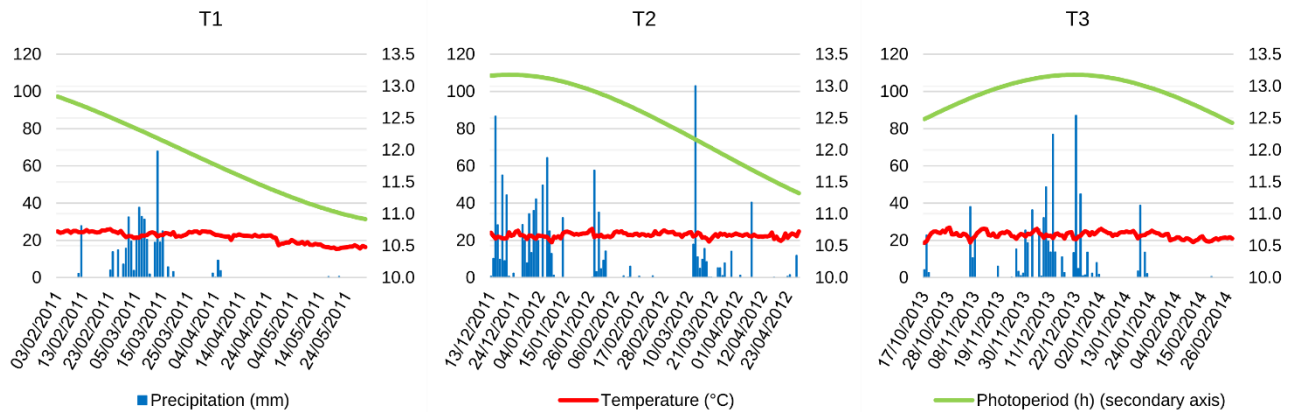
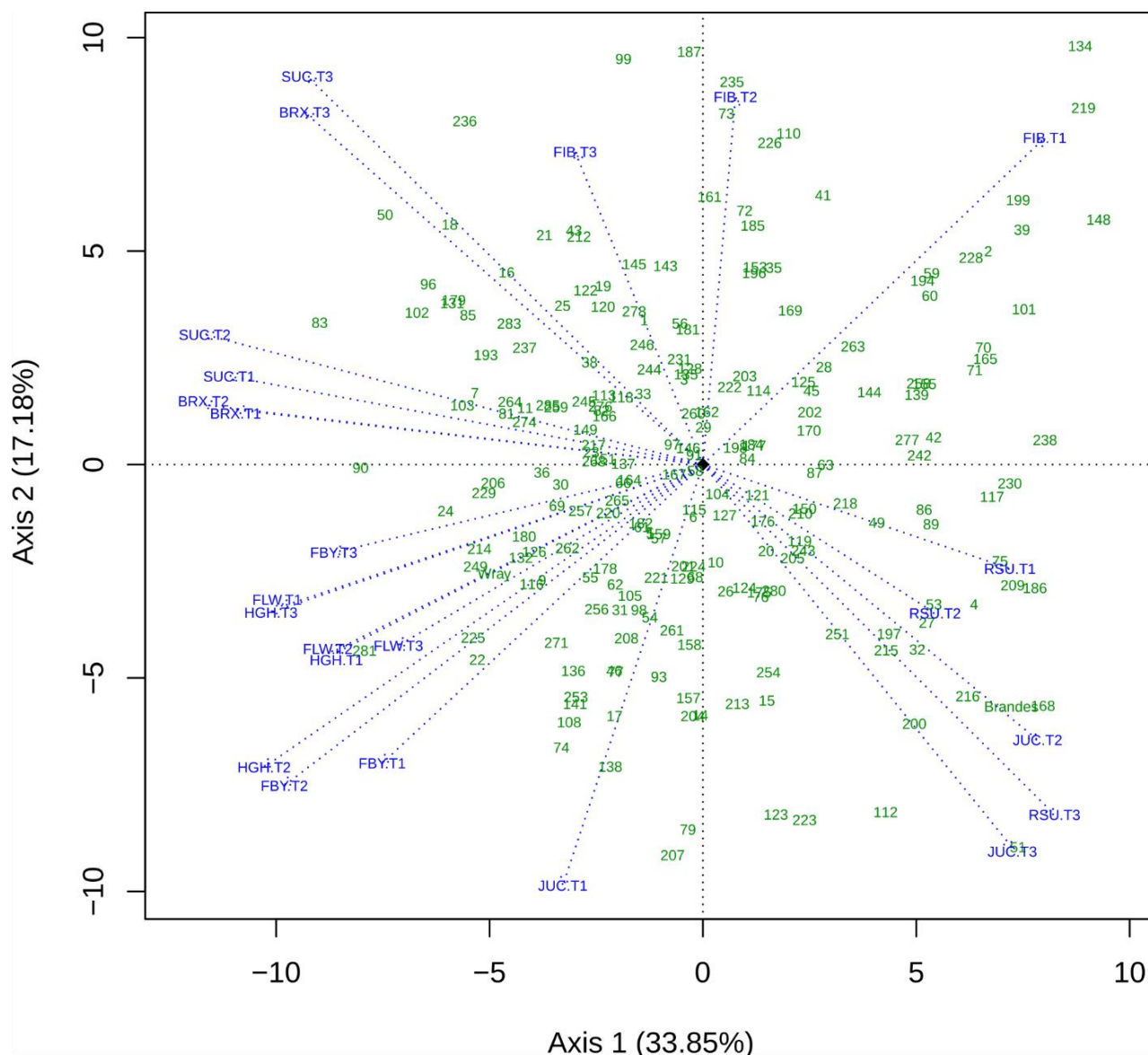


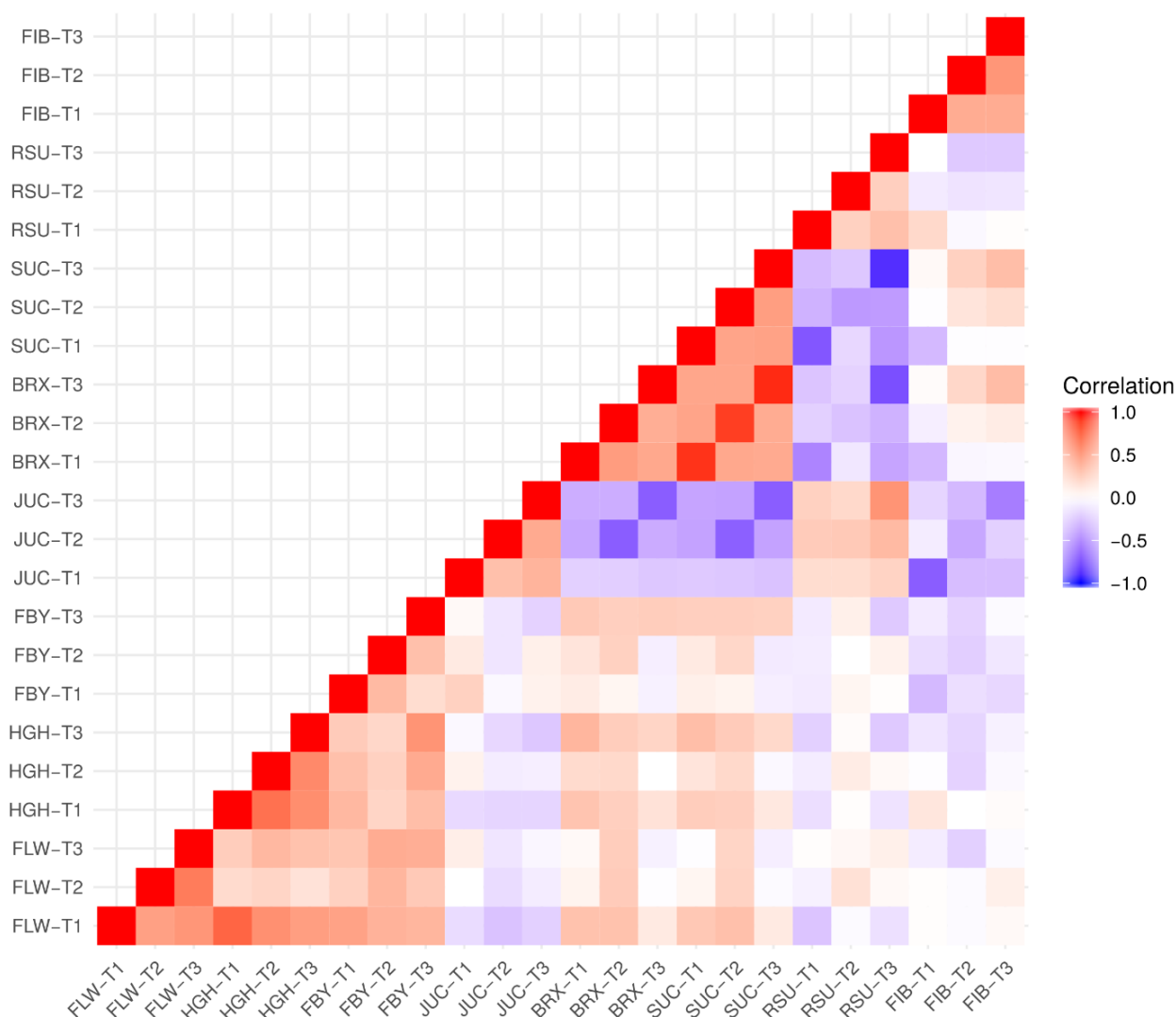
Supplementary Figures



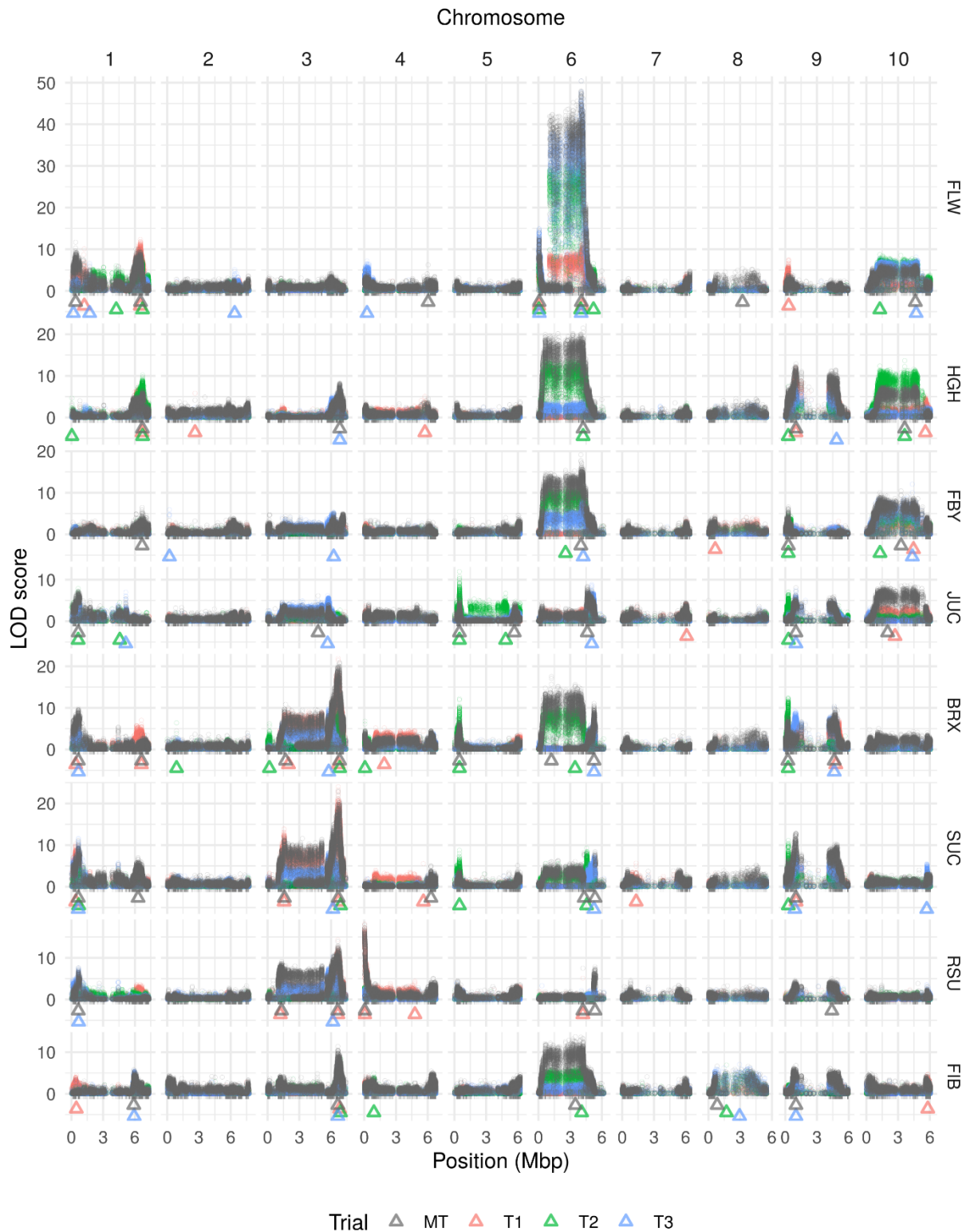
Supplementary Figure S1. Precipitation (mm) and average daily temperature (°C, left axis) and photoperiod (h, right axis) along the crop cycles of the three trials (T1, T2, T3) for Brandes × Wray sweet sorghum recombinant inbred lines. The climatic information was obtained from the meteorological station of Embrapa Maize and Sorghum, Sete Lagoas, Brazil.



