

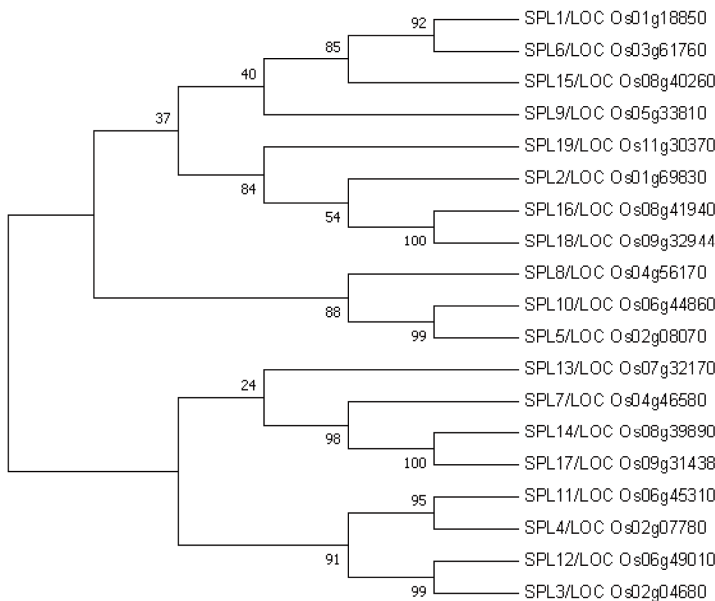
Transcriptional regulation of miR528 by *OsSPL9* orchestrates antiviral response in rice

Supplemental Figures and Supplemental figure legends

A

GCCGTAAGTGCGAACCTGCTCTGGCTCAATCGCATAGAGGGACGCGCTGCGCACAGCCCGATGCTTTTCTATA
 GTTCCATAGTCCACCGTTACCACATGGACGGATGGGATGATGGGAGAGTTTTCTGTAATGCTCACATTTATTGT
 ATCTTACTAAACCCACTTTTATAAATACATGACAGCATTGACTTTTGAACATATATTACTTAATTTTTAAAAATAA
 ATTAATTATTATTTTGTGGAGTTTTTTTATTGAAA **GTAC**TTTAAACATGATTTATTTTATGCAITTCGT
 AAAAAATTCTAATAAGACGAACAATGGTATGTATTAACGAGAGATTTAACATTTAATCT **GTAC**TATCAT
 TCGCGACAATTTTTTTTCAAATTGCGGAGTA **GTAC**TTACATATTGGCATGGA **GTAC**ATCAGACGATACTA
GTACAGCATACATGCTGGCGTTCAACTTGTGGAGATCTGATGCGATATAAATCGATCCTACGTCACATGAC
 AGACTGGACCCCTGTCAAAATTATGGATTGGATGATTAATCACTGATAGTA **GTAC**TAGTAGCAACTCAATCAC
 ACAAGCGAAGTGAGAAGAAAAGGAACCTTCTCCTGCATTAAGACAACGGCGACGGGTCACCTGAAAGTGAAGC
 CTGTGGCGCACACGACGACCTCCTCAACGGATCTGTGGCTTACCCGTGCGCGTTAGAGCGTTTGTCTCAAC
 GCTTCTGCA **GTAC**AAGA **GTAC**AGCTGAAAGCCATA **GTAC**ACTGATGATATTTGCAAGCCTGAA **GTAC**AAG
 CCGCCCTAACGATCTCCCCCATAT **GTAC**TGCAGCTAACTT **GTAC**TACTACCAGTGCCCATGGCCGGG
GTACAAATATGCCACCTTACCAATGGATGCATCAGCAGCCACAGCAAATTTGGTTTGGGATAGGTAG
 GTGTTATGTTAGGTCTGGTTTTTGGCTGTAGCAGCAGC

B



Supplemental Fig. 1 The promoter sequence of miR528 and a phylogenetic analysis of the 19 SPL proteins in rice. A. The promoter sequence of miR528. The SPL family protein binding motif “GTAC” is shown in red. **B.** Phylogenetic analysis of 19 SPL proteins in rice. An unrooted tree was constructed by aligning all SPL complete protein sequences in rice. The maximum likelihood method was used to generate the phylogenetic tree.

