

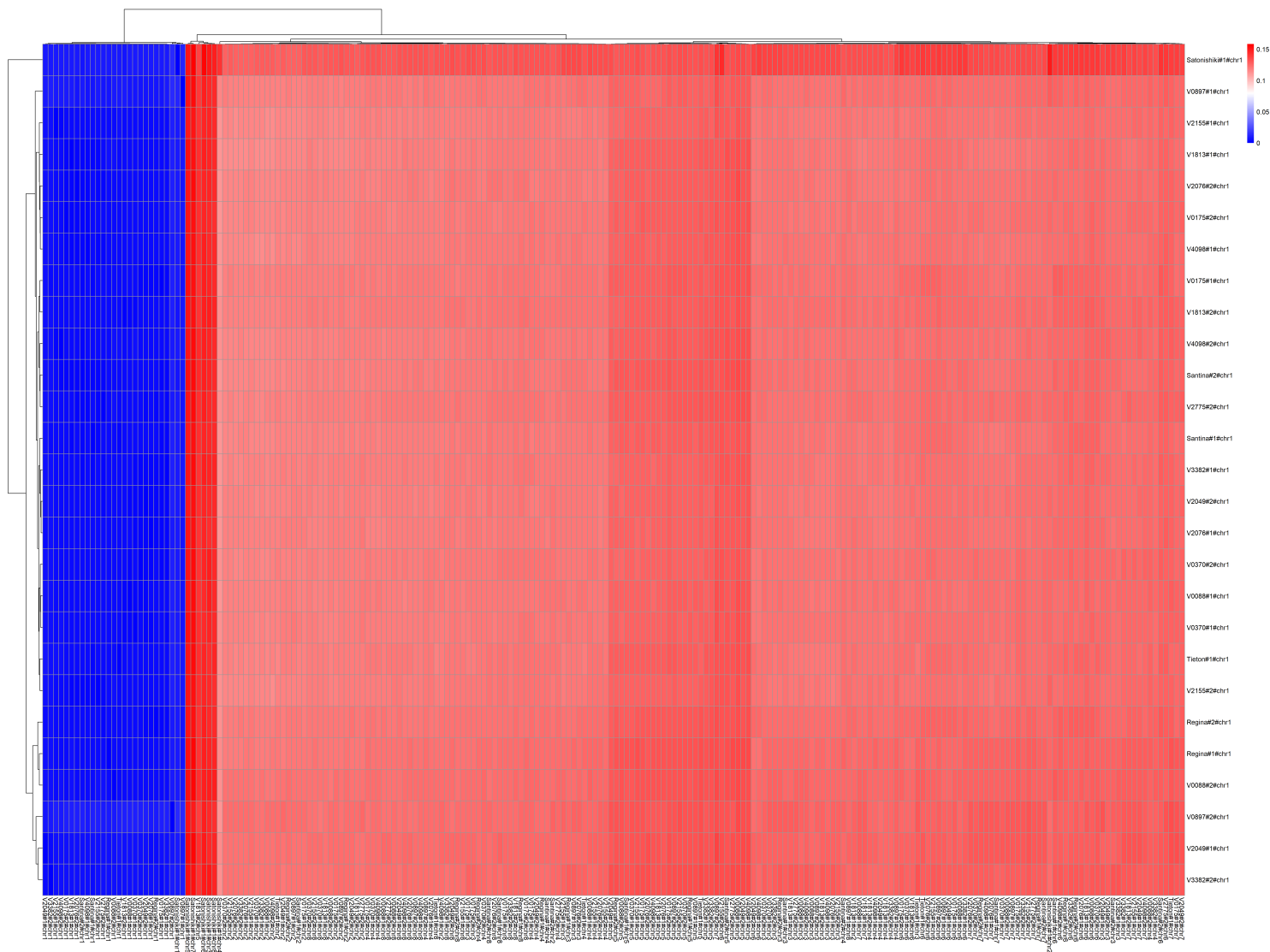


Fig. S1. Chromosome-wise alignment heatmap for chromosome 1 across sweet cherry genomes.

Alignments of chromosome 1 from each genome against all chromosomes from all genomes included in the pangenome are shown as a heatmap. Rows correspond to chr1 from each genome and columns to genomic coordinates across all chromosomes. Color intensity reflects alignment density, highlighting conserved macrosyntentic relationships and localized divergence.

