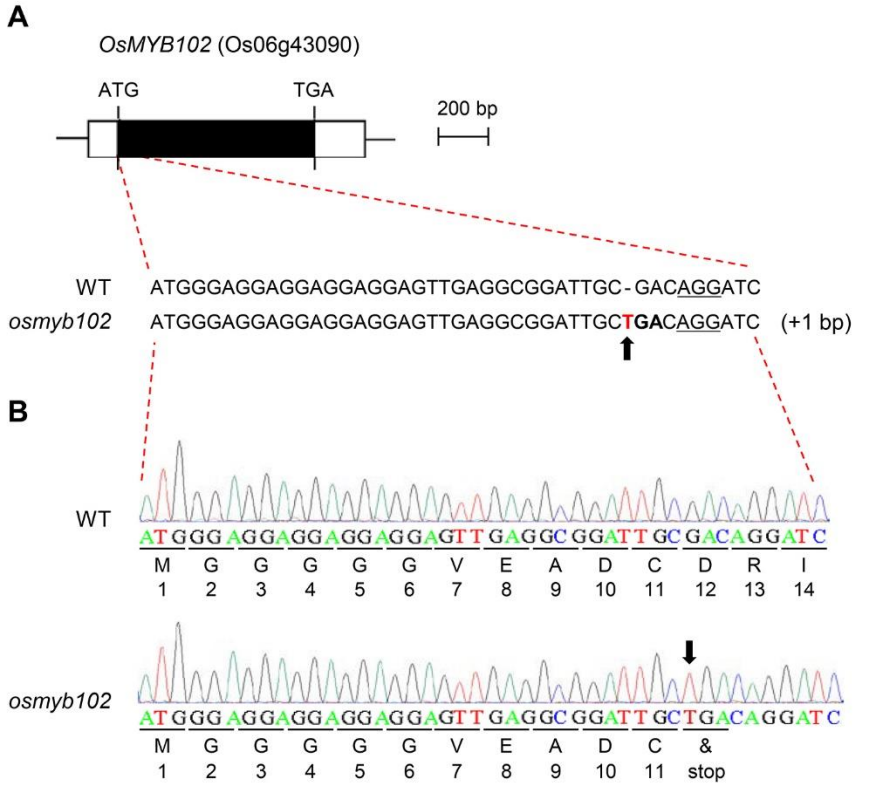
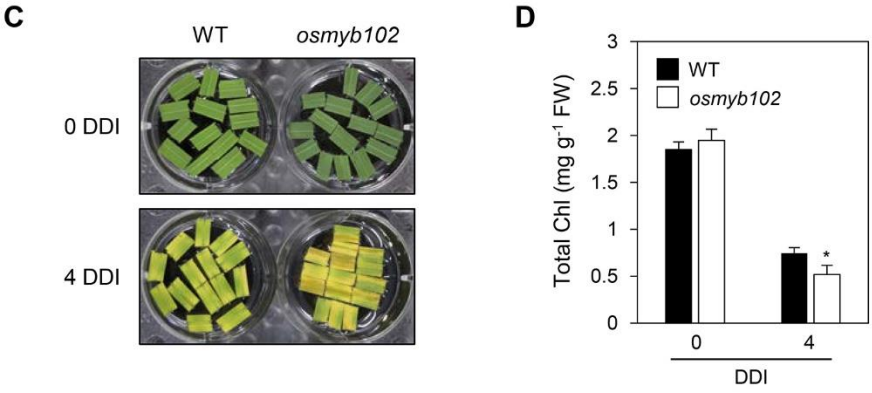
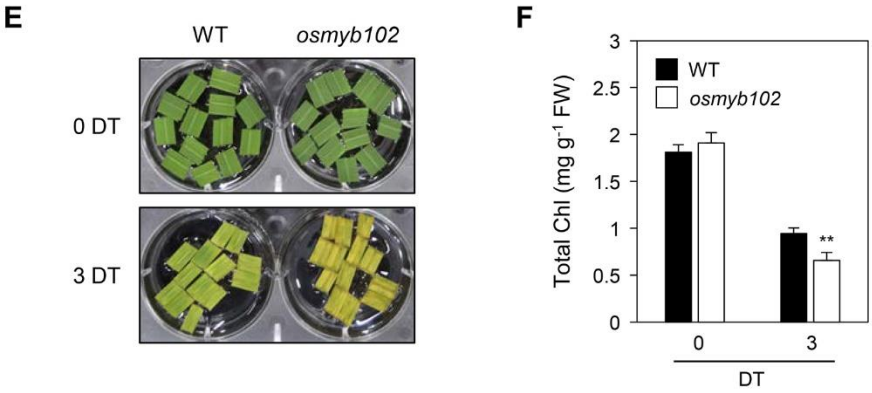
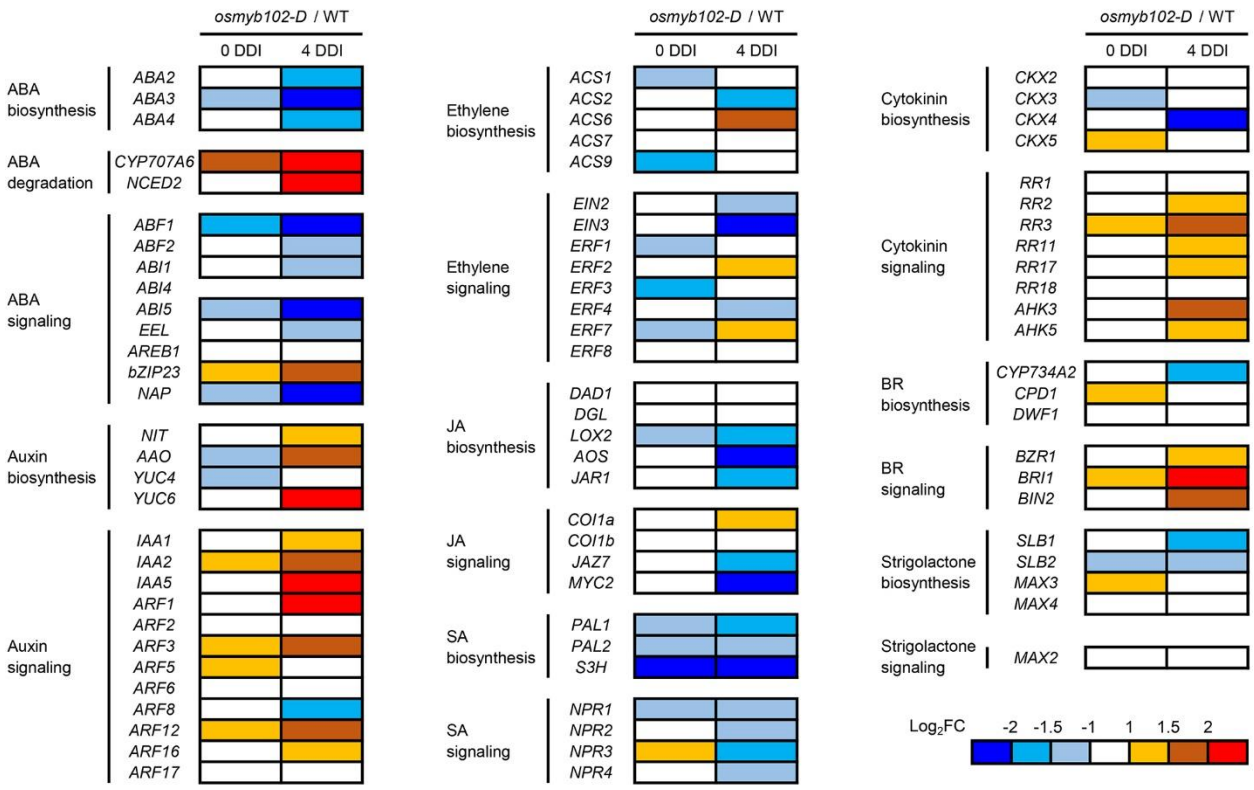
**Supplemental Information** – Piao et al.



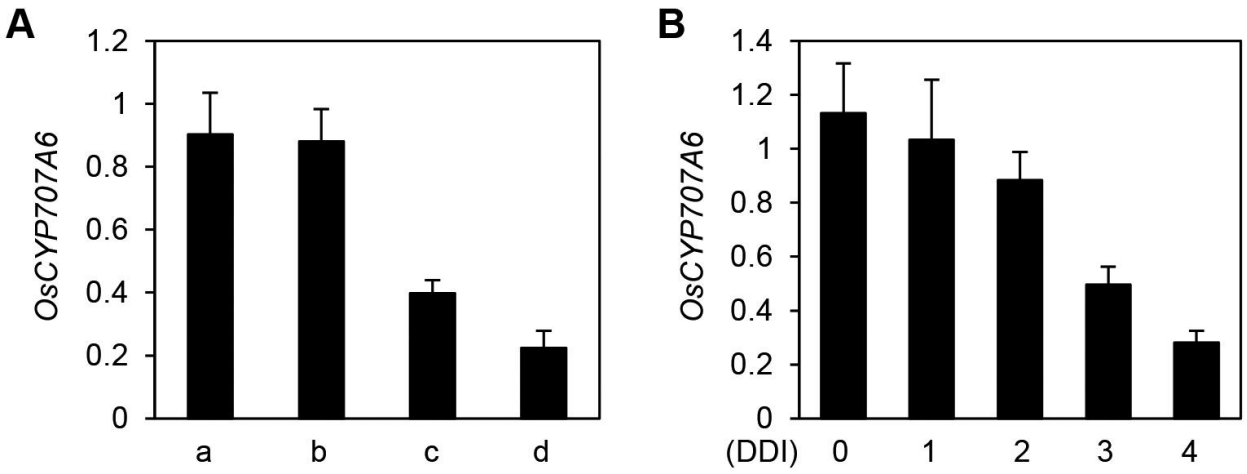



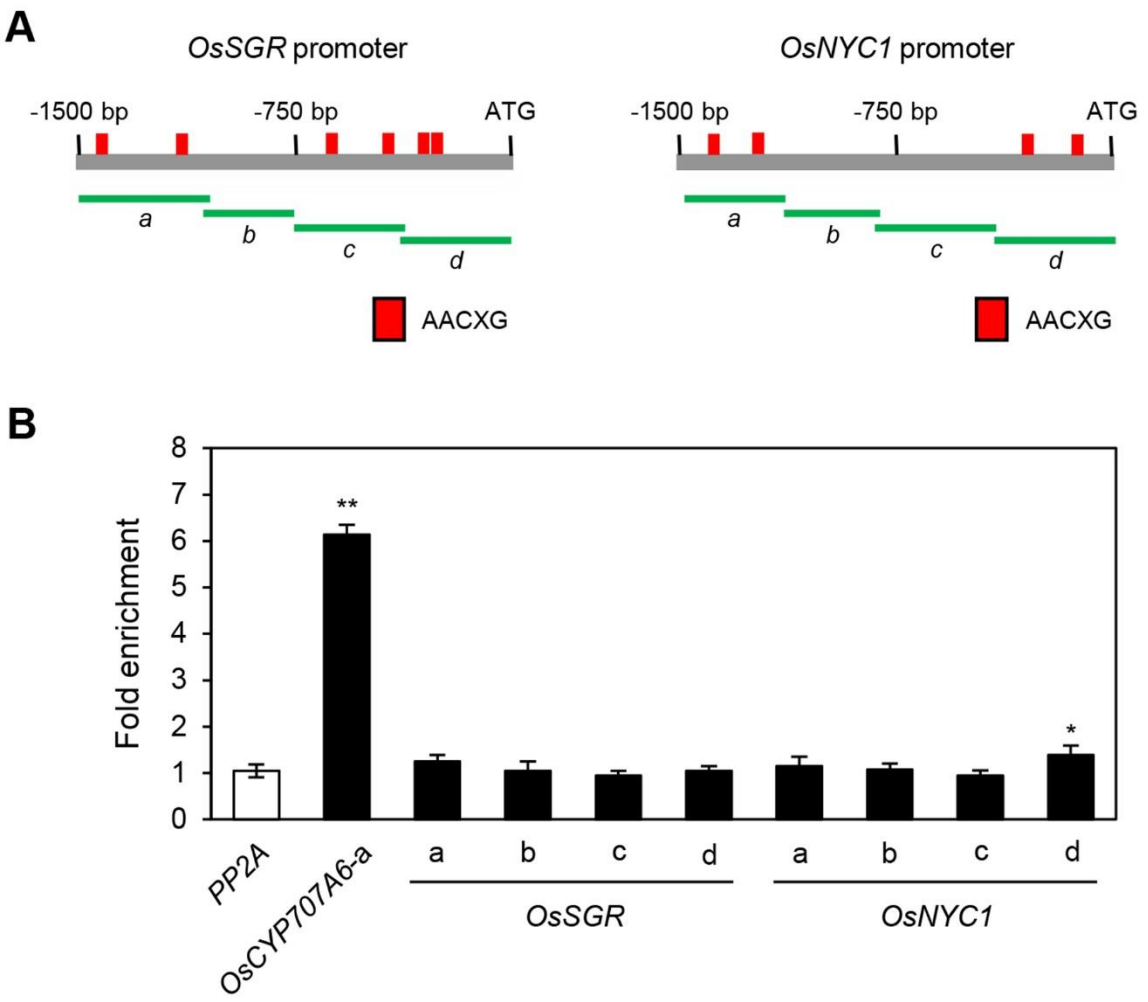
**Supplementary Fig. S1.** The *osmyb102* knockout mutant senesces faster than the wild-type during both dark- and ABA-induced senescence. (A) Editing the *OsMYB102* genomic sequence using the CRISPR/Cas9 system to generate the *osmyb102* knockout mutant. In a schematic diagram of *OsMYB102* gene structure, the UTRs and ORF of *OsMYB102* are indicated by open rectangles and a filled rectangle, respectively. The