A. ANOVA results N=800 populations

Table 1: ANOVA degrees of freedom (df), and F-statistics with significance of the MPP design, the number of parents, the QTL detection model, the QTL size and the QTL effect on TPR per QTL genetic model (cross-specific, parental, ancestral, bi-allelic, and MQE) for the N = 800 populations. Adjusted and cross-validation R2 of the models.

	df	Cr. sp.		Parental		Ancestral		Bi-allelic		MQE	
MPP des	3	91.9	***	2.6		1.4		3.4	*	15.6	***
Nb. par	1	188.6	***	131.8	***	37	***	22.4	***	97	***
Det. model	3	75.5	***	8.9	***	87.4	***	99	***	5	**
QTL size	1	693.3	***	845.1	***	1372.9	***	1167.8	***	824	***
QTL type	$0-3^a$	8.5	**	0		0				10.9	***
MPP des x Nb. par	3	9.7	***	1.8		1.3		0.1		3.4	*
MPP des x Det. model	9	4.5	***	1.2		1.9		1.5		0.5	
MPP des x QTL size	3	2.4		3.1	*	11.2	***	0.8		0.3	
Nb. par x Det. model	3	3.2	*	2.5		13.9	***	13.3	***	2.3	
Nb. par x QTL size	1	5.3	*	22	***	1.1		1.4		3.5	
Det. model x QTL size	3	22	***	6.3	***	17.8	***	17.3	***	0.2	
Residuals	$94-97^a$										
adj. R2 (%)		92		89		93		96		67	
CV R2 (%)		90		85		91		92		65	

* $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$

a. The df of the QTL type term is equal to 1, 1, 1, 0, 3 from the Cr. sp. to the MQE genetic model. The df of the residuals change according to the df of the QTL type term.

B. ANOVA results N=1600 populations

Table 2: ANOVA degrees of freedom (df), and F-statistics with significance of the MPP design, the number of parents, the QTL detection model, the QTL size and the QTL effect on TPR per QTL genetic model (cross-specific, parental, ancestral, bi-allelic, and MQE) for the N = 1600 populations. Adjusted and cross-validation R2 of the models.

	df	Cr. sp.		Parental		Ancestral		Bi-allelic		MQE	
MPP des	3	44.8	***	1		4.4	**	0.8		4.4	**
Nb. par	1	69.6	***	4.5	*	0		1.6		13.2	***
Det. model	3	122.2	***	9.6	***	113	***	125	***	0.3	
QTL size	1	328.3	***	623.8	***	2614.8	***	2217.6	***	952.7	***
QTL type	$0-3^a$	28.2	***	17.1	***	13	***			10.9	***
MPP des x Nb. par	3	19.9	***	0.5		4.5	**	4	*	5.9	***
MPP des x Det. model	9	5.9	***	1		5.5	***	3.5	**	0.3	
MPP des x QTL size	3	4.9	**	0.1		0.4		0.5		1.9	
Nb. par x Det. model	3	8.9	***	1		17.6	***	16.5	***	1.3	
Nb. par x QTL size	1	17.3	***	28.7	***	242.9	***	54.9	***	44.7	***
Det. model x QTL size	3	2.6		8.2	***	22.7	***	20	***	6.8	***
Residuals	$94-97^a$										
adj. R2 (%)		89		85		96		98		69	
CV R2 (%)		85		80		95		95		66	

* $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$

a. The df of the QTL type term is equal to 1, 1, 1, 0, 3 from the Cr. sp. to the MQE genetic model. The df of the residuals change according to the df of the QTL type term.