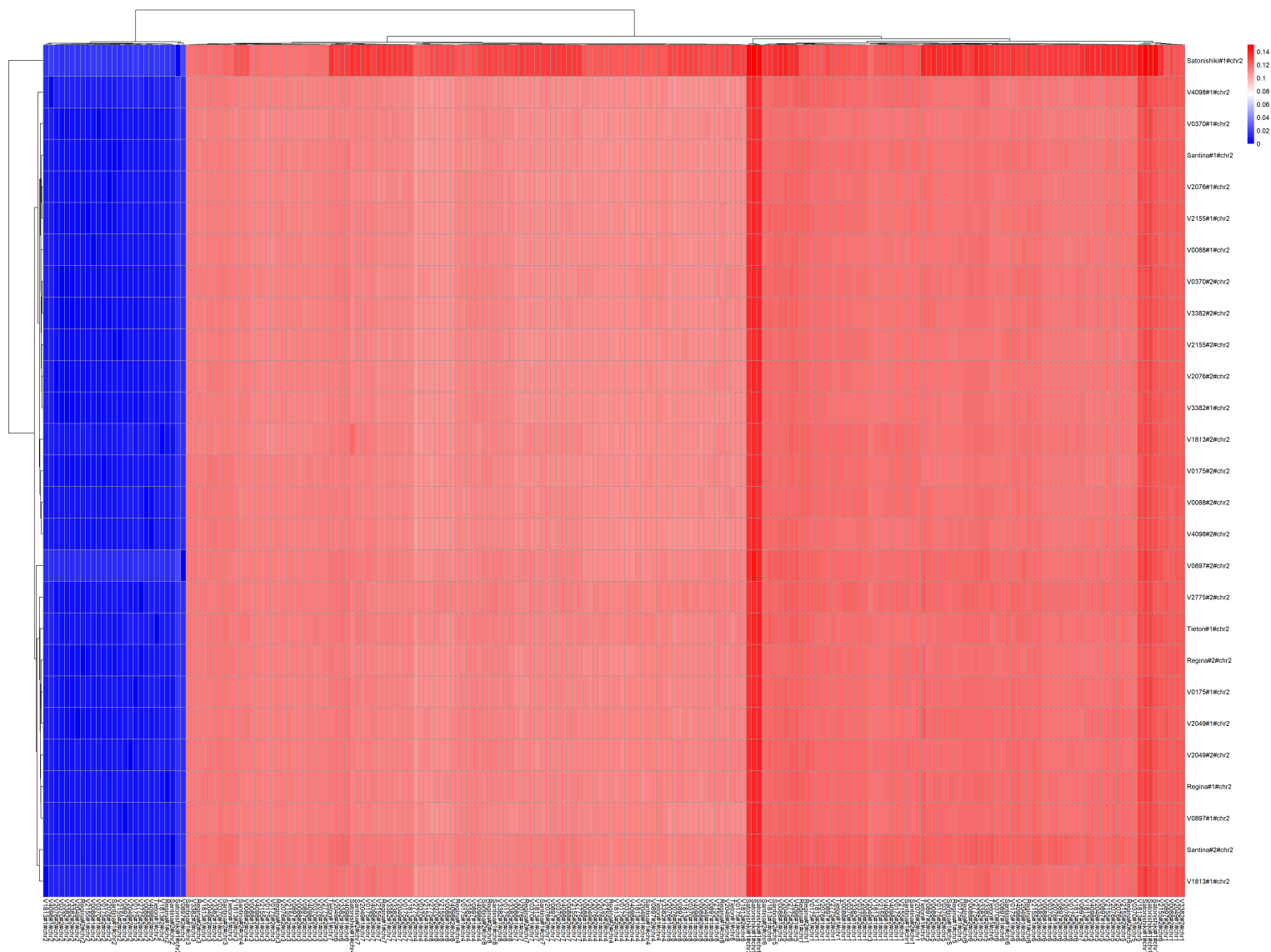


Fig. S2. Chromosome-wise alignment heatmap for chromosome 2 across sweet cherry genomes.

Alignments of chromosome 2 from each genome against all chromosomes from all genomes included in the pangenome are shown as a heatmap. Rows correspond to chr2 from each genome and columns to genomic coordinates across all chromosomes. Color intensity reflects alignment density, highlighting conserved macrosyntentic relationships and localized divergence.