A

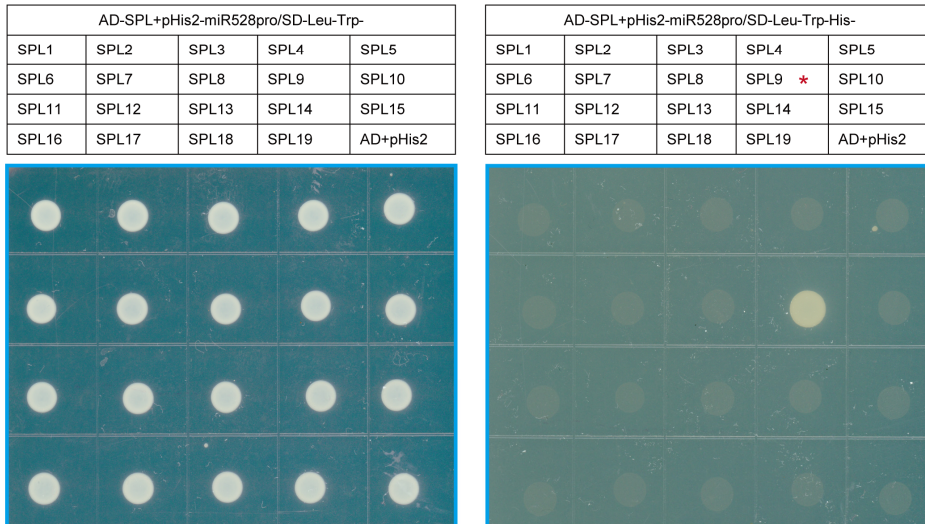
Effector construct



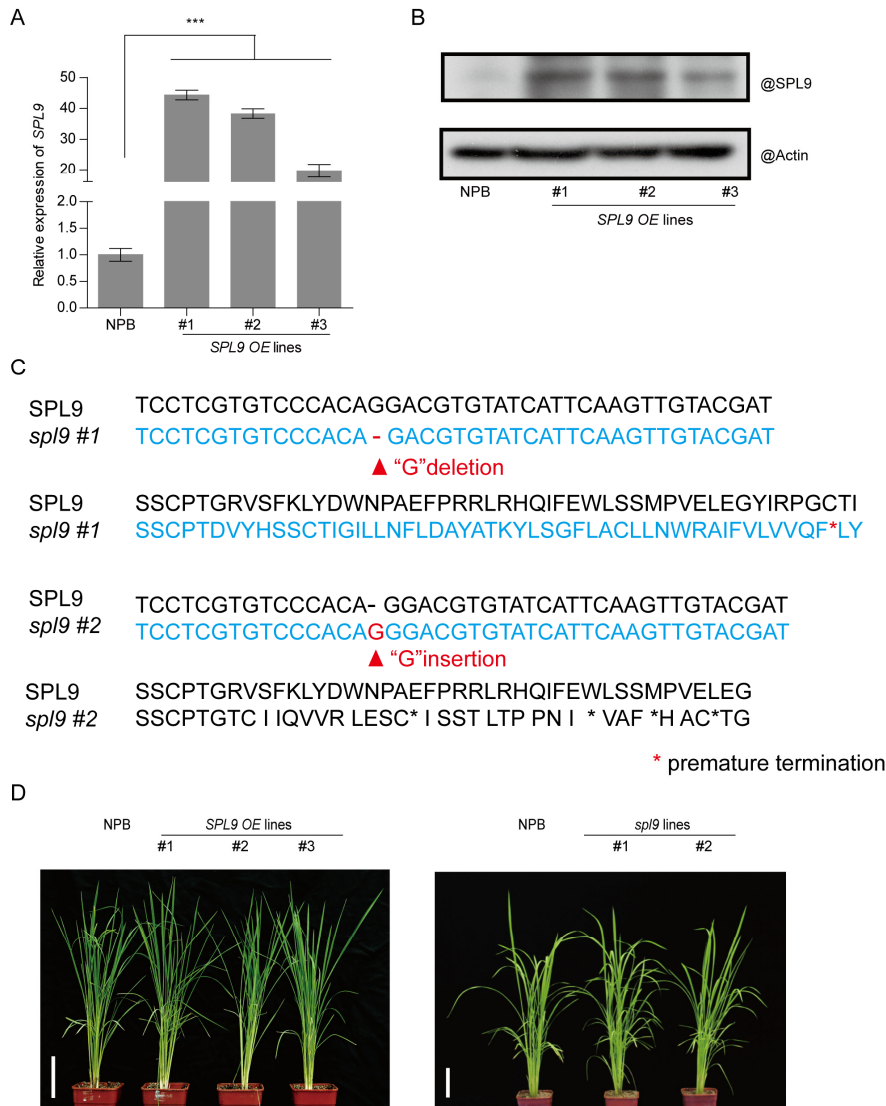
Report construct



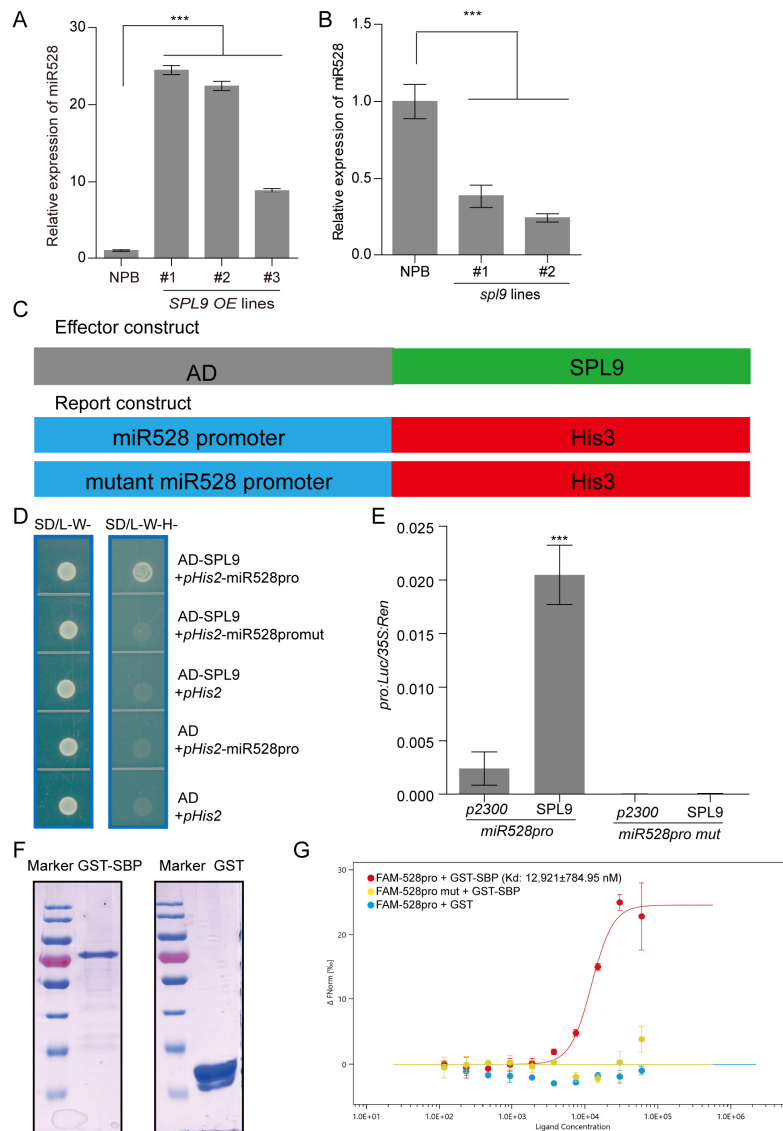
B



Supplemental Fig. 2 SPL9 specifically activates the miR528 promoter. **A.** Schematic diagrams of the effector and reporter constructs used in the yeast one-hybrid (Y1H) assays. **B.** Y1H assays. The full-length cDNAs of *SPL1-19* were cloned into the pGADT7Rec2 vector. The promoter of miR528 was cloned into reporter vector pHis2. The empty vectors were used as the negative control. Yeast cultures were spotted onto plates lacking Trp and Leu (SD/L-W-) and Trp, His, and Leu (SD/L-W-H).

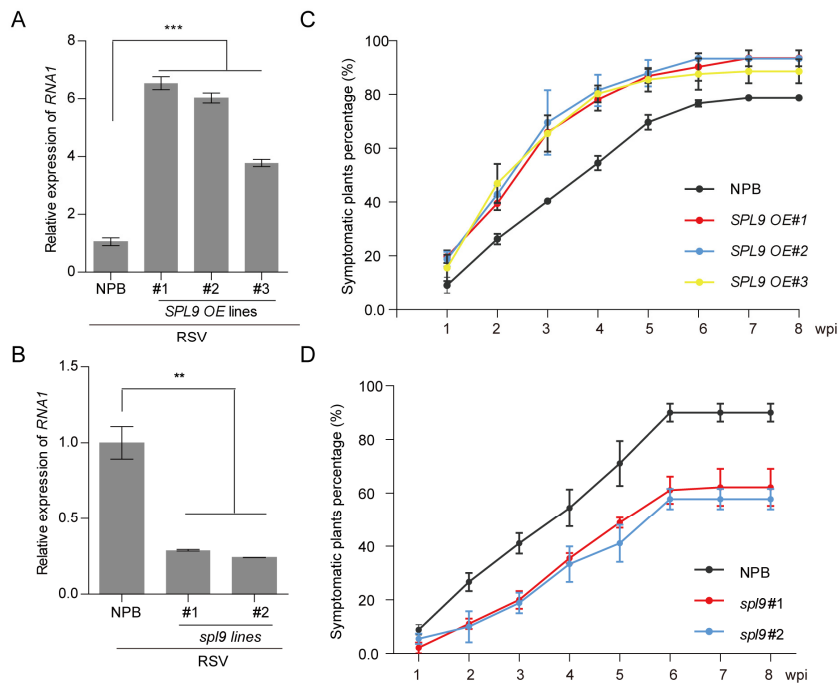


Supplemental Fig. 4 Generation of the *SPL9* overexpression and *sp19* knock-out mutant rice lines. **A.** Detection of the *SPL9* expression levels in the wild-type (NPB) and *SPL9* overexpression (*SPL9 OE*) lines using RT-qPCR. *EF* expression was used as a control. The average values (\pm standard deviation) from three biological repeats are shown. Asterisks mark significant differences to the wild type, according to Student's *t*-test; *** P value ≤ 0.001 . **B.** Detection of the *SPL9* protein levels in NPB and *SPL9 OE* using a western blot. Actin was probed as a loading control. **C.** The construction of the *sp19* knock-out mutant lines using CRISPR/Cas9. The DNA sequences of the two *sp19* mutant lines are shown. The mutations, a 'G' deletion in line *sp19*#1 and a 'G' insertion in line *sp19*#2, caused the premature termination of the *SPL9* amino acid sequence. **D.** Phenotypic comparison of indicated rice lines at six weeks after germination. Scale bar = 10 cm.



Supplemental Fig. 5 SPL9 activates the transcription of miR528. A–B. Detection of the expression levels of mature miR528 in wild-type (NPB), *SPL9 OE*, and *spl9* mutant rice lines using qPCR. U6 expression was used as a control. The average values (\pm standard deviation) from three biological repeats are shown. Asterisks mark significant differences from the wild type, according to Student’s *t*-test; *** P value ≤ 0.001 . C. Schematic diagrams of the effector and reporter constructs used in the yeast one-hybrid assays. In the mutant miR528 promoter, “GTAC” was mutated into “GATC”. D. Yeast one-hybrid assay. The full-length cDNA of *SPL9* was cloned into the *pGADT7Rec2* vector. The promoter of miR528 or the mutated miR528 promoter were cloned into the reporter vector *pHis2*. The empty vectors were used as the negative control. Yeast cultures were spotted onto plates lacking Trp and Leu (SD/L-W-) and lacking Trp, His, and Leu (SD/L-W-H-). E. Transient dual-luciferase reporter assay. *Agrobacterium* strain *GV3101* carrying the reporter plasmid (*miR528pro-LUC* or *miR528pro mut-LUC*) together with different combinations of effector plasmids (*p2300* or *p2300:SPL9*) was infiltrated into *N. benthamiana* leaves, and the luciferase activity at the sites of infiltration was measured 2 d after infiltration. The activities of firefly

luciferase and Renilla luciferase were measured sequentially, and the LUC:REN ratio was calculated as the final transcriptional activity. The average values (\pm standard deviation) from six biological repeats are shown. Asterisks mark significant differences from the wild type, according to Student's *t*-test; ** P value ≤ 0.01 . **F.** The purification of the SPL9-containing DNA-binding domain *in vitro*. The Coomassie Blue staining of the purified GST-SPL9 SBP and GST proteins is shown. **G.** SPL9 binds to the miR528 promoter. The promoter or mutant promoter of miR528 was labelled using FAM, and the microscale thermophoresis assays gave the Kd values.

