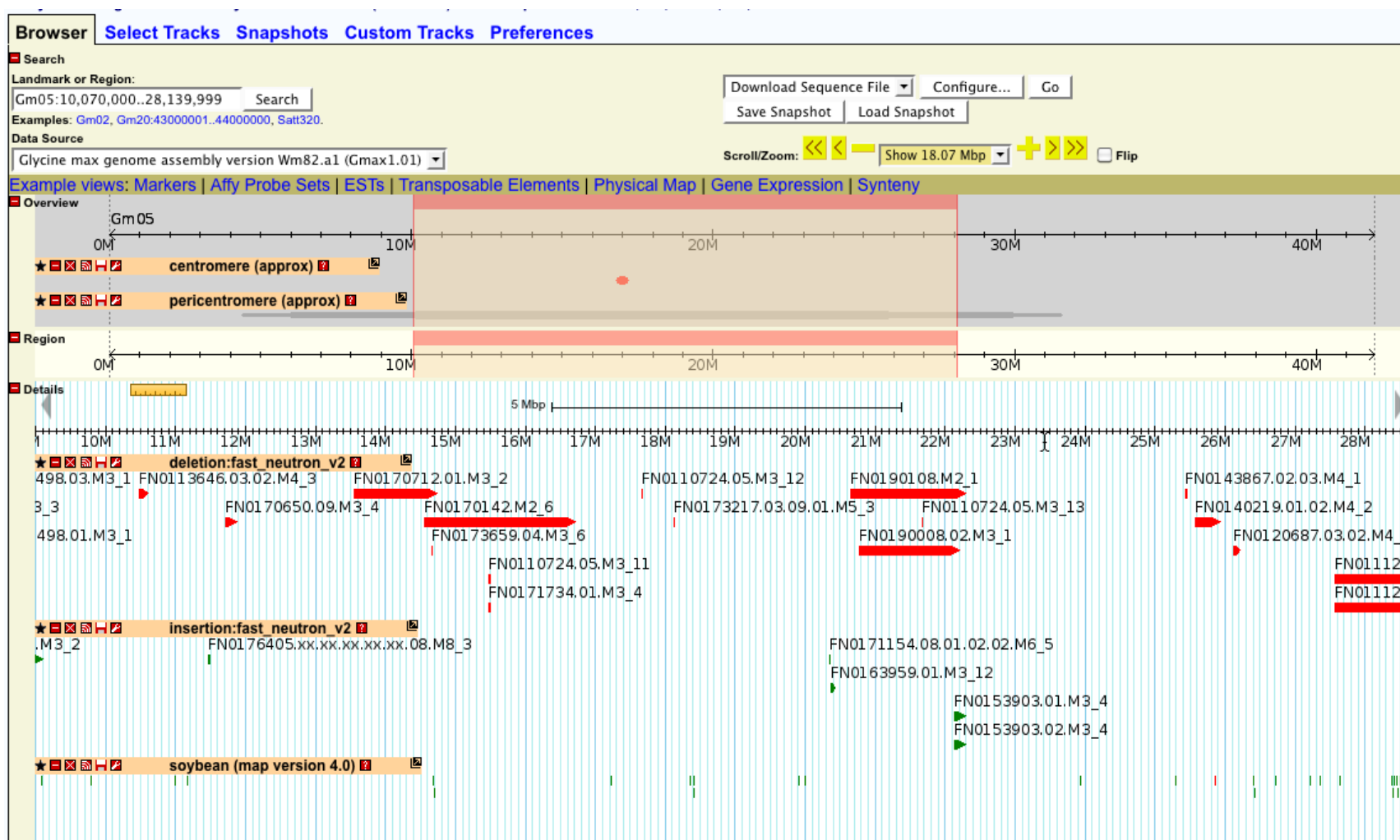
