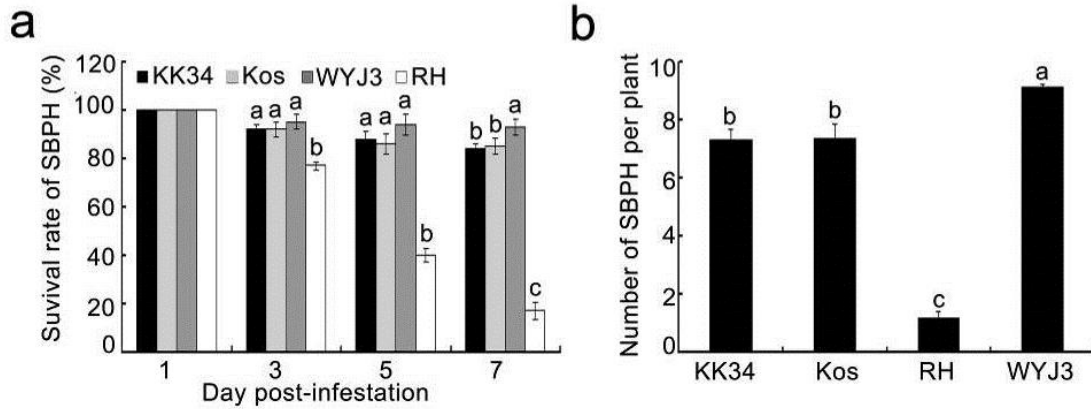
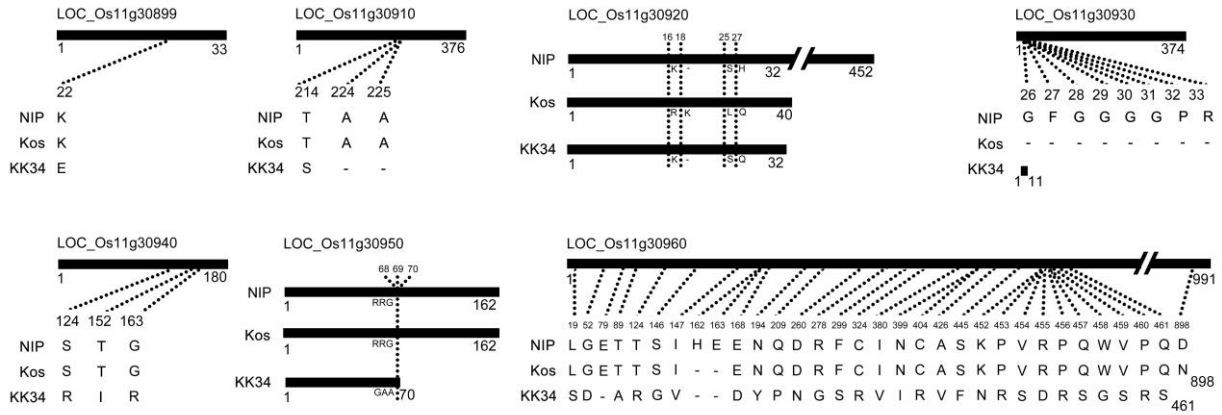


