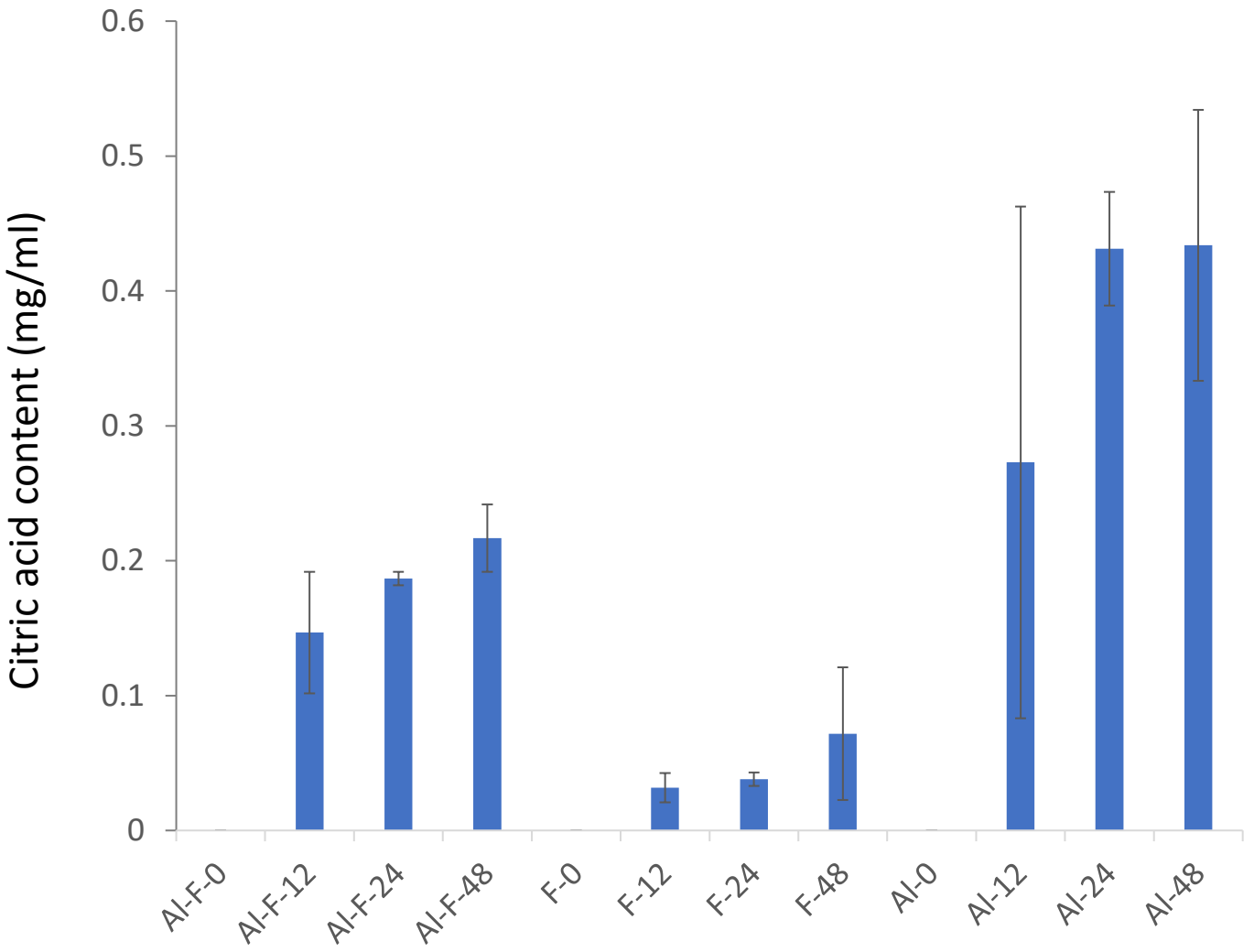
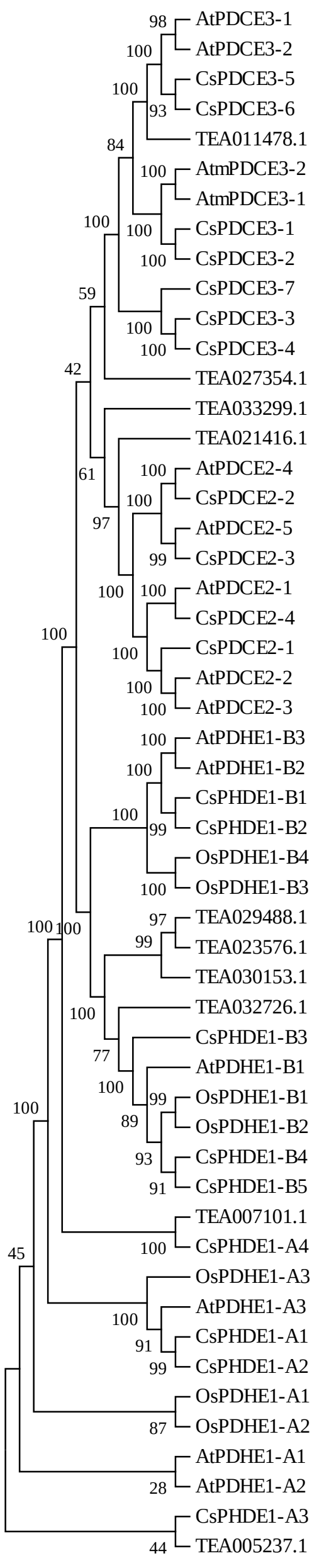


Figure S1. Trace levels of citric acid secretion into tea seedling culture media under Al and F treatments.

Media were collected at different time points after Al and F