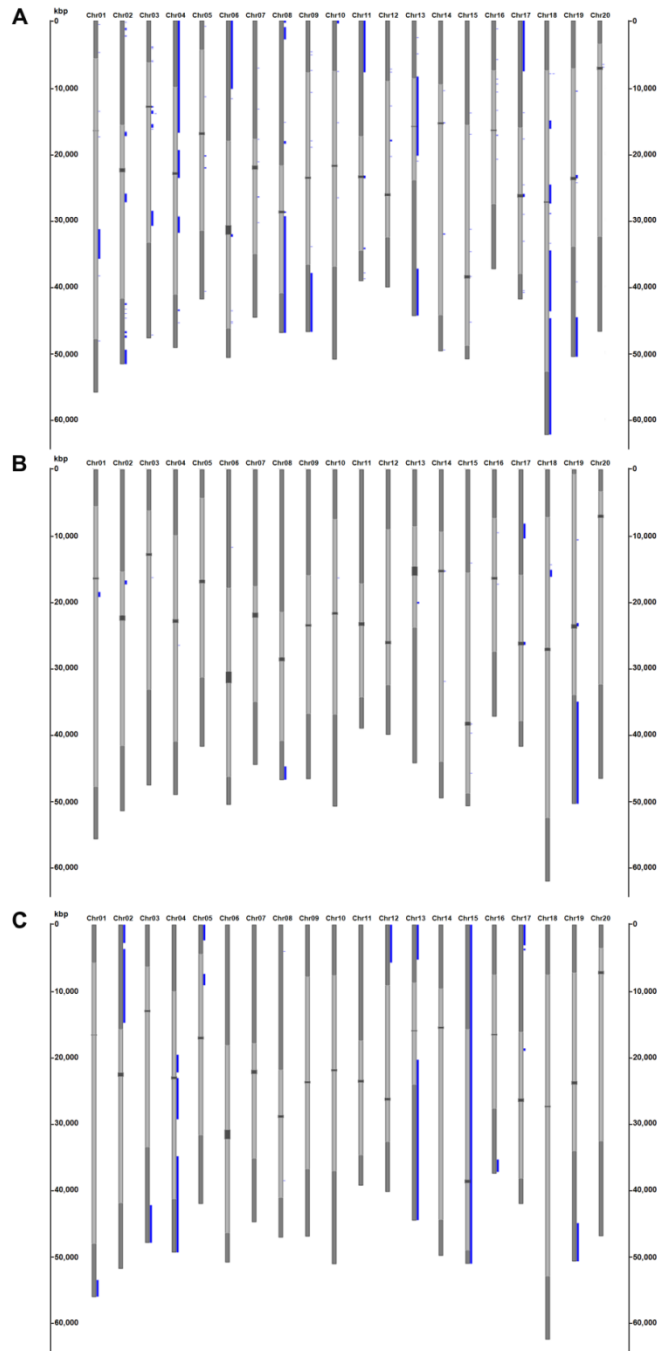


