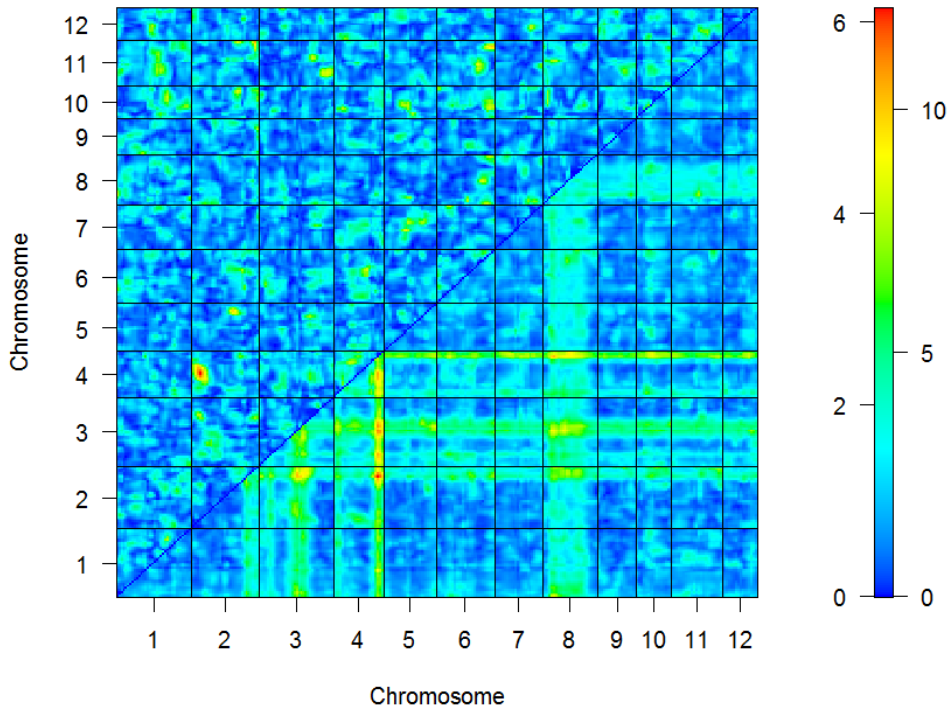
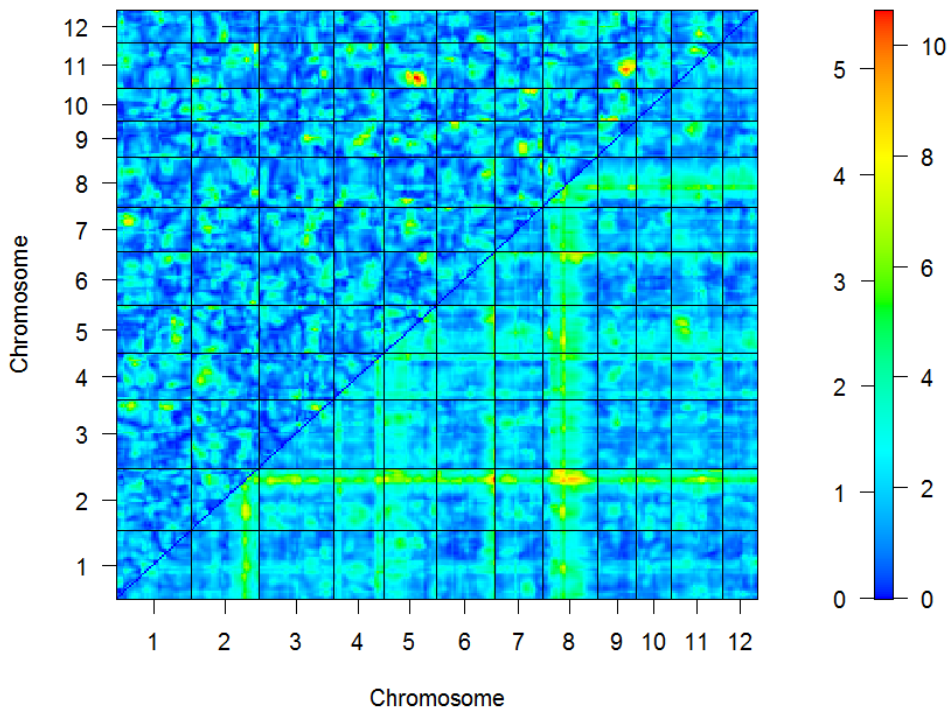


**a****b**

**Figure S5. Heat maps for a two-dimensional genome scan with a two-QTL model in YuK-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 = 5.57 for RDR50 and 5.81 for RDR70), and the full model on the right (LOD threshold = 8.51 for RDR50 and 8.89 for RDR70).