

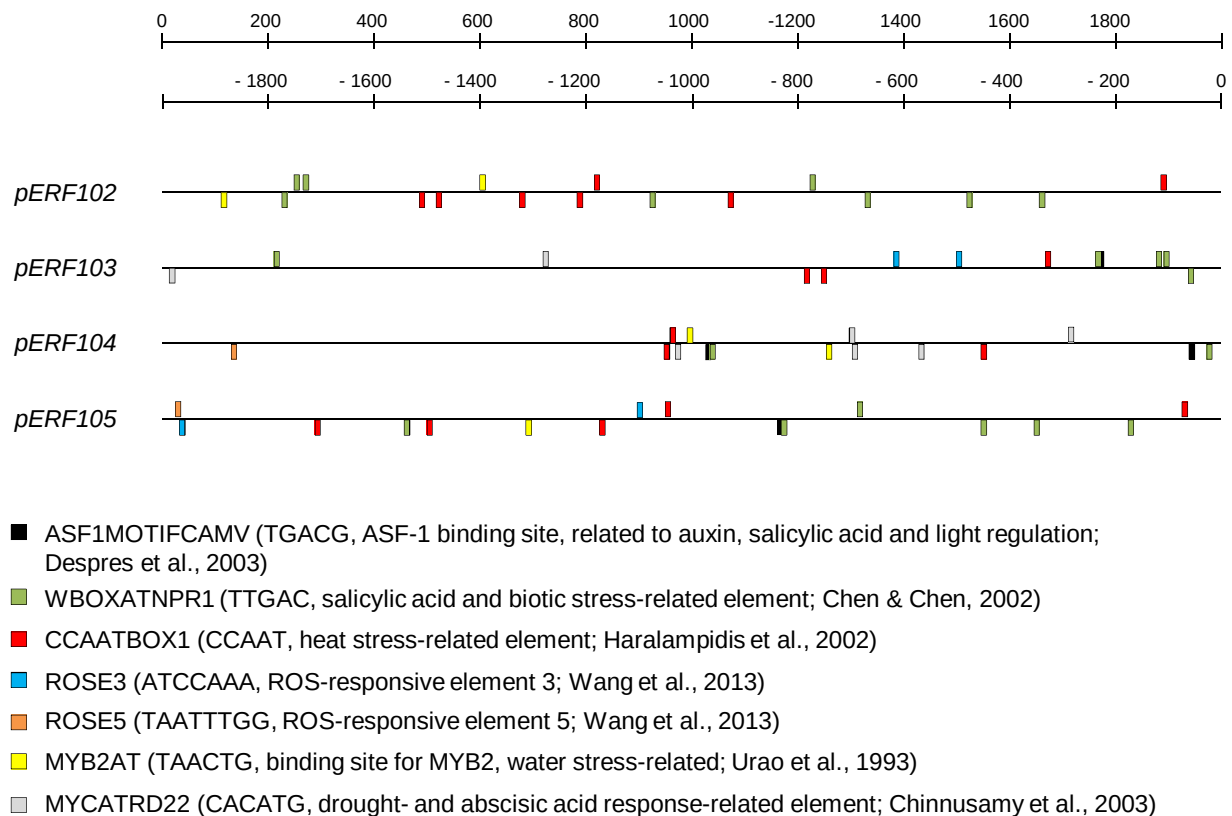


Fig. S1 *cis*-acting regulatory elements in the *ERF102* to *ERF105* promoters. Analysis of the *ERF102* to *ERF105* promoters for the presence of *cis*-acting regulatory elements (CAREs) was carried out using the PLACE website (<http://www.dna.affrc.go.jp/PLACE/>; Higo et al., 1998). The motifmapper of the TOUCAN2 workbench (Aerts et al., 2005) was used to visualize the location of CAREs. The 2 kb promoter regions are represented by black lines. Colored boxes shown above the black lines represent CAREs oriented in the 5' → 3' direction, colored boxes below the black lines indicate CAREs in the 3' → 5' direction. A selection of CAREs relevant for gene regulation by hormonal or environmental cues shown in Fig. 2 is shown. Additional CAREs found in the *ERF102* to *ERF105* promoters are shown in Table S2

