Fig. S1: Coincidence between short genomic regions of residual heterozygosity (grey lines, green blocks) and elevated recombination rates (pink).
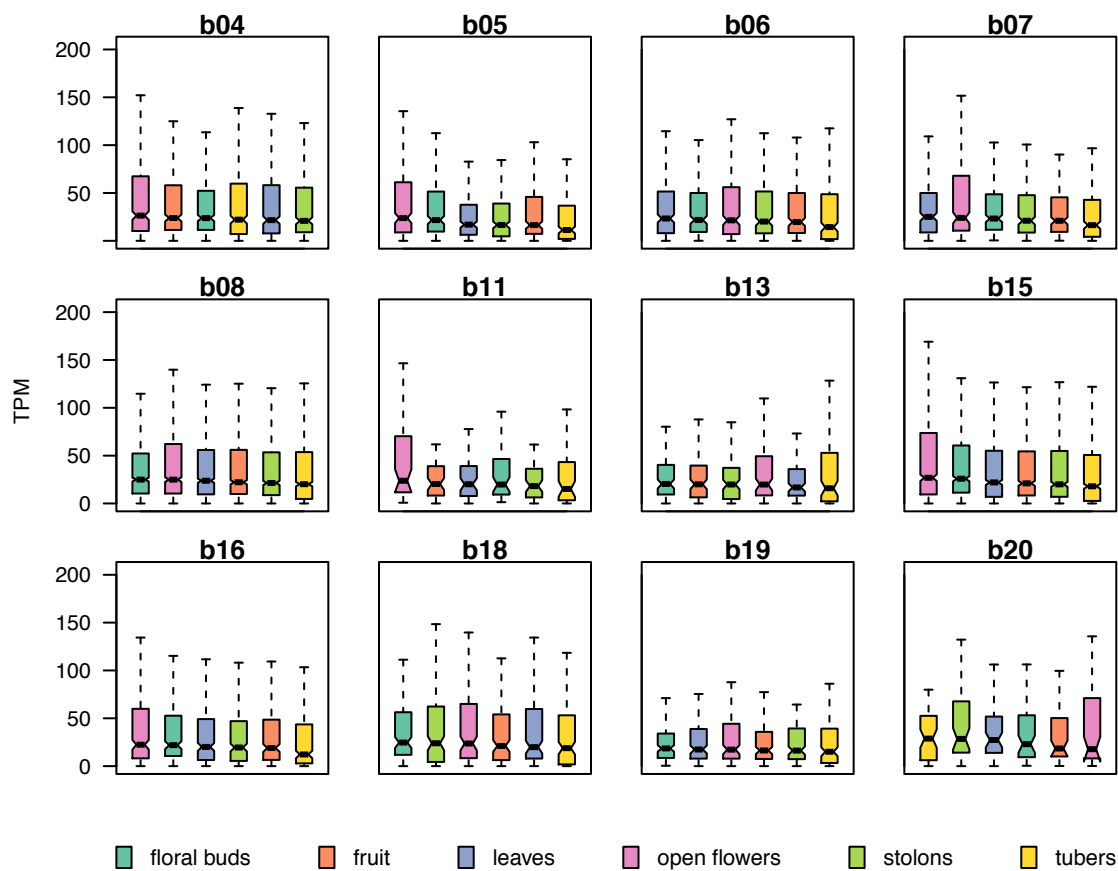
Fig. S2: Distribution of gene expression (TPM) across six tissues, and 12 blocks of residual heterozygosity. TPM, transcripts per million.
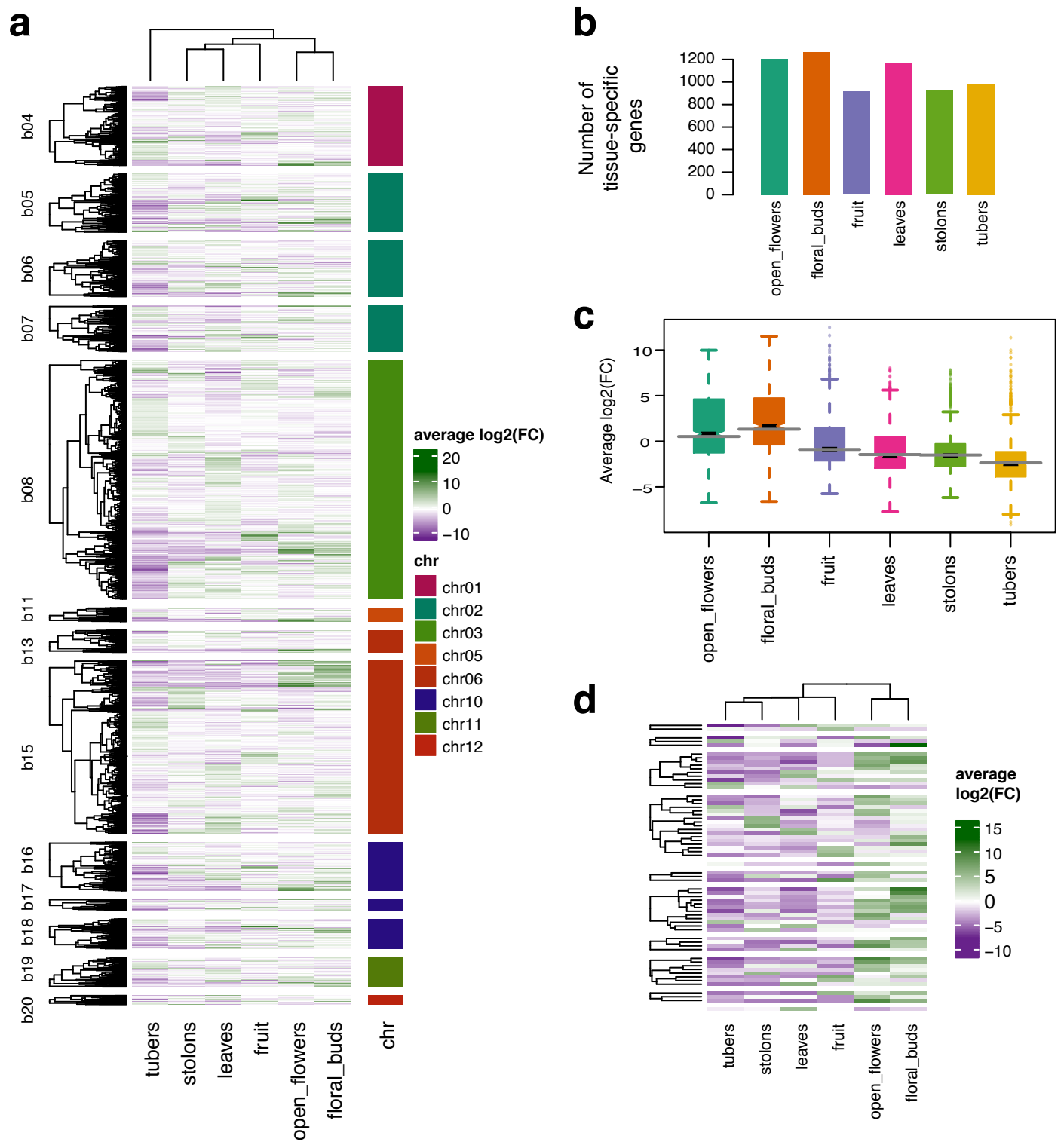
Fig. S3: Heterozygous blocks are associated with floral-specific gene expression. (**a**) Distribution of average log2(FC) from pairwise comparisons between all tissue types for each gene in every heterozygous block. (**b**) Counts of tissue-specific genes for each tissue type for genes underlying recalcitrant regions of heterozygosity. (**c**) Distribution of the average log2(FC) values by tissue compared to the genome-wide median (grey bars) for genes underlying heterozygous blocks. Only floral tissues have a greater median average