Supplimentary figures

Mechanisms Underlying the Enhanced Biomass and Abiotic Stress Tolerance Phenotypes of an Arabidopsis MIOX Over-expresser

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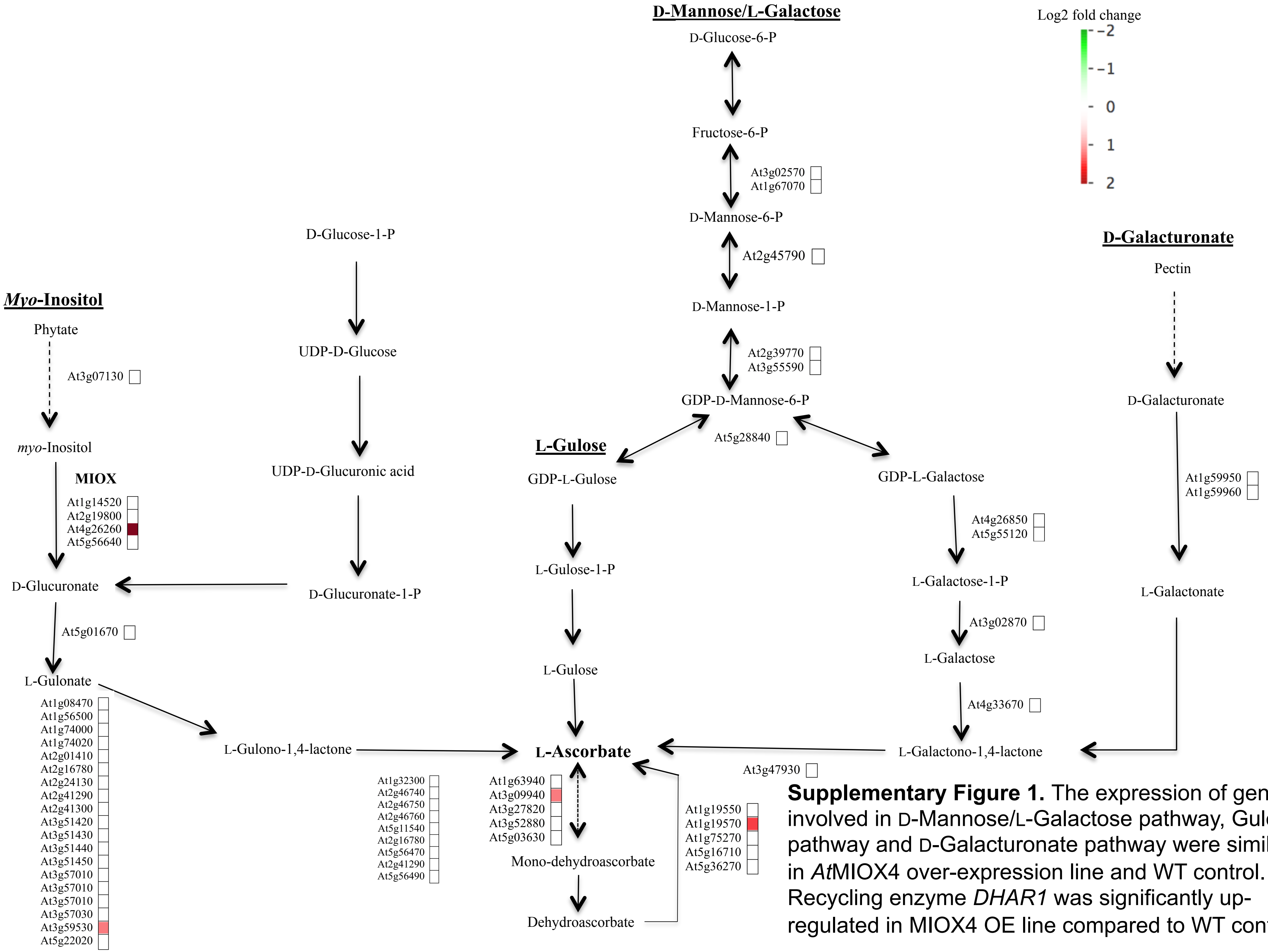
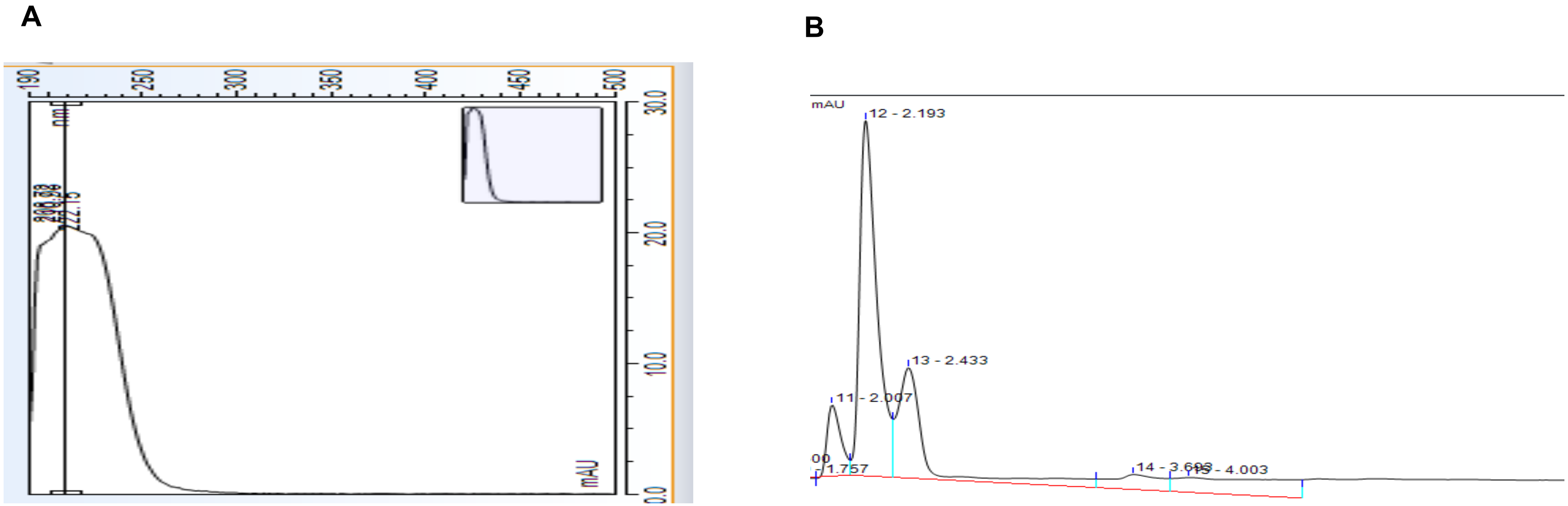
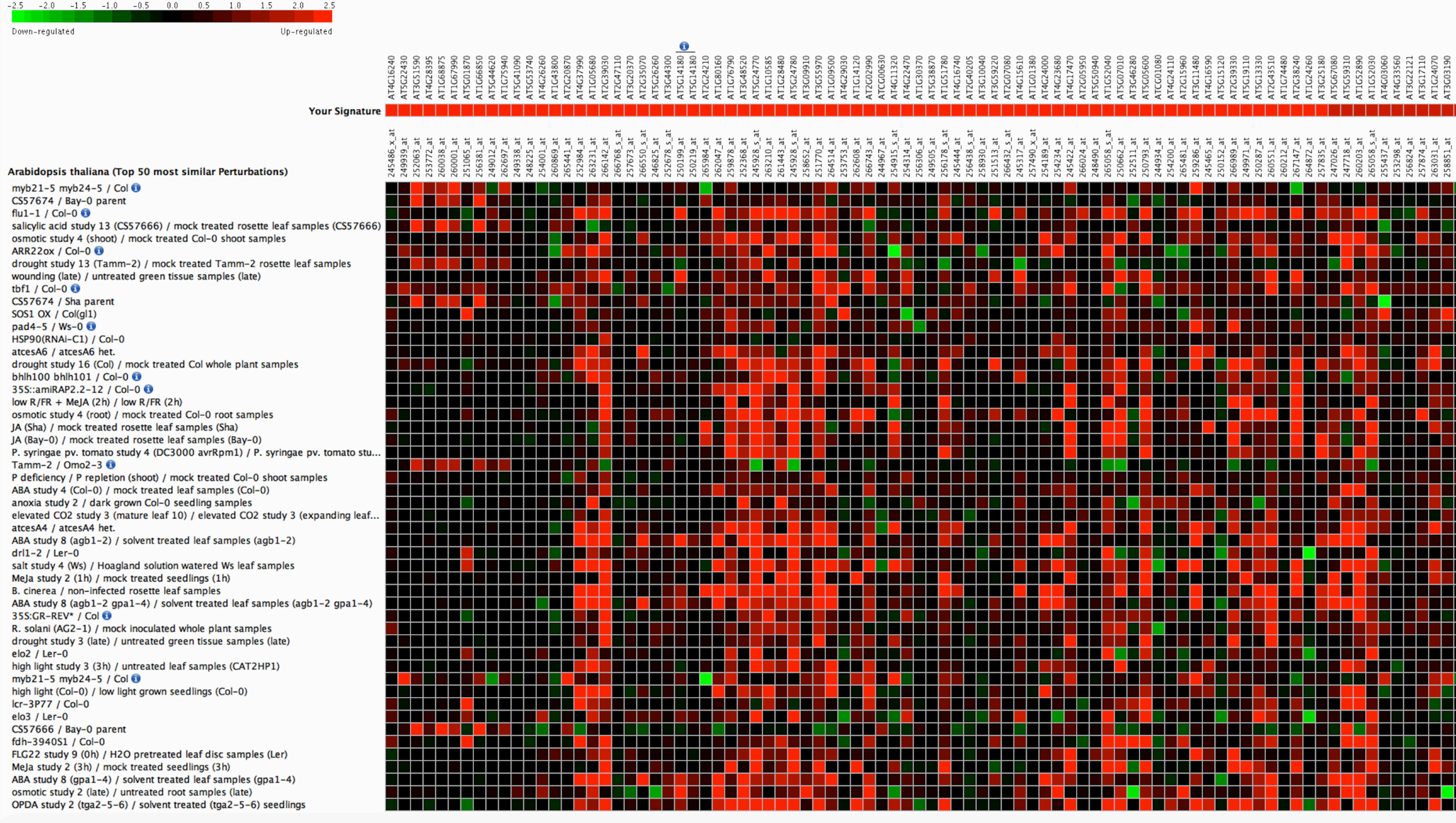


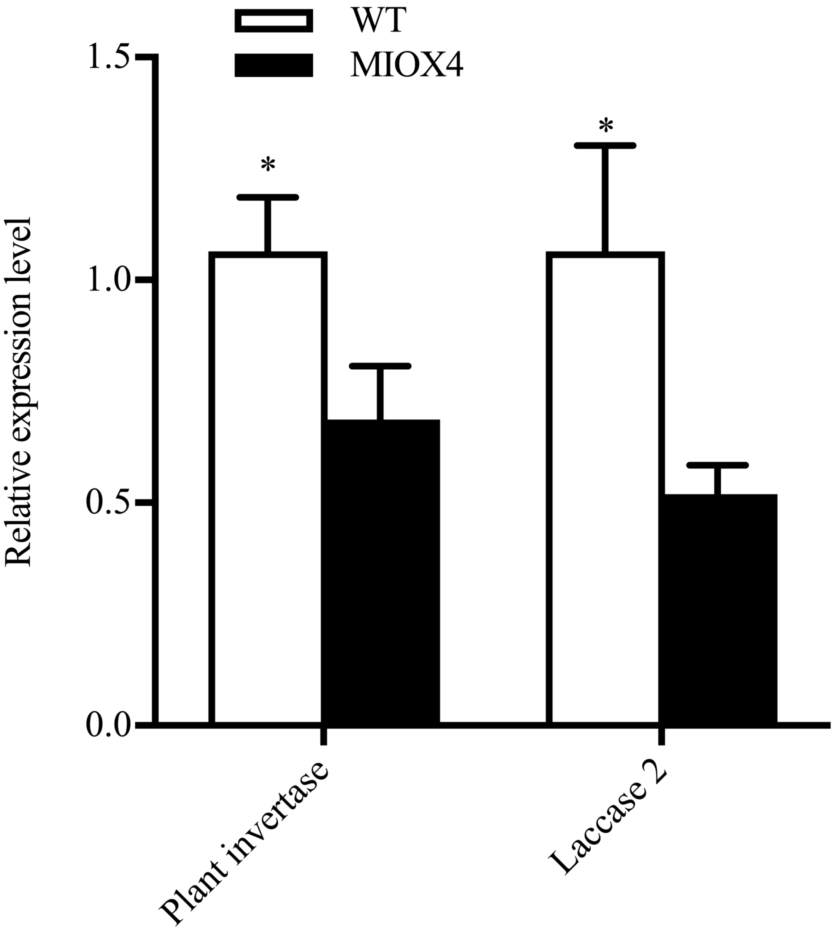
Supplementary Figure 1. The expression of genes involved in D-Mannose/L-Galactose