



Supplemental Figure 1: Cell Death Phenotypes of the *oscul3a* Mutant under Field Conditions. The top three leaves were collected from ZH11 and *oscul3a* and photographed at 60 dps.

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gDNA-OsCUL3a : ATGAGCGGGGGCGGGCCGCGAAGAAACGCAACTTCAAGATCGAGCTGTTC AAGCACCGCGTGGAGCTCGACCCCAAGTACGCGGAGCGGACATGGAAGGTCCTGGAGCAGCCATCCAC : 120
gDNA-oscul3a : ATGAGCGGGGGCGGGCCGCGAAGAAACGCAACTTCAAGATCGAGCTGTTC AAGCACCGCGTGGAGCTCGACCCCAAGTACGCGGAGCGGACATGGAAGGTCCTGGAGCAGCCATCCAC : 120
cDNA-OsCUL3a : ATGAGCGGGGGCGGGCCGCGAAGAAACGCAACTTCAAGATCGAGCTGTTC AAGCACCGCGTGGAGCTCGACCCCAAGTACGCGGAGCGGACATGGAAGGTCCTGGAGCAGCCATCCAC : 120
cDNA-oscul3a : ATGAGCGGGGGCGGGCCGCGAAGAAACGCAACTTCAAGATCGAGCTGTTC AAGCACCGCGTGGAGCTCGACCCCAAGTACGCGGAGCGGACATGGAAGGTCCTGGAGCAGCCATCCAC : 120

gDNA-OsCUL3a : GAGATCTACAACCACAACGCCAGTGGCCTCTCCTTCGAGGAGCTCTACAGTTGGTACAACCCCGGAGGCCCGCACTCCCATGATCCTCCGCTCCTGCCGTCGCGCTCGCGTTTCC : 240
gDNA-oscul3a : GAGATCTACAACCACAACGCCAGTGGCCTCTCCTTCGAGGAGCTCTACAGTTGGTACAACCCCGGAGGCCCGCACTCCCATGATCCTCCGCTCCTGCCGTCGCGCTCGCGTTTCC : 240
cDNA-OsCUL3a : GAGATCTACAACCACAACGCCAGTGGCCTCTCCTTCGAGGAGCTCTACAGTTGGTACAACCCCGGAGGCCCGCACTCCCATGATCCTCCGCTCCTGCCGTCGCGCTCGCGTTTCC : 171
cDNA-oscul3a : GAGATCTACAACCACAACGCCAGTGGCCTCTCCTTCGAGGAGCTCTACAGTTGGTACAACCCCGGAGGCCCGCACTCCCATGATCCTCCGCTCCTGCCGTCGCGCTCGCGTTTCC : 170

gDNA-OsCUL3a : CGCTTGGCGACCTAGATCCTACCGCCCCGGCCCTAACATGTGGTTAATTAGAAAAATTCAGTGTGCCAATTCCTAATAAGTTTGTCTCCTCTTGAGATGATTAATGATTATGATTAAGTAC : 360
gDNA-oscul3a : CGCTTGGCGACCTAGATCCTACCGCCCCGGCCCTAACATGTGGTTAATTAGAAAAATTCAGTGTGCCAATTCCTAATAAGTTTGTCTCCTCTTGAGATGATTAATGATTATGATTAAGTAC : 360
cDNA-OsCUL3a : ----- : -
cDNA-oscul3a : ----- : -

gDNA-OsCUL3a : GAACATTCCTGTCCGATATGTTGATGGTTGAAAGTGATTTCTTCGAGAGAATTCCTTTTAGTATTTGTGATCCTACAATTTTCGTTAAAAATACAGAATTTTATAGTCAACGATCAG : 480
gDNA-oscul3a : GAACATTCCTGTCCGATATGTTGATGGTTGAAAGTGATTTCTTCGAGAGAATTCCTTTTAGTATTTGTGATCCTACAATTTTCGTTAAAAATACAGAATTTTATAGTCAACGATCAG : 480
cDNA-OsCUL3a : ----- : -
cDNA-oscul3a : ----- : -

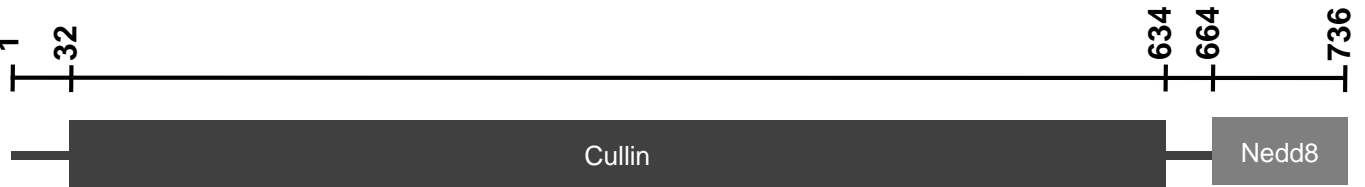
gDNA-OsCUL3a : TATTAGGGAGATTGGCGGATGTTAGGTGTTGGATATTGATGGGTTACTCCATCTAGTCATCTGTAGTATTGACTTAGTTGTTGGAAGCCATGCTTGTCCGCTCCTTTGGTCTGCACAGC : 600
gDNA-oscul3a : TATTAGGGAGATTGGCGGATGTTAGGTGTTGGATATTGATGGGTTACTCCATCTAGTCATCTGTAGTATTGACTTAGTTGTTGGAAGCCATGCTTGTCCGCTCCTTTGGTCTGCACAGC : 600
cDNA-OsCUL3a : ----- : -
cDNA-oscul3a : ----- : -

gDNA-OsCUL3a : AACTTGGTGATAAATAACTATTCTGAACCTCACTTGATTGTAATTTGCAATATTCCTTTCATCTGTGCAGGAGTCCCAAAACATGGTGTCCACAAGTATGGTGAGAAGCTATATGAT : 720
gDNA-oscul3a : AACTTGGTGATAAATAACTATTCTGAACCTCACTTGATTGTAATTTGCAATATTCCTTTCATCTGTGCAGGAGTCCCAAAACATGGTGTCCACAAGTATGGTGAGAAGCTATATGAT : 712
cDNA-OsCUL3a : ----- : 219
cDNA-oscul3a : ----- : 191

