

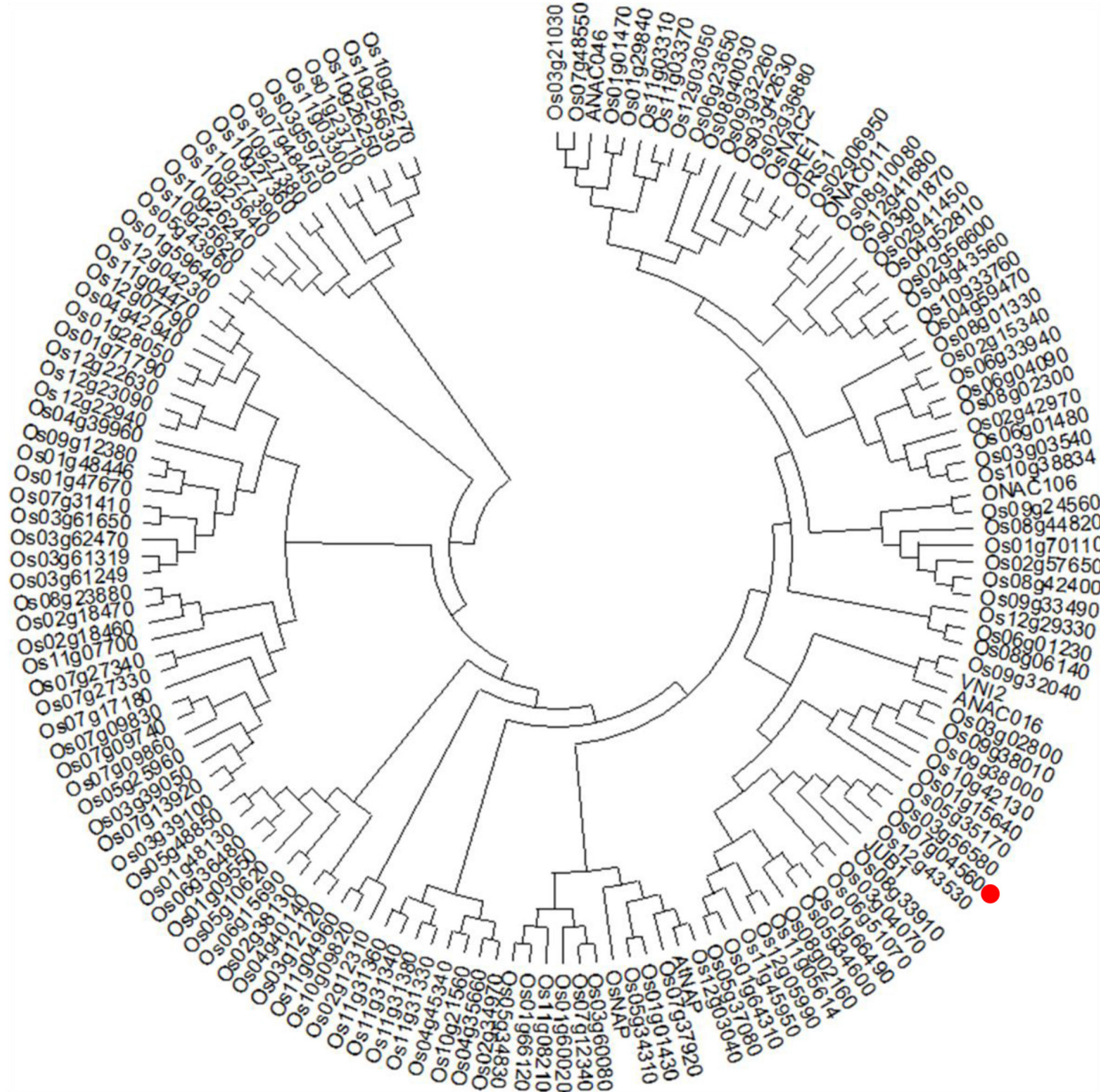


Figure S1. Phylogenetic analysis of *Arabidopsis* NAC and rice NAC protein sequences. The unrooted tree was generated using the ClustalX program with the neighbor-joining method. Bootstrap values from 1000 replicates are indicated at each node. The locus ID and names of *Arabidopsis* and rice NAC proteins were derived from the Rice Genome Annotation Project (<http://rice.plantbiology.msu.edu/index.shtml>) and various reports (OsNAP, Liang et al. 2014; ONAC106, Sakuraba et al. 2015; OsNAC2, Mao et al. 2017; ONAC011, El Mannai et al. 2017; Oresara1 (ORE1), Kim et al. 2009; Oresara1 sister1 (ORS1), Balazadeh et al. 2011; Jungbrunnen1 (JUB1), Wu et al. 2012; *Arabidopsis* NAC-like, activated by apetala3/pistillata (AtNAP), Guo et al. 2006; Vascular-related NAC-domain interacting (VNI2), Yang et al. 2011; ANAC016, Kim et al. 2013; ANAC046, Oda-Yamanizo et al. 2016). The red circle indicates ONAC096.

