

Figure S1 Evaluation of the repeatability and accuracy of SNPs in the 600K SoySNP array. (a) The consistency between two independent genotype calls produced by this array was calculated for six soybean accessions. (b) The consistency between genotype calls from this array and the in-depth resequencing method was evaluated for 13 parental lines.

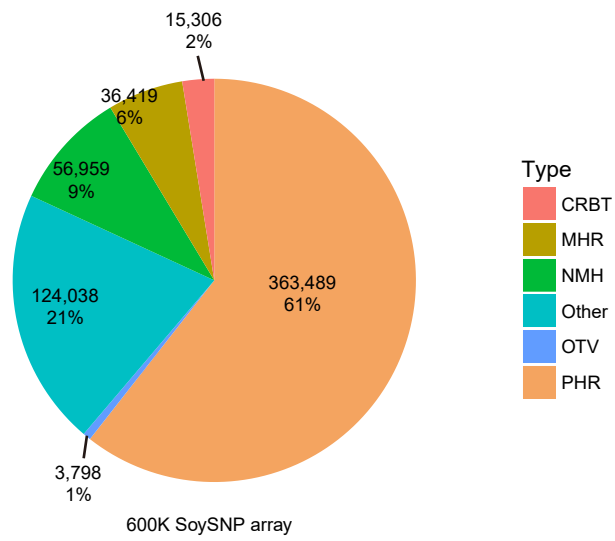


Figure S2 Classification of SNPs in the 600K SoySNP array. CRBT, CallRateBelowThreshold; MHR, MonoHighResolution; NMH, NoMinorHom; Other, several criteria not fulfilled; OTV, Off-Target Variant; PHR, PolyHighResolution.