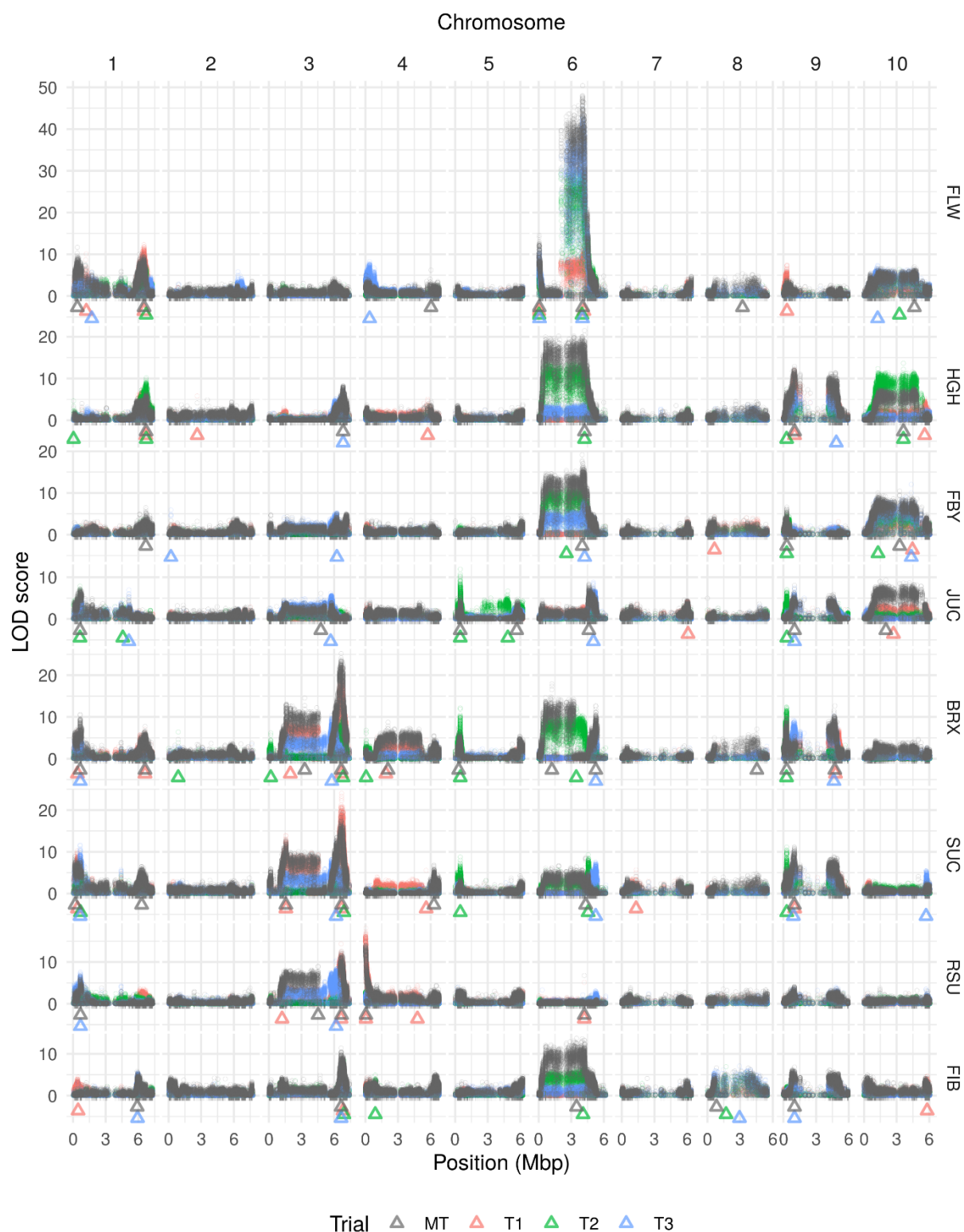
Supplementary Figure S2. GGE biplot of adjusted means of Brandes × Wray sweet sorghum recombinant inbred lines (in green), and the vectors of each trait-trial combination (in blue). Traits: days to flowering (FLW), plant height (HGH, in cm), fresh biomass yield (FBY, in $t \cdot ha^{-1}$), juice extraction yield (JUC, in %), total soluble solids (BRX, in $^{\circ}Brix$), sucrose content (SUC, in %), reducing sugar content (RSU, in %) and fibers (FIB, in %). Trials: T1, T2, T3.