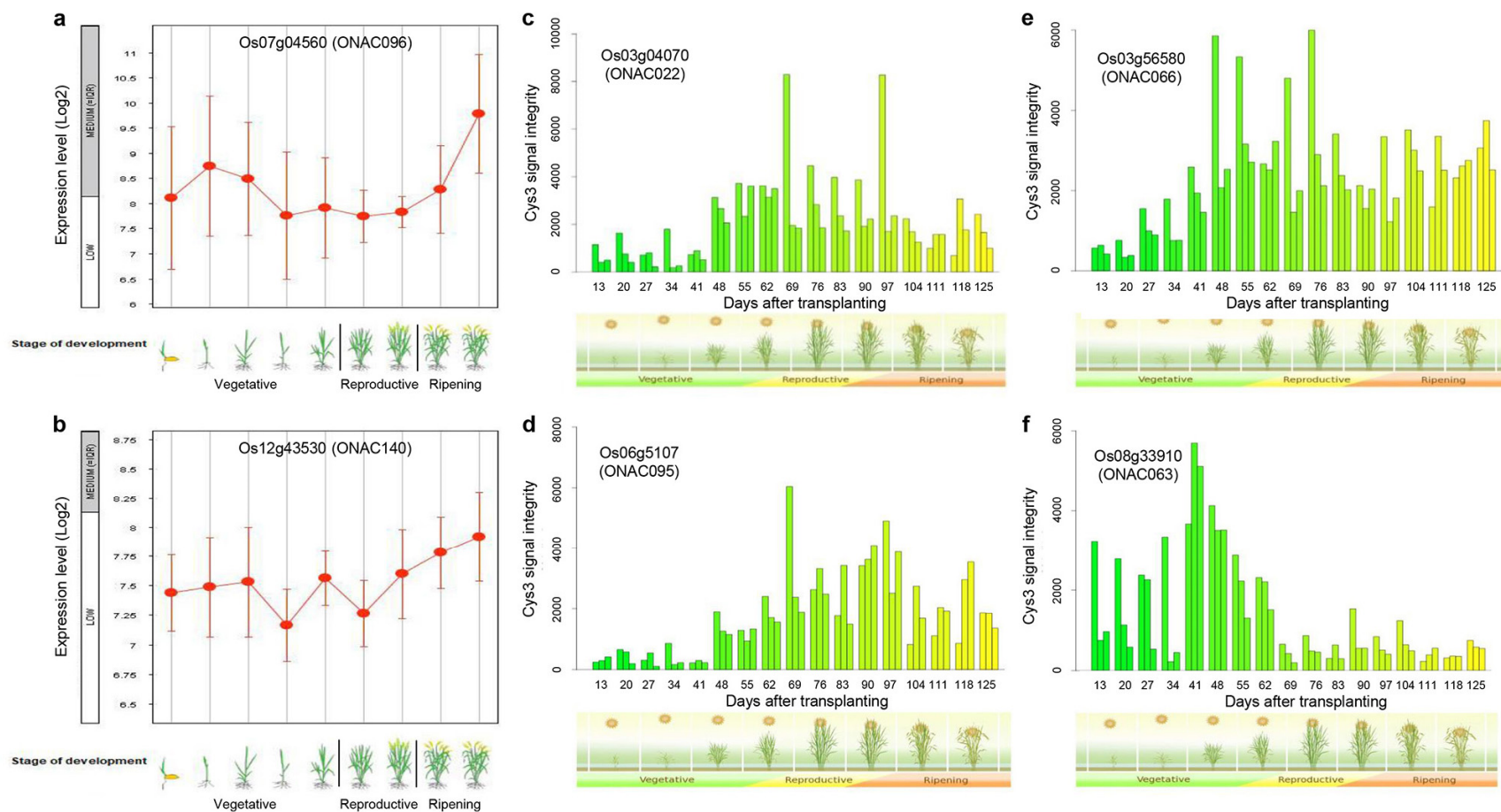


Figure S2. Expression profiles of rice NAC TFs throughout the growth period in the field. The data were obtained from GENEVESTIGATOR (<https://genevestigator.com/gv/>) (**a,b**) and RiceXPro (<http://ricexpro.dna.affrc.go.jp/>) (**c-f**).

ONAC096 1 -----MKR--GCEDELG-AGDV--ILRGVEEVEEEDDDDLVLPGRFRHPTDEELVT
 Arabidopsis thaliana 1 -----M-----SGEGNLGKDHEEENEAPLPGFRFHPTDEELLG
 Brachypodium distachyon 1 MVTYKEERDQNSIAMEKVKN-NGEV-----VLGEEDDAALPGYRFHPTDEELVT
 Sorghum bicolor 1 -----MAKEIVMAGEHG-EGE-----EVVLVEDEEEEDMLPGFRFHPTDEELVT
 Populus trichocarpa 1 -----MVEKIINMNSQDHL-RSTNY--KDDDDDEEVQLPGFRFHPTDEELVG
 Glycine max 1 -----MGVNEDFNQDIDYDHHEYVDDDDVPLPGFRFHPTDEELVS
 Solanum lycopersicum 1 -----MENTIV-----CESKIKNSDDDEENDLLPGFRFHPTDEELVG
 Gossypium hirsutum 1 -----MYLKVVKEIVRR-----IEMEVMEKMISEDEDVLPGFRFHPTDEELVG

ONAC096 47 FYLRRKIAEKRLSIELIKEMDIYKHDPDFLKTSTV--GSEKEWYFFCLRGRKYRNSIRP
 Arabidopsis thaliana 34 FYLRRKVENKTIKLELIKQIDYKYDPWDLERVSSV--GEKEWYFFCMRGRKYRNSVRP
 Brachypodium distachyon 50 FYLRRKVARKPLSIEVIREMDIYKHDPWDLPKASTV--GGEKEWYFFCLRGRKYRNSIRP