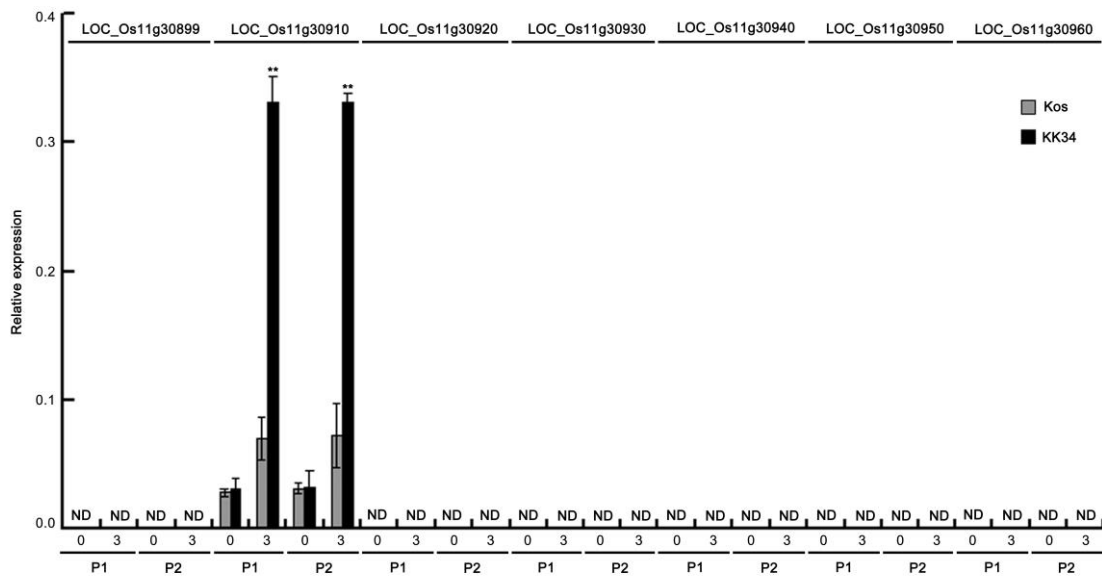
Supplementary Information



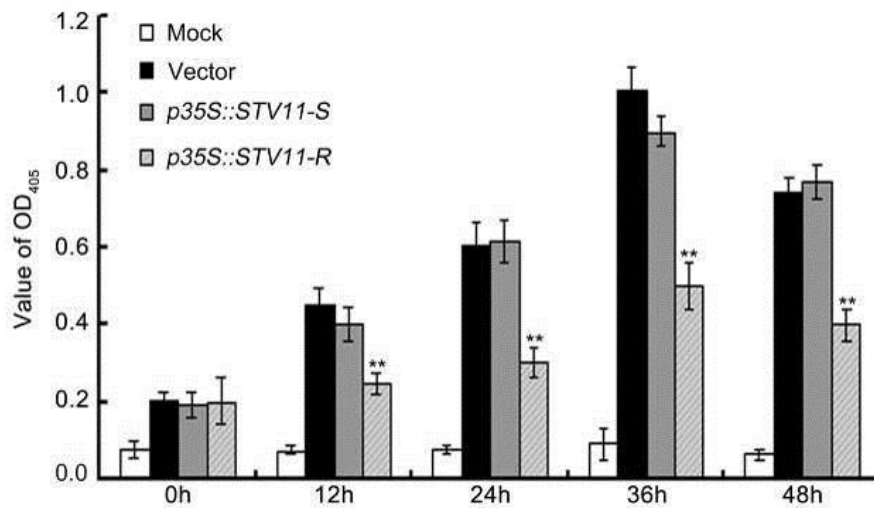
Supplementary Figure 1. KK34 and Kos are similarly susceptible to the insect vector SBPH. **(a)** Survival rates of SBPH on KK34 and Kos. **(b)** Feeding preferences of SBPH on KK34 and Kos. RH and WYJ3 were used as the resistant and susceptible controls, respectively. The error bars represent the s.e.m. Different letters on the top of each column indicate significant differences of $P < 0.01$, based on 3 replicates, by the Student's *t*-test.