stress treatments for HPLC analysis. Data are from three independent experiments.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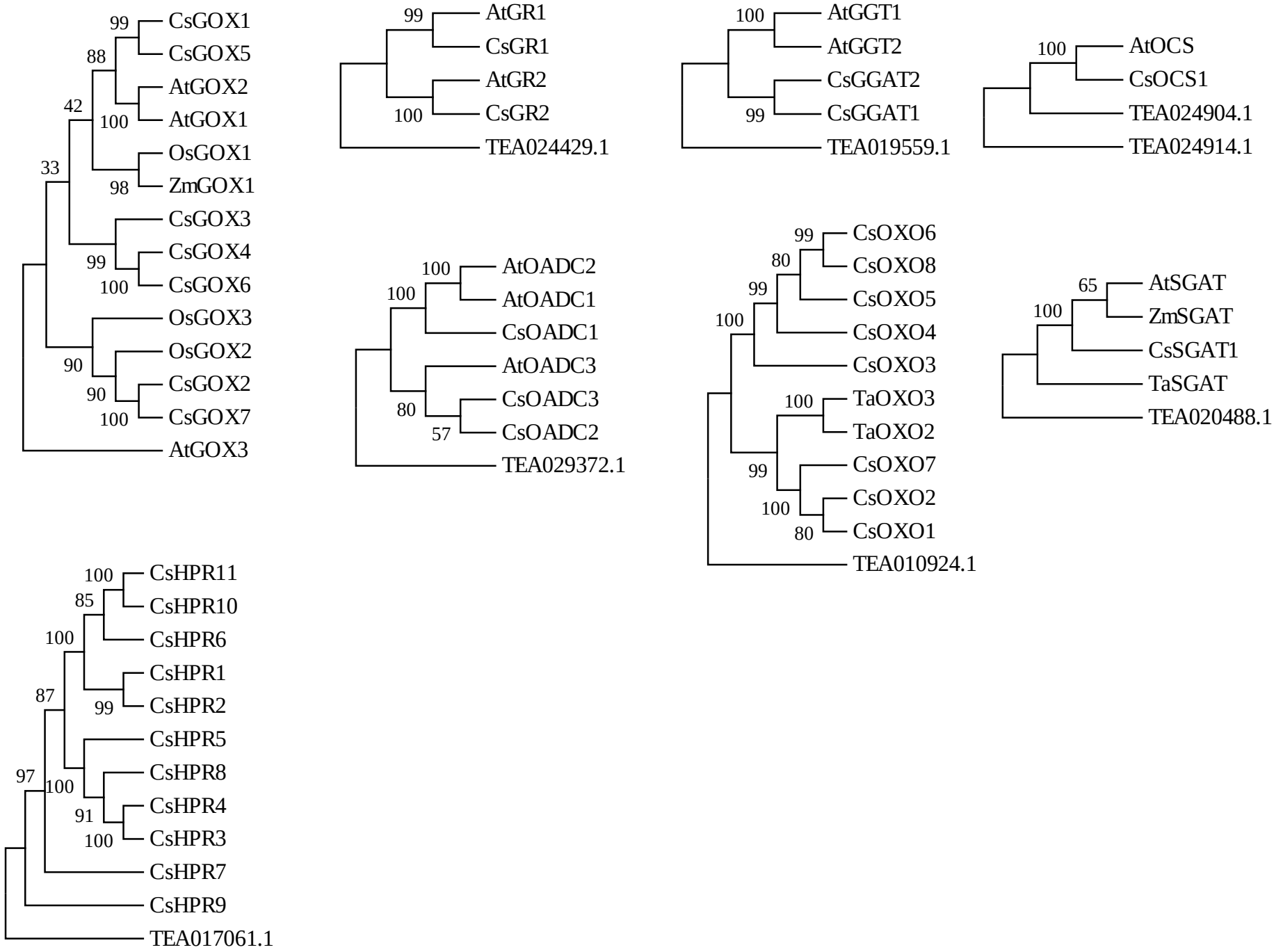


Figure S2. phylogenetic analysis of the key genes involved in oxalate biosynthesis.