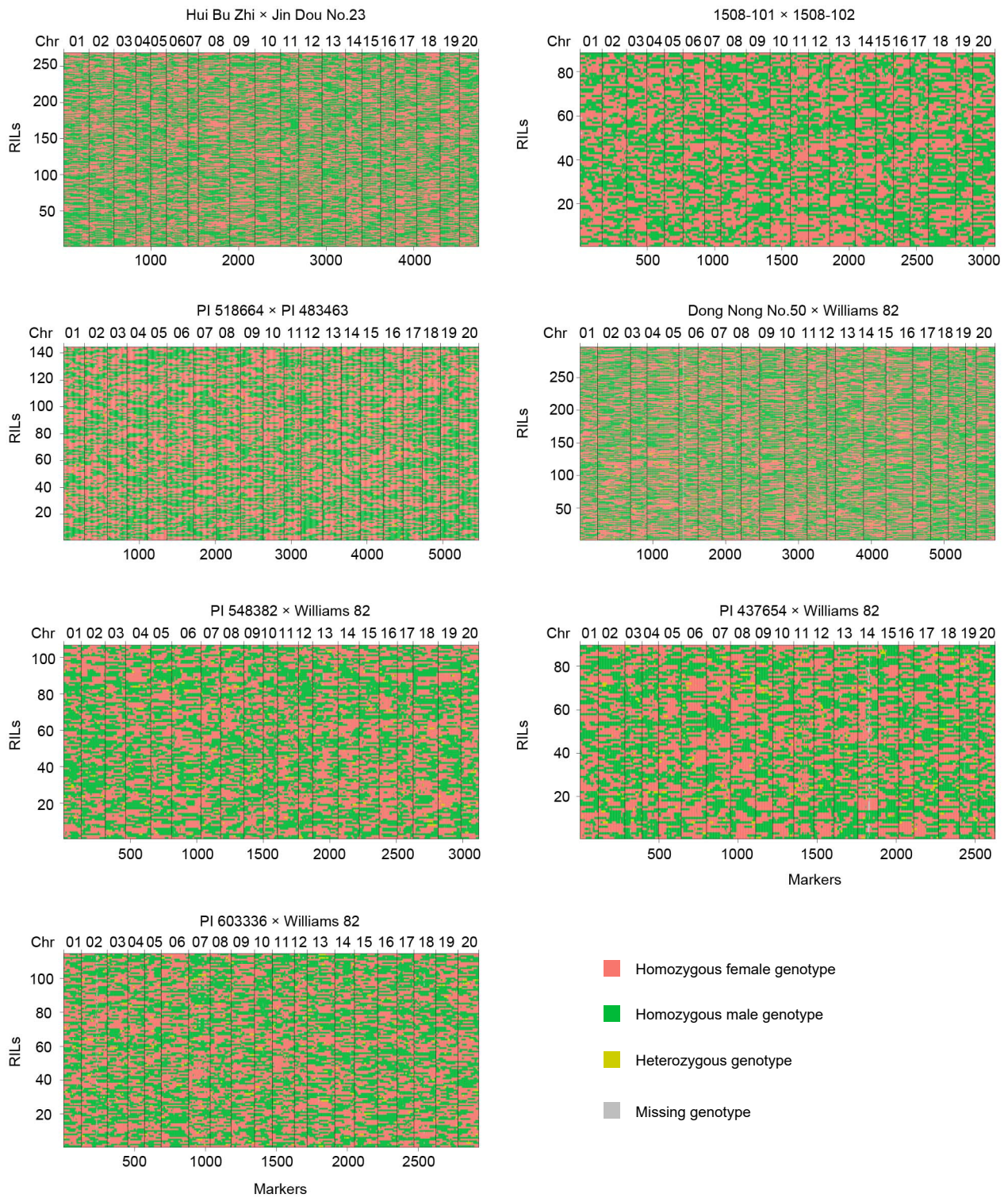


Figure S3 Recombination maps for soybean RIL populations. The color red represents the homozygous female genotype, green indicates the homozygous male genotype, yellow represents the heterozygous genotype, and gray indicates a missing genotype.

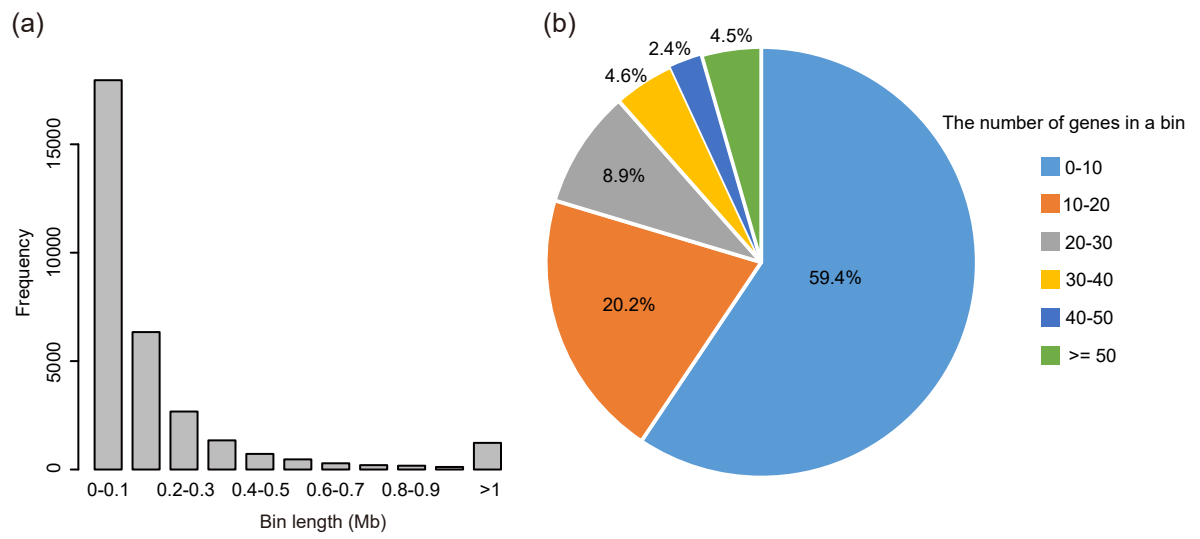


Figure S4 Features of bins in the recombination bin map. (a) The distribution of bin length in soybean RIL populations. (b) The proportion of bins containing different gene numbers based on Wm82 reference genome annotation (Wm82.a2.v1).

