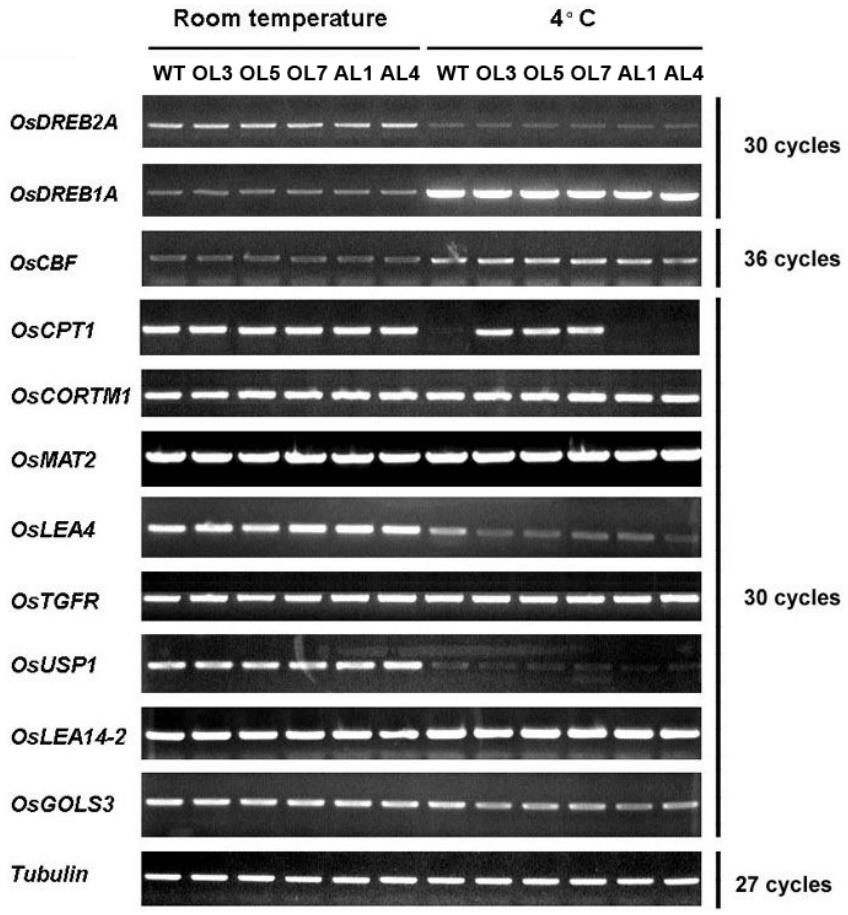
**Supplemental data files**




**Supplementary figure 1. RT-PCR results of rice DREB genes and the rice homologs of target genes of *Arabidopsis* DREBs in *OsMYB3R-2* transgenic rice plants.** The method of obtaining seedlings at the same stage is described in "Materials and methods". *Tubulin* was used as an internal control. WT: wild type; OL3, OL5, OL7: *OsMYB3R-2*-overexpressing lines; AL1, AL4: *OsMYB3R-2*-antisense lines. The results were repeated twice at least. Data represent means and SEs of experiments performed in triplicate.

**Supplementary table 1. The information of rice DREB genes and the rice homologs of target genes of Arabidopsis DREBs.**

