



Figure S7. Heat maps for a two-dimensional genome scan with a two-QTL model in TaK-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 scales indicate the values for the interaction model on the left (LOD threshold = 6.36 for RDR50 and 6.24 for RDR70), and the full model on the right (LOD threshold = 9.13 for RDR50 and 9.34 for RDR70).