



Figure S5 QTL detection power and distribution of genetic effects in simulation and real data. (A) The statistical power for population sizes of 100 (green), 500 (purple), 1,000 (blue) and 4,000 (red) F_2 individuals at a genome-wide significance threshold. The solid curves indicate detection power for additive QTL, the wide dashed curves indicate detection power for dominant QTL and the narrow dashed curves indicate detection power for QTL-QTL interactions. (B) The distribution of genetic effects and power to detect them using the mapping population of 3,756 F_2 individuals in this study.