Supplementary information

Heterologous overexpression of OsSalT enhances drought tolerance by regulating antioxidant enzyme activity and flavonoid biosynthesis in tomato

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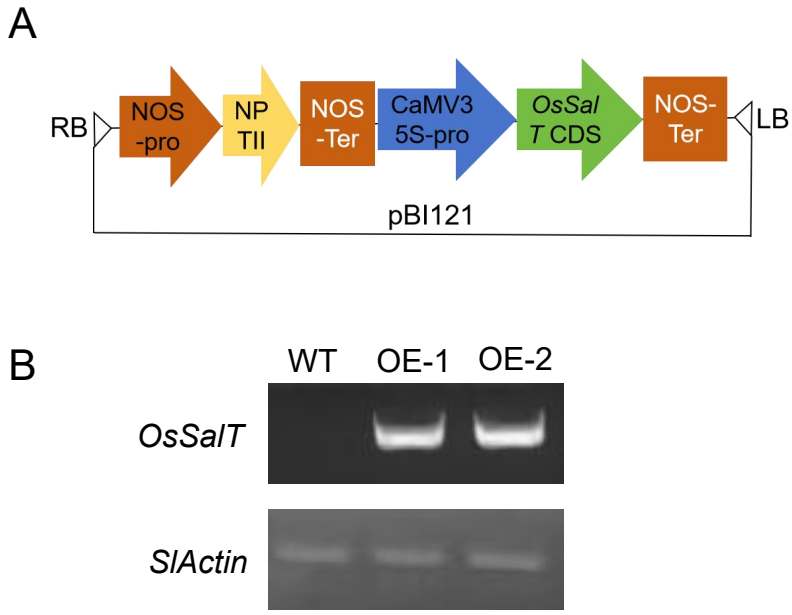

Fig. S1 Construction and identification of OsSalT overexpression transgenic plants. (A) Schematic representation of OsSalT coding sequence (CDS) transformation vector constructs. NPTII, neomycin phosphotransferase II gene; nos ter, nopa line synthase terminator. RB and LB, left and right T- DNA borders. (B) mRNA clone of OsSalT generated by amplification, The detailed primer information is shown in Table S1.

Fig. S2 Gene ontology (GO) classification of differentially expressed genes (DEGs).