log2(FC) than the genome-wide average across all genes. (**d**) Distribution of average log2(FC) from pairwise comparisons between all tissue types for genes under selection located within M6 heterozygous blocks.
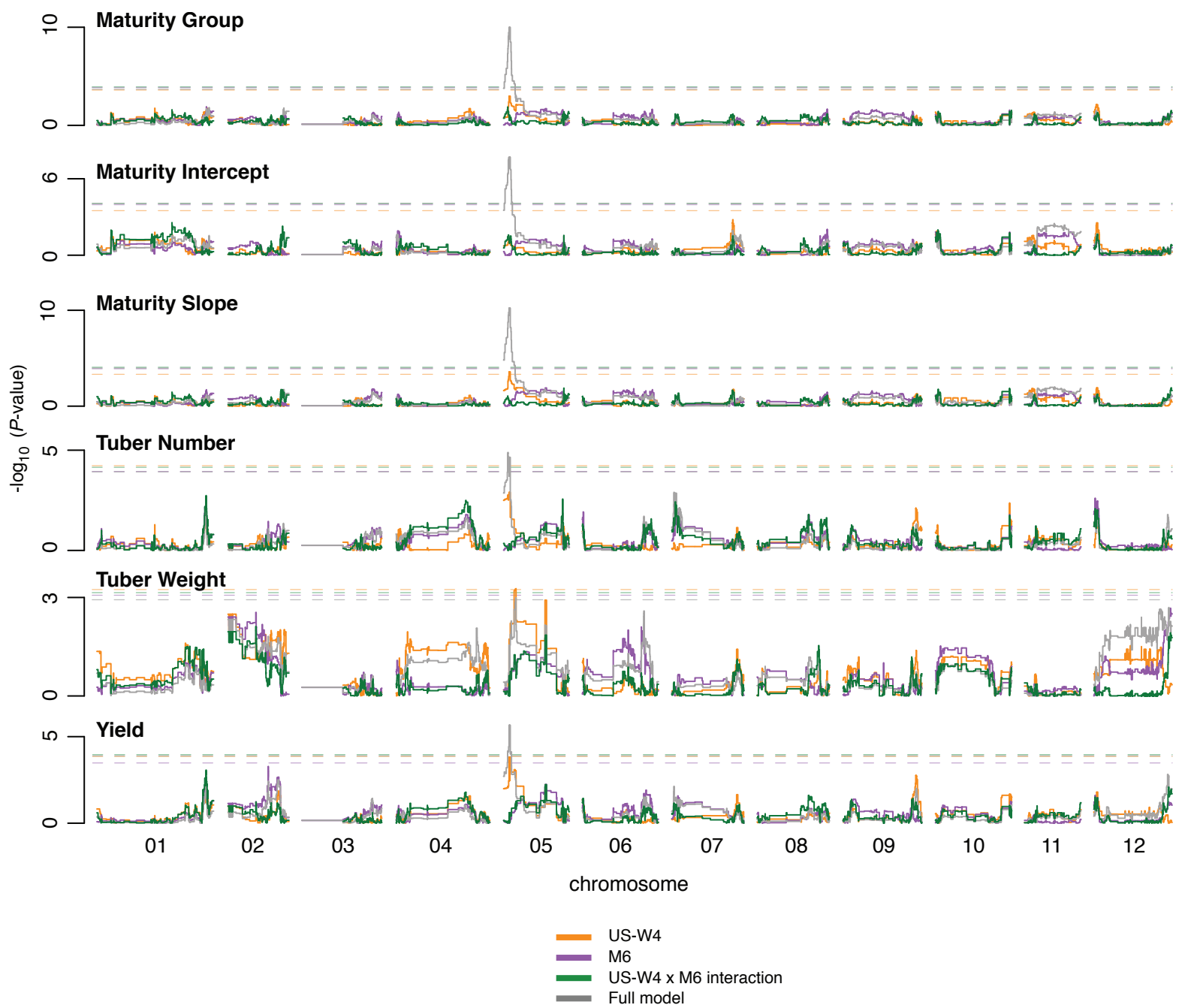
Fig. S4: Genome-wide mapping of three maturity components derived from random regression models, in addition to two yield components, and overall yield. All –log10(P-values) are shown for the parental effects of US-W4 (orange) and M6 (purple), the interaction between parental haplotypes (green), and the full model (grey). The previously reported maturity locus is highlight using a light blue window. Dashed lines indicate permutation significance thresholds (1,000 permutations) controlling for a false positive error rate of 0.05, and colored according to the respective model component.
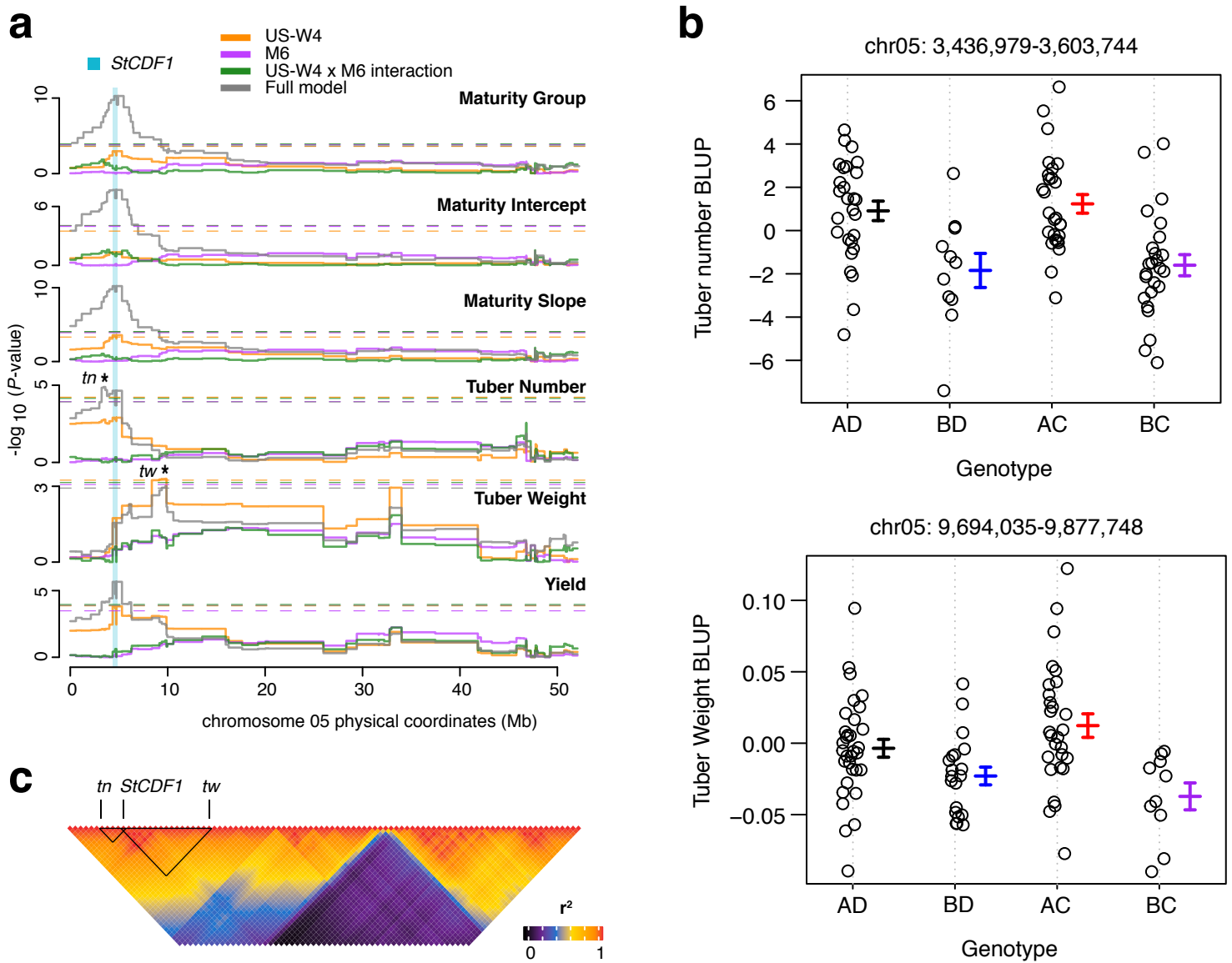
Fig. S5: QTL mapping of yield and growth habit traits. (**a**) QTL mapping results on chromosome 05. The –log10(P-values) are shown for the parental effects of US-W4 (orange) and M6 (purple), the interaction between parental haplotypes (green), and the full model (grey). The previously reported maturity locus is highlight using a light blue window. Dashed lines indicate permutation significance thresholds (1,000 permutations) controlling for a false positive error rate of 0.05, and colored according to the respective model component. (**b**) Effects plots for tn (top) and tw (bottom) loci. US-W4 alleles, A & B. M6 alleles, C & D. (**c**) Partial heatmap highlighting the degree of LD between the bins containing tn, tw and StCDF1. All bins on chromosome 05 are shown (top of heatmap), but restricted to nearby bins. Black lines illustrate the comparison of LD values for the three different denoted bins. LD, linkage disequilibrium.
