

Transcriptome analysis highlights key differentially expressed genes involved in cellulose and lignin biosynthesis of sugarcane genotypes varying in fiber content

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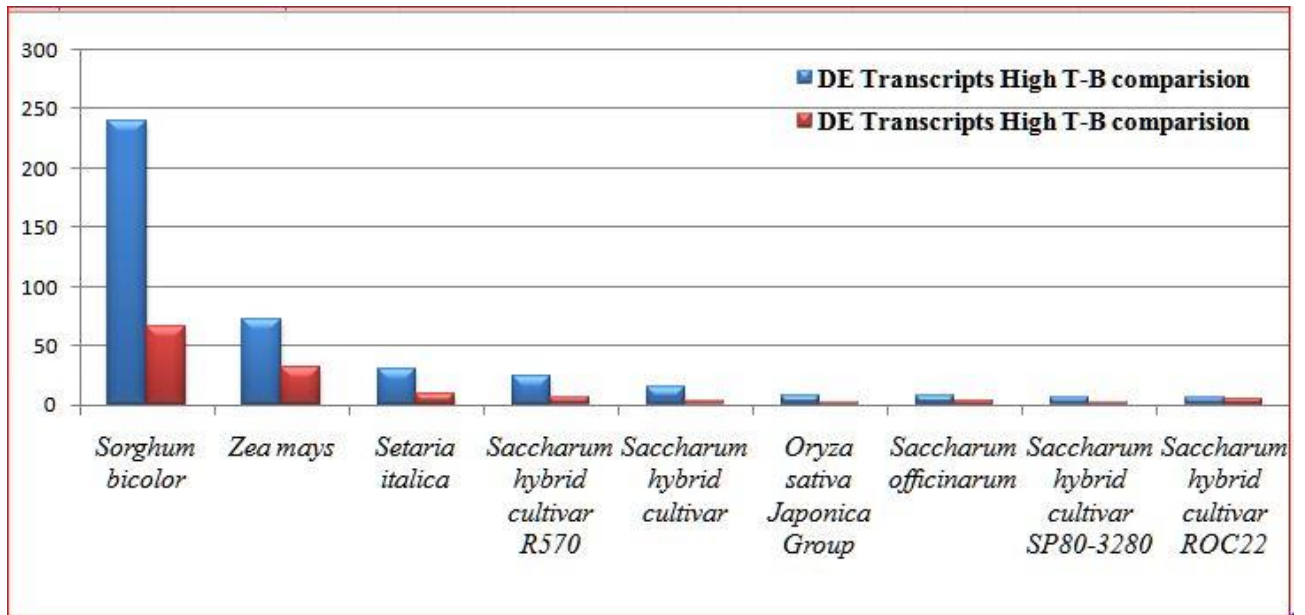
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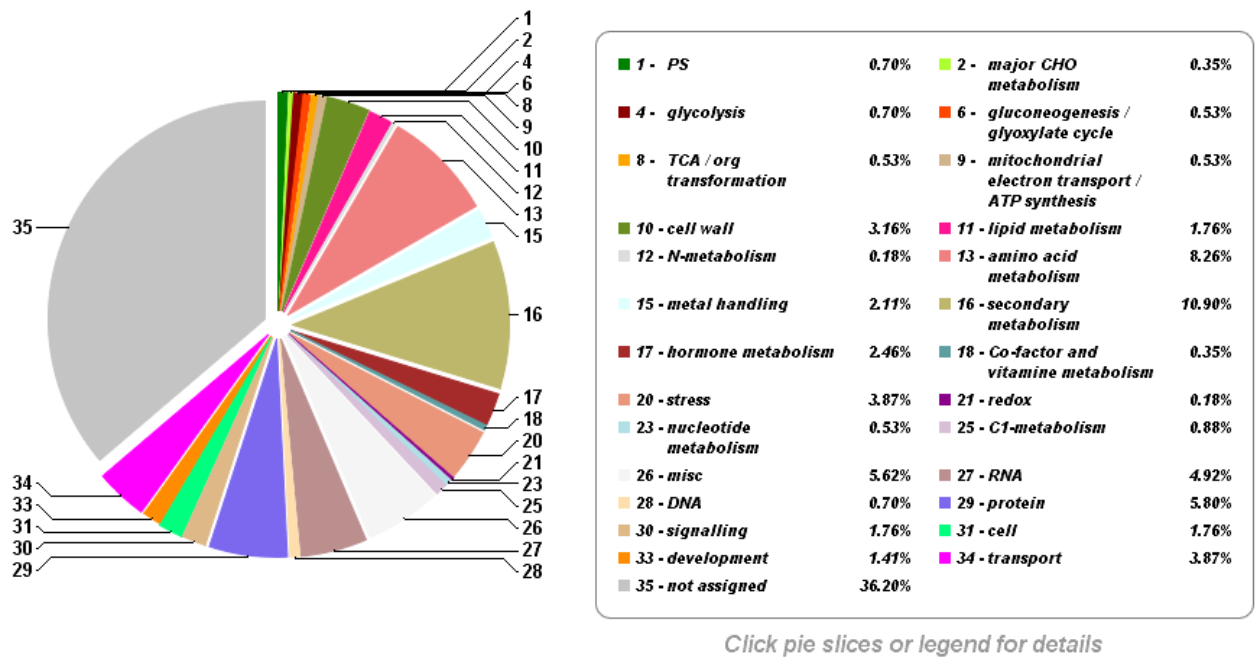
Email: f.botha@uq.edu.au