pathway, Gulose pathway and D-Galacturonate pathway were similar in *At*MIOX4 over-expression line and WT control. Recycling enzyme *DHAR1* was significantly up-regulated in MIOX4 OE line compared to WT control.



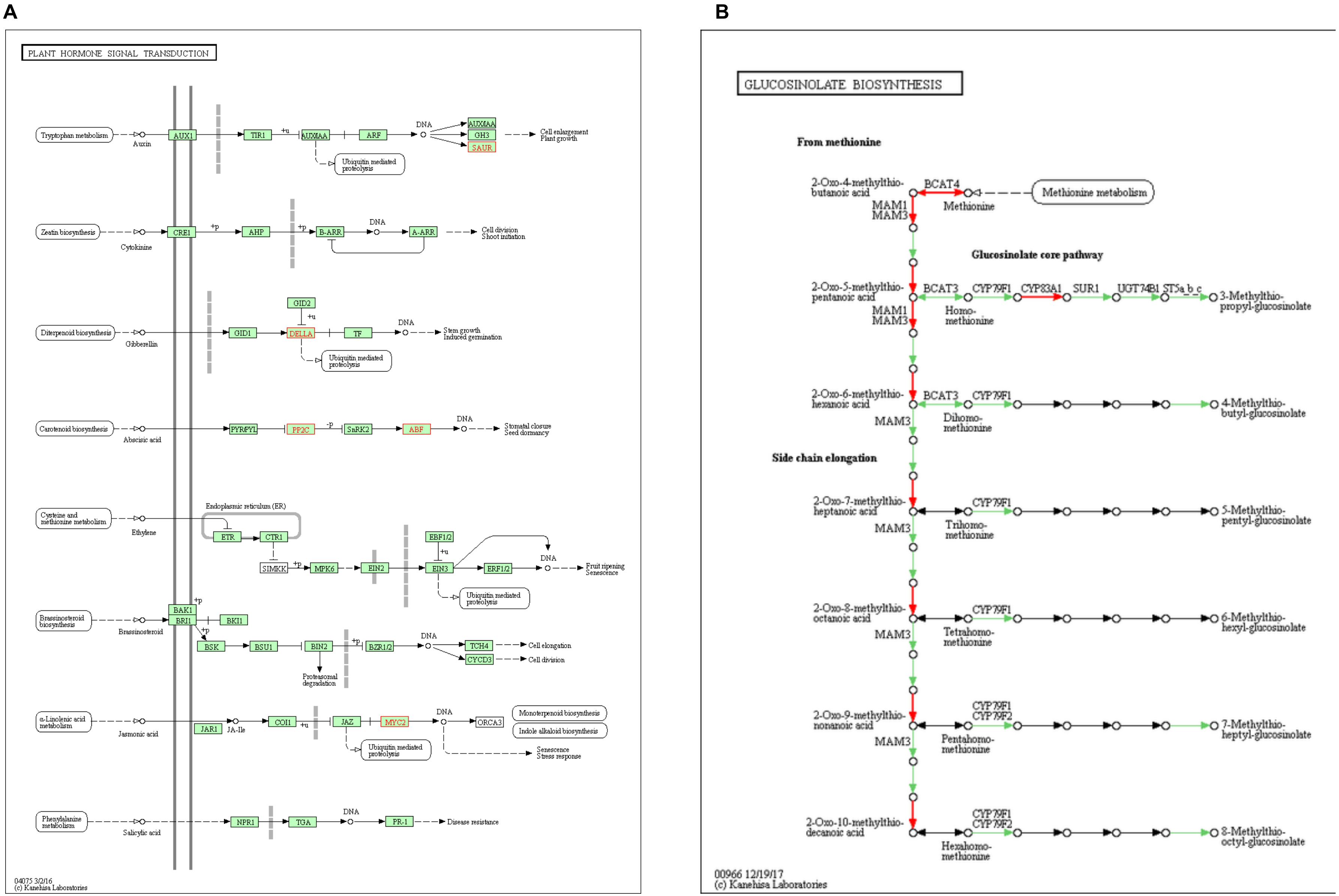
Supplementary Figure 2. A) UV-spectra of glucoerucin at 229nm B) Chromatogram of glucoerucin detected at 229nm.