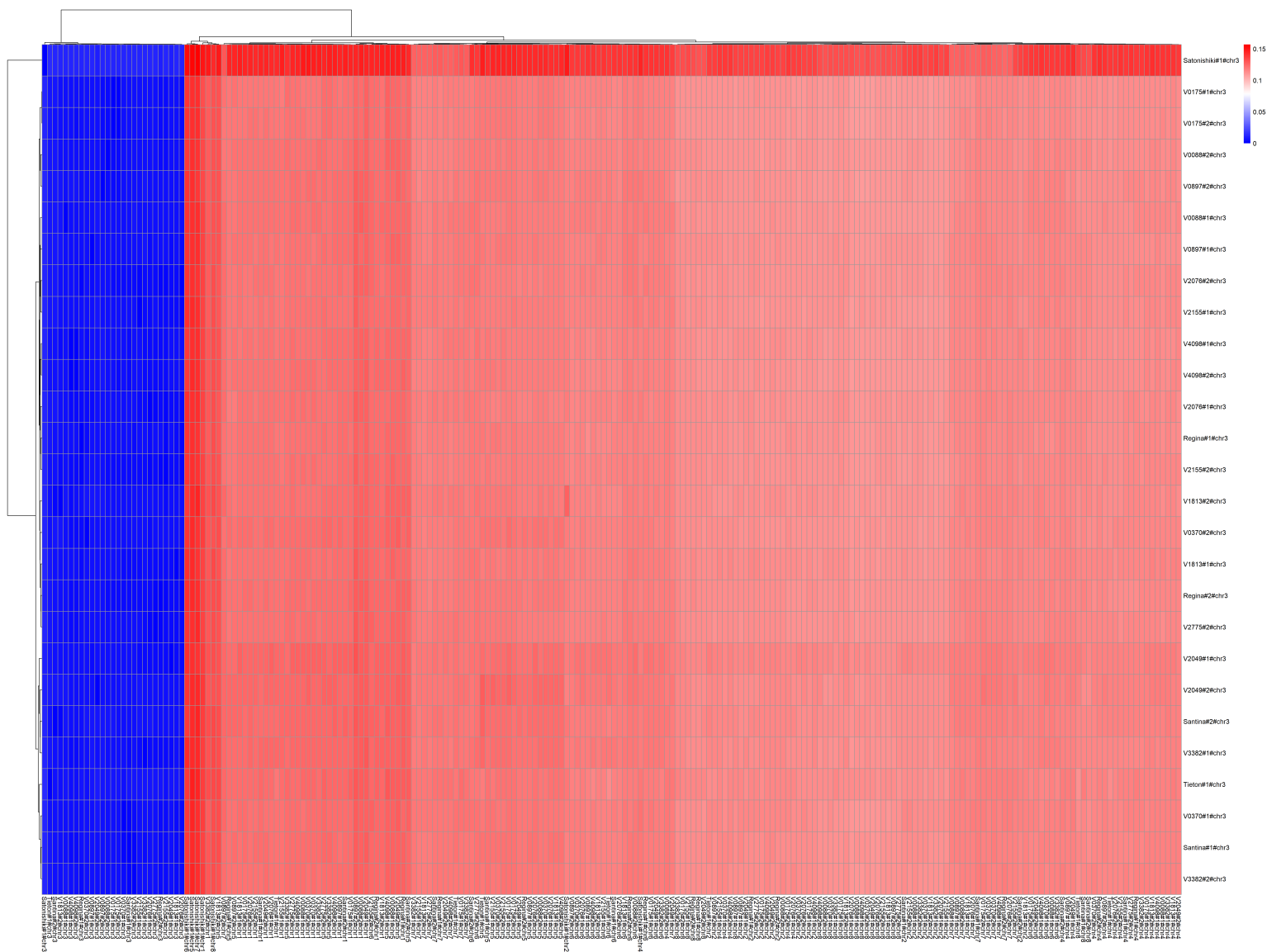


Fig. S3. Chromosome-wise alignment heatmap for chromosome 3 across sweet cherry genomes.

Alignments of chromosome 3 from each genome against all chromosomes from all genomes included in the pangenome are shown as a heatmap. Rows correspond to chr3 from each genome and columns to genomic coordinates across all chromosomes. Color intensity reflects alignment density, highlighting conserved macrosyntenic relationships and localized divergence.

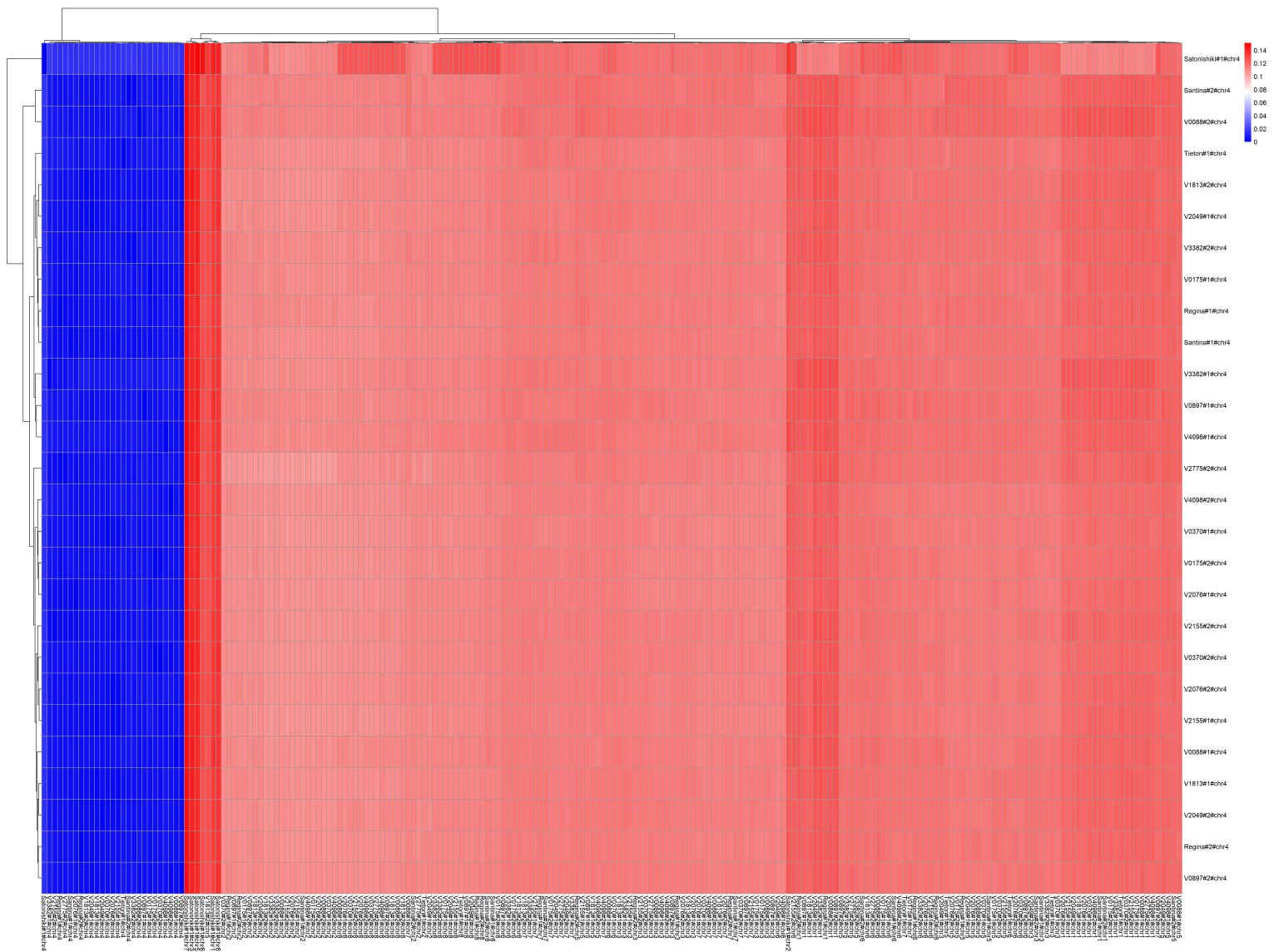


Fig. S4. Chromosome-wise alignment heatmap for chromosome 4 across sweet cherry genomes.