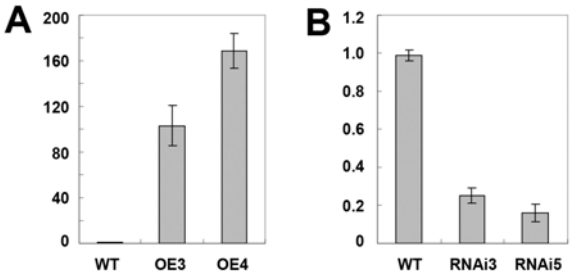
| Gene name | Primer sequence | PCR product | Accession no. and annotation |
|---|---|---|---|
| *OsDREB1A* | F 5' GATGTGCGGGATCAAGCAGGA3' | | Os09g0522200, supported by AK105599; |
| | R 5' GTACTCTAATAGGAGAAAAGGCT 3' | 718 bp | DRE-binding protein 1A. |
| *OsDREB2A* | F 5' GATGGAGCGGGGGGAGGGGAG 3' | | Os01g0165000, supported by AK121956; DRE binding protein 2, |
| | R 5' GTACTCTAATAGGAGAAAAGGCT 3' | 832 bp | drought and salt stress inducible transcriptional activator. |
| *OsCBF1* | F 5´GGGGAGGACCAAGTTCAGG 3´ | | AY327040; putative DREB protein, |
| | R 5´CGTAGTAGTAGGACGGCTGGTC3´ | 476 bp | transcription factor CBF1. |
| *OsCBF* | F 5´CGCGGTGACCGTTTCTGG 3´ | | Os06g0165600; CRT/DRE binding factor |
| | R 5´CGACGATGATGGCGAGGG 3´ | 606 bp | |
| *OsCPT1* | F 5´CGGTGGCAGTAGGAAAGTAG 3´ | | Os02g0629800, supported by AK121915; |
| | R 5´CATGAACAACAGACAAAGGAGA 3´ | 405 bp | Cp-thionin. |
| *OsCORTM1* | F 5´GCTAAAGGCACAGCCATACA 3´ | | OsCOR413-TM1, cold acclimation protein COR413-TM1. |
| | R 5´AACATCATCAAGGGGATAACTG3´ | 377 bp | |
| *OsMAT2* | F 5´GGAGTCTGTGAACGAGGGC 3´ | | Os05g0135700, supported by AK103157; S-adenosylmethionine |
| | R 5´GACACCGATGGCGTATGAT 3´ | 913 bp | synthetase 1. |
| *OsLEA4* | F 5´TCCAACAGGCGAGTGAGC 3´ | | Os05g0542500, supported by AK119713; Group 3 LEA (Type I) |
| | R 5´CCCGTCAGAAATCCTCCC 3´ | 310 bp | protein. |
| *OsTGFR* | F 5´ATTGGGCAAATTGAGGCA 3´ | | Os01g0913300, supported by AK100698; TGF-beta receptor, |
| | R 5´CACAAGACTGACATAGGCGATA3´ | 1202 bp | type I/II extracellular region family protein. |
| *OsUSP1* | F 5´CTCCATCTCGCCACATTCG 3´ | | Os05g0453700, supported by AK063881; Universal stress protein |
| | R 5´GCCACTACGGTAAGCTCCAA 3´ | 452 bp | (Usp) family protein. |
| *OsLEA14-1* | F 5´GCGAAAATCCCCAAGCC 3´ | | Os01g0624400; Late embryogenesis abundant protein 2 family |
| | R 5´CACGTAGTCGATGTCCCAGTC 3´ | 303 bp | protein. |
| *OsLEA14-2* | F 5´ATGGACAAGGCGAAAGGG 3´ | | Os05g0584200, supported by AK061818; Late embryogenesis |
| | R 5´GATCGGAGTTGGTTGATGAGA 3´ | 480 bp | abundant protein Lea14-A. |
| *OsGOLS3* | F 5´ACTGGAAGGGCGTCGTG 3´ | | Os07g0687900, supported by AK107065; WSI76 protein induced |
| | R 5´TTGGGGATGGGCTTGTAC 3´ | 595 bp | by water stress. |

F: forward primer, R: reverse primer.

