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Title: Transcriptome analysis and metabolic profiling reveal the key regulatory pathways in drought stress responses and recovery in tomato

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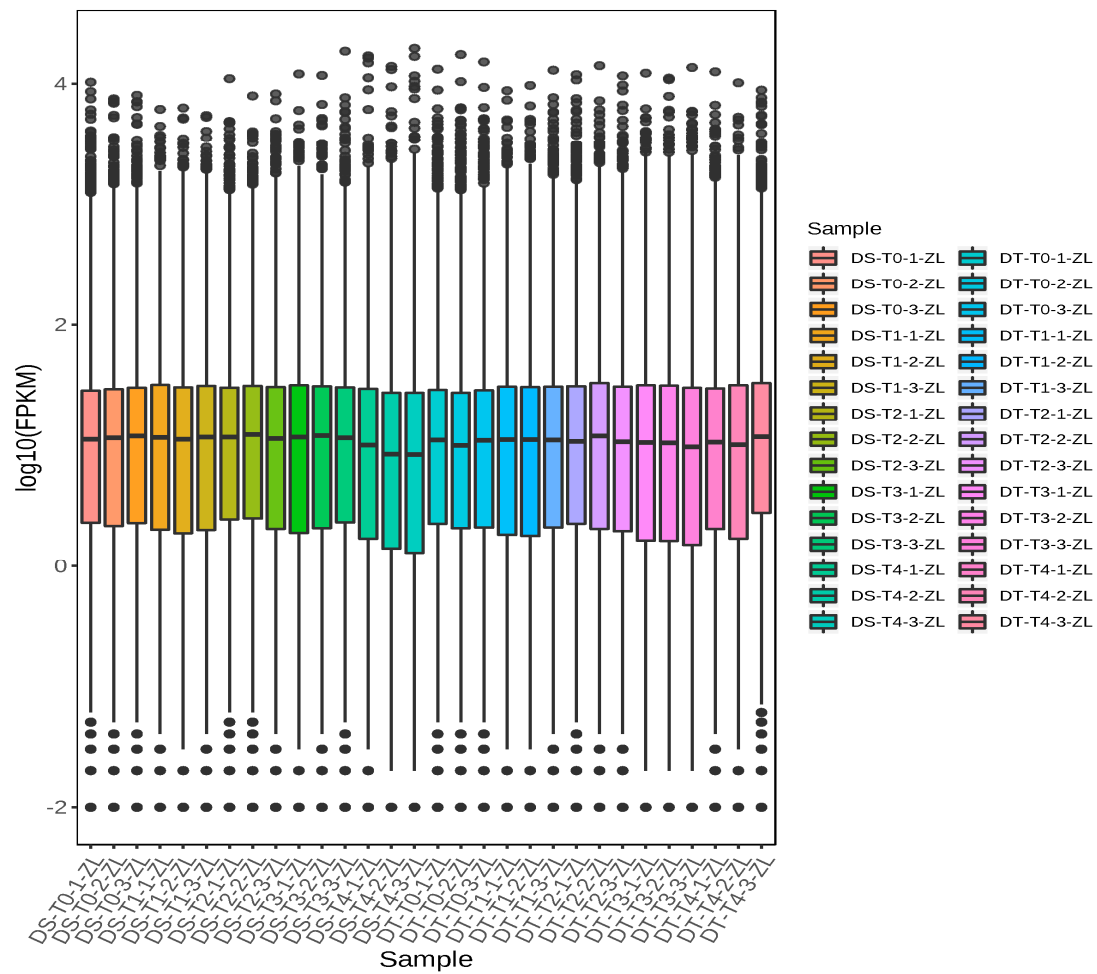