 Sorghum bicolor 45 FYLRRKVAGKRLSIELIKDFDIYKHDPWDLPKSSSI--LGEKEWYFFCLRGRKYRNSIRP
 Populus trichocarpa 45 FYLRRMVDKKPLRIELIKQVEIYKYDPWDLPKSSCV--GDKEGYFFCKRGRKYRNSIRP
 Glycine max 41 FYLQRLDKKPISIELIKQIDYKYDPWDLPKTSAT--GGEKEGYFFCRRGRKYRNSIRP
 Solanum lycopersicum 39 FYLKRKVENKRIKLDIKEVDIYKHDPWDLPMGRV--GDNKEWYFFSMRGRKYKNSVRP
 Gossypium hirsutum 45 FYLRRKVEKKLFSIDIKHVDIYKHDPWDLPKVSKLSSCTEKEWYFFCRRGRKYRNSIRP

ONAC096 105 NRVTGSGFWKATGIDRPICSAAGGGGDCIGLKKS LVYYRGSAGKGTCTDWMMEHFRLLP
 Arabidopsis thaliana 91 NRVTGSGFWKATGIDKPVYSN----LDCVGLKKS LVYYLGSAGKGTCTDWMMEHFRLLP
 Brachypodium distachyon 108 NRVTGSGFWKATGIDRPIYSAAAASSGESIGLKKS LVYYRGSAGKGTCTDWMMEHFRLLP
 Sorghum bicolor 103 NRVTGSGFWKATGIDRPIHSAASGRAGDPIGLKKS LVYYRGSAGKGTCTEWMMEHFRLLP
 Populus trichocarpa 102 NRVTGSGFWKATGIDKVEFSL--GGEGRDSIGLKKT LVYYRGSAGKGTCTDWMMEHFRLLP
 Glycine max 99 NRVTGSGFWKATGIDKPVYSH--GGEGRNDCIGLKKT LVYYRGSAGKGTCTDWMMEHFRLLP
 Solanum lycopersicum 97 NRVTGSGFWKATGIDKPVHSQ--SN--ELCIGLKKS LVYYRGSAGKGTCTDWMMEHFRLLP
 Gossypium hirsutum 105 NRVTGSGFWKATGIDKPIYSV--GGF--HDCIGLKKS LVYYKGSAGKGTCTDWMMEHFRLLP

