

# Supplimentary figures

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

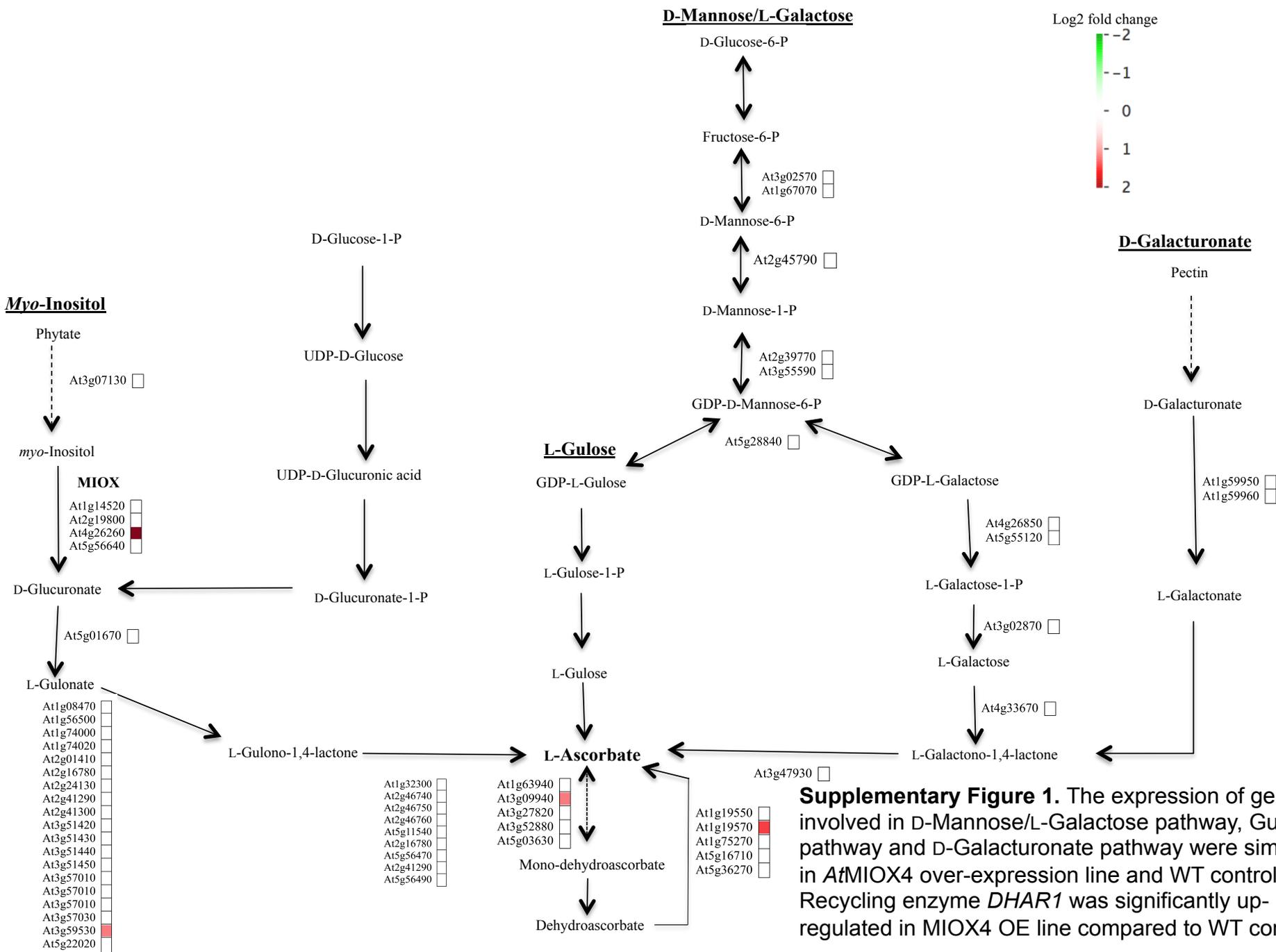
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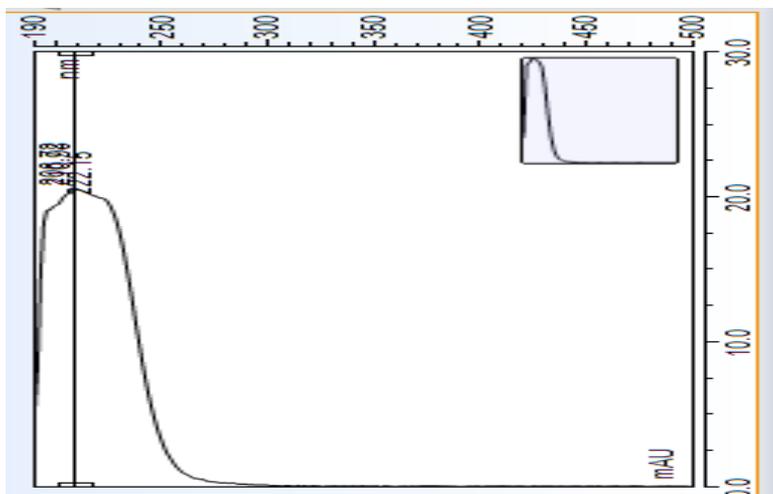
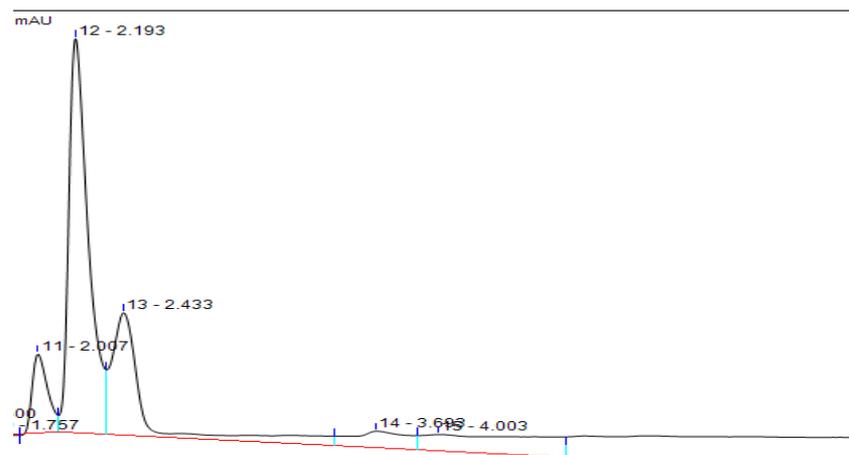
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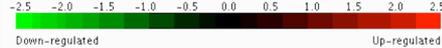
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**Supplementary Figure 1.** The expression of genes involved in D-Mannose/L-Galactose pathway, Gulose pathway and D-Galacturonate pathway were similar in *AtMIOX4* over-expression line and WT control. Recycling enzyme *DHAR1* was significantly up-regulated in *MIOX4* OE line compared to WT control.