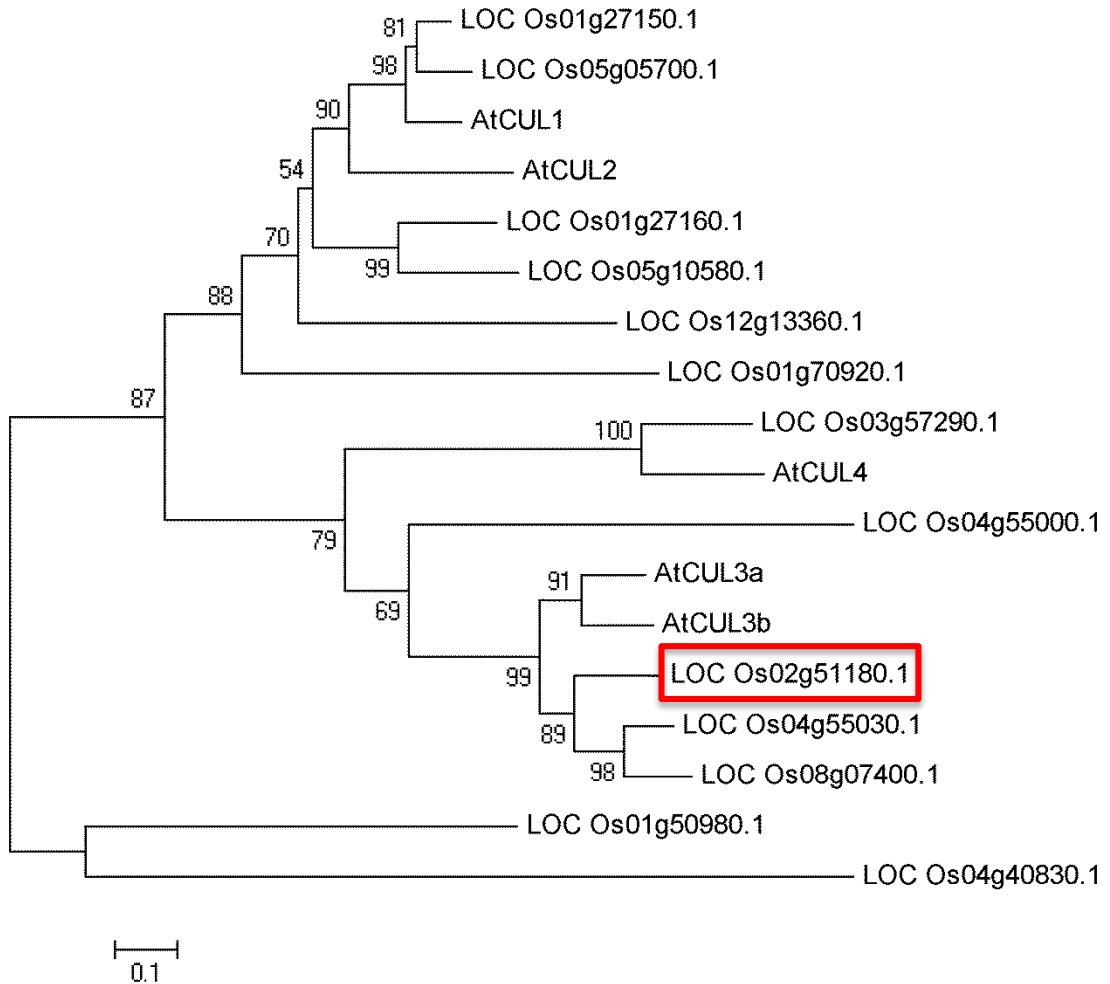
gDNA-OsCUL3a : GGCTGGAGAGAAGTATGACATGGCGCTTGAAGGAAATATCAAAATCAATAGAGGCTGCACAGGGTGGTTTGTCTTTCGGAGGAGCTGAATGCCAAGTGGATGGATCACAAATAAGGCATTG : 840
gDNA-oscul3a : GGCTGGAGAGAAGTATGACATGGCGCTTGAAGGAAATATCAAAATCAATAGAGGCTGCACAGGGTGGTTTGTCTTTCGGAGGAGCTGAATGCCAAGTGGATGGATCACAAATAAGGCATTG : 832
cDNA-OsCUL3a : GGCTGGAGAGAAGTATGACATGGCGCTTGAAGGAAATATCAAAATCAATAGAGGCTGCACAGGGTGGTTTGTCTTTCGGAGGAGCTGAATGCCAAGTGGATGGATCACAAATAAGGCATTG : 339
cDNA-oscul3a : GGCTGGAGAGAAGTATGACATGGCGCTTGAAGGAAATATCAAAATCAATAGAGGCTGCACAGGGTGGTTTGTCTTTCGGAGGAGCTGAATGCCAAGTGGATGGATCACAAATAAGGCATTG : 311

gDNA-OsCUL3a : CAGATGATCCGAGATATTCCTAATGTACATGGATCGAACATATGTCCCGCAATCCCGTAGAACACCTGTTTCATGAGCTTGGTTTGAATTTGTGGAGGGATCACATAATTCCAC : 951
gDNA-oscul3a : CAGATGATCCGAGATATTCCTAATGTACATGGATCGAACATATGTCCCGCAATCCCGTAGAACACCTGTTTCATGAGCTTGGTTTGAATTTGTGGAGGGATCACATAATTCCAC : 943
cDNA-OsCUL3a : CAGATGATCCGAGATATTCCTAATGTACATGGATCGAACATATGTCCCGCAATCCCGTAGAACACCTGTTTCATGAGCTTGGTTTGAATTTGTGGAGGGATCACATAATTCCAC : 450
cDNA-oscul3a : CAGATGATCCGAGATATTCCTAATGTACATGGATCGAACATATGTCCCGCAATCCCGTAGAACACCTGTTTCATGAGCTTGGTTTGAATTTGTGGAGGGATCACATAATTCCAC : 422
    
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Supplemental Figure 2: Sequence Alignments between ZH11 and the *oscul3a* Mutant.
 (A) Genomic DNA and cDNA of OsCUL3a were PCR amplified from ZH11 and *oscul3a* respectively. Sequence comparison was conducted using ClustalW software after sequencing.
 (B) Protein structure of OsCUL3a.