Figure S1 Box plot of RNA-seq samples in DS and DT genotypes

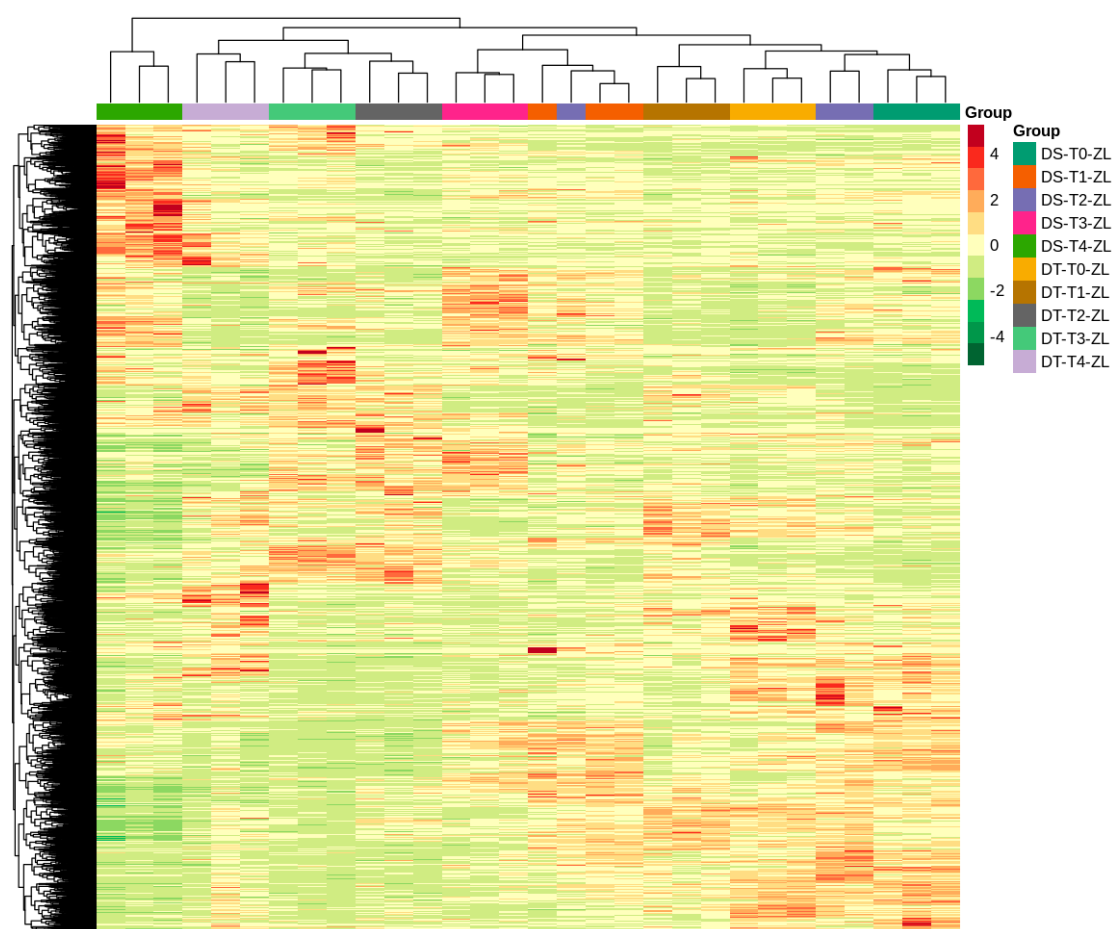


Figure S2 Cluster heat map of RNA-seq samples in DS and DT genotypes

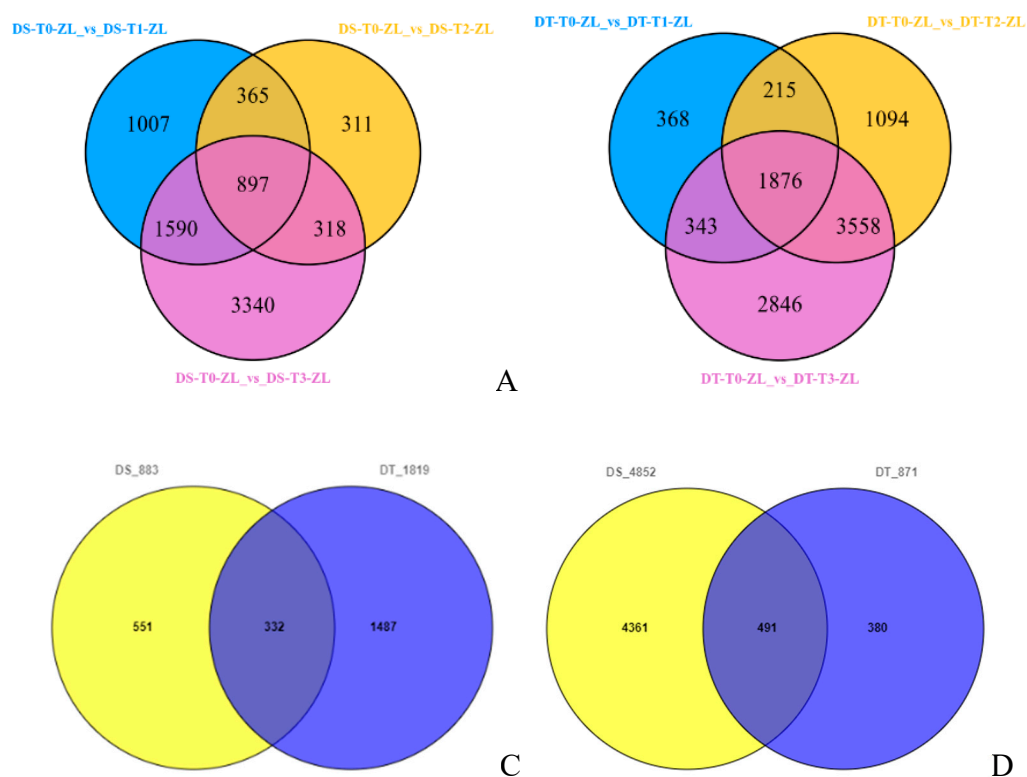


Figure S3 Venn diagrams of DEGs common to DS and DT under drought and recovery conditions. A: Venn diagram of DEGs in DS. B: Venn diagram of DEGs in DT. C: Venn diagram of the genes identified as DEGs at all drought stress time-points in DS and DT. D: Venn diagram of the genes identified as DEGs between DS and DT during rehydration.

