Figure S4 – Miami plot of marginal additive effects in genome-wide associations studies (GWAS). Open circles: $-\log_{10}(p)$ values for SNP effect in GWAS models (p: p-value from Wald tests); increasing size refers to lower FDR, as estimated by the method of Benjamini and Hochberg (1995). Lines: Pr(QTL), posterior inclusion probability from BSLMM.