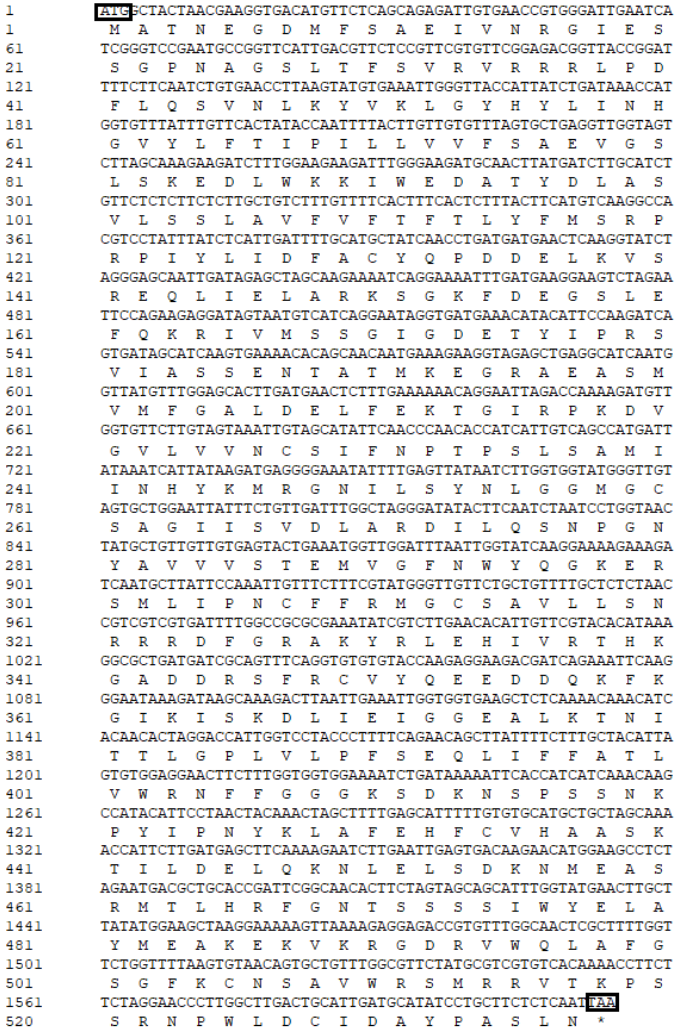
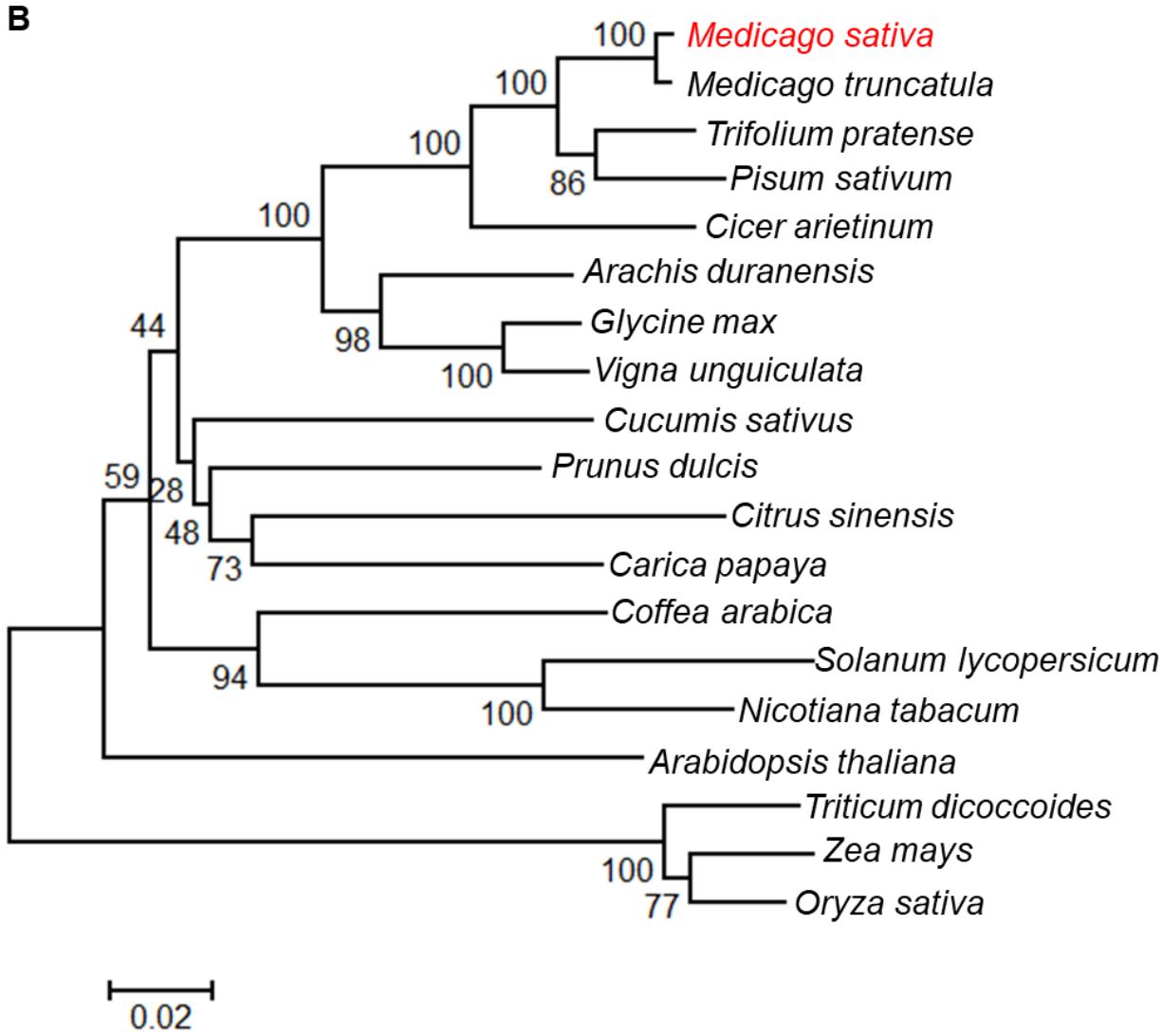


