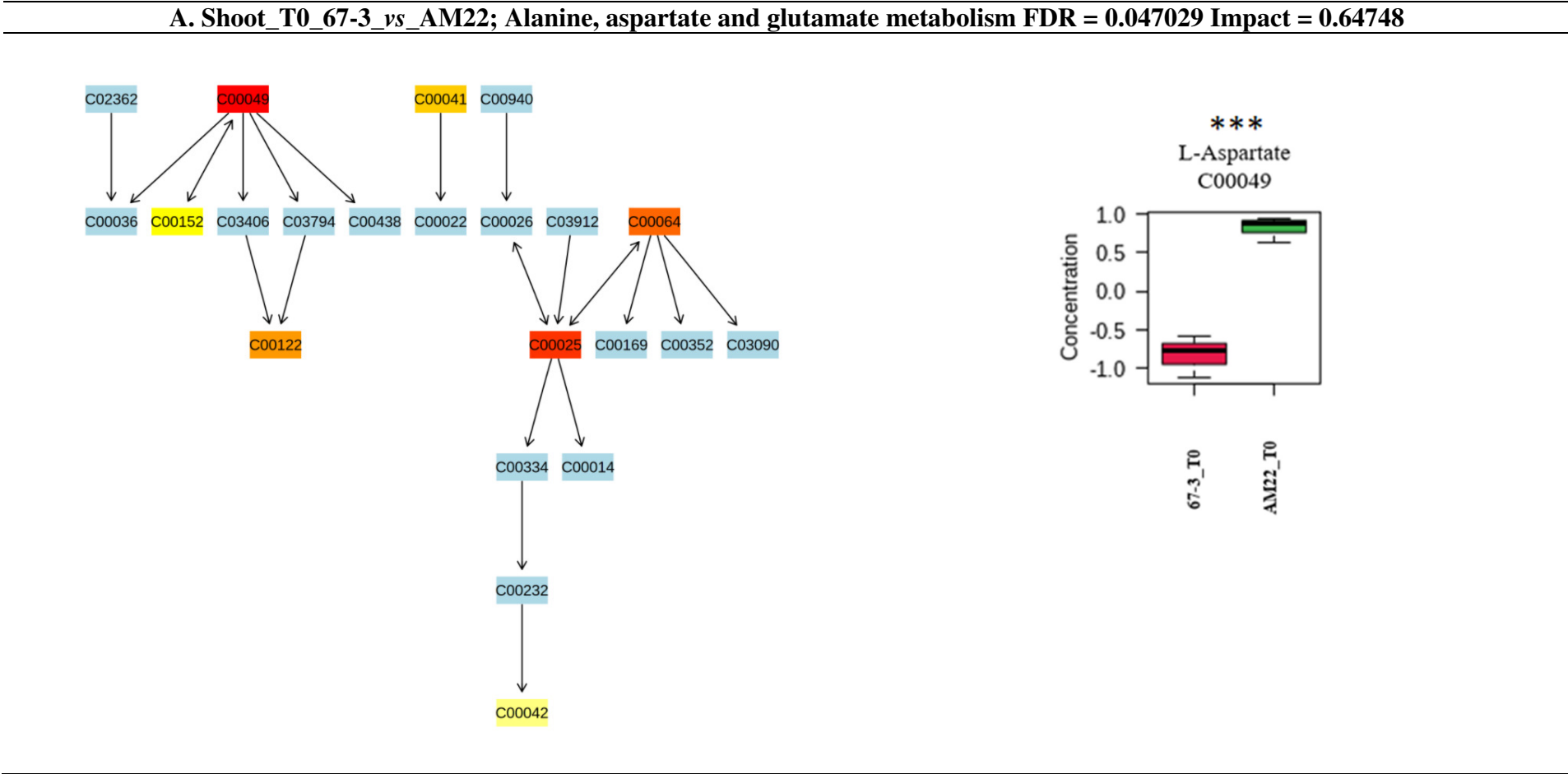
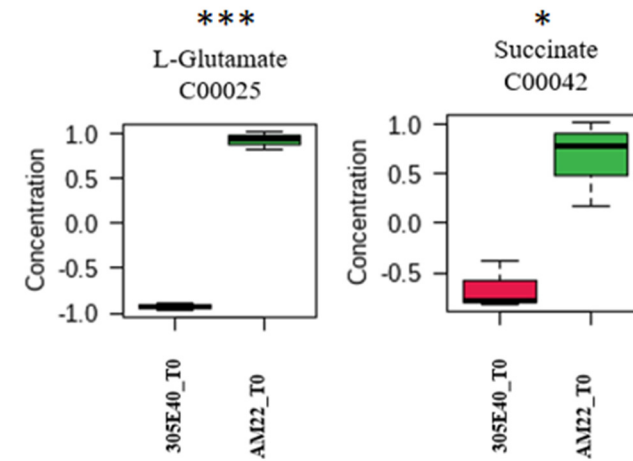
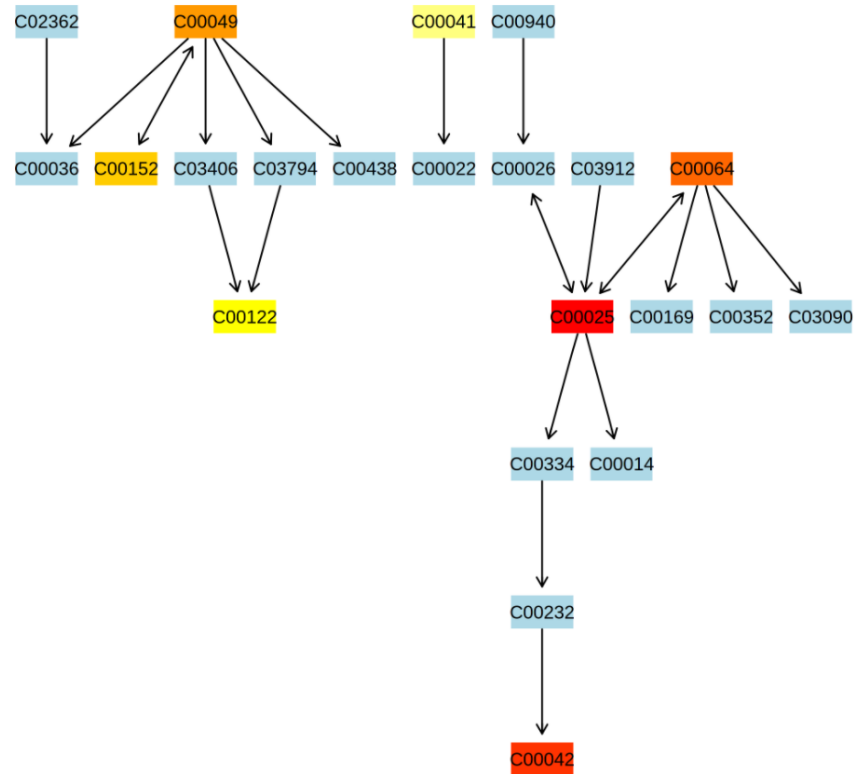


