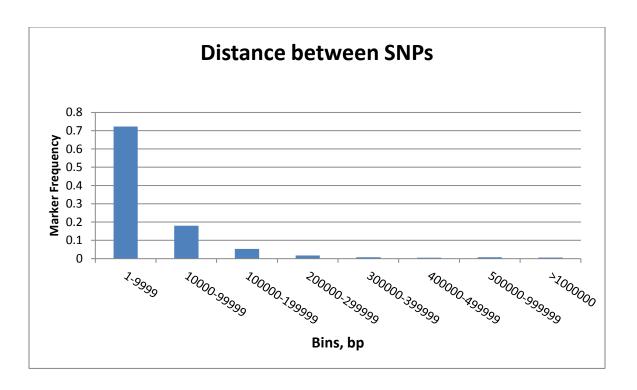


**Figure S1a** Distribution of SNPs utilized in this study across the 10 *Sorghum bicolor* chromosomes. The location of SNPs generated by genotyping-by-sequencing at *Fsel* cut-sites are represented by blue squares. The y-axis represents the physical location of the SNPs across the sorghum genome. The SNPs are well-distributed over the 10 chromosomes and cover predominantly euchromatic regions of the genome. Regions in which SNPs are absent represent the gene-poor pericentromeric heterochromatic regions.



**Figure S1b** Distance between SNPs utilized in this study. The x-axis represents ranges of base pair distances between adjacent SNPs. The y-axis represents the percentage of total SNPs that fall within a specific range. The figure shows that 72% of the SNPs fall within 10,000 base pairs of each other.