Figure S1



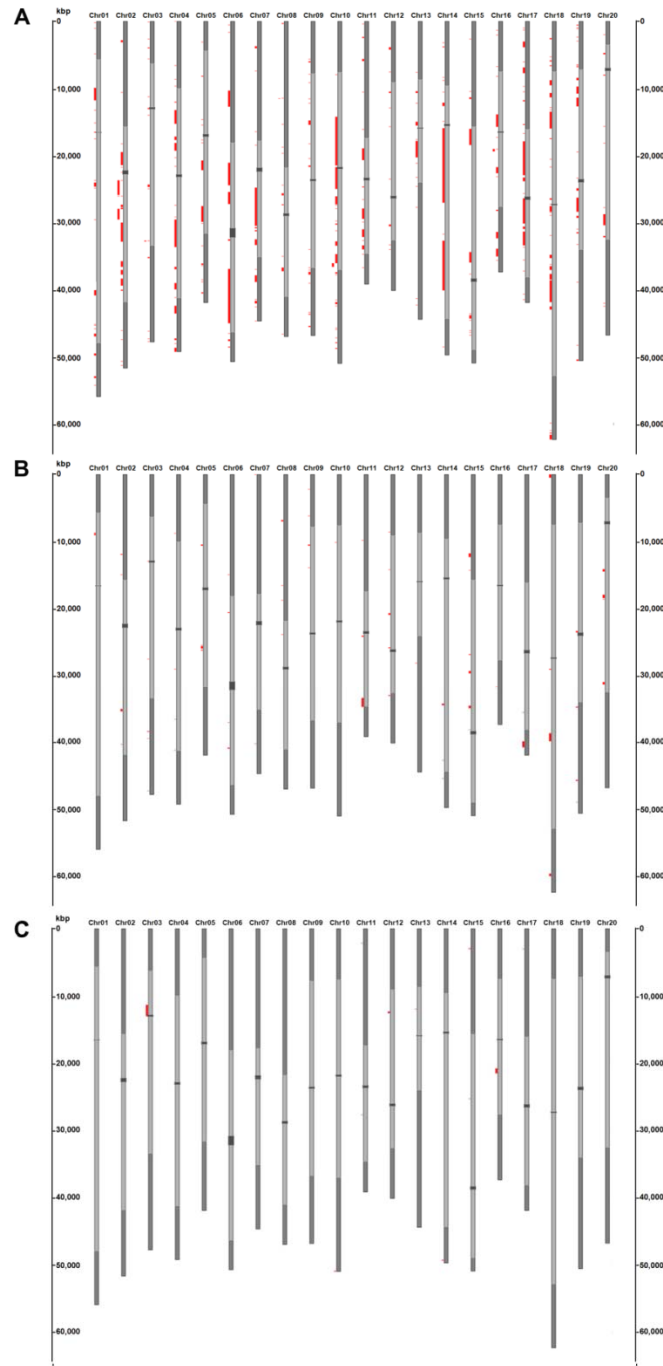
**Figure S1** Example genome browser view of fast neutron mutant duplication and deletion coverage. Data from this study is available on the online browser at [www.soybase.org](http://www.soybase.org).

Figure S2



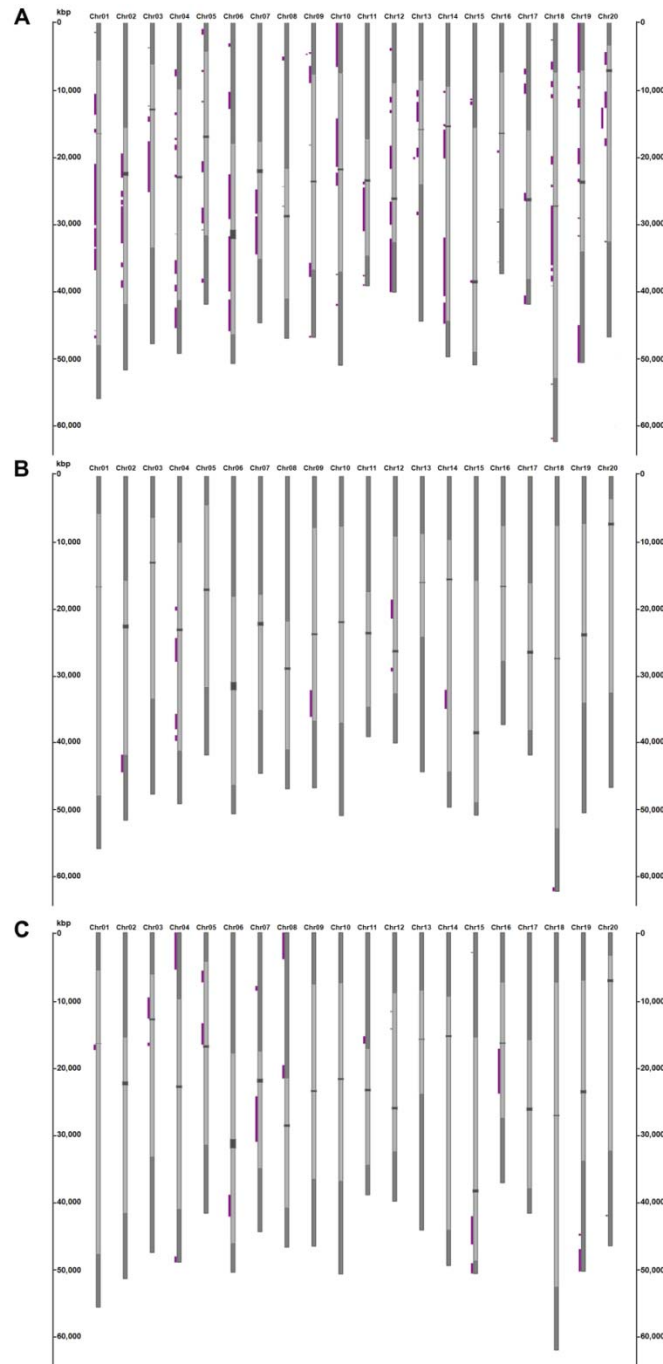
**Figure S2** Genome-wide view of segmental duplication coverage detected in fast neutron-irradiated soybean mutants for each selection category. Light gray lines indicate pericentromeric regions while euchromatic and centromeric regions are shown in dark gray. Segmental duplication events are shown as blue bars, detected in plants from the Forward Screen (A), No-Phenotype (B), and the Reverse Screen (C) classes.

