Figure S.5: Heat-map of the signals detected by each method in the third simulated example, SIM3, and averaged across the 25 replicates. In M-SPLS the significant (non-significant) transcript-marker association is recoded as 1 (0). From top to bottom, left to right: HESS, M-SPLS, MOM and BAYES. The symbol 'G' in the y-axis identifies groups of transcripts that are influenced by the same pattern of markers. Red triangles indicate where the hot-spots have been simulated.