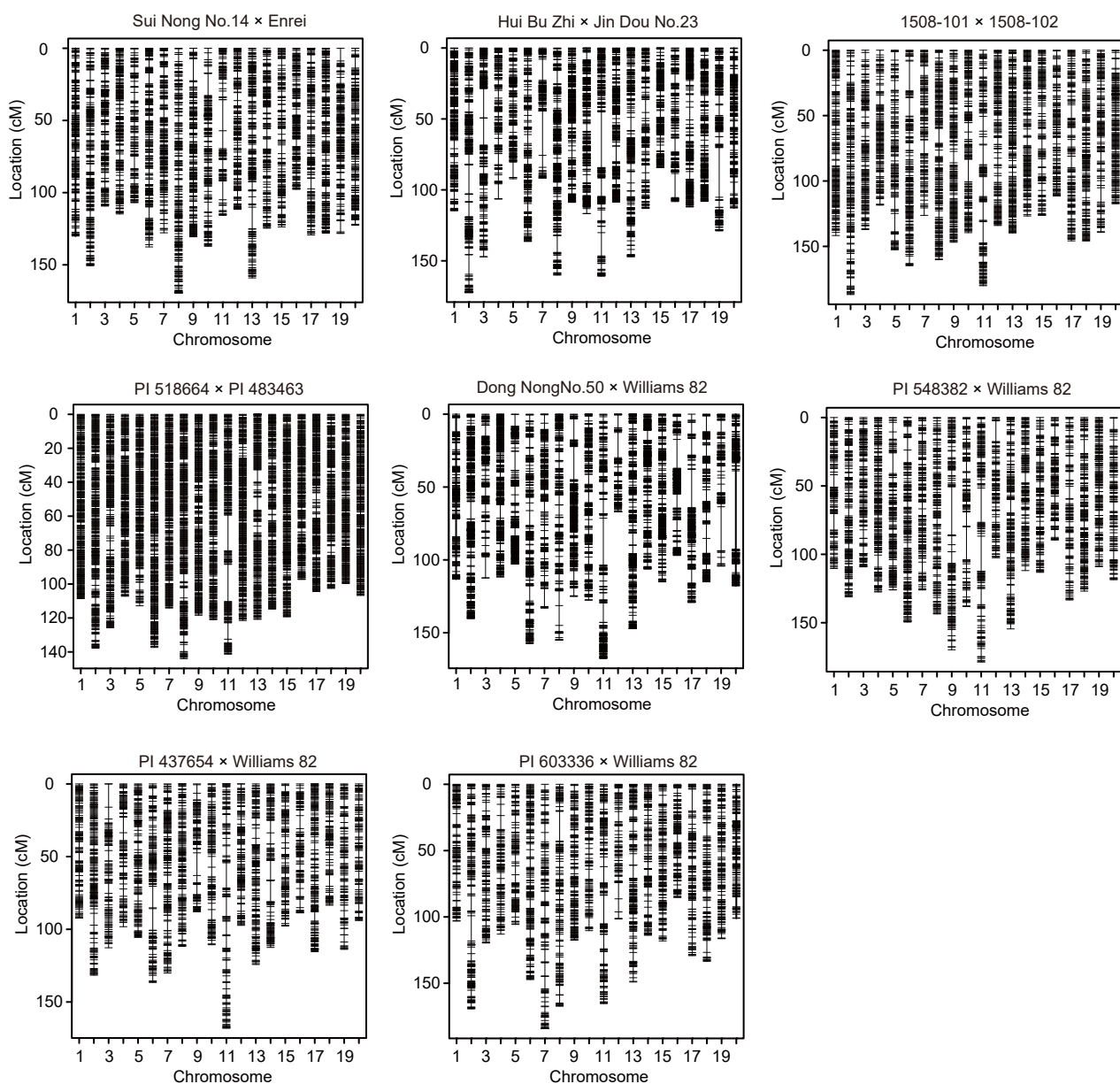


Figure S5 Linkage maps for eight soybean RIL populations using bins as genetic markers. Chromosomes and bins are represented by the vertical and short horizontal lines, respectively.