**A****B**

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

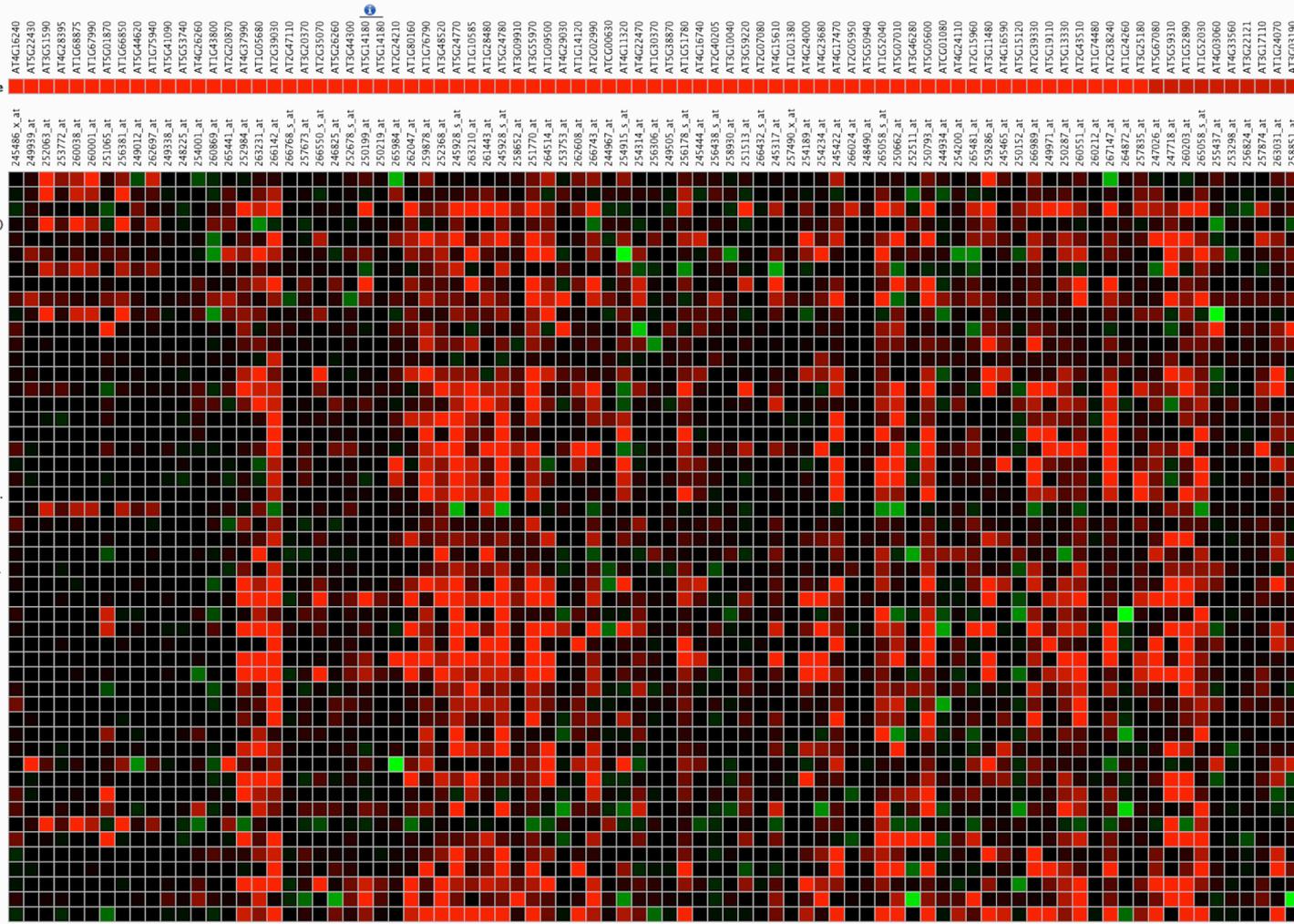


Down-regulated Up-regulated

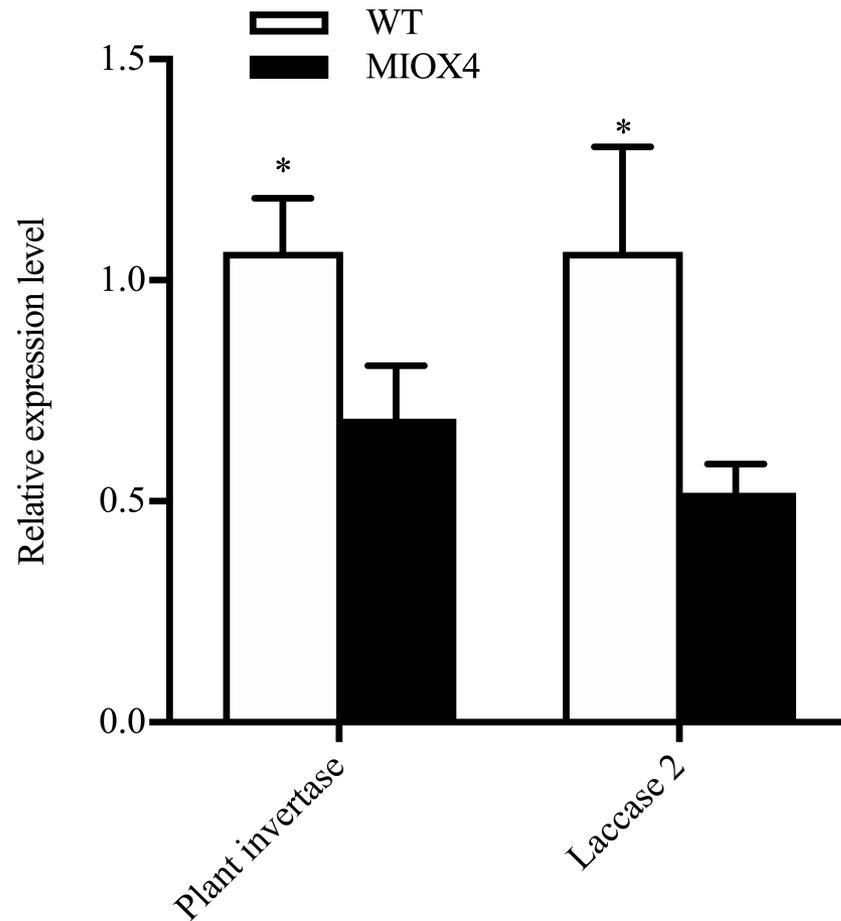
**Arabidopsis thaliana (Top 50 most similar Perturbations)**

- myb21-5 myb24-5 / Col [i](#)
- CS57674 / Bay-0 parent
- flu1-1 / Col-0 [i](#)
- salicylic acid study 13 (CS57666) / mock treated rosette leaf samples (CS57666)
- osmotic study 4 (shoot) / mock treated Col-0 shoot samples
- ARR22ox / Col-0 [i](#)
- drought study 13 (Tamm-2) / mock treated Tamm-2 rosette leaf samples
- wounding (late) / untreated green tissue samples (late)
- tbfl / Col-0 [i](#)
- CS57674 / Sha parent
- SOS1 OX / Col(g11)
- pad4-5 / Ws-0 [i](#)
- HSP90(RNAi-C1) / Col-0
- atcesA6 / atcesA6 het.
- drought study 16 (Col) / mock treated Col whole plant samples
- bhh100 bhh101 / Col-0 [i](#)
- 35S::amiRAP2.2-12 / Col-0 [i](#)
- low R/FR + MeJA (2h) / low R/FR (2h)
- osmotic study 4 (root) / mock treated Col-0 root samples
- JA (Sha) / mock treated rosette leaf samples (Sha)
- JA (Bay-0) / mock treated rosette leaf samples (Bay-0)
- P. syringae pv. tomato study 4 (DC3000 avrRpm1) / P. syringae pv. tomato stu...
- Tamm-2 / Omo2-3 [i](#)
- P deficiency / P repletion (shoot) / mock treated Col-0 shoot samples