PDK, Pyruvate dehydrogenase kinase; PHDE, pyruvate dehydrogenase; PDCE, dihydrolipoamide acetyltransferase; CSY, citrate synthase; IDH, isocitrate dehydrogenase; OGDC, 2-ketoglutarate dehydrogenase; SCS, succinyl-CoA synthase; ACO, aconitate; SDH, Succinate dehydrogenase; FH, fumarase hydratase; MDH, malate dehydrogenase; ACL, ATP-citrate synthase/lyase; ICL, isocitrate lyase; GOX, glycolate oxidase; GR, glyoxylate reductase; GGT, glutamate: glyoxylate aminotransferase ; OADC, oxaloacetate decarboxylase; OXO, oxalate oxidase; OCS, oxalyl-CoA reductase.

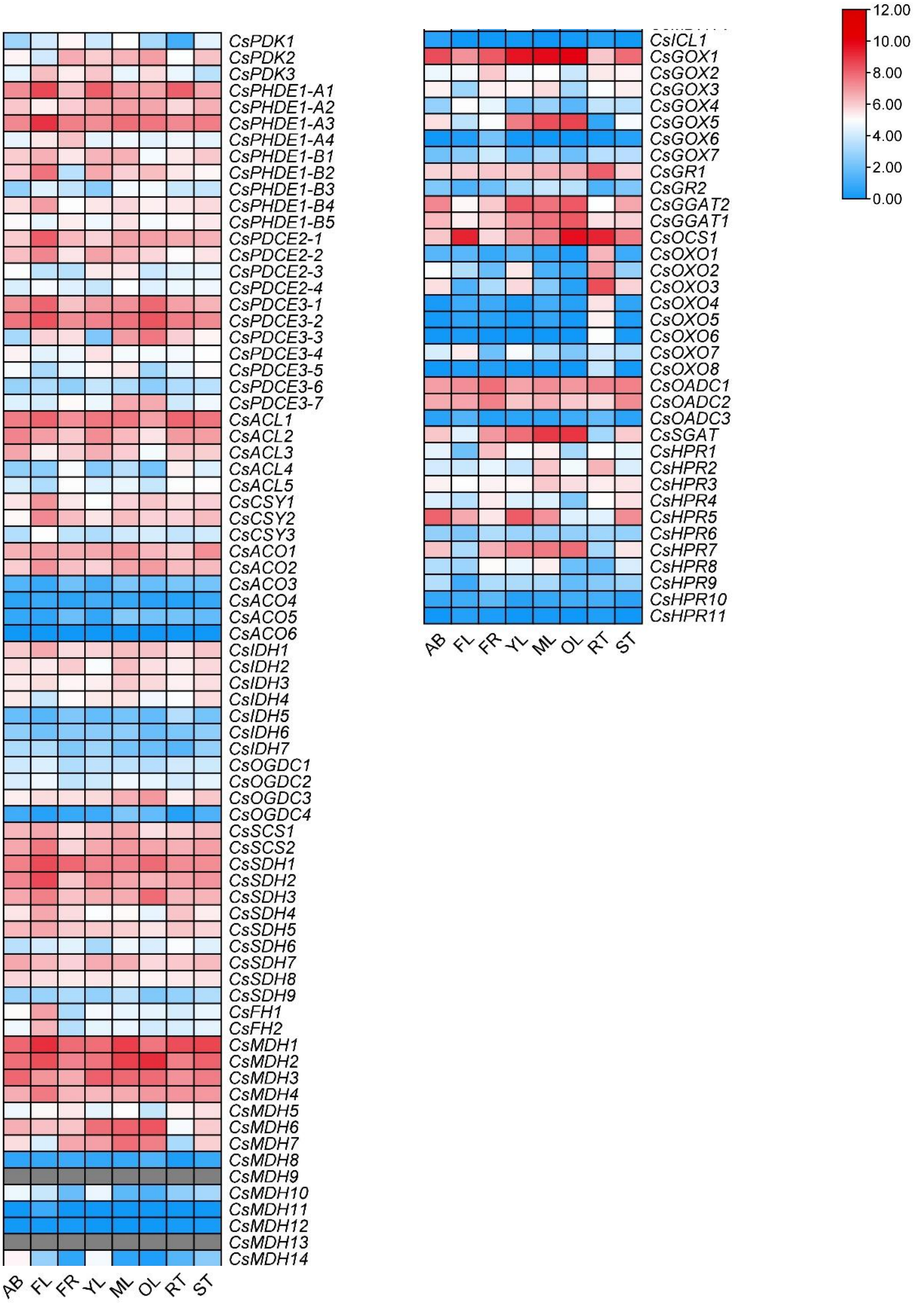
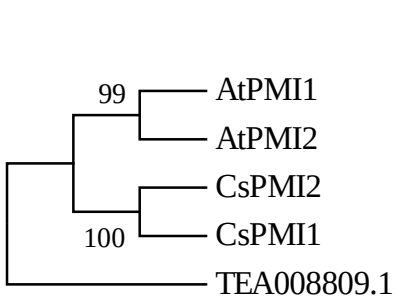


Figure S3. Heatmap analysis of the key genes involved in oxalate biosynthesis in various tissues.

Heatmap analysis of gene expression was made with these transcriptome data retrieved from previous transcriptome data, expressed as FPKM. The Tbtools software was used to structure the heat map.