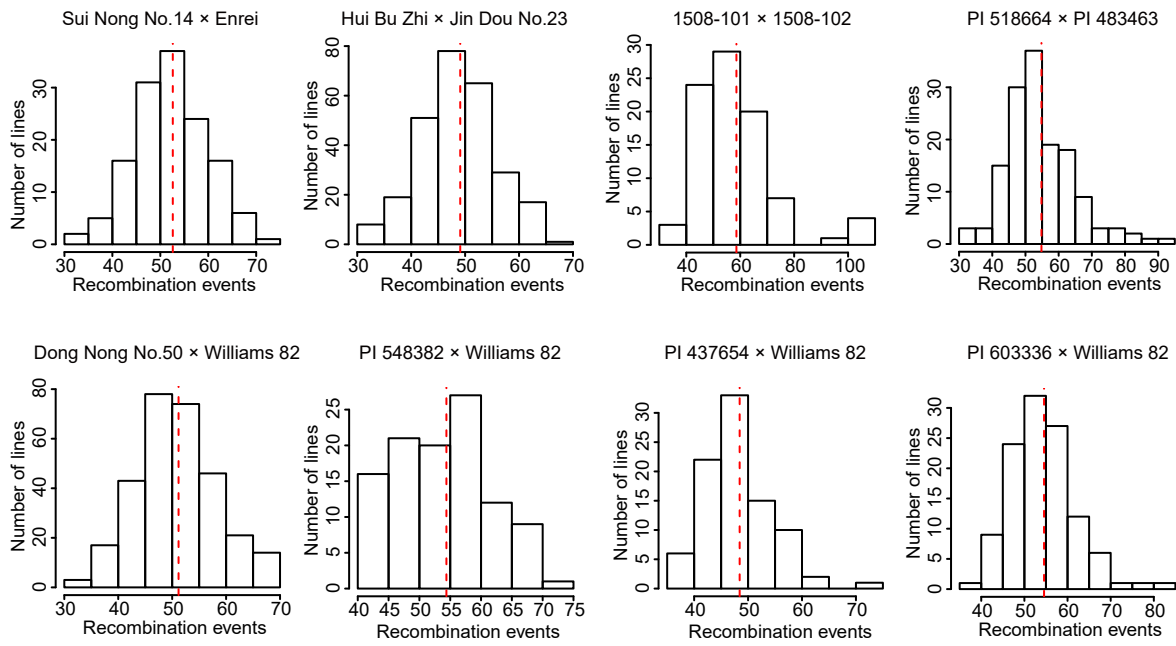


Figure S6 Distribution of recombination events identified in 8 soybean RIL populations. Red dashed lines indicate average recombination events per RIL for each population.

