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