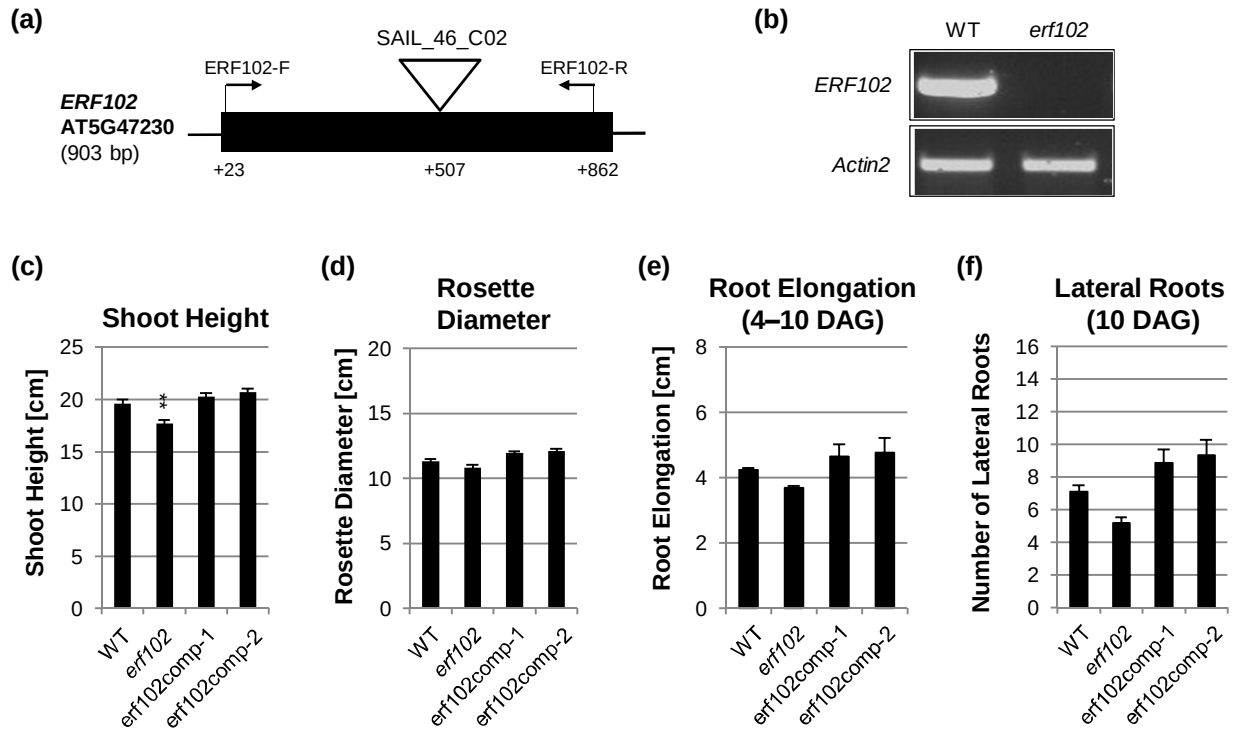


Fig. S2 Characterisation of the *erf102* mutant SAIL_46_C02. **(a)** Structure of the *Arabidopsis* *ERF102* (AT5G47230) gene. The black line denotes the untranslated region, the black box represents the exon, the T-DNA insertion at position +507 is shown by a triangle. The positions of primers that were used for RT-PCR are indicated by arrows. **(b)** RT-PCR analysis of *ERF102* expression using total RNA extracted from seedlings of wild type and *erf102*. The *Actin2* gene was used as internal control. **(c–f)** Complementation of the *erf102* mutant by introgression of the 35S:*ERF102* gene. Shoot height **(c)** and rosette diameter **(d)** of 35-day-old plants. **(e)** Elongation of the primary root and **(f)** number of lateral roots of plants grown on half-strength MS medium. Asterisks indicate significant differences to the wild type ($n \geq 30$), (*, $p < 0.05$; **, $p < 0.01$). Error bars represent SE

