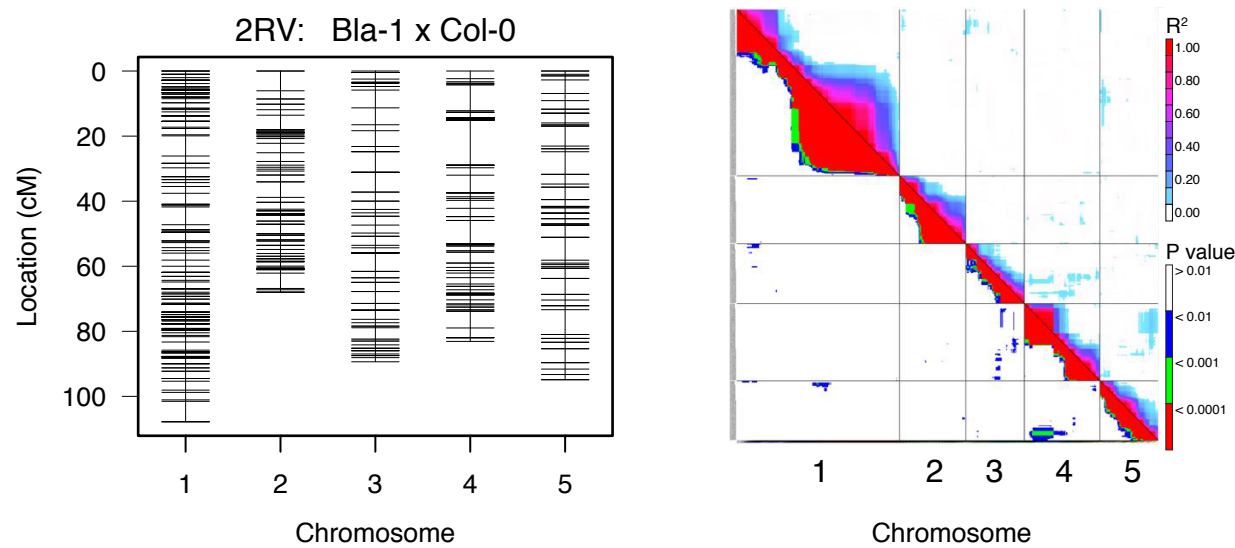
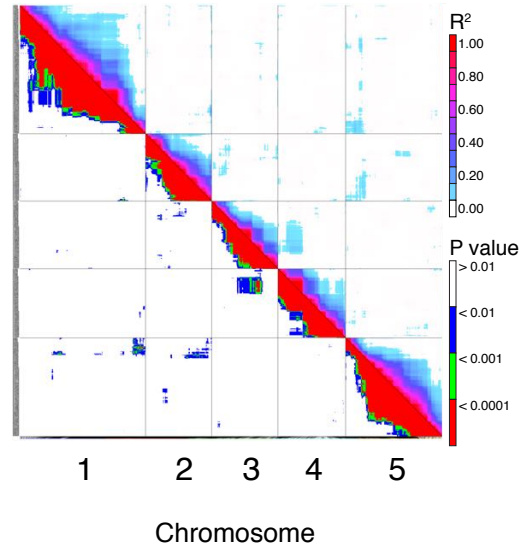
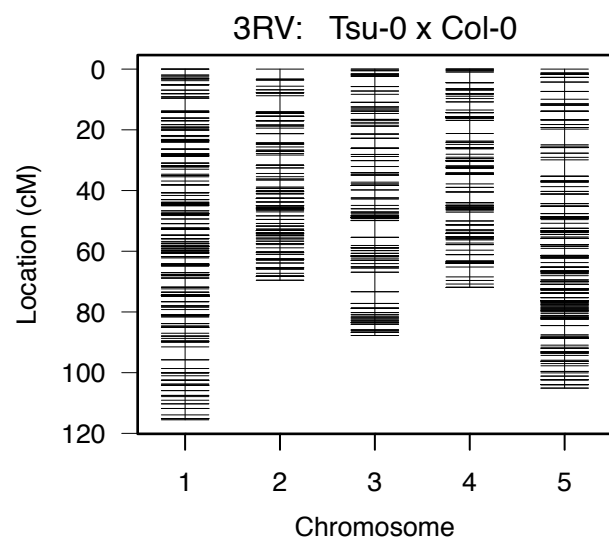
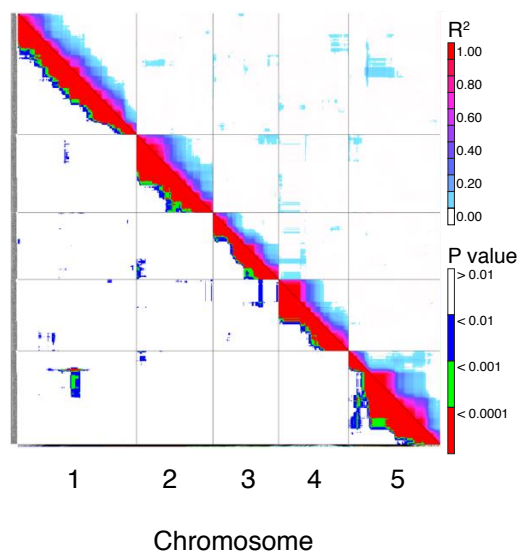
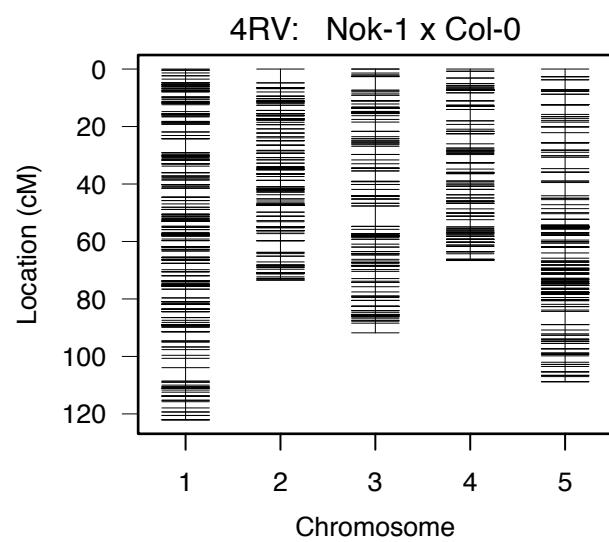
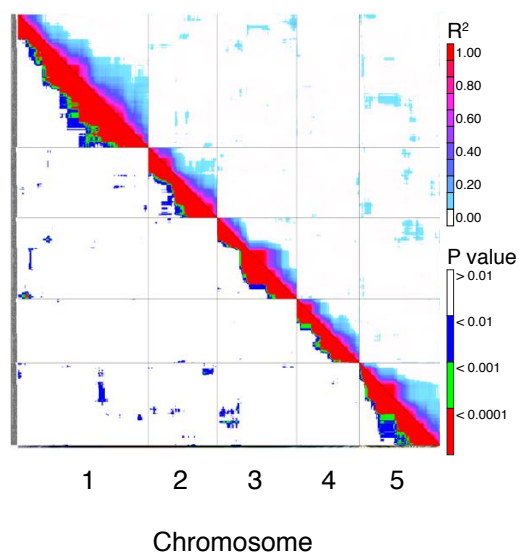