Supplemental Figure 3: Phylogenetic Analysis of CUL Proteins in Arabidopsis and Rice. The phylogenetic tree was generated by MEGA5 software using neighbor joining method. Numbers at nodes indicate bootstrap values. Scale bar indicates 0.1 substitutions.

Supplemental Data. Liu et al. (2017). Plant Cell 10.1105/tpc.16.00650

OsCUL3a : **MSGGGPPKRNFKIELEFKHRVLEDPKVAERLWKVLEHATHEIYNHNASGLSFEELYRSAYNMVLHKYGEKLYDGLERTVTRWLEKETS** : 100
 OsCUL3b : **MN---SOKKRSFKIEPPFRHRVDAADPKSIEDKSWKKLEDAIREIYNHNASGLSFEELYRTAYNLVLHKHGLKLYDKLTENIKGHLKEMCRSIEDAOGSLFLE** : 97
 OsCUL3c : **MS---SRKKPS-RIEFPRHKVETDPRFPEKAWRKLDDAIREIYNHNASGLSFEELYRTAYNLVLHKHGLKLYDKLTENMEDHLQEMRVSTEAAGGLFLV** : 96

OsCUL3a : **ELNAKMDHDKALQMIIRDILMYMDRIVVQSRRTPVHELEGLNLWRDHIITHSEMTIHSRLLDTLLELIHRERMGEMINRGLMRSITKMLMDLGAAYVQDDFE** : 200
 OsCUL3b : **ELQRRMADHDKALQMIIRDILMYMDRITFATNKKTPVFDLGLLEWRDIIVVRTPKIHGRLLDTLLELIHRERMGEMINRGLMRSITKMLMDLGSSVYHDDFE** : 197
 OsCUL3c : **ELQRKMDHDKALQMIIRDILMYMDRVFIFPTNKKTPVFDLGLLEWRDIIVRSPKIHGRLLDTLLELIHRERTGEVINRSGLMRSITKMLMDLGSSVYQDDFE** : 196

OsCUL3a : **KPFLEVSASFYSGESQDFIECCDCGNYLKKSERRLNEMERVSHYLDSGTEAKITSVVPEKEMIANHMHRLVHMENSGLVNMLVDDKMDDLARMYNLFRV** : 300
 OsCUL3b : **KPFLEVSASFYSGESQDFIECCDCGNYLKKAERRLAEELEERSVQYMDAKTADKITSVVDTEMLANHMORLIHMENSGLVNMLVDDKHEDLSRMYNLFRV** : 297
 OsCUL3c : **RPFLEVSASFYSGESQDFIECCSCGEYLKKAQRLEBAERVSQYMDAKTDEKITAIVVVKEMLANHMQRLIMENSGLVNMLVDDKMDLTMVYSLQRV** : 296

OsCUL3a : **FDGISTIRDMVTSVLRTEGKQLVVDPERLKPVEFVQRLNNEKDKHDKITINWAFGNDKIFQNALNSSFBYFINLNNSPEFISLYVDDKLRKGLKGA** : 400
 OsCUL3b : **FDGISTIRDMVTSVLRTEGKQLVVDPEKIKDPVEFVQRLNNEKDKYDDEITISISFNDKIFQNALNSSFBYFINLNNSPEFISLYVDDKLRKGVKGANEE** : 397
 OsCUL3c : **FDGISTIKSVMNSVVKTEGKQVMVMDPERLKPVEFVQRLNNEKDKYDSEIVTISFNDKIFQNALNSSFBYFINLNNSPEFISLYVDDKLRKGMKGANEE** : 396

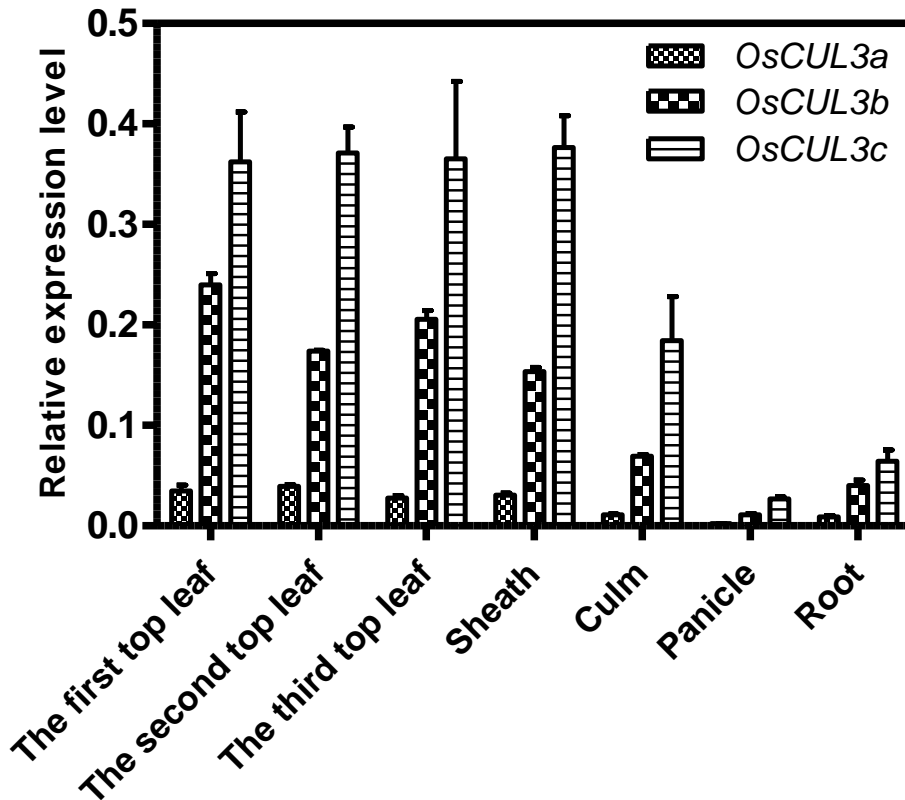
OsCUL3a : **DVEVIVLDKVMMLFRYLQEKDVFEEKYKQHLAKRLLSGKIVSDDAERSMIVKLVKTECGYQFTSKLEGMFIDMKTSQDTVIDFYAKKSEELGCGPTLDVHII** : 500
 OsCUL3b : **DVEVIVLDKVMMLFRYLQEKDVFEEKYKQHLAKRLLSGKIVTSDDAERSMIVKLVKTECGYQFTSKLEGMFIDLKTSHDTMGSFYANLS-GDTSPTISVQIIL** : 496
 OsCUL3c : **DVEVIVLDKVMMLFRYLQEKDVFEEKYKQHLAKRLLSGKIAASDSDAERSMIVKLVKTECGYQFTSKLEGMFIDLKTSHDTMGSFYAGTPT-DLGLDAPTISVQIIL** : 495