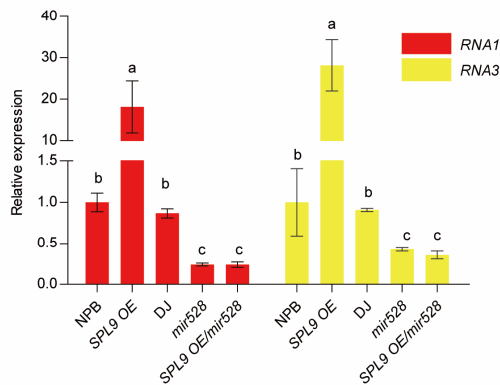


Supplemental Fig. 6 SPL9 negatively regulates the rice antiviral response during RSV infection. **A–B.** qRT-PCR analysis of the expression level of *RSV-RNA1* in the wild-type (NPB), *SPL9 OE*, and *spl9* mutant rice lines infected with RSV. The average values (\pm standard deviation) from three biological repeats are shown. Asterisks mark significant differences from the wild type, according to Student's *t*-test; ** P value ≤ 0.01 ; *** P value ≤ 0.001 . **C–D.** The incidences of infection determined by the visual disease symptoms at 1–8 wpi (weeks post infection) for the NPB, *SPL9 OE*, and *spl9* mutant lines. The average values (\pm standard deviation) from three biological repeats are shown.

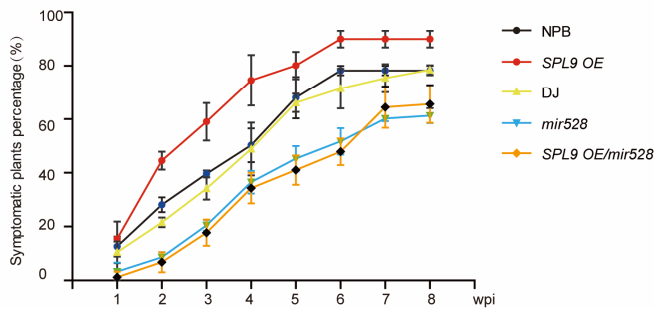
A



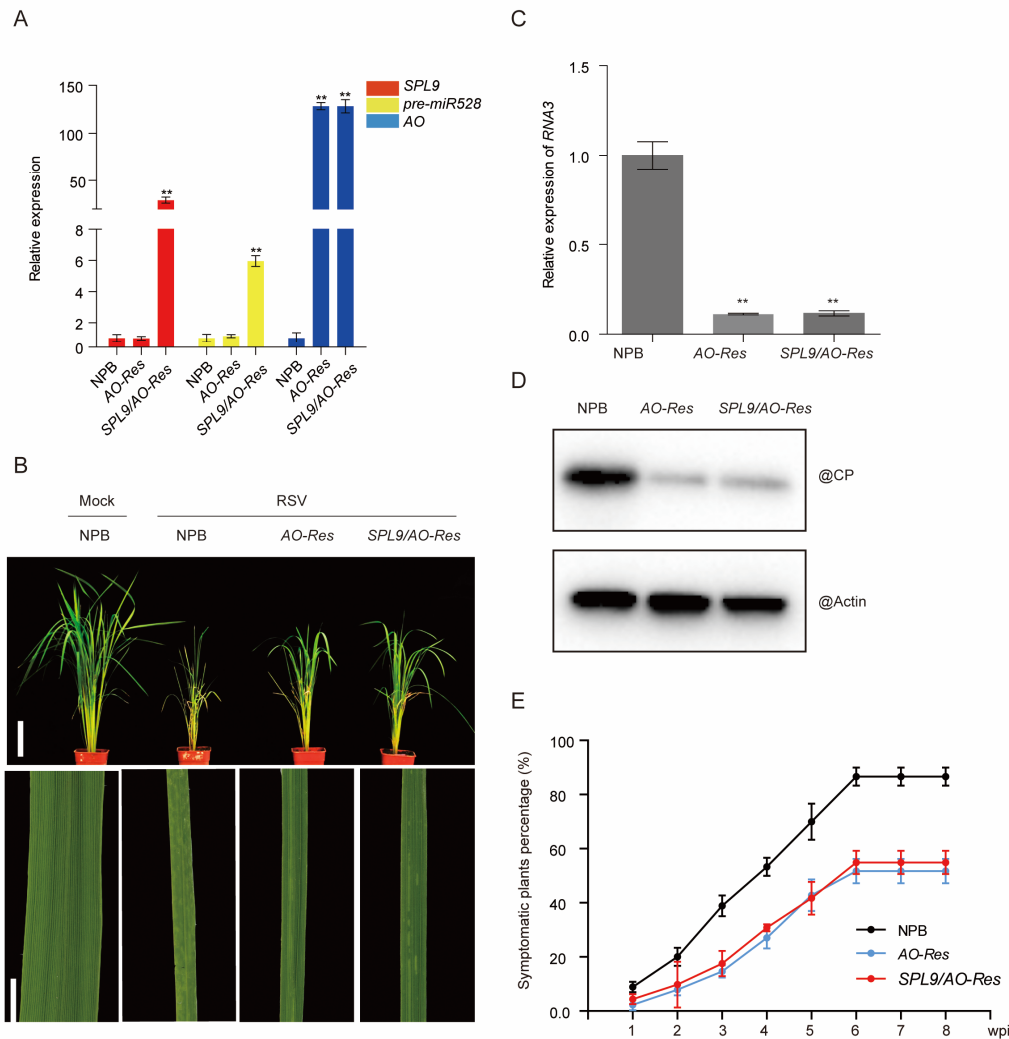
B



C



Supplemental Fig. 7 Both *SPL9 OE/mir528* and *mir528* are more tolerant of RSV infection than *SPL9 OE*. **A.** Phenotypic comparison of the indicated rice lines at six weeks after germination. Scale bar = 10 cm. **B.** qRT-PCR analysis of the levels of *RSV-RNA1* and *RSV-RNA3* in the indicated lines. The average values (\pm standard deviation) from three biological repeats are shown. For each gene, different letters indicate significant differences in expression according to Student's *t*-test; $P \leq 0.05$. **C.** The incidences of infection at 1–8 wpi (weeks post inoculation) for the indicated lines. The average values (\pm standard deviation) from three biological repeats are shown.



Supplemental Fig. 8 Both *SPL9 OE/AO-Res* and *AO-Res* are more tolerant of RSV infection than *SPL9 OE*. **A.** qRT-PCR analysis of the expression levels of *SPL9*, *pre-miR528*, and *AO* in the wild-type (NPB), *AO-Res*, and *SPL9 OE/AO-Res* lines. The average values (\pm standard deviation) from three biological repeats are shown. Asterisks mark significant differences to the wild type, according to Student's *t*-test; ** P value ≤ 0.01 . **B.** Symptoms of the mock-inoculated NPB or RSV-infected NPB, *AO-Res*, and *SPL9 OE/AO-Res* lines at 4 wpi (weeks post inoculation). Scale bars = 10 cm (upper panel) and 1 cm (lower panel). **C.** qRT-PCR analysis of the expression levels of *RSV-RNA3* in the indicated lines. The average values (\pm standard deviation) from three biological repeats are shown. Asterisks mark significant differences to the wild type, according to Student's *t*-test; ** P value ≤ 0.01 . **D.** Detection of RSV-CP in the NPB, *AO-Res*, and *SPL9 OE/AO-Res* lines using a western blot. Actin was probed as a loading control. **E.** The incidences of infection in the indicated lines from 1–8 wpi. The average values (\pm standard deviation) from three biological repeats are shown.

Supplemental files

Supplemental file 1

Supplemental file 1A. Record of the number of rice lines showing RSV symptoms (week post inoculation, wpi) for NPB, *SPL9 OE#1*, *SPL9 OE#2*, *SPL9 OE#3*.