Alignments of chromosome 4 from each genome against all chromosomes from all genomes included in the pangenome are shown as a heatmap. Rows correspond to chr4 from each genome and columns to genomic coordinates across all chromosomes. Color intensity reflects alignment density, highlighting conserved macrosyntentic relationships and localized divergence.

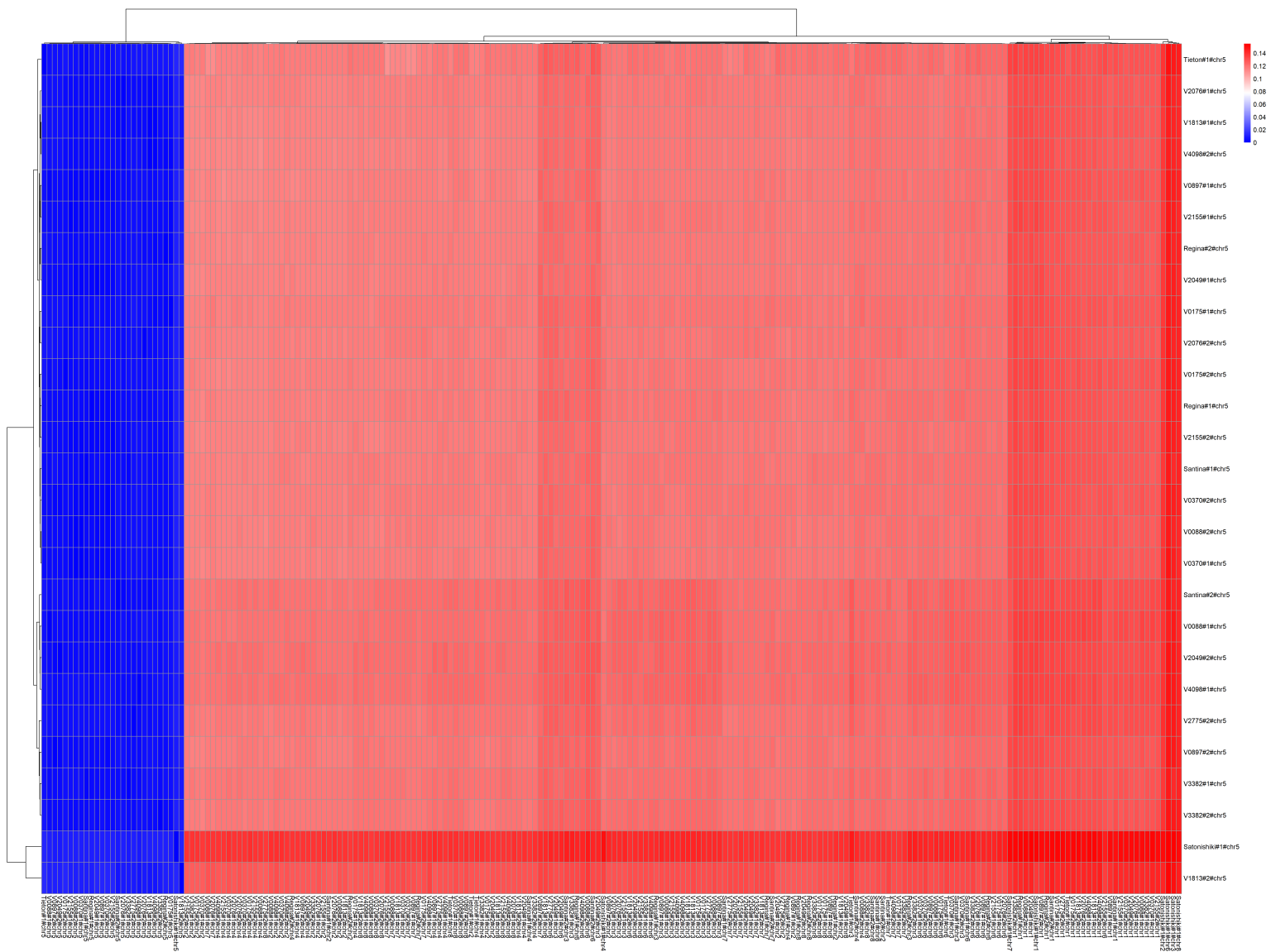


Fig. S5. Chromosome-wise alignment heatmap for chromosome 5 across sweet cherry genomes.

Alignments of chromosome 5 from each genome against all chromosomes from all genomes included in the pangenome are shown as a heatmap. Rows correspond to chr5 from each genome and columns to genomic coordinates across all chromosomes. Color intensity reflects alignment density, highlighting conserved macrosyntenic relationships and localized divergence.