OsCUL3a : **TTGSWPTQPCPECNLPEEILATCDNFRFTYYLGTHSGRRLTWQTNMGADIKATFGKCGKHELVNSTYQMCVLMFNSTDGLTYGDIEQDTAIPASDLKRC** : 600
 OsCUL3b : **TTGSWPTQPCPECKLPPEIVDISEKFRAFYLGTHNGRRLTWQTNMGADIKATFG-GRRHELVNSTYQMCVLMFNSTADGLTYGDIEQDTAIPASDLKRC** : 595
 OsCUL3c : **TTGSWPTQPCNTCNLPEEILCVSEMFRGFYLGTHNGRRLTWQTNMGADIKAVFGNCSKHELVNSTYQMCVLMFNSTADCLSYRDIEQDTAIPASDLKRC** : 595

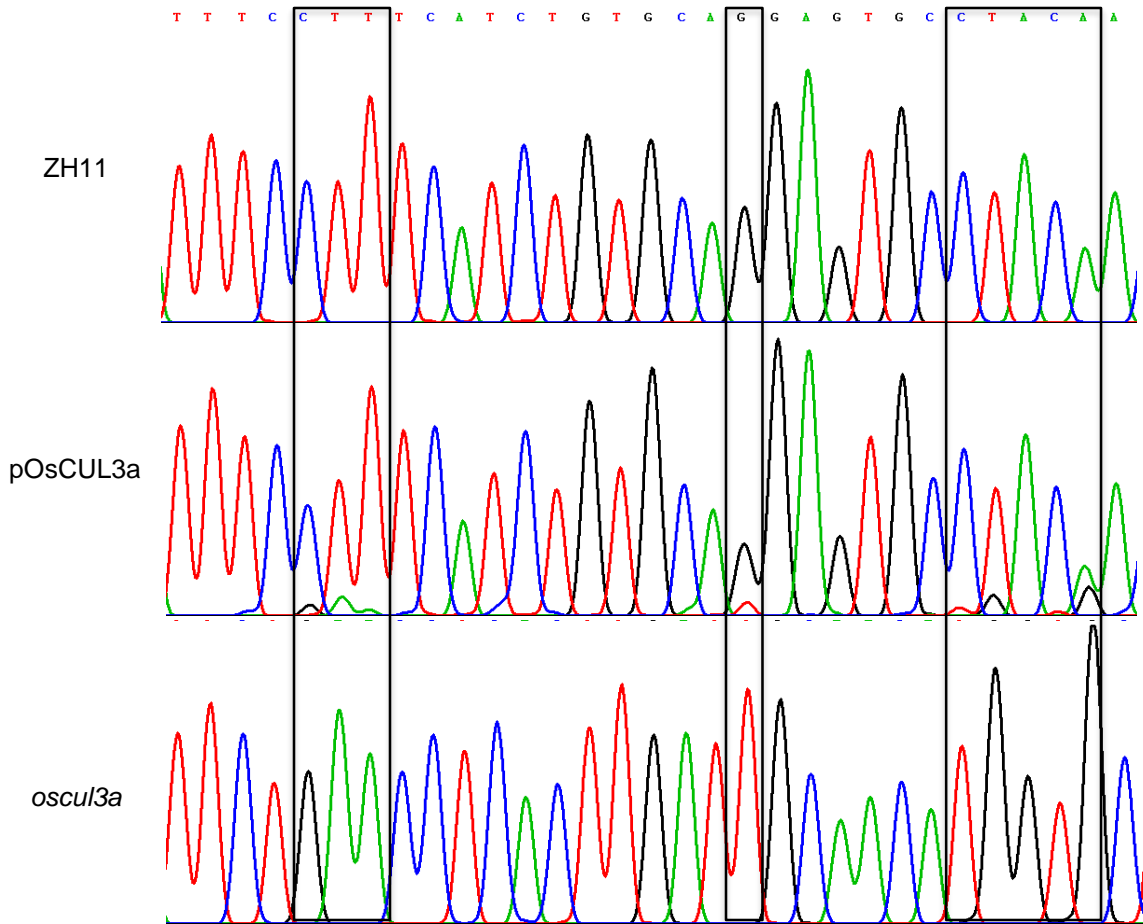
OsCUL3a : **LOS�AVKGNVLRKEPMSKDISDDTFYVNDKFTSKLVKVKIGTVVAQKESEPEKQETRQRVEEDRKPOIEAAIVRIMKSRRVLDHNSIVAEVTKQLQA** : 700
 OsCUL3b : **LOS�AVKGNVLRKEPMSKDISDDTFYVNDKFTSKLVKVKIGTVVAQKESEPEKQETRQRVEEDRKPOIEAAIVRIMKSRRVLDHNSIIEVTKQLQS** : 695
 OsCUL3c : **LOS�AVKGNVLRKEPMSRDISDDNFYVNDKFTSKLVKVKIGTVVATQKESEPEKQETRQRVEEDRKPOIEAAIVRIMKSRRVLDHNSIIEVTKQLQP** : 695

OsCUL3a : **RFMPNPVVIKKRIESLIBREFLERDKADRKLYRYLA** : 736
 OsCUL3b : **RFLPNPVIKKRIESLIBREFLERDKVDRKMYRYLA** : 731
 OsCUL3c : **RFMPNPVVIKKRVESLIBREFLERDKADRKLYRYLA** : 731

Supplemental Figure 4: Protein Alignment of OsCUL3a, OsCUL3b, and OsCUL3c.