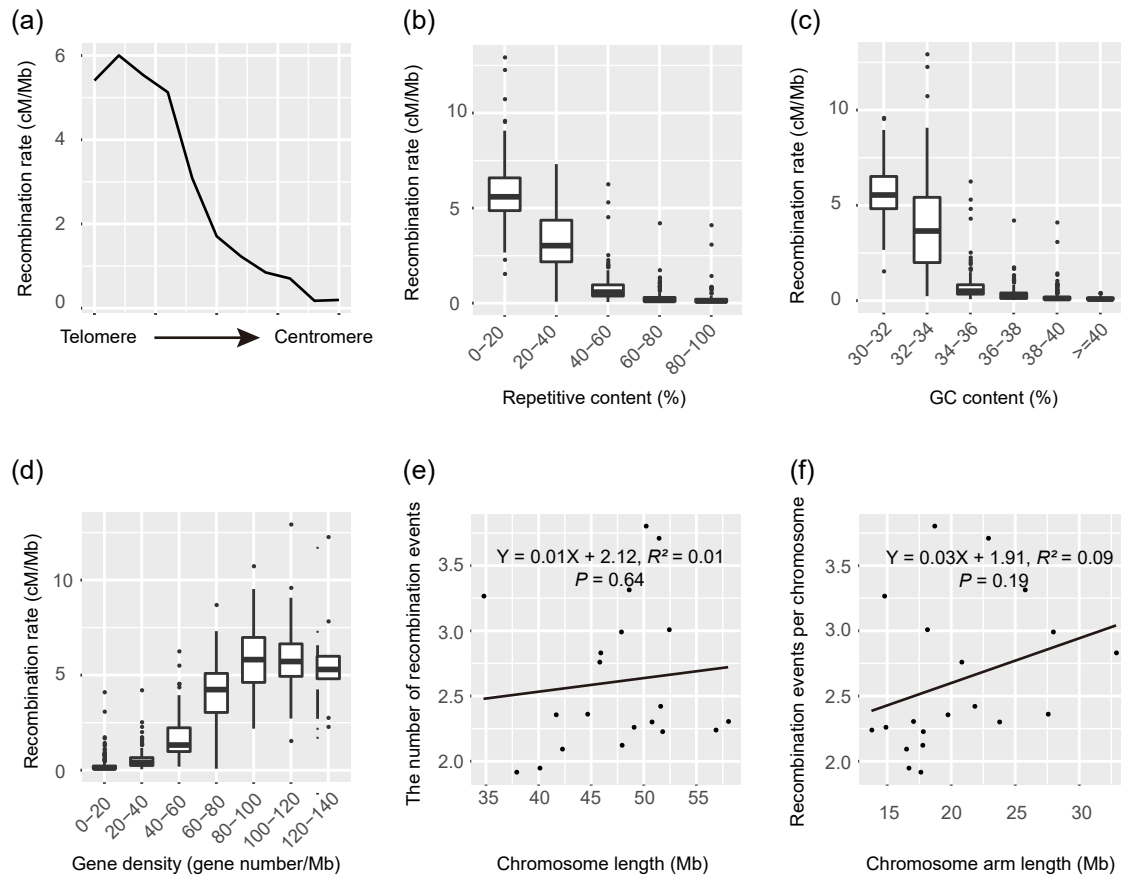


Figure S7 Genomic features of recombination events in soybean. (a) The distribution of recombination rate from telomere to centromere. (b-d) The association between recombination rate and repetitive content (b), GC content (c) and gene density (d). The center line of the boxes indicates the median recombination rate, and the lower and upper bounds of the boxes represent the first (Q1) and third (Q3) quartiles of the recombination rate, respectively. The whiskers denote $Q3 + 1.5 \times$ the interquartile range (IQR) and $Q1 - 1.5 \times$ IQR from the top, respectively, where $IQR = Q3 - Q1$. (e, f) Relationship between the average numbers of recombination events per chromosome and chromosome size (e) and chromosome arm length (f).

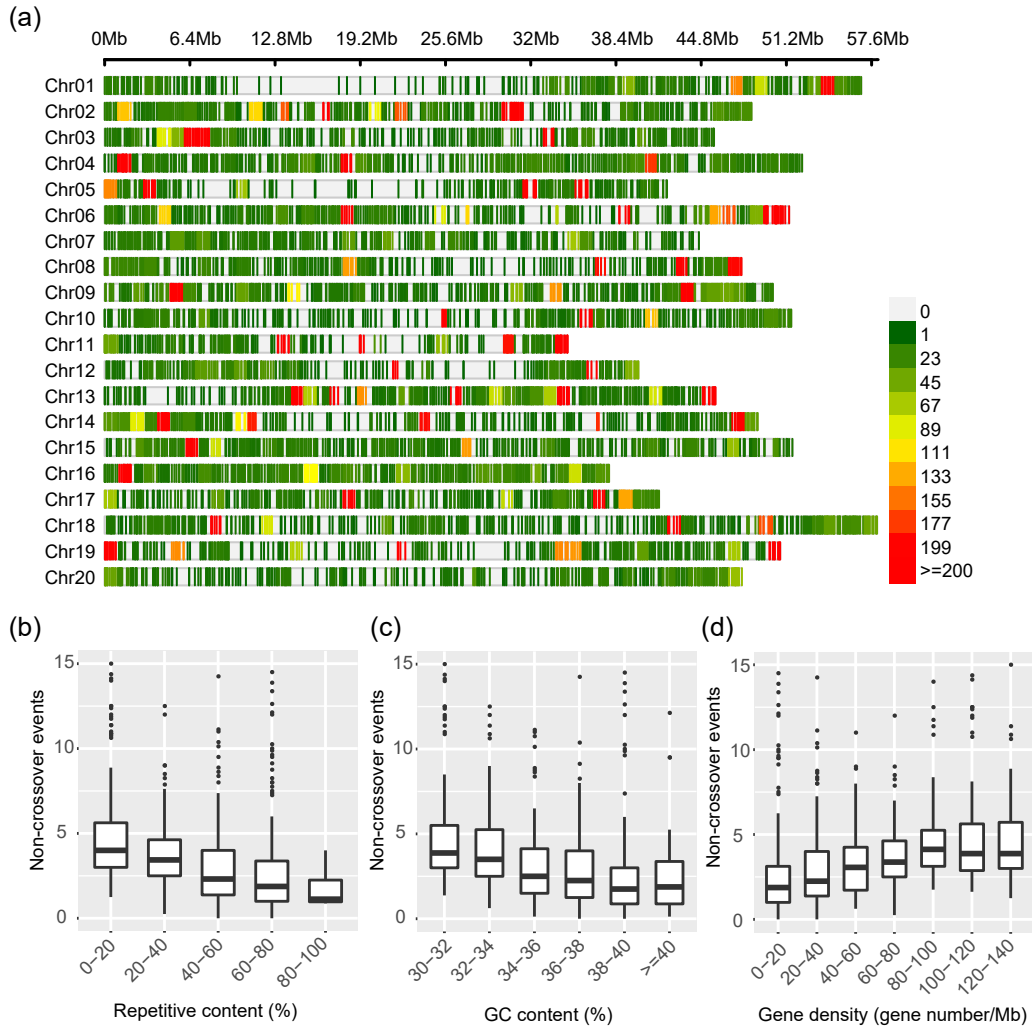


Figure S8 Non-crossover (NCO) events and their genomic features in soybean RIL populations. (a) The distribution of NCO events along the all chromosomes. Various color represents NCO density in a window of 1 Mb. (b-d) The association between NCO events and repetitive content (b), GC content (c) and gene density (d).