ONAC096 165 PPADDLAAGRSS--PPPSLQEA EVWTLCRIFQRNITHKKQPQ-PQLAVAA-----AA
 Arabidopsis thaliana 146 TTKTD-----SPAQQA EVWTLCRIFKRVTSQRNPTILPNRKPV-----
 Brachypodium distachyon 168 AAA-----AN--ASPSMQEA EVWTLCRIFRRNITYRKQQT-WRPPPA-----AV
 Sorghum bicolor 163 RAES-----AH--TSPSEQEA EVWTLCRIFRRNFTYKHPQ-QQIAGSSKVSAAATAA
 Populus trichocarpa 161 KDNSTSTATV--KAKISDQEA EVWTLCRIFKRNVSCKRYTPDLKQLSTT-----
 Glycine max 158 NTDNNNTNLRSSKNYVDVPQEAELWTLCRIFKRNVSORKHTPDLKQISAK-----
 Solanum lycopersicum 154 IWKTNTSNGQHLPNLNIAAEAEVWTLCRIFKRISNYKRFTPDWKQQQPV-----
 Gossypium hirsutum 163 PSTTTLSST-----NKDNLPEAEVWTLCRIFKRDVSSRKFFASDWQNKKNK-----

ONAC096 214 VPAPVPDATSSITGSLES DSAG-DD-VVEYM-----NTLQPP-PASNVNGGY-----S
 Arabidopsis thaliana 185 -I-----TLTDTC SKTSSLSDSHRTVD-----SMSHEPPLPQP--QNPYWNQHI--
 Brachypodium distachyon 210 STAVAADSSNTAGSFESSDGGGDD-YMAQA-----ATTGPPCIIPHVQQHGNLQ LGA
 Sorghum bicolor 214 VVTQTQGESSSVTGSLES DTGD-E-----YT-----NDLPQPTQAPAIVDGY-----D
 Populus trichocarpa 208 -PQQPPIDTSSKLCQVESNYTQES-YVNF GAPLIQHYDNKPPVH-----HVKE
 Glycine max 208 -RQSI-HDKSSRMSNVFENTTNQES-YINFGGHYHNEQ--KPTINYT-----NSDQ
 Solanum lycopersicum 204 -VKQSFVDTSSKACSVQSEISDDQSNVI-N-----FKKM-----ABF--QKSIMNASCGG
 Gossypium hirsutum 208 -QNTNTSAS SRACSVES ENSLKVENFGVLD-----DKGIE-----RKLQNDHF--

ONAC096 259 NQR-----YFQE QWNSSSNDNTTVFHQHA AAAAPPEPSEATAMAGFGHDQSVLSSPA---
 Arabidopsis thaliana 229 -----VGFNQPTY-T-----GNDNNL-----LMSFWNG--NG
 Brachypodium distachyon 263 TNGGFFSQFQGWSSVPPPTLPLDQKPL-----NEASAPIAFHLNDHSLA-----
 Sorghum bicolor 256 YDYG YGDQQQGWNSHA-----LHAAATAPLSPTMAAFHH--SVLSSPAAGG
 Populus trichocarpa 255 -----RKPLHVDQL-----SYVAQPPSM-----ASSLNI--SS
 Glycine max 254 -----RNQYHVMTHQLCA---PVAQQH-----QQPQQLTSP-----SSNFWI--NN
 Solanum lycopersicum 251 -----NLNYQVDQRNSYYNNSQLITTMP-----DQ--SEFTSS-----NSIFWNT--RA
 Gossypium hirsutum 251 -----LGGNQLFAAT-----TQVLPS-----YLSFSNP--NA--