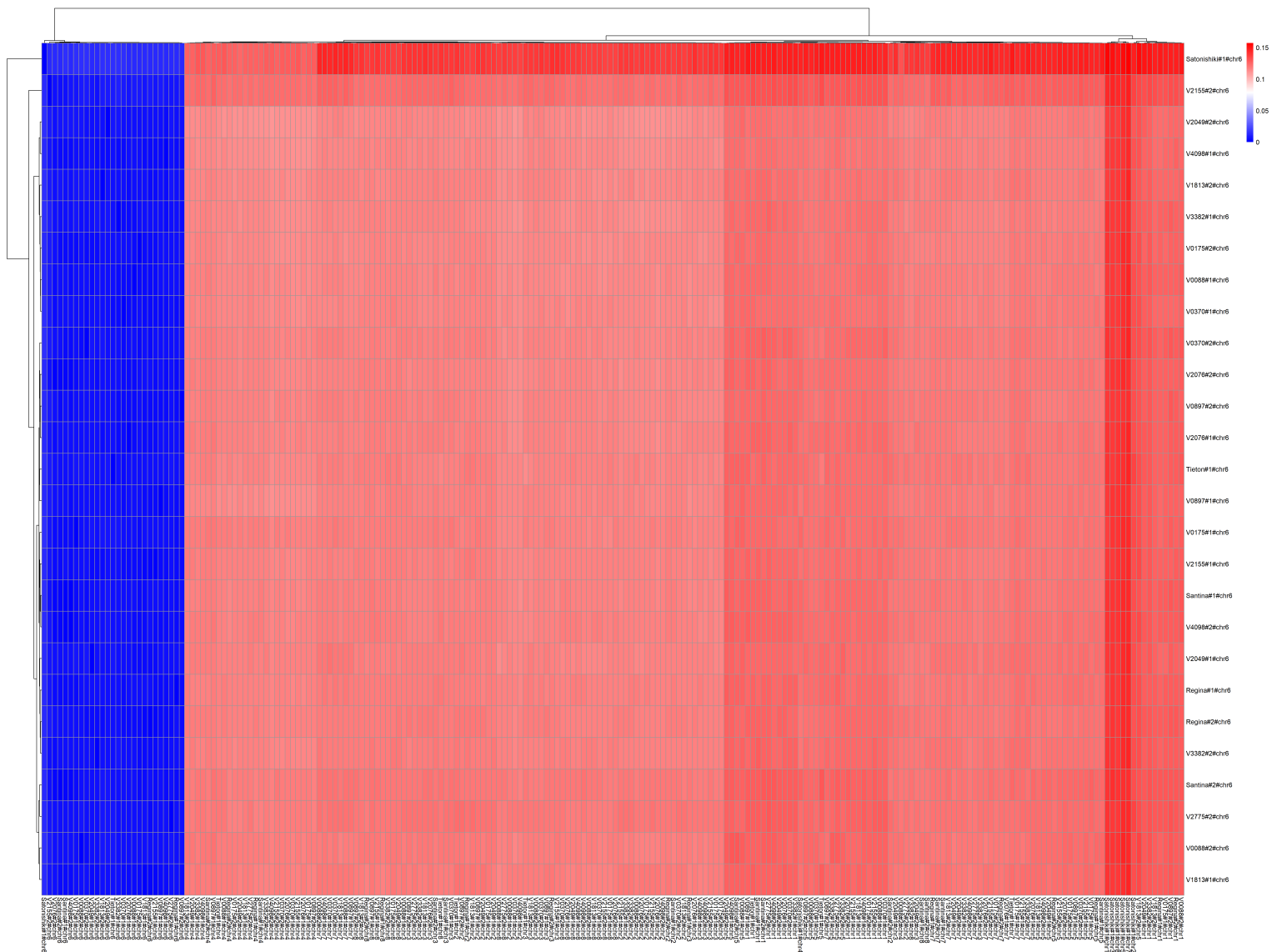


Fig. S6. Chromosome-wise alignment heatmap for chromosome 6 across sweet cherry genomes. Alignments of chromosome 6 from each genome against all chromosomes from all genomes included in the pangenome are shown as a heatmap. Rows correspond to chr6 from each genome and columns to genomic coordinates across all chromosomes. Color intensity reflects alignment density, highlighting conserved macrosyntentic relationships and localized divergence.