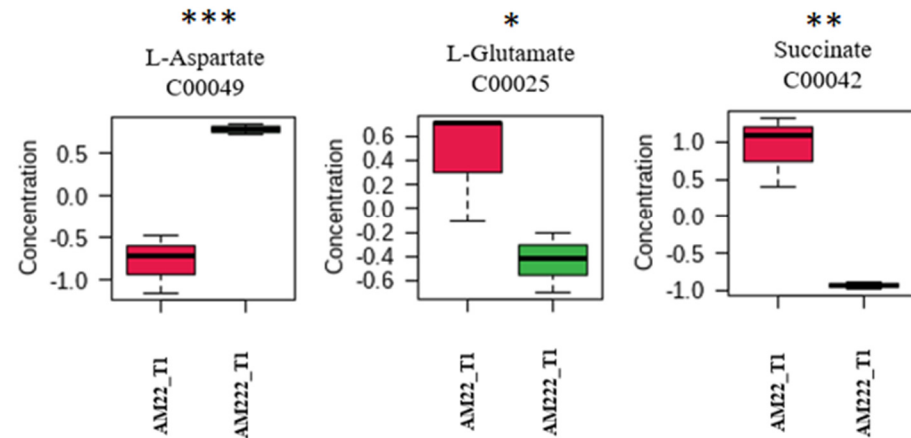
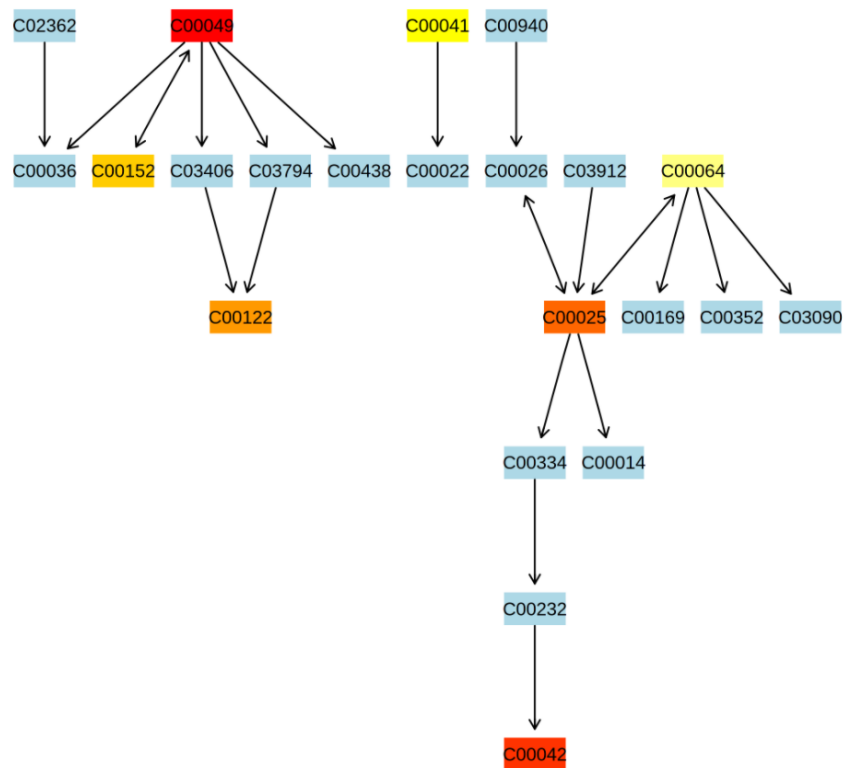
Figure S1. Interactive visualization system and detailed results from the pathway analysis in shoot are presented graphically for AM222, 67-3 and 305E40 vs. AM22: A) and B) to T0; C), D) and E) to T1; F), G), and H) to T2. Paths with FDR <0.05 and with a higher Impact value were highlighted. A P-value of less than 0.05, 0.01, and 0.001 was designated with one (*), two (**) or three (***) asterisks, respectively.



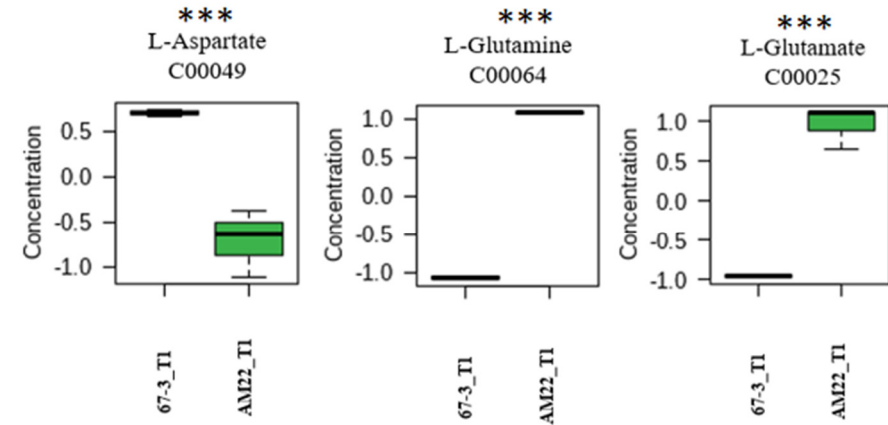
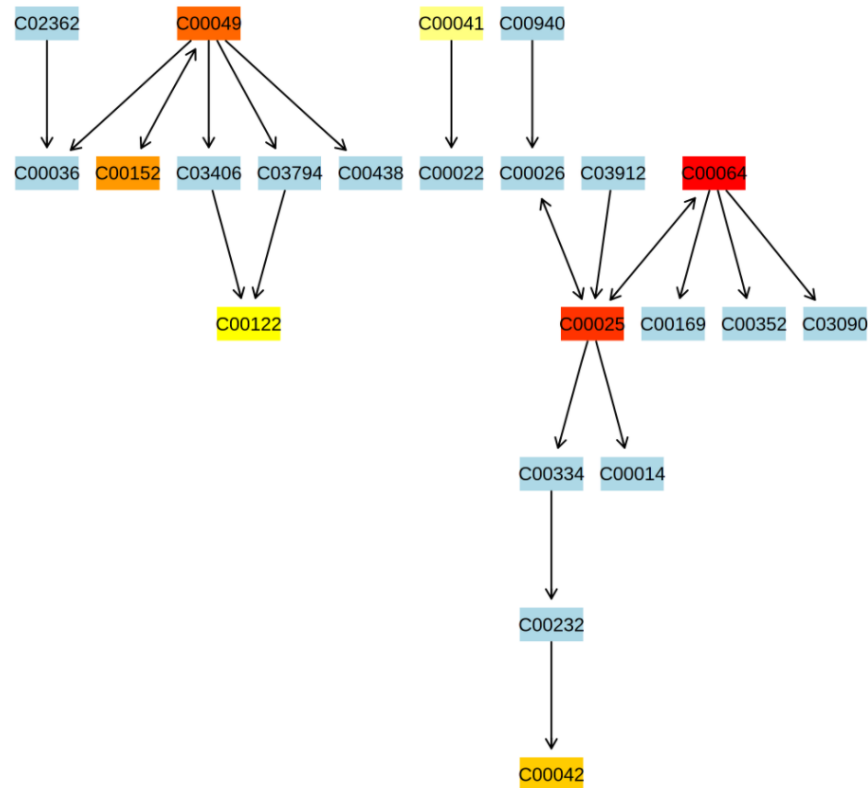
B. Shoot_T0_305E40_vs_AM22; Alanine, aspartate and glutamate metabolism FDR = 0.0094 Impact = 0.64748