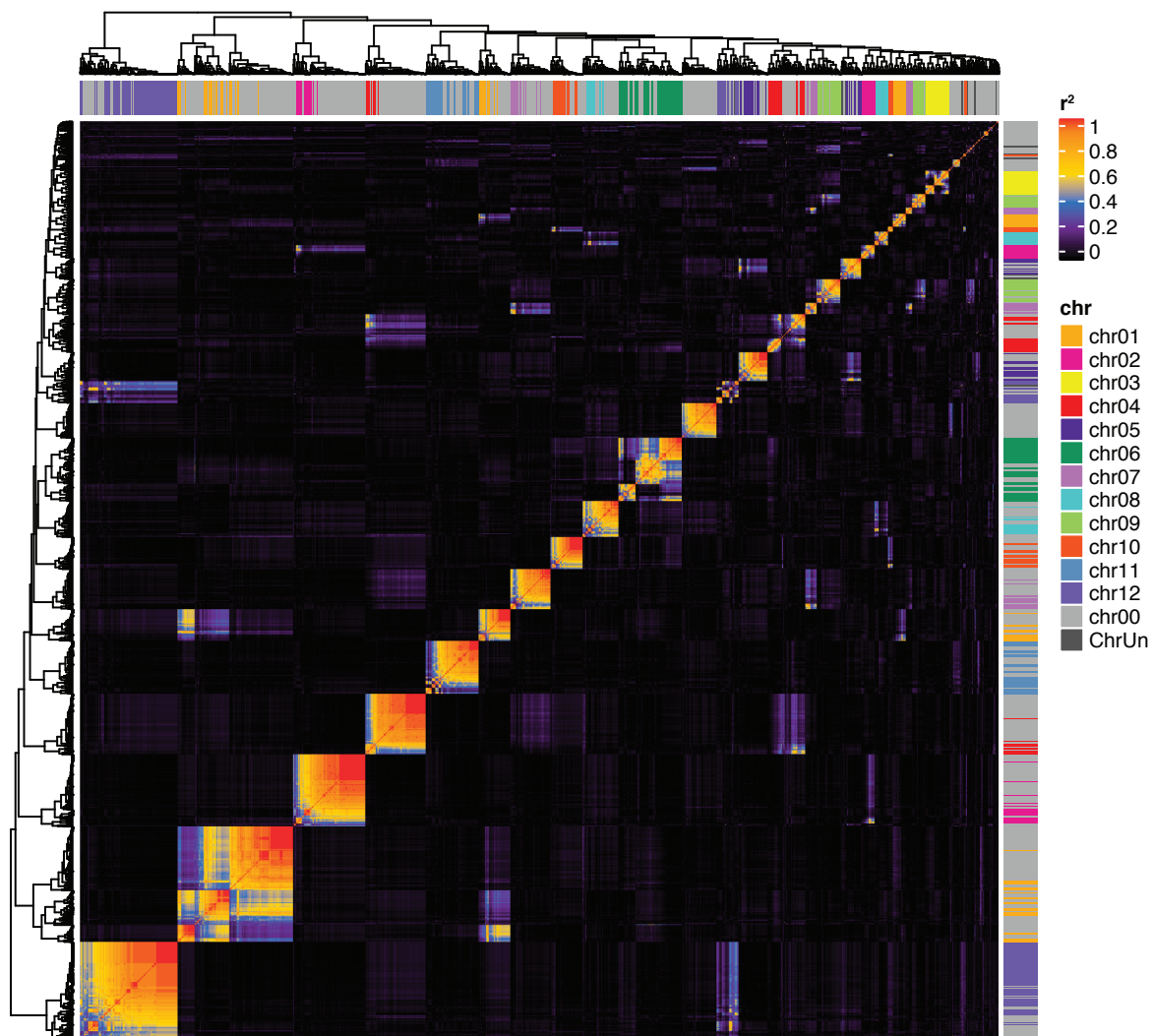
Fig. S6: Pairwise estimates of linkage disequilibrium (r^2) across all unique recombination bins.