ORF of *OsMYB102* is 936 bp long and encodes a protein with 311 amino acids. However, the *osmyb102* mutant generated by CRISPR/Cas9 contains a thymine insertion, shown by the black arrow, between positions 33 and 34 of the *OsMYB102* ORF. This mutation alters the reading frame, leading to a premature stop codon at position 12 of the protein. The premature stop codon is highlighted in bold type, and the PAM sequence is underlined. (B) Chromatograms of direct sequencing of genomic PCR products in the WT and *osmyb102* mutant. The *OsMYB102* genomic sequences around the single guide RNA (sgRNA) binding site were amplified by PCR using specific primers (see Supplementary Table S1), and the resulting PCR products were subjected to direct sequencing. The *osmyb102* mutant has a homozygous thymine insertion, shown by the black arrow, in the coding sequence of *OsMYB102* gene. The added thymine causes a premature stop codon, producing a truncated OsMYB102 protein with only 11 amino acids. This short peptide likely does not have OsMYB102 function, and thus, *osmyb102* is considered a knockout mutant. Numbers denote the position of amino acid residues. (C–D) The changes in leaf color (C) and total chlorophyll content (D) of the leaf discs from the WT and *osmyb102* mutant during dark-induced senescence. The leaves of one-month-old WT and *osmyb102* mutants grown under long-day conditions (14.5 h-light, 30℃/9.5 h-dark, 24℃) were detached and incubated on 3 mM MES (pH 5.8) buffer with the abaxial side up at 30℃ in darkness. (E–F) The changes in leaf color (E) and total chlorophyll content (F) of the leaf discs from the WT and *osmyb102* mutant during ABA-induced leaf senescence. The leaves of one-month-old WT and *osmyb102* mutants grown under long-day conditions (14.5 h-light, 30℃/9.5 h-dark, 24℃) were detached and incubated on 3 mM MES (pH 5.8) buffer containing 100 μM ABA with the abaxial side up at 30℃ in continuous light conditions. (D, F) The mean and SD values are shown as values and error bars, respectively ($n$ = 4). Student's $t$-test was performed for statistical analysis (*$P$< 0.05, **$P$< 0.01).



