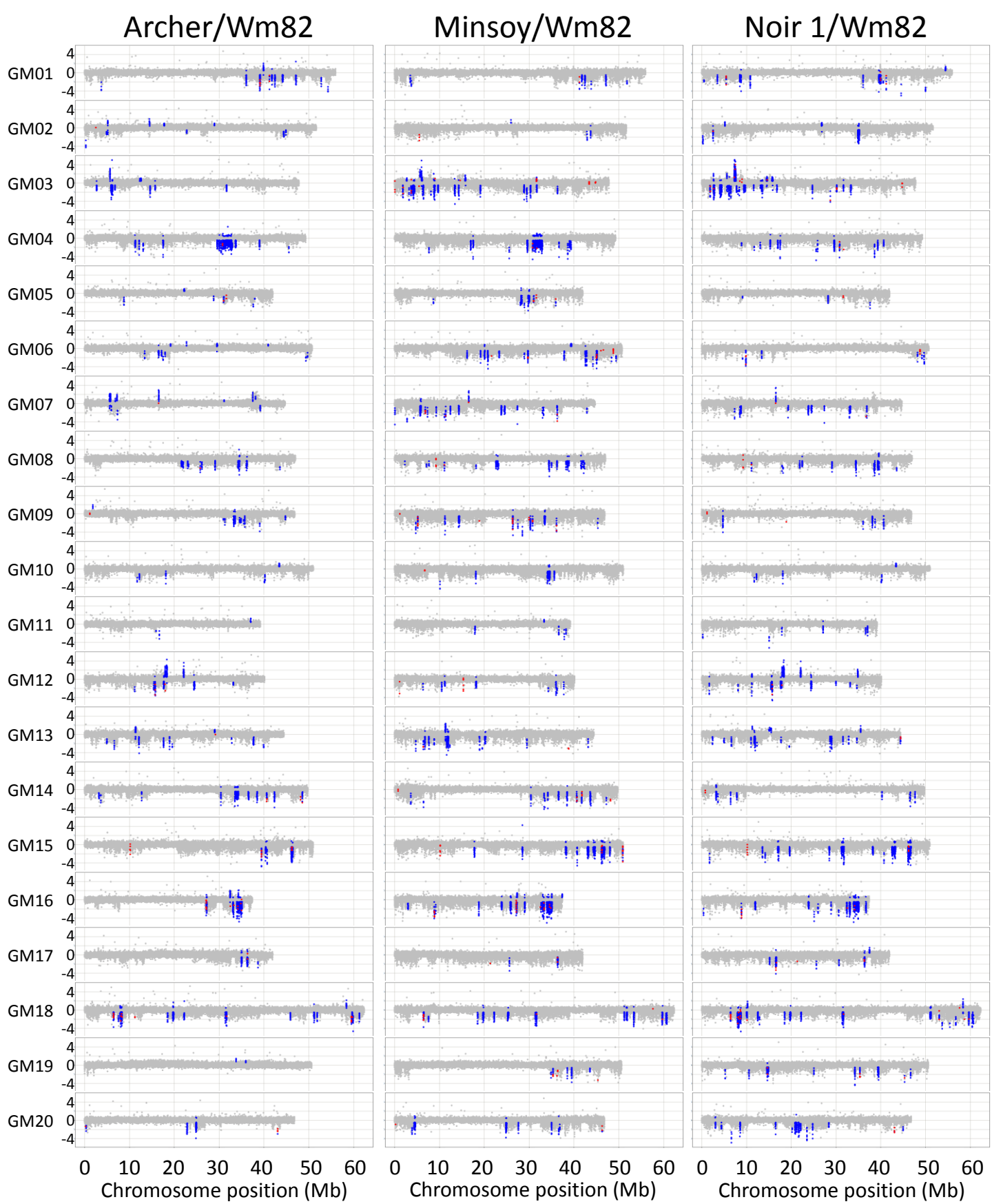
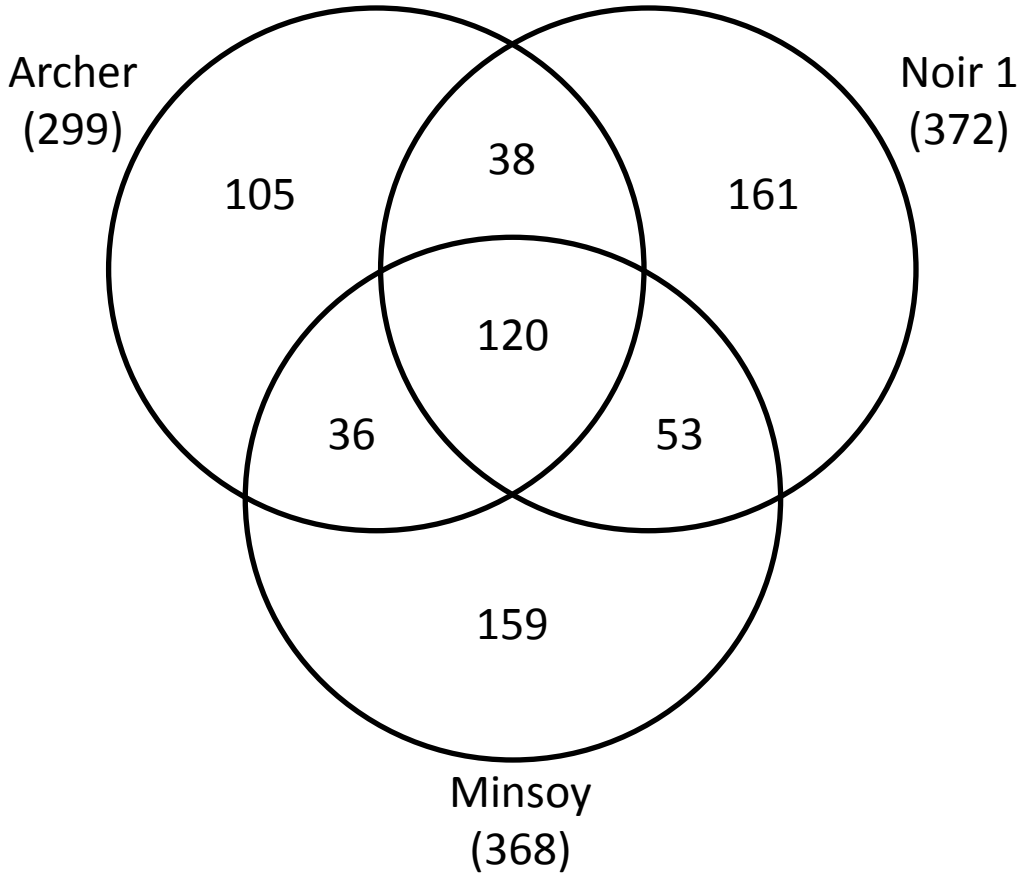
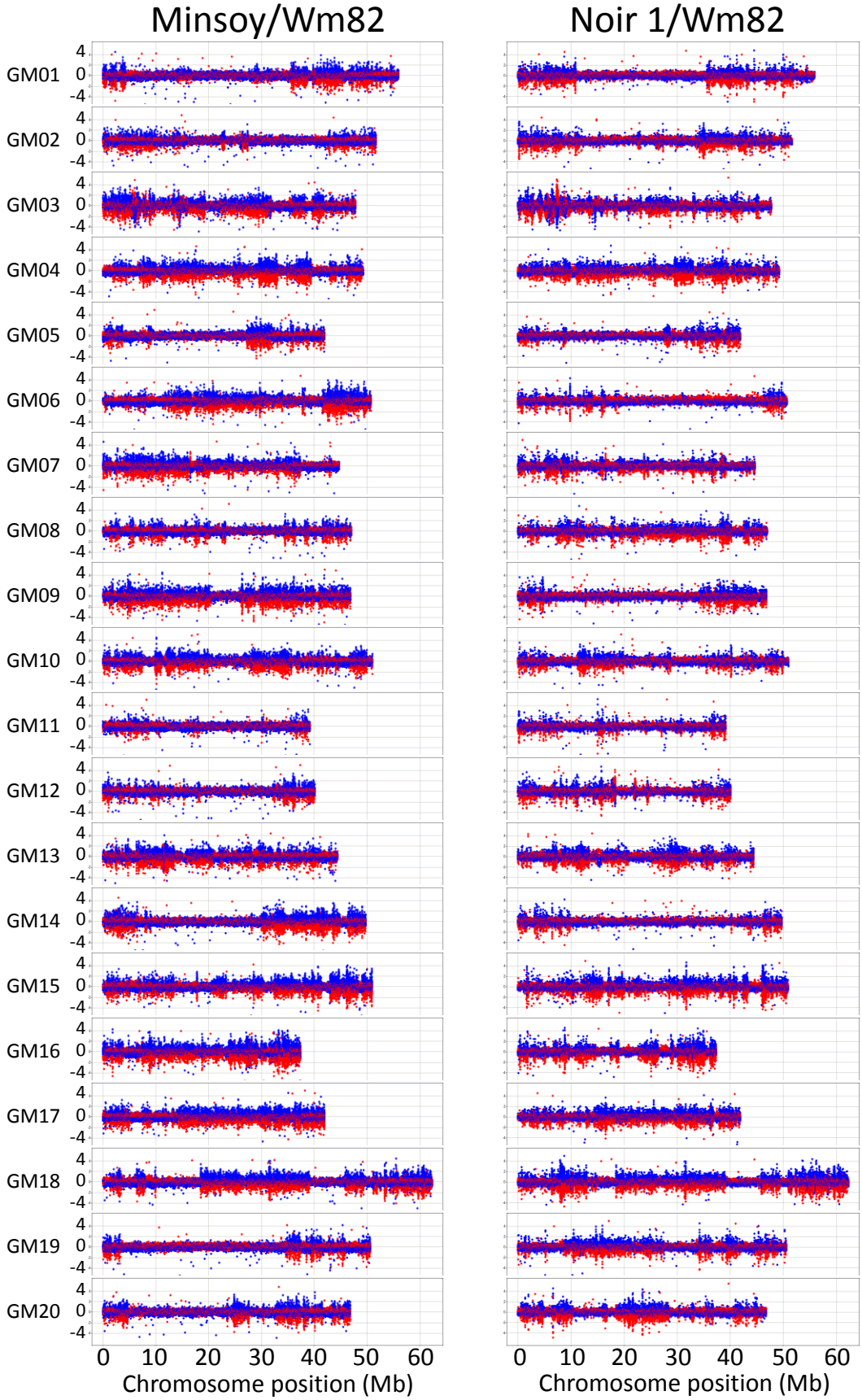


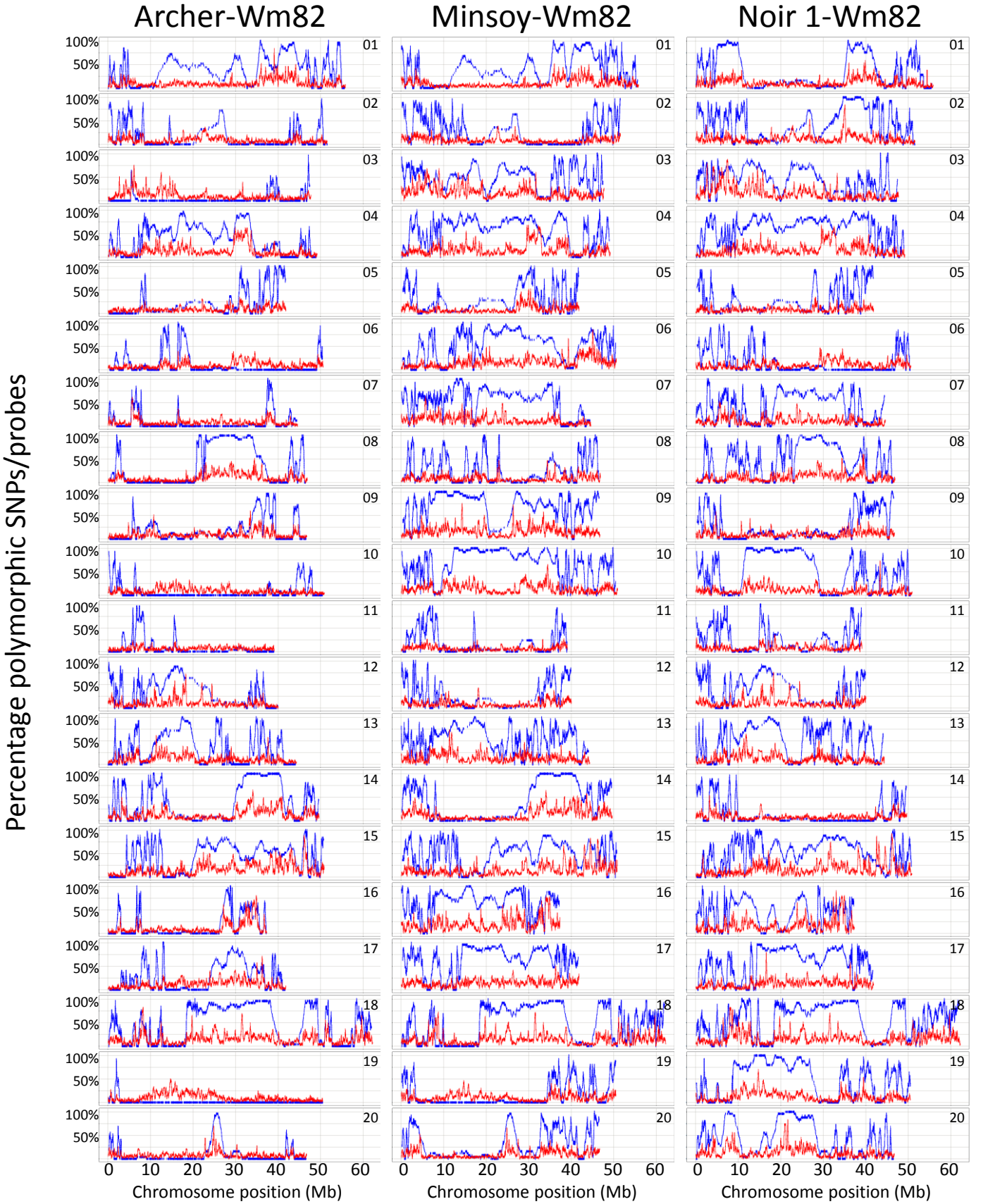