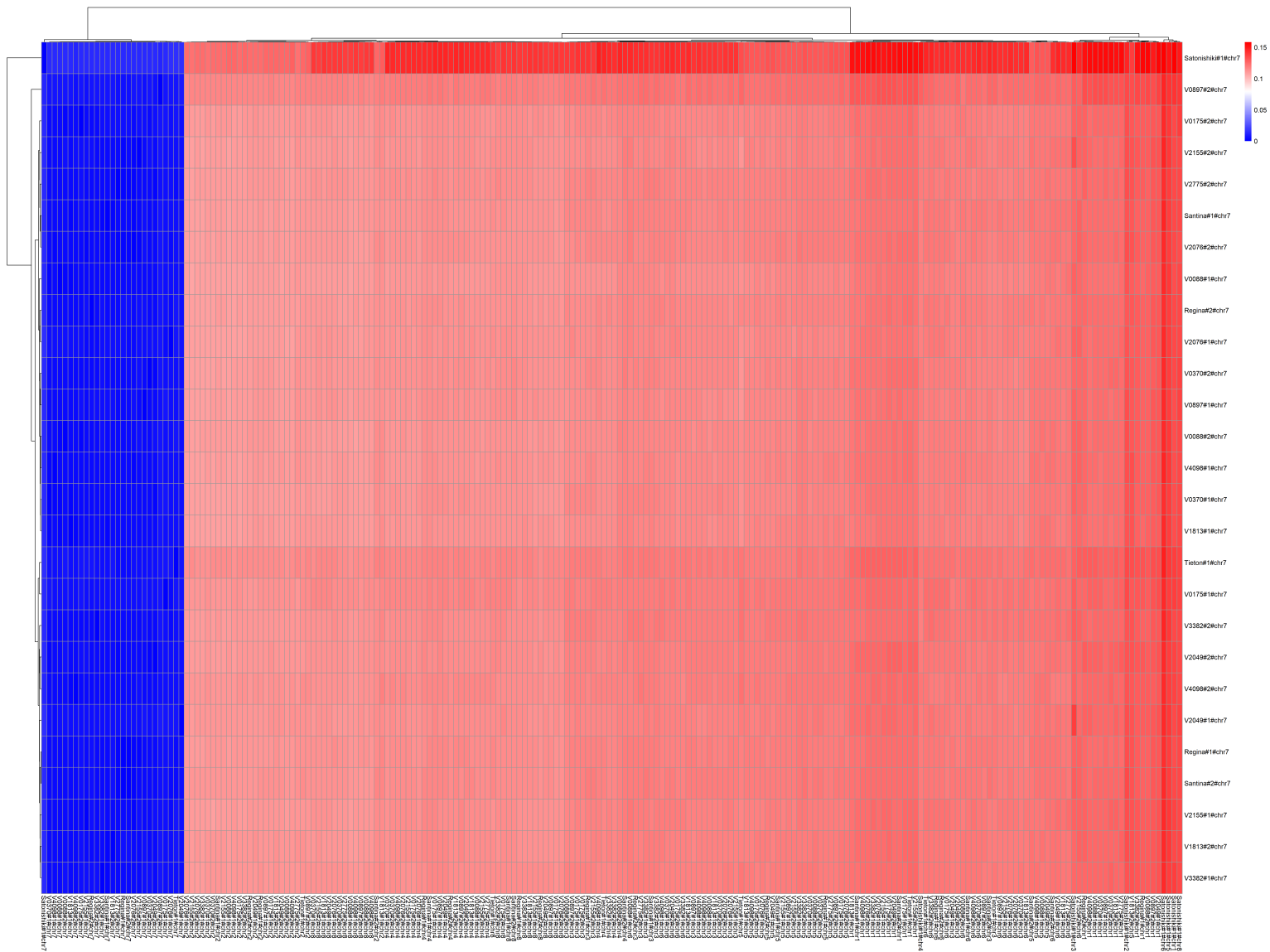


Fig. S7. Chromosome-wise alignment heatmap for chromosome 7 across sweet cherry genomes.

Alignments of chromosome 7 from each genome against all chromosomes from all genomes included in the pangenome are shown as a heatmap. Rows correspond to chr7 from each genome and columns to genomic coordinates across all chromosomes. Color intensity reflects alignment density, highlighting conserved macrosyntentic relationships and localized divergence.

