Figure S7

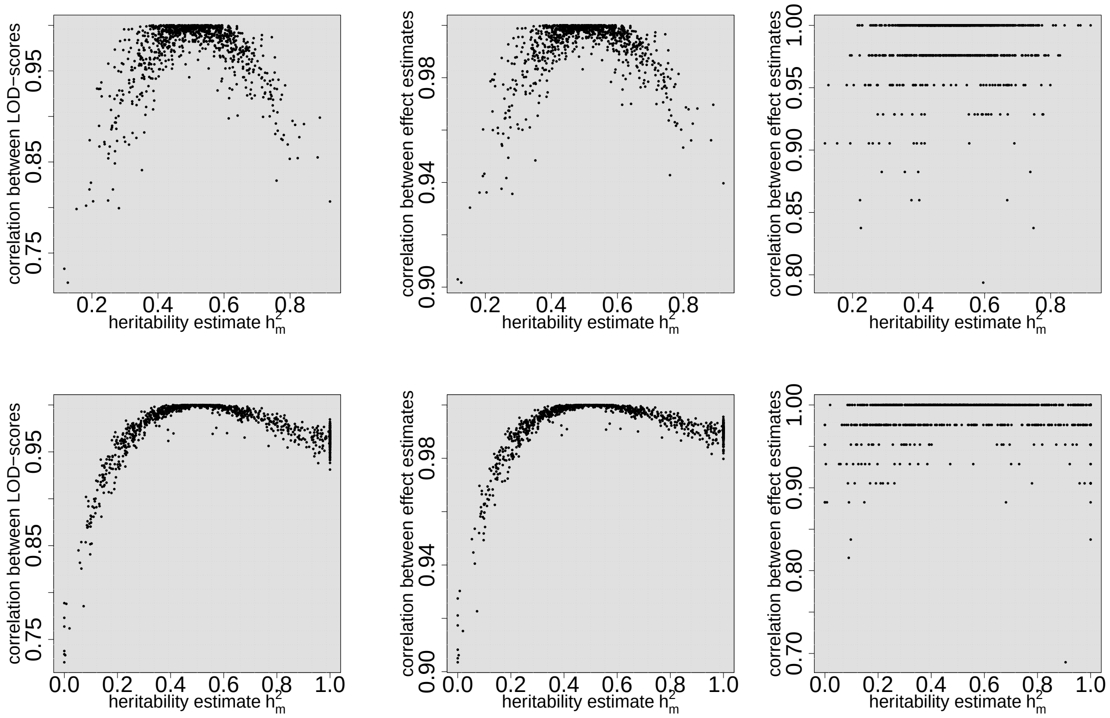

Figure S7 : **Rank correlation (Spearman ρ^2) between effect-size estimates obtained with a one- and two-stage approach, versus the heritability estimates obtained in the two-stage approach ($\hat{h}_m^2$).** 1000 traits were simulated for the Structured RegMap (first row) and the HapMap (second row), with a simulated heritability of 0.5. 10 QTLs were simulated, which explained 75% of the genetic variance. Left column: rank correlation between LOD-scores of all SNPs. Middle column: rank correlation between effect-size estimates for all SNPs. Right column: rank correlation between effect-size estimates for the 10 simulated QTLs.