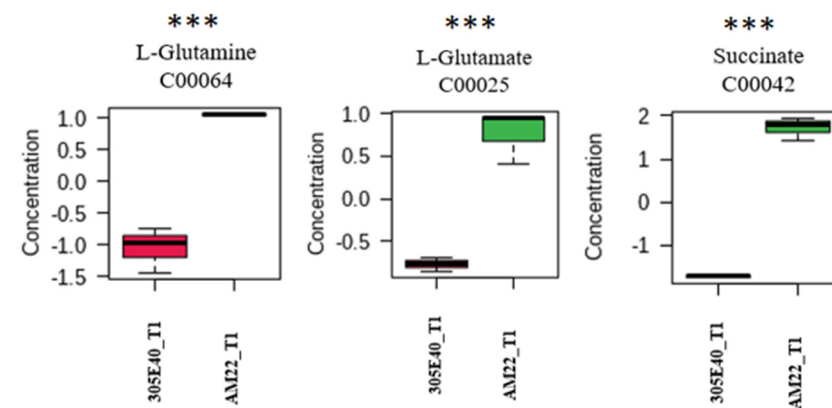
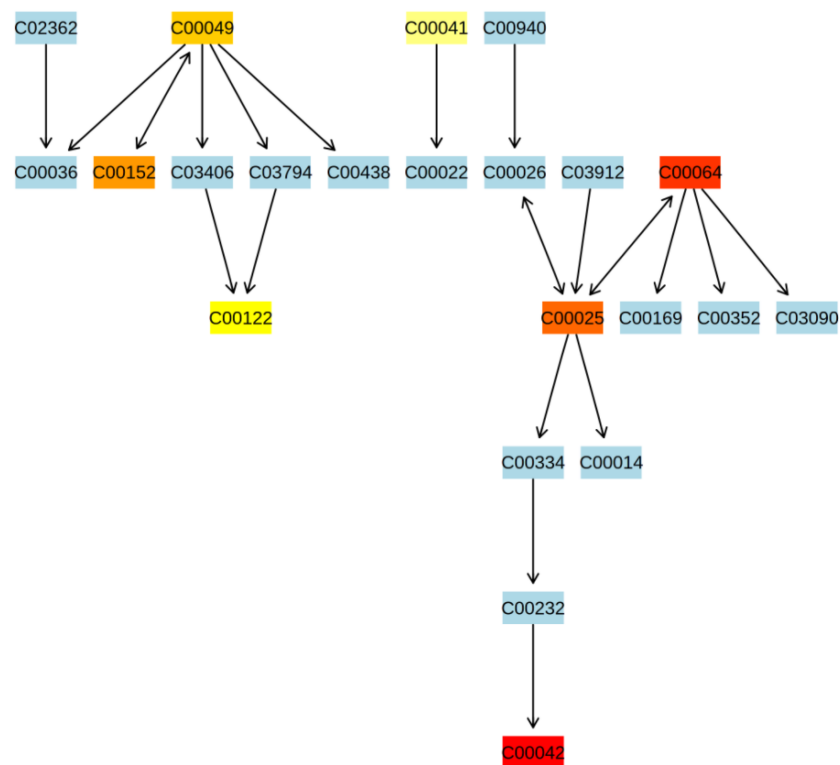
C. Shoot_T1_AM222_vs_AM22; Alanine, aspartate and glutamate metabolism FDR = 0.010616 Impact = 0.64748



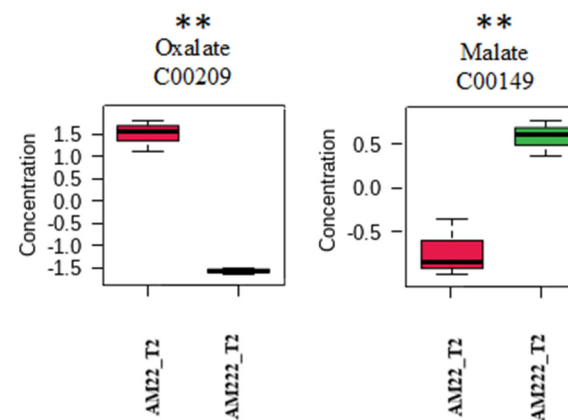
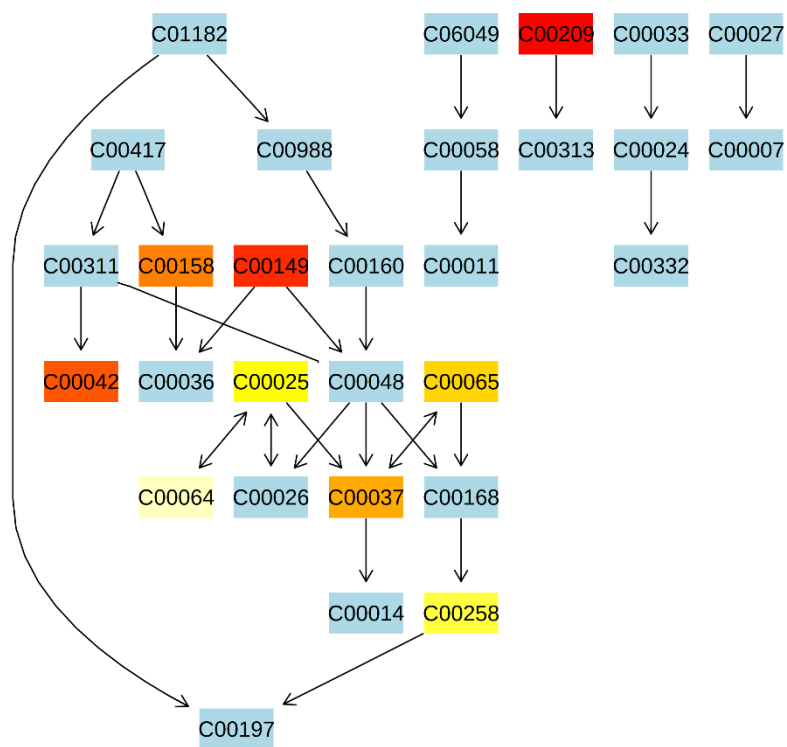
D. Shoot_T1_67-3_vs_AM22; Alanine, aspartate and glutamate metabolism FDR = 0.00020894 Impact = 0.64748