Supplementary Figure 1. Blast top hit species distribution

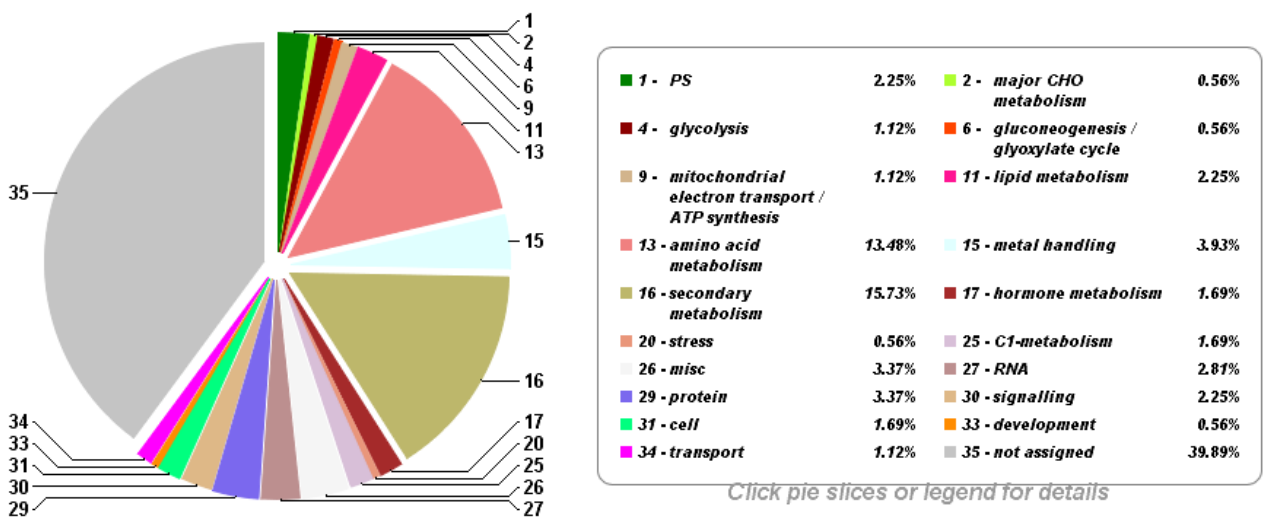


Supplementary Figure 2. Map man annotation bins

(a) DE transcripts between top and bottom internodes of high fiber

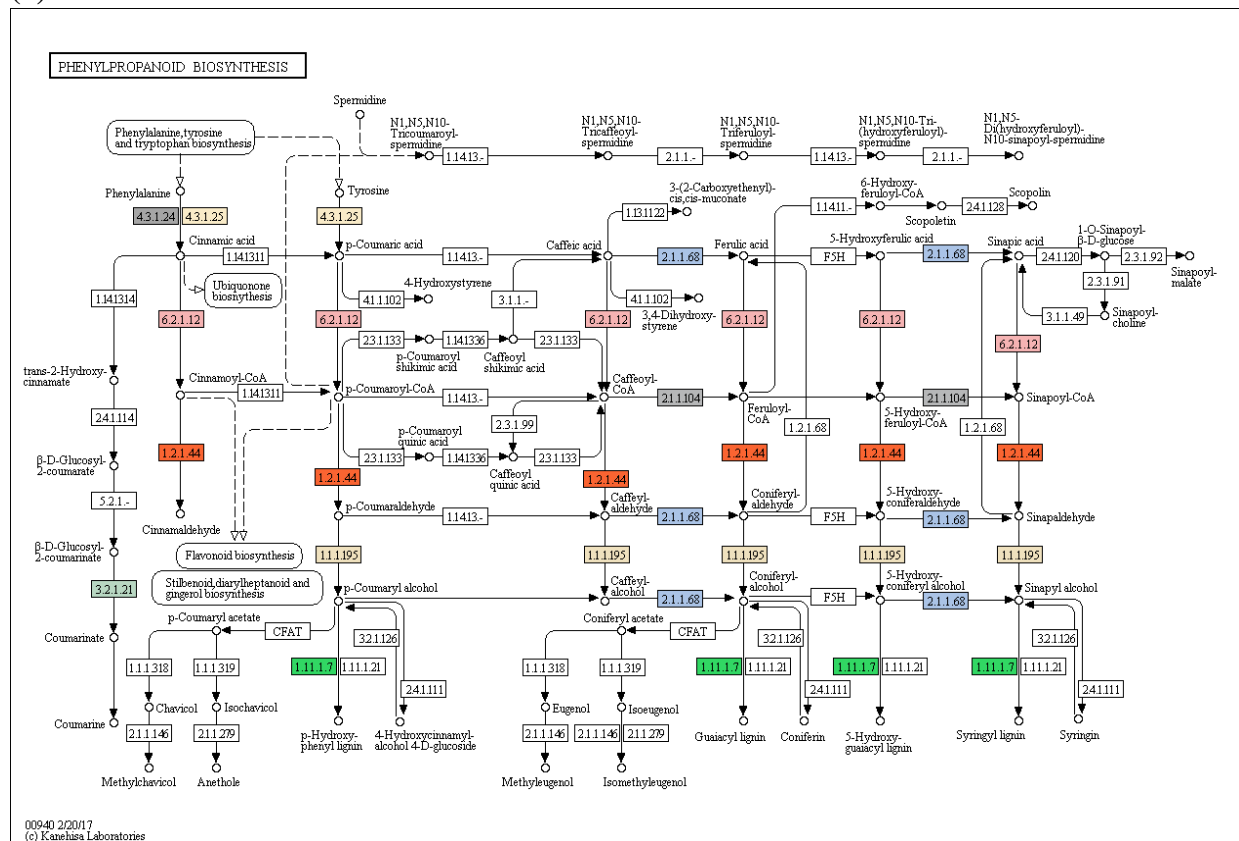


(b) DE transcripts between top and bottom internodes of Low fiber

