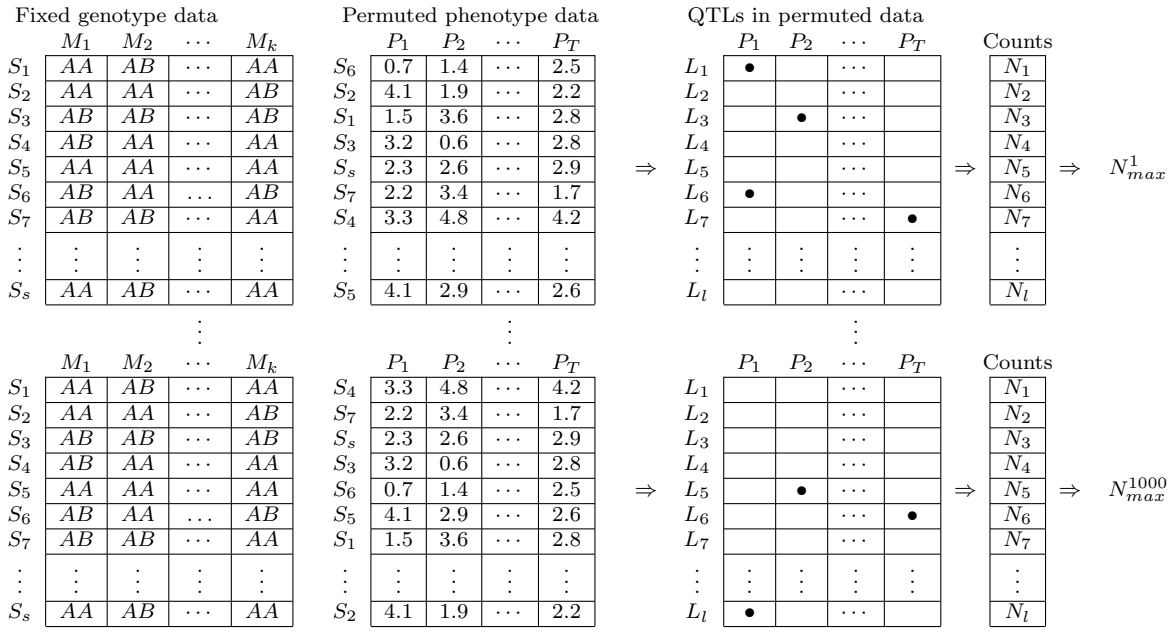

Figure S3 A permutation scheme that preserves the correlation among the phenotypes. Breitling et al. (2008) proposed a permutation scheme where the rows of the phenotype data matrix are permuted, while the genotype data matrix is kept intact. The idea is to break the connection between the genotype and phenotype data, but to preserve the correlation structure among the phenotypes. The permutation null distribution of hotspot sizes is derived as follows. For each one of the, say 1000, permutations we: (i) permute the rows of the phenotype data matrix, while keeping the genotype data intact (note the different row orderings of the permuted phenotype data matrices in relation to original phenotype matrix in Figure 1); (ii) perform mapping analysis of the T phenotypes, using a predetermined LOD threshold, λ, to determine a new QTL matrix (note that all QTLs detected with the permuted data are false positives); (iii) for each genomic location $L_1, \ldots, L_l$ we record the number of QTLs, $N_1, \ldots, N_l$; (iv) we record the maximum count $N^{per}_{max} = \max\{N_1, \ldots, N_l\}$. The permutation null distribution for the chosen λ threshold is then given by the distribution of the 1,000 N^{per}_{max} values.