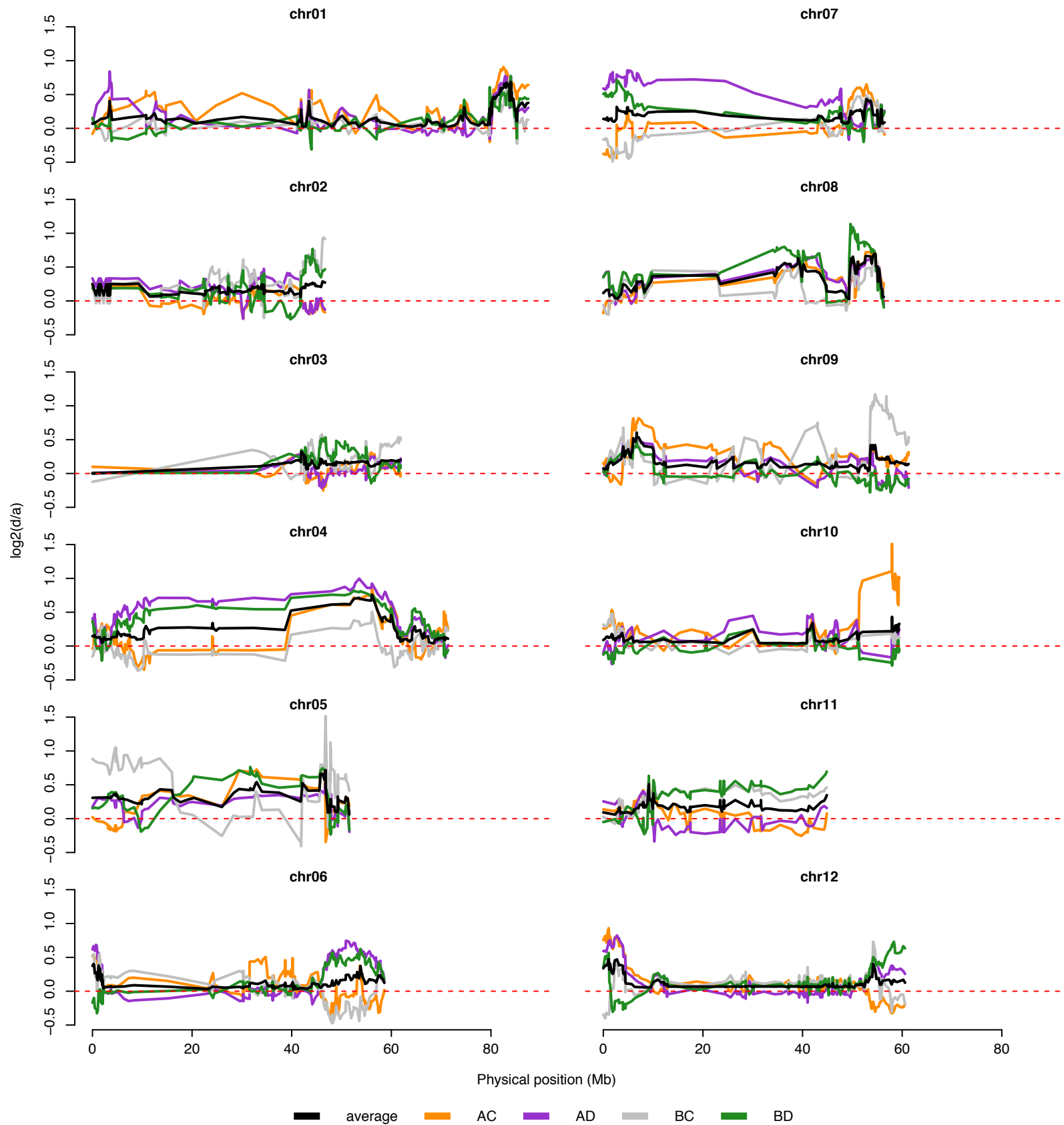
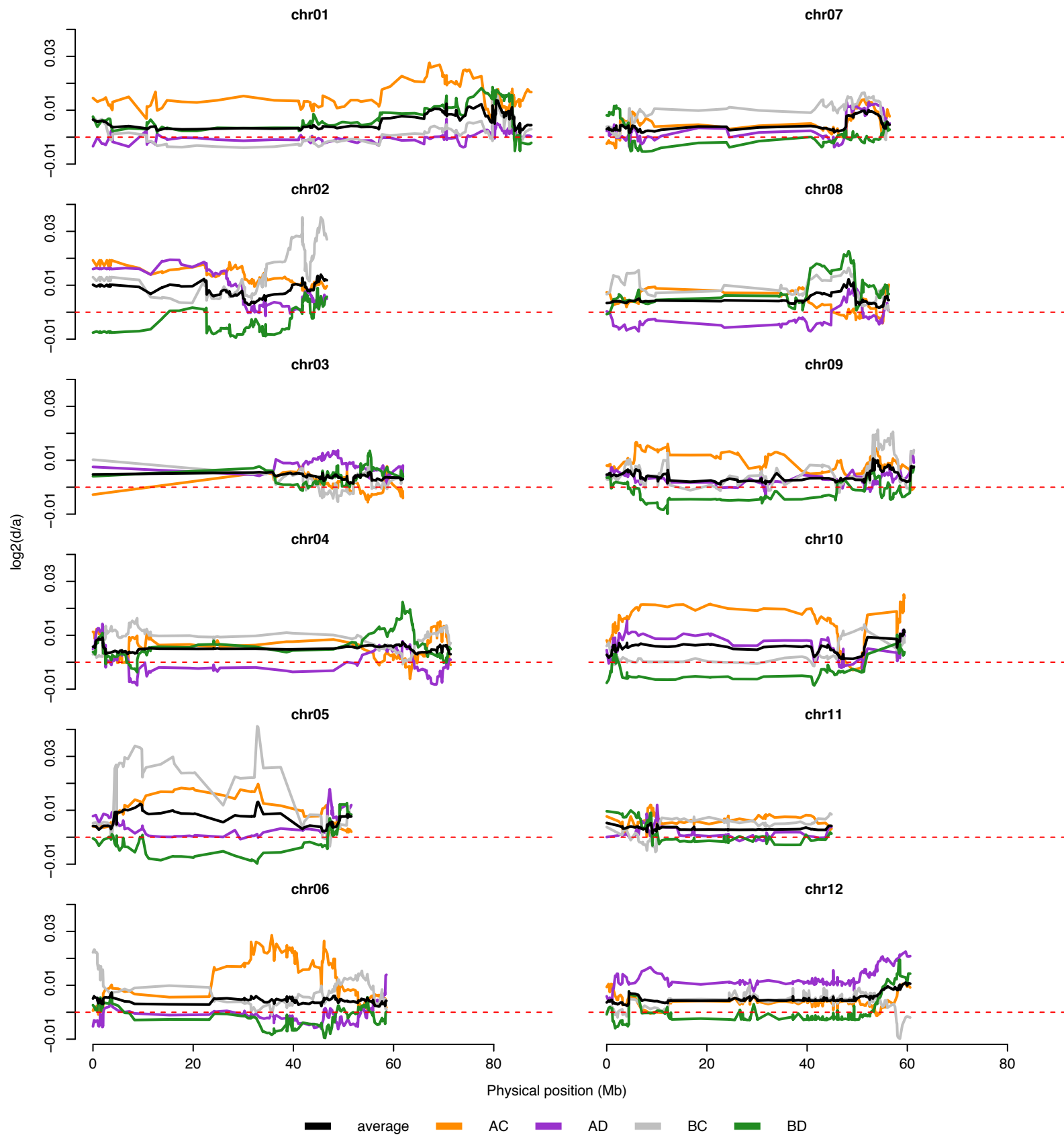**Fig. S7:** Genome-wide distribution of relative dominance values (log2(dominance/additive)) for tuber number.