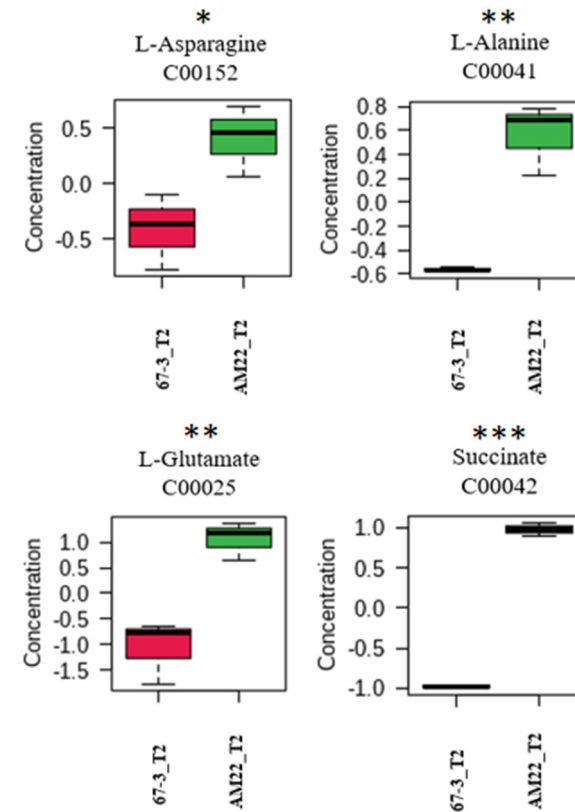
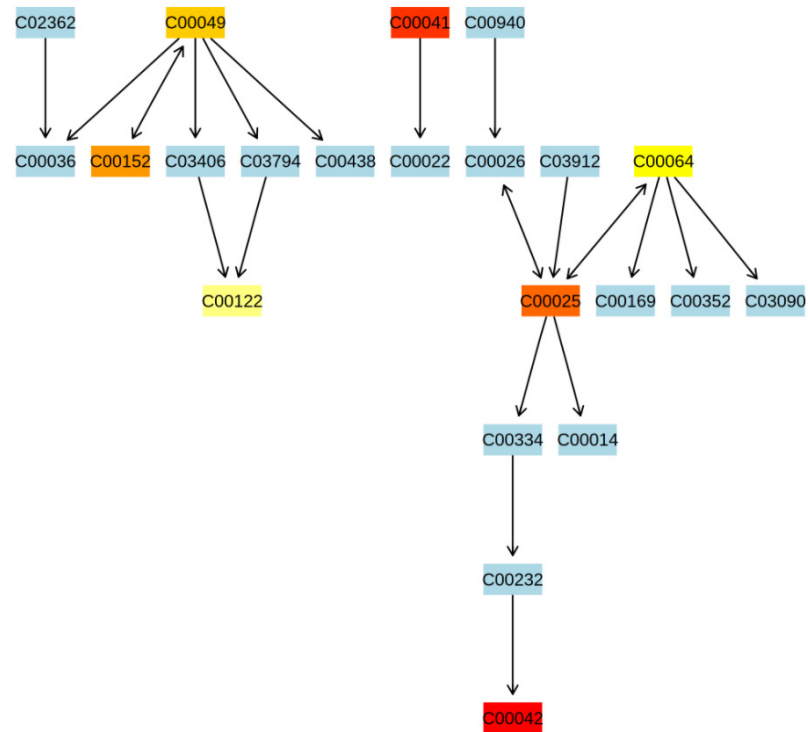
E. Shoot_T1_305E40_vs_AM22; Alanine, aspartate and glutamate metabolism FDR = 0.00029036 Impact = 0.64748



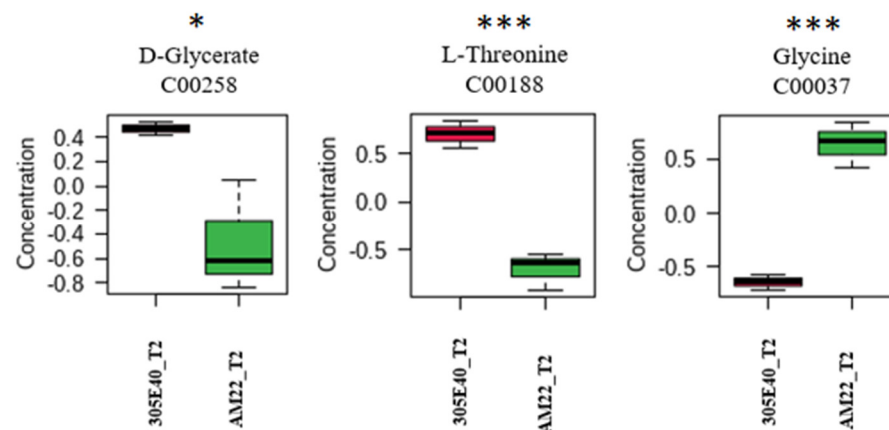
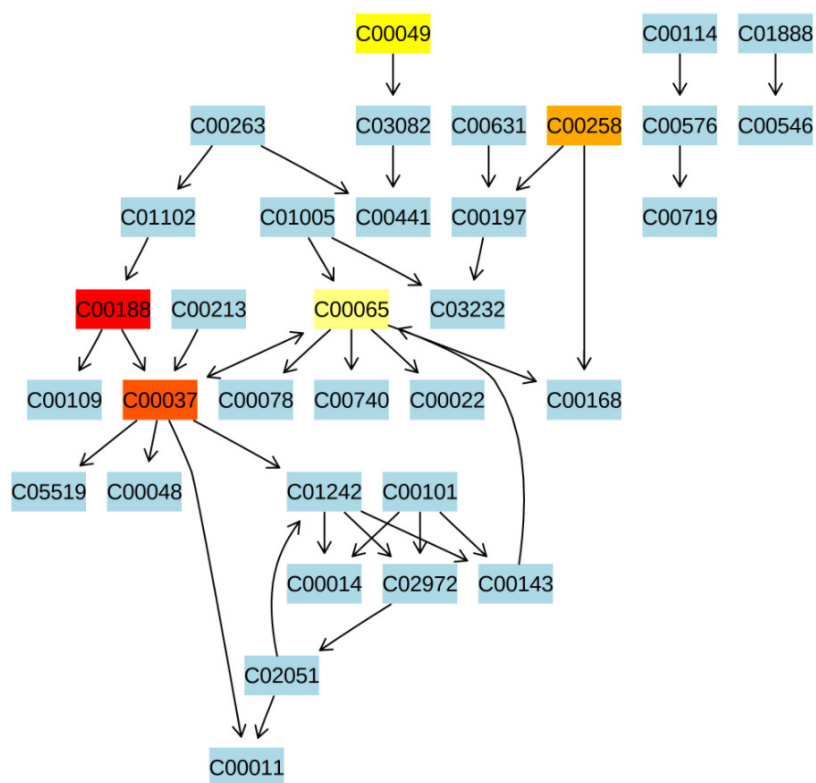
F. Shoot_T2_AM222_vs_AM22; Glyoxylate and dicarboxylate metabolism FDR = 0.018191 Impact = 0.28209



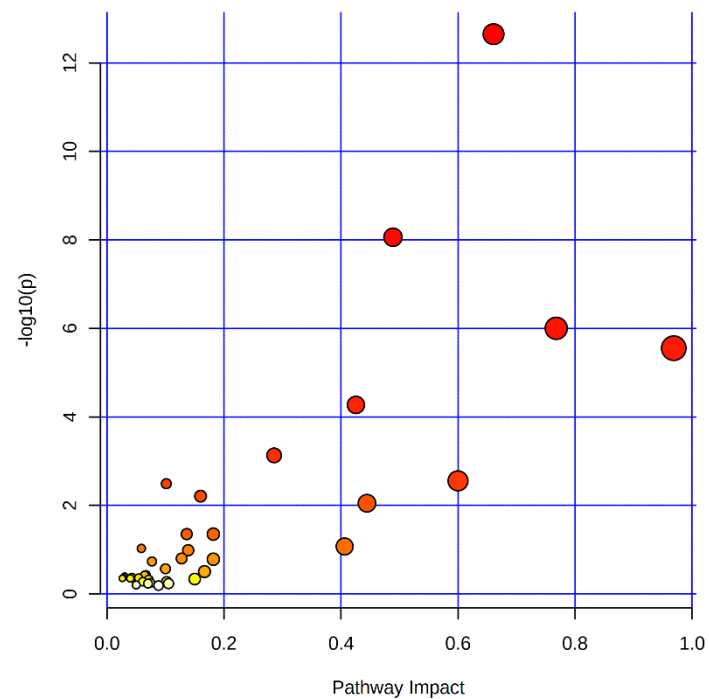
G. Shoot_T2_67-3_vs_AM22; Alanine, aspartate and glutamate metabolism FDR = 0.0032463 Impact = 0.64748