- ABA study 4 (Col-0) / mock treated leaf samples (Col-0)
- anoxia study 2 / dark grown Col-0 seedling samples
- elevated CO2 study 3 (mature leaf 10) / elevated CO2 study 3 (expanding leaf...
- atcesA4 / atcesA4 het.
- ABA study 8 (agb1-2) / solvent treated leaf samples (agb1-2)
- dr1-2 / Ler-0
- salt study 4 (Ws) / Hoagland solution watered Ws leaf samples
- Meja study 2 (1h) / mock treated seedlings (1h)
- B. cinerea / non-infected rosette leaf samples
- ABA study 8 (agb1-2 gpa1-4) / solvent treated leaf samples (agb1-2 gpa1-4)
- 35S:GR-REV\* / Col [i](#)
- R. solani (AG2-1) / mock inoculated whole plant samples
- drought study 3 (late) / untreated green tissue samples (late)
- elo2 / Ler-0
- high light study 3 (3h) / untreated leaf samples (CAT2HP1)
- myb21-5 myb24-5 / Col [i](#)
- high light (Col-0) / low light grown seedlings (Col-0)
- lcr-3P77 / Col-0
- elo3 / Ler-0
- CS57666 / Bay-0 parent
- fdh-3940S1 / Col-0
- FLG22 study 9 (0h) / H2O pretreated leaf disc samples (Ler)
- Meja study 2 (3h) / mock treated seedlings (3h)
- ABA study 8 (gpa1-4) / solvent treated leaf samples (gpa1-4)
- osmotic study 2 (late) / untreated root samples (late)
- OPDA study 2 (tga2-5-6) / solvent treated (tga2-5-6) seedlings

