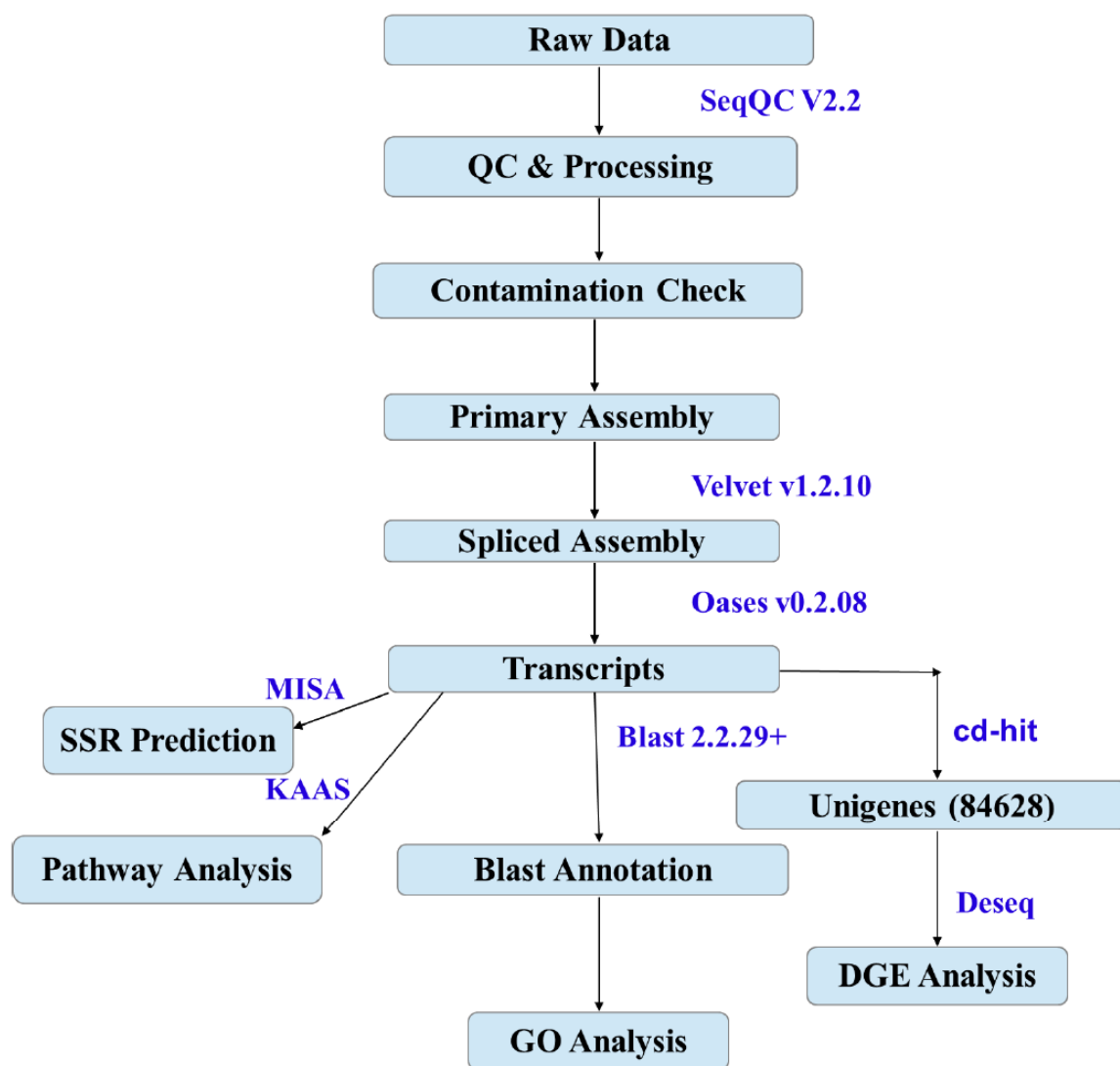
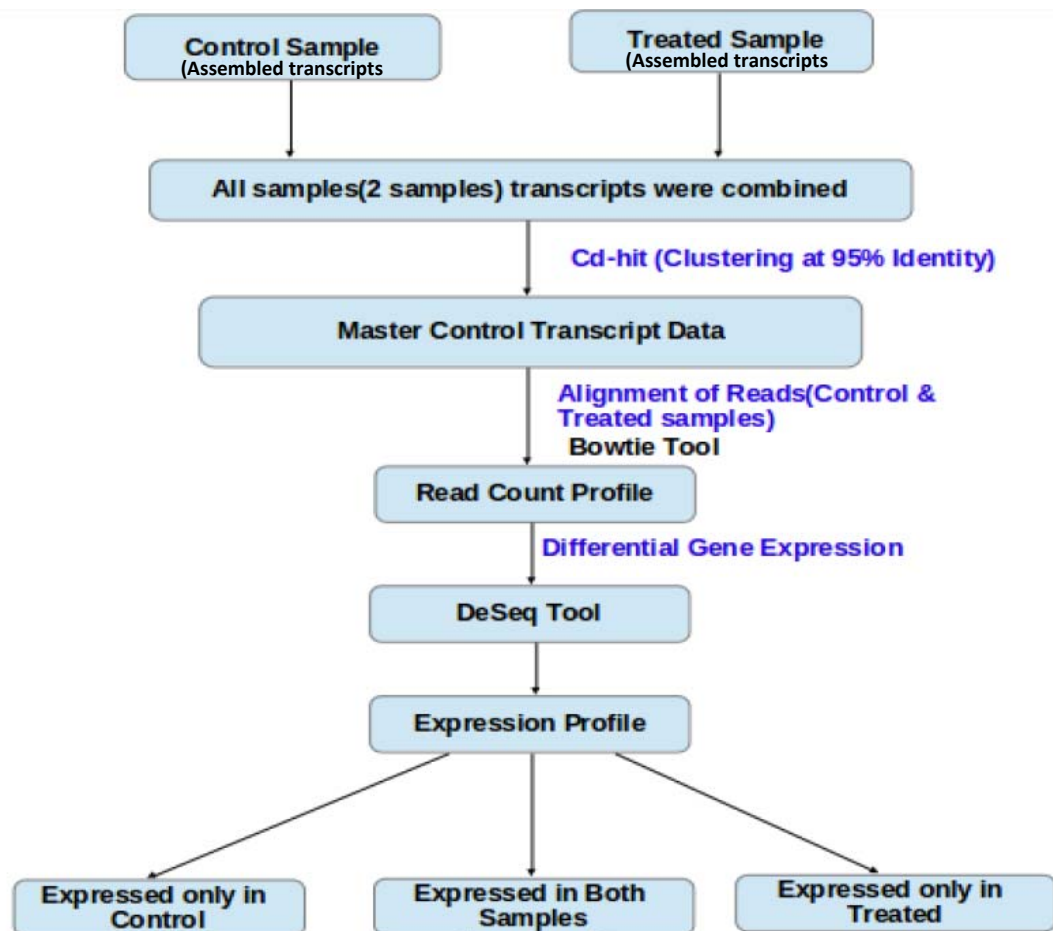
