

Figure S1. Effects of KAR<sub>1</sub> on electrolyte leakage of creeping bentgrass under control and drought-stressed conditions. Columns marked with different letters indicate significant differences among water and KAR<sub>1</sub> treatment under a given condition based on the LSD value ( $P < 0.05$ ), bars represent standard error ( $n = 3$ ).

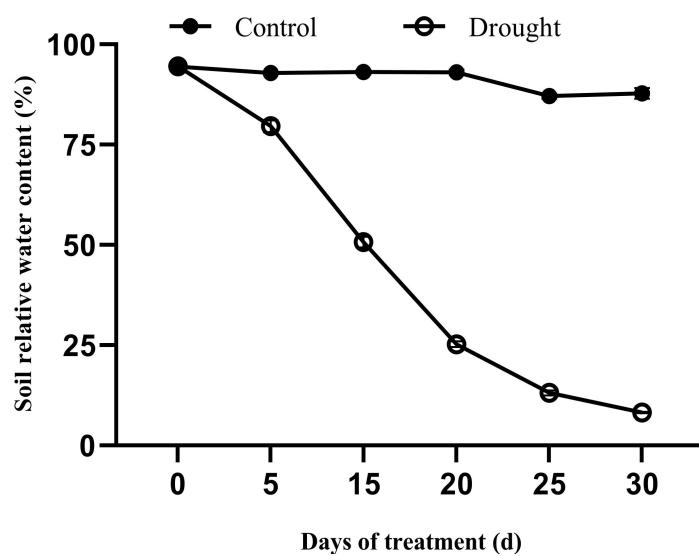


Figure S2. Temporal trend of soil relative water content under control and drought-stressed conditions

