4,26	3,33
		AUB17	d	7	100	15,9	76,4	34,6	19,2
		AUB17	d_{DD}	1	100	3,3	3,3	3,3	-
		AUB17	d_{DF}	67	100	1,66	57,8	8,45	7,96
		SOU17	d_{DF}	11	100	1,03	42,3	7,88	11,7
		SOU17	d_{FF}	2	100	24,3	24,3	24,3	0
		SMH16	d	1	100	97,3	97,3	97,3	-
		SMH16	d_{DD}	4	100	2,48	2,48	2,48	0
		SMH16	d_{DF}	6	100	1,61	16,8	9,66	5,79
		SMH17	d_{DD}	2	100	1,64	2,23	1,94	0,42
		MULTI	d_{DD}	9	100	1,49	12,9	3,58	3,58
		MULTI	d_{DF}	123	100	1,24	9,32	7,08	1,45
	Hum	JAR16	d	8	100	4,14	10,1	4,89	2,09
		JAR16	d_{DD}	1	100	8,14	8,14	8,14	-
		JAR16	d_{FF}	25	100	1,38	77,9	4,98	15,4
		AUB17	d	2	100	2,47	4,35	3,41	1,32
		AUB17	d_{DD}	29	100	1,39	330	21,8	75,1
		AUB17	d_{FF}	2	100	5,44	23,2	14,3	12,5

		SOU17	d	1	100	20,2	20,2	20,2	-
		SOU17	d_{DD}	2	100	1,82	4,1	2,96	1,62
		SOU17	d_{FF}	2	100	3,53	6,25	4,89	1,92
		SMH16	d	1	100	4,82	4,82	4,82	-
		SMH16	d_{DD}	1	100	3,64	3,64	3,64	-
		SMH16	d_{FF}	6	100	1,2	4,69	2,18	1,27
		SMH17	d	22	100	1,26	91,4	6,07	19,1
		SMH17	d_{FF}	72	100	1,06	216	9,72	26,2
		MULTI	d_{DD}	8	100	5,11	5,11	5,11	0
		JAR16	d_{DF}	4	100	2,42	5,94	3,67	1,59
		AUB17	d_{DF}	107	100	1,24	3,39	2,15	0,455
		SOU17	d	1	100	211	211	211	-
	GY	SOU17	d_{DF}	78	100	1,42	111	22,1	20,6
		SMH16	d_{DF}	28	100	1,48	12,6	4,02	3,44
		SMH17	d_{DF}	9	100	5,13	7,46	5,57	0,712
		MULTI	d_{DF}	16	100	2,41	7,17	6,47	1,14
		AUB15	d_{DF}	5	100	1,41	6	3,14	1,7
		MOR14	d_{DF}	2	100	2,51	3,05	2,78	0,382
		VIL15	d_{DF}	21	100	1,74	64,2	4,71	13,6
	FloF	SMH14	d_{DF}	2	100	1,29	3,45	2,37	1,53
		SMH15	d_{DF}	1	100	7,73	7,73	7,73	-
		CAU14	d_{DF}	13	100	1,8	3,76	2,1	0,542
		CON15	d_{DF}	5	100	1,11	28,9	7,92	11,9
		MOR14	d_{DF}	3	100	1,11	1,61	1,33	0,255
Het1	FloM	SMH14	d_{DF}	1	100	2,94	2,94	2,94	-
		CAU14	d_{DF}	13	100	1,07	3,16	1,8	0,527
		VIL15	d_{DF}	1	100	14,6	14,6	14,6	-
	Hum	SMH14	d_{DF}	3	100	1,15	1,79	1,58	0,37
		SMH15	d_{DF}	6	100	1,19	1,7	1,33	0,204
		AUB15	d_{DF}	12	100	1,07	23,1	3,47	6,2
		VIL15	d_{DF}	3	100	1,8	1,8	1,8	0
	GY	SMH14	d_{DF}	13	100	1,49	13,7	3,37	4,59
		SMH15	d_{DF}	2	100	2,69	2,91	2,8	0,154
		CON15	d_{DF}	1	100	2,01	2,01	2,01	-

Number of significant dominance QTLs for each panel, trait and environment. The percentage of overdominance QTLs is the proportion of dominance QTLs with a ratio |d/a| superior to 1.