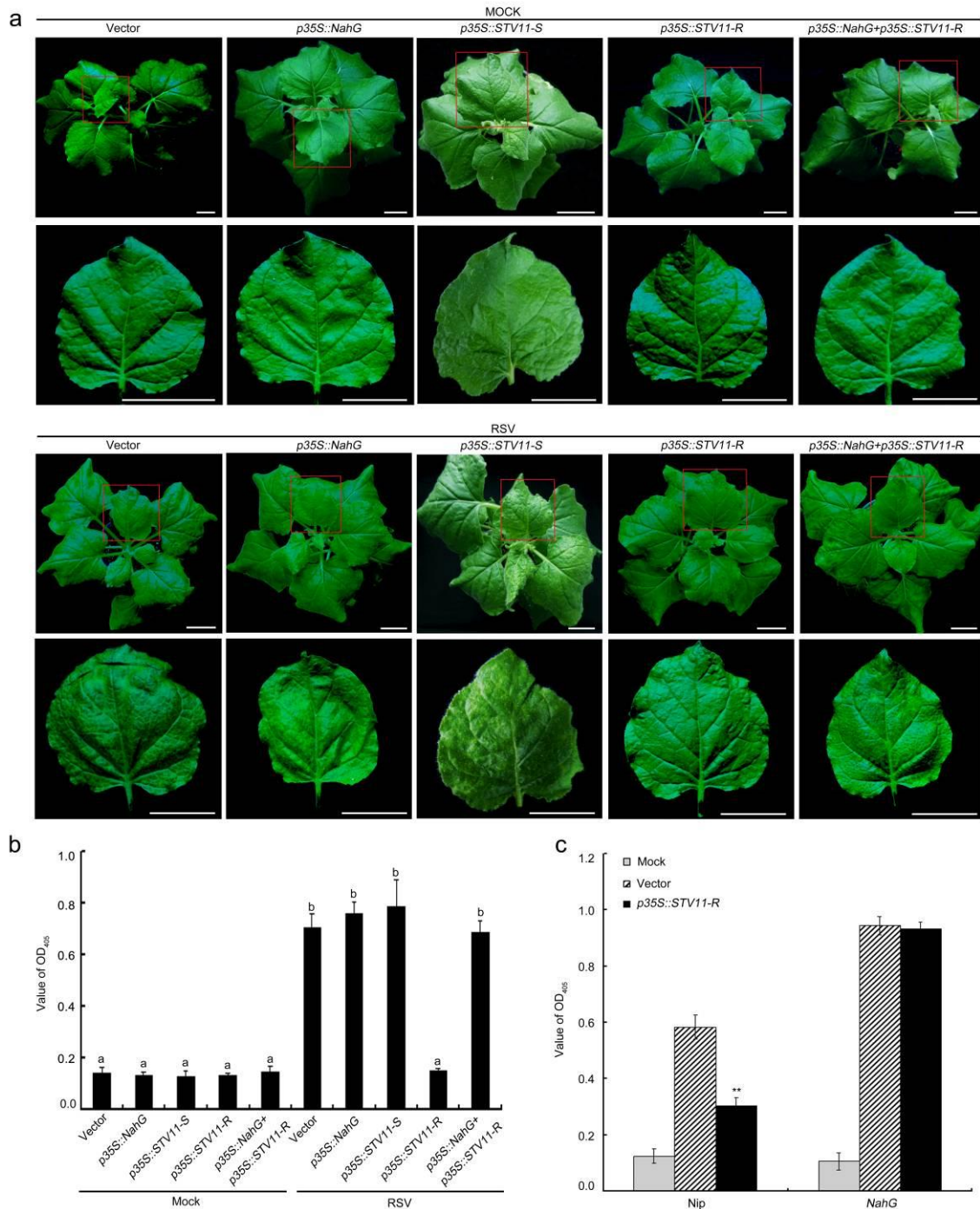
Supplementary Figure 2. Protein sequence comparison of the seven predicted gene products in the fine-mapped 39.2-kb region among Nipponbare (NIP), Kos and KK34. Amino acid changes are shown. One nucleotide substitution (position 929) and deletion (position 306) in *Loc_Os11g30920* lead to premature termination in Kos and KK34, respectively. A 36 nucleotides substitution (position 1-36) in *Loc_Os11g30930* leads to premature termination in KK34. One nucleotide deletion (position 201) in *Loc_Os11g30950* leads to premature termination in KK34. One nucleotide insertion (position 4370) and 16 nucleotides deletion (position 1663-1678) in *Loc_Os11g30960* result in truncated protein in Kos (898 amino acids) and KK34 (461 amino acids), respectively.



Supplementary Figure 3. Real time RT-PCR analysis of the seven predicted genes in the fine-mapped 39.2-kb region using Kos and KK34 seedling samples at 0 and 3 days post inoculation with RSV. The expression level is shown as the ratio to that of the rice *Ubiquitin-1* (Os06g0681400). Two pairs of primers (P1 and P2) were used to detect the expression of each gene. The mean \pm s.e.m was obtained from three technical repeats and three biological repeats. ND: not detectable. Error bars represent s.e.m; ** indicates significant differences between Kos and KK34 at $P < 0.01$ by the Student's t -test ($n = 3$).

