Supplementary Information 1

Comparative morphology and transcriptome analysis reveals distinct functions of the primary and secondary laticifer cells in the rubber tree

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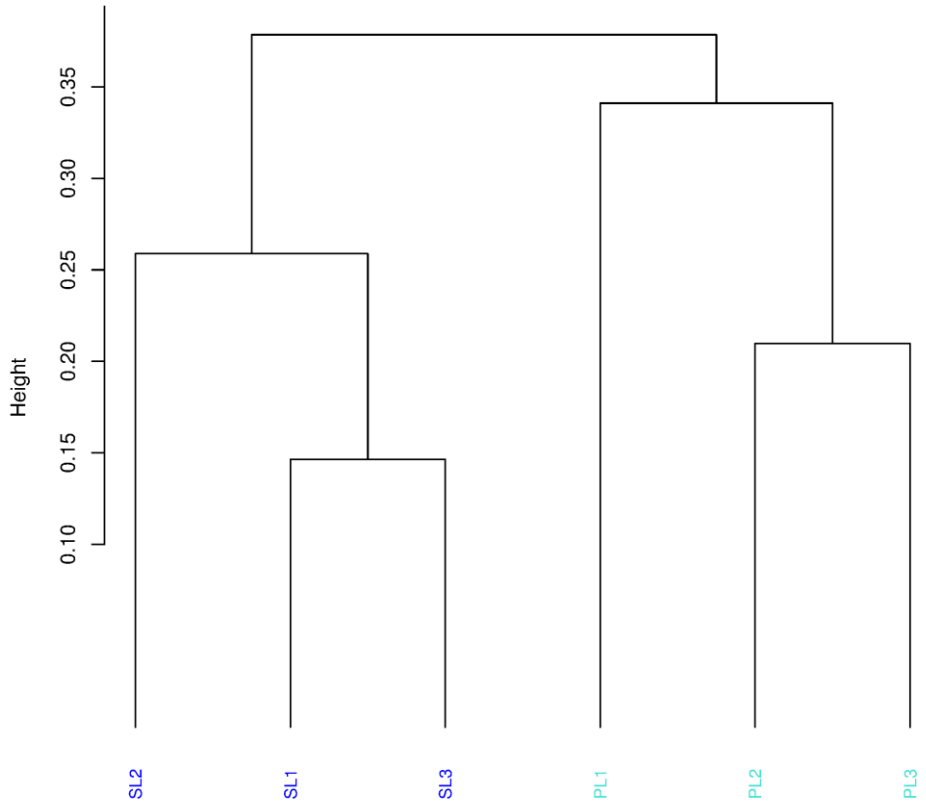
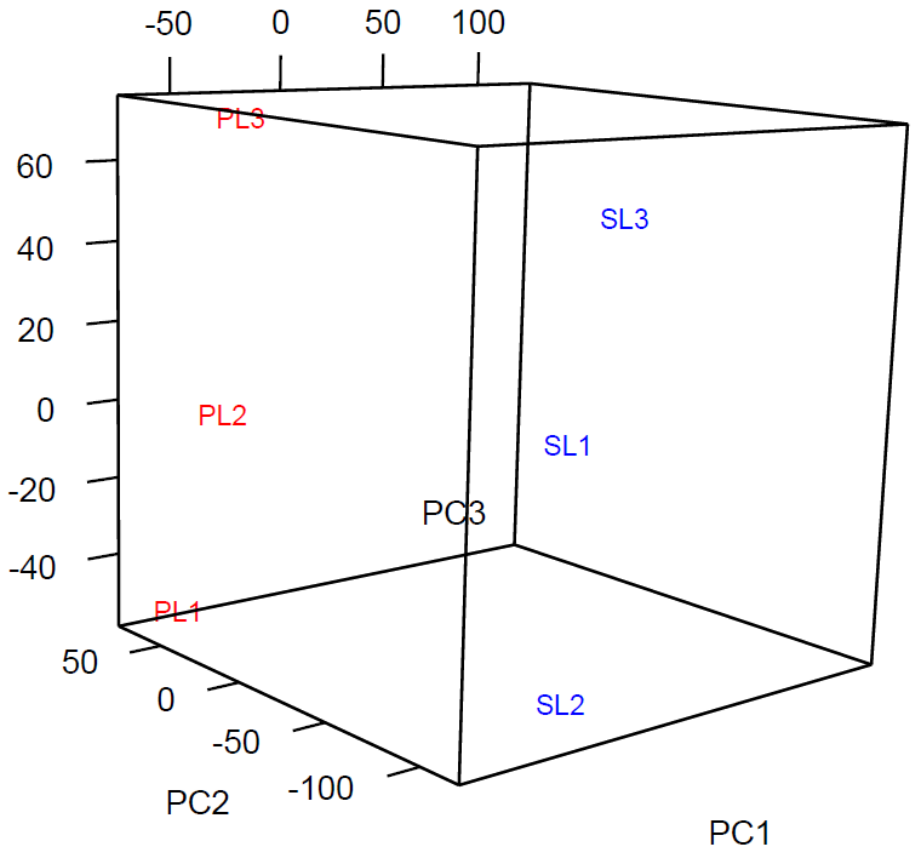
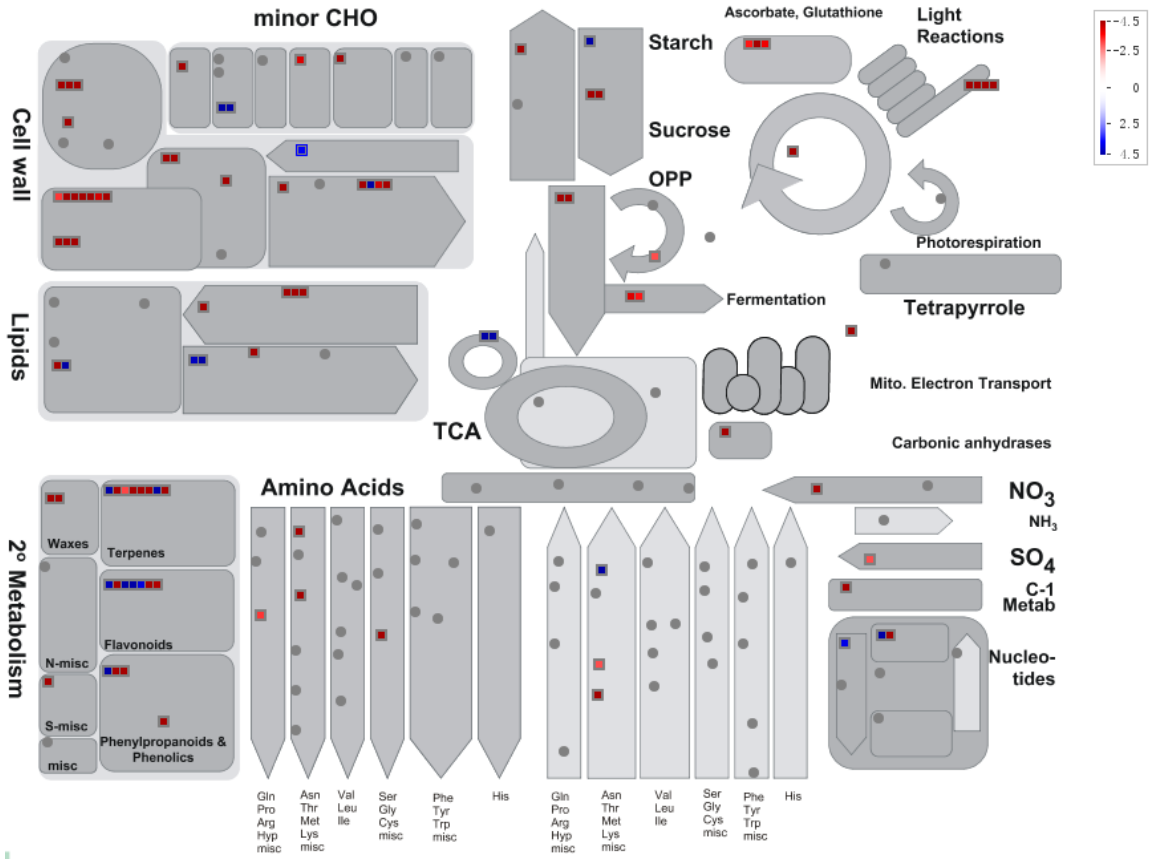


