



**Figure S2** Permutation scheme adopted by West et al. (2007) and Wu et al. (2008). In this permutation scheme we take the QTL matrix and, for each fixed phenotype (column in the QTL matrix), we permute the QTL locations (the row cells at each fixed column). This figure depicts the result of two permutations of the observed QTL matrix. The permutation null distribution of hotspot sizes is derived as follows. For each one of the, say 1000, permutations we: (i) permute the genomic positions of the QTLs for each one of the phenotypes separately; (ii) for each genomic location we record the number of QTLs; (iii) record the maximum count  $N_{max}^{per}$ . The permutation null distribution (for the  $\lambda$  threshold used to derive the observed QTL matrix) is then given by the distribution of the 1,000  $N_{max}^{per}$  values.