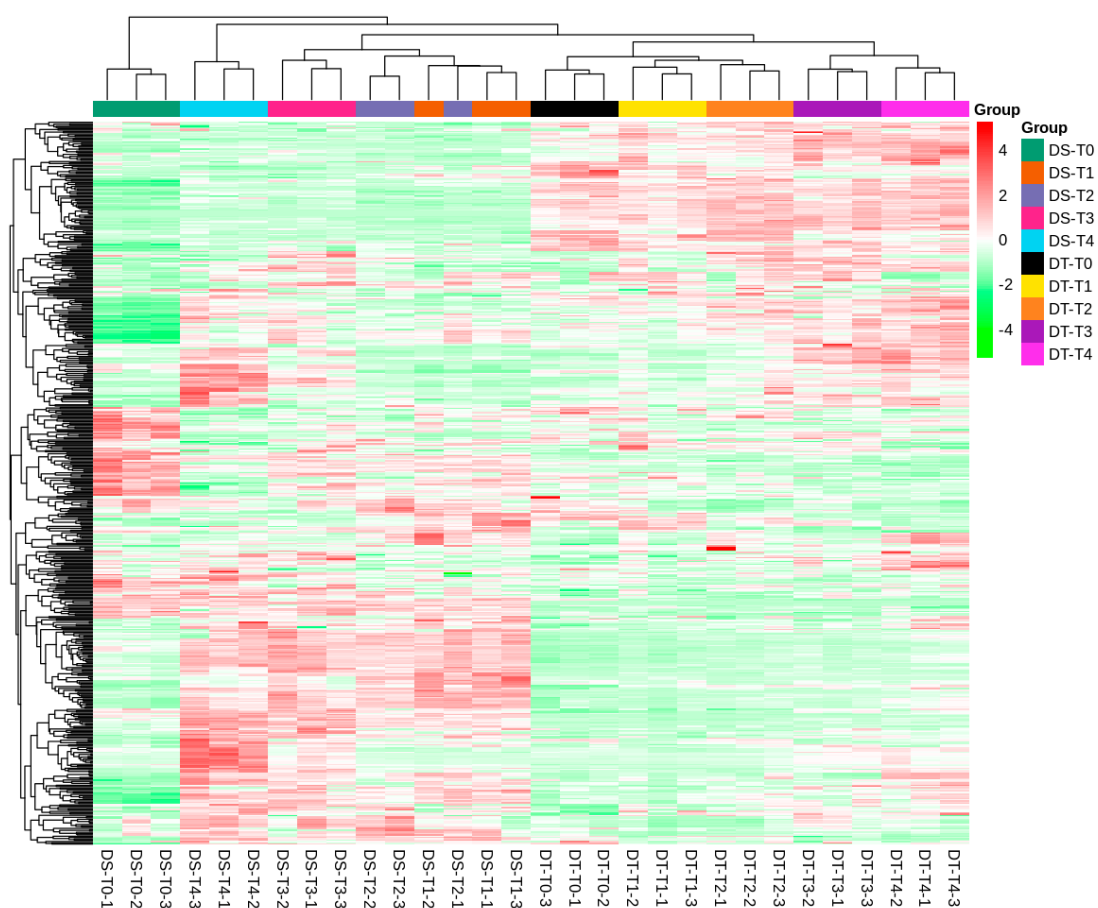


Figure S4 Correlations among 30 metabolome samples in the DS and DT genotypes.

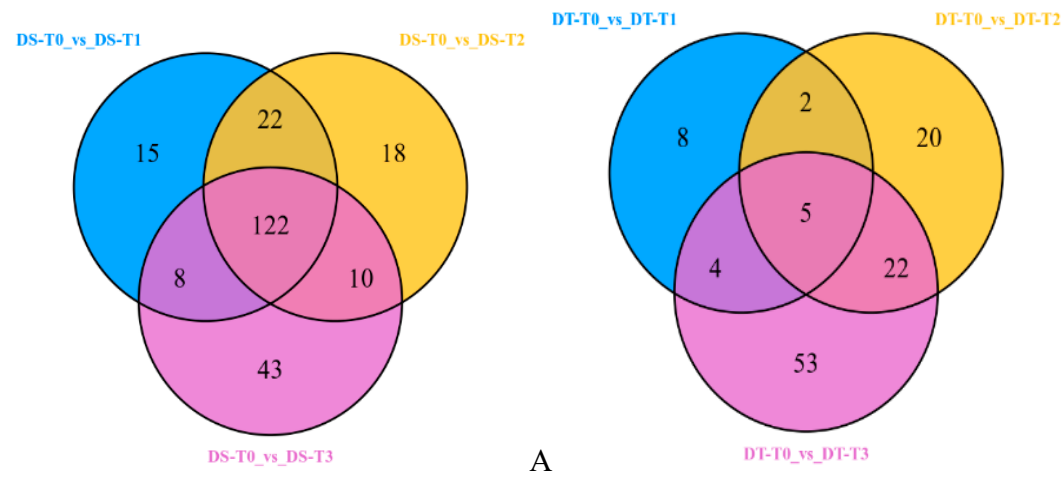


Figure S5 Venn diagram of the differentially abundant metabolites in DS and DT under drought conditions. A: Venn diagram of differentially abundant metabolites in DS. B: Venn diagram of differentially abundant metabolites in DT.