		NPB	<i>SPL9 OE#1</i>	<i>SPL9 OE#2</i>	<i>SPL9 OE#3</i>
1wpi	Repeat1	2	5	5	4
	Repeat2	3	6	6	7
	Repeat3	4	7	6	4
2wpi	Repeat1	9	12	13	13
	Repeat2	9	11	12	15
	Repeat3	8	13	14	17
3wpi	Repeat1	13	19	18	19
	Repeat2	14	20	23	24
	Repeat3	13	21	22	20
4wpi	Repeat1	18	24	24	25
	Repeat2	19	23	25	26
	Repeat3	17	24	25	26
5wpi	Repeat1	23	26	28	27
	Repeat2	24	26	27	27
	Repeat3	22	27	25	28
6wpi	Repeat1	25	27	30	28
	Repeat2	26	28	27	27
	Repeat3	25	27	28	29
7wpi	Repeat1	25	28	30	28
	Repeat2	27	28	27	28
	Repeat3	26	29	28	29
8wpi	Repeat1	25	28	30	28
	Repeat2	27	28	27	28
	Repeat3	26	29	28	29
Number of inoculated plants	Repeat1	32	29	32	32
	Repeat2	34	30	29	33
	Repeat3	33	32	30	31

Supplemental file 1B. Record of the number of rice lines showing RSV symptoms (week post inoculation, wpi) for NPB, *spl9 #1* , *spl9 #2*.

		NPB	<i>spl9#1</i>	<i>spl9#2</i>
1wpi	Repeat1	3	1	2
	Repeat2	2	0	2
	Repeat3	3	1	1
2wpi	Repeat1	8	3	2
	Repeat2	7	4	5
	Repeat3	9	3	2
3wpi	Repeat1	13	6	5
	Repeat2	11	5	7
	Repeat3	13	7	5
4wpi	Repeat1	18	10	12
	Repeat2	14	11	10
	Repeat3	17	11	8
5wpi	Repeat1	24	15	14
	Repeat2	19	15	13
	Repeat3	21	14	10
6wpi	Repeat1	27	20	18
	Repeat2	26	17	16
	Repeat3	28	18	18
7wpi	Repeat1	27	21	18
	Repeat2	26	17	16
	Repeat3	28	18	18
8wpi	Repeat1	27	21	18
	Repeat2	26	17	16
	Repeat3	28	18	18
Number of inoculated plants	Repeat1	30	30	30
	Repeat2	30	30	30
	Repeat3	30	30	30

Supplemental file 1C. Record of the number of rice lines showing RSV symptoms (week post inoculation, wpi) for NPB, *SPL9 OE*, *DJ*, *mir528* and *SPL9 OE/mir528*.

		NPB	<i>SPL9 OE</i>	DJ	<i>mir528</i>	<i>SPL9 OE</i> <i>/mir528</i>
1wpi	Repeat1	3	4	2	1	0
	Repeat2	4	3	4	0	0
	Repeat3	5	7	4	2	1
2wpi	Repeat1	8	14	8	3	1
	Repeat2	10	13	7	2	2
	Repeat3	9	13	6	3	3
3wpi	Repeat1	13	19	10	6	7
	Repeat2	13	18	12	7	5
	Repeat3	12	16	11	6	4
4wpi	Repeat1	16	22	14	13	12
	Repeat2	15	25	15	10	11
	Repeat3	17	20	18	11	8
5wpi	Repeat1	21	24	22	13	14
	Repeat2	21	25	21	14	13
	Repeat3	23	23	21	15	10
6wpi	Repeat1	25	26	23	15	16
	Repeat2	26	28	22	16	14
	Repeat3	24	27	24	17	13
7wpi	Repeat1	25	26	26	19	22
	Repeat2	26	28	23	19	19
	Repeat3	24	27	24	18	17
8wpi	Repeat1	25	26	26	19	22
	Repeat2	26	28	23	18	19
	Repeat3	24	27	24	19	17
Number of inoculated plants	Repeat1	32	29	34	32	30
	Repeat2	34	30	33	31	32
	Repeat3	30	31	30	30	28

Supplemental file 1D. Record of the number of rice lines showing RSV symptoms (week post inoculation, wpi) for NPB, *AO-Res* and *SPL9 OE/AO-Res* lines.

		NPB	<i>AO-Res</i>	<i>SPL9OE/AO-Res</i>
1wpi	Repeat1	3	1	1
	Repeat2	2	0	2
	Repeat3	3	1	1
2wpi	Repeat1	6	2	2
	Repeat2	5	2	6
	Repeat3	7	3	1
3wpi	Repeat1	11	4	5
	Repeat2	11	4	7
	Repeat3	13	5	4
4wpi	Repeat1	15	7	9
	Repeat2	16	8	10
	Repeat3	17	9	9
5wpi	Repeat1	23	11	12
	Repeat2	19	13	15
	Repeat3	21	14	11
6wpi	Repeat1	26	14	17
	Repeat2	25	14	18
	Repeat3	27	16	15
7wpi	Repeat1	26	14	17
	Repeat2	25	14	18
	Repeat3	27	16	15
8wpi	Repeat1	26	14	17
	Repeat2	25	14	18
	Repeat3	27	16	15
Number of inoculated plants	Repeat1	30	30	30
	Repeat2	30	30	31
	Repeat3	30	29	30

Supplemental file 2

Supplemental file 2A. Constructs, Related to Experimental Procedures

Use	Construct	Plasmid name	Insert Fragment	Primers	Template	Plasmid backbone	Cloning method
Transgenic rice	Actin1::SPL9	<i>p2300:Actin1::SPL9</i>	SPL9	SPL9F1 SPL9R1	Rice cDNA	<i>pCAMBIA2300</i>	<i>Xba I</i> <i>Sal I</i>
	Actin1::FLAG-SPL9	<i>p2300:Actin1::FLAG-SPL9</i>	FLAG-SPL9	SPL9F2 SPL9R1	Rice cDNA	<i>pCAMBIA2300</i>	<i>Xba I</i> <i>Sal I</i>
Y1H	SPL1~19-AD	<i>AD-SPL1~19</i>	SPL1~19	SPL1~19F SPL1~19R	Rice cDNA	<i>pGADT7Rec2</i>	<i>Homology Recombination</i>
	miR528pro-His	<i>pHis2-miR528pro</i>	miR528 promoter	528pro-F1 528pro-R1	Rice DNA	<i>pHis2</i>	<i>Homology Recombination</i>
	miR528promut-His	<i>pHis2-miR528promut</i>	miR528 promoter mut	528pro-F1 528pro-R1	Gene synthesis	<i>pHis2</i>	<i>Homology Recombination</i>
Protein purification	SBP-GST	<i>pGEX4T-1-SBP</i>	SBP	SBPF1 SBPR2	<i>p2300:Actin1::SPL9</i>	<i>pGEX4T-1</i>	<i>Homology Recombination</i>

Supplemental file 2B. Primers for Plasmids Constructions, Related to Experimental Procedures

