a

b

Figure S3. Heat maps for a two-dimensional genome scan with a two-QTL model in MoK-F2

(**a**) RDR50, (**b**) RDR70. Upper left triangle: maximum LOD score for the interaction model. Lower right triangle: maximum LOD score for the full model (two QTLs plus an interaction). Color-coded scale indicates values for the interaction model (LOD threshold = 6.10 in RDR50 and 5.93 in RDR70) on the left, and the full model (LOD threshold = 8.80 in RDR50 and 9.05 in RDR70) on the right.