MdDof54 MDP0000308863 Consensus	MFTDPTVKQMLQCPPSGQGQFMMMEMKRPWNKSHIEVAPNCPRCASSNTKFCYYNNYSLSQPRYFCKGCRRYWTKGGSLRNVPVGGGCRKNRRGKA <mark>A</mark> RLS MFTDPTVKQMLQCPPSGQGQFMMMEMKRPWNKSHIEVAPNCPRCASSNTKFCYYNNYSLSQPRYFCKGCRRYWTKGGSLRNVPVGGGCRKNRRGKATRLS mftdptvkqmlqcppsgqgqfmmmemkrpwnkshievapncprcassntkfcyynnyslsqpryfckgcrrywtkggslrnvpvgggcrknrrgkarls	100 100
MdDof54 MDP0000308863 Consensus	QTD <mark>R</mark> ASLSYFQHHNSSSGTEDDPSGNNQPGGSNASDIDLAVVFAKFLNHNSTTPDDHYHDPNLVISSSALNDHDGSQNSSKA <mark>D</mark> DLVEAVDHYLLEGHQQS QTD <mark>S</mark> ASLSYFQHHNSSSGTEDDPSGNNQPGGSNASDIDLAVVFAKFLNHNSTTPDDHYHDPNLVISSSALNDHDGSQNSSKA <mark>G</mark> DLVEAVDHYLLEGHQQS qtd aslsyfqhhnsssgteddpsgnnqpggsnasdidlavvfakflnhnsttpddhyhdpnlvisssalndhdgsqnsska dlveavdhylleghqqs	200 200
MdDof54 MDP0000308863 Consensus	H <mark>EENVQTFMGINHNDDMNIHEFELQGL<mark>LG</mark>DEDQVVQDVFWSDDATMSSLASSTASFTWQPMVHLQELDCSLPSDDDQMKISTNLCGDNWSTFDFSGFEVF QEENVQTFMGINHNDDMNIHEFELQGL<mark>PV</mark>DEDQVVQDVFWSDDATMSSLASSTASFTWQPMVHLQELDCSLPSDDDQMKISTNLCGDNWSTFDFSGFEVF eenvqtfmginhnddmnihefelqgl dedqvvqdvfwsddatmsslasstasftwqpmvhlqeldcslpsdddqmkistnlcgdnwstfdfsgfevf</mark>	300 300
MdDof54 MDP0000308863 Consensus	SR 	302 300

Dof domain

Supplementary Figure 1. Protein alignment of MdDof54 from apple genome. The Dof domain is indicated with a red box.



Supplementary Figure 2. Generation of *MdDof54* RNAi plants.

MdDof54 mRNA levels were detected in the MdDof54 RNAi plants.

Error bars indicate standard deviation (n = 3).



Supplementary Figure 3. Leaf area of *MdDof54* RNAi plants under long-term drought stress. Two-month-old plants were transferred to a greenhouse for one additional month and then exposed to a moderate drought treatment for two months. Oven-dried leaf (A) and leaf area (B) of GL-3 and *MdDof54* RNAi plants after drought stress. Asterisks indicate significant differences between GL-3 and transgenic lines based on one-way ANOVA and Tukey's test (*, p < 0.05; **, p < 0.01; ***, p < 0.001). Error bars indicate standard deviation (n = 15).

Supplementary Figure 4. Gene Ontology (GO) analysis of differentially expressed genes in MdDof54 RNAi plants under drought stress. The adjusted *p*-values indicate which pathways are more likely to have p.adjust biological significance. The red dots 1e-14 indicate low adjusted *p*-values (high 2e-14 enrichment), and the blue dots indicate 3e-14 high adjusted *p*-values (low enrichment). Count Gene Ratio indicates the ratio of gene 30 40 numbers annotated to a pathway among 50 Supplementary data 3. Count: count of 60 70 genes.





Supplementary Figure 5. Generation of *MdDof54* overexpression plants.

MdDof54 mRNA levels were detected in the *MdDof54* overexpression plants.

Error bars indicate standard deviation (n = 3).



Supplementary Figure 6. Leaf area of *MdDof54* overexpression plants under drought. Two-month-old plants were transferred to a greenhouse for one additional month and then exposed to a moderate drought treatment for two months. Oven dried leaf (A) and leaf area (B) of GL-3 and *MdDof54* OE plants. Error bars indicate standard errors (n = 15). Asterisks indicate significant differences between GL-3 and transgenic lines based on one-way ANOVA and Tukey'S test (*, p < 0.05; **, p < 0.01; ***, p < 0.001). Error bars indicate standard deviation. OE, overexpression.



Supplementary Figure 7. Root development and hydraulic conductivity of *MdDof54* OE plants under long-term drought stress. Two-month-old plants were transferred to a greenhouse for one additional month and then exposed to a moderate drought treatment for two months. (A) Morphological characteristics of roots from GL-3 and *MdDof54* RNAi plants after drought stress. Bar = 5cm. (B)–(C) Root dry weight (B) and root hydraulic conductivity (C) of GL-3 and *MdDof54* OE plants after drought stress. Asterisks indicate significant differences between GL-3 and transgenic lines based on one-way ANOVA and Tukey's test (*, p < 0.05; **, p < 0.01; ***, p < 0.001). Error bars indicate standard deviation (n = 15). OE, overexpression.