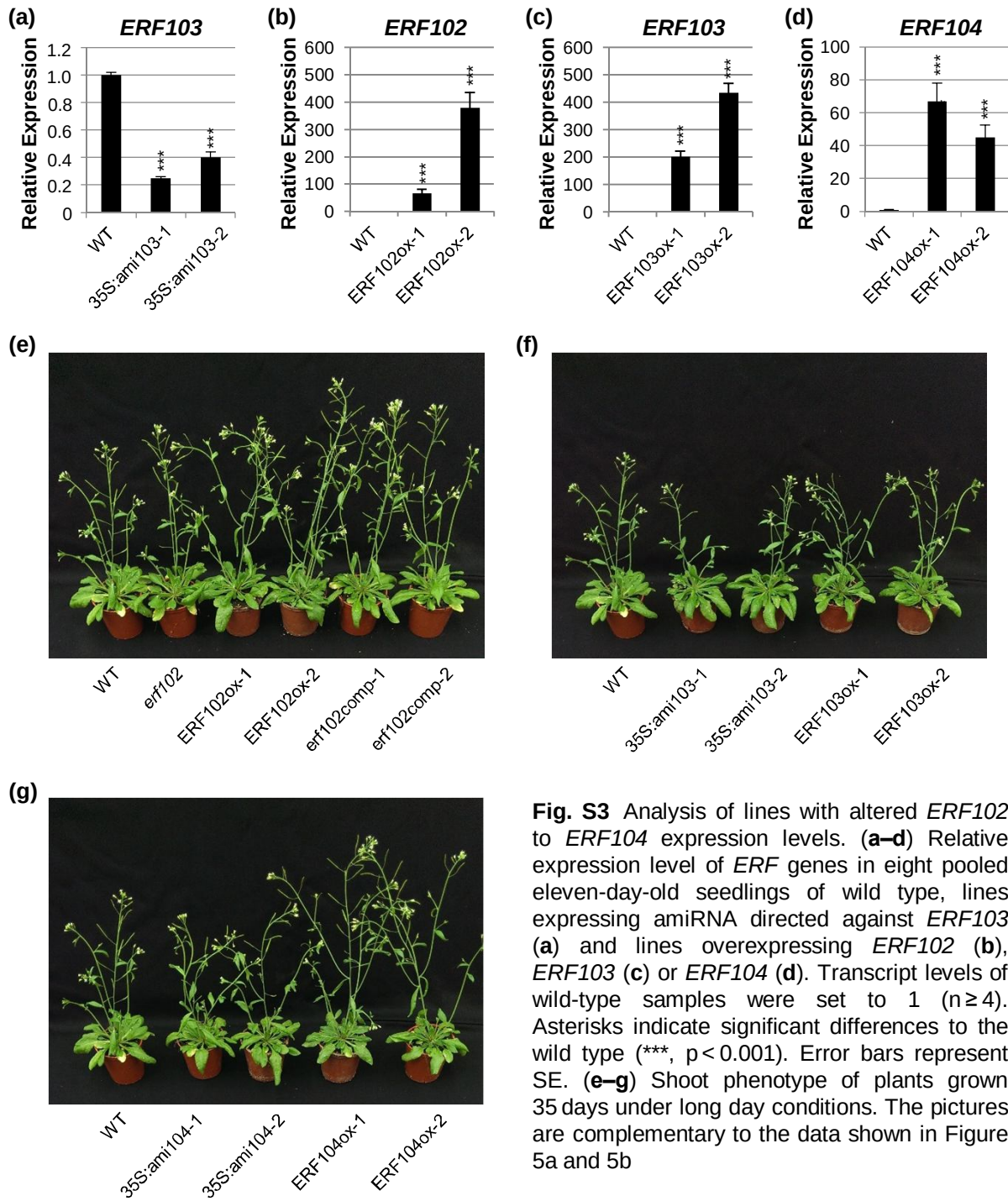


Fig. S3 Analysis of lines with altered *ERF102* to *ERF104* expression levels. **(a–d)** Relative expression level of *ERF* genes in eight pooled eleven-day-old seedlings of wild type, lines expressing amiRNA directed against *ERF103* **(a)** and lines overexpressing *ERF102* **(b)**, *ERF103* **(c)** or *ERF104* **(d)**. Transcript levels of wild-type samples were set to 1 ($n \geq 4$). Asterisks indicate significant differences to the wild type (***, $p < 0.001$). Error bars represent SE. **(e–g)** Shoot phenotype of plants grown 35 days under long day conditions. The pictures are complementary to the data shown in Figure 5a and 5b

