File S4: Simulation results for a different genetic architecture.

Table 1: **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 the Structured regmap and Hapmap. A single QTL was simulated, which explained 90 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
Structured regmap			
$h^2 = 0.2$			
broad-sense (H^2)	-0.00127	0.04787	1.00000
replicates (h_r^2)	-0.00066	0.05102	1.06585
means (h_m^2)	0.00782	0.08626	1.80191
$h^2 = 0.5$			
broad-sense (H^2)	-0.00279	0.04500	1.00000
replicates (h_r^2)	-0.00571	0.07001	1.55569
means (h_m^2)	0.01295	0.16461	3.65791
$h^2 = 0.8$			
broad-sense (H^2)	-0.00257	0.02458	1.00000
replicates (h_r^2)	-0.01163	0.05404	2.19850
means (h_m^2)	0.00337	0.20855	8.48496
Hapmap			
$h^2 = 0.2$			
broad-sense (H^2)	-0.00110	0.04344	1.00000
replicates (h_r^2)	-0.00098	0.04320	0.99453
means (h_m^2)	0.06629	0.26168	6.02448
$h^2 = 0.5$			
broad-sense (H^2)	-0.00123	0.03437	1.00000
replicates (h_r^2)	-0.00187	0.03736	1.08695
means (h_m^2)	0.03062	0.33527	9.75477
$h^2 = 0.8$			
broad-sense (H^2)	-0.00027	0.01633	1.00000
replicates (h_r^2)	-0.00106	0.02029	1.24235
means (h_m^2)	-0.07852	0.33486	20.50621

Table 2: **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 structured regmap (top) and Hapmap (bottom). A single QTL was simulated, which explained 90 percent of the genetic variance. The simulated heritability was 0.2, 0.5 and 0.8.

	coverage	interval width
Structured regmap		
$h^2 = 0.2$		
broad-sense	0.940	0.178
replicates (standard)	0.945	0.201
replicates (log-transformed)	0.962	0.202
means (standard)	0.911	0.315
means (log-transformed)	0.960	0.321
$h^2 = 0.5$		
broad-sense	0.926	0.160
replicates (standard)	0.837	0.194
replicates (log-transformed)	0.847	0.192
means (standard)	0.814	0.446
means (log-transformed)	0.886	0.427
$h^2 = 0.8$		
broad-sense	0.914	0.084
replicates (standard)	0.674	0.097
replicates (log-transformed)	0.666	0.097
means (standard)	0.714	0.437
means (log-transformed)	0.840	0.547
Hapmap		
$h^2 = 0.2$		
broad-sense	0.961	0.178
replicates (standard)	0.961	0.181
replicates (log-transformed)	0.972	0.182
means (standard)	0.807	0.537
means (log-transformed)	0.899	0.675
$h^2 = 0.5$		
broad-sense	0.979	0.160
replicates (standard)	0.971	0.164
replicates (log-transformed)	0.975	0.163
means (standard)	0.800	0.766
means (log-transformed)	0.967	0.819
$h^2 = 0.8$		
broad-sense	0.990	0.084
replicates (standard)	0.963	0.085
replicates (log-transformed)	0.964	0.085
means (standard)	0.820	0.840
means (log-transformed)	0.849	0.903

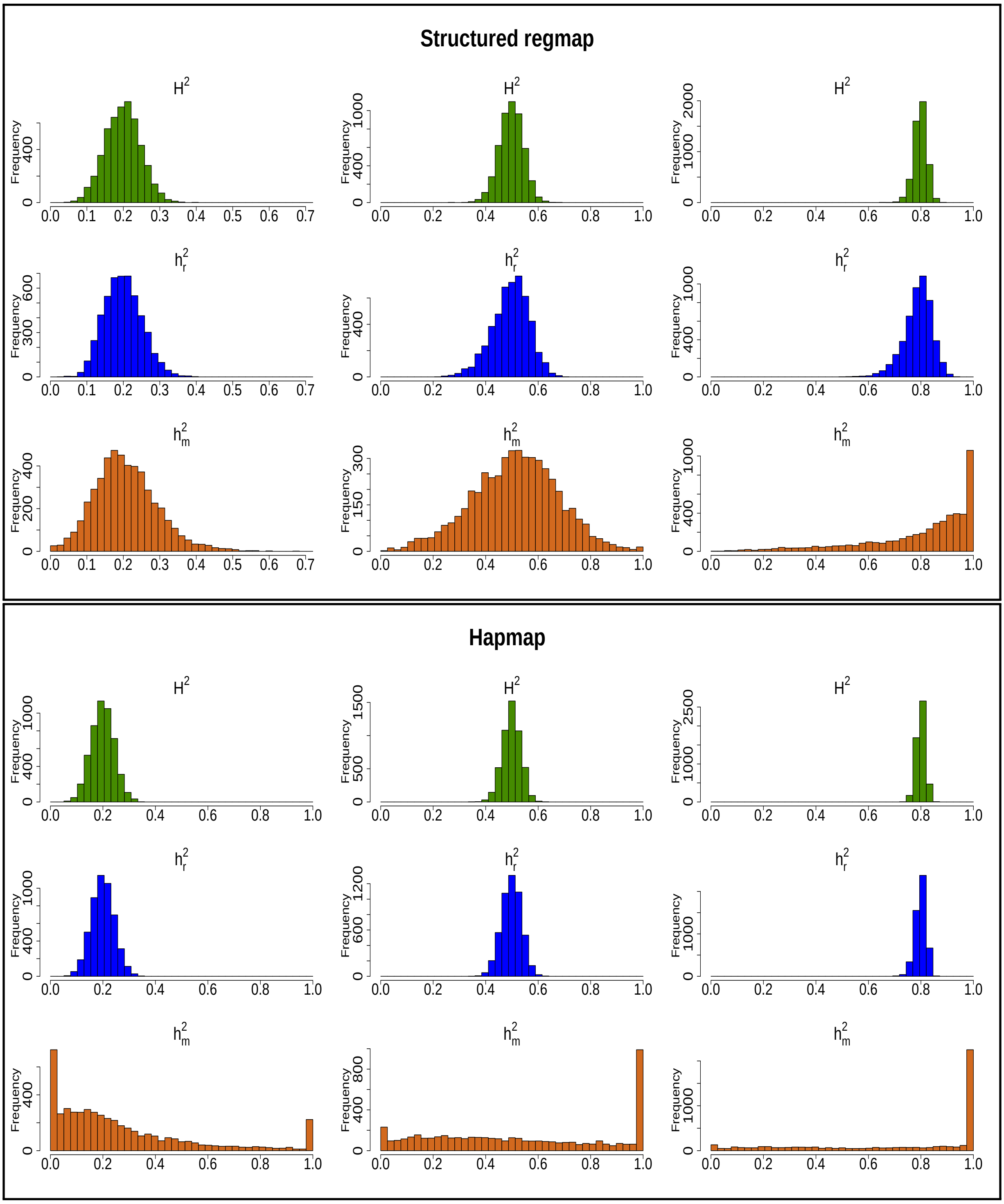

Figure 1: **Heritability estimates for 5000 simulated traits for random samples of 200 accessions drawn from the Structured regmap (top panel) and the Hapmap (bottom panel).** 1 QTL was simulated, which explained 90% of the genetic variance. The simulated heritability was 0.2 (left column), 0.5 (middle column) and 0.8 (right column). Within each panel, the first row shows the ANOVA-based estimates of broad-sense heritability, the second row the mixed model based estimates based on the individual data, and the third row the mixed model based estimates based on genotypic means.