Primer name	Primer Sequence 5'-3'
SPL9F1	ATATCTAGAATGGACGCCCCCGGCGGCG
SPL9R1	ATAGTCGACCTATGATGAGTAGTTCCTAGACAAGTACCTC
SPL9F2	ATAATGGATTACAAGGATGACGACGATAAGTCTAGAATGGACGCCCCCGGCGGCG
SPL1F	TGGCCATGGAGGCCAGTGAATTCATGTCGAGTGGGCTCAAGAAG
SPL1R	CGTATCGATGCCACCCTCTAGATCACTTGGGGCCTGAACGCAAAG
SPL2F	ATGGCCATGGAGGCCAGTGAATTCATGGATTGGGACGCAAGATG
SPL2R	CGTATCGATGCCACCCTCTAGACTACCACGATGAGAAAGGAA
SPL3F	ATGGCCATGGAGGCCAGTGAATTCATGGGTTCTTTGGGATGGA
SPL3R	CGTATCGATGCCACCCTCTAGATCAGTTCATCTGATCATAGTGG
SPL4F	ATGGCCATGGAGGCCAGTGAATTCATGGATTGGATGCTCCTCC
SPL4R	CGTATCGATGCCACCCTCTAGATTAATGAAATGACATGCAGC
SPL5F	ATGGCCATGGAGGCCAGTGAATTCATGGCGGTGCCAGCGGCGG
SPL5R	CGTATCGATGCCACCCTCTAGACTAGATGAAATCCACCTCGA
SPL6F	ATGGCCATGGAGGCCAGTGAATTCATGGAGGCTGCCGGGTC
SPL6R	CGTATCGATGCCACCCTCTAGATCACATTGGTCCACGTCT
SPL7F	ATGGCCATGGAGGCCAGTGAATTCATGGAAAGGAAACGGCTGCG
SPL7R	CGTATCGATGCCACCCTCTAGATCAGACCACGGGGCGCCCTC
SPL8F	ATGGCCATGGAGGCCAGTGAATTCATGATGAACGTTCCATCC
SPL8R	CGTATCGATGCCACCCTCTAGACTAGTGATCGAAGTCGAGA
SPL9F	ATGGCCATGGAGGCCAGTGAATTCATGGACGCCCCCGGCGGCG
SPL9R	CGTATCGATGCCACCCTCTAGACTATGATGAGTAGTTCCTAGAC
SPL10F	ATGGCCATGGAGGCCAGTGAATTCATGATGAGCGGTAGGATG
SPL10R	CGTATCGATGCCACCCTCTAGACTACATGAAGTCGACCTCGA
SPL11F	ATGGCCATGGAGGCCAGTGAATTCATGGAGTGAACCCCGTCTC
SPL11R	CGTATCGATGCCACCCTCTAGATCAATGTATCTGGTTCAGAC
SPL12F	ATGGCCATGGAGGCCAGTGAATTCATGGCTTCTTTGGGATG
SPL12R	CGTATCGATGCCACCCTCTAGATCAGTGCAGATGGCCATAGC

SPL13F	ATGGCCATGGAGGCCAGTGAATTCATGGACCGCAAGGACAAGG
SPL13R	CGTATCGATGCCACCCTCTAGA TTATCTGATCTGGAACGGCG
SPL14F	ATGGCCATGGAGGCCAGTGAATTCATGGAGATGGCCAGTGGAGG
SPL14R	CGTATCGATGCCACCCTCTAGACTACAGAGACCAATCCATCGTG
SPL15F	ATGGCCATGGAGGCCAGTGAATTCATGCAGAGGGGAAGTGGGG
SPL15R	CGTATCGATGCCACCCTCTAGATTATATCGTACCAAAATCCAG
SPL16F	ATGGCCATGGAGGCCAGTGAATTCATGGAGTGGGATCTCAAGA
SPL16R	CGTATCGATGCCACCCTCTAGACTACTGCCATGAGAACGGCAG
SPL17F	ATGGCCATGGAGGCCAGTGAATTCATGGCGACCGGCGGCAGCGG
SPL17R	CGTATCGATGCCACCCTCTAGACTACAGAGACCAGTTCATGG
SPL18F	ATGGCCATGGAGGCCAGTGAATTCATGGATTGGGATCTCAAG
SPL18R	CGTATCGATGCCACCCTCTAGACTACTGCCACGAGAATGGGAG
SPL19F	ATGGCCATGGAGGCCAGTGAATTC ATGGAGTGGGCGGCGGCGG
SPL19R	CGTATCGATGCCACCCTCTAGACTACACCTGCCAAGAGAATG
528 _{pro} -F1	CGGAATTCGACGGATGGGATGATGGGAGAG
528 _{pro} -R1	GCGAGCTCCATTGGTGAAGGGTGGCATAT
SBPF1	TGGTTCCGCGTGGATCCCCGGAATTCATGGACGCCCCCGGCGGCGG
SBPR2	GTCACGATGCGGCCGCTCGAGTCGACCCACAGGTGTTCCCTGTCCA

Supplemental file 2C. Primers for EMSA, qRT-PCR, and MST, Related to Experimental Procedures

Primer name	Primer Sequence 5'-3'	Use
EF1 α -F	GCACGCTCTTCTTGCTTTCCTCT	QRT-PCR
EF1 α -R	GCACGCTCTTCTTGCTTTCCTCT	
SPL9-F	AGCAGATGGTAGTGGTGATG	
SPL9-R	CAGAAGCAGCGAAAGTCA	
AO-F	CGAGAACGTGGAGACCTGCGTCGA	
AO-R	CCACCACCGTCATCTTGTGCCCTTG	
pre-miR528-F	CAGAGGAGCAGGAGATCA	
pre-miR528-R	AAACTTCCACAGAACAGCCT	
RSV-RNA1-F	GCACCCAATAGGTATCTCCTTGAT	
RSV-RNA1-R	CAAATGACCCTACTAGATGGACGA	
RSV-RNA3-F	TATATGGGCACCAACAAGCCAGCC	
RSV-RNA3-R	TATGACTTAGGGAGTGAGTTGTGCAGT	
MST-528 _{pro} -F	FAM- CAGTACAAGAGTACAGCTGAAAGCCATAGTACTACTGATGAT ATTTGCAAGCCTGAAGTAC	
MST-528 _{pro} -R	FAM- GTACTTCAGGCTTGCAAATATCATCAGTGTACTATGGCTTTC AGCTGACTCTTGTACTG	
MST-528 _{pro} mut-F	FAM- CAGATCAAGAGATCAGCTGAAAGCCATAGTACTACTGATGAT ATTTGCAAGCCTGAAGATC	

MST-528pro mut-R	FAM- GATCTTCAGGCTTGCAAATATCATCAGTGATCTATGGCTTTC AGCTGATCTCTTGATCTG	
Lablled-miR528pro-F	Biotin- CAGTACAAGAGTACAGCTGAAAGCCATAGTACACTGATGAT ATTTGCAAGCCTGAAGTAC	EMSA
Lablled-miR528pro-R	Biotin- GTACTTCAGGCTTGCAAATATCATCAGTGTACTATGGCTTTC AGCTGTACTCTTGACTG	
unlablled-miR528pro-F	AGTACAAGAGTACAGCTGAAAGCCATAGTACAC	
unlablled-miR528pro-R	GTGTACTATGGCTTTCAGCTGTACTCTTGACT	
mutant-miR528pro-F	AGATCAAGAGATCAGCTGAAAGCCATAGATCAC	
mutant-miR528pro-R	GTGATCTATGGCTTTCAGCTGATCTCTTGATCT	
P1-F	GTACTTCACATATTGGCATG	
P1-R	GTGATTGAGTTGCTACTAGT	
P2-F	GCTCCAACGCTTCTGCAGTA	
P2-R	ATGCATCCATTGGTGAAGGG	
C-F	GCAGCCACAGCAAAATTTGGT	
C-R	GATGCCATGGACGATTAACC	

Supplemental file 3

General information about genes in this study

SPL1 LOC_Os01g18850
 SPL2 LOC_Os01g69830
 SPL3 LOC_Os02g04680
 SPL4 LOC_Os02g07780
 SPL5 LOC_Os02g08070
 SPL6 LOC_Os03g61760
 SPL7 LOC_Os04g46580
 SPL8 LOC_Os04g56170
 SPL9 LOC_Os05g33810
 SPL10 LOC_Os06g44860
 SPL11 LOC_Os06g45310
 SPL12 LOC_Os06g49010
 SPL13 LOC_Os07g32170
 SPL14 LOC_Os08g39890
 SPL15 LOC_Os08g40260
 SPL16 LOC_Os08g41940
 SPL17 LOC_Os09g31438
 SPL18 LOC_Os09g32944
 SPL19 LOC_Os11g30370
 MIR528 LOC_Os03g03724
 AO LOC_Os06g37150