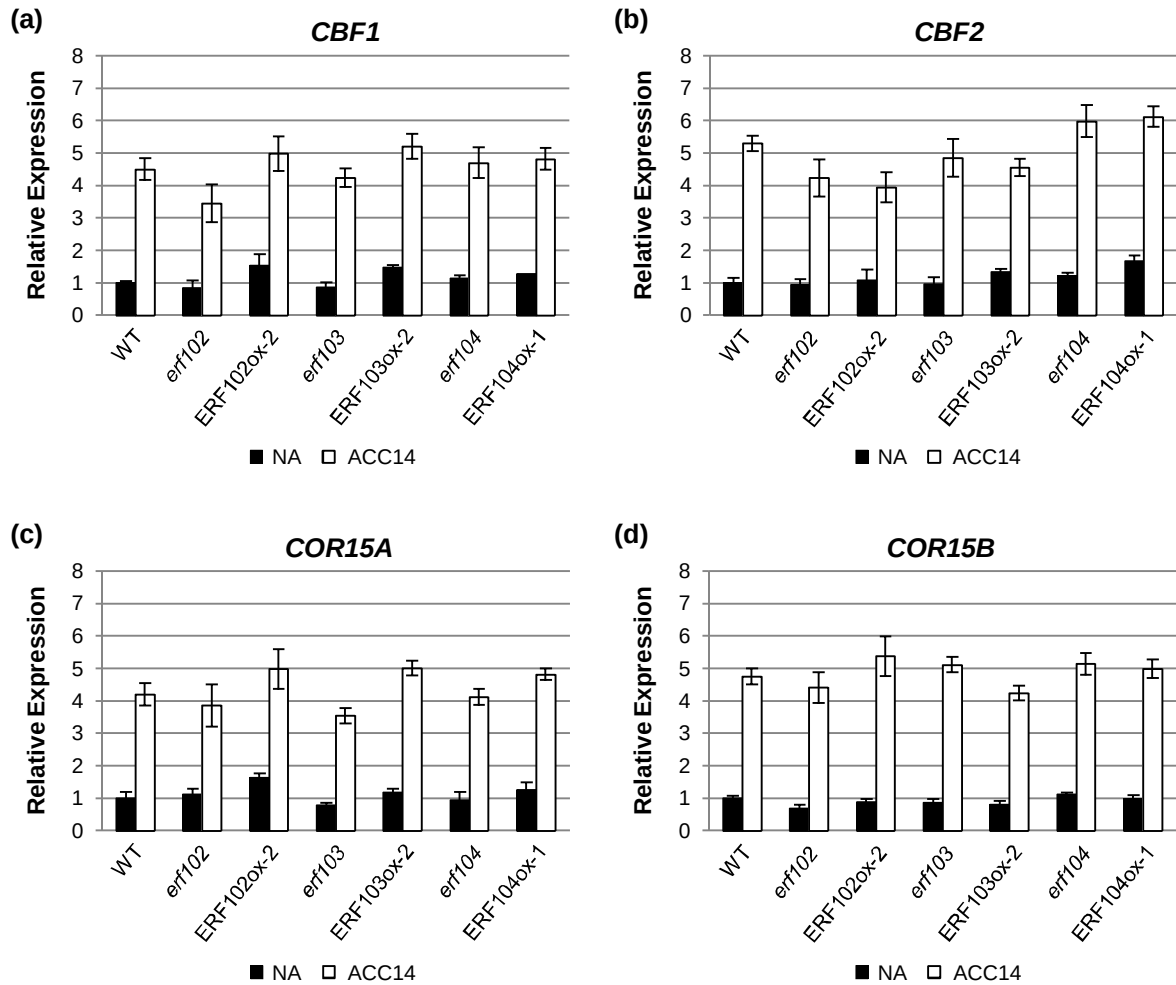


Fig. S4 Expression of selected cold-responsive genes in lines with reduced or enhanced *ERF102* to *ERF104* expression. Relative expression of *CBF1* (a), *CBF2* (b), *COR15A* (c), and *COR15B* (d) genes in six-week-old lines with reduced or enhanced *ERF102* to *ERF104* expression before (non-acclimated, NA) and after 14 days (acclimated, ACC14) of cold acclimation at 4 °C. Transcript levels of wild-type samples under non-acclimated conditions were set to 1 ($n \geq 4$). Error bars represent SE

