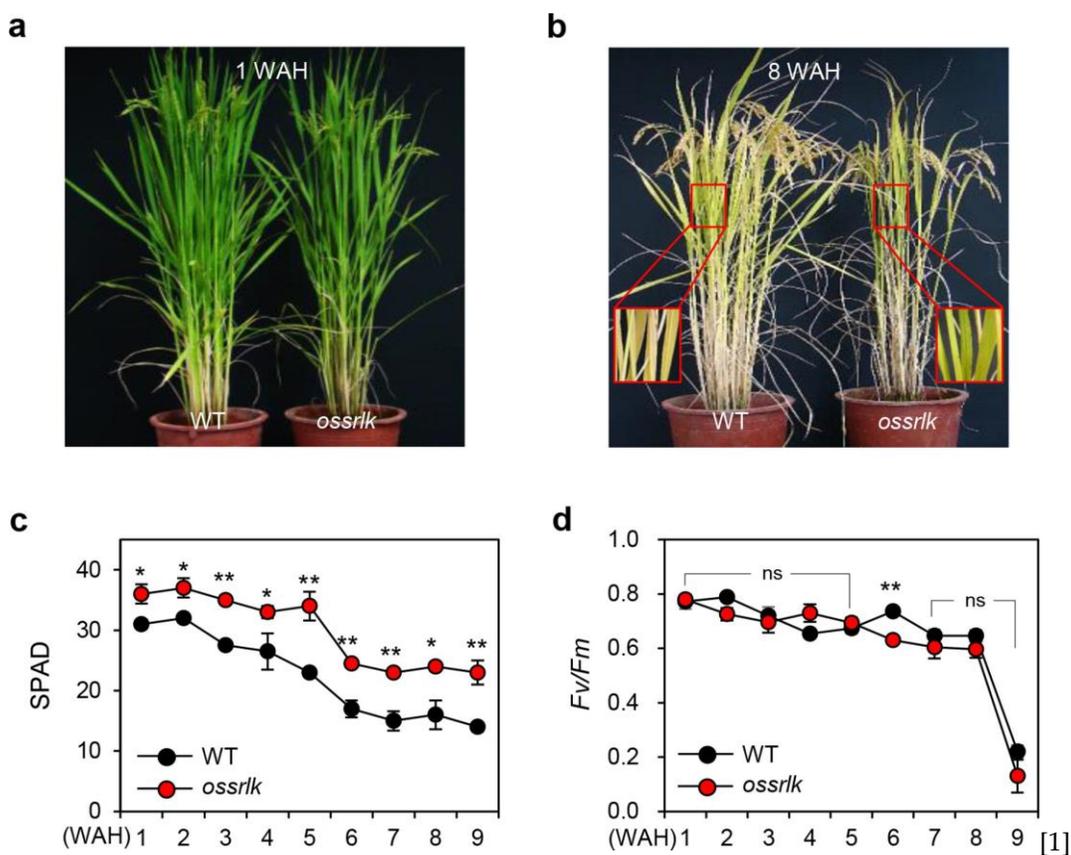


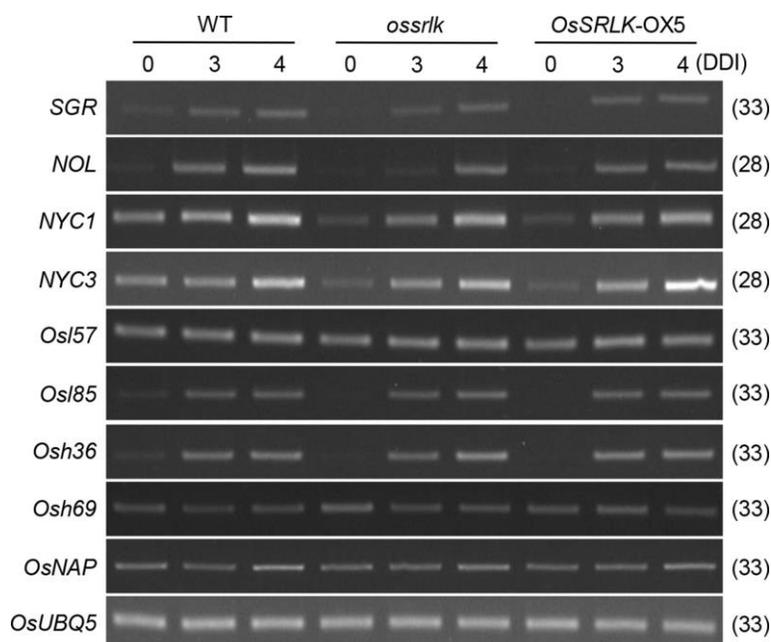
## Supplementary

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 Brachypodium distachyon 1 ---MPPRLPC---AAFLALAVVV--VCAEPPADARRAALDFLAGVGGRA--GRINW  
 Triticum turgidum 1 ---MPPRLPC---AAFLALAVVV--VCAEPPADARRAALDFLAGVGGRA--GRINW  
 Hordeum vulgare 1 ---MPPRLPC---AAFLALAVVV--VCAEPPADARRAALDFLAGVGGRA--GRINW  
 Zea mays 1 MPTPLGAGLLRCLRLCLSLRPR--LASEPPADKAAALDFLAGVGGRA--GRINW  
 Sorghum bicolor 1 MPTPLGAGLLRCLRLCLSLRPR--LASEPPADKAAALDFLAGVGGRA--GRINW  
 Panicum millicium 1 ---MPPRLPC---AAFLALAVVV--VCAEPPADARRAALDFLAGVGGRA--GRINW  
 Setaria italica 1 ---MPPRLPC---AAFLALAVVV--VCAEPPADARRAALDFLAGVGGRA--GRINW  
  
