Figure S4. Principal component analysis (PCA) of transcript abundance for the 21 samples collected from leaf 8 of maize inbred B73 in the LM-RNAseq analysis. The first two principal components (PCs) correspond to developmental stage (PC1) and tissue type (PC2). Each point corresponds to an RNAseq sample. From left to right, each color corresponds to a specific developmental stage (youngest to oldest part of the leaf). From bottom to top, circles represent epidermal tissues, and triangles represent internal tissues. The orange dot and triangle points that are encompassed by a black circle were considered an outlier for stage 2 (interval 4 - 6 cm), thus these samples were removed.