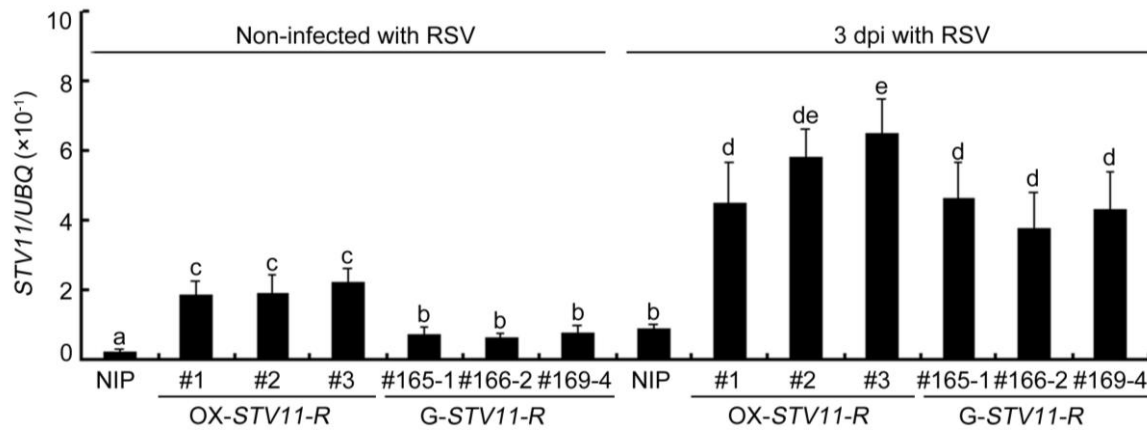


Supplementary Figure 4. RSV replication in NIP protoplasts transfected with the empty vector, p35S::STV11-S or p35S::STV11-R, together with RSV. Mock, the protoplasts not transfected with RSV. Data are shown as means \pm s.e.m. (n = 3). ** indicates significant differences at $P < 0.01$ from the empty vector control, by the Student's *t*-test, based on 3 replicates.

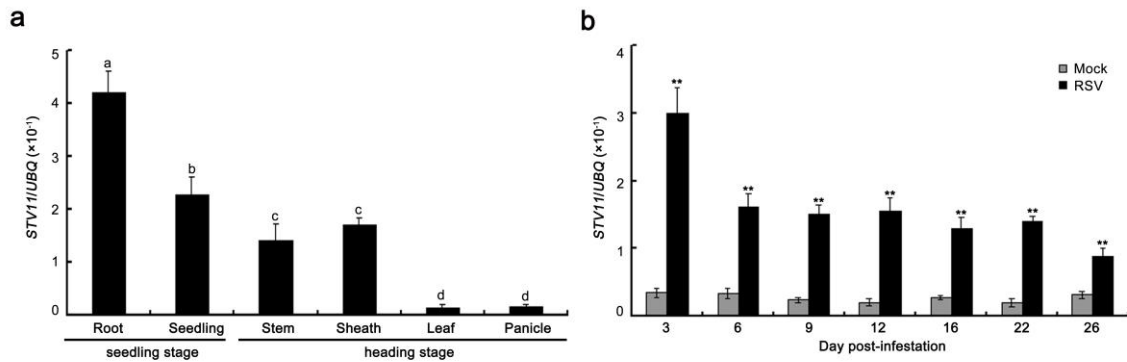


Supplementary Figure 5. The antagonistic effect of *NahG* expression on *STV11*-mediated RSV resistance in *N. benthamiana* and rice protoplasts. (a) Preantepenultimate leaves of 4-week-old *N. benthamiana* plants injected with *Agrobacterium* cells carrying the empty vector, p35S::NahG, p35S::STV11-S,

