Figure S3

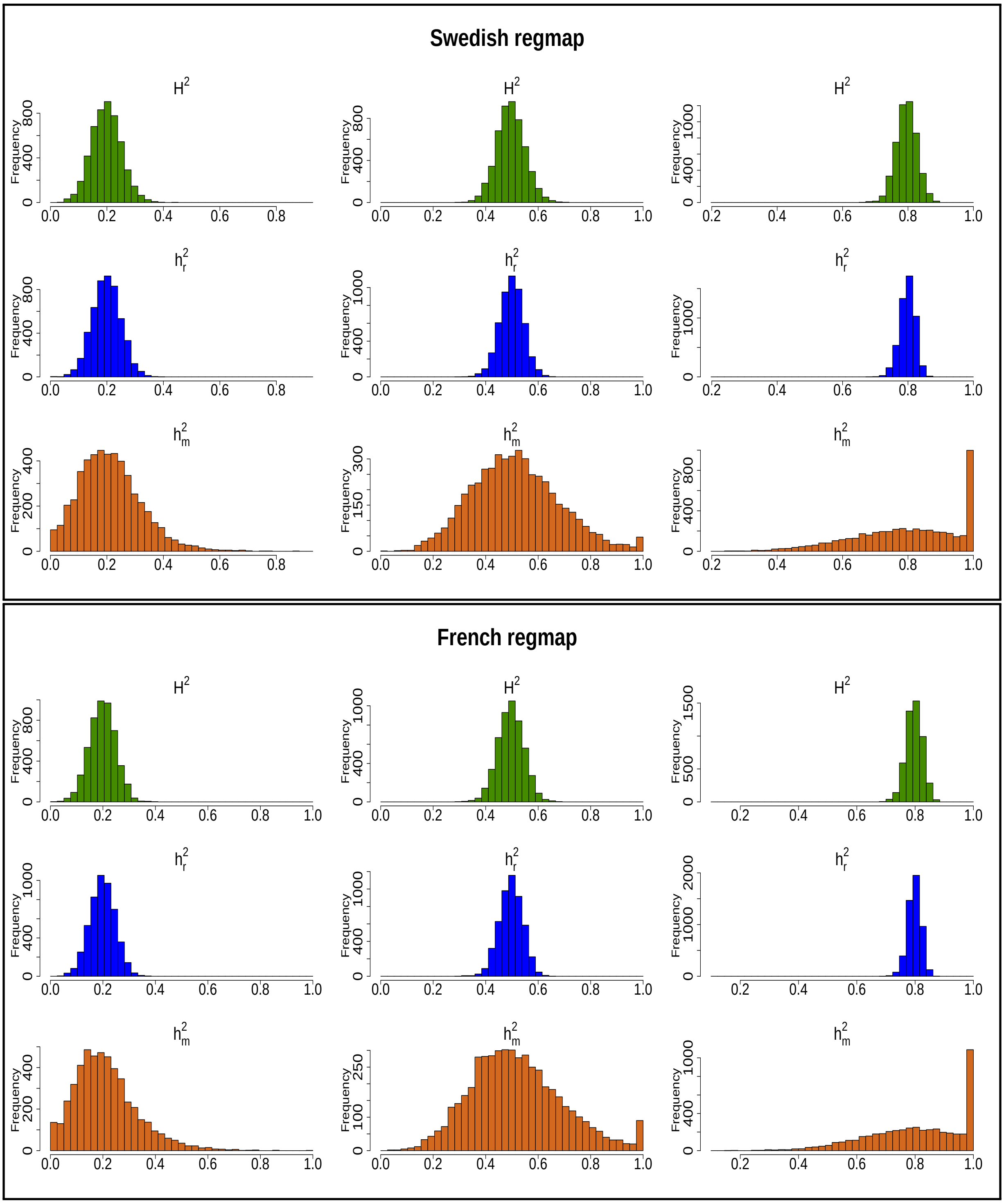

Figure S3 : **Heritability estimates for 5000 simulated traits for random samples of 200 accessions drawn from the Swedish regmap (top panel) and the French regmap (bottom panel).** 20 QTLs were simulated, which explained half of the genetic variance. The simulated heritability was 0.2 (left column), 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.