H. Shoot_T2_305E40_vs_AM22; Glycine, serine and threonine metabolism FDR = 0.0055903 Impact = 0.53598



C. Pathway enrichment analysis and pathway impact



	Total	Expected	Hits	Raw p	$-\log(p)$	Holm adjust	FDR	Impact
Glyoxylate and dicarboxylate metabolism	57	0.84534	13	2.24E-13	12.649	2.15E-11	2.15E-11	0.66071
Alanine, aspartate and glutamate metabolism	46	0.6822	9	8.70E-09	8.0605	8.27E-07	4.18E-07	0.48889
Starch and sucrose metabolism	57	0.84534	8	9.95E-07	6.0024	9.35E-05	3.18E-05	0.76786
Glycine, serine and threonine metabolism	65	0.96398	8	2.80E-06	5.5535	0.00026	6.71E-05	0.96875
Cyanoamino acid metabolism	48	0.71186	6	5.34E-05	4.2723	0.0049145	0.001026	0.42553
Butanoate metabolism	29	0.43008	4	0.000741	3.1304	0.067397	0.01185	0.28571
Citrate cycle (TCA cycle)	41	0.60805	4	0.002783	2.5556	0.25043	0.038161	0.6
Aminoacyl-tRNA biosynthesis	70	1.0381	5	0.00323	2.4909	0.28743	0.038754	0.10145

Figure S3. Heatmap of correlations in eggplant accession between metabolites and transcripts by the Pearson's correlation coefficient ($p < 0.05$) at T0. Correlations between eggplant metabolites and transcripts are based on 70 variables in shoot (A) and root (B).

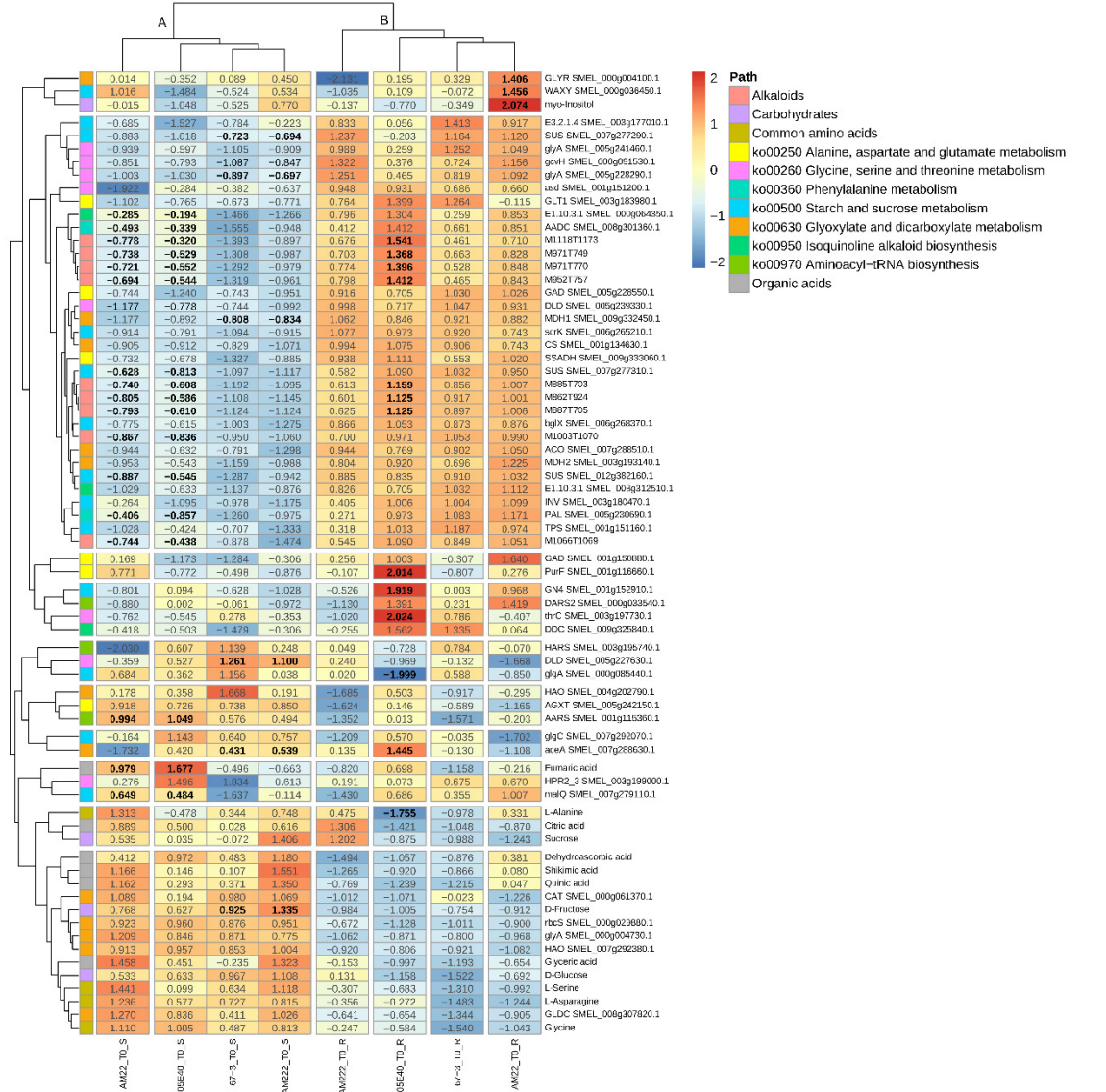


Figure S4. Heatmap of correlations in eggplant accession between metabolites and transcripts by the Pearson's correlation coefficient ($p < 0.05$) at T1. Correlations between eggplant metabolites and transcripts are based on 70 variables in shoot (A) and root (B).