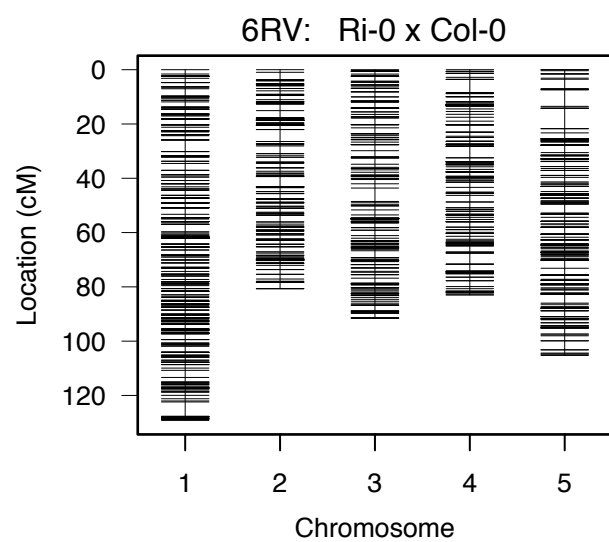


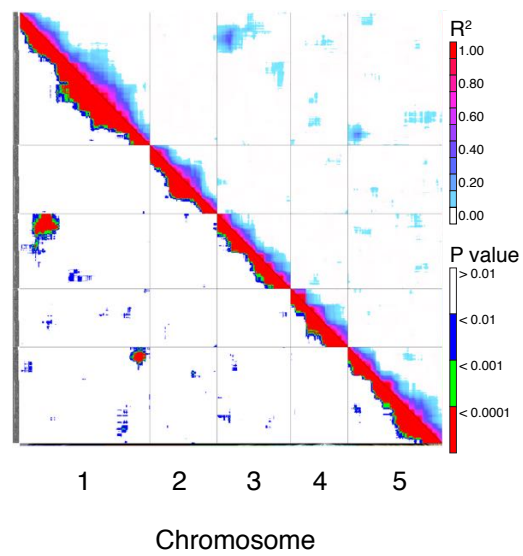
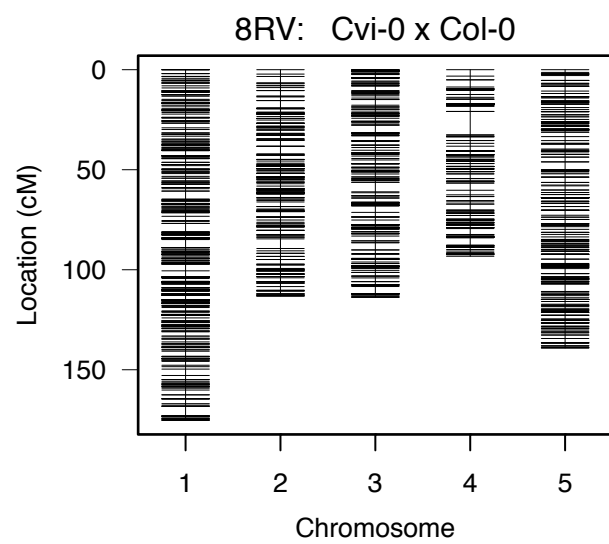
Fig. S1

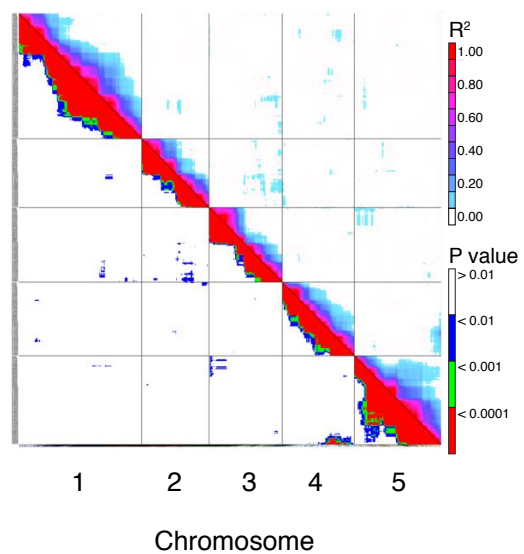
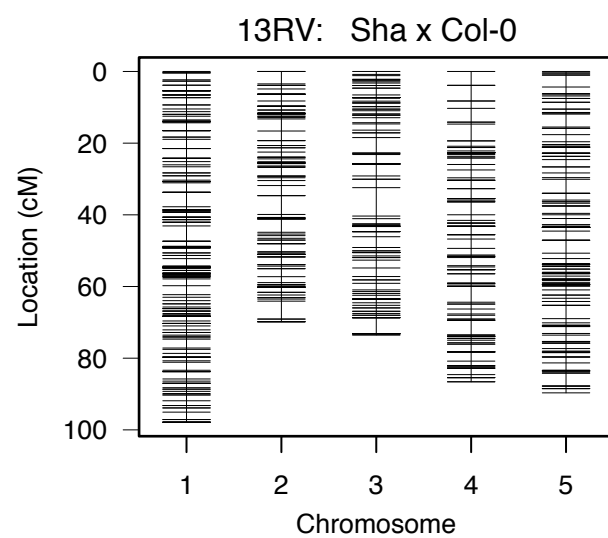


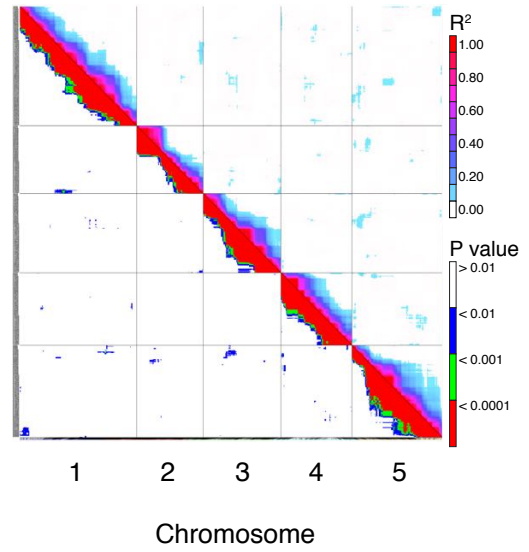
