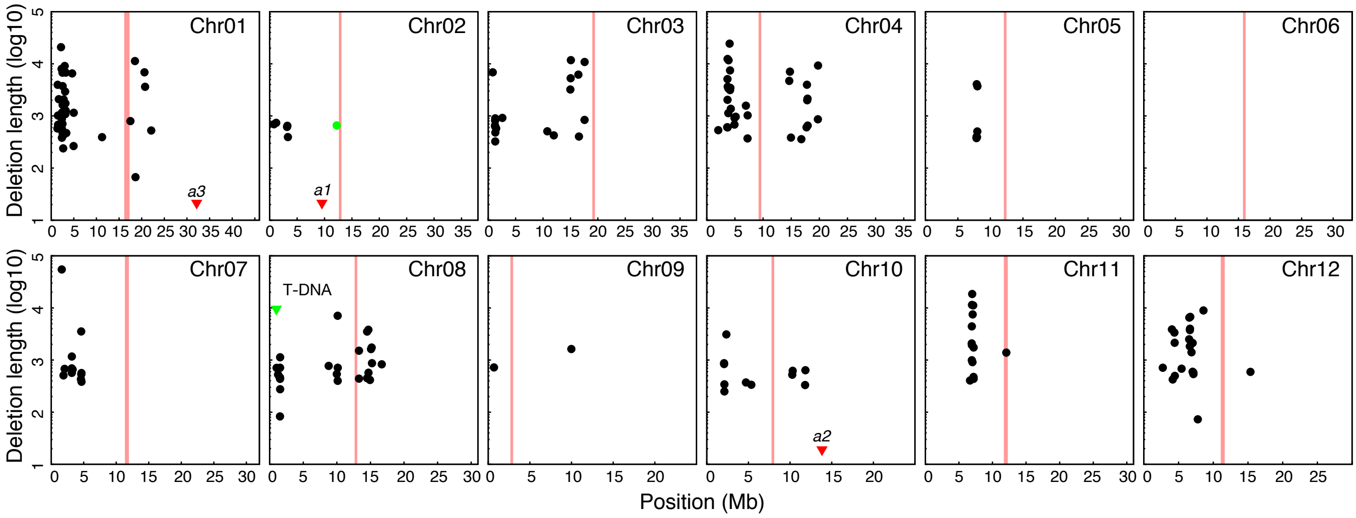
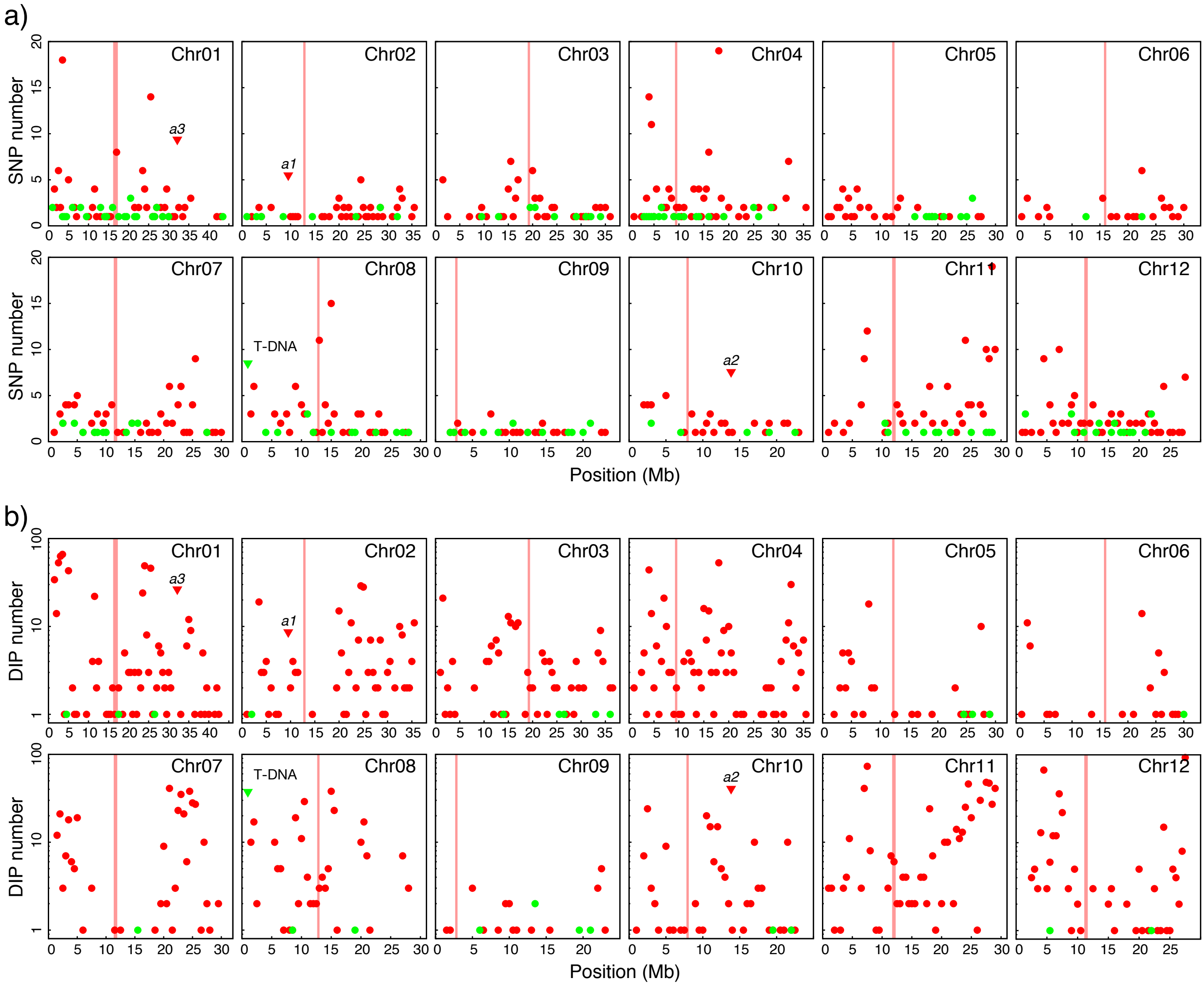
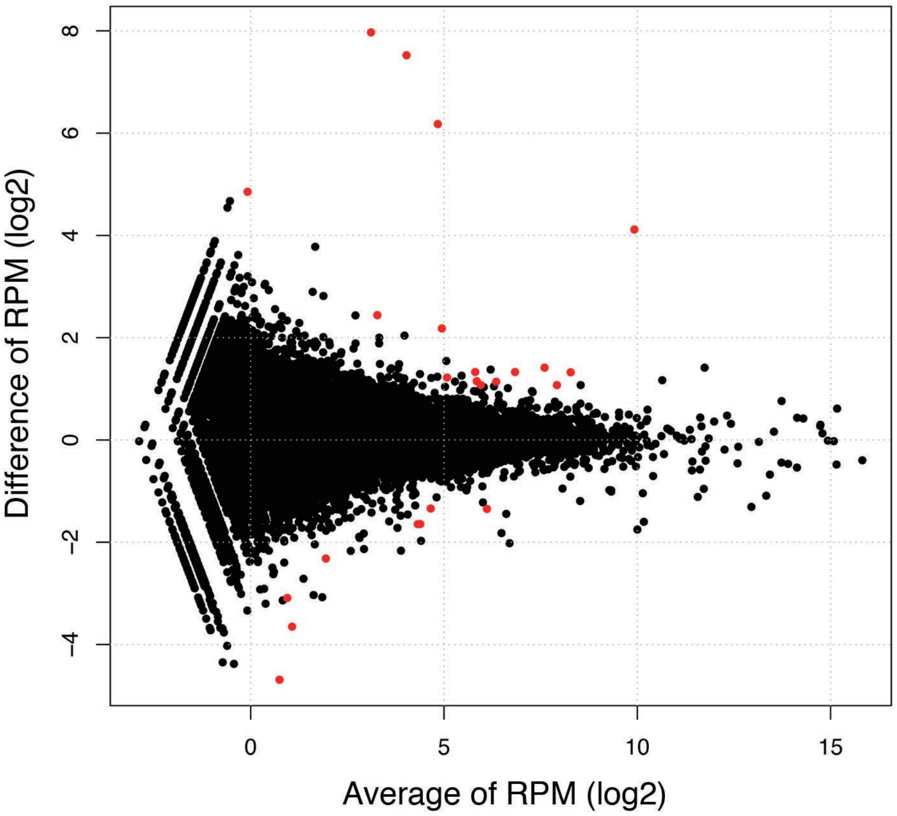


Supplemental Figure S1. Genome-wide and size distribution of structural variation candidates. X-axis indicates chromosomal location, and Y-axis indicates deletion size in log10 phase. Black dots indicate large deletions in all three lines (Koshihikari, a123 and OSCR11). Green dot indicates deletion confirmed in OSCR11. Light pink bars indicate centromeres. Red arrowheads indicate mutations corresponding to a123. Green arrowhead indicates T-DNA integration site in OSCR11.



Supplemental Figure S2. Genome-wide distribution of mutations. A. Single base substitutions. B. Deletions and insertions. X-axis indicates chromosomal location, and Y-axis indicates number of mutations within 500kb window. Red and green dots indicate mutagenesis and transformation specific mutations, respectively. Light pink bars indicate centromeres. Red arrowheads indicate mutations corresponding to a123. Green arrowhead indicates T-DNA integration site in OSCR11.



Supplemental Figure S3. Comparison of transcriptomes in developing endosperm. X-axis indicates average expression level between a123 and OSCR11. Y-axis indicates differential expression ratio of OSCR11 to a123. Black dots indicate each gene. Red dots indicate differentially expressed gene between a123 and OSCR11, identified by DESeq (FDR < 5%).