Figure S3



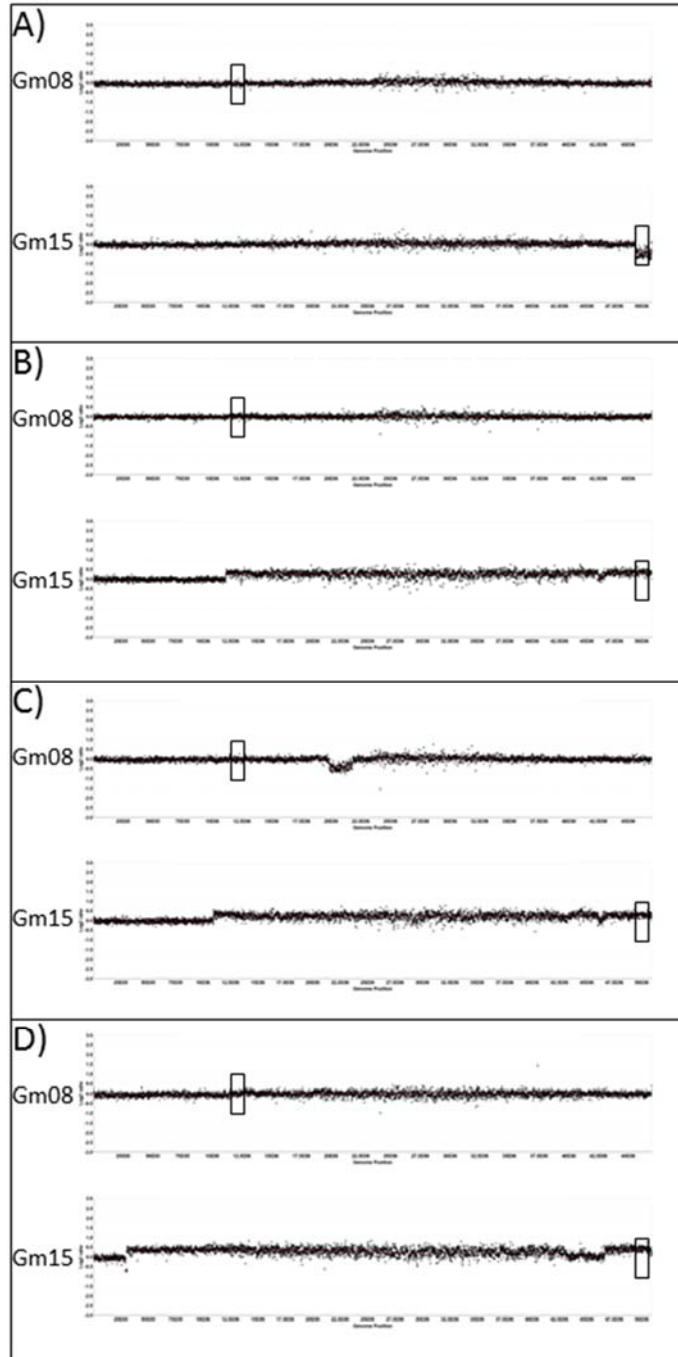
**Figure S3** Genome-wide view of homozygous deletion coverage detected in fast neutron-irradiated soybean mutants for each selection category. Light gray lines indicate pericentromeric regions while euchromatic and centromeric regions are shown in dark gray. Homozygous deletion events are shown as red bars, detected in plants from the Forward Screen (A), No-Phenotype (B), and the Reverse Screen (C) classes.