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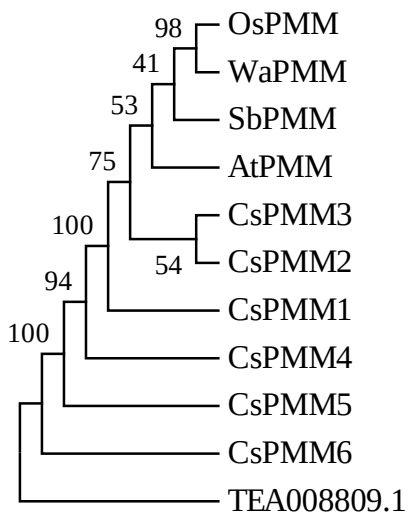
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WaPMM
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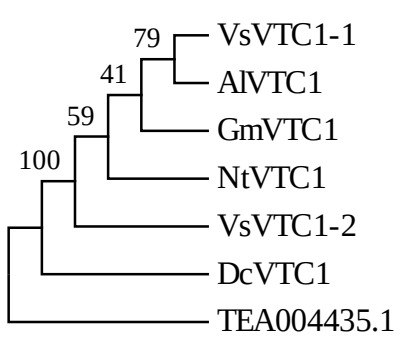
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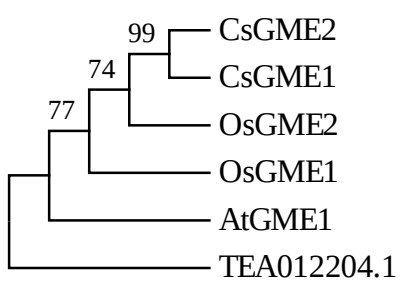
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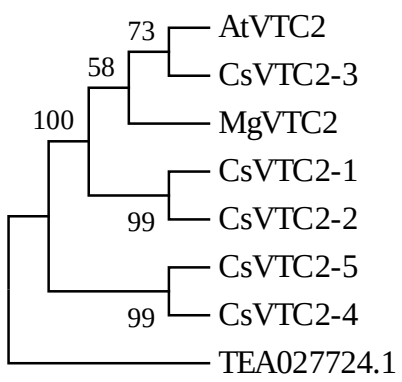
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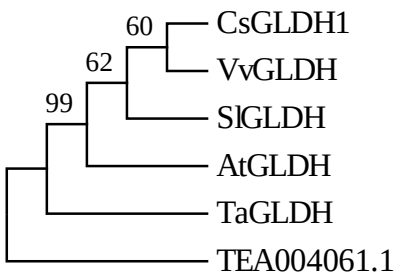
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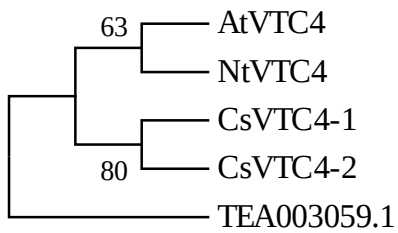
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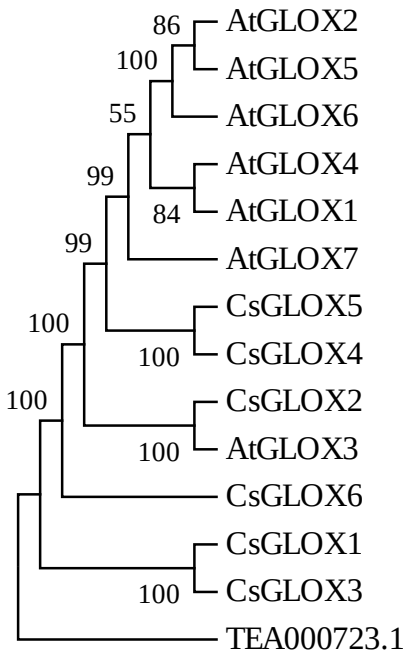
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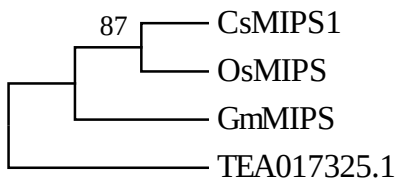