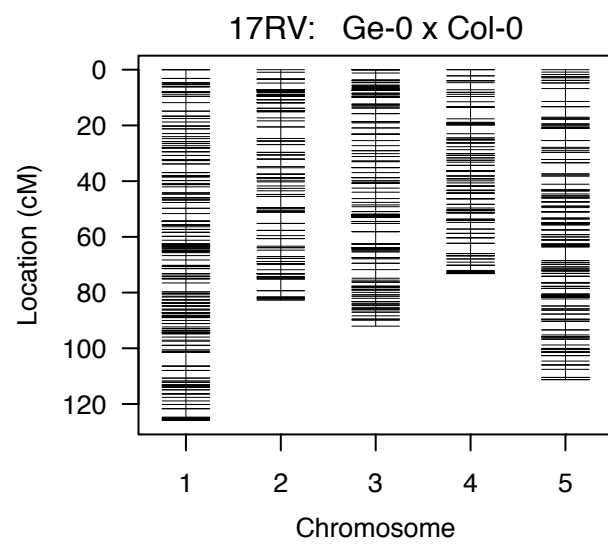


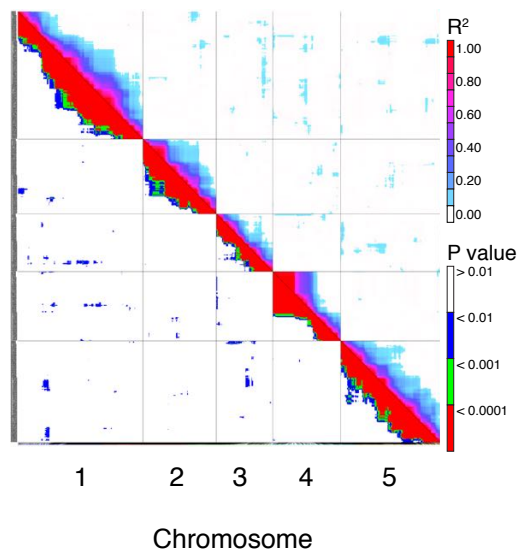
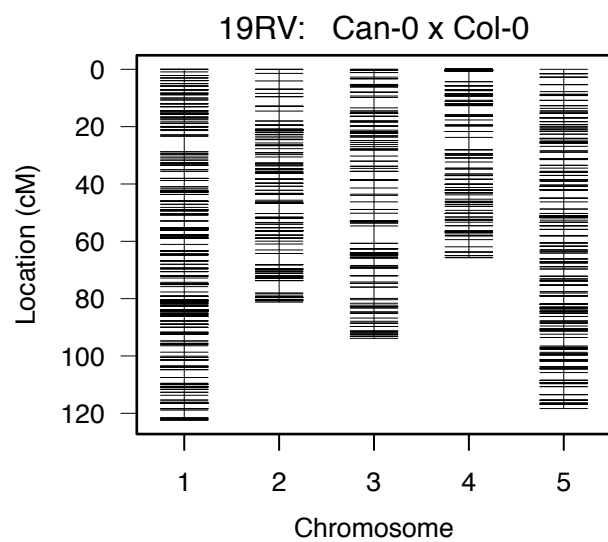


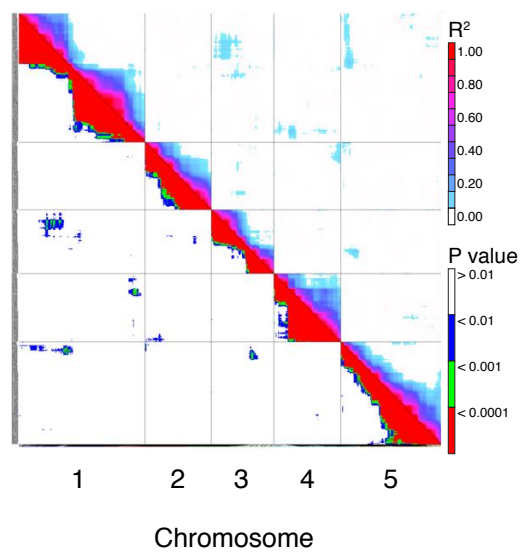
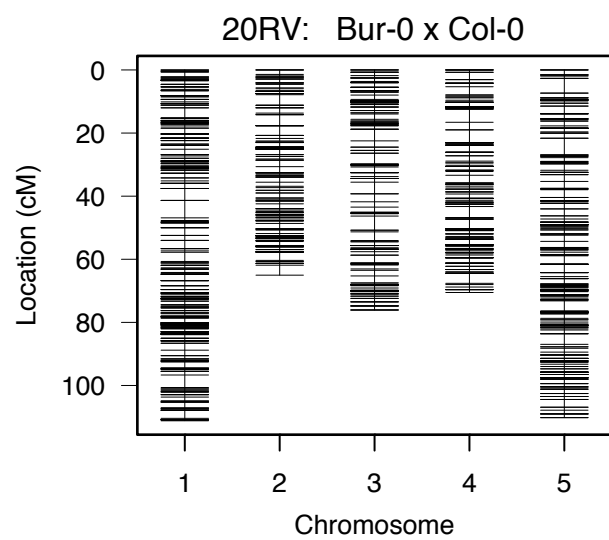


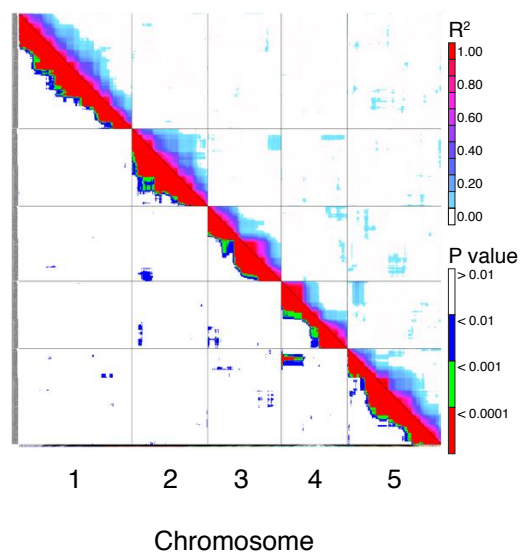