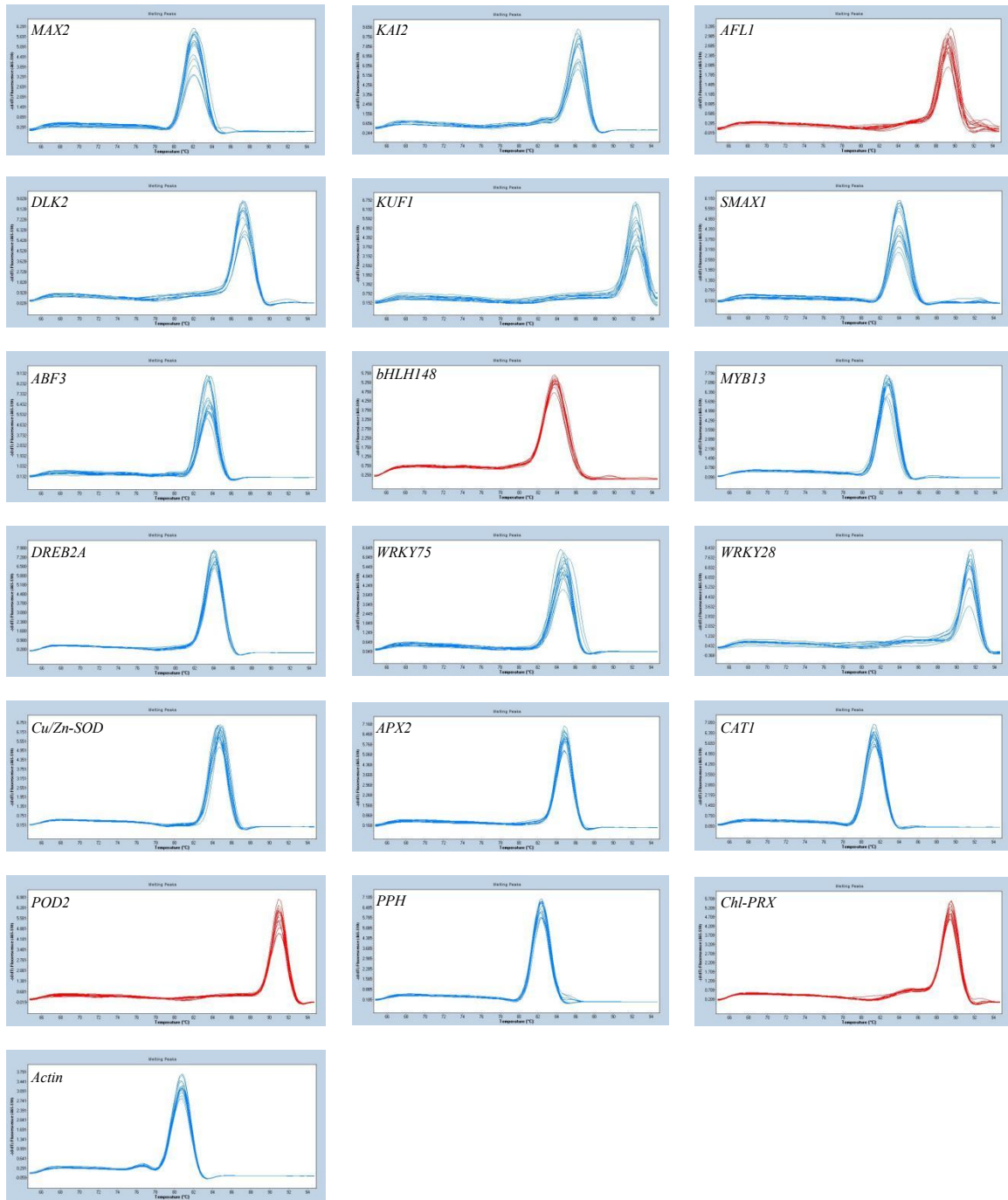


Figure S3. The melting curves of 19 genes by RT-PCR



Figure S4. Effects of KAR<sub>1</sub> on plant performance of creeping bentgrass under control or drought stress for 30 d. C-W: water- treated control; C-KAR<sub>1</sub>: KAR<sub>1</sub>-treated control; D-W: water treatment of drought stress; D-KAR<sub>1</sub>: KAR<sub>1</sub> treatment of drought stress. The white bar represents 5 cm.

Table S1 Primer sequences used for RT-PCR analysis

Gene*	Forward primer (5'-3')	Reverse primer (5'-3')
<i>MAX2</i>	GCGGGGCACATTGATCTTTC	CACATCCCTGTCTTGGGGTG
<i>KAI2</i>	GTCGCTTGCCACATTGTTCA	GGCATGACCTCAACGATGGA
<i>AFL1</i>	CCCTTCACCGACGAGTTCTT	GCGAAGATGACGCTTGACAC
<i>DLK2</i>	TACACGTTCTCCAGGTTTCGC	CCTGATGGAAGCAATGCACC
<i>KUF1</i>	GCGACACGATCTTCCTGGT	CCACGACCACCACCTTCTTG
<i>SMAX1</i>	TCTCGATTGGGGACAAGCAC	ATGGCCACCGGACAATTCTT
<i>ABF3</i>	ATCTGCCTGCGGAGGACACT	TGAAGCATCGGAACAGTGGC
<i>bHLH148</i>	CAGTCCGCCGCCAACTA	TCCGAAACGTGACTGGAGTT
<i>MYB13</i>	CATTCAAGTTTACCCGAGTGCG	CATAAAACATGACCCATCACAGCT
<i>DREB2A</i>	CGATTCGGTCGCTGAAAT	GCCATGCACCCTTTCTT
<i>WRKY75</i>	TGGTGGTGACGACATACGAGG	GGTTGGTAAAGGTTGAGGAGGTG
<i>WRKY28</i>	GGCAGCAACAACAACAAC	GCGAAGGTATGGTGGTTC
<i>Cu/Zn-SOD</i>	CACTGGACCTCACTTCAAC	GTAGCAACACCATCCACTC
<i>APX2</i>	AGGACATTGTTGCCCTTTC	GCTCCGTGAAGTAAGAGTTG
<i>CAT1</i>	TTGCCAATAAGAGGGAGAATG	CGAAGCCGAGCATGTAAG
<i>POD2</i>	CTTCGACAACGCCTACTAC	TTTGCCCATGTTACCA
<i>PPH</i>	TCCGGAAGCACCTTATTATC	CCCTCAGACTCCACATTCTTA
<i>Chl-PRX</i>	CCCAACCTACAGGACATCGT	GGAAGCAGTCGTGGAAGAAG
<i>ACT</i>	CCTTTTCCAGCCATCTTTCA	GAGGTCCTTCCTGATATCCA

\**MAX2*, More axillary growth 2; *KAI2*, Karrikin insensitive 2; *AFL1*, At14a-Like1; *DLK2*, D14-Like 2; *KUF1*, Karrikin-up-regulated F-box1; *SMAX1*, Suppressor of MAX2-1; *ABF3*, ABRE binding factor 3; *bHLH148*, Basic helix-loop-helix transcription factor 148; *MYB13*, MYB transcription factor 13; *DREB2A*, Dehydration-responsive element-binding protein 2A; *WRKY75*, WRKY transcription factor 75; *WRKY28*, WRKY transcription factor 28; *Cu/Zn-SOD*, Cu/Zn-Superoxide dismutase; *APX2*, Ascorbate peroxidase 2; *CAT1*, Catalase 1; *POD2*, Peroxidase 2; *PPH*, Pheophytinase; *Chl-PRX*, Chl-degrading peroxidase; *ACT*, Actin.