Supplemental Figure 1. Copy number variation (CNV) among soybean genotypes. Log2 ratios between each genotype relative to the Wm82 reference are shown. Blue spots indicate probes within significant CNV segments with values beyond threshold. Red spots indicate probes within present-absent variant (PAV) genes as determined by exome resequencing analysis.



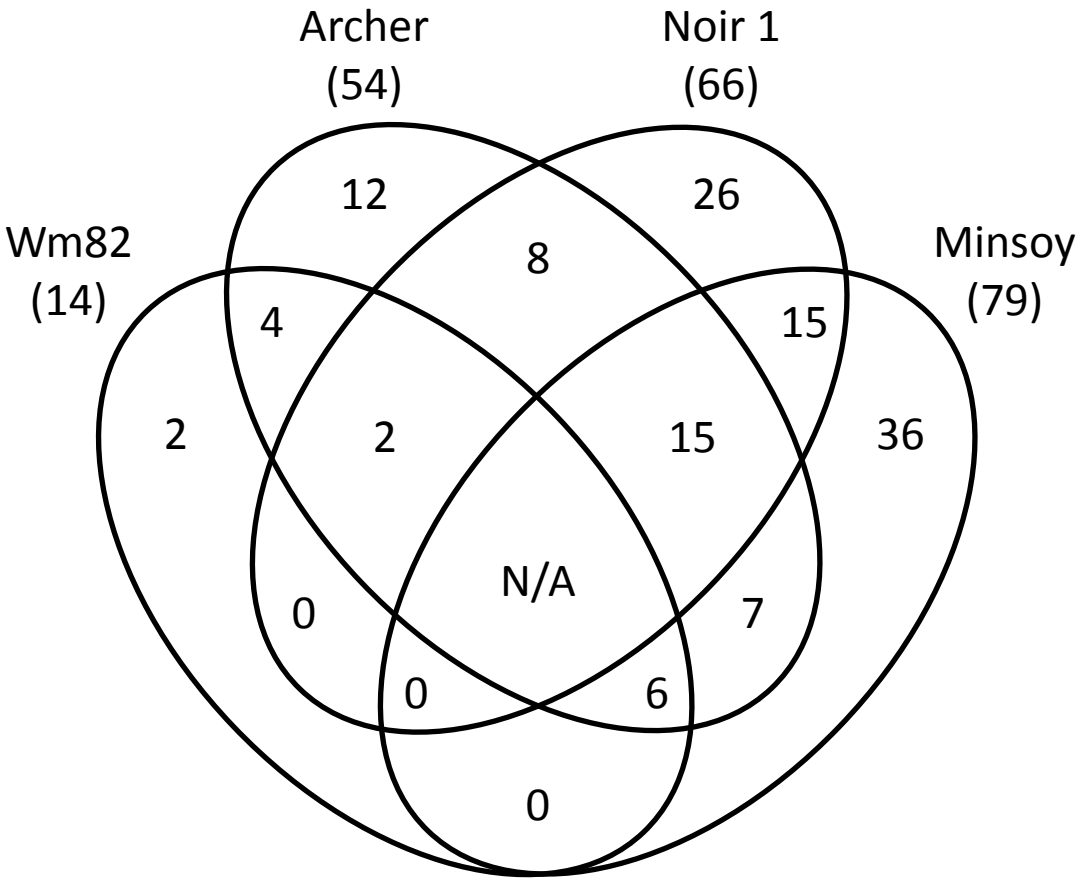
Supplemental Figure 2. Frequency of shared and unique CNV associated with soybean gene models. The values indicate the number of gene models associated with significant CNV compared to Wm82 within each genotype.



