Table S3

Table S3: : **Marker-based estimation of heritability: width and coverage confidence intervals obtained from the individual plant data and the genotypic means.** Results for broad sense heritability intervals are reported for comparison. We simulated 5000 traits, for random samples of 200 accessions drawn from the Swedish regmap (top) and French (bottom). 20 unlinked QTLs were simulated, which explained 50 percent of the genetic variance. The simulated heritability was 0.2, 0.5 and 0.8.

	coverage	interval width
Swedish regmap		
$h^2 = 0.2$		
broad-sense	0.912	0.178
replicates (standard)	0.933	0.188
replicates (log-transformed)	0.961	0.189
means (standard)	0.899	0.381
means (log-transformed)	0.968	0.405
$h^2 = 0.5$		
broad-sense	0.864	0.160
replicates (standard)	0.946	0.176
replicates (log-transformed)	0.950	0.175
means (standard)	0.921	0.594
means (log-transformed)	0.970	0.560
$h^2 = 0.8$		
broad-sense	0.823	0.085
replicates (standard)	0.945	0.088
replicates (log-transformed)	0.947	0.088
means (standard)	0.960	0.635
means (log-transformed)	0.938	0.748
French regmap		
$h^2 = 0.2$		
broad-sense	0.929	0.178
replicates (standard)	0.941	0.184
replicates (log-transformed)	0.962	0.185
means (standard)	0.898	0.396
means (log-transformed)	0.960	0.431
$h^2 = 0.5$		
broad-sense	0.898	0.160
replicates (standard)	0.953	0.173
replicates (log-transformed)	0.956	0.171
means (standard)	0.927	0.619
means (log-transformed)	0.976	0.585
$h^2 = 0.8$		
broad-sense	0.866	0.084
replicates (standard)	0.947	0.088
replicates (log-transformed)	0.947	0.088
means (standard)	0.966	0.652
means (log-transformed)	0.948	0.767