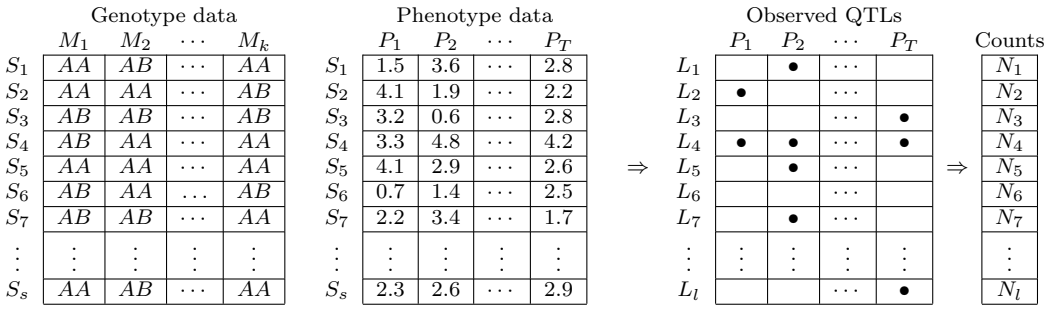

Figure S1 Hotspot analysis in a genetical genomics study. The data is composed by genotypes and phenotypes on s subjects, $S_1, \ldots, S_s$, from a segregating population. The genotype data is composed by the genotypes of k markers, $M_1, \ldots, M_k$. The phenotype data is composed by measurements on T quantitative phenotypes, $P_1, \ldots, P_T$. The output of the analysis is a QTL matrix, where rows represent l genomic positions, $L_1, \ldots, L_l$, and columns the phenotypes. A significant QTL is represented by a bullet, for example, phenotype P_1 maps to QTLs located at the L_2 and L_4 genomic positions. For each genomic position, $L_1, \ldots, L_l$, we count the number of significant QTLs, $N_1, \ldots, N_l$. We say we detected a significant hotspot at a genomic location, L_j, when the respective count, N_j, is higher than what is expected by chance at a pre-determined genome wide error rate.