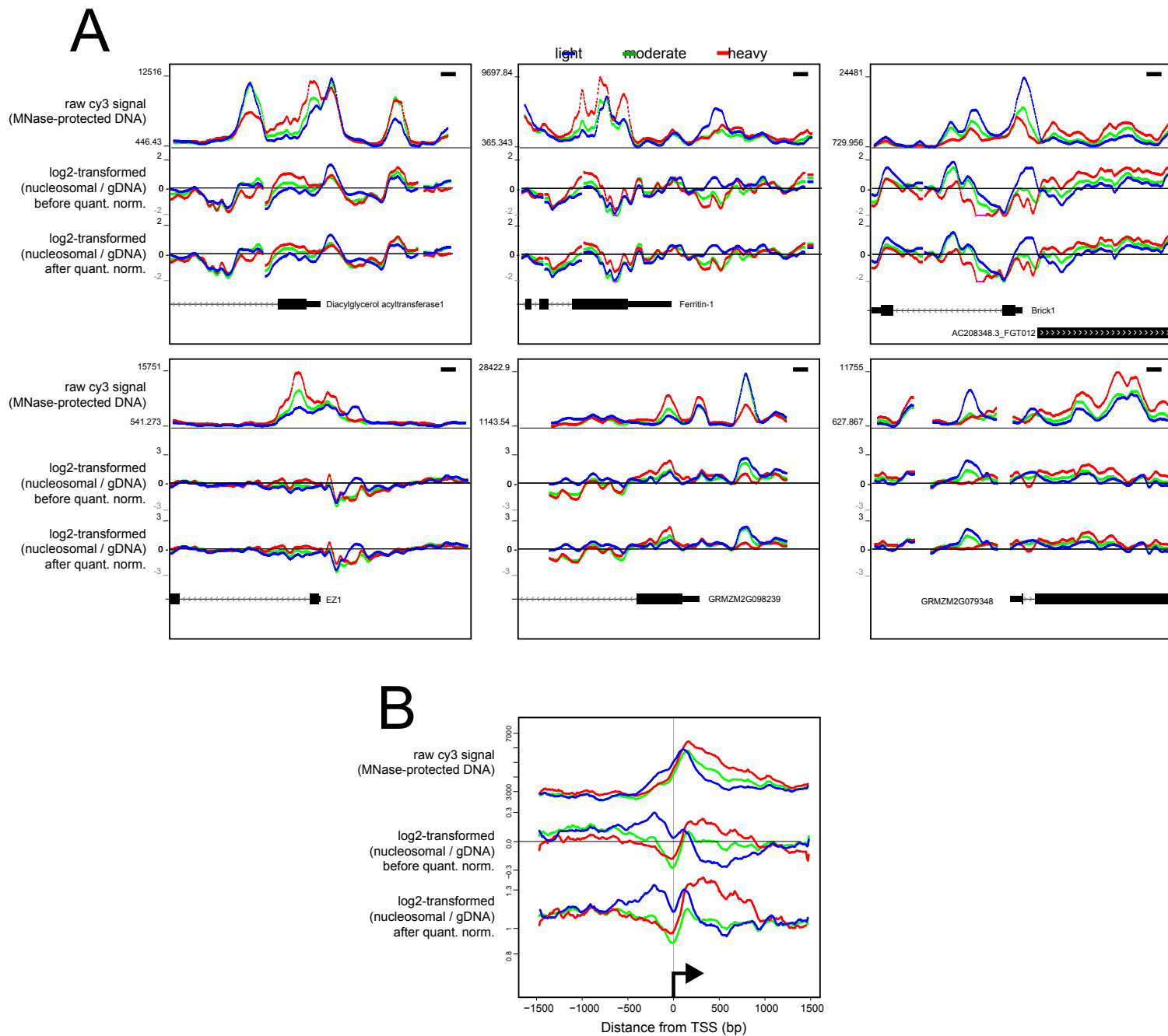
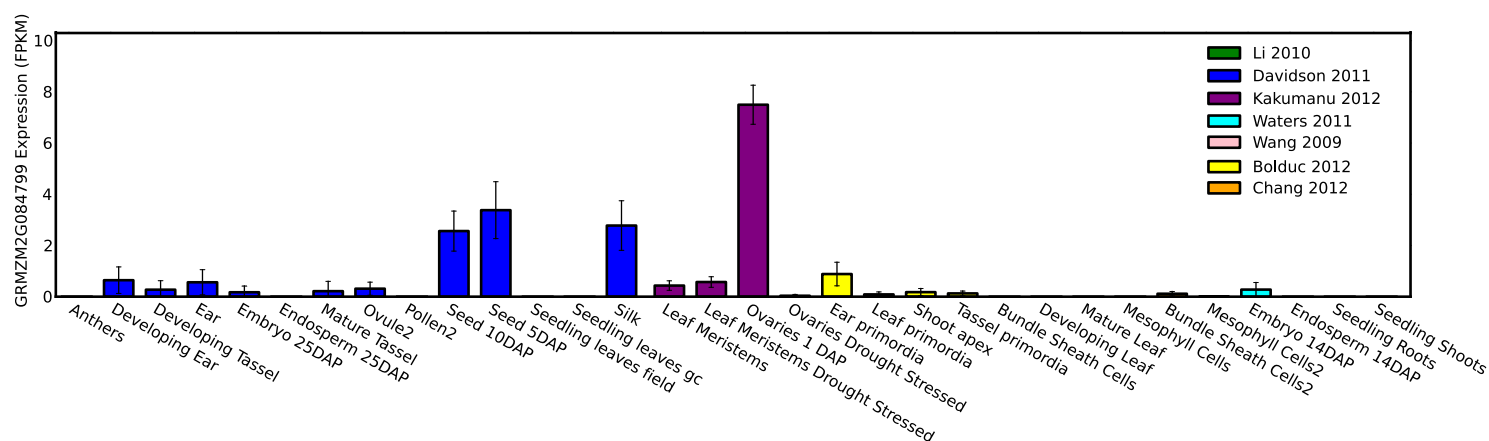