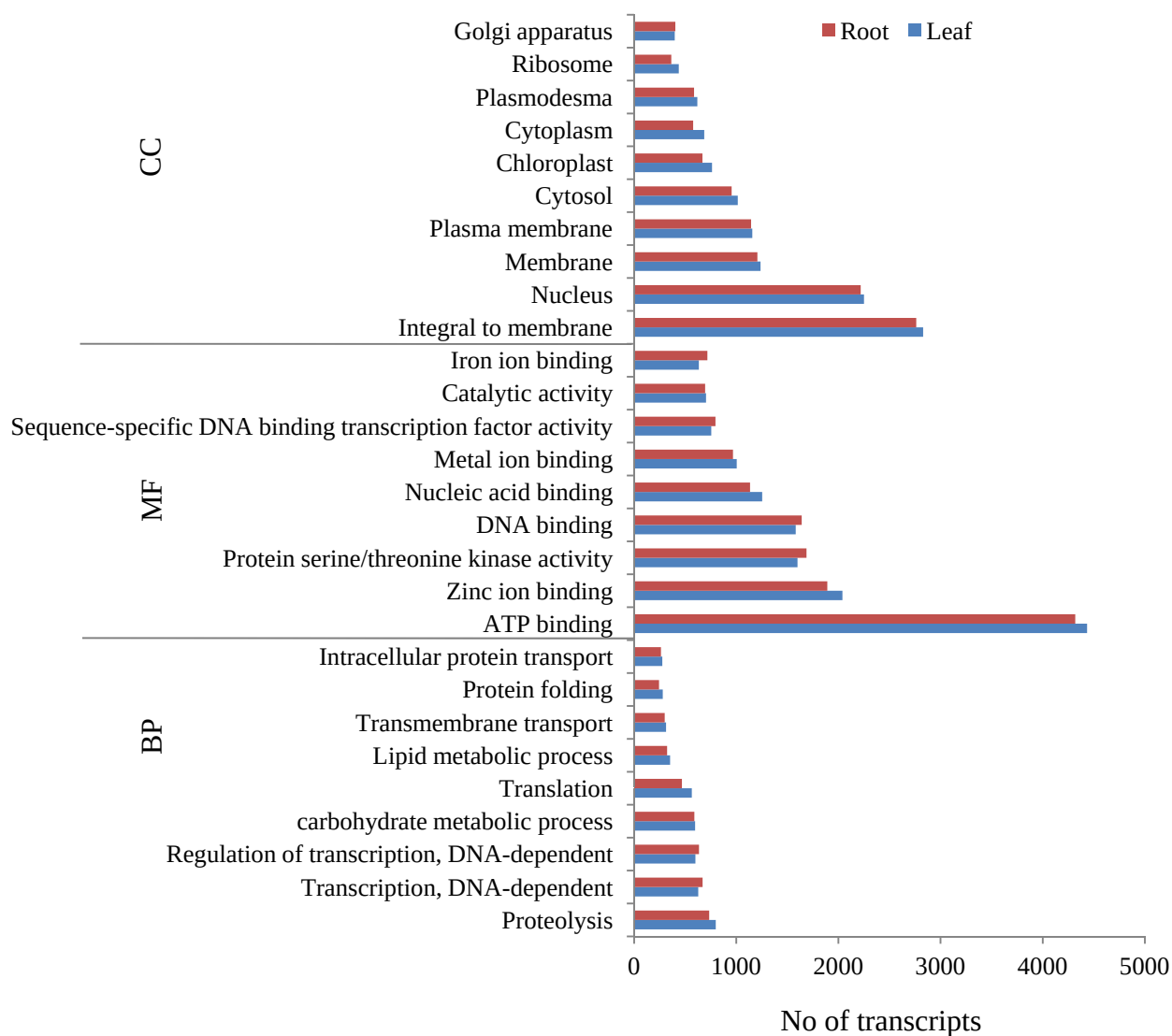