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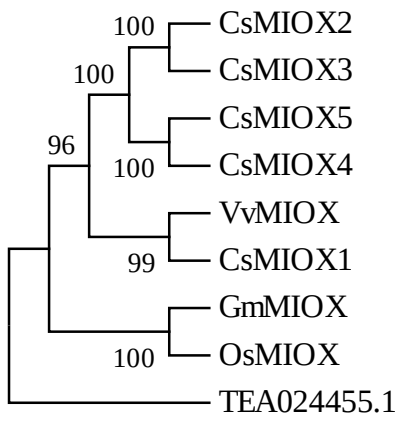
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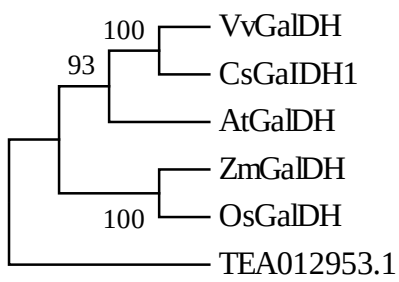
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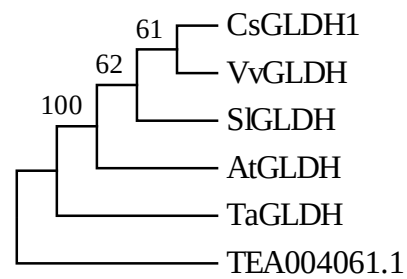
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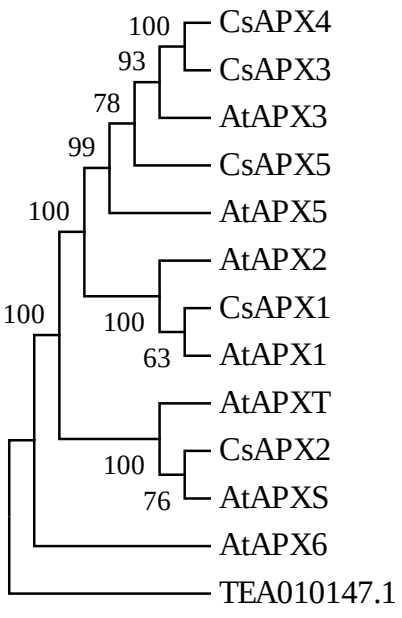
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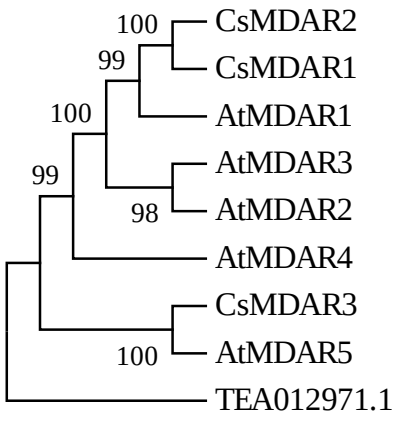
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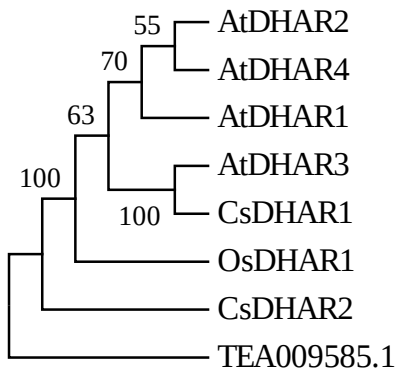
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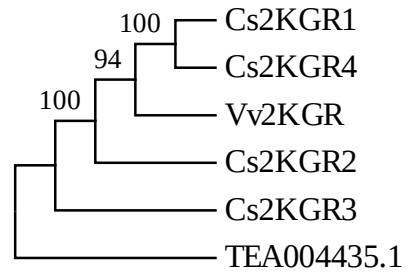
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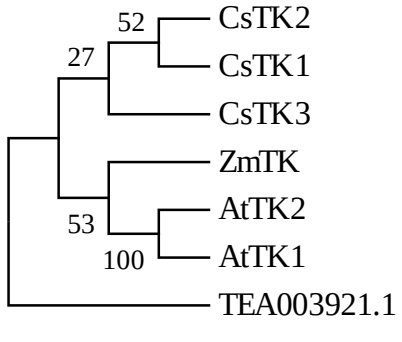
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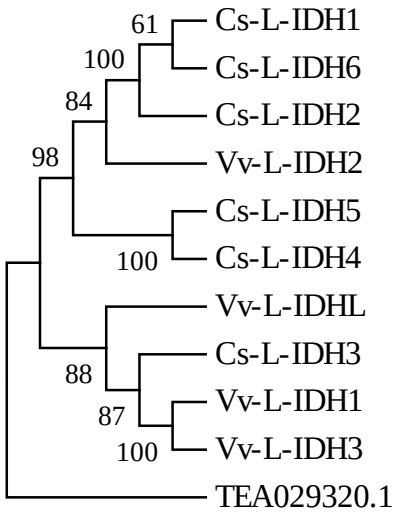
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Vv-L-IDHL
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Cs-L-IDH3
87
Vv-L-IDH1
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Vv-L-IDH3
TEA029320.1

Figure S4. Identification of the key genes involved in tartaric acid biosynthesis in tea plants.

A-R. the key gene's phylogenetic analysis including PMI, Phosphomannose isomerase; PMM, phosphomannomutase; VTC1, GDP-D-mannose pyrophosphorylase; GME, GDP-D-mannose epimerase; VTC2, GDP-L-galactose phosphorylase; VTC4, L-galactose-1-phosphate phosphatase; L-GalDH, L-galactose dehydrogenase; GLDH, L-galactono-1,4-lactone dehydrogenase; MIPS, myo-inositol-3-phosphate synthase; MIOX, myo-inositol oxidase; GLOX, L-gulonolactone oxidase; MDAR, monodehydroascorbate reductase; DHAR, Dehydroascorbate reductase; APX, ascorbate peroxidase; 2KGR, 2-keto-L-gulonate reductase; L-IDH, L-idonate dehydrogenase; TK, transketolase.