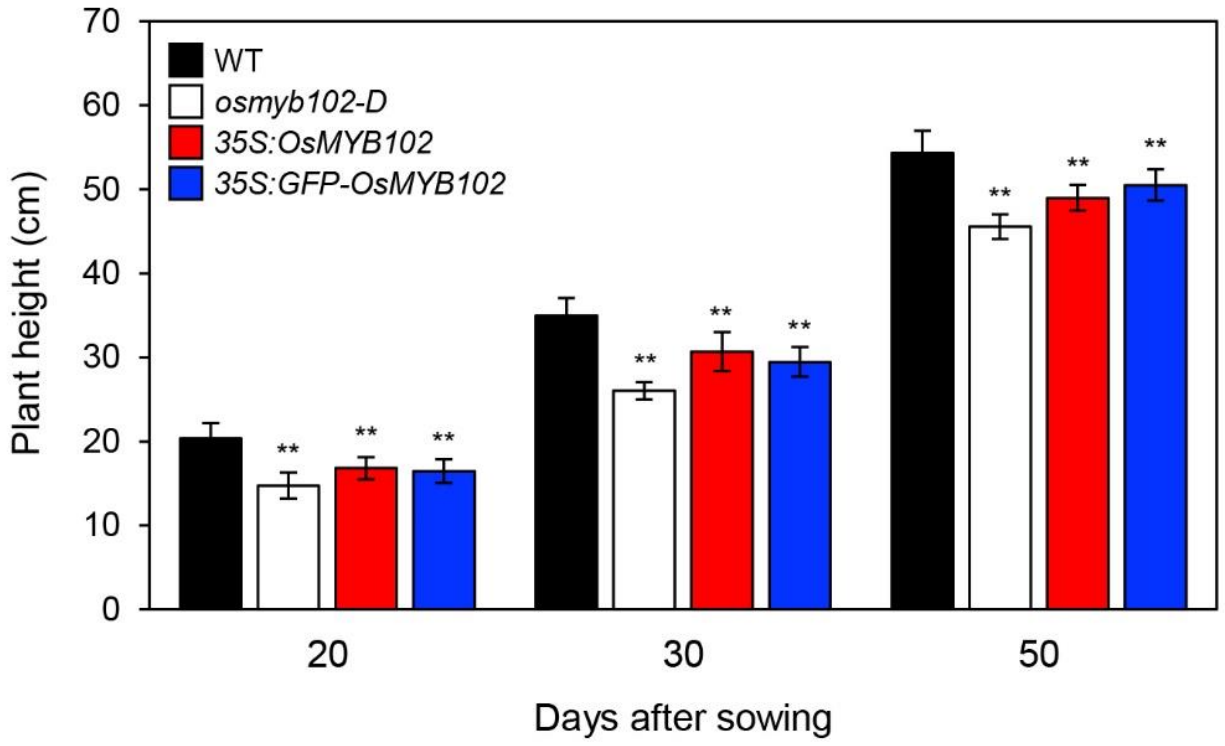

**Supplementary Fig. S2.** Phytohormone biosynthesis and signaling genes were differentially expressed in *osmyb102-D* leaf discs during DIS. The ratios of expression levels (*osmyb102-D*/WT) for known or putative phytohormone-associated genes at 0 and 4 DDI are illustrated. The information on these genes was obtained from Oryzabase (http://shigen.nig.ac.jp/rice/oryzabase/). One-month-old plants grown in the growth chamber under LD (14.5 h light/day) conditions were used. DDI, day(s) of dark incubation.