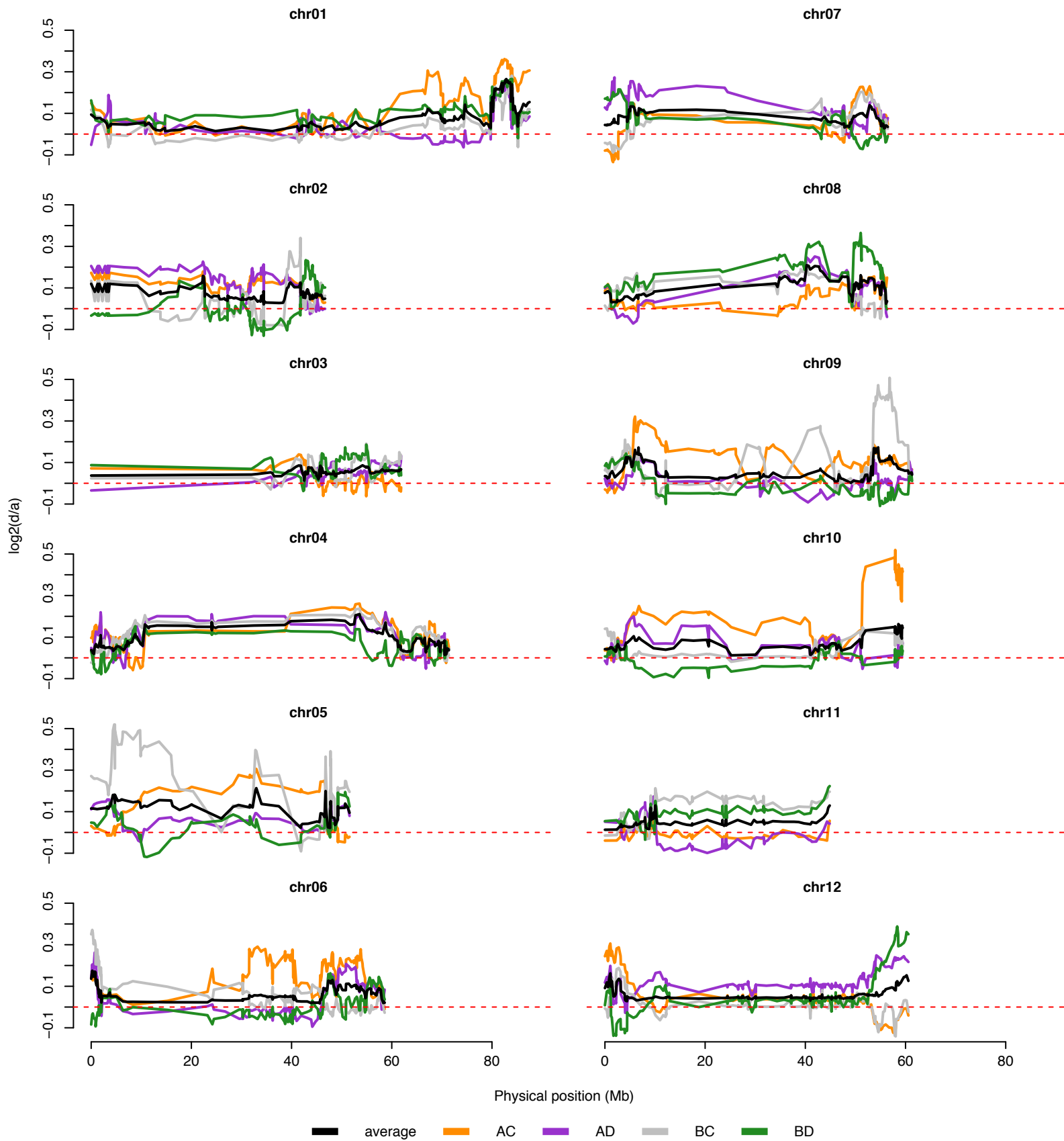**Fig. S8:** Genome-wide distribution of relative dominance values (log2(dominance/additive)) for tuber weight.

