Table S1 List of primers used in this study

Primer name	Primer sequence	
CoBBX24-ORF-F	ATGAAGATCCAGTGTGATG	clone
CoBBX24-ORF-F	ACCTAGATCAGGAACAGTG	clone
RT-CoBBX24-F	GCTGCTCCTTCAATCCCTCT	qRT-PCR
RT-CoBBX24-R	CTCATCACAATCCCGACAGA	qRT-PCR
TUBα-3-F	CCATGCCTTGGATCACATTT	qRT-PCR
TUBα-3-R	TGGGGCCATTAATGTAGACG	qRT-PCR
Actin2-F	GGTAACATTGTGCTCAGTGGTGG	qRT-PCR
Actin2-R	AACGACCTTAATCTTCATGCTGC	qRT-PCR
AtABF4-RT-F	AGCTAGTTACGGAGGAACCG	qRT-PCR
AtABF4-RT-R	AGCACATACGGAACTGGTGA	qRT-PCR
AtSAG12-RT-F	TGATGAGCAAGCACTGATGA	qRT-PCR
AtSAG12-RT-R	TGCACTCTCCAGTGAACACA	qRT-PCR
AtSAG29-RT-F	AACGTTGCCTTCTTCTCGTT	qRT-PCR
AtSAG29-RT-R	TTTATCACACGAGCCACGAT	qRT-PCR
AtNYE1-RT-F	GCAAGGATGGGCAAATAGG	qRT-PCR
AtNYE1-RT-R	CACCGCTTATGTGACAATGAAC	qRT-PCR
AtNYE2-RT-F	GACGAAGTAGTGGGCGAGTG	qRT-PCR
AtNYE2-RT-R	CGATGAGATTCAAGAAGAAGTGG	qRT-PCR
AtNYC1-RT-F	TATAGTTGGCTTGGTGGAA	qRT-PCR
AtNYC1-RT-R	GATTCAGAACTGCGAGATG	qRT-PCR
BD-CoBBX24-F	GGAATTCATGAAGATCCAGTGTGATG	Y2H
BD-CoBBX24-R	GCGGATCCCGGCATCAGAGTTGG	Y2H

CoBBX24 ORF:

ATGAAGATCCAGTGTGATGTGTGTGAGAAAGCTCCAGCAACTGTGATCTGTTGCGCTG
ATGAGGCTGCCCTATGTGCAAAATGTGACATAGAAGTTCATGCAGCAAACAAGCTTGC
AAGCAAGCACCAGAGGCTGCTCCTTCAATCCCTCTCCAACAAACTCCCTCCATGTGAC
ATATGTCAAGAGAAGGCAGCTTTCATTTTTTGTGTGGAAGACAGGGCTCTCTTCTGTCG
GGATTGTGATGAGCCAATCCATTCTGCTAGTAGCCTCTCTGCAAACCACCAGCGGTTTC
TTGCCACCGGAATCCGAGTTGCTCTCACTTCAAGTTGCACGAAGGACAGTGAGAAGA
GCAACCAAGATCCAGAGCCAGAGCCACCTAATCATAATGCACAATCGGTTAGCATCAA
AATGCCCACACAGCAATCTTCAAGCTTCACTTCACCATCGTGGGCTGTTGATGACTTAT
TGCATCTCTCAGATATTGAATCTTCTGATAAGAAAGAACAACTTGAGTTTGGAGAGCTA
GAATGGTTCACAGACATTGGTCTCTTTGGTGAGCAAGTTCCTCGCGAGGCGTTAGCTC
TTGCTGAAGTGCCTCAGCTTCCAGTGCCACAGTTAAGCAATGCCACTTCATACAGACC
CACCAAATTGAACATGCCCTACAAGAAGCCTAGAATTGAAATCACGGATGAGGATGAT
GAGTATTTCACTGTTCCTGATCTAGGT

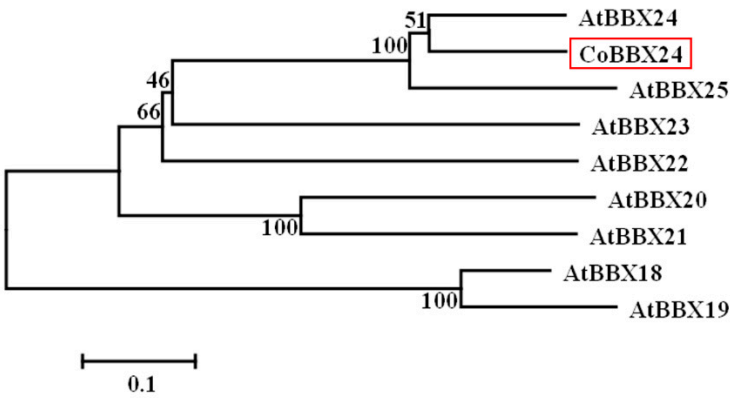

Figure S1. The phylogenetic tree of the *Arabidopsis* BBX family and CoBBX24. The phylogenetic trees were derived using the neighbor-joining (NJ) method with a bootstrap value of 1,000 replicates. Bootstrap values indicate the divergence of each branch, with the scale representing the branch length.