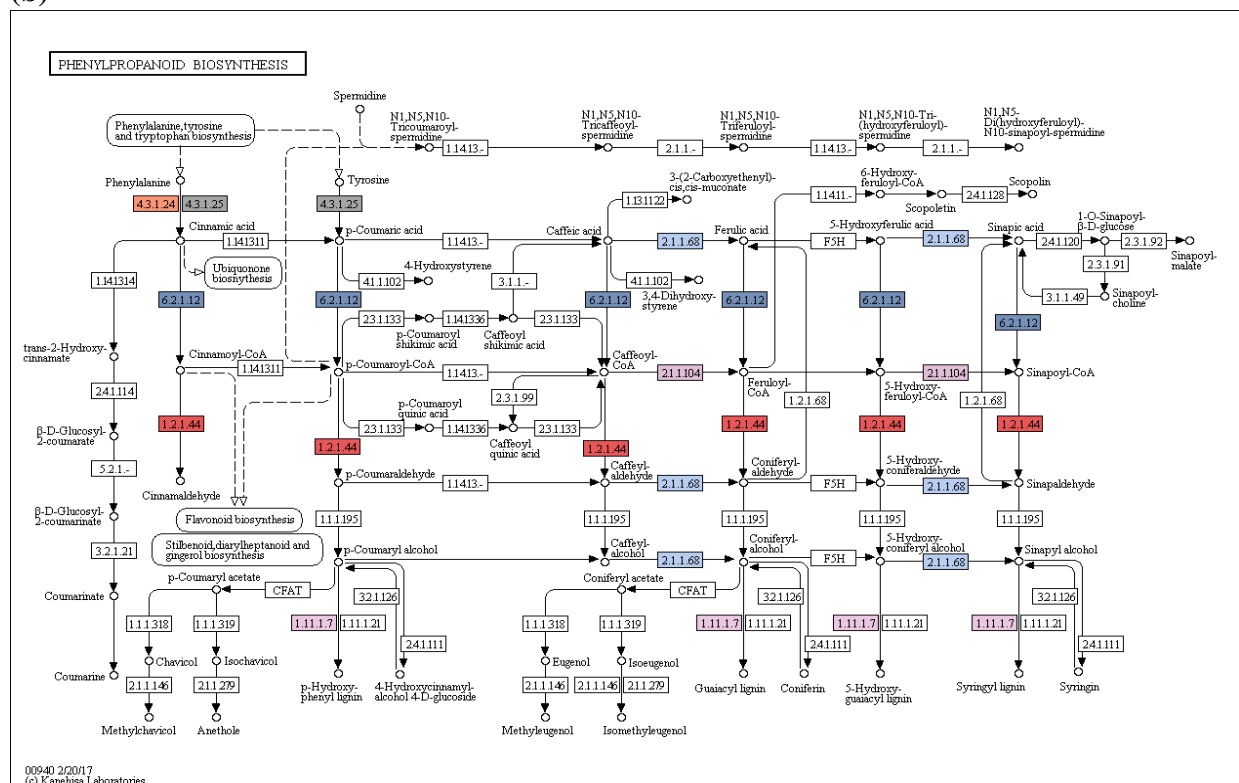


Supplementary Figure 3. KEGG maps of phenylpropanoid pathway (a) DE transcript between top and bottom internodes of High fiber, (b) DE transcript between top and bottom internodes of low fiber (<http://www.kegg.jp/kegg/kegg1.html>).