Fig. S1 Coding DNA sequence (CDS) and deduced amino acid sequence of MsKCS10. The start codon and stop codon are boxed.

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Fig. S2 The deduced amino acid sequence analysis of MsKCS10. Multiple alignments of the deduced amino acid sequence of MsKCS10 with homologous KCS10 from other plants (A). Phylogenetic tree of MsKCS10 and homolog from other plants (B). Identical residues are shaded in the same colors. The predicted conserved domain (3-ketoacyl-CoA synthase superfamily) is indicated with black lines. The phylogenetic tree was constructed using the neighbor-joining method with 1 000 bootstraps. The species and corresponding GenBank accession number are as follows: *M. sativa* (QEX52173.1), *M. truncatula* (XP_003603250.1), *T. pratense* (XP_045803743.1), *A. duranensis* (XP_015945536.1), *G. max* (XP_003522322.1), *V. unguiculata* (XP_027942061.1), *C. sinensis* (XP_006474532.1), *A. thaliana* (NP_180193.1), *Z. mays* (NP_001149405.2), *S. lycopersicum* (XP_004245205.1), *N. tabacum* (XP_016491550.1), *P. sativum* (XP_050884701.1), *C. arietinum* (XP_004501406.1), *P. dulcis* (XP_034199250.1), *C. sativus* (XP_004141352.1), *C. papaya* (XP_021894386.1), *C. arabica* (XP_027084762.1), *T. dicoccoides* (XP_037419554.1), and *O. sativa* (XP_015632380.1).

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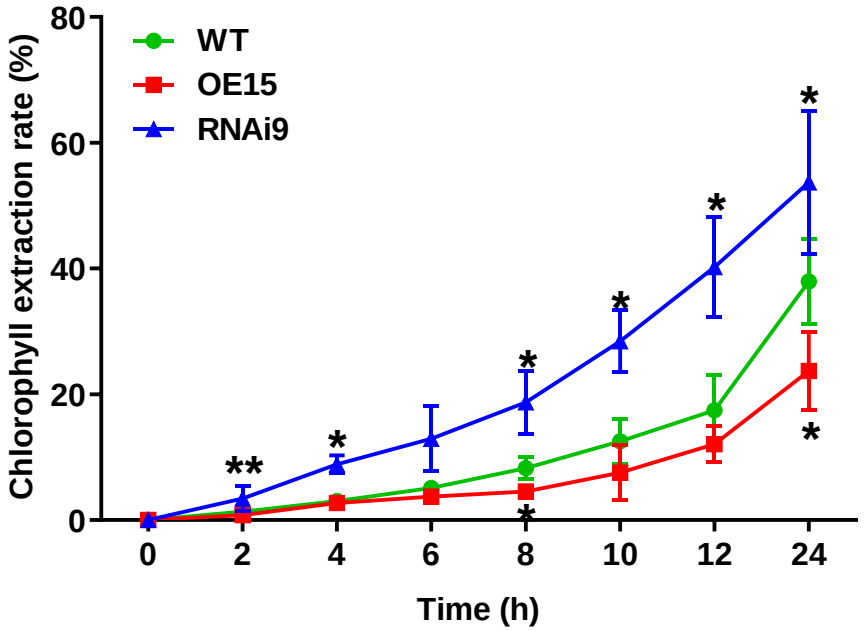


Fig. S3 Chlorophyll extraction rate from detached leaves of alfalfa WT, OE, and RNAi plants. * and ** indicate a significant difference between OE lines and WT at $P < 0.05$ and $P < 0.01$, respectively. The fourth to sixth trifoliate were harvested from 2-month-old alfalfa plants and used for the chlorophyll leaching assay.