**Your Signature**

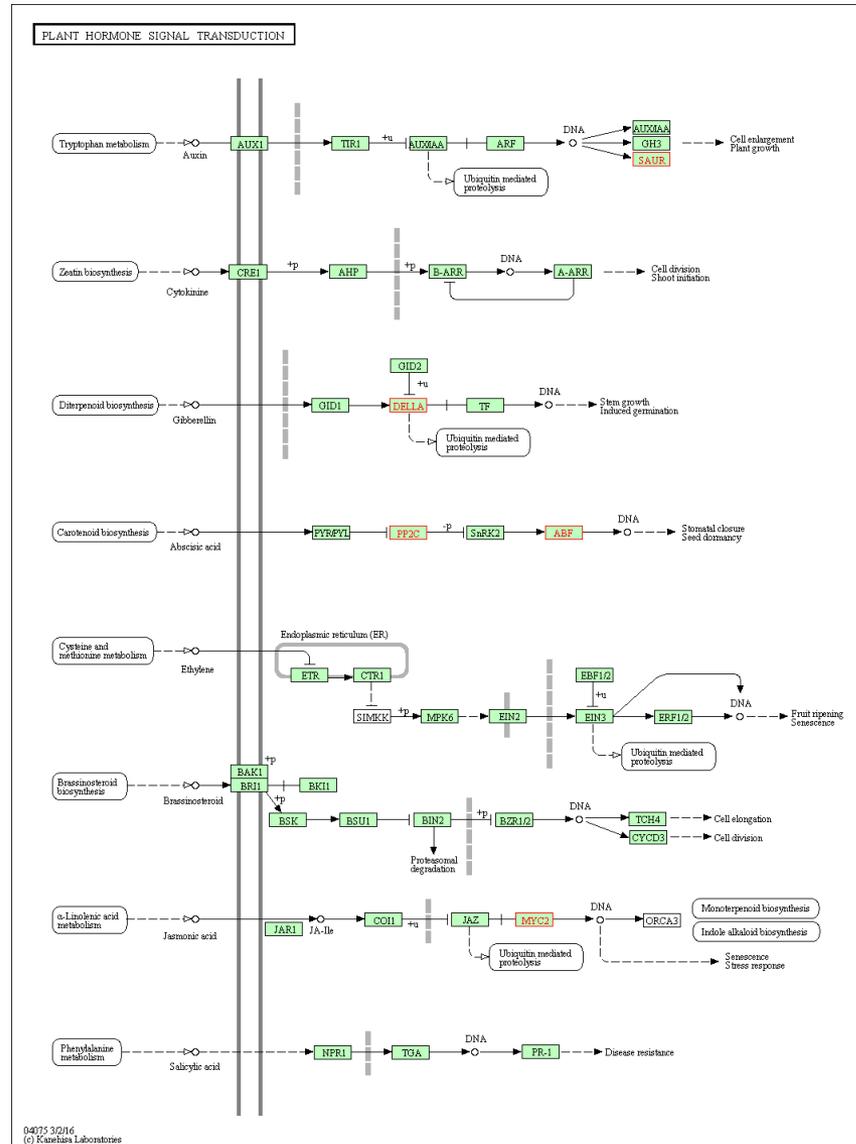


**Supplementary Figure 3.** GeneVestigator analysis of top 200 up-regulated transcripts ( $\log_2$ fold > 1.75) were compared with signature expression transcripts from 50 abiotic and biotic stress perturbations. *ATCAD8*, *GLY17* and *NAC019* were also highly expressed in most of the abiotic stress (heat, salt, drought cold) tolerance experiments.