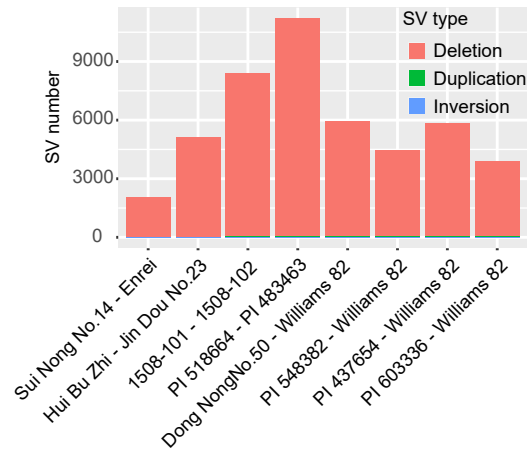


Figure S9 SVs detected between the parental lines of each RIL population. SVs included deletion, insertion and inversion.

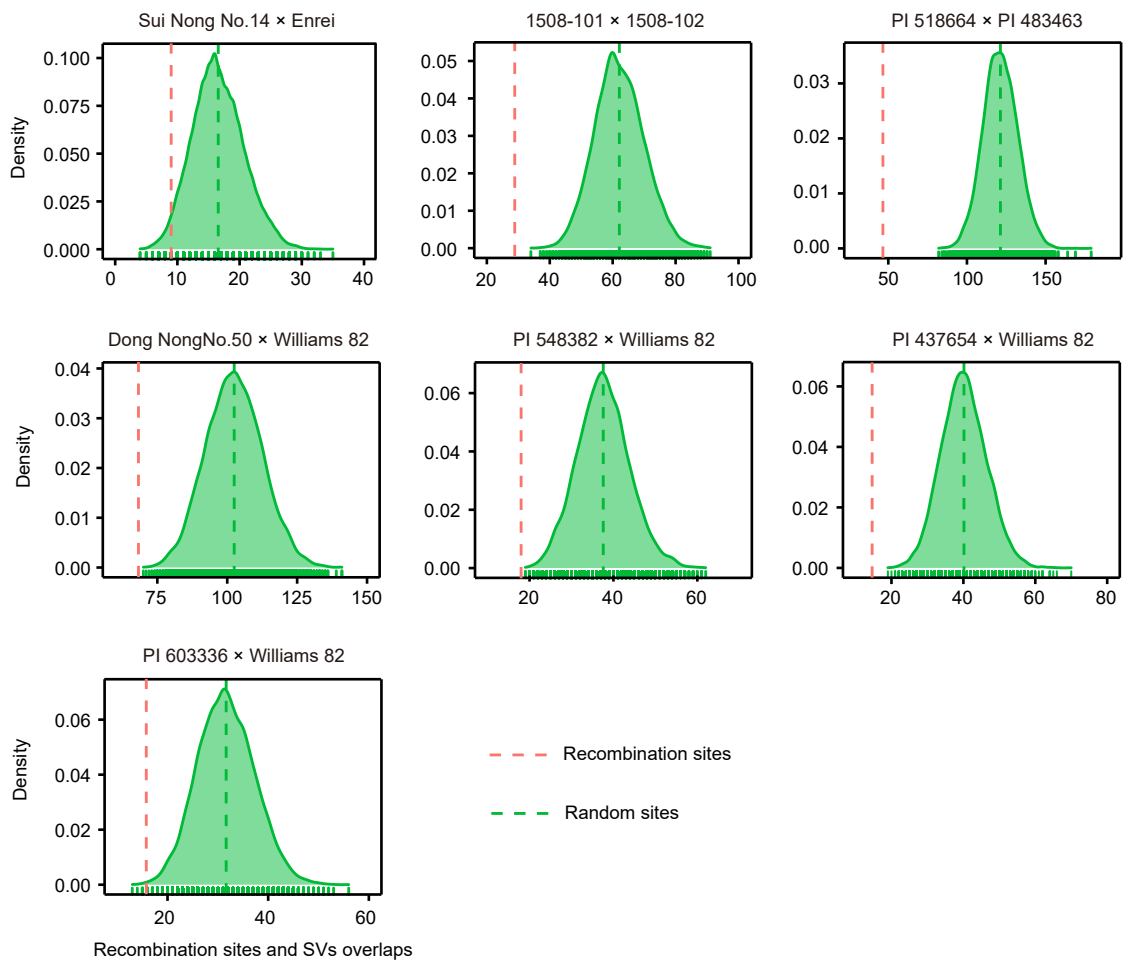


Figure S10 Overlaps between SVs and recombination events for each population. Dashed red lines indicate the average overlaps between SVs and recombination events, while dashed green lines indicate the average overlaps between SVs and MC random sites.