Supplementary Figure 3. GeneVestigator analysis of top 200 up-regulated transcripts ($\log_2$fold > 1.75) were compared with signature expression transcripts from 50 abiotic and biotic stress perturbations. *ATCAD8* , *GLYI7* and *NAC019* were also highly expressed in most of the abiotic stress (heat, salt, drought cold) tolerance experiments.

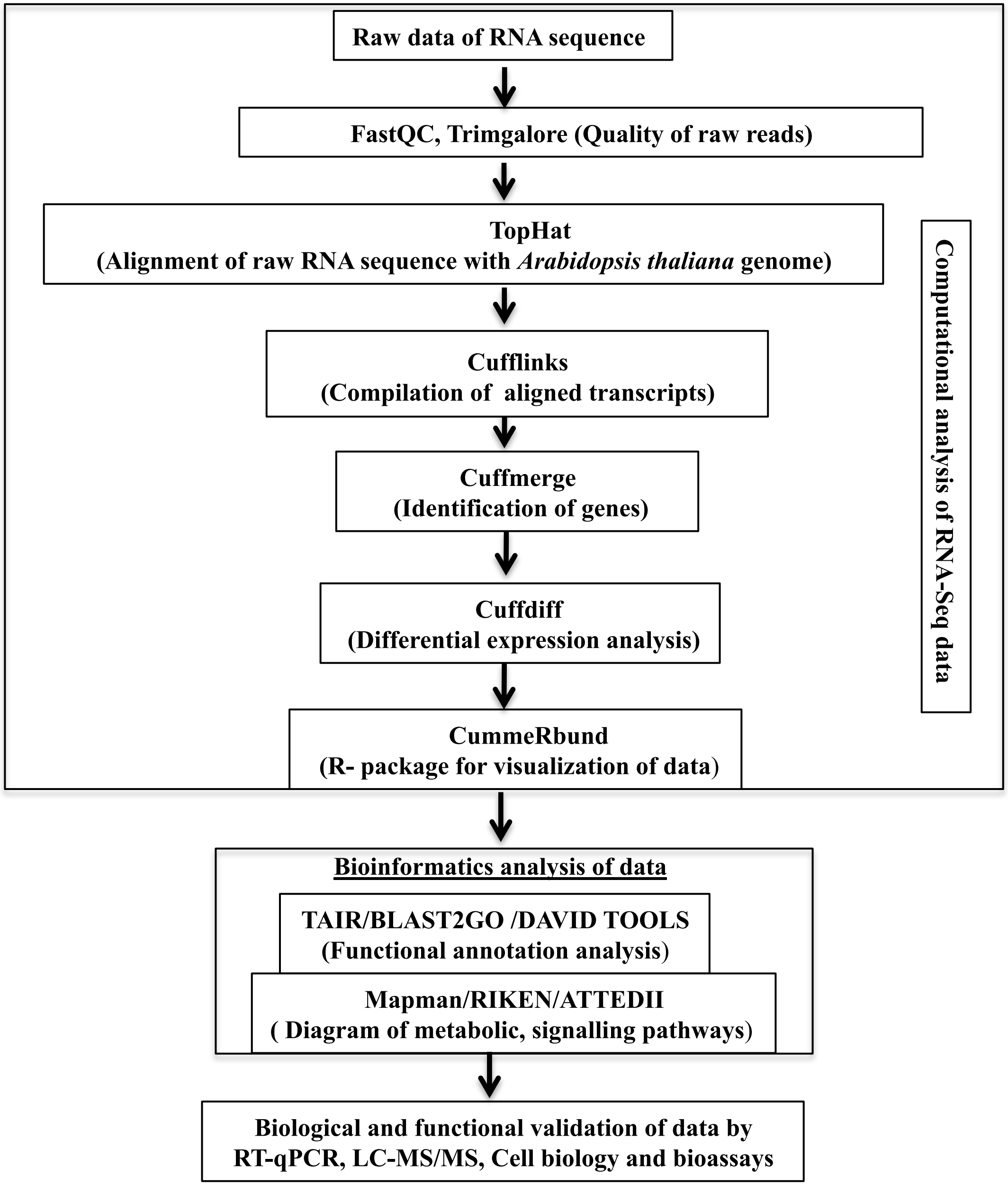


Supplementary Figure 4. Down-regulation of cell wall metabolism transcripts. Validation of down-regulation