Table 1 Suppl. Nucleotide sequences of primers used for reverse transcription quantitative PCR analysis.

Gene names (seqence ID)	Forward primers 5′ - 3′	Reverse primers 5′ - 3′
AtDREB1A	AGGCGGTGATTATATTCCGACGCT	TCAGCGGTTTGAAATGTTCCGAGC
P5CS (NM_001246978.2)	CCATCAGCAATCTCCGTTCT	TGCACTGGAAGCAAATGAAA
CAT	TTCCATCACTGCAGCTTTGCTTCG	TTTGTTTGGGCCAGCTTCTCTCTC
SOD	CCATCCAGTTCGTCCAAGAT	GTATCGCCAAGAGCATGGAT
LPO	ATCCATCCCACCACACTCGTCAAT	TCCATGTCAAGTCACTCCCAGTGT
Actin	AAGCTGCAGGTATCCACGAGACTA	ACGGTCAGCAATACCAGGGAACAT

Table 2 Suppl. Morphological observations of transgenic and wild-type plants under control and cold stress (4 °C for 5 d) applied to 25-d-old wild-type (H86) and transgenic (D86) seedlings. CH86 - wild type cold treated plants, CD86 - transgenic cold treated plants. Means ± SEs, $n = 3$, values followed by the same letter are not significantly different ($P > 0.05$) according to the Duncan multiple range test.

Parameters	H86	CH86	D86	CD86
Shoot fresh mass (SFM) [g plants^{-1}]	9.09 ± 0.645^{a}	7.80 ± 0.250^{b}	7.68 ± 0.41^{b}	8.74 ± 0.810^{a}
Shoot dry mass (SDM) [g plants^{-1}]	0.86 ± 0.027^{bc}	1.01 ± 0.060^{b}	0.73 ± 0.067^{c}	1.22 ± 0.074^{a}
Ratio (SFM/SDM)	10.60 ± 0.888^{a}	10.50 ± 1.05^{a}	10.50 ± 1.05^{a}	7.19 ± 0.373^{b}
Root fresh mass (RFM) [g plants^{-1}]	1.86 ± 0.090^{b}	1.76 ± 0.090^{c}	1.76 ± 0.090^{c}	2.26 ± 0.130^{a}
Root dry mass (RDM) [g plants^{-1}]	0.16 ± 0.004^{b}	0.16 ± 0.008^{b}	0.16 ± 0.008^{b}	0.20 ± 0.030^{a}
Ratio (RFM/RDM)	11.50 ± 1.170^{a}	10.90 ± 0.848^{a}	10.90 ± 0.848^{a}	11.30 ± 1.26^{a}
Root length [cm plants^{-1}]	13.20 ± 0.457^{a}	12.40 ± 1.05^{a}	12.40 ± 1.050^{a}	13.00 ± 1.33^{a}
Shoot length [cm plants^{-1}]	13.00 ± 0.637^{b}	14.20 ± 1.79^{b}	14.20 ± 1.79^{b}	17.20 ± 2.34^{a}