

Supplementary figure legends:

Figure S1. Map-based cloning of *RSN1*.

(A) The positions of the mapping markers. The *rsn1* mutations are flanked between markers F24M12 and T5P19.

(B) Gene structure of *RSN1* and the mutation sites in *RSN1*. Exons are indicated with gray boxes and introns with lines. Arrows indicates the mutation sites of *rsn1* mutants.

Figure S2. Alignment of RSN2 and its homologs from other eukaryotes. Amino acid sequences of hSPF45 from human, SPF45 from *Drosophila*, F58B3.7 from *C.elegans*, OsDRT111 from rice and RSN2 were aligned with Clustal Omega program (<http://www.ebi.ac.uk/Tools/msa/clustalo/>) and the alignment result was shaded with BOXSHADE program (http://www.ch.embnet.org/software/BOX_form.html).

Figure S3. flg22-induced ROS burst in wild type and *rsn2-1* plants. Four-week-old soil-grown plants were used in this assay.

Supplementary Table S1. Primers used in this study.

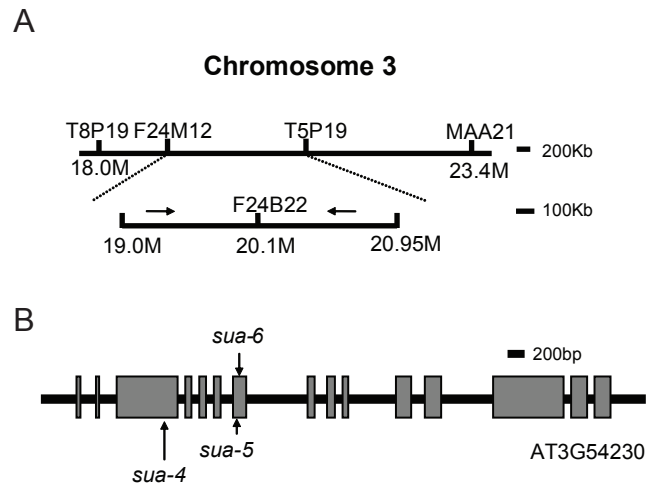


Figure S1. Map-based cloning of *RSN1*.

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F58B3.7 1 ----MYNDEDDVPQGPPAAKQAKPMHNIQMAFMQSQLAQRKAALQQAARQLVKSSAP
RSN2 1 MLGGLYGDLPPPTDDEKPSGNS--SSVWSSSTKMAPPTLRKPPAF-AP-----
OSDRT111 1 MLGGLYGDLPPPSSSADDDKPS-AAGWSSAAKMAPPTLRKPPATFAP-----
hSPF45 1 --MSLYDDLGVETSD-----SK-TEGWSKNFKLLQSQLQVKKAALTQAK-SQRTKQSTVL
SPF45 1 --MDLYDGIDTRARS-----SQ-IDGWSSGIKMLQTQLAVKMAVK-----PLM

F58B3.7 57 PVIDLSTRNRTITTAVTSKSFQIPIRANPVSDNISFLPKAATDESVMLFGEEHVKCEYYP
RSN2 46 -PQTILRPLNKPKPIVSAPYKPPPSNSSQSVLIPANESAPSHQPALVGVTSSVIEEYDP
OSDRT111 47 -PPSVLRN-SRPAPKAPAAQPPPPTL-----PIETTTSTSFQPALVAVQSTVMEEYDP
hSPF45 52 APVIDLKRGGSSDDRQIV-DT-PPHVAAGLKDPVPSGFSAG-----EVLIPLADEYDP
SPF45 42 TPVNLRSKRLADPEVTC-FA-P--ITTVVSKPLISGKALPSILERINRGDWDVADEYDP

F58B3.7 117 MTPNNYEVWAKEINDRKQREKTAREVAKRLQR-----EHEEEDDKKRS-----
RSN2 105 ARPNDYEEYKREKKRKATEAEMKREMDKRRQEDEERDKREREEREKERERDNSDPSR---
OSDRT111 99 ARPNDYEDYRKDKLKRAKEAEVRKELERRRRREEEERERE-REL-----REREGRDA---
hSPF45 103 MFPNDYEKVVKRQREE---RQRQRELER-----QKEIEEREKRRK-DR-----
SPF45 98 QRPNEYEKLKEKSNGS---DKNRAGVSD-----REDRDDKEKDRKRGRVRGREFYR

F58B3.7 159 -----KGA-----AIAPPTMLMEPEPEV
RSN2 162 -----LNISGE-----EA-W--KRRAAMSGGSGGKRSSSPPGNVDGFSI--
OSDRT111 149 -----LNISGE-----EA-W--KRRAAMSGSAA---PRPSSSPHGDFAI--
hSPF45 142 -----HEASGFARRPDPDSDEDEDEYERRRKRSMGGAA-----IAPPTSLVEKDKEL
SPF45 146 DEVSAPNLKISGFGHRQND---DDMYLPSPGLVAKQGGAT-----IAPPPSLQEMST--

F58B3.7 177 IKNTNENQDEKPH----SSFMPPPSFL-----PAFGKATSRGLGIAANIMKR
RSN2 200 -----GKSETSGLGVGAGGQMTAAQRMMAK
OSDRT111 184 -----GNSSSSGLGLGAGGQMTAAQRMMAR
hSPF45 189 PRDFPYEDSRPRSQSSKAAIPPPVYEEQDRPRSPTGPSNSF---LANMGGTVAHKIMQK
SPF45 195 -----DS--GCEATNT---MPYSASSVAAKIMAK