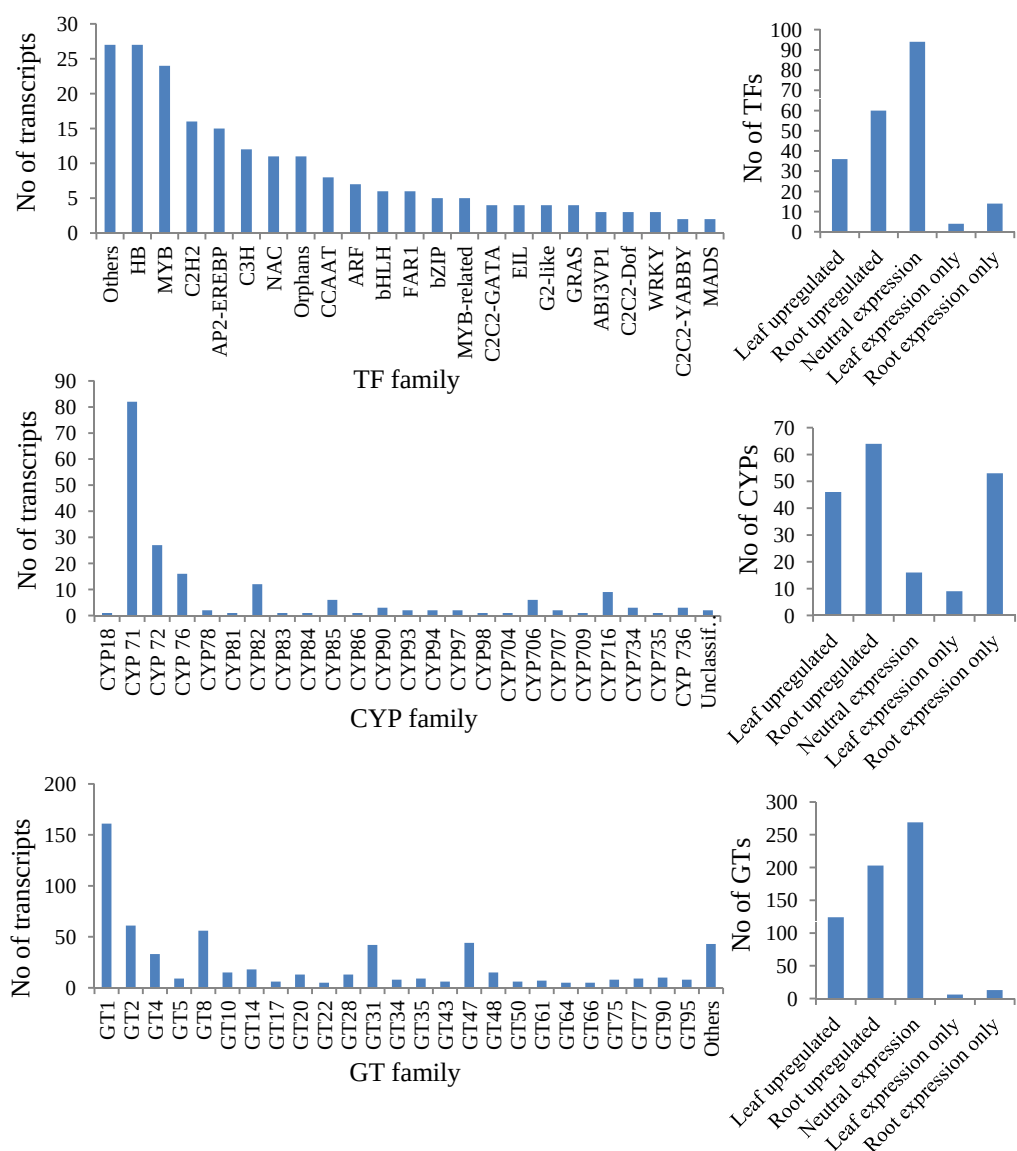
Supplementary Figure S1. Flow chart displaying strategies employed for *de novo* transcriptome analysis.