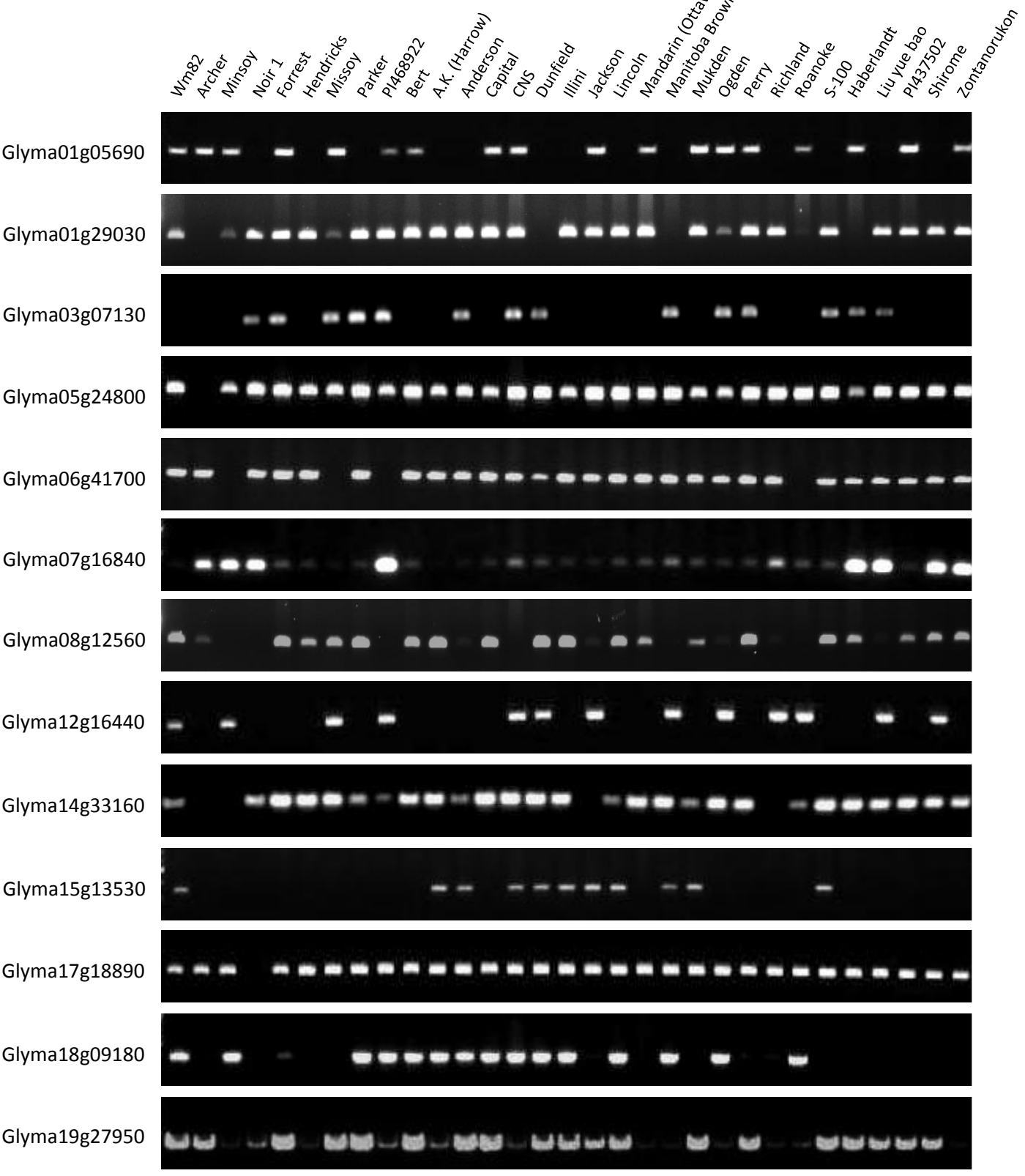
Supplemental Figure 3. CGH profiles among technical replications of the Minsoy/Wm82 and Noir1/Wm82 hybridizations. Log2 ratios between each genotype relative to the Wm82 reference are shown. All data points are shown in color. Red spots indicate data points from the original hybridization experiments. Blue spots indicate data points from the technical replication experiments. Reciprocal values are shown for the technical replication data points (blue), such that validated peaks appear as mirror images across the x-axis.