Supplemental file 4

A. Sequence of miR528 promoter

GCCGTAAGTGCGAACCTGCTCTGGCTCAATCGCATAGAGGGACGCGCTGCGCACAGCCCGATGCTTTTC
 TATAGTTCCATAGTCCACCGGTTACCACATGGACGGATGGGATGATGGGAGAGTTTTCTGTAATGCTCA
 CATTATTGTATCTTACTAAACCCACTTTTATAAATACATGACAGCATTGACTTTTGAACATATATTAT
 CTTAATTTTTAAAAATAAATTAATTATTATTTATTTTGTGTGAGTTTTTTTTTATTGAAAGTACTTTA
 AACATGATTTTATATTTTATGCATTTTCGTAAAAATATTCTAATAAGACGAACAATGGTATGTATTA
 AAAAAACGAGAGTATTTAACATTTTAATCTGTACTATCATTCGCGACAATTTTTTTTTTCAAAATTGCGGAGTAG
 TACTTCACATATTGGCATGGAGTACATCAGACGATACTAGTACAGCATAACATGTCGTGGCGTTCAACTT
 GTTGGAGATCTGATGCGATATAAATCGATCCTACGTCACATGACAGACTGGACCTTGTCAAAATTATG
 GATTGGATGATTAATCACTGATAGGTAGTACTAGTAGCAACTCAATCACACAAGCGAAGTGAGAAGAAA
 AGGAACCTCTTCTGCATTAAGACAACGGCGACGGGGTCACTGAAAGTGAAGCCTGTGGCGCACACGAC
 ACGACCTCCTCAACGGATCTGTGGCTTACCCGTCGCCGTTAGAGCGTTTGTCTCAACGCTTCTGCAGTA
 CAAGAGTACAGCTGAAAGCCATAGTACACTGATGATATTTGCAAGCCTGAAGTACAAGCCGCCCTAAC
 GATCTCCCCCATATGTACTGCAGCTAACTTGTACTACTACCAGTGCACCATGGCCGGGGTACAAATA
 TGCCACCCTTACCAATGGATGCATCAGCAGCAGCCACAGCAAAATTTGGTTTGGGATAGGTAGGTGTT
 ATGTTAGGTCTGGTTTTTTTGGCTGTAGCAGCAGC

B. Binding sites predicted by New PLACE

(<https://sogo.dna.affrc.go.jp/cgi-bin/sogo.cgi?sid=&pj=0&lang=en&action=page&page=analysis>)

Factor or Site Name	Loc. (Str.)	Signal Sequence	SITE #
CACTFTPPCA1	7 (-) YACT		S000449
CAATBOX1	27 (+) CAAT		S000028
ARR1AT	28 (-) NGATT		S000454
CGCGBOXAT	42 (-) VCGCGB		S000501
CGCGBOXAT	42 (+) VCGCGB		S000501
DOFCOREZM	64 (-) AAAG		S000265
POLLEN1LELAT52	66 (-) AGAAA		S000245
BOX1INTPATPB	67 (-) ATAGAA		S000296
MYBCORE	88 (+) CNGTTR		S000176
EBOXBNNAPA	95 (-) CANN TG		S000144
MYCCONSENSUSAT	95 (-) CANN TG		S000407
MYCATERD1	95 (-) CATGTG		S000413
EBOXBNNAPA	95 (+) CANN TG		S000144
MYCATRD22	95 (+) CACATG		S000174
MYCCONSENSUSAT	95 (+) CANN TG		S000407
CMSRE1IBSPOA	99 (+) TGGACGG		S000511
PALBOXAPC	100 (-) CCGTCC		S000137
POLLEN1LELAT52	124 (-) AGAAA		S000245
GTGANTG10	136 (-) GTGA		S000378
POLASIG1	141 (-) AATAAA		S000080
CAATBOX1	144 (-) CAAT		S000028

GATABOX	148 (-) GATA	S000039
CACTFTPPCA1	153 (+) YACT	S000449
SEF3MOTIFGM	158 (+) AACCCA	S000115
CACTFTPPCA1	162 (+) YACT	S000449
DOFCOREZM	164 (-) AAAG	S000265
TATABOX2	168 (+) TATAAAT	S000109
BIHD10S	178 (-) TGTCA	S000498
WRKY710S	178 (+) TGAC	S000447
CAATBOX1	185 (-) CAAT	S000028
WBOXATNPR1	186 (+) TTGAC	S000390
WBOXHVIS01	187 (+) TGACT	S000442
WRKY710S	187 (+) TGAC	S000447
WBOXNTERF3	187 (+) TGACY	S000457
DOFCOREZM	190 (-) AAAG	S000265
ROOTMOTIFTAPOX1	201 (+) ATATT	S000098
GT1CONSENSUS	203 (-) GRWAAW	S000198
IBOXCORE	204 (-) GATAA	S000199
GATABOX	205 (-) GATA	S000039
SEF4MOTIFGM7S	212 (+) RTTTTTR	S000103
TATABOX5	221 (-) TTATTT	S000203
POLASIG1	222 (+) AATAAA	S000080
HDZIP2ATATHB2	229 (-) TAATMATTA	S000373
POLASIG3	231 (-) AATAAT	S000088
POLASIG3	234 (-) AATAAT	S000088
TATABOX5	235 (+) TTATTT	S000203
POLASIG1	238 (-) AATAAA	S000080
TATABOX5	239 (+) TTATTT	S000203
RAVIAAT	245 (-) CAACA	S000314
GTGANTG10	249 (+) GTGA	S000378
MARTBOX	255 (+) TTWTWTTT	S000067
POLASIG1	259 (-) AATAAA	S000080
CAATBOX1	262 (-) CAAT	S000028
DOFCOREZM	266 (+) AAAG	S000265
CACTFTPPCA1	268 (-) YACT	S000449
CURECORECR	269 (-) GTAC	S000493
CURECORECR	269 (+) GTAC	S000493
CACTFTPPCA1	270 (+) YACT	S000449
NTBBF1ARROLB	271 (+) ACTTTA	S000273
DOFCOREZM	272 (-) AAAG	S000265
TAAAGSTKST1	272 (-) TAAAG	S000387
ARRIAT	281 (+) NGATT	S000454
TATABOX2	283 (-) TATAAAT	S000109
MARARS	283 (+) WTTTATRRTTW	S000064
LECPLEACS2	287 (-) TAAAATAT	S000465

ROOTMOTIFTAPOX1	287 (+) ATATT	S000098
SEF4MOTIFGM7S	304 (-) RTTTTTR	S000103
ROOTMOTIFTAPOX1	308 (-) ATATT	S000098
ROOTMOTIFTAPOX1	309 (+) ATATT	S000098
-10PEHVPSBD	310 (+) TATTCT	S000392
CPBCSPOR	314 (-) TATTAG	S000491
CAATBOX1	327 (+) CAAT	S000028
S1FBOXSORPS1L21	329 (+) ATGGTA	S000223
CACTFTPPCA1	351 (-) YACT	S000449
TATABOXOSPAL	353 (+) TATTAA	S000400
ARR1AT	366 (-) NGATT	S000454
CURECORECR	371 (-) GTAC	S000493
CURECORECR	371 (+) GTAC	S000493
CACTFTPPCA1	372 (+) YACT	S000449
GATABOX	375 (-) GATA	S000039
PRECONSCRHSP70A	383 (+) SCGAYNRNNNNNNNNNNNNNNHHD	S000506
CAATBOX1	387 (+) CAAT	S000028
GT1CONSENSUS	394 (-) GRWAAW	S000198
GT1GMSCAM4	394 (-) GAAAAA	S000453
CAATBOX1	403 (-) CAAT	S000028
CACTFTPPCA1	410 (-) YACT	S000449
CACTFTPPCA1	413 (-) YACT	S000449
CURECORECR	414 (-) GTAC	S000493
CURECORECR	414 (+) GTAC	S000493
CACTFTPPCA1	415 (+) YACT	S000449
GTGANTG10	419 (-) GTGA	S000378
ROOTMOTIFTAPOX1	423 (+) ATATT	S000098
CAATBOX1	425 (-) CAAT	S000028
CCAATBOX1	425 (-) CCAAT	S000030
CACTFTPPCA1	435 (-) YACT	S000449
CURECORECR	436 (-) GTAC	S000493
CURECORECR	436 (+) GTAC	S000493
GATABOX	447 (+) GATA	S000039
CACTFTPPCA1	449 (+) YACT	S000449
CACTFTPPCA1	453 (-) YACT	S000449
CURECORECR	454 (-) GTAC	S000493
CURECORECR	454 (+) GTAC	S000493
SORLIP1AT	470 (-) GCCAC	S000482
RAV1AAT	483 (-) CAACA	S000314
GATABOX	500 (+) GATA	S000039
TATABOX2	502 (+) TATAAAT	S000109
ARR1AT	506 (-) NGATT	S000454
TGACGTMAMY	516 (-) TGACGT	S000377
ACGTATERD1	516 (-) ACGT	S000415