Supplemental Figure 5: *OsCUL3a*, *OsCUL3b*, *OsCUL3c* Are Constitutively Expressed in Rice. Different tissues were collected from ZH11 plants at the flowering stage for total RNA isolation. *OsCUL3a/b/c* mRNA level were analyzed by qRT-PCR. Error bars represent the SEM, n=3.



Supplemental Figure 6: Confirmation of the pOsCUL3a Plants by Sequencing. Sequence chromatograms obtained for the region around the mutation site in ZH11, pOsCUL3a and *oscul3a* plants indicated by pane.

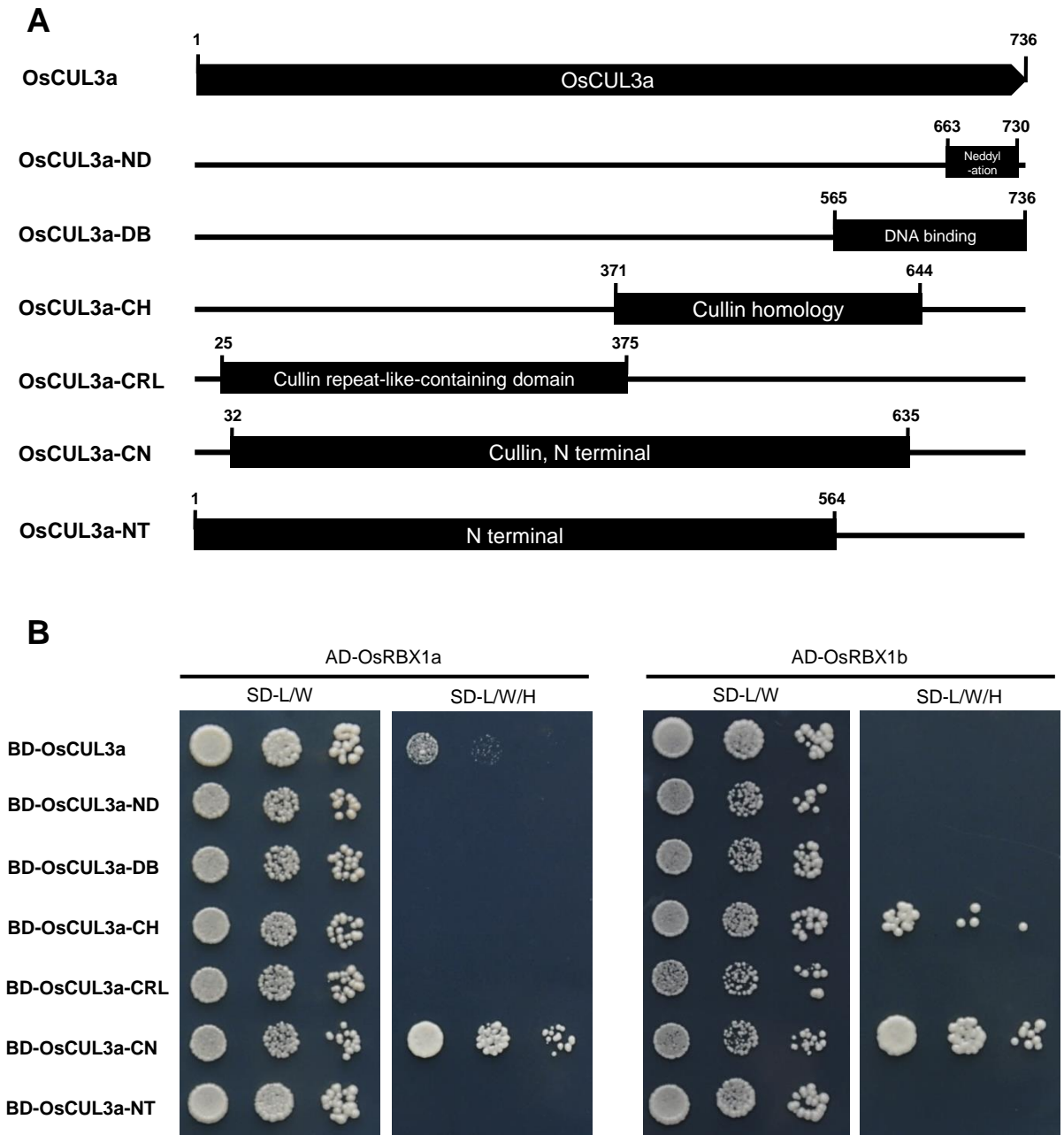


Supplemental Figure 7: Cell Death Phenotype of *oscul3a* is Rescued by OsCUL3a.
(A) ZH11, *oscul3a*, and pOsCUL3a plants were grown in summer field and photographed at the filling stage.
(B) Flag leaves collected from (A).

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AtRBX1 : MATLDSVDVTMIPA-----GEASSSVAASSSNKMAKRFETIKKWSAVLWAWDIVVDNCAICRNHIMDLCTECQ : 67
OsRBX1A : MDKGDVAVAVPP-----SIAGASSSGAKKGRFETIKKWNVSLWAWDIVVDNCAICRNHIMDLCTECQ : 63
OsRBX1B : MSAMETDINAPPPAPAPAGAGEGSSSAAGPSSRKPGRFETIKKWNVSLWAWDIVVDNCAICRNHIMDLCTECQ : 75