Figure S4



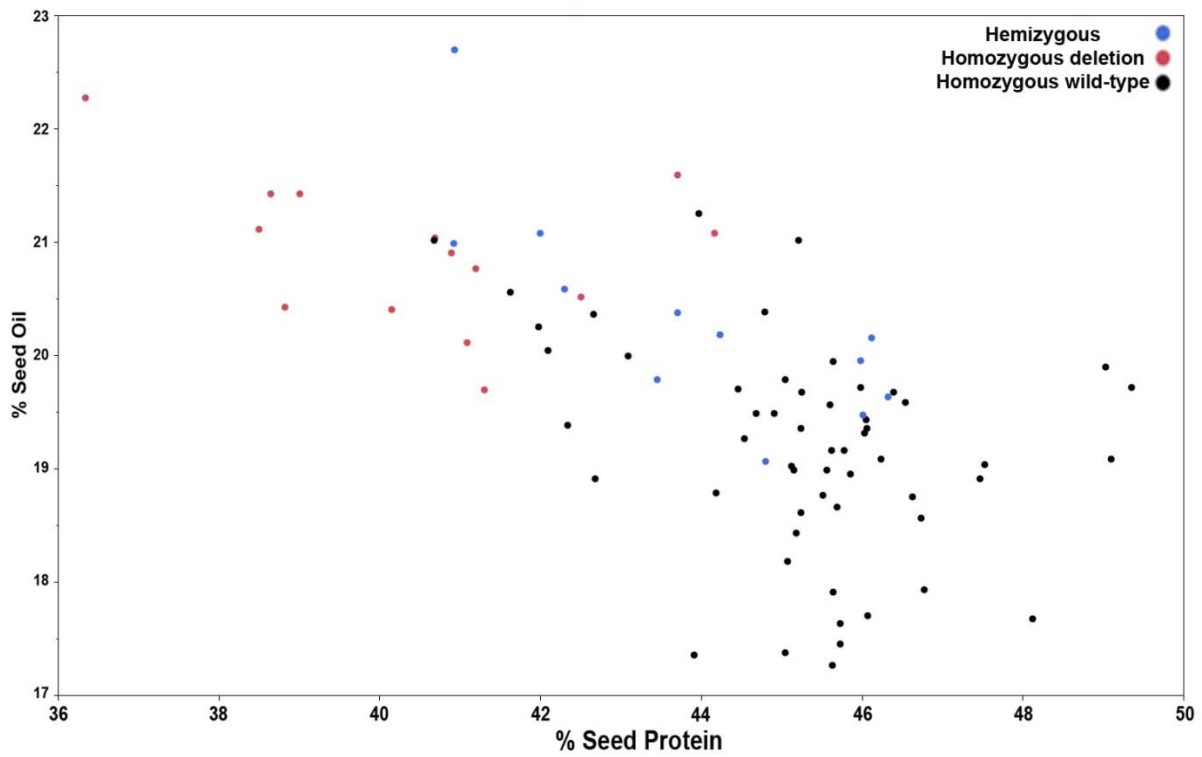
**Figure S4** Genome-wide view of hemizygous deletion coverage detected in fast neutron-irradiated soybean mutants for each selection category. Light gray lines indicate pericentromeric regions while euchromatic and centromeric regions are shown in dark gray. Hemizygous deletion events are shown as purple bars, detected in plants from the Forward Screen (A), No-Phenotype (B), and the Reverse Screen (C) classes.