ONAC096 311 -PSDFYK DGC--NDDIYRM MELADPSLFYDHIYA-----
 Arabidopsis thaliana 253 --GDFIGDS--ASWDELRSVIDGNTKP-----
 Brachypodium distachyon 310 AASDLYKVDGY--LEEIAR-MMEVTDPHPAAIYDYRYA---
 Sorghum bicolor 303 GLDDMYKDGSSSWDDIGRMV MELTDPSPGVFSFYDTRS YV
 Populus trichocarpa 281 PYGNQILTH--GDWDELTSVVDCAFD PFLV-----
 Glycine max 291 PPGNDFFTF--DNWDELGSLVKFAVDSPSL-----
 Solanum lycopersicum 291 EDQEYLF SH--GNWDELKSVVDLAIDPRS LFGFK-----
 Gossypium hirsutum 276 --ADEYFGQ--EHWDELRPVVDYTI AKSLQYS DW-----

Figure S3. Amino acid sequence alignment of ONAC096 proteins. The amino acid sequences of ONAC096 from rice and other plant species homologous to ONAC096 were obtained from NCBI through BLAST analysis. Sequence alignment was performed using ClustalW with default parameters. The sequences are as follows: *Arabidopsis*, XP_015646514, *Brachypodium distachyon*, XP_003559373; *Sorghum bicolor*, XP_002459331; *Populus trichocarpa*, XP_024461145; *Glycine max*, NP_001241333; *Solanum lycopersicum*, XP_004243883; *Gossypium hirsutum*, XP_016753414. The black bars represent the conserved NAM domains of NAC proteins.

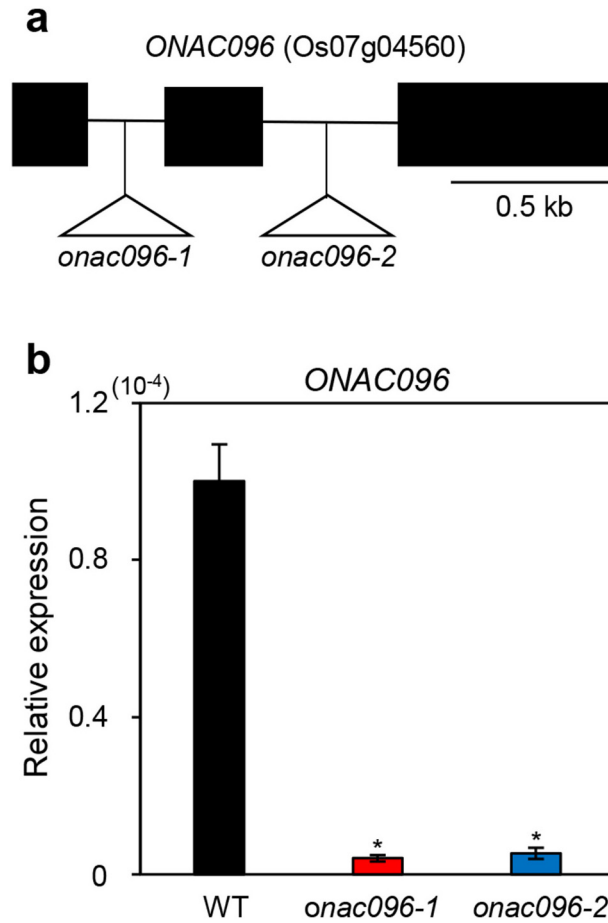


Figure S4. T-DNA insertion *onac096* mutants. **(a)** Schematic diagram of the positions of the T-DNA insertion in two independent *onac096* mutants. The black boxes and lines represent exons and introns, respectively. The white triangles indicate the positions of T-DNA insertions (*n096-1*, PFG_1B-02928 and *n096-2*, PFG_3A-08770). **(b)** *ONAC096* expression in wild-type (WT) and *onac096* plants. Total RNA was isolated from the leaves of 3-week-old plants grown in paddy soil under long-day conditions. *ONAC096* transcript levels were measured by RT-qPCR and normalized to that of *OsUBQ5*. Relative expression was calculated using the $\Delta\Delta C_T$ method. Asterisks indicate statistically significant differences between *onac096* and the WT, as determined by Student's *t*-test (* $p < 0.05$). The experiments were repeated twice with similar results.