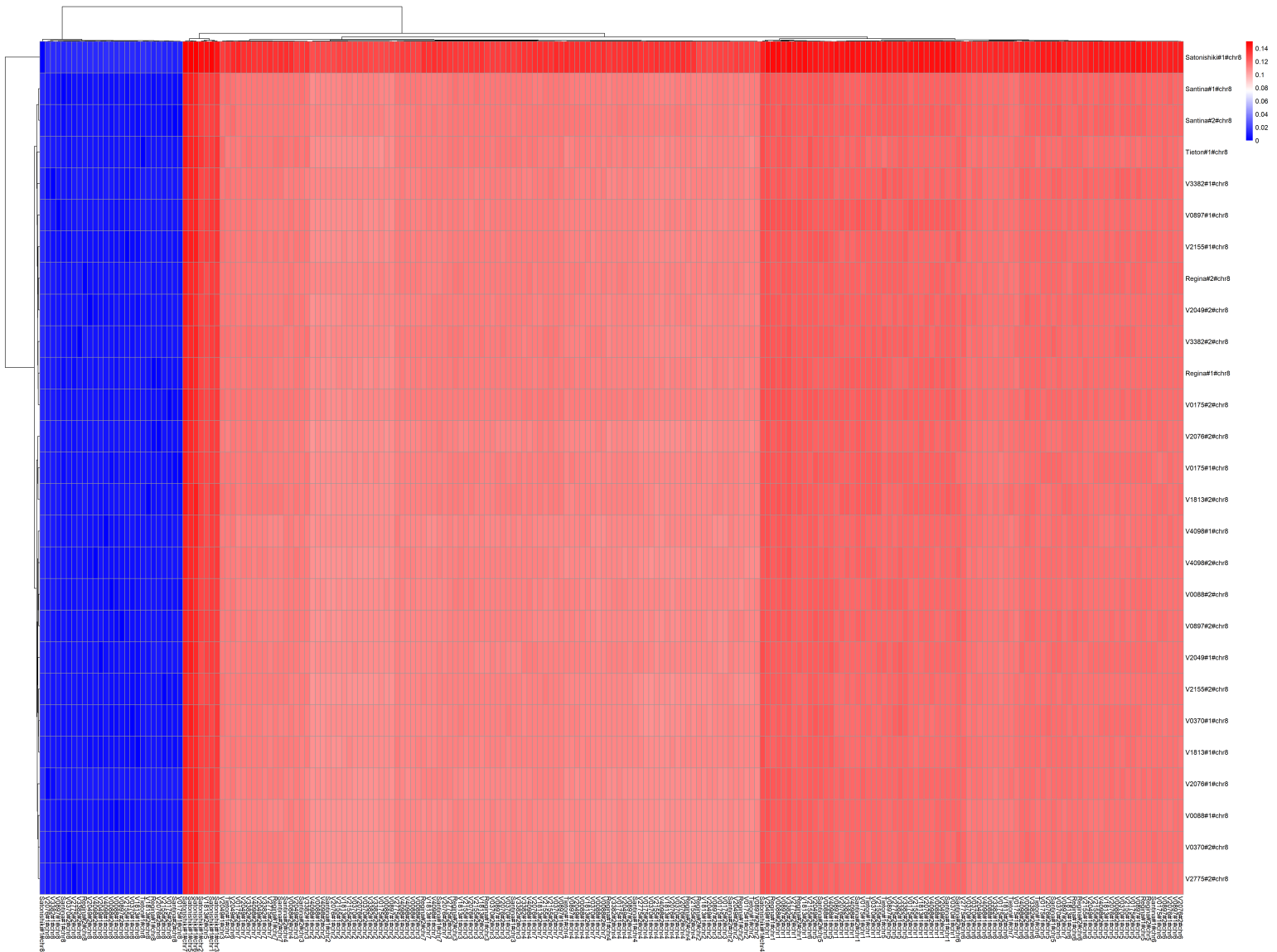


Fig. S8. Chromosome-wise alignment heatmap for chromosome 8 across sweet cherry genomes.

Alignments of chromosome 8 from each genome against all chromosomes from all genomes included in the pangenome are shown as a heatmap. Rows correspond to chr8 from each genome and columns to genomic coordinates across all chromosomes. Color intensity reflects alignment density, highlighting conserved macrosyntenic relationships and localized divergence.

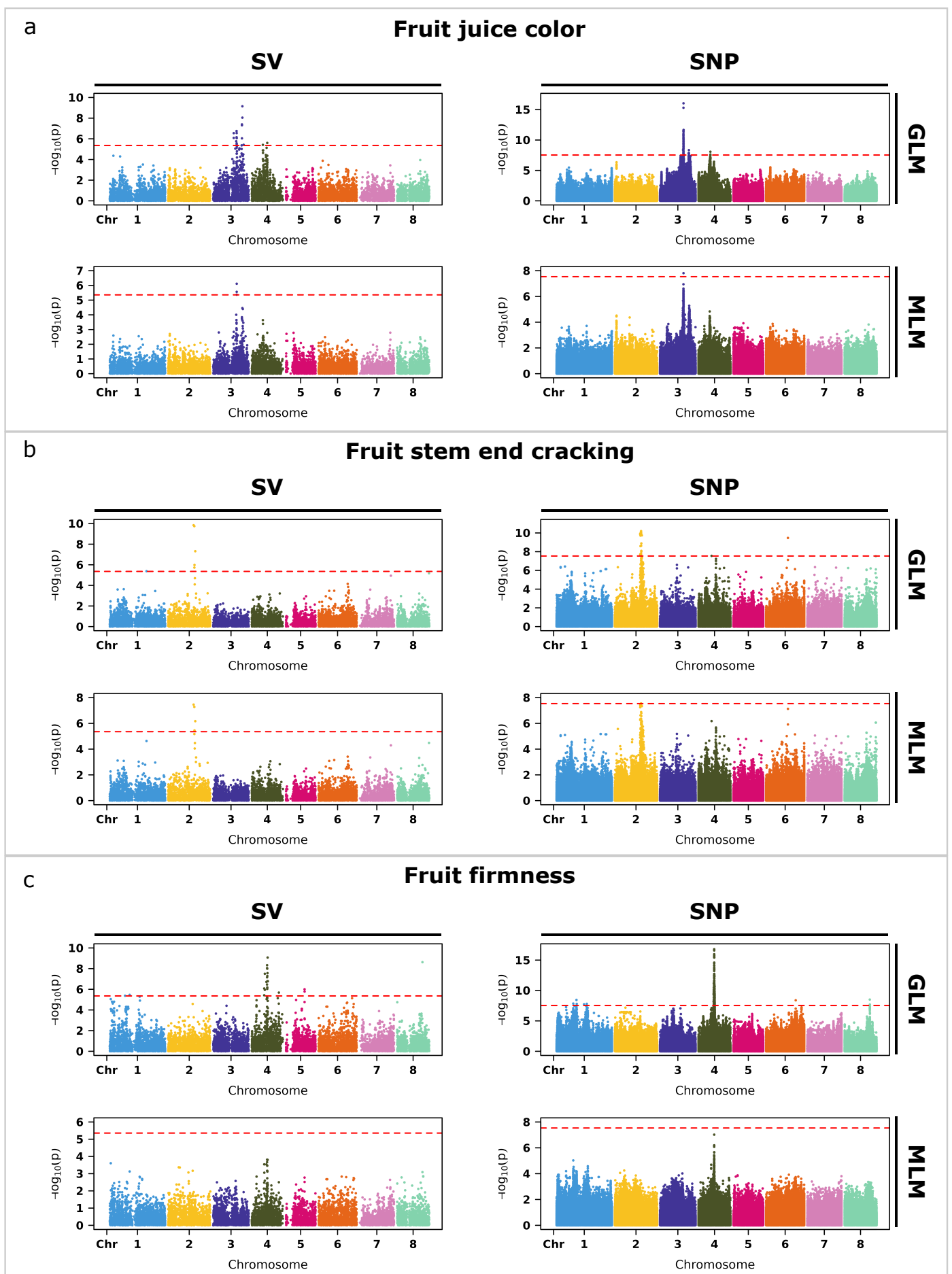


Fig. S9. Genome-wide association analyses for additional fruit traits using SNPs and structural variants.