AtRBX1 : ANQASATSEECTVAWEDDQNNCNKYFCILDSCMKDDHLEGVCNHAFHFHCISRWLKTRQVCPLDNSEWEFQKYGH : 142
OsRBX1A : ANQASATSEECTVAW-----GVCNHAFHFHCISRWLKTRQVCPLDNSEWEFQKYGH : 114
OsRBX1B : ANQASATSEECTVAW-----GVCNHAFHFHCISRWLKTRQVCPLDNSEWEFQKYGH : 126
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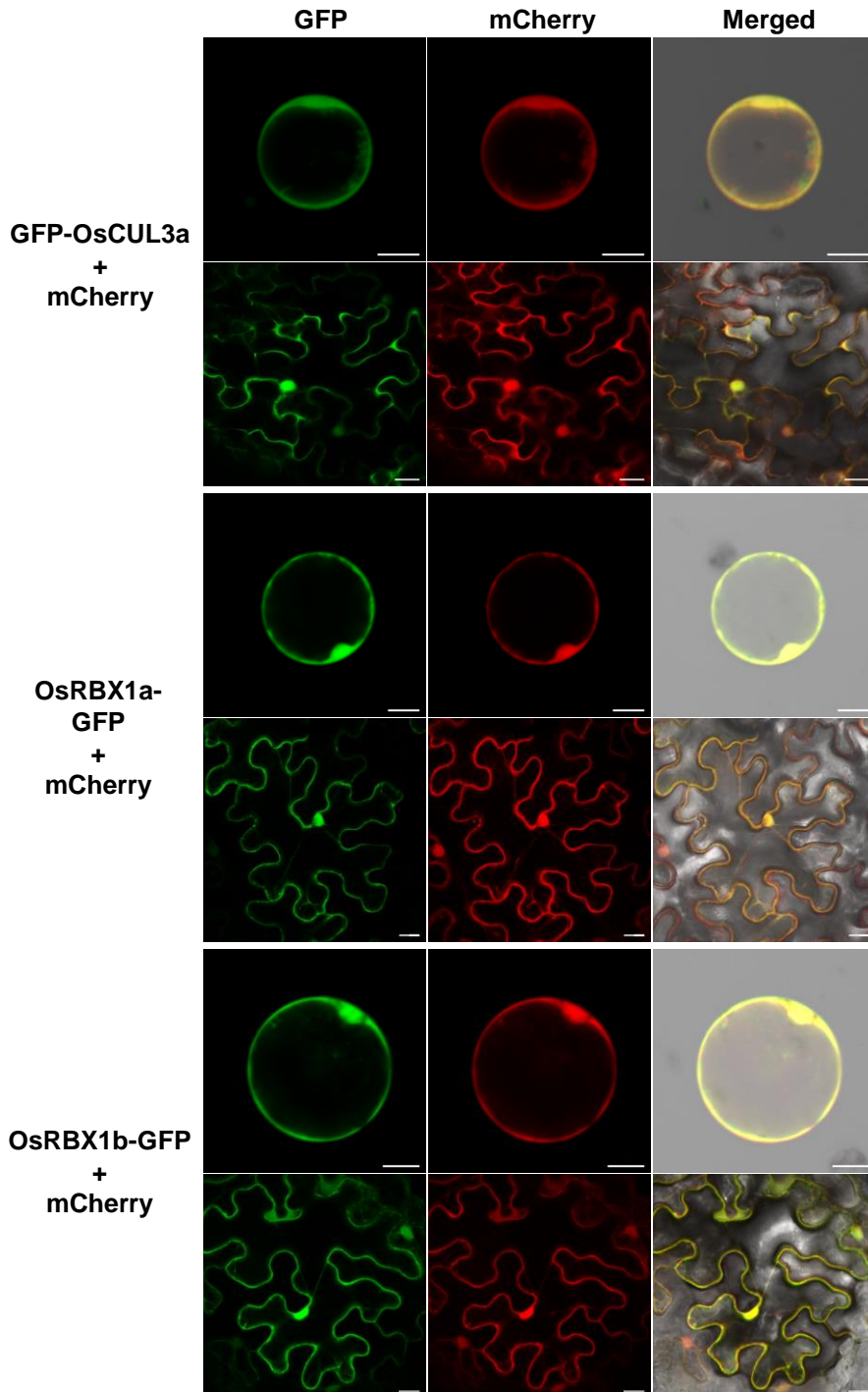
Supplemental Figure 8: Protein Alignment between AtRBX1, OsRBX1a, and OsRBX1b.



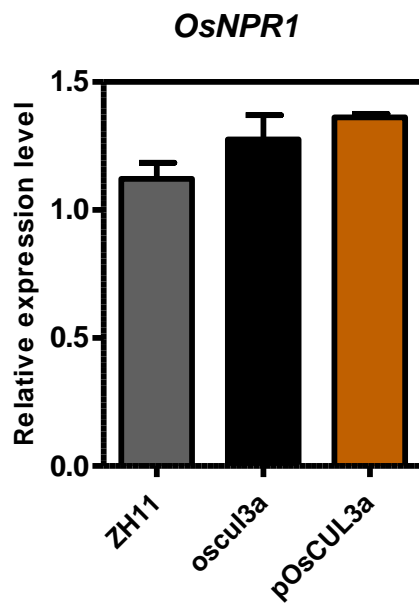
Supplemental Figure 9: OsCUL3a Interacts with OsRBX1a and OsRBX1b in Yeast.

(A) Schematic diagrams of full-length or truncated OsCUL3a proteins.

(B) Protein interactions as indicated by the ability of yeast cells to grow on synthetic dropout medium lacking L, W, and H in the presence of 2.5 mM 3-amino-1,2,4-triazole.