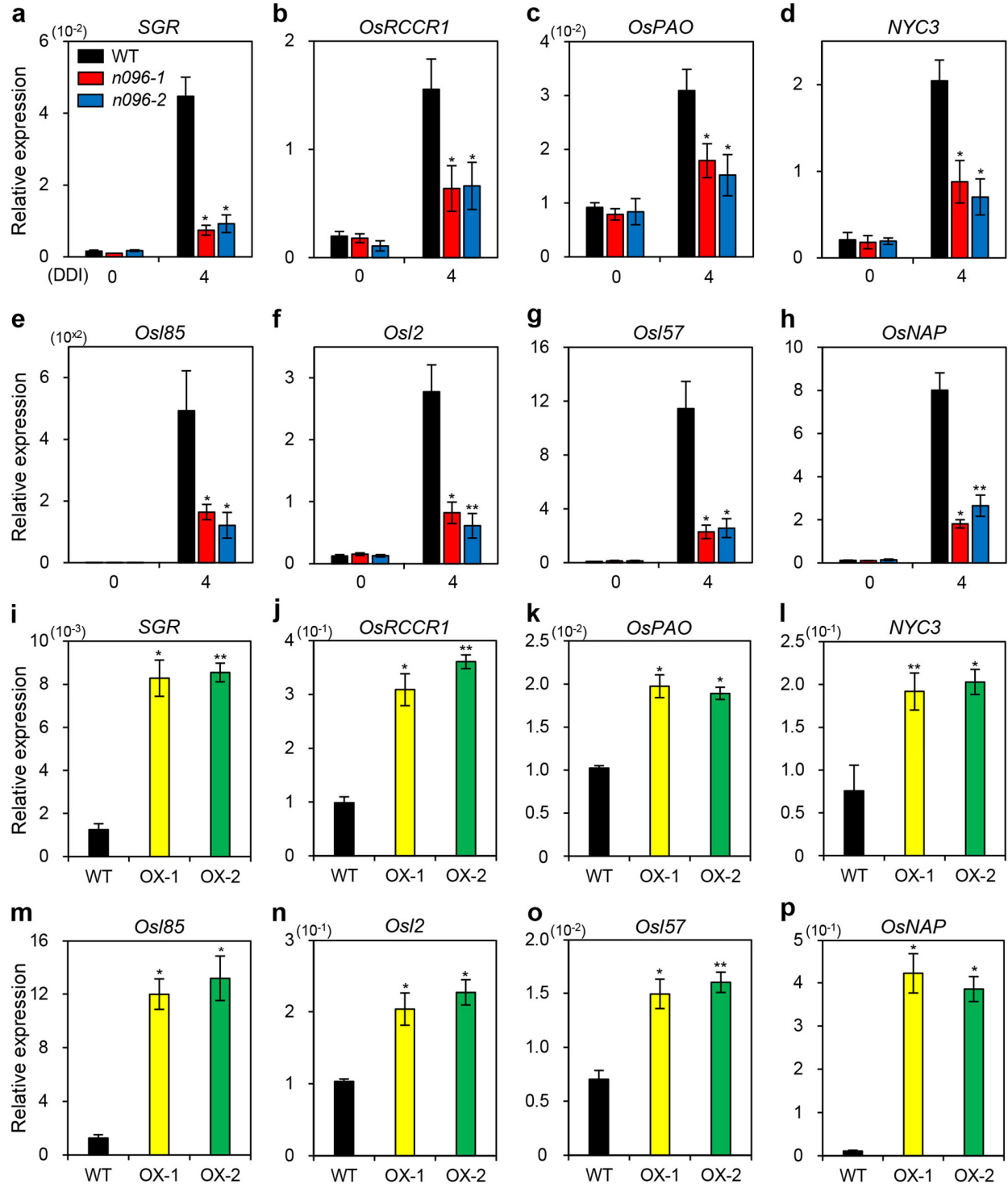


Figure S5. Altered expression of CDGs and SAGs in *onac096* and *ONAC096*-OX plants. Total RNA was isolated from the detached leaves of 3-week-old WT and *onac096* plants (*n096-1* and *n096-2*) incubated in 3 mM MES buffer (pH 5.8) in complete darkness at 28 °C (a-h) under long-day conditions (14.5 h light per day) or the attached leaves of WT and *ONAC096*-OX plants (OX-1 and OX-2) grown in paddy soil, for 3 weeks under NLD conditions (i-p). The transcript levels of chlorophyll degradation genes (CDGs; a-d, i-l) and senescence-associated genes (SAGs; e-h, m-p) were measured by RT-qPCR and normalized to that of

OsUBQ5. Relative expression was calculated using the $\Delta\Delta\text{CT}$ method. Mean and standard deviations were obtained from three biological repeats. Asterisks indicate statistically significant differences between *onac096* mutants and *ONAC096-OX* compared to the WT according to Student's *t*-test (* $p < 0.05$ and ** $p < 0.01$). The experiments were repeated twice with similar results. DDI, day(s) of dark incubation.

Table S1. Primers used in this study.

A. Primers for verification of T-DNA insertion		
Primer names	Left primers (5' → 3')	Right primers (5' → 3')
PFG_1B-02928	CATTAAAGCTGGACCAGATGG	AACCACTTGCGGATTAATGC