S17 Table: QTL stability across environments in Het1

Contrast	Trait	Tot	Gso-MULTI only	Gso-MULTI and Gso-MONO							Gso-MONO only						
				1	2	3	4	5	6	7	1	2	3	4	5	6	7
	FloF	63	0	42	6	2	1	0	0	0	6	1	2	2	0	1	0

Additivity	FloM	36	0	30	3	0	0	0	0	0	0	1	0	0	0	1	1
	Hum	63	0	62	1	0	0	0	0	0	0	0	0	0	0	0	0
	GY	22	0	22	0	0	0	0	0	0	0	0	0	0	0	0	0
Dominance	FloF	19	0	18	1	0	0	0	0	0	0	0	0	0	0	0	0
	FloM	8	0	8	0	0	0	0	0	0	0	0	0	0	0	0	0
	Hum	7	0	7	0	0	0	0	0	0	0	0	0	0	0	0	0
	GY	13	0	13	0	0	0	0	0	0	0	0	0	0	0	0	0

"Contrast" terms correspond respectively to the Additivity (a_{DF}) and the Dominance (d_{DF}) QTLs. "Gso-MONO" counts for the number of times a QTL has been observed in single environments models. "Gso-MULTI and Gso-MONO" counts for the number of times a QTL has been observed in single environment and multiple environment models. "Gso-MULTI" only refers to QTLs only identified with multiple environment model. "Total" indicates the total number of QTLs. The nominal FDR level is fixed at 0.2.

S18 Table. Correlation of additive effect between Gad and Gso.

Panel	Trait	Env	$cor(a, \alpha)$	$cor(d, \delta)$	$cor(Pval_a, Pval_\alpha)$	$cor(Pval_d, Pval_\delta)$
Het1	FloF	AUB15	0.998	0.939	0.992	0.852
		MOR14	0.997	0.946	0.989	0.867
		VIL15	0.997	0.942	0.991	0.848
		SMH14	0.997	0.944	0.99	0.86
		SMH15	0.997	0.943	0.991	0.861
		CAU14	0.997	0.946	0.989	0.864
		CON15	0.998	0.945	0.992	0.86
		MULTI	0.995	0.928	0.987	0.851
	FloM	AUB15	0.998	0.944	0.992	0.86
		MOR14	0.998	0.941	0.992	0.854
		VIL15	0.998	0.942	0.992	0.85
		SMH14	0.998	0.947	0.991	0.863
		SMH15	0.998	0.946	0.992	0.862
		CAU14	0.997	0.946	0.99	0.865
		CON15	0.997	0.943	0.991	0.856
		MULTI	0.996	0.93	0.988	0.856
	Hum	AUB15	0.997	0.938	0.989	0.846
		MOR14	0.998	0.941	0.992	0.852
		VIL15	0.998	0.936	0.992	0.841
		SMH14	0.997	0.944	0.991	0.858
		SMH15	0.998	0.941	0.994	0.852
		CAU14	0.998	0.939	0.993	0.846
		CON15	0.998	0.944	0.993	0.855
		MULTI	0.993	0.93	0.984	0.849
	GY	AUB15	0.998	0.934	0.994	0.835
		MOR14	0.999	0.939	0.995	0.848
		VIL15	0.998	0.935	0.994	0.833
		SMH14	0.999	0.946	0.995	0.855
		SMH15	0.999	0.942	0.996	0.86
		CAU14	0.999	0.945	0.995	0.852

		CON15	0.999	0.936	0.994	0.843
		MULTI	0.997	0.933	0.991	0.848
Het2	FloF	AUB15	0.998	0.939	0.992	0.852
		MOR14	0.997	0.943	0.99	0.861
		VIL15	0.997	0.942	0.991	0.848
		SMH14	0.997	0.946	0.991	0.859
		SMH15	0.997	0.943	0.991	0.861
		CAU14	0.996	0.948	0.989	0.866
		CON15	0.998	0.945	0.992	0.86
		MULTI	0.995	0.928	0.987	0.851
	FloM	AUB15	0.998	0.944	0.992	0.86
		MOR14	0.998	0.941	0.992	0.854
		VIL15	0.998	0.942	0.992	0.85
		SMH14	0.998	0.947	0.991	0.863
		SMH15	0.998	0.946	0.992	0.862
		CAU14	0.997	0.946	0.99	0.865
		CON15	0.997	0.943	0.991	0.856
		MULTI	0.996	0.93	0.988	0.856
	Hum	AUB15	0.997	0.938	0.989	0.846
		MOR14	0.998	0.941	0.992	0.852
		VIL15	0.998	0.936	0.992	0.841
		SMH14	0.997	0.944	0.991	0.858
		SMH15	0.998	0.941	0.994	0.852
		CAU14	0.998	0.939	0.993	0.846
		CON15	0.998	0.944	0.993	0.855
		MULTI	0.993	0.93	0.984	0.849
	GY	AUB15	0.998	0.934	0.994	0.835
		MOR14	0.999	0.939	0.995	0.848
		VIL15	0.998	0.935	0.994	0.833
		SMH14	0.999	0.946	0.995	0.855
		SMH15	0.999	0.942	0.996	0.86
		CAU14	0.999	0.945	0.995	0.852
		CON15	0.999	0.936	0.994	0.843
		MULTI	0.997	0.933	0.991	0.848

$cor(\alpha, a)$ (or $cor(\delta, \mathrm{d})$) indicates the correlation between additive effects α and a (or between dominance effects δ and d). $cor(Pval_{\alpha}, Pval_{a})$ indicates the correlation between additive Pvalues for effects α and a (and between dominance effects δ and d). All correlations are calculated over all candidate markers for each panel, trait and environment.