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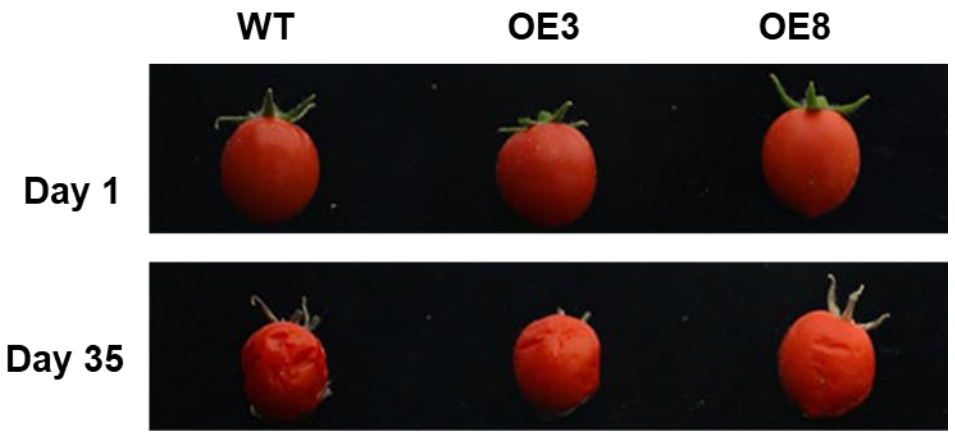


Fig. S4 Phenotype of tomato fruit WT and OE lines after storage in a constant temperature and windless environment for 35 days.

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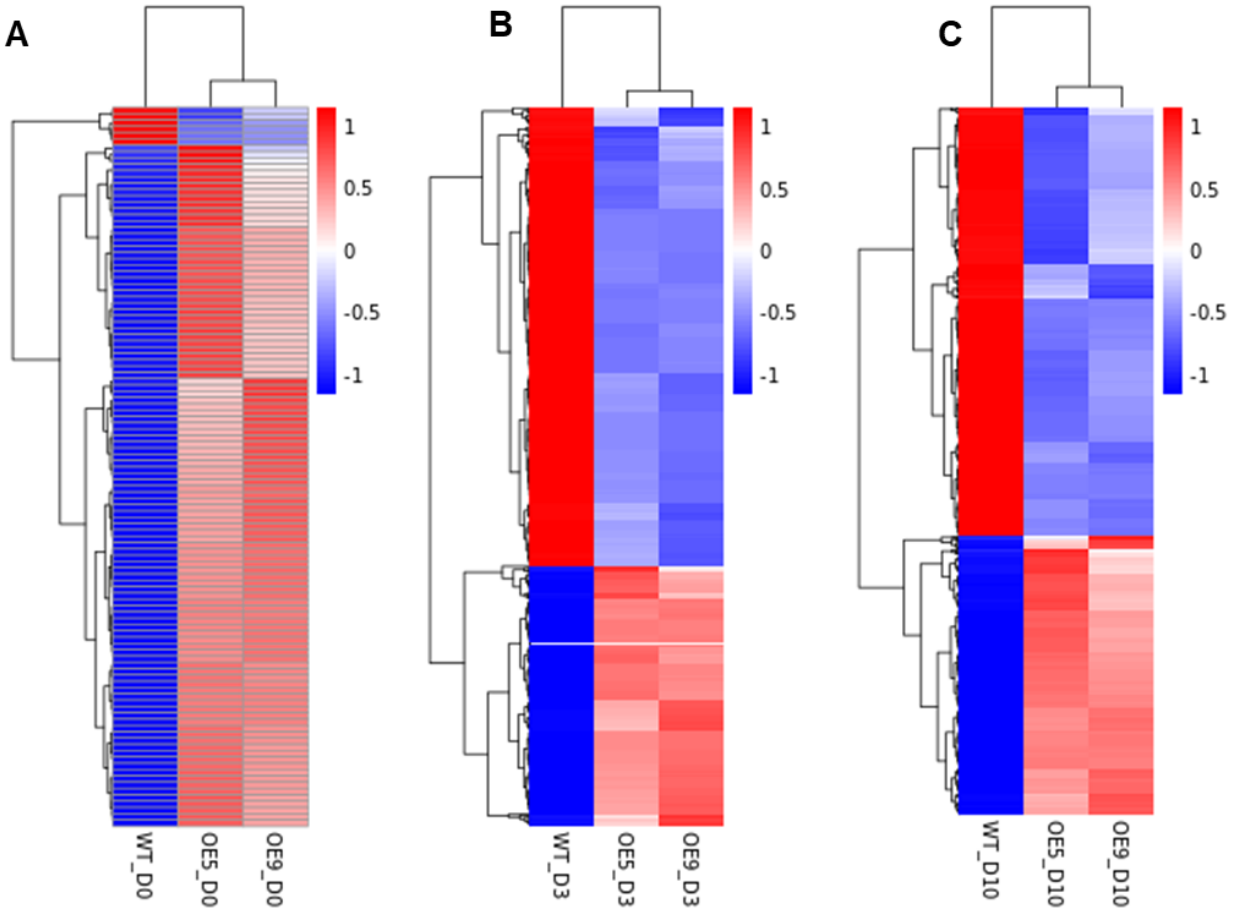


Fig. S5 Heatmap of the differentially expressed genes (DEGs) between OE lines and WT under normal growth conditions (A), drought stress for 3 days (B), and drought stress for 10 days (C).

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