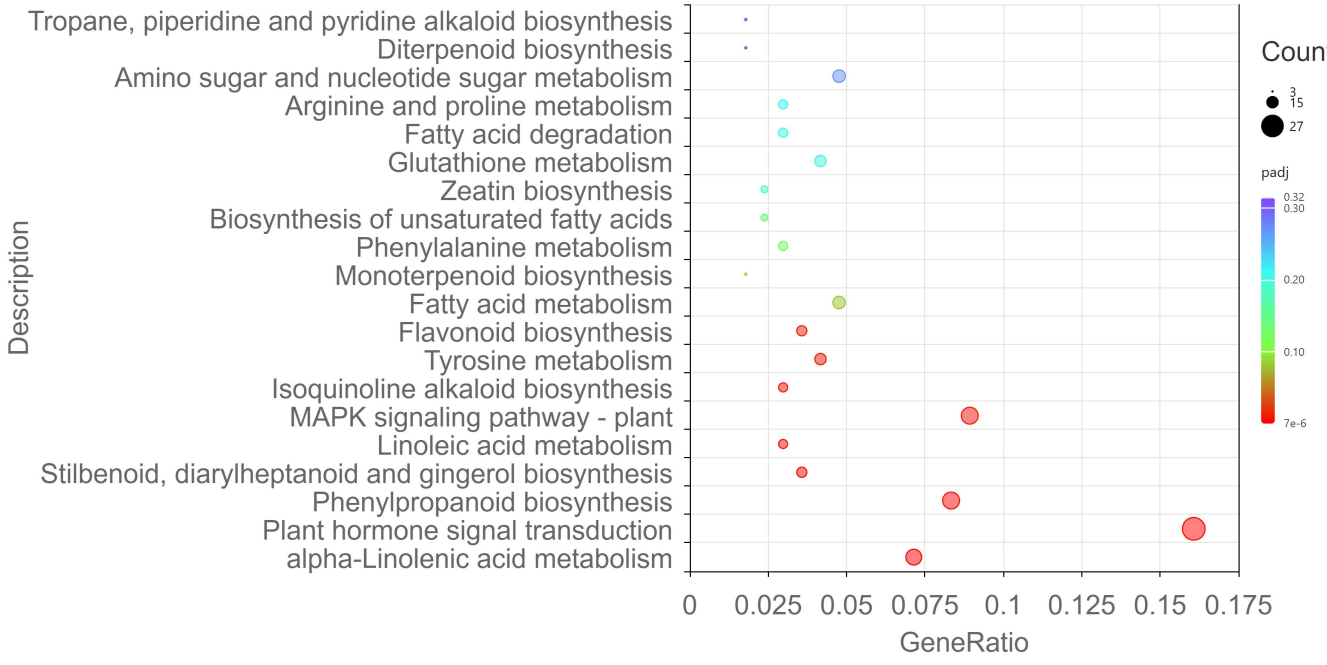

Fig. S3 KEGG enrichment pathways of down regulated genes in OsSalT-OE lines.

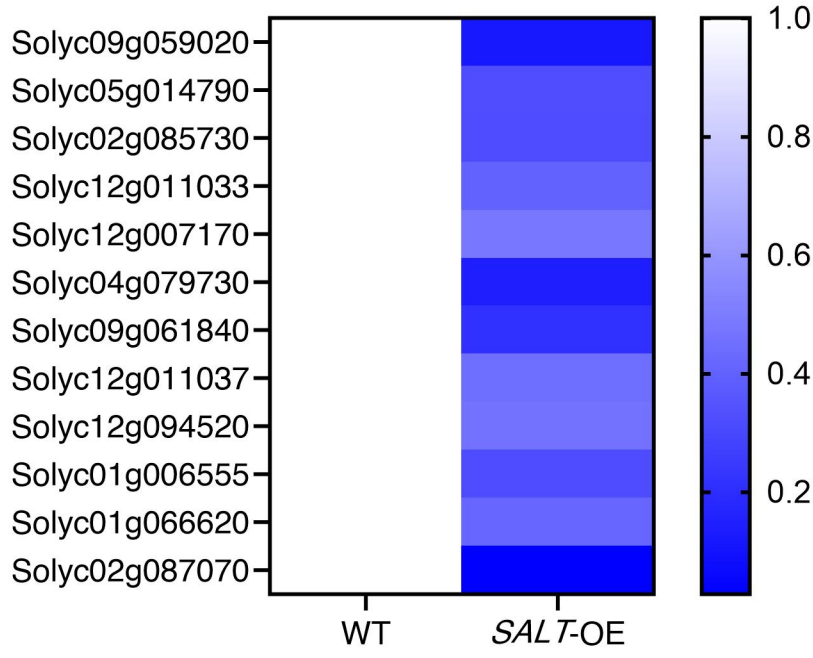

Fig. S4 Expression profile of genes related to 'alpha-Linolenic acid metabolism' metabolic pathways.