(a)

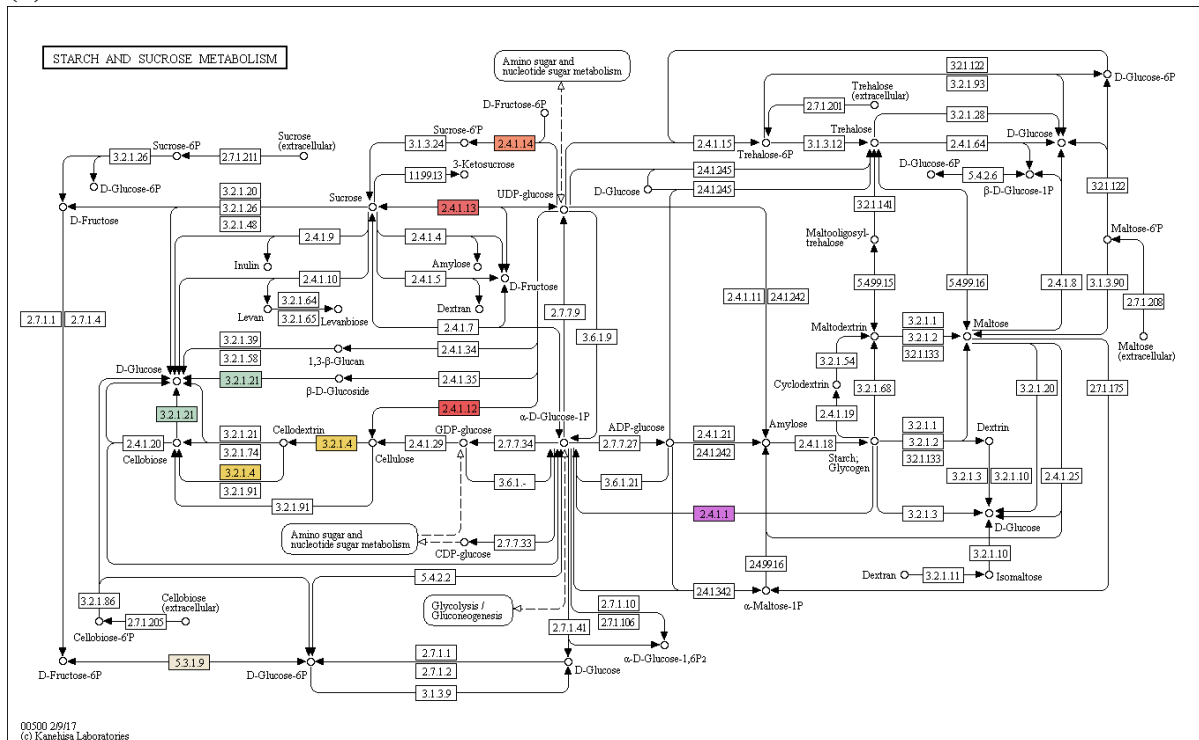


(b)



Supplementary Figure 4. KEGG maps of starch and sucrose pathway (a) DE transcript between top and bottom internodes of High fiber, (b) DE transcript between top and bottom internodes of Low fiber (<http://www.kegg.jp/kegg/kegg1.html>).

(a)



(b)