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 Oryza sativa 49 ASS-PR-----VCGNWTGVTCSADGRVRLRPLGLSGVFRGTLGRITAOVLSLR  
 Brachypodium distachyon 48 SSTAR-----VCGNWTGVTCSADGRVRLRPLGLSGVFRGTLGRITAOVLSLR  
 Triticum turgidum 46 AAA-RP-----VCNNTGVTCSADGRVRLRPLGLSGVFRGTLGRITAOVLSLR  
 Hordeum vulgare 48 SA-RP-----VCGNWTGVTCSADGRVRLRPLGLSGVFRGTLGRITAOVLSLR  
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 Oryza sativa 103 ANLSGPFPRVVEKDAFTVPCNNISGLDFDFVWKNITGVNLSNFGNPTPSSL  
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 Brachypodium distachyon 162 SNLIRKIQSNLANNLSCDIPDLVLSLGHIDLNNYDAFFIDMRRPFSSYTD  
 Triticum turgidum 159 SNLIRKIQSNLANNLSCDIPDLVLSLGHIDLNNYDAFFIDMRRPFSSYTD  
 Hordeum vulgare 161 SNLIRKIQSNLANNLSCDIPDLVLSLGHIDLNNYDAFFIDMRRPFSSYTD  
 Zea mays 178 SNLIRKIQSNLANNLSCDIPDLVLSLGHIDLNNYDAFFIDMRRPFSSYTD  
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 Brachypodium distachyon 569 NIEEEMVEMLOIAMCVSRTPERRPKMSVVRMLIEVGRNDT-----GTRPSTEA---  
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 Hordeum vulgare 569 NIEEEMVEMLOIAMCVSRTPERRPKMSVVRMLIEVGRNDT-----GTRPSTEA---  
 Zea mays 592 NIEEEMVEMLOIAMCVSRTPERRPKMSVVRMLIEVGRNDT-----GTRPSTEA---  
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 Panicum millicium 583 NIEEEMVEMLOIAMCVSRTPERRPKMSVVRMLIEVGRNDT-----GTRPSTEA---  
 Setaria italica 578 NIEEEMVEMLOIAMCVSRTPERRPKMSVVRMLIEVGRNDT-----GTRPSTEA---  
  
 Arabidopsis thaliana 631 ETSTPSEI-----SSAAH---  
 Oryza sativa 624 --STFVGEARSKAES-----SSAAH---  
 Brachypodium distachyon 620 --STFVGEARSKAES-----SSAAH---  
 Triticum turgidum 617 --STFVGEARSKAES-----SSAAH---  
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 Zea mays 649 --STFVGEARSKAES-----SSAAH---  
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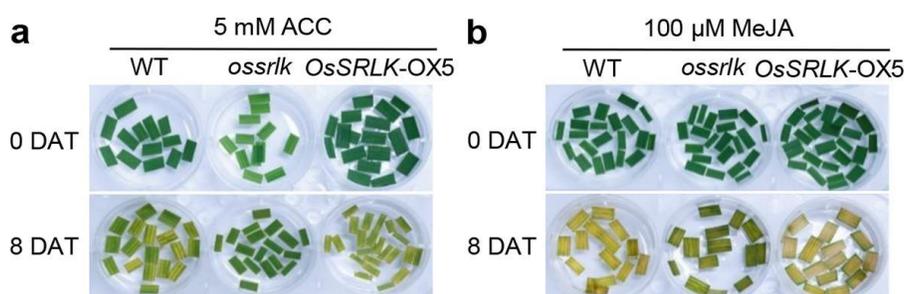
**Figure S1.** Amino acid sequence alignment of RLK protein. The amino acid sequences for OsSRLK proteins of other plant species homologous to rice SRLK were obtained from NCBI through BLAST analysis. Sequence alignment was performed using ClustalW with default parameters. The sequences are as follows: *Arabidopsis thaliana*, NM\_118505.5; *Oryza sativa*, LOC\_Os01g12390.1; *Brachypodium distachyon*, XP\_003565740; *Triticum turgidum*, VAH59131; *Hordeum vulgare*, BAJ86409; *Zea mays*, NP\_001168844; *Sorghum bicolor*, XP\_021312403; *Panicum miliaceum*, RLN23550; *Setaria italic*, XP\_004967473. Red and blue bars represent the leucine rich repeats and catalytic domain of serine/threonine kinases, respectively.



