

AdditionalFile5. Variance component estimation results from bivariate analysis for simulated and real data for the trait polledness.

Table 1. Estimated variance components for the trait polledness from bivariate models for real data (performance and reproduction traits).

Trait	Model	σ_a^2	σ_v^2	σ_e^2	QTL- h^2	h^2 (SE) (polygenic + QTL)
MY	<i>Basic</i> ^(bivariate)	0.191		0.025		0.884 (0.031)
	<i>QTL</i> ^(bivariate)	0.800e-06	0.032	0.132e-07	1.000	1.000 (0.040)
F%	<i>Basic</i> ^(bivariate)	0.191		0.025		0.883 (0.031)
	<i>QTL</i> ^(bivariate)	0.146e-06	0.032	0.292e-09	1.000	1.000 (0.041)
P%	<i>Basic</i> ^(bivariate)	0.191		0.025		0.883 (0.031)
	<i>QTL</i> ^(bivariate)	0.105e-06	0.011	0.591e-09	1.000	1.000 (0.039)
SCS	<i>Basic</i> ^(bivariate)	0.191		0.025		0.883 (0.031)
	<i>QTL</i> ^(bivariate)	0.252e-06	0.032	0.507e-06	1.000	1.000 (0.041)
NRR-56	<i>Basic</i> ^(bivariate)	0.191		0.025		0.883 (0.031)
	<i>QTL</i> ^(bivariate)	0.148e-06	0.032	0.476e-08	1.000	1.000 (0.041)
DFS*	<i>Basic</i> ^(bivariate)	0.191		0.025		0.883 (0.031)
	<i>QTL</i> ^(bivariate)	/	0.032	0.187e-08	1.000	1.000 (0.002)
DO	<i>Basic</i> ^(bivariate)	0.190		0.026		0.880 (0.031)
	<i>QTL</i> ^(bivariate)	0.158e-06	0.032	0.485e-08	1.000	1.000 (0.041)

σ_a^2 = additive genetic variance based on A , σ_v^2 = additive genetic variance based on A_v , σ_e^2 = residual variance, QTL- h^2 = QTL heritability calculated as $\sigma_v^2 / (\sigma_a^2 + \sigma_v^2 + \sigma_e^2)$, h^2 (SE) = overall heritability and standard error (in brackets) calculated as $\sigma_v^2 + \sigma_a^2 / (\sigma_a^2 + \sigma_v^2 + \sigma_e^2)$, *The full bivariate model including A and A_v for the trait DFS did not fully converge. Therefore, we present the results for a model excluding A in the model for polledness.

Table 2. Estimated variance components for the trait polledness from bivariate models for all simulated scenarios.

Trait h ² 0.30	Model	σ_a^2	σ_v^2	σ_e^2	QTL-h ²	h^2 (SE) (polygenic + QTL)
QTL-h ² = 0.1	<i>Basic</i> ^(bivariate)	0.752		0.003		0.996 (0.022)
	<i>QTL</i> ^(bivariate)	0.001e-07	0.569	0.722e-04	1.000	1.000 (0.015)
QTL-h ² = 0.05	<i>Basic</i> ^(bivariate)	0.862		0.002		0.997 (0.027)
	<i>QTL</i> ^(bivariate)	0.002e-06	0.696	0.503e-04	1.000	1.000 (0.053)
QTL-h ² = 0.025	<i>Basic</i> ^(bivariate)	0.945		0.001		0.999 (0.024)
	<i>QTL</i> ^(bivariate)	0.003e-07	0.766	0.968e-06	1.000	1.000 (0.018)
Trait h ² 0.05	Model	σ_a^2	σ_v^2	σ_e^2	QTL-h ²	h^2 (SE) (polygenic + QTL)
QTL-h ² = 0.025	<i>Basic</i> ^(bivariate)	0.944		0.002		0.998 (0.017)
	<i>QTL</i> ^(bivariate)	0.001e-05	0.772	0.396e-04	1.000	1.000 (0.011)
QTL-h ² = 0.01	<i>Basic</i> ^(bivariate)	0.757		0.727e-03		0.999 (0.016)
	<i>QTL</i> ^(bivariate)	0.001e-07	0.585	0.630e-04	1.000	1.000 (0.012)

σ_a^2 = additive genetic variance based on A , σ_v^2 = additive genetic variance based on A_v , σ_e^2 = residual variance, $QTL-h^2$ = QTL heritability calculated as $\sigma_v^2 / (\sigma_a^2 + \sigma_v^2 + \sigma_e^2)$, h^2 (SE) = overall heritability and standard error (in brackets) calculated as $(\sigma_a^2 + \sigma_v^2) / (\sigma_a^2 + \sigma_v^2 + \sigma_e^2)$.