Figure S5



**Figure S5** aCGH mapping of fast neutron-induced deletions and duplications on chromosomes 8 and 15 for plants identified by the Reverse Screen. A) FN0170255, B) FN0170228, C) FN0170522, D) FN0170712. The  $\log_2$  ratio of the mutant versus the control is plotted. Values that plot above zero indicate duplications and values that plot below zero indicate deletions. Each data point represents the average feature ratio across adjacent probes within 11-kb windows. The rectangles indicate the homoeologous regions on Gm08 and Gm15 that were initially Reverse Screened by Sequenom MassARRAY. The rectangles are vertically centered at the  $\log_2$  value of zero to clearly show the downward shift representing a deletion (chromosome 15 in FN0170255) and the upward shifts representing duplications (chromosome 15 in FN0170228, FN0170522, and FN0170712).

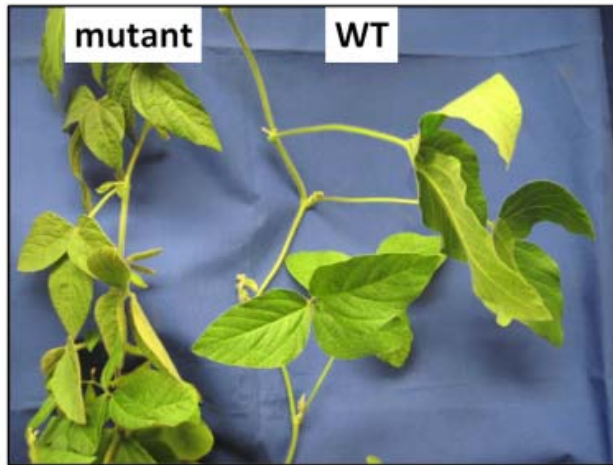
Figure S6



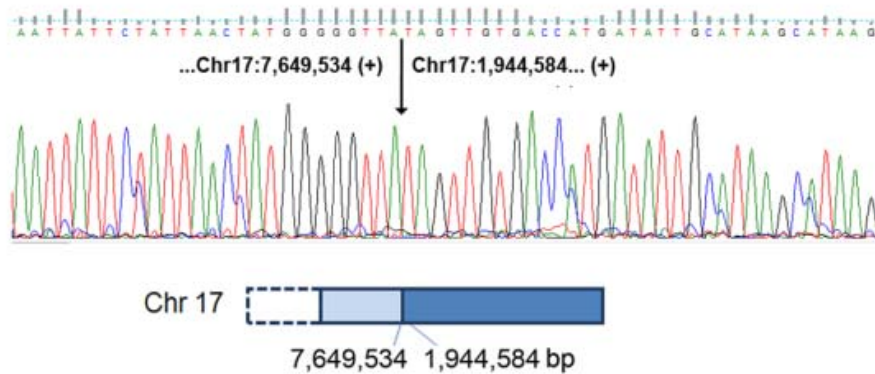
**Figure S6** Scatter plot representation of a genetic association of a  $\sim 1.3$  Mb deletion in mutant FN0172932 with quantitative changes in seed composition. Individual  $BC_1F_3$  plants are represented by color code for the presence of the wild-type allele (black) and homozygous (red) or hemizygous (blue) deletion allele on chromosome 10 and graphed on a percent oil by percent protein basis.

Figure S7

**A**



**B**



**Figure S7** Phenotype and sequence analysis of mutant FN0163764. (A) A photograph of representative mutant vs. wild-type plants show the shorter petiole lengths in the FN0163764 mutant. (B) Sequencing evidence for the tandem duplication junction on chromosome 17 in the short petiole FN0163764 mutant.

#### **Tables S1-S4**

Available for download as Excel files at <http://www.genetics.org/lookup/suppl/doi:10.1534/genetics.114.170340/-/DC1>

**Table S1** Primer sequences for Sequenom MassARRAY assays used for reverse screening of 760 fast neutron M2 plants. Large deletions and/or duplications between ten syntenic paralogous pairs between chromosomes 03 and 19 could be detected with this method.

**Table S2** Identification, description, and categorization of 264 soybean fast neutron mutants and 2 wild-type controls selected for comparative genomic hybridization.

**Table S3** Natural structural variation (i.e. heterogeneous regions) identified within the cv. 'M92-220'.

**Table S4** SV events (1216) detected among the 264 soybean fast neutron mutants by comparative genomic hybridization.