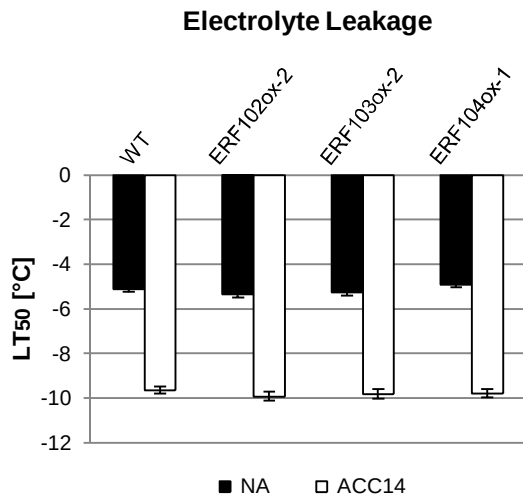


Fig. S5 Electrolyte leakage assays of lines with enhanced *ERF102* to *ERF104* expression. Electrolyte leakage assays on detached leaves of lines overexpressing *ERF102*, *ERF103* or *ERF104* before (non-acclimated, NA) and after 14 days (acclimated, ACC14) of cold acclimation at 4 °C. The bars represent the means $\pm$ SE from four replicate measurements where each replicate comprised leaves from three plants

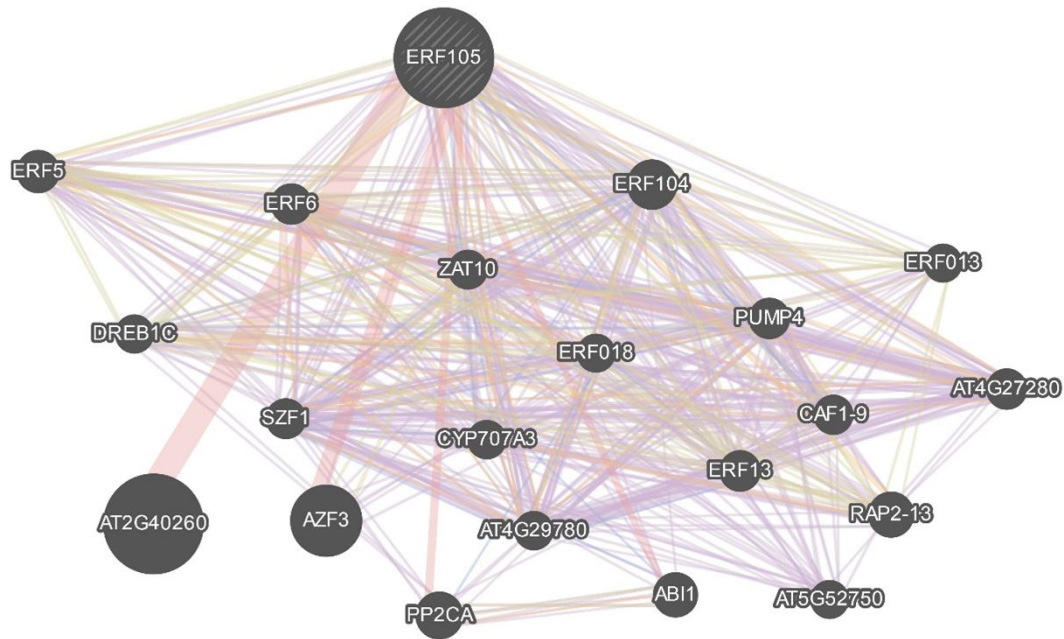


Fig. S6 Network of co-localisation, co-expression, genetic and physical interactions of ERF105. The blue connecting lines between two genes represent co-localisation, purple lines co-expression, green lines genetic interactions and red lines physical interactions. ABI1 = ABA INSENSITIVE 1; AZF3 = ZINC-FINGER PROTEIN 3; CAF1-9 = CCR4-ASSOCIATED FACTOR 1 HOMOLOG 9; CYP707A3 = CYTOCHROME P450, FAMILY 707, SUBFAMILY A, POLYPEPTIDE 3; DREB1C (CBF2) = DEHYDRATION-RESPONSE ELEMENT-BINDING PROTEIN 1C/C-REPEAT-BINDING FACTOR 2; ERF = ETHYLENE RESPONSE FACTOR, PP2CA = PROTEIN PHOSPHATASE 2CA; PUMP4 = PLANT UNCOUPLING MITOCHONDRIAL PROTEIN 4; RAP2-13 (RAP2.4/WIND) = RELATED TO AP2 13; SZF1 = SALT-INDUCIBLE ZINC-FINGER; ZAT10 (STZ) = ZINC FINGER PROTEIN 10 (SALT TOLERANCE ZINC FINGER). Analysis was done using GeneMania (Wardle-Farley et al., 2010)