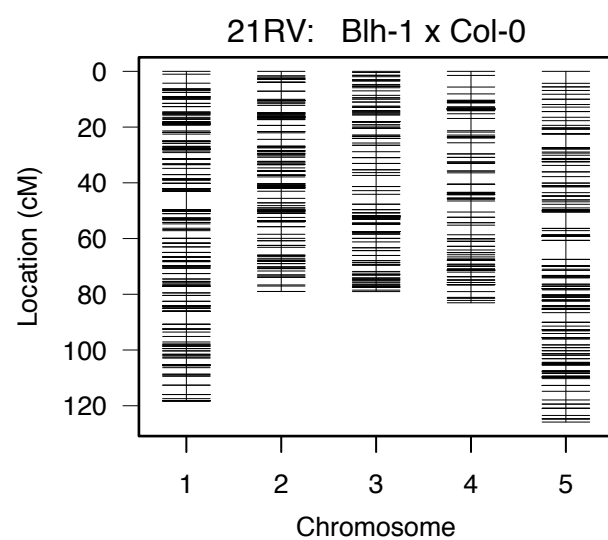


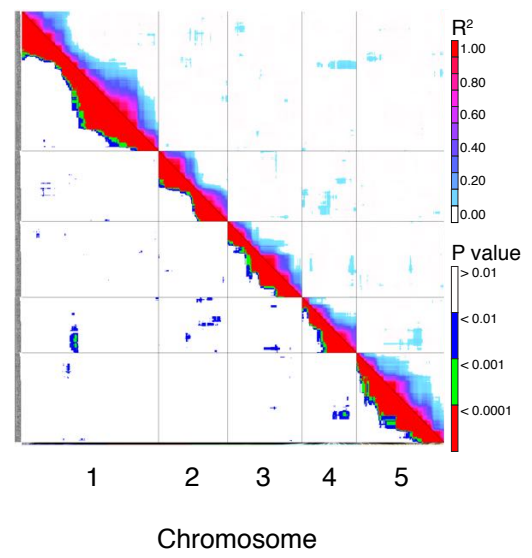
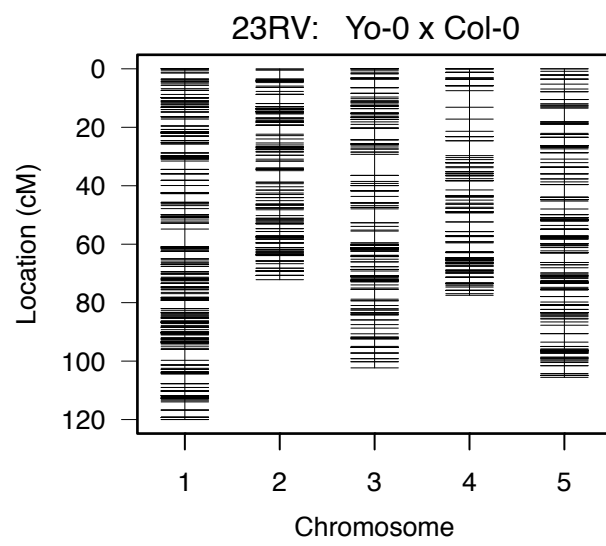


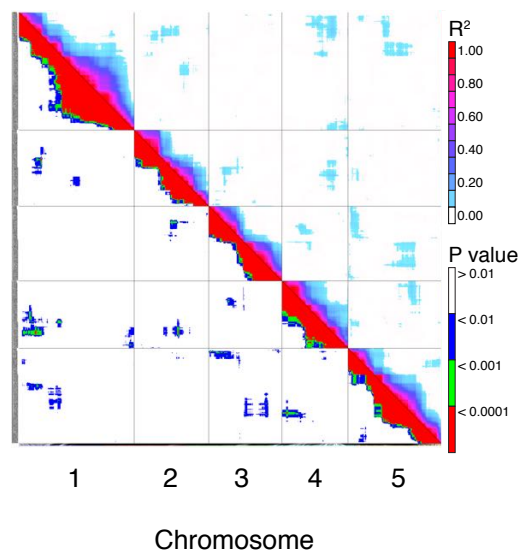
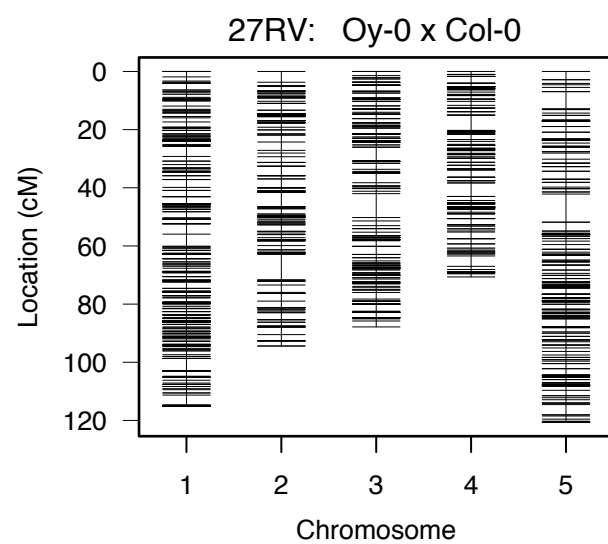


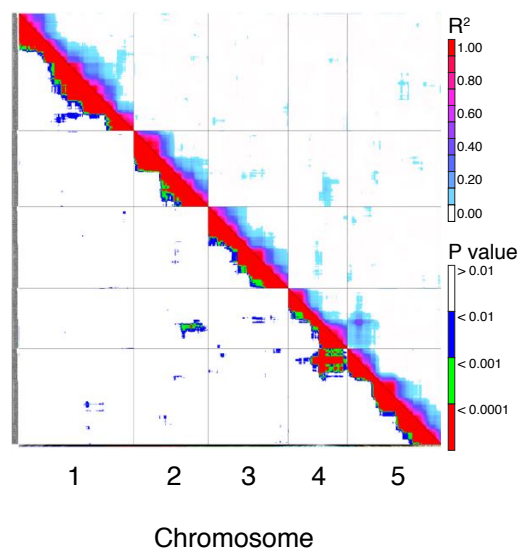