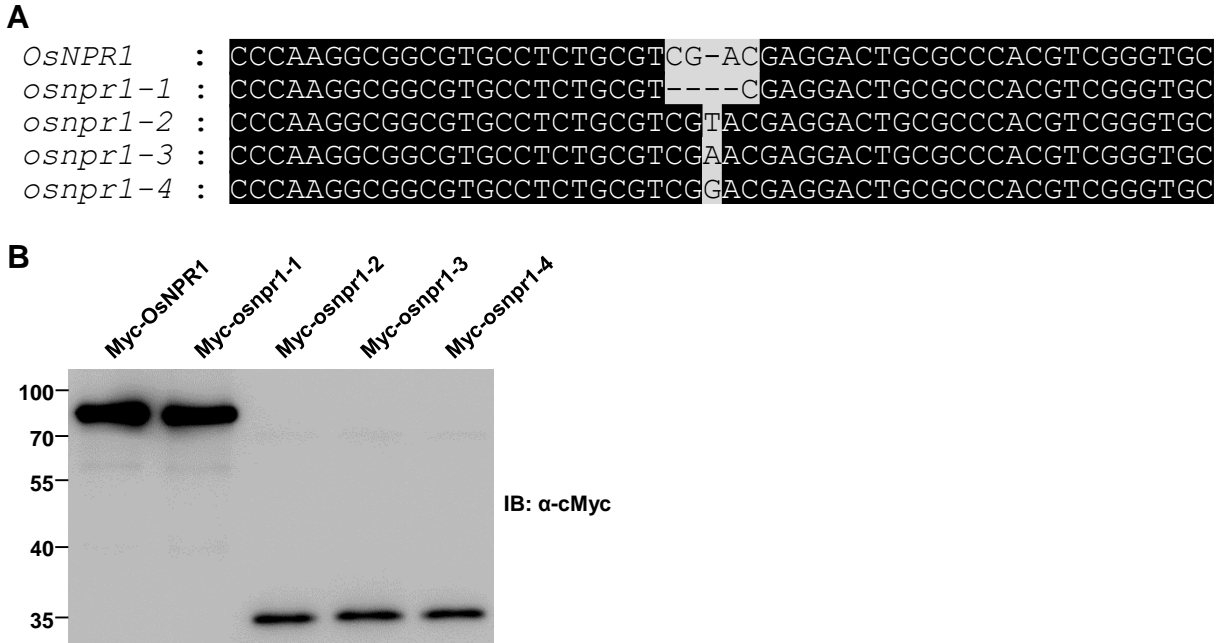


Supplemental Figure 10: Subcellular Localization of OsCUL3a, OsRBX1a, and OsRBX1b. GFP tagged OsCUL3a, OsRBX1a, and OsRBX1b were transiently expressed in rice protoplast or *Nicotiana benthamiana* leaves. GFP signal were detected using ZEISS confocal microscope at 36 h or 72 h post transfection. Bar=10 μ m.



Supplemental Figure 11: *OsNPR1* Transcriptional Level in ZH11, *oscul3a* Mutant, and pOsCUL3a Plants.

Total RNA was isolated from the second top leaves of ZH11, *oscul3a*, and pOsCUL3a plants at 60 dps. *OsNPR1* mRNA level was analyzed by qRT-PCR.



Supplemental Figure 12: Characterization of Different Types of the *osnpr1* Mutants Created by CRISPR/Cas9.

(A) Genomic DNA sequence alignment of *osnpr1s* flanked the mutation site.

(B) *osnpr1s* created by Crispr/Cas9 method encode 2 types *osnpr1* proteins. The full length cDNA of wild-type *OsNPR1* and 4 *osnpr1* mutants were PCR amplified and fused with Myc tag. The recombinant protein were transiently expressed in rice protoplast for western blot analysis with anti-cMyc antibody.

Supplemental Table 1

Primer name	Primer sequence (5'-3')	Enzyme	Vectors
Primers for qRT-PCR			
qMoPot2	F: ACGACCCGTCTTTACTTATTTGG		
	R: AAGTAGCGTTGGTTTTGTTGGAT		
qPR1a	F: CGTGTCGGCGTGGGTGT		
	R: GGCGAGTAGTTCAGGTGATG		
qPR1b	F: TACGCCAGCCAGAGGAGC		
	R: GCCGAACCCAGAAGAGG		
qPR10	F: GTCCGGGCACCATCTACACC		
	R: CAAGCTTCGTCTCCGTCGAGT		
qPAL1	F: TTCAACGCCGACACCT		
	R: GTAGAGCGGATACGACCTG		
qAOS2	F: AAGCTGCTGCAATACGTGTACTGG		
	R: CGACGAGCAACAGCCTTCCG		
qWRKY45	F: GCCGACGACCAGCACGATCACC		
	R: ACGAGCCGACGCCGCCCTC		
qACTIN	F: CAGGCCGTCTCTCTCTGTA		
	R: AAGGATAGCATGGGGGAGAG		
Primers for genotyping			
ZN7	F: GCGTGAAACGGAGGGA		
	R: CAAAGGGGACCAAACATTAT		
ZN26	F: AGGAGACATAGCCTGAGGACACT		
	R: CTTTGAGCCAATCCACAATACAT		
ZN30	F: GCCTGTTGAAGTTGGTAGCG		
	R: AGGGACTGCGGGATGGA		
ZN32	F: CTAACCTTGCCAAATTCGCTAC		
	R: TCGTGGTTACATTTAAGATGCA		
ZN34	F: GTGGTTCAGTCAAAGATGCCA		
	R: ACTCTAACCCCTCAGGAGTACATACC		
ZN35	F: GCTCGGCTAAGATTCATACATC		
	R: GGTTATCACATACCGTGGTTTC		