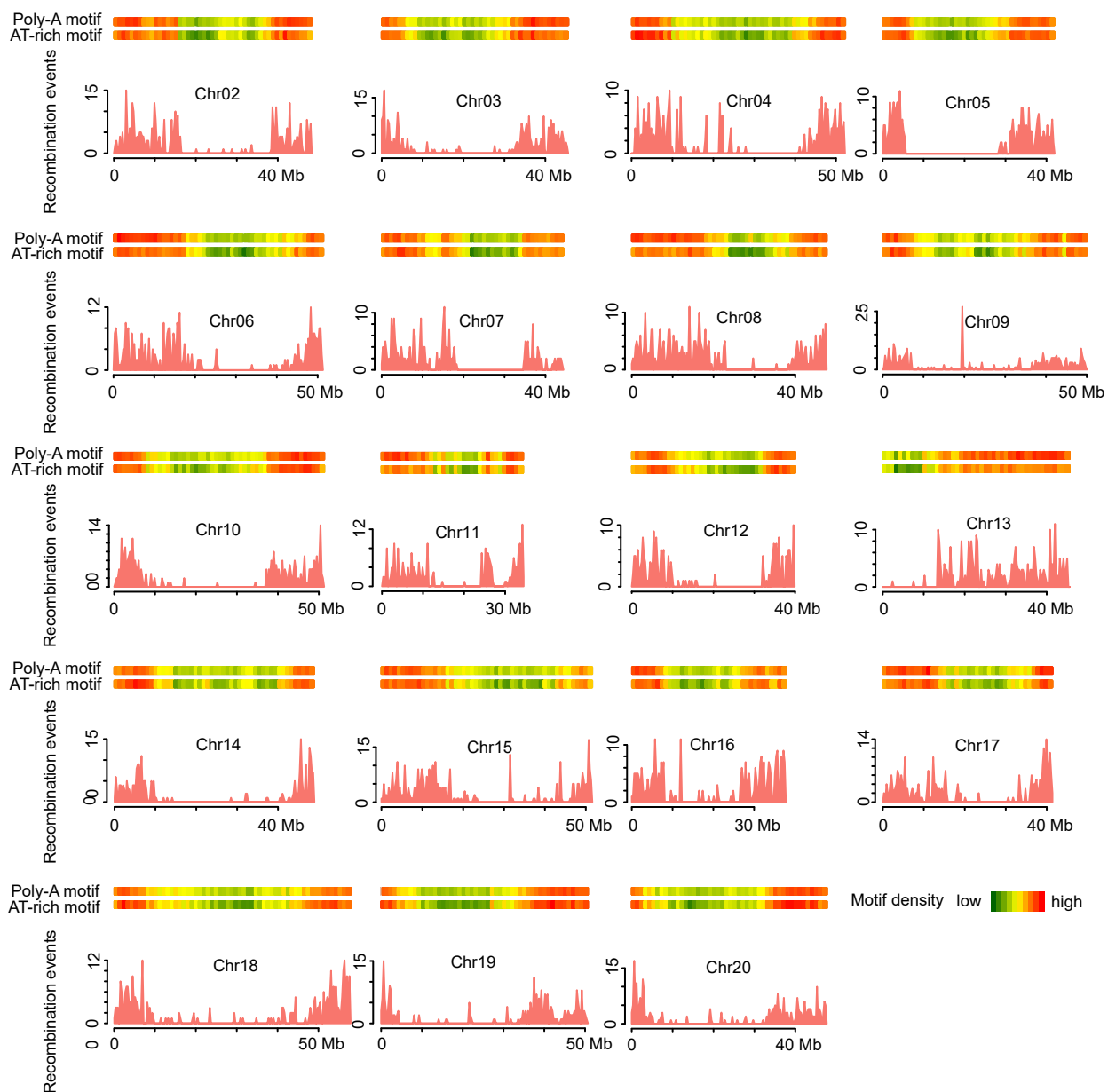


Figure S11 Poly-A and AT-rich motifs associated with the distribution of high-resolution recombination events along Chr02 to Chr20. The colors from green to red represent increasing motif density.