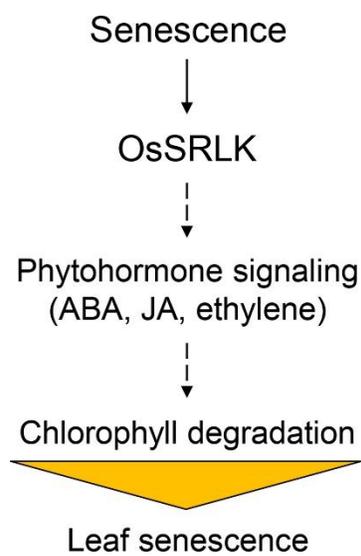
**Figure S2.** The senescence phenotype of *ossrlk* under natural senescence conditions in the field. The plants were photographed 1 week after heading (WAH) (a) and 8 WAH (b). SPAD value (c) and  $F_v/F_m$  (efficiency of photosystem II) (d) were measured in WT and *ossrlk* every 1 week from 1 WAH to 9 WAH. Mean and standard deviation values were obtained from 10 measurements. Asterisks indicate a significant difference between WT and *ossrlk* mutant (Student's *t*-test, \* $P < 0.05$ , \*\* $P < 0.01$ ). n.s., not significant.



**Figure S3.** Expression of CDGs and SAGs in *ossrlk* and *OsSRLK-OX5* during DIS. Total RNA was isolated from the detached leaves of WT, *ossrlk*, and *OsSRLK-OX5* plants under DIS, as presented in Figure 2 (2 c,h). Transcripts of CDGs (*SGR*, *NOL*, *NYC1*, and *NYC3*) and SAGs (*Osl57*, *Osl85*, *Osh36*, *Osh69*, and *OsNAP*) were determined by reverse-transcriptase PCR analysis. *OsUBQ5* was used as a loading control. Numbers in parentheses indicate the numbers of PCR cycles. DDI, day(s) of dark incubation.



**Figure S4.** Phytohormone hyposensitivity of *ossrlk*. Detached leaves of 3-week-old WT, *ossrlk*, and *OsSRLK-OX5* plants were treated with 3 mM MES buffer (pH 5.8) containing 5 mM ACC (1-aminocyclopropane-1-carboxylic acid) (a) and 100 μM MeJA (b) under continuous light conditions at 28 °C. DAT, day(s) after treatment.



**Figure S5.** Proposed model for the role of OsSRLK in leaf senescence. Solid and dashed arrows represent direct and indirect activation, respectively.

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

A. Primers for verification of T-DNA insertion		
Primer name	Left primers (5' → 3')	Right primers (5' → 3')
PFG_1A-15835	TCTCCCTCATCAAAACGTCC	AGTGAGAGGAGCTCCTCCG
pGA2717	ACGCTGAACTTGTGGCCGTT	AACGCTGATCAATTCCACAG
B. Primers for RT-qPCR		
Genes	Forward primers (5' → 3')	Reverse primers (5' → 3')
<i>OsSRLK</i>	GACGTCGAGCTGATGAGGTA	CACCACGTCCGACATCTTAG
<i>OsUBQ5</i>	ACCACTTCGACCGCCACTACT	ACGCCTAAGCCTGCTGGTT
C. Primers for RT-PCR		
Genes	Forward primers (5' → 3')	Reverse primers (5' → 3')
<i>OsSRLK</i>	TTGTGGACAGATTCAAGAA	ATAGAGACTACTGTGAAACA
<i>SGR</i>	AGGGGTGGTACAACAAGCTG	GCTCCTTGCGGAAGATGTAG
<i>NOL</i>	GAAAGGGTAGAATCTGCGGTG	CTGCAGAGATTTTGTAAGGTG
<i>NYC1</i>	GAATCCGTAATTGGGCTGAA	CTGGAAGAGGTCCACCTGAG
<i>NYC3</i>	TGCTGCATCCTGTCCACACCTTG	GATGCAAATGATGCAGCAGCTGC
<i>Os157</i>	ACCCTAAAGTAAATGAAGTC	CCTGCTCTTGTCTTGTTA
<i>Os185</i>	CGTCACGGACACGTTCGC	GCAAGAACATGGCTGCTGC
<i>Osh36</i>	GTTGAGGCGATGGTCAACC	CAGTGTAAGCCGGGCAATC
<i>Osh69</i>	CCTGCTCTTGTCTTGTTA	GGTGAACACTATGGAACA
<i>OsNAP</i>	AACCATTTCATCGCGAACAAC	CAGTGACGATCCCTGCAAGG
<i>OsUBQ5</i>	ACCACTTCGACCGCCACTACT	ACGCCTAAGCCTGCTGGTT
D. Primers for plant transformation		
Primer name	Forward primer (5' → 3') <sup>a</sup>	Reverse primer (5' → 3') <sup>a</sup>
<i>OsSRLK_HindIII</i> and <i>HpaI</i>	<u>AAGCTT</u> ATGCCGCGCCGAGGCTG	<u>GTTAACT</u> CAGAGGAGCTCCTCCG

<sup>a</sup>The underlined nucleotides represent the restriction site for restriction enzymes.