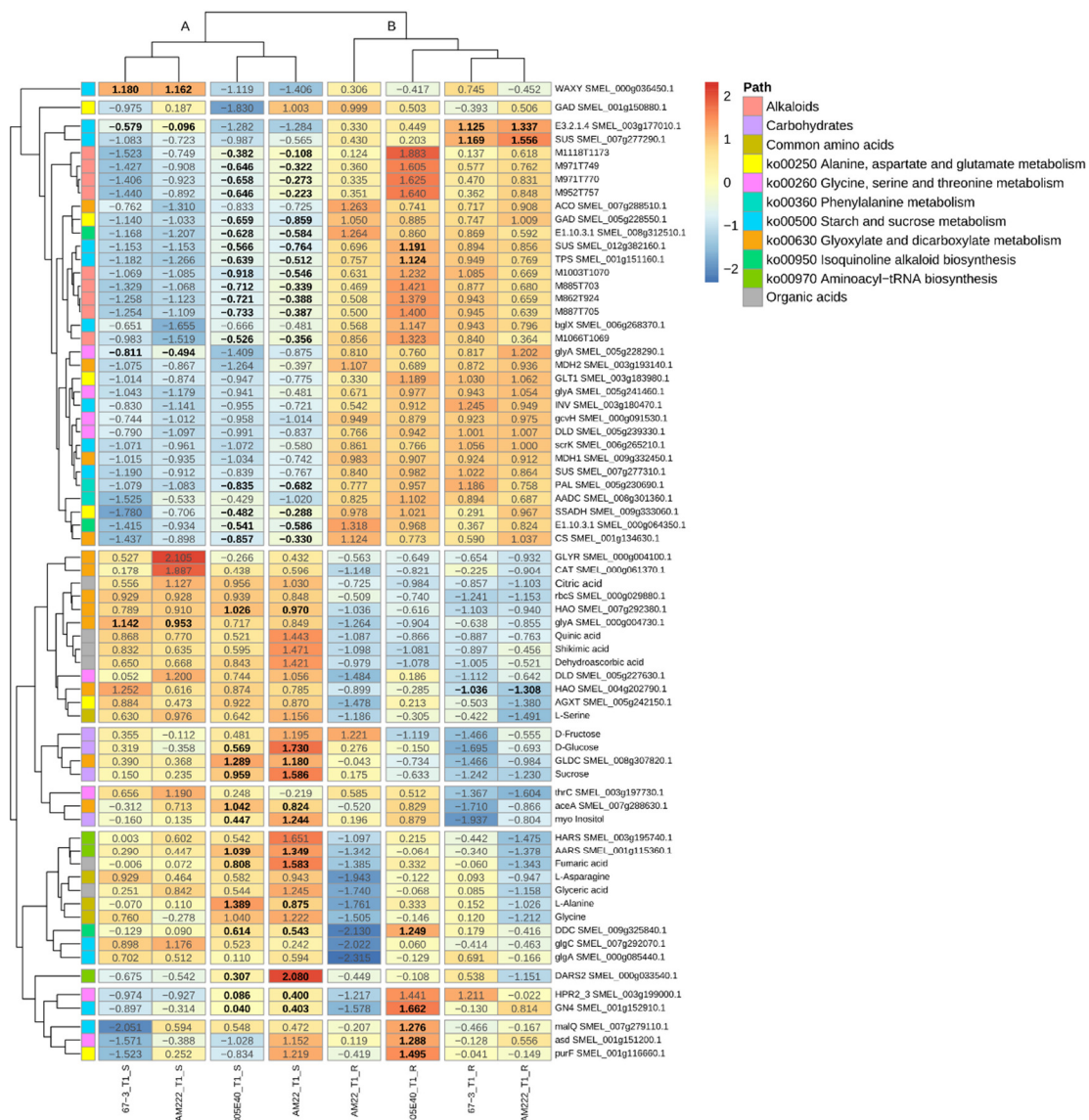


Figure S5. Heatmap of correlations in eggplant accession between metabolites and transcripts by the Pearson's correlation coefficient ($p < 0.05$) at T2. Correlations between eggplant metabolites and transcripts are based on 70 variables in shoot (A) and root (B).