Primer name	Primer sequence (5'-3')	Enzyme	Vectors
Primers for genotyping			
ZN36	F: TAGCACAATCAAAGGAACATGC		
	R: GCCCCTCAAACAACCTCAATCT		
ZN9	F: GTCAGCGTCTAGGCAAGG		
	R: GAATCGATATGAACCGACAAT		
ZN19	F: CACAACCTTCAACACGAGAACC		
	R: TGCCCAAAGCAATAGCC		
Primers used for vector construction			
1300-OsCUL3a	F: GGCCAGTGCC <u>AGCTTTTT</u> GTCAAGGCTGAATAACGA	Hind III	pCAMBIA1300
	R: CCATGATTAC <u>GAATTC</u> TAGCCTCAAATTC AACCCGTA	EcoR I	
GFP-OsCUL3a	F: GCTTGATATC <u>GAATTC</u> ATGAGCGGGGGCGGGC	EcoR I	pYBA1152
	R: CGGGCTGCAG <u>GAATTC</u> TGCAAGATAGCGATATAACTTCCTA	EcoR I	
OsRBX1a-GFP	F: TGGCGGCCGCTC <u>TAG</u> AATGGACAAGGGCGACGT	Xba I	pYBA1132
	R: CGGTATCGATA <u>AAGCTT</u> GTGACCATACTTCTGGA ACTCCC	Hind III	
OsRBX1b-GFP	F: TGGCGGCCGCTC <u>TAG</u> AATGTGGCCATGGAGACCG	Xba I	pYBA1132
	R: CGGTATCGATA <u>AAGCTT</u> GTGCCATATTTCTGAAATTC CC	Hind III	
BD-OsCUL3a	F: CATGGAGGCC <u>GAATTC</u> AAGAGCGGGACCTCACC	EcoR I	pGBKT7
	R: GGATCCCCGG <u>GAATTC</u> GACCTTCTATGCAAGATAGCG	EcoR I	
BD-OsCUL3a-CN	F: AGGAGGACCTGCATATGTGGAAGGTCCTGGAGCA	Nde I	pGBKT7
	R: GGATCCCCGG <u>GAATTC</u> CTTGTGCTTGAAGTAGAATGT	EcoR I	
BD-OsCUL3a-ND	F: AGGAGGACCTGCATATGTTACAAGCAAGCTTGTTAAG	Nde I	pGBKT7
	R: GGATCCCCGG <u>GAATTC</u> TGCAAGATAGCGATATAACTTCC	EcoR I	
BD-OsCUL3a-NT	F: AGGAGGACCTGCATATGATGAGCGGGGGCGGGC	Nde I	pGBKT7
	R: GGATCCCCGG <u>GAATTC</u> TACATTTAGTTCATGCTTCTGACC	EcoR I	
BD-OsCUL3a-CRL	F: AGGAGGACCTGCATATGAAACGCAACTTCAAGATCGAG	Nde I	pGBKT7
	R: GGATCCCCGG <u>GAATTC</u> GTTTAAAGTTGATGAAGTACTC	EcoR I	
BD-OsCUL3a-CH	F: AGGAGGACCTGCATATGTTCACTTAAACAACAGG	Nde I	pGBKT7
	R: GGATCCCCGG <u>GAATTC</u> CCCAATCTTGACCTTAACAAG	EcoR I	
BD-OsCUL3a-DB	F: AGGAGGACCTGCATATGTCCAATTATCAGATGTGTGTT	Nde I	pGBKT7
	R: GGATCCCCGG <u>GAATTC</u> CTATGCAAGATAGCGATATAAC	EcoR I	

Primer name	Primer sequence (5'-3')	Enzyme	Vectors
Primers used for vector construction			
AD-OsNPR1	F: GGAGGCCAGTGAATTCATGGAGCCCGACCAGCC	EcoR I	pGADT7
	R: CACCCGGGTGGAATTCATCTCCTTGGTGAATG	EcoR I	
AD-OsRBX1a	F: GGAGGCCAGTGAATTCATGGACAAGGGCGACGT	EcoR I	pGADT7
	R: CACCCGGGTGGAATTCCTAGTGACCATACTTCTGGAATC	EcoR I	
AD-OsRBX1b	F: GGAGGCCAGTGAATTCATGTCGGCCATGGAGACCG	EcoR I	pGADT7
	R: CACCCGGGTGGAATTCCTAGTGCCCATATTTCTGAAATC	EcoR I	
OsCUL3a-NLuc	F: CGGGGACGAGCTCGGTACCAAGAGCGGGACCTCACC	Kpn I	p35S::NLuc
	R: ACGAGATCTGGTCTGACTGCAAGATAGCGATATAACTTC	Sal I	
CLuc-OsNPR1	F: ACGCGTCCCGGGGCGGTACCATGGAGCCCGACCAGCC	Kpn I	p35S::CLuc
	R: AGCTCTGCAGGTCGACTCATCTCCTTGGTGAATG	Sal I	
CLuc-OsRBX1a	F: ACGCGTCCCGGGGCGGTACCATGGACAAGGGCGACGT	Kpn I	p35S::CLuc
	R: AGCTCTGCAGGTCGACTAGTGACCATACTTCTGGAATC	Sal I	
CLuc-OsRBX1b	F: ACGCGTCCCGGGGCGGTACCATGTCGGCCATGGAGACCG	Kpn I	p35S::CLuc
	R: AGCTCTGCAGGTCGACTAGTGCCCATATTTCTGAAATC	Sal I	
YN-OsCUL3a	F: GCCTACTAGTGGATCCATGAGCGGGGGCGGGC	BamH I	pSPYNE (R) 173
	R: GAGCGGTACCCTCGAGCTATGCAAGATAGCGATATAAC	Xho I	
YN-OsCUL3a-NT	F: GCCTACTAGTGGATCCATGAGCGGGGGCGGGC	BamH I	pSPYNE (R) 173
	R: GAGCGGTACCCTCGAGTACATTTAGTTCATGCTTCTGACC	Xho I	
YC-OsRBX1a	F: CGCCACTAGTGGATCCATGGACAAGGGCGACGT	BamH I	pSPYCE (M)
	R: GAGCGGTACCCTCGAGGTGACCATACTTCTGGAATCCC	Xho I	
YC-OsRBX1b	F: CGCCACTAGTGGATCCATGTCGGCCATGGAGACCG	BamH I	pSPYCE (M)
	R: GAGCGGTACCCTCGAGGTGCCCATATTTCTGAAATCCC	Xho I	
4HA-OsCUL3a	F: AGATTACGCTGGATCCATGAGCGGGGGCGGGC	BamH I	Ubi::HA
	R: CCGCACTAGTAAGCTTCTATGCAAGATAGCGATATAAC	Hind III	
4Myc-OsNPR1	F: CTTGAATTCGGGATCCATGGAGCCCGACCAGCC	BamH I	Ubi::Myc
	R: CCGCACTAGTAAGCTTTCATCTCCTTGGTGAATG	Hind III	
C-OsNPR1	F: GGCGTGCCTCTGCGTGCACG		pOsU3-sgRNA
	R: CGTCGACGCAGAGGCACGCC		
CS-OsNPR1	F: CCGCCTCTCCGACAACCTC		
	R: GAGTCGCATCCACACGTTCA		