F58B3.7 220 HGYKEGAGLGKSEQGMSTALSIEKTGVRGGNIVAEAPKAP-T-----
RSN2 225 MGWKQGQGLGKSEQGITTPLMAKKTDRRAGVIVNASENKSS-----
OSDRT111 209 MGWKEGQGLGKQEQGITAPLVAKKTDRRGGVIVDENS-----
hSPF45 246 YGFFEGQGLGKHEQLSTALSVEKTSKRGGKIIVGDATEK-----
SPF45 219 YGFKQGQGLGKSEQGMAIALQVEKTSKRGGRIIHEKDVFLPPLALSPPSIGSQIGTSPSH

F58B3.7 261 -----FATNSMEAVQNATKILQLWNITDLSEVSGEEGKEFADEIKEE
RSN2 267 -----AEKKVVKSVNINGEPTRVLLLRNMVGPGQV-----DDELEDEVGGE
OSDRT111 247 -----KQEKKPKSVNFDGPPTRVLLLRNMVGPGEV-----DDELEEEVASE
hSPF45 286 -----DASKKSDSNPLTEILKCPTKVVLLRNMVGAGEV-----DEDLEVETKEE
SPF45 279 KAMPPPQMVDTAAESGDIGYSITEIMKSPSKVVLLRNMVGPGDV-----DEELEPEVKDE

F58B3.7 304 ME-KCQVVNVIVHVDE--SQEEDRQVRVFVEFTNNAQAIKAFVMMNGRFFGGRSVSAGF
RSN2 308 CG-KYGTVTRVLIFEITEPNFVHEAVRIFVQFSRPETTKALVDLDGRYFGGRTVRATF
OSDRT111 288 CS-KYGTVLRVLIFEITQADFPAEAVRIFILFERAEEATKAMIDLEGRFFGGRVVRATF
hSPF45 330 CE-KYGKVGKCVIFEIP--GAPDDEAVRIFLEFERVESAIKAVVDLNGRYFGGRVVKACF
SPF45 334 CNTKYGEVNSVIIHESF--GTVPEDAVKIFVEFRRIESAIKAVVDLNGRFFGGRQVRAGF

F58B3.7 361 QNVSDYNNREF-----
RSN2 367 YDEEKFSKNELAPVPGEIPGY-
OSDRT111 347 FDEERFGKNQLAPMPGEVAGFD
hSPF45 387 YNLDKFRVLDLAEQV-----
SPF45 392 YNYDKFKCFQLH-----

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Figure S2. Alignment of RSN2 and its homologs from other eukaryotes.

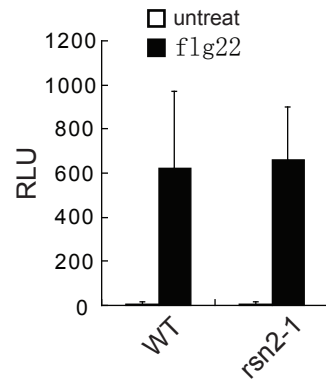


Figure S3. flg22-induced ROS burst in wild type and *rsn2-1* plants.

Table S1. Primers used in this study

Primer	5'-3' sequence	Purpose
<i>SNC4</i> -RT-F	cttcgcagatgaaactgttg	Real-time PCR
<i>SNC4</i> -RT-R	gtggaataagagccttcagc	Real-time PCR
<i>CERK1</i> -RT-F	gcacaatttcagctacag	Real-time PCR
<i>CERK1</i> -RT-R	caacaagccacaatcactcc	Real-time PCR
<i>CERK1</i> -SPL-1R	ggtgcattccaccattc	Alternative splicing
<i>AtSR1/SRp34</i> -F	aggagcagaagtccaaggc	Alternative splicing
<i>AtSR1/SRp34</i> -R	ccttctgaacagaaggtagag	Alternative splicing
<i>UI-70K</i> -F	cccaataatgatccaatgc	Alternative splicing
<i>UI-70K</i> -R	cttatatgcagctttcatgtc	Alternative splicing
<i>RSN1</i> -F	gagcgggtaccaccaccatcatcccag	Complementation
<i>RSN1</i> -R	cgcggggatccatagccaggattccactgc	Complementation
F17F8-F1	ggaagaggattgactcaagagc	InDel marker
F17F8-R1	gcagcaaacacgtacgtgagc	InDel marker
F1K23-F	gcaaatccataggaagtgagtc	InDel marker
F1K23-R	gatctgtatctgaaacctgggaa	InDel marker
F13K9-F	ttctgctgaaccaaggtgc	InDel marker
F13K9-R	ataatatgatgcgcgctagg	InDel marker
F14M2-F	cgcatacgtgtcaccgtgag	InDel marker
F14M2-R	tgtccgggactgcctttagc	InDel marker
T8P19-F1	agaacacgcaaaaggacacg	InDel marker
T8P19-R1	gcttagtataactggttttgg	InDel marker
F24M12-F1	tgaagattctacctcgcgtg	InDel marker
F24M12-R1	gttgatctggtgaccaatcc	InDel marker
T5P19-F1	cgtattaaaagtttgagatgttac	InDel marker
T5P19-R1	aatagactgcaaaggtttttgac	InDel marker
MAA21-F1	gtcacccatgatgcaaagg	InDel marker
MAA21-R1	gcaattgaagcagactcaacc	InDel marker
F24B22-F1	gtgttgatgtatgcctgagc	InDel marker
F24B22-R1	cctaaagtacaatccaagagc	InDel marker