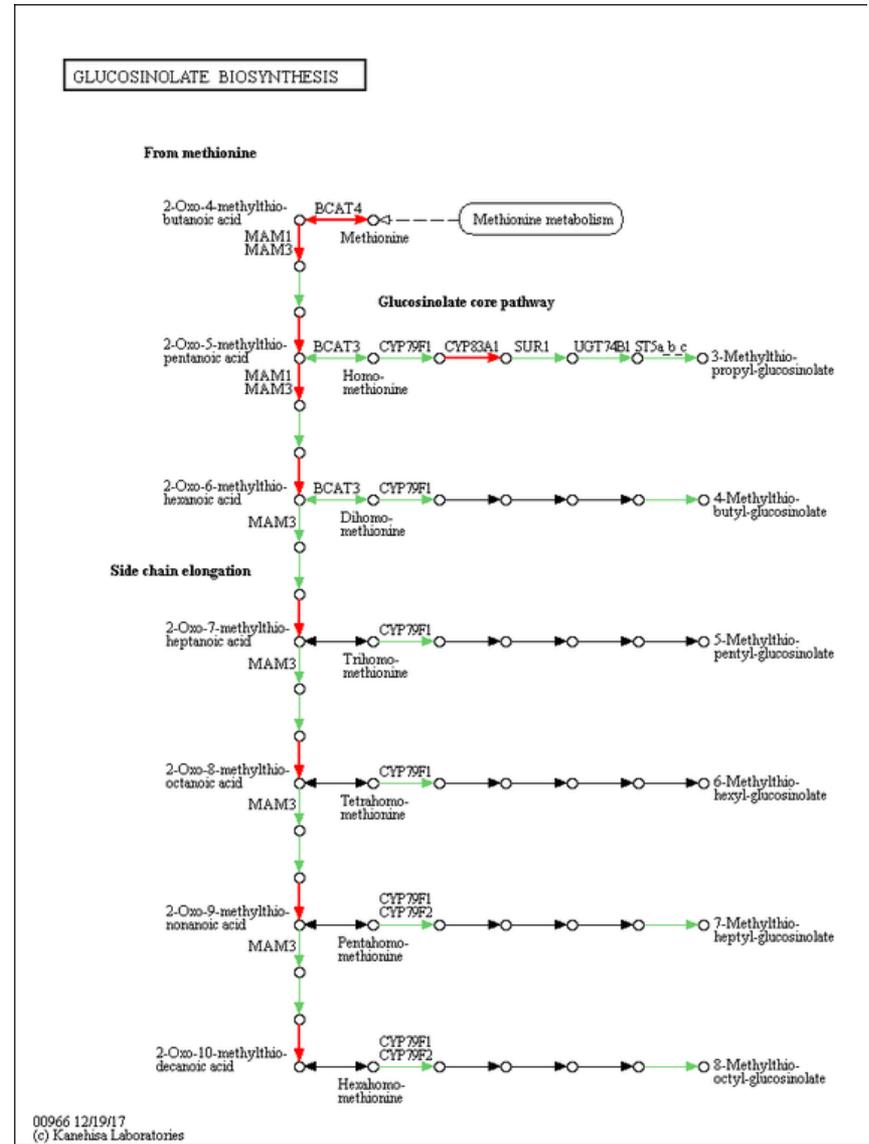


**Supplementary Figure 4.** Down-regulation of cell wall metabolism transcripts. Validation of down-regulation of plant invertase/pectinmethylesterase superfamily protein and Laccase 2 in *AtMIOX4* OE line using RT-qPCR. \* indicated  $p < 0.05$  at 0.05 significance level. Data was mean  $\pm$  SEM (n=3).