Supplemental Figure 1



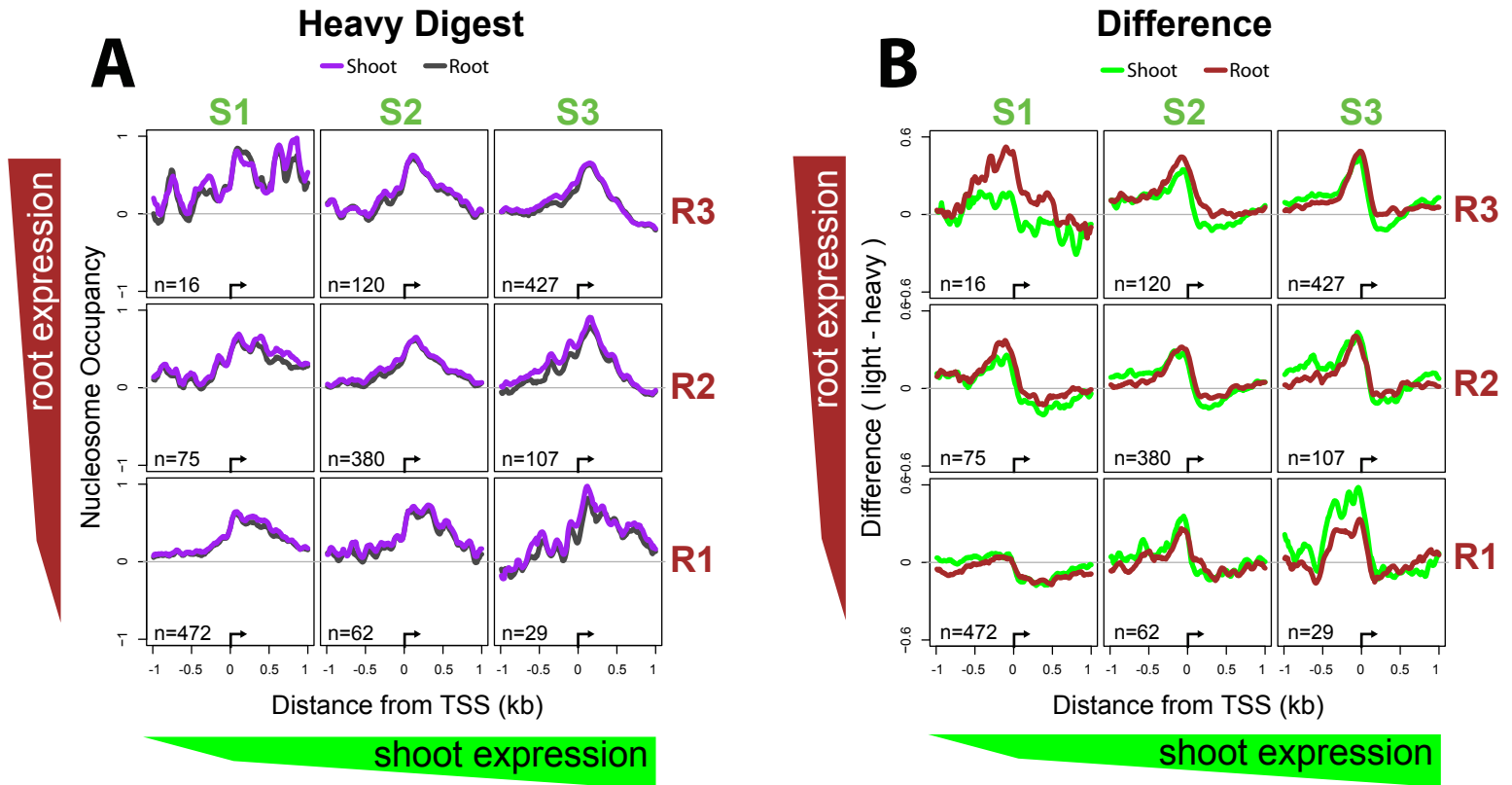
Supplemental Figure 1. MNase-sensitive and MNase-resistant footprints are observed in raw and unnormalized data. (A) Six example loci from the TSS-based microarray with data tracks for raw cy3 signal intensities (fluorescence signal for MNase-protected regions), log₂-transformed fluorescence intensities (log₂(nucleosomal/genomic)), and quantile-normalized log₂-transformed data. Black scale bar = 150 bp. (B) The same data as shown in (A) but averaged at the 389 genes aligned by their transcription start sites.

Supplemental Figure 2



Supplemental Figure 2. Pericarp color1 gene expression levels in various maize tissues. Bar plot of Fragments per Kilobase per Million (FPKM) values derived from RNA-seq data of the maize gene pericarp color1 from 7 published sources.

Supplemental Figure 3



Supplemental Figure 3. Average nucleosome occupancy and difference profiles at genes grouped by their expression levels in seedling shoot and roots. Each of the 1,688 genes represented on the microarray were grouped into expression tertiles for seedling shoots and roots (S1-S3 and R1-R3). Each group of genes were aligned by their TSS and average heavy-digest nucleosome occupancy profiles (A) and difference profiles (light - heavy, B) were calculated. The number of genes in each group are indicated by "n=".