of plant invertase/ pectinmethylestarase superfamily protein and Laccase 2 in *At*MIOX4 OE line using RT-qPCR. * indicated $p<0.05$ at 0.05 significance level. Data was mean ± SEM (n=3).



Supplementary Figure 5. ATTEDII analysis of up-regulated transcripts. A) Mapping of up-regulated transcripts in plant hormone signaling pathway, B) Mapping of up-regulated transcripts in glucosinolates biosynthesis pathway.

Supplementary Figure 6. Pageman analysis of differentially expressed transcripts. The transcripts associated with light reactions of photosynthesis, lipid metabolism, secondary metabolism and hormone metabolism are up-regulated whereas transcripts related to cell wall metabolism are down-regulated in *At*MIOX4 transcriptome. The functional enrichment analysis was performed using binwise wilcoxon test, no multiple corrections, and over representation value 3.



Supplementary Figure 7. Schematic representation of RNA-Seq data analysis. Raw RNA Sequence data was analyzed by using TopHat, Cufflink, Cuffmerge, Cuffdiff and CummeRbund algorhitms. Functional annotation and metabolic pathways of transcriptomics datasets were analyzed by BLAST2gOv3.1 and Mapman. RT-qPCR validation of hallmark genes expression, quantification of metabolites by LC-MS/MS and completion of data analysis.