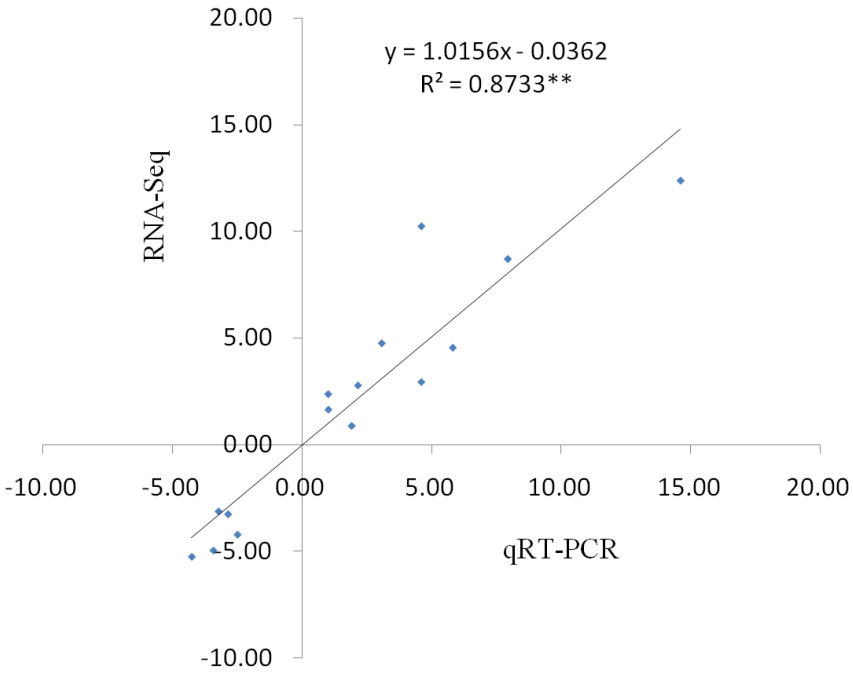
Supplementary Figure S1. Sample-clustering of the transcriptome replicates of the primary laticifer cells (PL) and the secondary laticifer cells (SL). The tree was constructed based on the Pearson correlations of gene expression values in each sample.



Supplementary Figure S2. PCA plot analysis of the transcriptome data. The transcriptome profile replicates of the primary laticifer cells (PL) and the secondary laticifer cells (SL) are well separated. The analysis was performed with 'prcomp' function in R software.



Supplementary Figure S3. Metabolism overview of genes differentially expressed between the primary and secondary laticifer cells. The analysis was performed in the MapMan software, and log2(SL/PL) values were used. Blue indicates up-regulation in gene expression, and red indicates down-regulation.



Supplementary Figure S4. Correlation analysis of the expression levels of representative genes as estimated by RNA-Seq and qRT-PCR methods. The significance of correlation was analyzed using IBM SPSS Statistics Version 24, and the correlation curves were created with Excel 2007 (Microsoft Inc., USA).