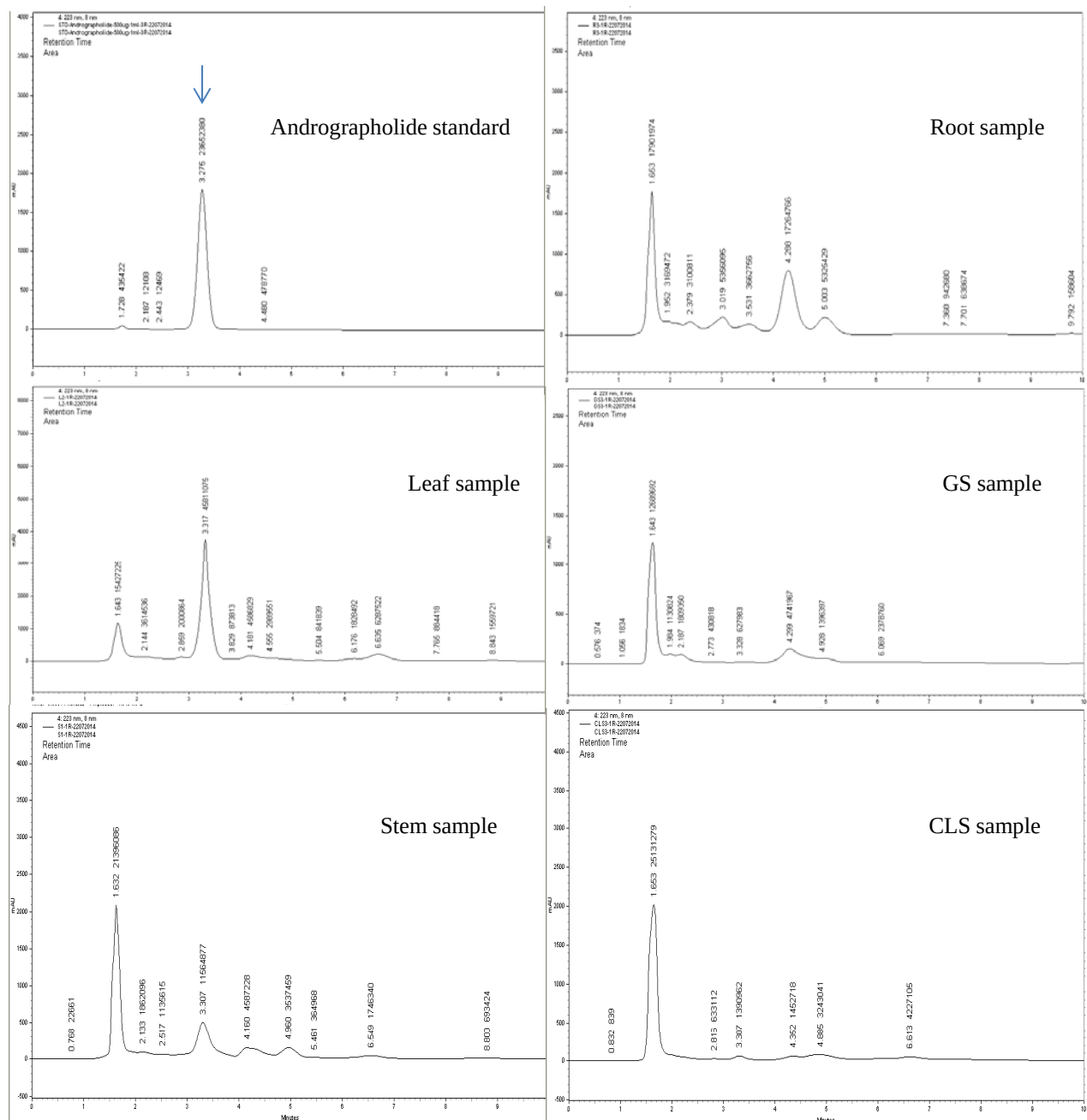
Supplementary Figure S2. Flow chart displaying strategies employed for digital gene expression analysis.



Supplementary Figure S3. Gene ontology classification of root and leaf transcripts. BP- biological process, MF- molecular function, CC- cellular component.



Supplementary Figure S4. Transcription factor, cytochrome P450 monooxygenase and glycosyltransferase families. Expression patterns of the transcripts are based on DGE. Leaf upregulated, root upregulated and neutral expression denote log2FoldChange (leaf vs root) of ≥ 1 , ≤ -1 and between 1 and -1, respectively.



Supplementary Figure S6. HPLC chromatograms of metabolites extracted from andrographolide-accumulating (Leaf and stem) and non-accumulating (root, GS, CLS) tissues of *A. paniculata*. Methanol extracts were analyzed as described in Methods.