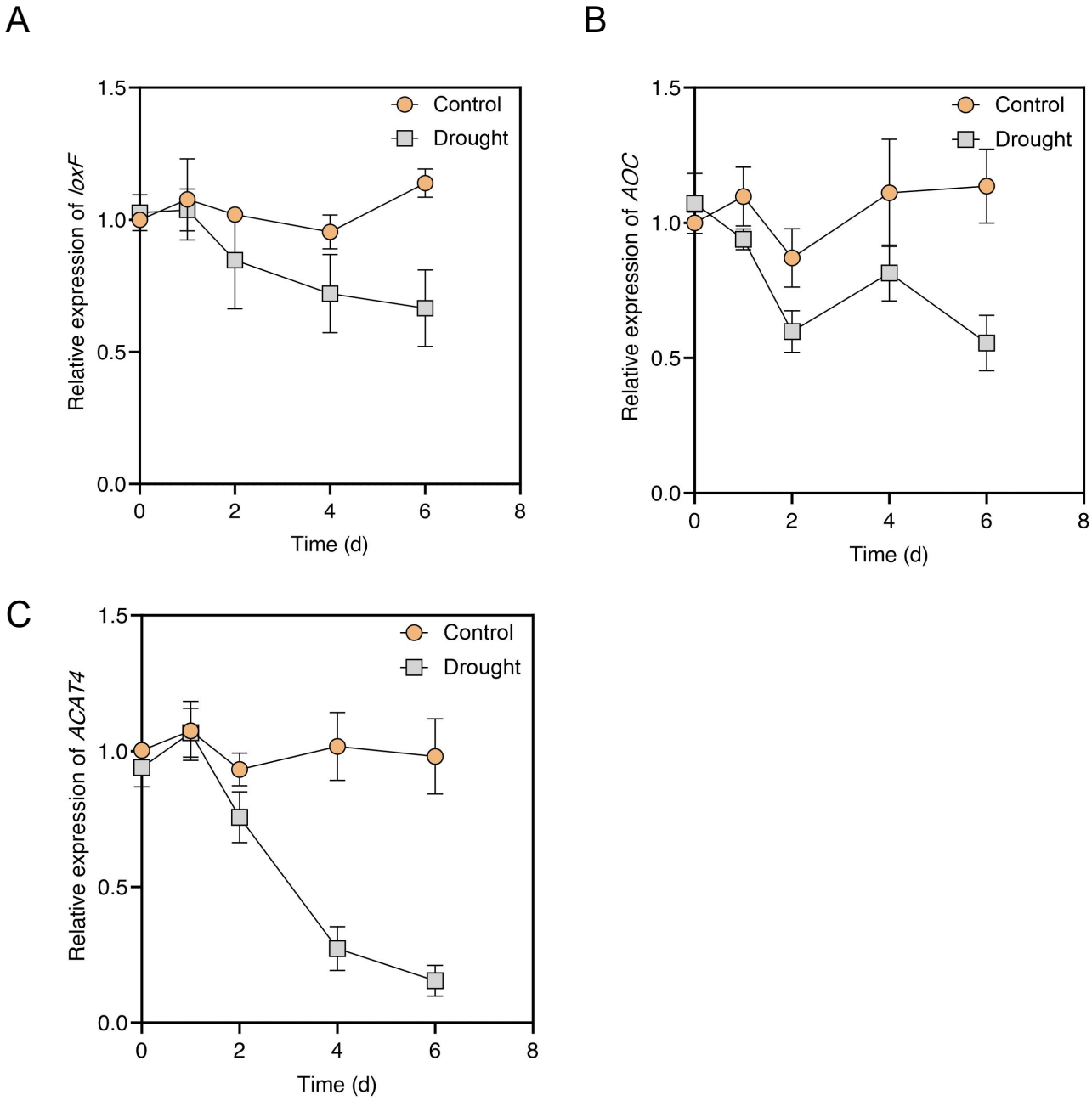

Fig. S5 qRT-PCR analysis of alpha-Linolenic acid metabolism-related gene expression profiles by time crossing. The relative expression levels of three DEGs encoding loxF, AOC and ACAT4 were calculated according to the 2−ΔΔCt method using the ToUBQ gene as an internal reference gene. The leaves of tomato exposed to 0, 1, 2, 4, 6 days drought treatment were used for RNA extraction and RT-qPCR. The experiments were repeated three independent biological replicates. The detailed primer information is shown in Table S1.