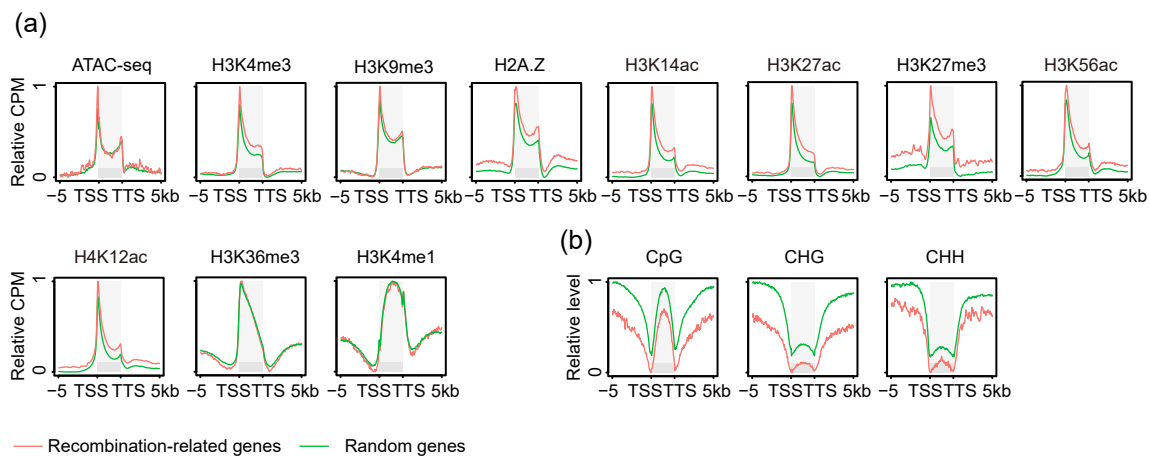


Figure S12 Epigenetic modifications across recombination-related genes and random genes obtained from permutations and in their flanking regions. (a) The distribution of normalized read counts for ATAC-seq, histone modifications and histone variant H2A.Z across recombination-related genes and in their flanking regions compared to random genes. (b) The distribution of normalized DNA methylation levels across recombination-related genes and in their flanking regions compared to random genes. CPM, counts per million; TSS, transcription start site; TTS, transcription termination site.

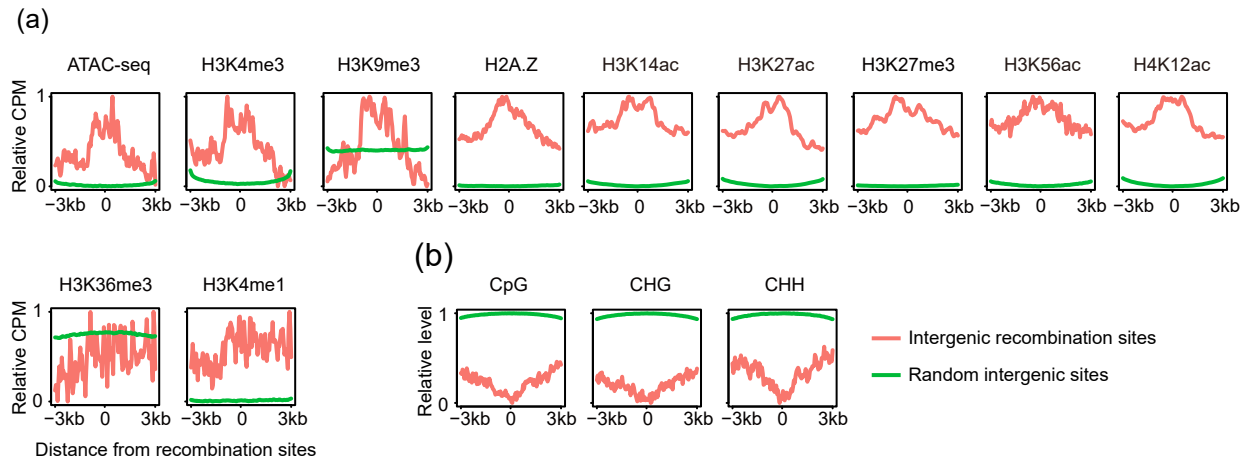


Figure S13 The distribution of read counts for chromatin states, histone modifications, histone variant H2A.Z and DNA methylation levels along intergenic recombination sites and their flanking regions compared to random sites. (a) The distribution of normalized read counts for ATAC-seq, histone modifications and histone variant H2A.Z along intergenic recombination sites and their flanking regions compared to random sites. (b) The distribution of normalized DNA methylation levels along intergenic recombination sites and their flanking regions compared to random genes. CPM, counts per million.