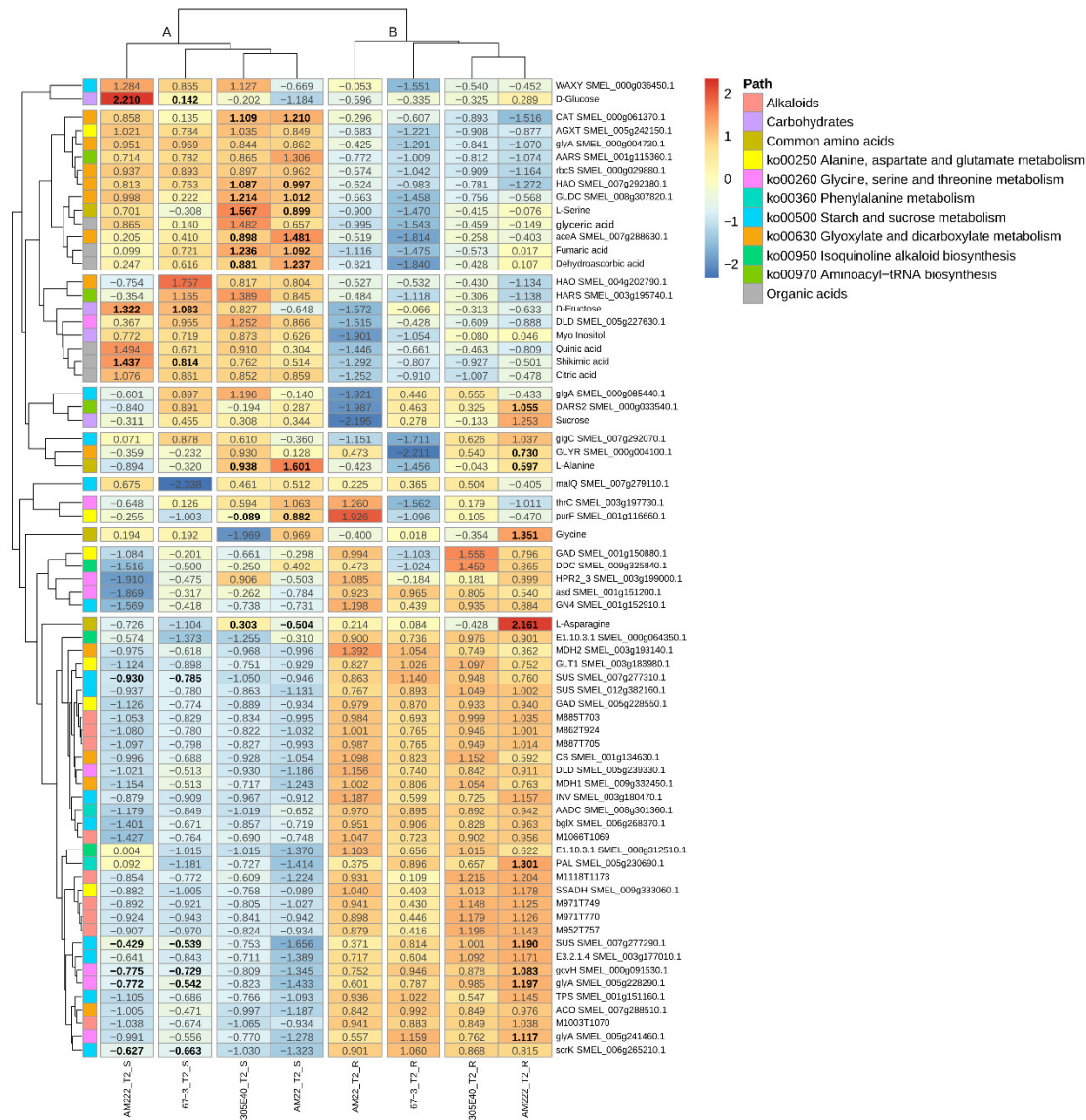
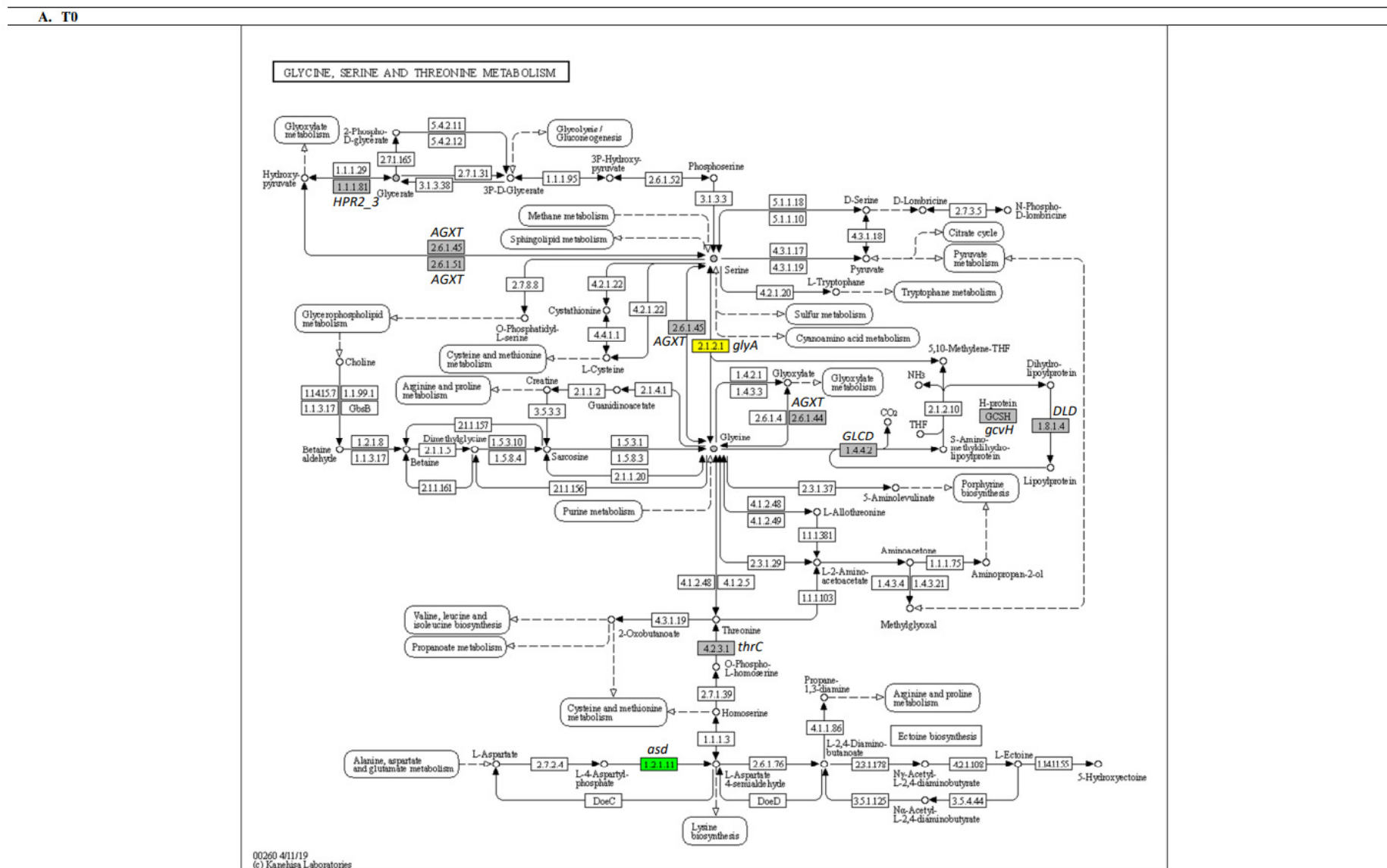
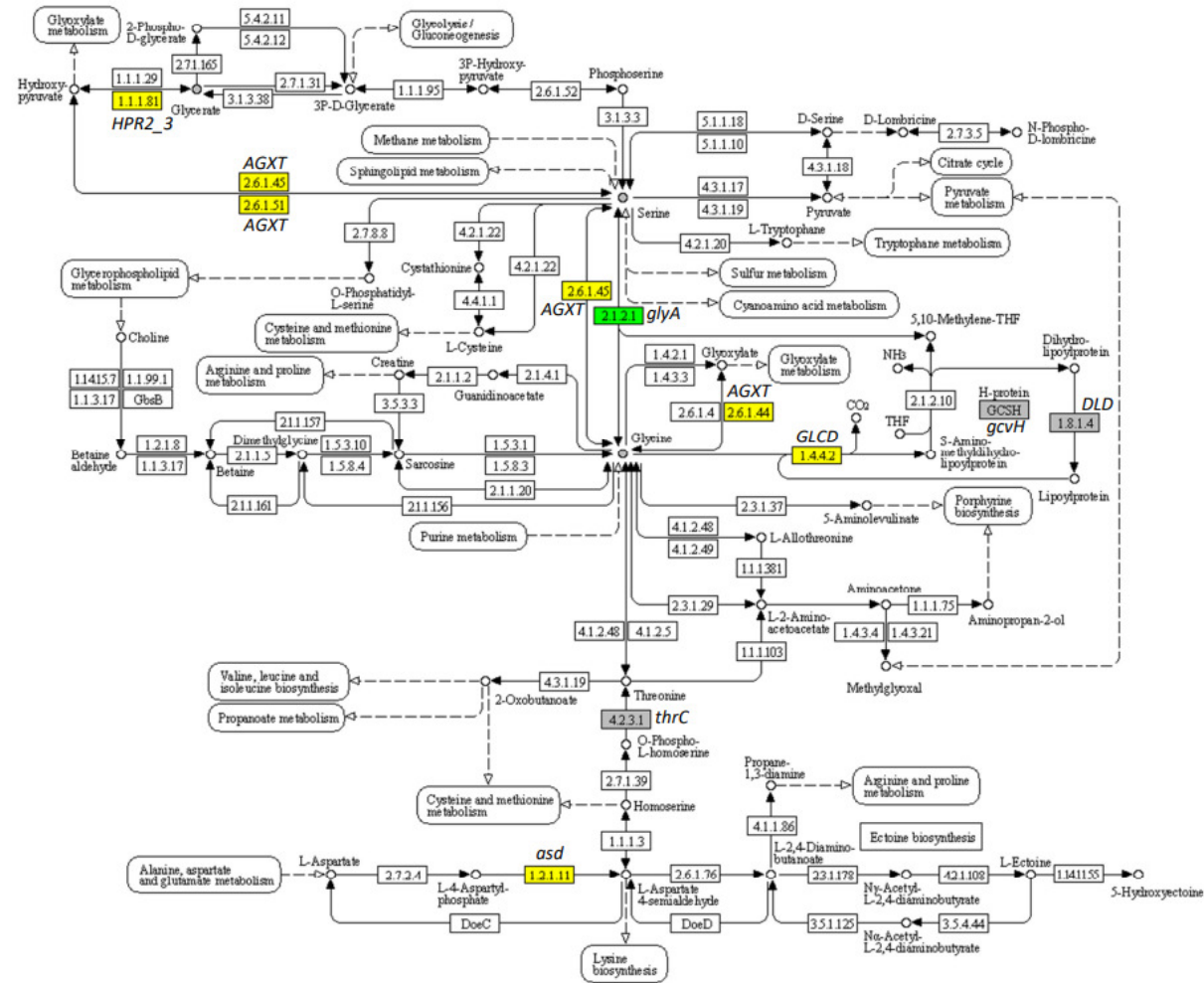


Figure S6. Exemplary scheme of Glycine, serine and threonine metabolism between efficient vs inefficient genotypes in shoots: A. T0, B. T1 and C. T2. In gray the metabolites and metabolic genes identified and not statistically different, in green the up-regulated and in yellow the down-regulated.