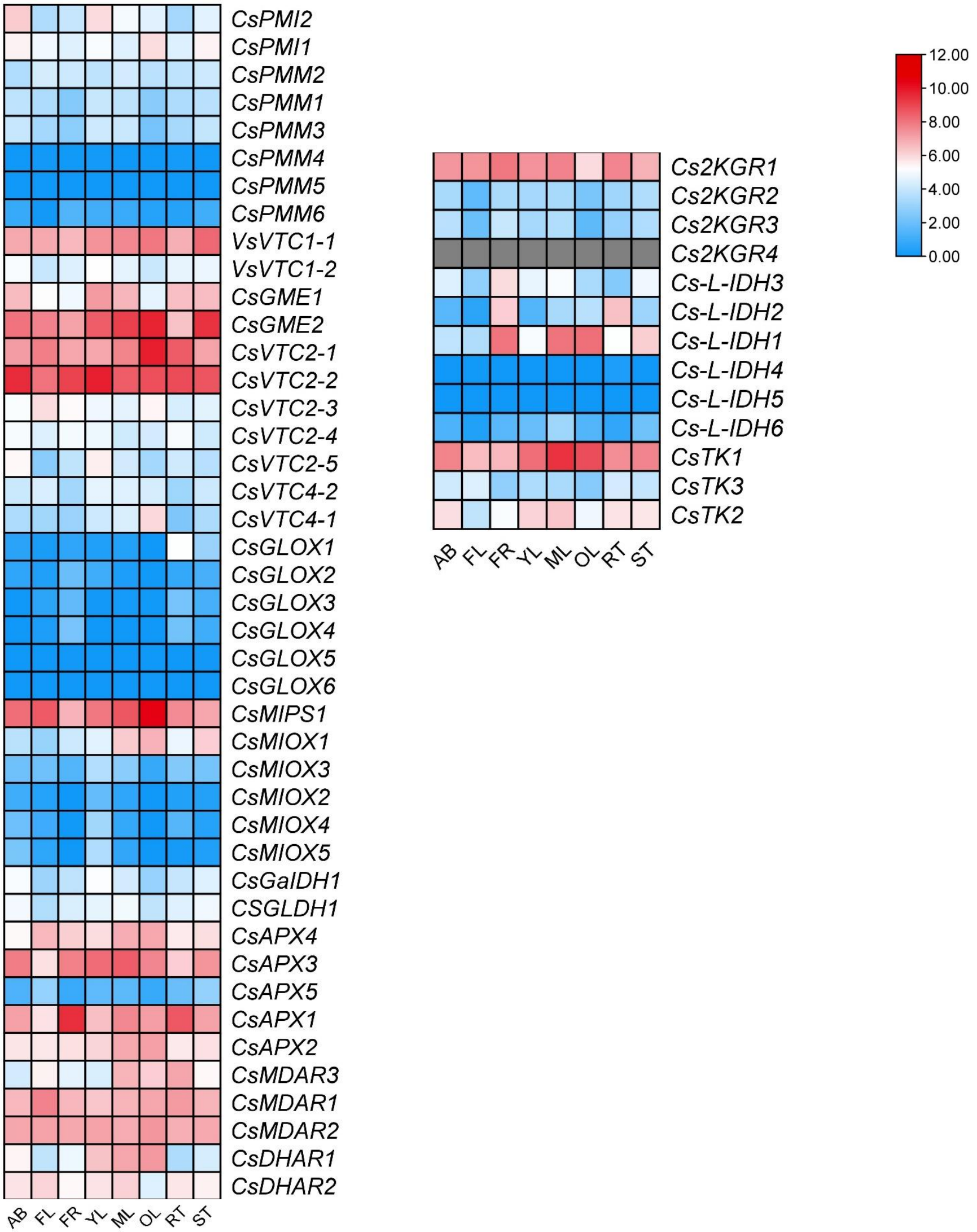

Figure S5. Heatmap analysis of the key genes involved in tartaric acid biosynthesis in various tissues. Heatmap analysis of gene expression was made with these transcriptome data retrieved from previous transcriptome data, expressed as FPKM. The Tbtools software was used to structure the heat map.