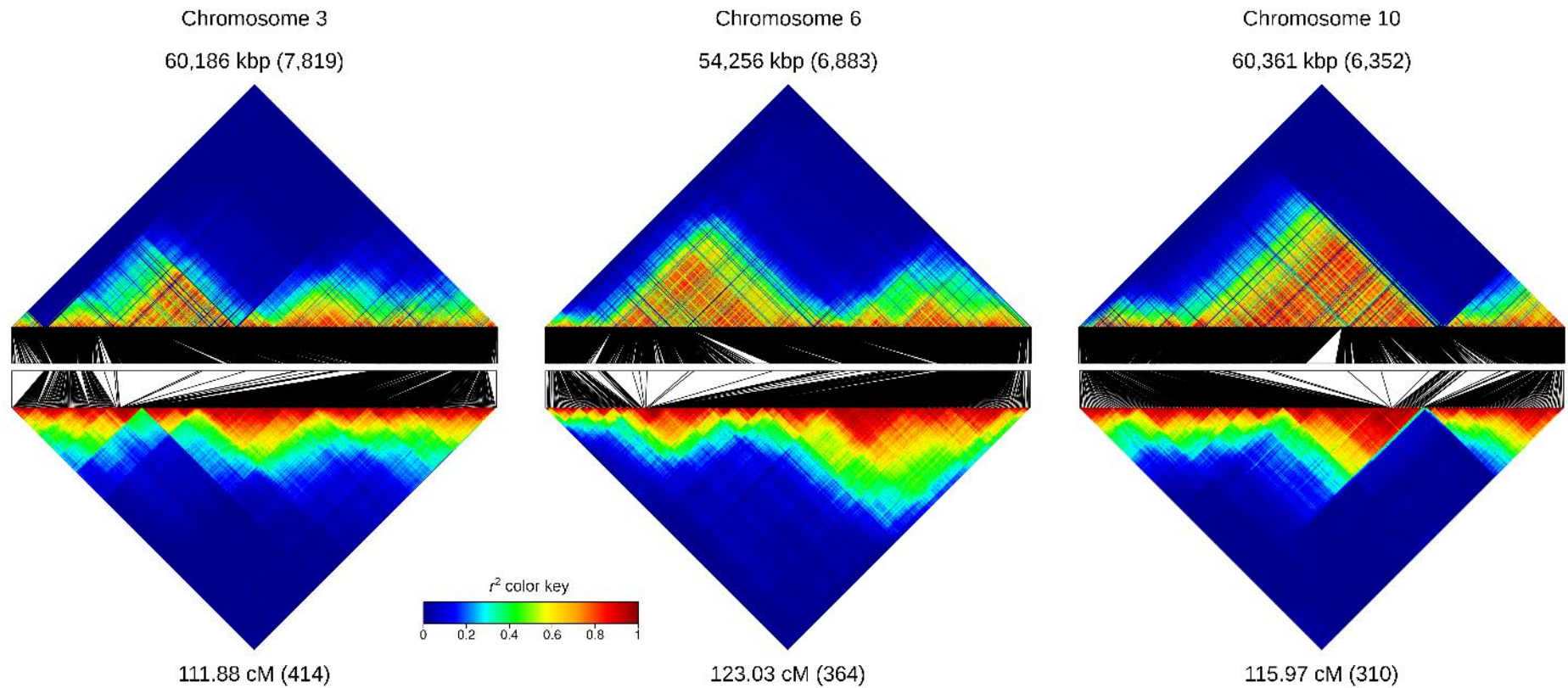
Supplementary Figure S3. Heatmap of correlations between adjusted means of Brandes × Wray sweet sorghum recombinant inbred lines evaluated across three trials (T1, T2, T3). Traits: days to flowering (FLW), plant height (HGH, in cm), fresh biomass yield (FBY, in $\text{t} \cdot \text{ha}^{-1}$), juice extraction yield (JUC, in %), total soluble solids (BRX, in $^{\circ}\text{Brix}$), sucrose content (SUC, in %), reducing sugar content (RSU, in %) and fibers (FIB, in %).



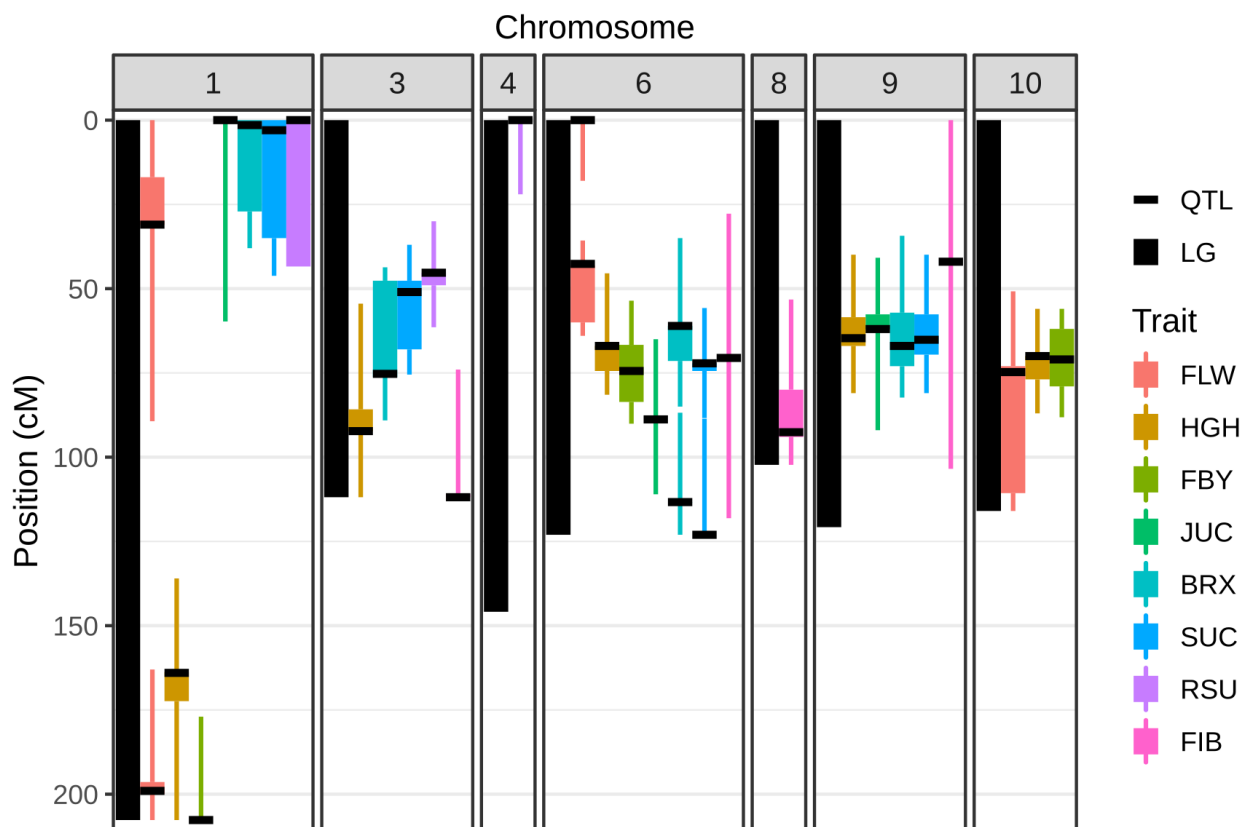