**Supplementary Fig. S3.** *OsCYP707A6* transcript levels decreased during natural and dark-induced leaf senescence. (A, B) The relative transcript levels of *OsCYP707A6* in the total RNA samples of Fig. 1A (A) or Fig. 1B (B) were determined by RT-qPCR and normalized to the transcript levels of *UBQ5*. The mean and SD values were obtained from more than three biological samples. DDI, day(s) of dark incubation.




**Supplementary Fig. S4.** OsMYB102 does not bind to the promoters of *OsSGR* or *OsNYC1*. (A) The positions of the AACXG sequence in the promoters of *OsSGR* and *OsNYC1*, and the promoter fragments used for the ChIP assay (green horizontal lines). (B) The OsMYB102 binding affinity to the promoter region of *OsSGR* and *OsNYC1 in planta* examined by ChIP assays. OsMYB102-MYC was transiently expressed in protoplasts isolated from 10-d-old WT seedlings. Fold enrichment of the promoter fragments was measured by immunoprecipitation with an anti-MYC antibody (see Methods). *PP2A* was used as a negative control, and *OsCYP707A6* was used as a positive control. The mean and SD values were obtained from more than three biological replicates. Asterisks indicate a significant difference compared to the negative control (Student's *t*-test, **P* < 0.05, ***P* < 0.01).




**Supplementary Fig. S5.** Overexpression of *OsMYB102* decreases plant height. Plant height of WT (DJ cultivar, black bars), *osmyb102-D* (white bars), *35S:OsMYB102* (red bars), and *35S:GFP-OsMYB102* (blue bars) plants at 20, 30, and 50 days after sowing. The mean and SD values were obtained from more than six plants. Asterisks indicate a significant difference compared to the WT (Student's *t*-test, $^{**}P < 0.01$).

**Supplementary Table S1.** Primers used in this study.

| | Forward primer (5'→3') | **Reverse primer (3'→5')** |
|---|---|---|
| A. Cloning for generating *OsMYB102* overexpressor | | |
| *OsMYB102* | ATGGGAGGAGGAGGAGGAGTTGAGG | TCAGTGCATCCTCCCGACGCGCTC |
| B. Genotyping the *osmyb102* knockout mutant generated by CRISPR/Cas9 | | |
| *OsMYB102* | CACCACCACCACTCGCGAACTA | TGGTTCTTCACGGCGTTGTCGG |
| C. Y1H assay | | |
| OsMYB102 | GAATTCATGGGAGGAGGAGGAGGAGTTGAG | CTCGAGTCAGTGCATCCTCCCGACGCGC |
| proOsCYP707A6 | GTCGAC GGTACAAACTACTGAAACT | CTCGAGCCTTAAATTAGCTCTCAAGAATC |