Fig. S9: Genome-wide distribution of relative dominance values (log2(dominance/additive)) for overall yield.
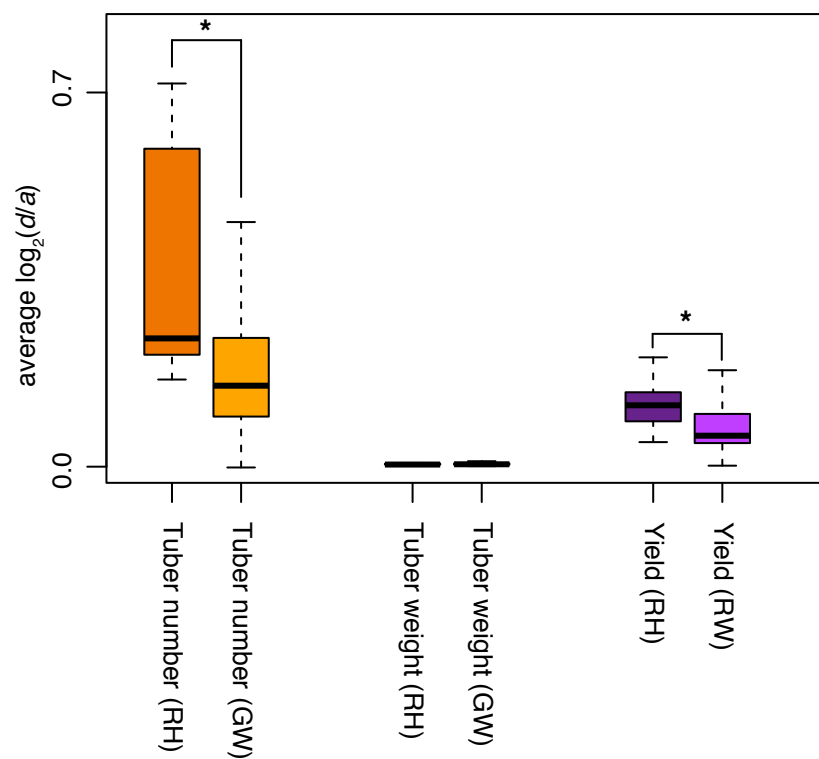
Fig. S10: Comparison of relative dominance values at regions of residual heterozygosity (RH) and genome-wide estimates (GW), for tuber number, tuber weight, and overall yield.