Manhattan plots showing GWAS results obtained with structural variants (SV) and SNPs for three fruit traits: (a) fruit juice color, (b) fruit stem end cracking, and (c) fruit firmness. For each trait, results from the GLM and MLM models are shown. The x-axis represents chromosomal position across the eight chromosomes, and the y-axis shows $-\log_{10}(P)$. The red dashed line indicates the genome-wide significance threshold.

LD decay in the sweet cherry selection dataset

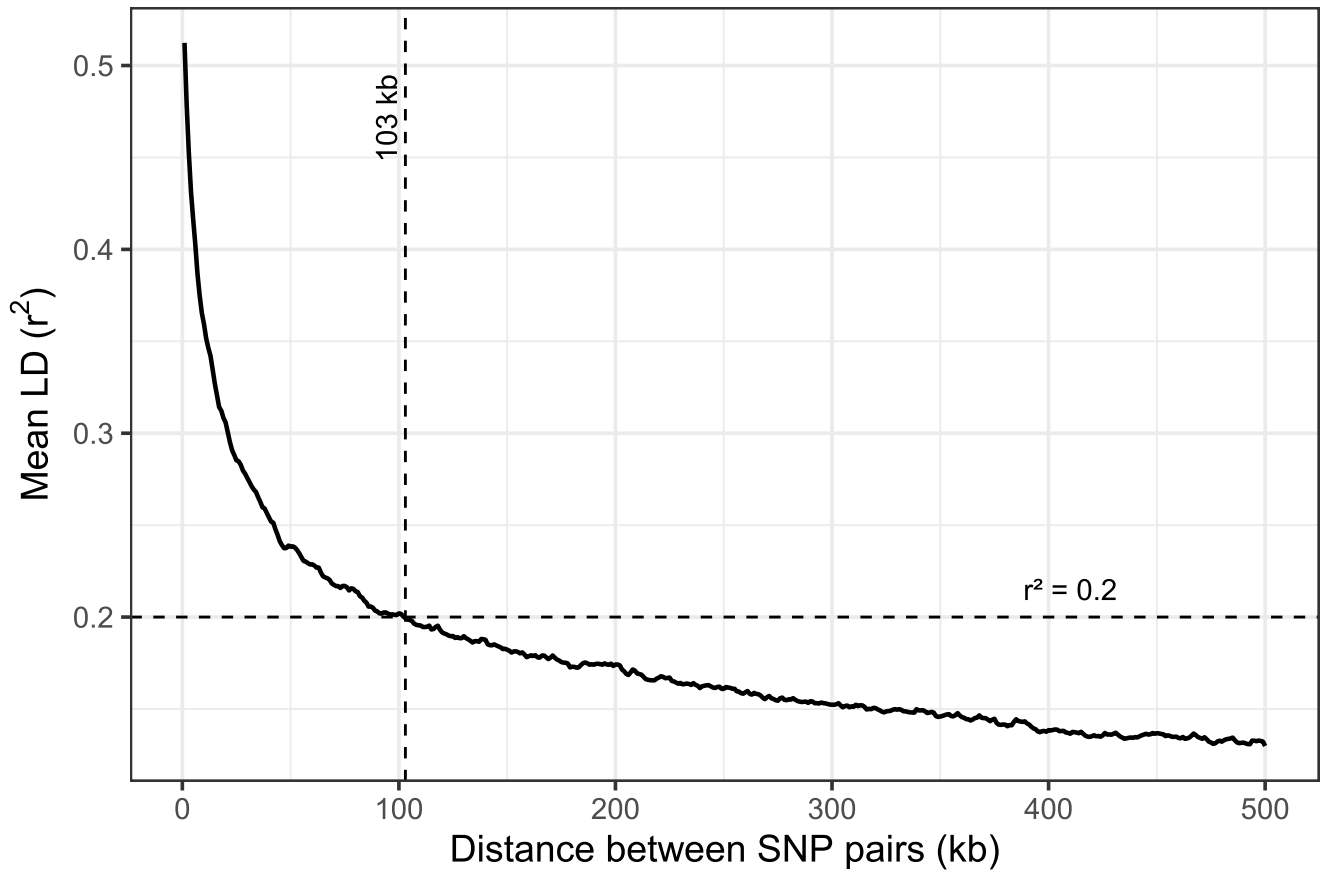


Fig. S10. Genome-wide linkage disequilibrium (LD) decay in the sweet cherry selection dataset.

Mean pairwise LD (r^2) was calculated as a function of physical distance between SNPs using PLINK v1.9. LD decayed rapidly within the first ~100 kb, reaching $r^2 \approx 0.2$ at ~100 kb, and decreased more gradually at larger distances. The dashed horizontal line indicates $r^2 = 0.2$, a commonly used threshold for linkage equilibrium, while the dashed vertical line marks the corresponding distance. These results support the use of a 100 kb window size for F_{ST} analyses. A zoomed view of the first 200 kb is also provided to highlight short-range LD decay.