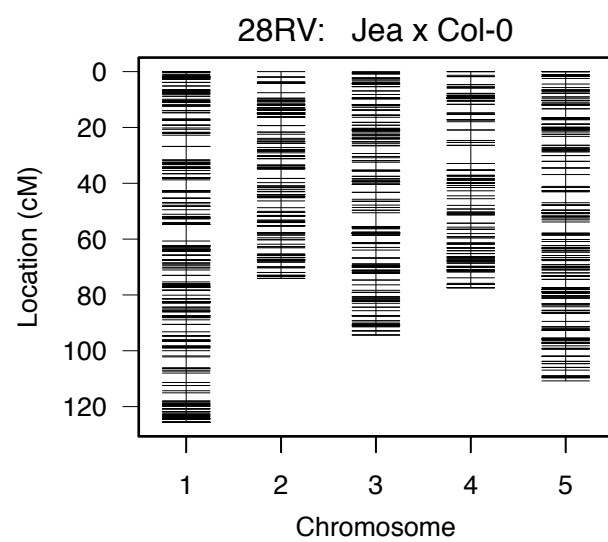












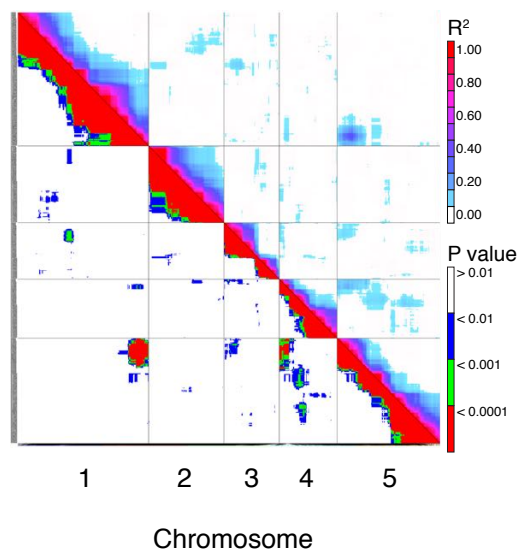
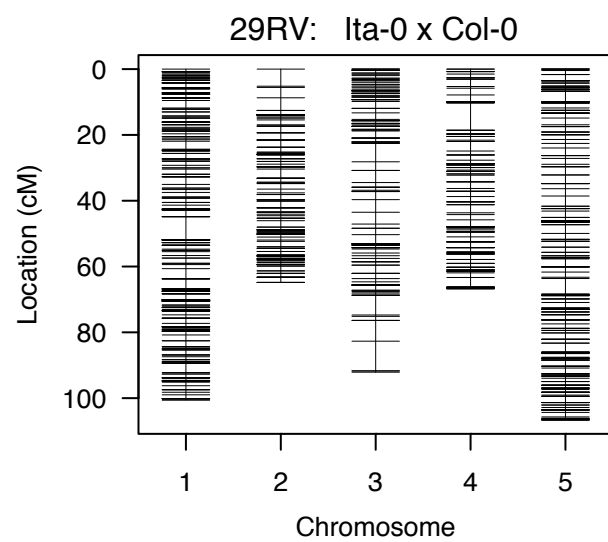


Fig. S1. Linkage maps (left) and linkage disequilibrium plots (right) for remaining 13 *Arabidopsis thaliana* RIL populations (population identified top left). Linkage maps were generated using both original INRA and newly identified GBS SNPs (see Figure 1 for remaining population of 14 total RIL sets). Linkage disequilibrium plots of intra- and inter-chromosomal LD as measured by SNP-SNP Pearson product moment correlation coefficients (r^2 ; top right of diagonal) with associated significance tests (p-value; lower left of diagonal). See Table 1 for SNP numbers, interval metrics, and missing data pre- and post-imputations for each population.