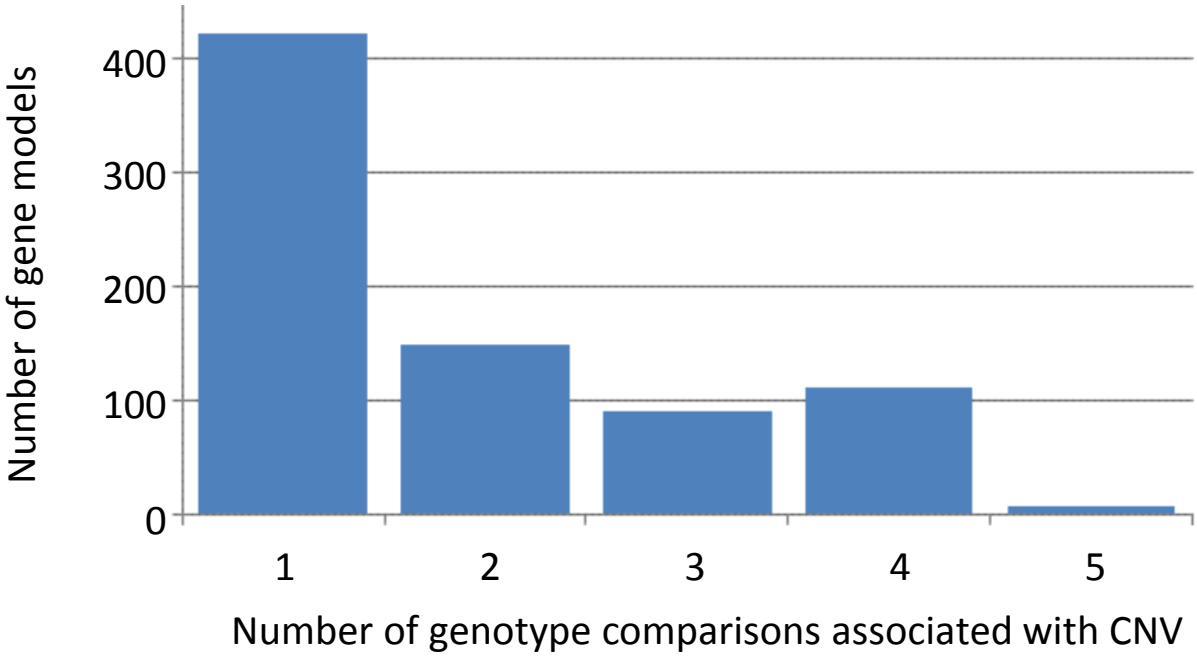
Supplemental Figure 4. Relationship between genomic structural variation and nucleotide SNP polymorphism among soybean genotypes. The blue lines represent the percentage of polymorphic SNPs for each genotype pairwise comparison along a sliding window of 25 adjacent SNPs, as assayed on the soybean Illumina Infinium platform. To assess structural variation, Archer, Minsoy and Noir 1 were each independently hybridized to the CGH microarray, with Wm82 serving as the reference. The red lines represent the percentage of probes above or below the significance threshold for each genotype pairwise comparison along a sliding window of 100 probes. The chromosome number is shown in the upper right corner of each display.



Supplemental Figure 5. Distribution of presence-absence gene content variants among the four soybean genotypes. The numbers indicate the number of "absent" genes within each genotype from the high-confidence list of 133 present-absent gene variation.



Supplemental Figure 6. Distribution of presence-absence gene content variants among 31 diverse accessions.



Supplemental Figure 7. Frequency of shared and unique CNV associated with soybean gene models across five comparisons using Wm82 as the reference genotype (experimental genotypes are Archer, Minsoy, Noir 1, Essex and Richland). The y-axis values indicate the number of gene models associated with significant CNV in one comparison, two comparisons, etc.