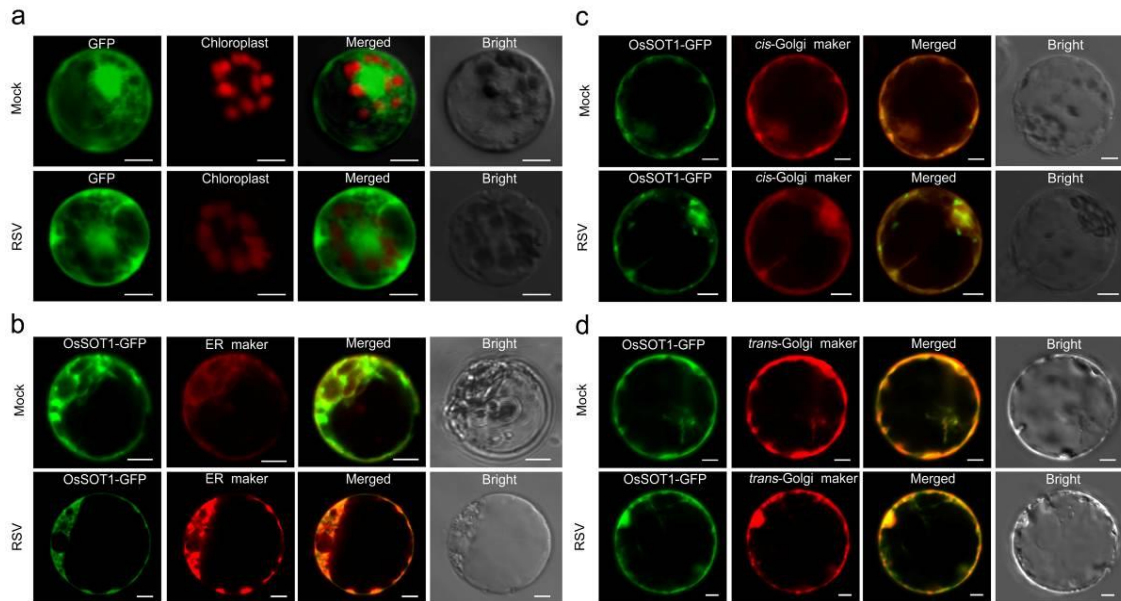
p35S::*STV11-R* or a mixture of p35S::*NahG* and p35S::*STV11-R*, were infected without (Mock, upper panel) or with (lower panel) RSV. The chlorosis and yellowing symptoms in the systemic leaves were visible at 15 dpi. Scale bar, 2 cm. **(b)** ELISA assay showing replication of RSV in systemic leaves of *N. benthamiana* plants at 15 dpi. Data are shown as means \pm s.e.m. (n = 3). Different letters indicate significant differences at $p < 0.01$ by the Student's *t*-test, based on 3 replicates. **(c)** The protoplasts were collected from Nipponbare (NIP) and transgenic Nipponbare plants carrying p35S::*NahG* at 16 h after infection by RSV. Mock, the protoplasts were not infected with RSV. Data are shown as means \pm s.e.m. (n = 3). ** indicates significant differences from the empty vector control at $P < 0.01$ by the Student's *t*-test, based on 3 replicates.



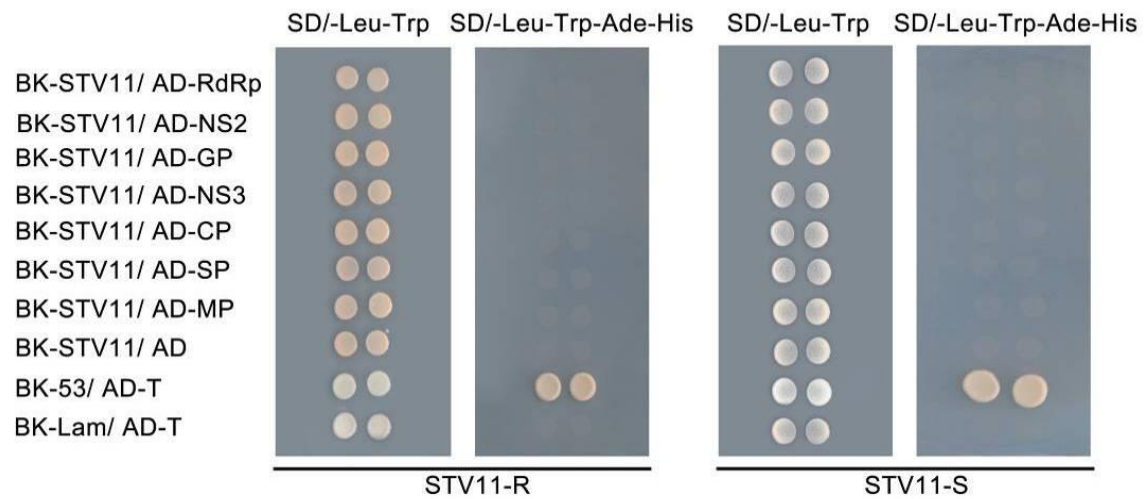
Supplementary Figure 6. RNA levels of *STV11* in transgenic lines. OX-*STV11-R*, transgenic lines over-expressing *STV11-R* driven by the maize *Ubiquitin-1* promoter; G-*STV11-R*, transgenic lines transformed with a genomic sequence of *STV11-R*. The expression level of *STV11* is shown as the ratio to that of rice *Ubiquitin-1* (Os06g0681400). The mean \pm s.e.m. was obtained from three repeats. Error bars represent s.e.m. Different letters on the top of each column indicate significant differences of $P < 0.05$ by the Student's *t*-test. The increased expression of *STV11* in the OX-*STV11-R* plants might be due to the stress responsiveness of the maize *Ubiquitin* promoter^{1,2}.



