

Genotype data					Phenotype data					Observed QTLs					Counts
	$M_1$	$M_2$	$\dots$	$M_k$		$P_1$	$P_2$	$\dots$	$P_T$		$P_1$	$P_2$	$\dots$	$P_T$	
$S_1$	AA	AB	$\dots$	AA	$S_1$	1.5	3.6	$\dots$	2.8	$L_1$		•	$\dots$		$N_1$
$S_2$	AA	AA	$\dots$	AB	$S_2$	4.1	1.9	$\dots$	2.2	$L_2$	•		$\dots$		$N_2$
$S_3$	AB	AB	$\dots$	AB	$S_3$	3.2	0.6	$\dots$	2.8	$L_3$			$\dots$	•	$N_3$
$S_4$	AB	AA	$\dots$	AA	$S_4$	3.3	4.8	$\dots$	4.2	$L_4$	•	•	$\dots$	•	$N_4$
$S_5$	AA	AA	$\dots$	AA	$S_5$	4.1	2.9	$\dots$	2.6	$L_5$		•	$\dots$		$N_5$
$S_6$	AB	AA	$\dots$	AB	$S_6$	0.7	1.4	$\dots$	2.5	$L_6$			$\dots$		$N_6$
$S_7$	AB	AB	$\dots$	AA	$S_7$	2.2	3.4	$\dots$	1.7	$L_7$		•	$\dots$		$N_7$
$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$
$S_s$	AA	AB	$\dots$	AA	$S_s$	2.3	2.6	$\dots$	2.9	$L_l$			$\dots$	•	$N_l$

**Figure S1** Hotspot analysis in a genetical genomics study. The data is composed by genotypes and phenotypes on  $s$  subjects,  $S_1, \dots, S_s$ , from a segregating population. The genotype data is composed by the genotypes of  $k$  markers,  $M_1, \dots, M_k$ . The phenotype data is composed by measurements on  $T$  quantitative phenotypes,  $P_1, \dots, P_T$ . The output of the analysis is a QTL matrix, where rows represent  $l$  genomic positions,  $L_1, \dots, L_l$ , 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,  $L_1, \dots, L_l$ , we count the number of significant QTLs,  $N_1, \dots, N_l$ . 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.