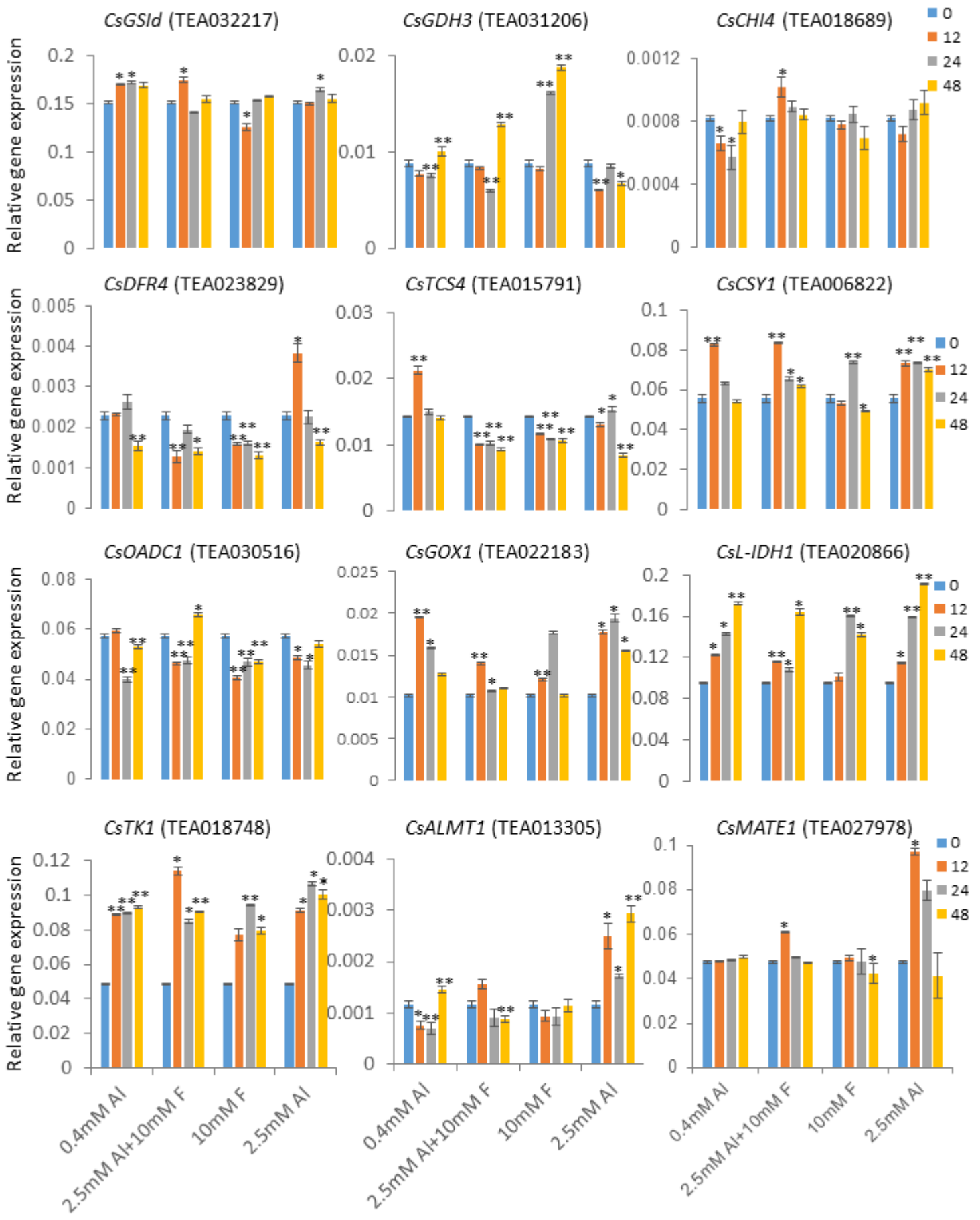

Figure S6. qRT-PCR validation of gene expression patterns in transcriptome.

Tea roots under normal SK medium containing 0.4 mM Al, or Al stress with 2.5 mM Al, F stress medium containing 10 mM F, and combined treatment with 2.5 mM Al and 10 mM NaF (Al+F), were sampled at interval times of treatments for RNA analysis. Both *CsACTIN* and *CsGAPDH* were used as internal references in qRT-PCR analyses. Data were from three experiments (n=3) and expressed as means ±s.d, and the significant differences between comparison was analyzed by using Student's t-test in a two-tailed comparison (*$P < 0.05$ and **$P < 0.01$).