Supplementary Figure S4. Physical map-based LOD scores of multiple interval mapping (MIM) for individual (T1, T2, T3) and multiple trials (MT) for Brandes \times Wray sweet sorghum recombinant inbred lines using a mapping window size of 100 kbp. Triangles represent mapped QTLs. Traits: days to flowering (FLW), plant height (HGH, in cm), fresh biomass yield (FBY, in $t \cdot ha^{-1}$), juice extraction yield (JUC, in %), total soluble solids (BRX, in $^{\circ}$ Brix), sucrose content (SUC, in %), reducing sugar content (RSU, in %) and fibers (FIB, in %).



Supplementary Figure S5. Physical map-based LOD scores of multiple interval mapping (MIM) for individual (T1, T2, T3) and multiple trials (MT) for Brandes \times Wray sweet sorghum recombinant inbred lines using a mapping window size of 200 kbp. Triangles represent mapped QTLs. Traits: days to flowering (FLW), plant height (HGH, in cm), fresh biomass yield (FBY, in $\text{t} \cdot \text{ha}^{-1}$), juice extraction yield (JUC, in %), total soluble solids (BRX, in $^{\circ}\text{Brix}$), sucrose content (SUC, in %), reducing sugar content (RSU, in %) and fibers (FIB, in %).



Supplementary Figure S6. Heatmap of linkage disequilibrium measures as squared correlation coefficients (r^2) between pairs of markers in the physical (top) and genetic (bottom) maps for chromosomes 3, 6, and 10. Physical and genetic distances are shown together with the number of markers (in parentheses).



Supplementary Figure S7. Multi-trait multiple interval mapping (MT-MIM) for Brandes × Wray sweet sorghum recombinant inbred lines. QTL peaks are represented as horizontal black lines, and their respective support intervals are represented by vertical-colored lines. Vertical bars represent the chromosomes (Chr, black) or the limits of co-located QTLs from MIM analyses (separate trials, colored). Traits: days to flowering (FLW), plant height (HGH, in cm), fresh biomass yield (FBY, in $\text{t} \cdot \text{ha}^{-1}$), juice extraction yield (JUC, in %), total soluble solids (BRX, in $^{\circ}\text{Brix}$), sucrose content (SUC, in %), reducing sugar content (RSU, in %) and fibers (FIB, in %).