

Tausta et al.

SUPPLEMENTAL DATA LEGENDS

Supplementary Dataset S1. All BS and M DE genes.

This sheet is the list of 7,994 genes determined to be DE in BS or M cells for three developmental sections of maize leaf blade. For each gene, Mapman annotations and best rice and *Arabidopsis* homologs are given. The \log_2 transformed BS/M expression ratio is found in columns H, I, J followed by the average of the upper quartile-normalized expression values from 2 biological isolations of LM-isolated RNA from either BS or M cells in L-Q. FDR values for each section are in columns S,T,U.

Supplementary Dataset S2. DE gene lists for C4, TIM, GS-PK, Aquaporin, IAA, Methionine salvage.

The dataset contains genes mentioned in the body of the paper. Activity was inferred primarily from Mapman annotation. Included in all are the \log_2 BS/M values determined in this analysis. For the TIM, GS-PK, Aquaporin, IAA lists the normalized data for each cell type and section and the whole section data from (Li *et al.*, 2010) is also included. Blue shading of values of 1 (2 fold) or higher indicates a BS-biased ratio and green indicates values of -1 (2 fold) or lower and an M-biased ratio. For the methionine salvage pathway-related genes only the tip data is presented in addition to the \log_2 BS/M values.

Supplementary Dataset S3. The top 100 most highly expressed DE genes in each section.

DE gene lists were filtered for the 100 genes with the highest expression in a cell type at one developmental time and are provided here. The genes that were found in only one section from the top 100 lists are also included.

Supplementary Dataset S4. DE genes expressed in only one section.

The DE list was filtered for genes that were expressed only in one developmental section. Expression in the other 2 sections was restricted to less than 0.2.

Supplementary Dataset S5. Transcription factor identification comparison.

The whole section transcription factor list identified by Li et al., 2010 was converted to B73 RefGen_v2 resulting in a final list of 885 genes which was compared to genes identified as potentially having transcription factor activity from the DE list. Column A contains the mapman annotation for the genes identified in the whole section data listed in column B. Column C shows any matches to BS-biased genes and D any M-biased genes. Note a few genes have annotations in both BS and M columns denoting a switch from one cell type bias to the other over the developmental sections.

The second page compares the BS and M-biased transcription factors with datasets from Wang et al., 2013, Chang et al., 2012 and Pick et al., 2011. Column G in blue denotes the matches with our BS-biased results and column H in green denotes the matches with our M-biased data. Columns D, E, F are the log₂BS/M ratios for each of the sections.

Supplemental Figure 1: Metabolism-related Transcripts Remain DE from SST.

Heat maps representing DE gene expression for select C4-related metabolic pathways. Columns represent leaf sections from youngest to oldest left to right and rows represent different genes with the predicted activities indicated on the left. Green signifies an M-biased ratio and blue represents a BS-biased ratio. The color scale represents the log₂BS/M value and is from -3 (green) to +3 (blue) where 0 (white) represents no difference in BS and M values.