GLYCINE, SERINE AND THREONINE METABOLISM



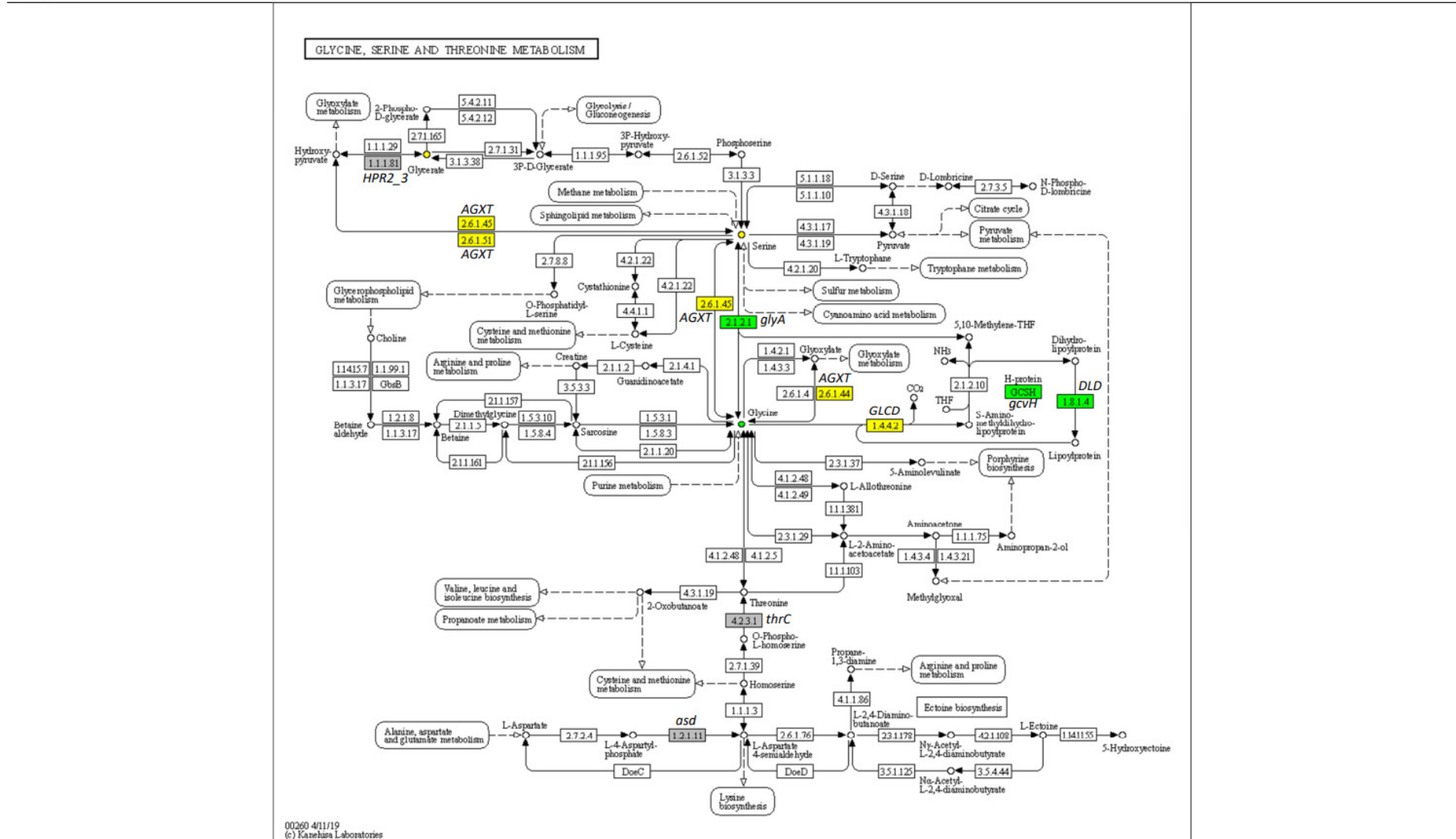
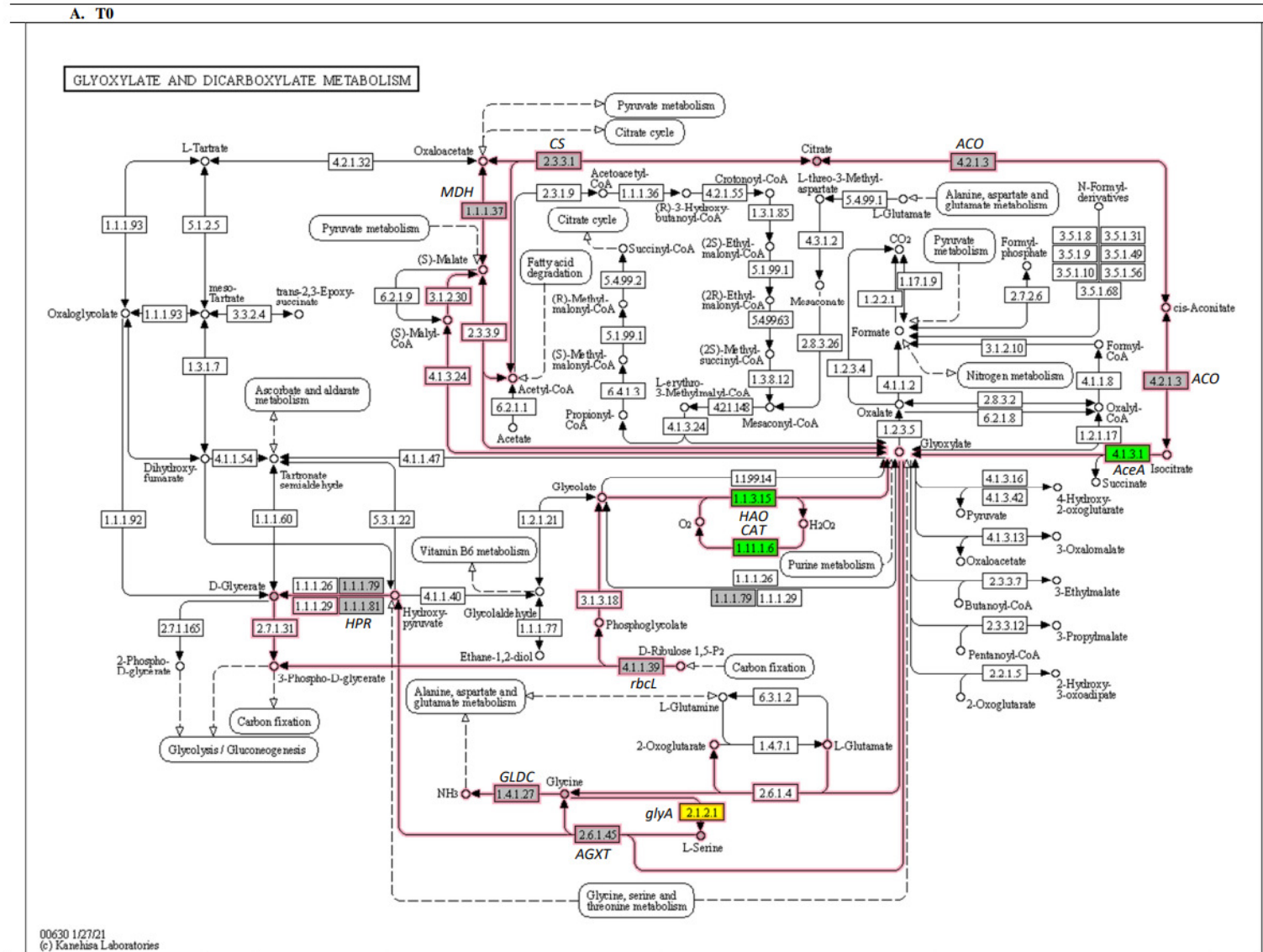


Figure S7. Exemplary scheme of Glyoxylate and dicarboxylate metabolism between efficient vs inefficient genotypes in shoots: A. T0, B. T1, C. T2. In gray the metabolites and metabolic genes identified and not statistically different, in green the up-regulated and in yellow the down-regulated. In red the pathway modules relating to the Glyoxylate cycle and Photorespiration.



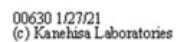




Figure S8. Exemplary scheme of Starch and sucrose metabolism between efficient vs inefficient genotypes in shoots: A. T0, B. T1, C. T2. In gray the metabolites and metabolic genes identified and not statistically different, in green the up-regulated and in yellow the down-regulated. In red the pathway modules relating to the Glycogen biosynthesis and Trehalose biosynthesis.