**Supplementary table 2. Primer sets used for RT-PCR of cell cycle genes**

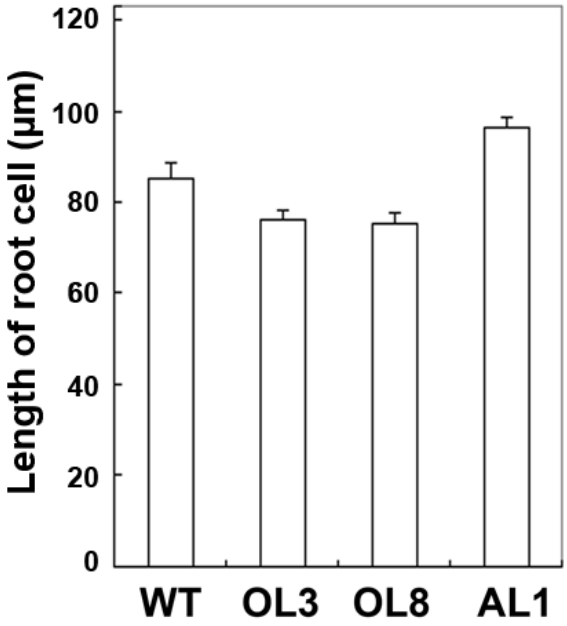
| Gene name | Accession no. | Annotation | Primer sequence | PCR product |
|---|---|---|---|---|
| *Tubulin* | DQ683569 | alpha-tubulin | F 5´ TCAGATGCCCAGTGACAGGA 3´,<br>R 5´ TTGGTGATCTCGGCAACAGA 3´ | 777 bp |
| *OsCycB1;1* | Os01g59120, supported by AK111939 | cyclin IaZm, putative, expressed | F 5´TCATCAACACCCTCACCTCC 3´<br>R 5´AGTGCCACTCCTCCAAGC 3´ | 874 bp |
| *OsCycB2;1* | Os04g47580, supported by AK070211 | cyclin B2, putative, expressed | F 5´TTGACCATCAGGTTTCCGTG 3´<br>R 5´TGCTGGCAACGAGTGAGA 3´ | 787 bp |
| *OsCycB2;2* | Os06g51110, supported by AK070518 | cyclin IIIZm, putative, expressed | F 5´GTGTTTCAATGGAGGGCGTCA 3´<br>R 5´GGCGAGCAGCATGGCAGT 3´ | 710 bp |
| *OsCDC20.1* | Os02g0700100, supported by AK102954 | WD-repeat protein | F 5´CAAGAAGGACAAGGAGAACGC 3´<br>R 5´ATGGGACGGACGATGCC 3´ | 728 bp |

F: forward primer, R: reverse primer.




**Supplementary figure 2. Molecular Identification of *OsCycB1;*1 transgenic rice**

A, Real-time RT-PCR of the expression of *OsCycB1;*1 in overexpression lines. B, Real-time RT-PCR of the expression of *OsCycB1;*1 in RNAi lines. WT: wild type; OE3, OE4: overexpression lines of *OsCycB1*;1 transgenic rice; RNAi3 and RNAi5: RNAi lines of *OsCycB1*;1 transgenic rice. Primers used for real-time RT-PCR analysis were as follows: *OsCycB1*:1 primers for overexpressed transgenic plants (Forward, 5´AATCTCACCGTTCCTACAGC3´; Reverse, 5´AGTAGAGTGCGAGGTAACAG 3´), and *OsCycB1:1* primers for RNAi transgenic plants (Forward, 5´AATCTCACCGTTCCTACAGC3´; Reverse, 5´AGTAGAGTGCGAGGTAACAAG3´). The rice *actin* gene was used as a positive internal control with a pair of primers (Forward, 5´GTATCCATGAGACTACATACAACT3´; Reverse, 5´ACTCAGCCTTGGC-AATCCACA 3´). $T_1$ generation of *OsCycB1*;1 transgenic lines was taken to do the real-time RT-PCR as the method described previously (Dai et al., 2007), and the experiments were repeated twice.




**Supplementary figure 3. The length of root cell in *OsMYB3R-2* transgenic rice.**

The shelled seeds of wild type and *OsMYB3R-2* $T_2$ transgenic rice lines were disinfected with 0.1% $HgCl_2$ and germinated at 30℃ in dark for 7 days. The tips of primary root were taken with GUS staining positive seedlings. Cell length with 500 root cells for each sample were observed and taken pictures under DIC microscope. The experiments on the length of root cell in *OsMYB3R-2* transgenic rice were repeated twice at least. Data represent means and SEs of experiments performed in triplicate. WT: wild type; OL3, OL8: *OsMYB3R-2*-overexpressing lines; AL1: *OsMYB3R-2*-antisense lines.