| D. ChIP assay | | |
| proOsCYP707A6-a | AAAACACTTCTATTGCAAAAATCTTGCAGAT | AAGGTGTCCACTGTTCAGTTAATTCAAC |
| proOsCYP707A6-b | GTTGAATTAACTGAACAGTGGACACC | GCTCTCAAAATTAGTTCTGGGCTAATC |
| proOsCYP707A6-c | GAGAGTAATATTTAGTAATGAATTGGTAGGCTAA | ATGGACGGCATGATGCTCATTAGAAA |
| proOsCYP707A6-d | GAGCATCATGCCGTCCATGAG | GTGTGTGTCTCCTTGTCCAAACAACT |
| proOsNAP-a | GGAAACGTCTCATTCAGTATTAGGTTC | GGGCATTTTGGAAGTGTCAAGAATG |
| proOsNAP-b | CATTCTTGACACTTCCAAAATGCCCTTA | GGTTACAGTGAACAGGAACACAGTTG |
| proOsNAP-c | CTGTGTTCCTGTTCACTGTAACCAAACTTC | GTGGGTTTGGTCCGTTATCCCT |
| proOsNAP-d | AAGCGCCGGAAACCACAGAAAA | GGCAGTCACCCACACACAACA |
| proOsABF4-a | TTTTGGTACAACTTGGTTCTCCAATCAC | CCCAACTATTATTGTTCAGGCTACACAA |
| proOsABF4-b | GTGTAGCCTGAACAATAATAGTTGGGG | CTTATGAAAATCAGGTGAGATTCATGT |
| proOsABF4-c | CATGAATCTCACCTGATTTTCATAAGAATTG | GGCTTCCGGACAAAAATATCGT |
| proOsABF4-d | TTTTTGTCCGGAAGCCGCC | CTTGCAACGCACCACGC |
| proOsSGR-a | CGTTCATCCTGTTTGGTCACGTG | CGTTCCAAACACGATTCCAACTTC |
| proOsSGR-b | CCAACGATCACTCTGAAGTTTGATCCA | CGTACCACACACCTACTTATCTGTAAC |
| proOsSGR-c | GTAACAGATAAGTAGGTGTGTGGTACG | TGGAGTGAGGGGTCGGGAAA |
| proOsSGR-d | ACCACGCGTGCACACCAA | GTCTGCTCCCTCGGATCTCTTA |
| proOsNYC1-a | CTGATGCATGCATCGAGAAATTCTACT | TGACCCGGACGGGTCA |
| proOsNYC1-b | GCTCAGTTGCGTGTGCGTG | CTCCTCTCTCTGCCTCCC |

| | | |
|---|---|---|
| proOsNYC1-c | GGCGACCCCAAAAAGCTAAAG | CACACTTAAAGTACTATGAGTGATAAAAC |
| proOsNYC1-d | GACGAATGGTCAAATATGTGTAG | TCGCCGCGAGCGGATAA |
| E. RT-qPCR analysis | | |
| *OsMYB102* | GGTTCGGGCAGATTTTCCGG | GAGAGCGAGGTGAAGGGATC |
| *OsABA2* | GTTGGTGGTGAAGCAAACCT | GTAAAGCCACCATCCACCAT |
| *OsABA3* | TGAGATGCTCAAGCTCCAAGT | GCCGACTATTGAGGTCAGAGA |
| *OsABF1* | GCATGATCAAGAACCGTGAGT | GAACCGTCTTCTCTGCCTCTT |
| *OsABF4* | CGAAGCTGAACTGAACTATC | CTGGCTGCCACCCCTATTTG |
| *OsNAP* | AACCATTTCATCGCGAACAAC | CAGTGACGATCCCTGCAAGG |
| *OsSGR* | GGAGTGGAAGAAGGTGCAG | CCTTGCGGAAGATGTAGTAG |
| *OsNYC1* | GAATCCGTAATTGGGCTGAA | CTGGAAGAGGTCCACCTGAG |
| *OsEIN3* | ATCTTCCCGGCAACCTACAA | CATGATCGTGGCATTGTCGT |
| *OsLhcb1* | CCATGTTCTCCATGTTCGGCTTCT | TAGGCCCAGGCGTTGTTGTTGA |
| *OsLhcb3* | TACCTGCAGTTCGAGCTGGAC | AGGCCGAACACCTCGGTGTA |
| *OsLhca1* | GGCCGACCCTTACACTCTCT | TCTCGAGGCCGAGGAAGTA |
| *UBQ5* | ACCACTTCGACCGCCACTACT | ACGCCTAAGCCTGCTGGTT |