PFG_3A-08770	TTGGATGCCTGATTAAGGTTG	CCGTTCTTGACATTACAC
pGA2715	CTAGAGTCGAGAATTCAGTACA	TTGGGGTTTCTACAGGACGTAAC
B. Primers for RT-qPCR		
Genes	Forward primers (5' → 3')	Reverse primers (5' → 3')
<i>ONAC096</i>	CAAGCATGATCCCTCCGACT	TCCCTCGAAGGCAGAAGAAG
<i>SGR</i>	AGGGGTGGTACAACAAGCTG	GCTCCTTGCGGAAGATGTAG
<i>NYC3</i>	TGTCGTTGCCATGTGAAGAT	TTGGTCACGCCACAAATCTA
<i>OsPAO</i>	GGAAATCCTAGCCAAGAAGTGTT G	CGCAGGAATCCCAGCAGTT
<i>OsRCCR1</i>	CGCATTTCTCATGGAATTT	CTTCTCACGCTGTTTGTCCA
<i>OsI2</i>	CGCAGACAACAAATCGCCAA	CTCCAGCAACTCTAACCAGCA
<i>OsI85</i>	GAGCAACGGCGTGAGAGA	GCGGCGGTAGAGGAGATG
<i>OsI57</i>	ACCCTAAAGTAAATGAAGTC	CCTGCTCTTGTCTTGTTA
<i>OsNAP</i>	CAAGAAGCCGAACGGTTC	GTTAGAGTGGAGCAGCAT
<i>OsCKX2</i>	CCGGGATAGCCTACAAGCAG	CCAGAGATTGGCACCGAAGT
<i>OsPIN2</i>	GAGGTACGACTTCCATGGGC	TTGAGGTACGGCTTGACAC
<i>OsTB1</i>	CCCAGCTTGAAGCTTTTGCT	ACAACACTGCAACTATCCCTATCA CT
<i>OsPIN5b</i>	GGGCTTCATGCCGATGTACT	TAGACAAAGCCCAGAACCGC
<i>OsTIR</i>	TCCAGGTGCTCCGCCTCGTCTCCT	CCGGGAAGAGGCTGAGCCAATGA A
<i>OsABI5</i>	CGAAGCTGAACTGAACTATC	CTGGCTGCCACCCCTATTTG
<i>OsEEL</i>	GCAGAAGCGCATGATCAAGA	GACGCAGCTAGGGAATGTTG
<i>OsUBQ5</i>	ACCACTTCGACCGCCACTACT	ACGCCTAAGCCTGCTGGTT
C. Primers for plant transformation		
Primer names	Forward primers (5' → 3')	Reverse primers (5' → 3')
ONAC096	ATGAAGAGGGGTTGTGAAGATG A	TTAAGCATATATATGATCATAGAA C
35S promoter	CTATCCTTCGCAAGACCCTTC	