HEXMOTIFTAH3H4	516 (+) ACGTCA	S000053
ACGTATERD1	516 (+) ACGT	S000415
ASF1MOTIFCAMV	517 (-) TGACG	S000024
WRKY710S	518 (-) TGAC	S000447
GTGANTG10	519 (-) GTGA	S000378
EBOXBNNAPA	520 (-) CANNTG	S000144
MYCCONSENSUSAT	520 (-) CANNTG	S000407
MYCATERD1	520 (-) CATGTG	S000413
EBOXBNNAPA	520 (+) CANNTG	S000144
MYCATRD22	520 (+) CACATG	S000174
MYCCONSENSUSAT	520 (+) CANNTG	S000407
BIHD10S	524 (-) TGTCA	S000498
WRKY710S	524 (+) TGAC	S000447
BIHD10S	540 (+) TGTCA	S000498
WBOXATNPR1	541 (-) TTGAC	S000390
WRKY710S	541 (-) TGAC	S000447
CARGCW8GAT	543 (-) CWWWWWWWG	S000431
CARGCW8GAT	543 (+) CWWWWWWWG	S000431
ARR1AT	552 (+) NGATT	S000454
CAATBOX1	554 (-) CAAT	S000028
CCAATBOX1	554 (-) CCAAT	S000030
ARR1AT	560 (+) NGATT	S000454
ARR1AT	565 (-) NGATT	S000454
GTGANTG10	567 (-) GTGA	S000378
CACTFTPPCA1	568 (+) YACT	S000449
GATABOX	572 (+) GATA	S000039
CACTFTPPCA1	579 (-) YACT	S000449
CURECORECR	580 (-) GTAC	S000493
CURECORECR	580 (+) GTAC	S000493
CACTFTPPCA1	581 (+) YACT	S000449
CACTFTPPCA1	585 (-) YACT	S000449
EECCRAH1	589 (-) GANTNC	S000494
CIACADIANLELHC	590 (+) CAANNNATC	S000252
CAREOSREP1	590 (+) CAACTC	S000421
CAATBOX1	595 (+) CAAT	S000028
ARR1AT	596 (-) NGATT	S000454
GTGANTG10	598 (-) GTGA	S000378
DPBFCOREDCDC3	600 (+) ACACNG	S000292
INRNTPSADB	608 (-) YTCANTYY	S000395
CACTFTPPCA1	610 (-) YACT	S000449
GTGANTG10	611 (+) GTGA	S000378
POLLEN1LELAT52	617 (+) AGAAA	S000245
PYRIMIDINEBOXOSRAMY1A	619 (-) CCTTTT	S000259
DOFCOREZM	620 (+) AAAG	S000265

NODCON2GM	628 (+) CTCTT	S000462
OSE2ROOTNODULE	628 (+) CTCTT	S000468
INTRONLOWER	633 (-) TGCAGG	S000086
MYBCORE	645 (-) CNGTTR	S000176
MYB2CONSENSUSAT	645 (+) YAACKG	S000409
MYBCOREATCYCB1	646 (+) AACGG	S000502
PRECONSCRHSP70A	650 (+) SCGAYNRNNNNNNNNNNNNNNHHD	S000506
HEXAMERATH4	651 (-) CCGTCG	S000146
CGACGOSAMY3	651 (+) CGACG	S000205
WBOXNTERF3	657 (-) TGACY	S000457
WRKY710S	658 (-) TGAC	S000447
GTGANTG10	659 (-) GTGA	S000378
CACTFTPPCA1	660 (+) YACT	S000449
INRNTPSADB	665 (-) YTCANTYY	S000395
DOFCOREZM	665 (+) AAAG	S000265
CACTFTPPCA1	667 (-) YACT	S000449
GTGANTG10	668 (+) GTGA	S000378
SORLIP1AT	677 (-) GCCAC	S000482
MYBCORE	701 (-) CNGTTR	S000176
MYB2CONSENSUSAT	701 (+) YAACKG	S000409
MYBCOREATCYCB1	702 (+) AACGG	S000502
SORLIP1AT	711 (-) GCCAC	S000482
HEXAMERATH4	720 (+) CCGTCG	S000146
CGACGOSAMY3	721 (-) CGACG	S000205
MYB2CONSENSUSAT	726 (-) YAACKG	S000409
MYBCOREATCYCB1	726 (-) AACGG	S000502
MYBCORE	726 (+) CNGTTR	S000176
CACTFTPPCA1	756 (-) YACT	S000449
CURECORECR	757 (-) GTAC	S000493
CURECORECR	757 (+) GTAC	S000493
NODCON2GM	761 (-) CTCTT	S000462
OSE2ROOTNODULE	761 (-) CTCTT	S000468
CACTFTPPCA1	764 (-) YACT	S000449
CURECORECR	765 (-) GTAC	S000493
CURECORECR	765 (+) GTAC	S000493
EBOXBNNAPA	768 (-) CANNTG	S000144
MYCCONSUSAT	768 (-) CANNTG	S000407
EBOXBNNAPA	768 (+) CANNTG	S000144
MYCCONSUSAT	768 (+) CANNTG	S000407
DOFCOREZM	774 (+) AAAG	S000265
CACTFTPPCA1	782 (-) YACT	S000449
CURECORECR	783 (-) GTAC	S000493
CURECORECR	783 (+) GTAC	S000493
CACTFTPPCA1	786 (+) YACT	S000449

GATABOX	793 (+) GATA	S000039
ROOTMOTIFTAPOX1	794 (+) ATATT	S000098
CACTFTPPCA1	810 (-) YACT	S000449
CURECORECR	811 (-) GTAC	S000493
CURECORECR	811 (+) GTAC	S000493
AGCBOXNPGLB	816 (+) AGCCGCC	S000232
GCCCORE	817 (+) GCCGCC	S000430
EBOXBNNAPA	840 (-) CANNTG	S000144
CATATGGMSAUR	840 (-) CATATG	S000370
MYCCONSENSUSAT	840 (-) CANNTG	S000407
EBOXBNNAPA	840 (+) CANNTG	S000144
CATATGGMSAUR	840 (+) CATATG	S000370
MYCCONSENSUSAT	840 (+) CANNTG	S000407
CURECORECR	845 (-) GTAC	S000493
CURECORECR	845 (+) GTAC	S000493
CACTFTPPCA1	846 (+) YACT	S000449
CURECORECR	861 (-) GTAC	S000493
CURECORECR	861 (+) GTAC	S000493
CACTFTPPCA1	862 (+) YACT	S000449
CACTFTPPCA1	865 (+) YACT	S000449
CACTFTPPCA1	872 (-) YACT	S000449
CURECORECR	889 (-) GTAC	S000493
CURECORECR	889 (+) GTAC	S000493
ROOTMOTIFTAPOX1	894 (-) ATATT	S000098
SORLIP1AT	899 (+) GCCAC	S000482
GTGANTG10	907 (-) GTGA	S000378
CCAATBOX1	910 (+) CCAAT	S000030
CAATBOX1	911 (+) CAAT	S000028
ANAERO2CONSENSUS	924 (+) AGCAGC	S000478
ANAERO2CONSENSUS	927 (+) AGCAGC	S000478
SORLIP1AT	931 (+) GCCAC	S000482
REALPHALGLHCB21	944 (-) AACCAA	S000362
MYB1AT	945 (-) WAACCA	S000408
MYBST1	952 (+) GGATA	S000180
GATABOX	953 (+) GATA	S000039
MYBPLANT	957 (-) MACCWAMC	S000167
MYBPZM	957 (-) CCWACC	S000179
BOXLCOREDPCAL	957 (-) ACCWWCC	S000492
MYB1AT	977 (-) WAACCA	S000408
ANAERO2CONSENSUS	992 (+) AGCAGC	S000478
ANAERO2CONSENSUS	995 (+) AGCAGC	S000478

C. Binding sites predicted by PlantCARE

(<http://bioinformatics.psb.ugent.be/webtools/plantcare/html/>)

Site Name	Organism	Position	Strand	Matrix score.	sequence	function
	organism	50	-	4	motif_sequence	short_function
	organism	486	-	4	motif_sequence	short_function
	organism	435	-	4	motif_sequence	short_function
	organism	842	+	4	motif_sequence	short_function
	organism	194	-	4	motif_sequence	short_function
	organism	764	-	4	motif_sequence	short_function
	organism	453	-	4	motif_sequence	short_function
	organism	627	+	4	motif_sequence	short_function
	organism	116	-	4	motif_sequence	short_function
	organism	829	+	4	motif_sequence	short_function
	organism	368	+	4	motif_sequence	short_function

Site Name	Organism	Position	Strand	Matrix score.	sequence	function
A-box	Petroselinum crispum	99	-	6	CCGTCC	cis-acting regulatory element