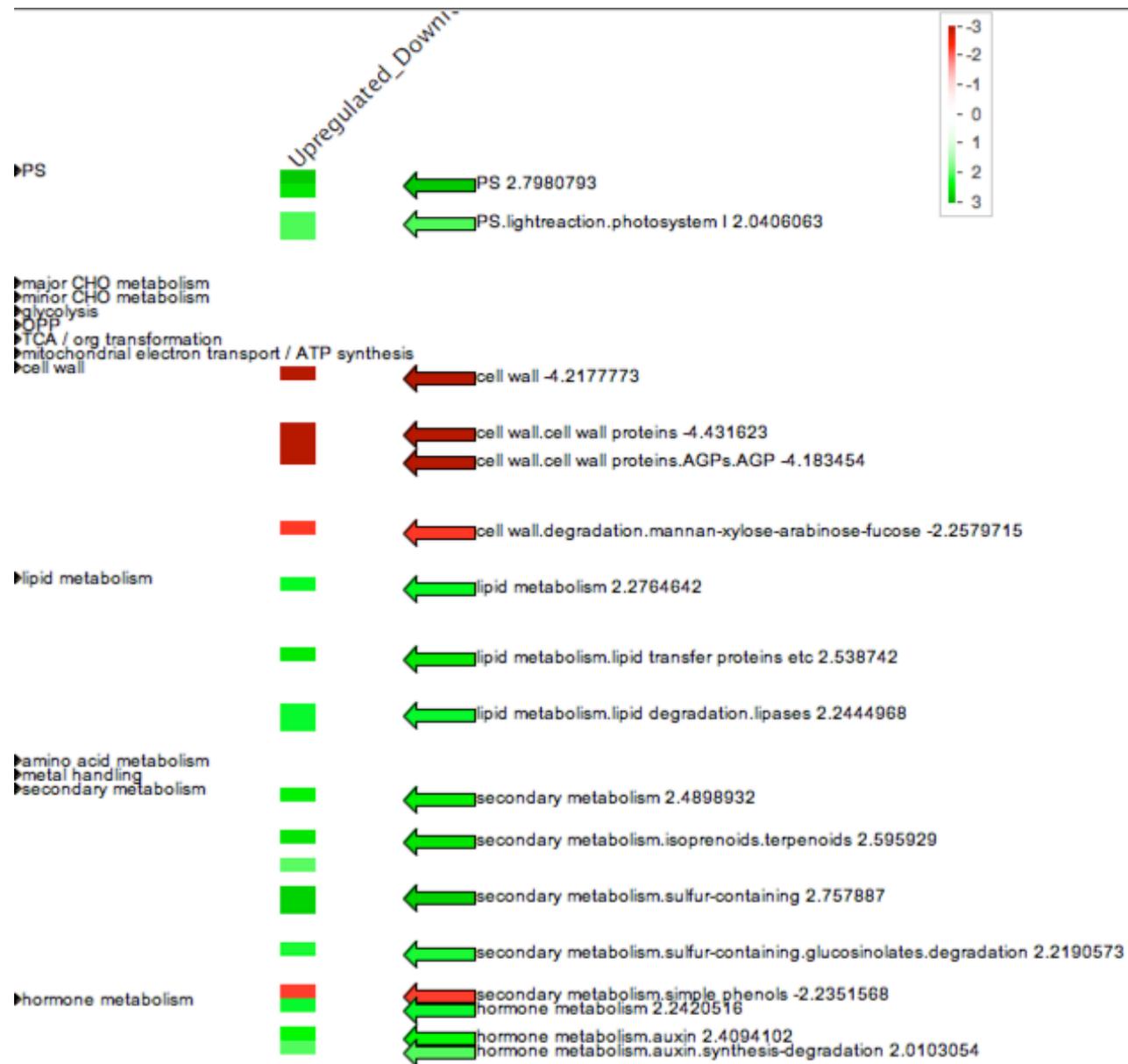
A



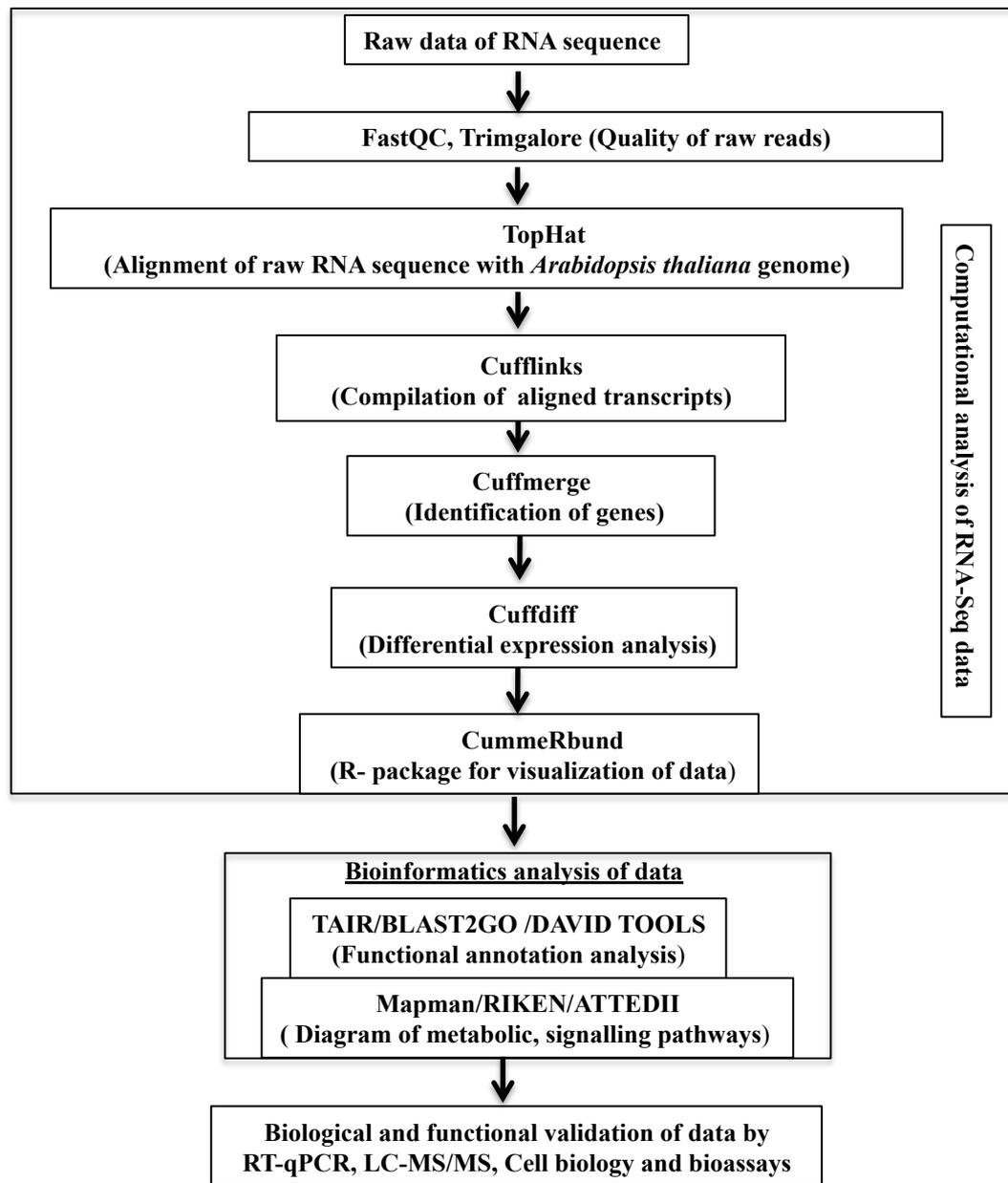
B



**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 *AtMIOX4* 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 algorithms. 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.