

Figure S1 Multiple alignment of deduced amino acid sequences of *MfWRKY7* the some highly homologous WRKYs from different plant species. Identical and similar amino acids are shaded in same color; Red line represented WRKY domain, red triangles represented zinc finger structure, and the altered amino acid residue is indicated by an arrow.

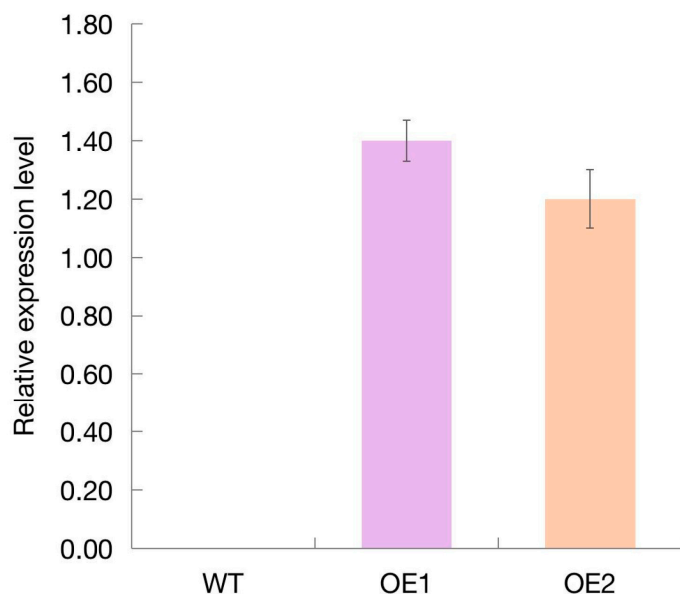


Figure S2 Quantification of expression level of *MfWRKY7* by quantitative real-time PCR (qRT-PCR). Leaves from transgenic and WT plants growing to 4-week-old were sampled. Total RNA was extracted with Plant RNA Kit (Omega Bio-tek, Norcross, GA, United States), which was also purified with RNase-Free DNase I (Omega Bio-tek) and reverse transcribed into cDNA by use of Uscrip II (Innovagene biotech, Hunan, China). The qRT-PCR amplification was performed in 25 μ l reaction mixture (innovagene biotech) including 12.5 μ l 2 \times Taq SYBR Green qPCR Mix, 0.5 μ l of 10 μ M of each primer, 4 μ l 5-fold-diluted cDNA, and 7.5 μ l of Nuclease-free H₂O, which was performed using the real-time PCR instrument CFX Connect (Bio-Rad, Hercules, CA, USA). Amplification conditions were devised that 94°C for 3 min, 42 cycles of degeneration at 94°C for 8 s, annealing/extension at 60°C for 60 s. The relative expression quantity of the target gene was evaluated based on the method of $2^{-\Delta\Delta CT}$ [1]. And the results were normalized by an internal reference gene *Actin2* for quantitative analysis of relative genes. Each RT-qPCR experiment was reproduced at least three times. The gene-specific amplification primers were: *Actin2F*: 5'-GGAAGGATCTGTACGGTAAC-3' and *Actin2R*: 5'-TGTGAACGATTCCTGGACCT-3' for *Actin2*, and *MfWRKY7F*: 5'-GGGCGCCTTTACCTTCTTCT-3' and *MfWRKY7R*: 5'-AGCGTTGAATTGGCGTAGGA-3' for *MfWRKY7*, respectively.

- [1] Livak, K.J.; Schmittgen, T.D.. Analysis of relative gene expression data using real-time quantitative PCR and the $2^{-(\Delta\Delta C(T))}$ Method. *Methods San Diego Calif* **2001**, *25*, 402–408, doi:10.1006/meth.2001.1262.

Table S1 The GenBank accession numbers of the sequences used in Fig. 1b and Fig. S1.

Genes Name	Accession numbers
SIWRKY7	XP_004238130.1_probable
StWRKY2	NP_001275001.1
CaWRKY7	XP_016568783.1
NbWRKY17	AIR74899.1
SiWRKY7	XP_011074403.1
OeWRKY7	XP_022868232.1
LbWRKY1	ACT55331.1
DkWRKY2	AVL95372.1
NnWRKY7	XP_010263444.1
PeWRKY7	XP_011005809.1
PtWRKY7	XP_006380693.1
VvWRKY7	XP_002284966.1
JcWRKY7	XP_020533746.1