Detection of Light-regulation Alternative Splicing in Maize

• The third replicate didn't correlate well with other replicates.

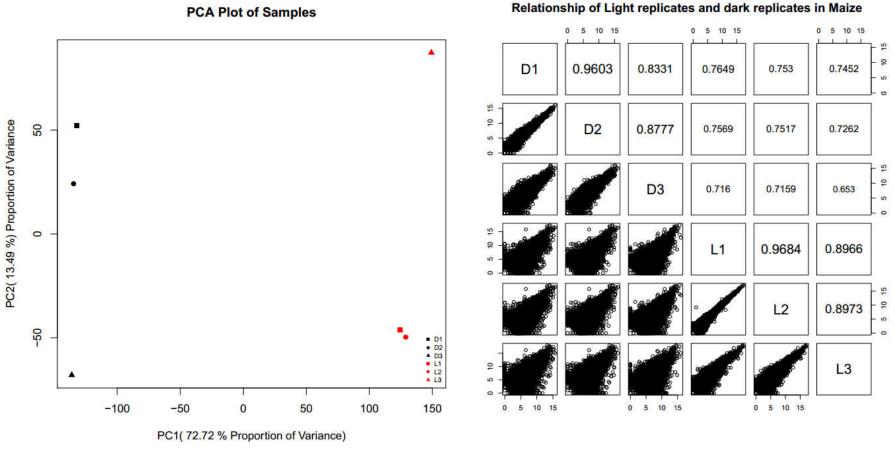
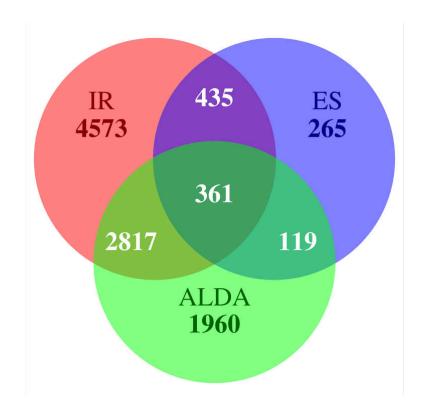


Fig1 PCA plot for the 6 samples

Fig2 Scatter plot to show the correlation of each sample

Detection of AS events using two replicates

- 1. A total of 11.12 and 11.28 million uniquely mapped reads for dark and light plants.
- 2. Under dark condition, a total of 20,379 splicing junction(SJ)-containing genes (out of a total 26,081 detected genes). In samples from light condition plants, a comparable but lower number (18,198) of SJ-containing genes was identified from a total of 23,258 detected genes.
- 3. All four major types of AS (intron retention, exon skipping, Alternative accepted and donated sites) were investigated in dark and light condition.(Fig3 and Fig4)



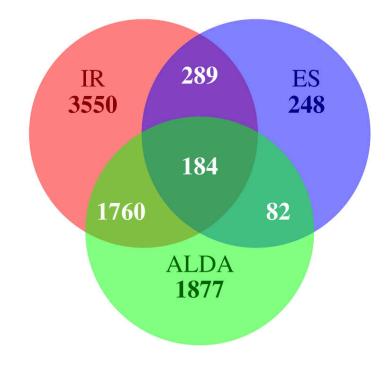
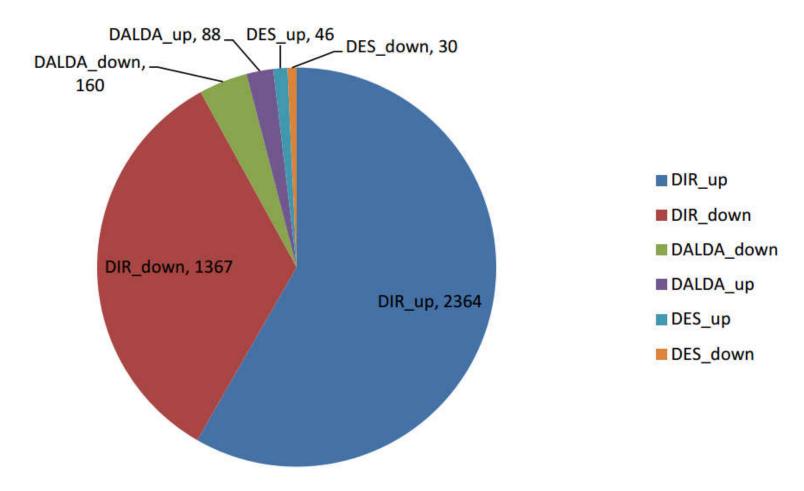


Fig3 Types of AS in plants grown in dark.

Fig4 Types of AS in plants grown in light.

Numbers represent alternatively spliced genes. ES, exon-skipping; IR, intron retention. ALDA, alternative donated and accepted sites.

Differential Alternative Splicing under Light Condition



- Alternatively Splice and Differentially Expressed Genes Are Separately Regulated
 - 1.1150(11.2% total) genes are both DAS genes and DE genes which take small portion of all DAS or DE genes.
 - Functional categorization of these 1150 revealed that they are enriched in some functional pathways, (photosynthesis, fructose metabolic process, drug transmembrane transport, carbohydrate metabolic process, superoxide metabolic process)
 - 2. Given the fact that most of DE and DAS genes are separately regulated. The functional categories showed that some post-transcriptional regulation gene are separately alternatively spliced.