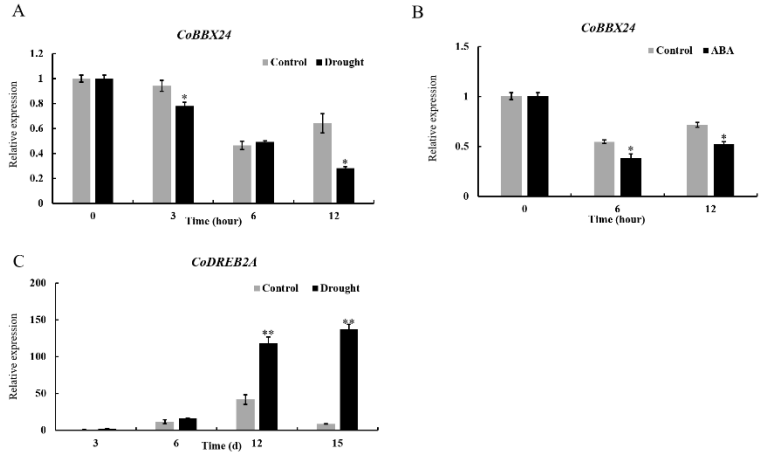

Figure S2. Transcriptional profiling of *CoBBX24* and *CoDREB2A* under drought stress or ABA treatment. (A) For assays on the effects of water deficit, plants were exposed to air drying at room temperature, the control group was cultured normally, samples were harvested 0, 3, 6, and 12 h after the water deficit. (B) For ABA assay of oil tea trees, 100 μM of ABA was sprayed, and the control group was sprayed with water containing an equal amount of ethanol. The sample was harvested 0, 6, and 12 h after spraying the ABA. (C) Transcriptional profiling of *CoDREB2A* under drought stress.

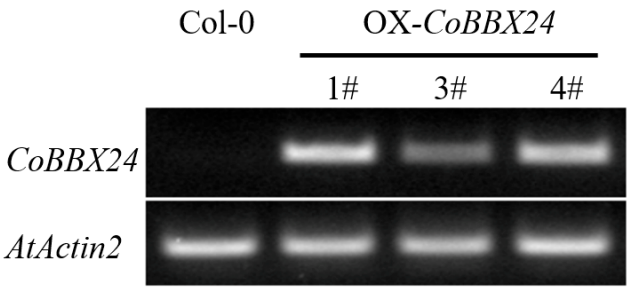

Figure S3. RT-PCR analysis of *CoBBX24* expression in WT and transgenic lines. *Actin2* was used as the reference gene.

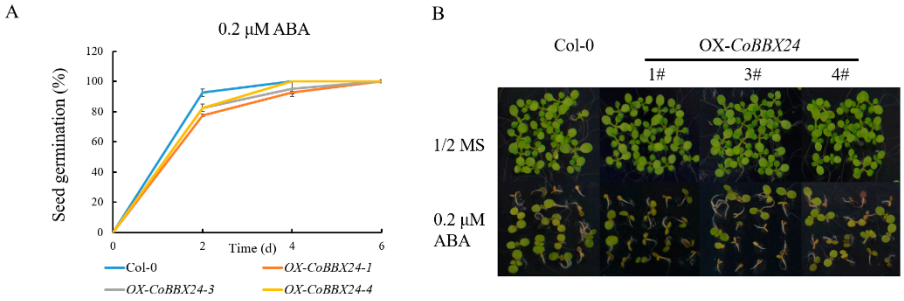

Figure S4. Overexpression of *CoBBX24* in *Arabidopsis* enhanced seedling sensitivity to ABA treatment. (A) The effect of the ABA treatment on germination in the presence of 0.2 μM of ABA. Whiskers indicate the SE (n=3). (B) The appearance of seedlings of WT and three transgenic lines grown for 5 days on solidified medium containing 0.2 μM of ABA.

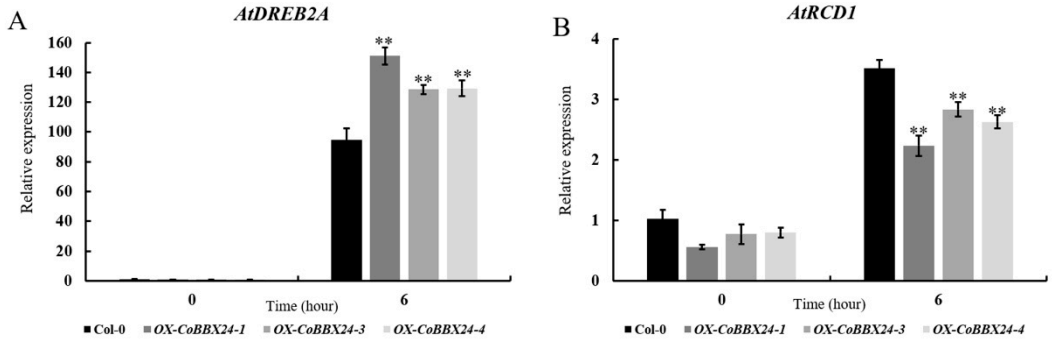

Figure S5. qRT-PCR assay to examine the expression of genes in *CoBBX24ox* and WT plants under drought treatment. The *OX-CoBBX24* transgenic lines and WT plants were exposed to air drying at room temperature, samples were harvested 0 and 6 h after the water deficit. The *Arabidopsis Actin2* was used as the reference gene for normalization. Error bars indicated the SD, (n = 3). Significant differences were determined by Duncan's test (* $P < 0.05$, ** $P < 0.01$).