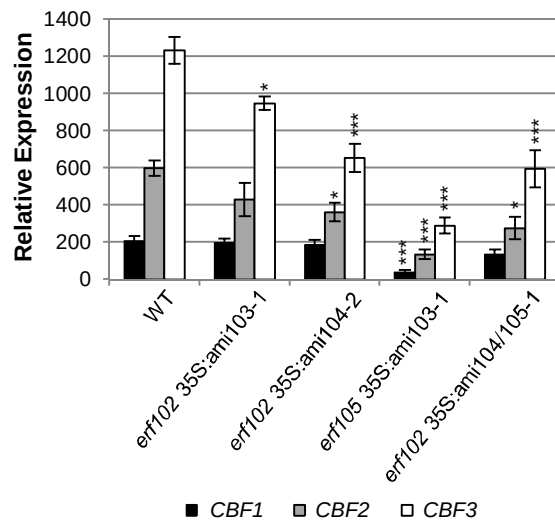


Fig. S7 Expression of selected cold-responsive genes in lines with reduced *ERF102* to *ERF105* expression. Relative expression of *CBF1*, *CBF2* and *CBF3* genes in eleven-day-old seedlings of wild type and lines with reduced *ERF102* to *ERF105* after 4 hours of cold treatment at 4 °C. Transcript levels of wild-type samples under control conditions were set to 1 ($n \geq 4$). Asterisks indicate significant differences to the wild type (*, $p < 0.05$; ***, $p < 0.001$). Error bars represent SE

Table S2 Sequences of primers used for cloning. Small letters in the primer sequences indicate the integrated *attB4*- or *attB1*-sites for cloning DNA fragments into the vector pDONR P4-P1R. Small italic letters in the primer sequences indicate the integrated *attB1*- or *attB2*-sites for cloning DNA fragments into the vector pDONR221. Underlined letters are the nucleotides added to keep the sequence in the right frame

Amplification of	Primer sequences (5'–3')
Promoter of <i>ERF102</i> (AT5G47230)	F: ggggacaactttgtatagaaaagttgCGTTGATTCTTCTACAAACCAG R: ggggactgctttttgtacaaaacttgTGATAAAATTTTCAAAAAGC
Promoter of <i>ERF103</i> (AT4G17490)	F: ggggacaactttgtatagaaaagttgGTTGTGGATTCTGGCATTG R: ggggactgctttttgtacaaaactgtTTTGGAGGAAACAGAGAATTG
Promoter of <i>ERF104</i> (AT5G61600)	F: ggggacaactttgtatagaaaagttgTGATGAGTGGTCGCTTCTTT R: ggggactgctttttgtacaaaactgCTTCACTCTACTTGATTGAC
<i>ERF102</i> (AT5G47230) for N-terminal fusion	F: <i>ggggacaagttgtacaaaaaagcaggct</i> <u>CA</u> ATGGCGACTCCTAACGAAG R: <i>ggggaccactttgtacaagaaagctgggt</i> <u>G</u> TAATCAAACAACGGTCAACTGG
<i>ERF103</i> (AT4G17490) for N-terminal fusion	F: <i>ggggacaagttgtacaaaaaagcaggct</i> <u>CG</u> GAAATGGCTACACCAAACGAA R: <i>ggggaccactttgtacaagaaagctgggt</i> <u>C</u> TCAAACAACGGTCAATTGTG
<i>ERF104</i> (AT5G61600) for N-terminal fusion	F: <i>ggggacaagttgtacaaaaaagcaggct</i> <u>CG</u> ATGGCAACTAAACAAGAAGCTTTA R: <i>ggggaccactttgtacaagaaagctgggt</i> <u>C</u> GTTTTAAGTGACGGAGATAACGGAAA