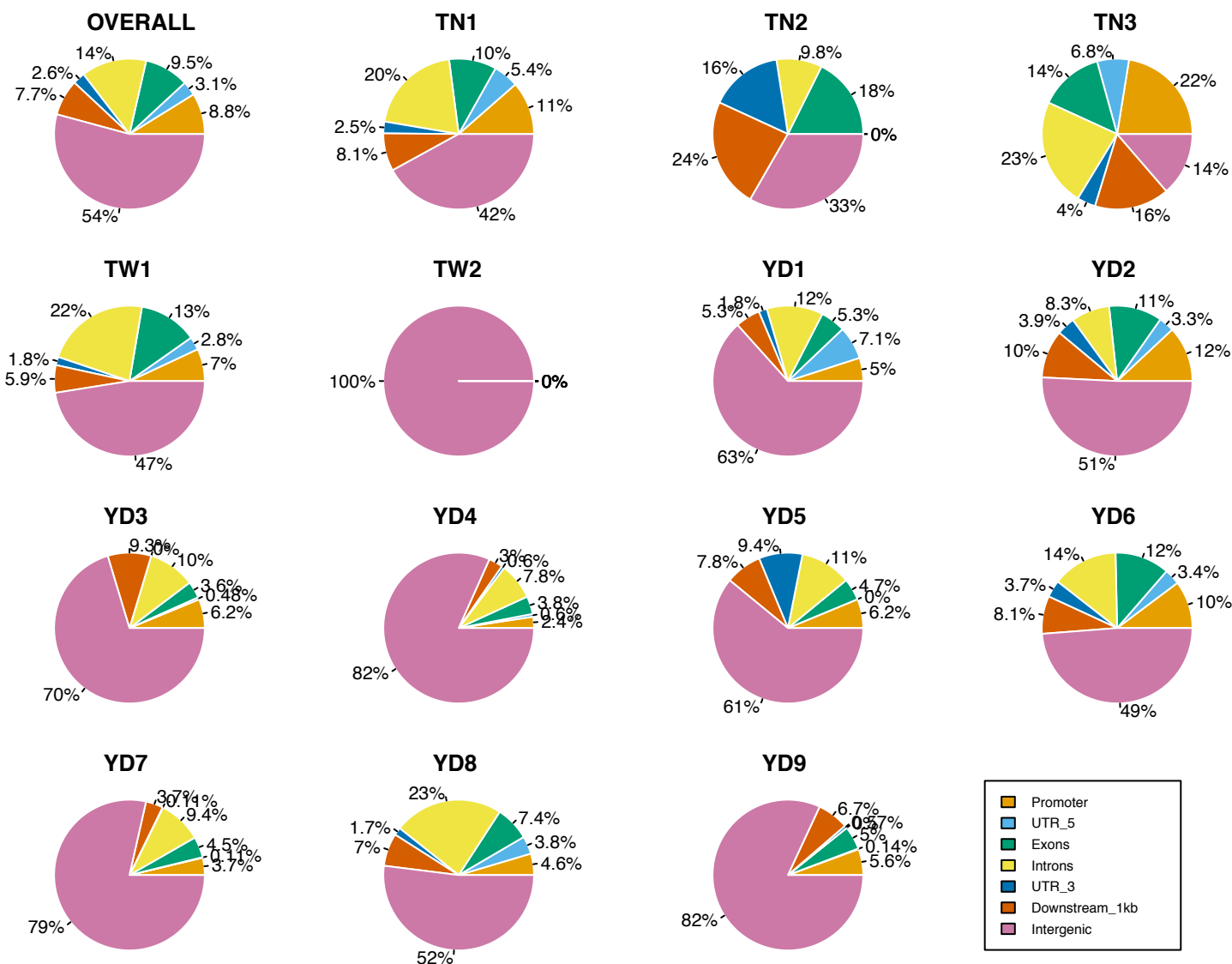
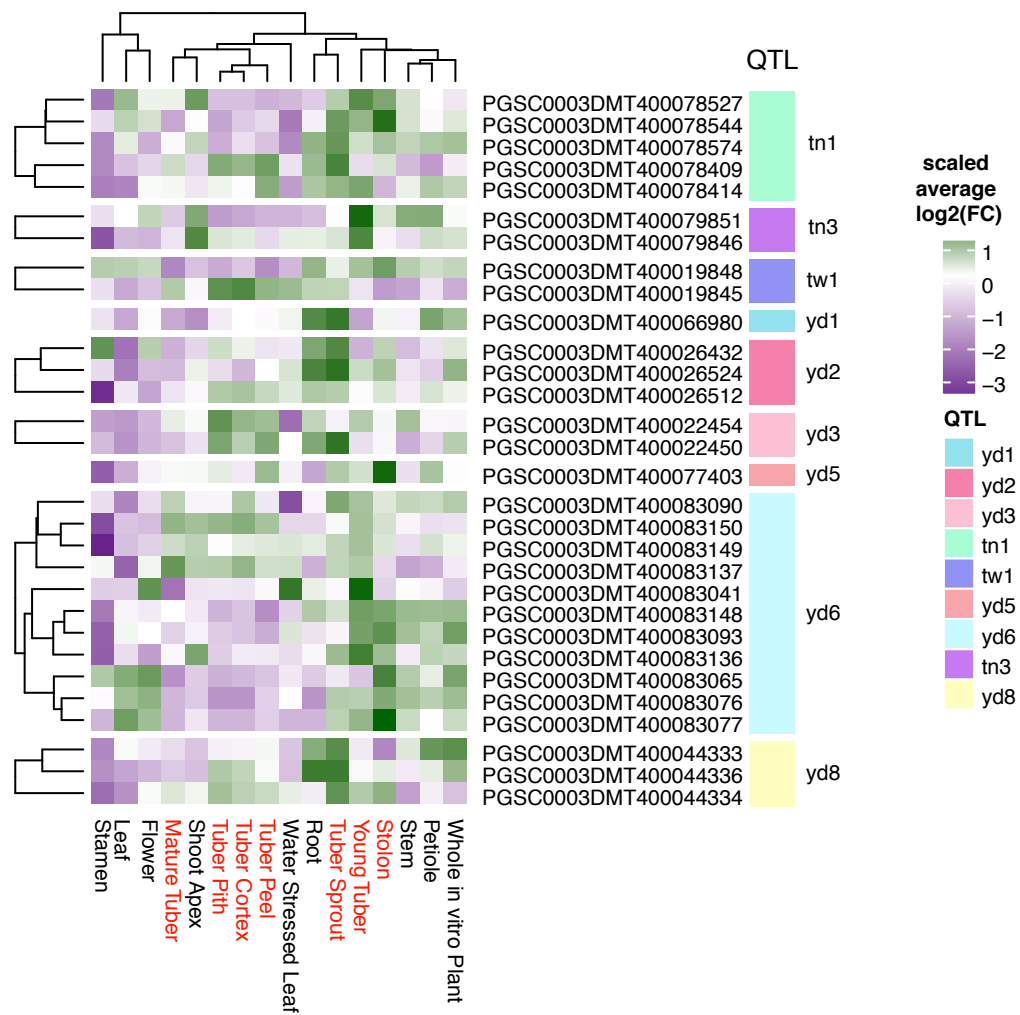**Fig. S11:** Distribution of SNV effects across all 14 QTL regions.

Fig. S12: Normalized (scaled average log2[fold-change]) gene expression patterns for QTL genes (rows) demonstrating tuber- or stolon-specific expression. Columns represent different tissue-types.