Site Name	Organism	Position	Strand	Matrix score.	sequence	function
ACE	Petroselinum crispum	459	-	9	GACACGTATG	cis-acting element involved in light responsiveness

Site Name	Organism	Position	Strand	Matrix score.	sequence	function
ARE	Zea mays	944	-	6	AAACCA	cis-acting regulatory element essential for the anaerobic induct
ARE	Zea mays	976	-	6	AAACCA	cis-acting regulatory element essential for the anaerobic induct

Site Name	Organism	Position	Strand	Matrix score.	sequence	function
AT1-motif	Solanum tuberosum	229	+	13	AATTATTTTTATT	part of a light responsive module

Site Name	Organism	Position	Strand	Matrix score.	sequence	function
Box 4	Petroselinum crispum	561	-	6	ATTAAT	part of a conserved DNA module involved in light responsiveness
Box 4	Petroselinum crispum	226	+	6	ATTAAT	part of a conserved DNA module involved in light responsiveness

Site Name	Organism	Position	Strand	Matrix score.	sequence	function
CAAT-box	Nicotiana glutinosa	26	+	4	CAAT	
CAAT-box	Arabidopsis thaliana	553	-	5	CCAAT	common cis-acting element in promoter and enhancer regions
CAAT-box	Nicotiana glutinosa	326	+	4	CAAT	
CAAT-box	Arabidopsis thaliana	909	+	5	CCAAT	common cis-acting element in promoter and enhancer regions
CAAT-box	Nicotiana glutinosa	261	-	4	CAAT	
CAAT-box	Pisum sativum	795	-	5	CAAAT	common cis-acting element in promoter and enhancer regions
CAAT-box	Nicotiana glutinosa	402	-	4	CAAT	
CAAT-box	Pisum sativum	941	-	5	CAAAT	common cis-acting element in promoter and enhancer regions
CAAT-box	Nicotiana glutinosa	143	-	4	CAAT	
CAAT-box	Nicotiana glutinosa	594	+	4	CAAT	
CAAT-box	Nicotiana glutinosa	386	+	4	CAAT	
CAAT-box	Nicotiana glutinosa	910	+	4	CAAT	
CAAT-box	Nicotiana glutinosa	184	-	4	CAAT	
CAAT-box	Pisum sativum	891	+	5	CAAAT	common cis-acting element in promoter and enhancer regions
CAAT-box	Arabidopsis thaliana	424	-	5	CCAAT	common cis-acting element in promoter and enhancer regions

Site Name	Organism	Position	Strand	Matrix score.	sequence	function
CCAAT-box	Hordeum vulgare	644	+	6	CAACGG	MYBHv1 binding site
CCAAT-box	Hordeum vulgare	700	+	6	CAACGG	MYBHv1 binding site

Site Name	Organism	Position	Strand	Matrix score.	sequence	function
CCGTCC motif	Nicotiana tabacum	99	-	6	CCGTCC	

Site Name	Organism	Position	Strand	Matrix score.	sequence	function
CCGTCC-box	Petroselinum hortense	99	-	6	CCGTCC	

Site Name	Organism	Position	Strand	Matrix score.	sequence	function
CGTCA-motif	Hordeum vulgare	516	+	5	CGTCA	cis-acting regulatory element involved in the MeJA-responsiveness

Site Name	Organism	Position	Strand	Matrix score.	sequence	function
G-box	Zea mays	466	-	6	CACGAC	cis-acting regulatory element involved in light responsiveness:
G-box	Zea mays	689	+	6	CACGAC	cis-acting regulatory element involved in light responsiveness:
G-box	Zea mays	684	+	6	CACGAC	cis-acting regulatory element involved in light responsiveness:

+ MSA-like						
Site Name	Organism	Position	Strand	Matrix score.	sequence	function
MSA-like	Catharanthus roseus	722	-	8.5	(T/C)C (T/C)AACGG (T/C) (T/C) A	cis-acting element involved in cell cycle regulation
+ MYB recognition site						
Site Name	Organism	Position	Strand	Matrix score.	sequence	function
MYB recognition site	Arabidopsis thaliana	644	-	6	CGGTTG	
MYB recognition site	Arabidopsis thaliana	700	-	6	CGGTTG	
+ MYC						
Site Name	Organism	Position	Strand	Matrix score.	sequence	function
MYC	Arabidopsis thaliana	519	-	6	CATGTG	
MYC	Arabidopsis thaliana	94	-	6	CATGTG	
+ NON						
Site Name	Organism	Position	Strand	Matrix score.	sequence	function
NON	Nicotiana tabacum	644	+	10	CAACGGCCACG	
+ STRE						
Site Name	Organism	Position	Strand	Matrix score.	sequence	function
STRE	Arabidopsis thaliana	820	-	5	AGGGG	
+ Sp1						
Site Name	Organism	Position	Strand	Matrix score.	sequence	function
Sp1	Oryza sativa	817	-	6	GGGGGG	light responsive element
+ TATA-box						
Site Name	Organism	Position	Strand	Matrix score.	sequence	function
TATA-box	Arabidopsis thaliana	69	+	4	TATA	core promoter element around -30 of transcription start
TATA-box	Brassica juncea	282	-	7	TATAAAT	core promoter element around -30 of transcription start
TATA-box	Arabidopsis thaliana	167	+	4	TATA	core promoter element around -30 of transcription start
TATA-box	Arabidopsis thaliana	499	+	9	taTATAAAAtc	core promoter element around -30 of transcription start
TATA-box	Helianthus annuus	165	-	6	TATAAA	core promoter element around -30 of transcription start
TATA-box	Arabidopsis thaliana	284	-	5	TATAA	core promoter element around -30 of transcription start
TATA-box	Arabidopsis thaliana	199	+	4	TATA	core promoter element around -30 of transcription start
TATA-box	Arabidopsis thaliana	501	-	4	TATA	core promoter element around -30 of transcription start
TATA-box	Pisum sativum	164	-	7	TATAAAA	core promoter element around -30 of transcription start
TATA-box	Helianthus annuus	283	-	6	TATAAA	core promoter element around -30 of transcription start
TATA-box	Brassica napus	198	+	6	ATATAT	core promoter element around -30 of transcription start
TATA-box	Brassica oleracea	500	+	6	ATATAA	core promoter element around -30 of transcription start
TATA-box	Arabidopsis thaliana	166	-	5	TATAA	core promoter element around -30 of transcription start
TATA-box	Arabidopsis thaliana	285	+	4	TATA	core promoter element around -30 of transcription start
TATA-box	Arabidopsis thaliana	281	-	9	taTATAAAAtc	core promoter element around -30 of transcription start
+ TATC-box						
Site Name	Organism	Position	Strand	Matrix score.	sequence	function
TATC-box	Oryza sativa	949	-	7	TATCCCA	cis-acting element involved in gibberellin-responsiveness
+ TCT-motif						
Site Name	Organism	Position	Strand	Matrix score.	sequence	function
TCT-motif	Arabidopsis thaliana	149	+	6	TCTTAC	part of a light responsive element
+ TGACG-motif						
Site Name	Organism	Position	Strand	Matrix score.	sequence	function
TGACG-motif	Hordeum vulgare	516	-	5	TGACG	cis-acting regulatory element involved in the MeJA-responsiveness
+ Unnamed_1						
Site Name	Organism	Position	Strand	Matrix score.	sequence	function
Unnamed_1	Zea mays	468	+	5	CGTGG	
+ Unnamed_2						
Site Name	Organism	Position	Strand	Matrix score.	sequence	function
Unnamed_2	Zea mays	883	-	6	CCCCGG	
+ Unnamed_4						
Site Name	Organism	Position	Strand	Matrix score.	sequence	function
Unnamed_4	Petroselinum hortense	116	-	4	CTCC	
Unnamed_4	Petroselinum hortense	695	+	4	CTCC	
Unnamed_4	Petroselinum hortense	432	-	4	CTCC	
Unnamed_4	Petroselinum hortense	831	+	4	CTCC	
Unnamed_4	Petroselinum hortense	407	-	4	CTCC	
Unnamed_4	Petroselinum hortense	740	+	4	CTCC	
Unnamed_4	Petroselinum hortense	486	-	4	CTCC	
+ as-1						
Site Name	Organism	Position	Strand	Matrix score.	sequence	function
as-1	Arabidopsis thaliana	516	-	5	TGACG	