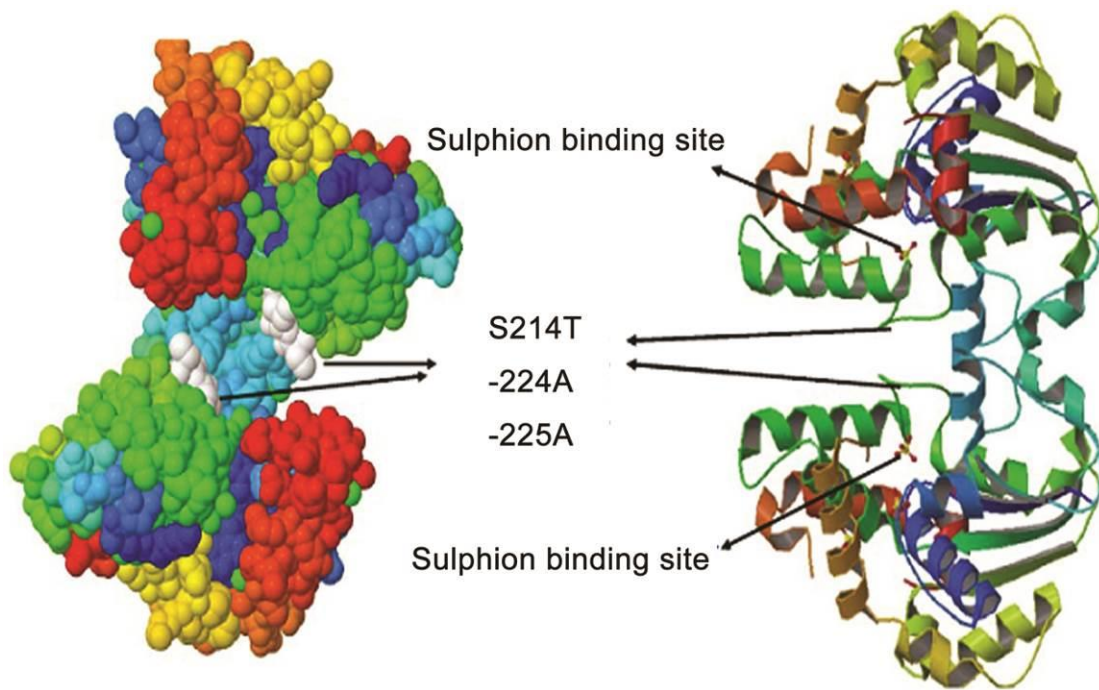
Supplementary Figure 7. Expression patterns of *STVII* in KK34. **(a)** Differential expression of *STVII* in different tissues at the seedling or heading stage. The expression level of *STVII* is shown as the ratio to that of rice *Ubiquitin-1* (Os06g0681400). The mean \pm s.e.m. was obtained from three technical repeats and three biological repeats. Error bars represent s.e.m. Different letters on the top of each column indicate significant differences at $P < 0.05$ by the Student's *t*-test. **(b)** Induced expression of *STVII* by RSV infection. Mock, seedlings were infested with RSV-free SBPH. The expression level of *STVII* is shown as the ratio to that of rice *Ubiquitin-1* (Os06g0681400). The mean \pm s.e.m. was obtained from three technical repeats and three biological repeats. Error bars represent s.e.m. ** indicates significant differences from mock at $P < 0.01$ by the Student's *t*-test.



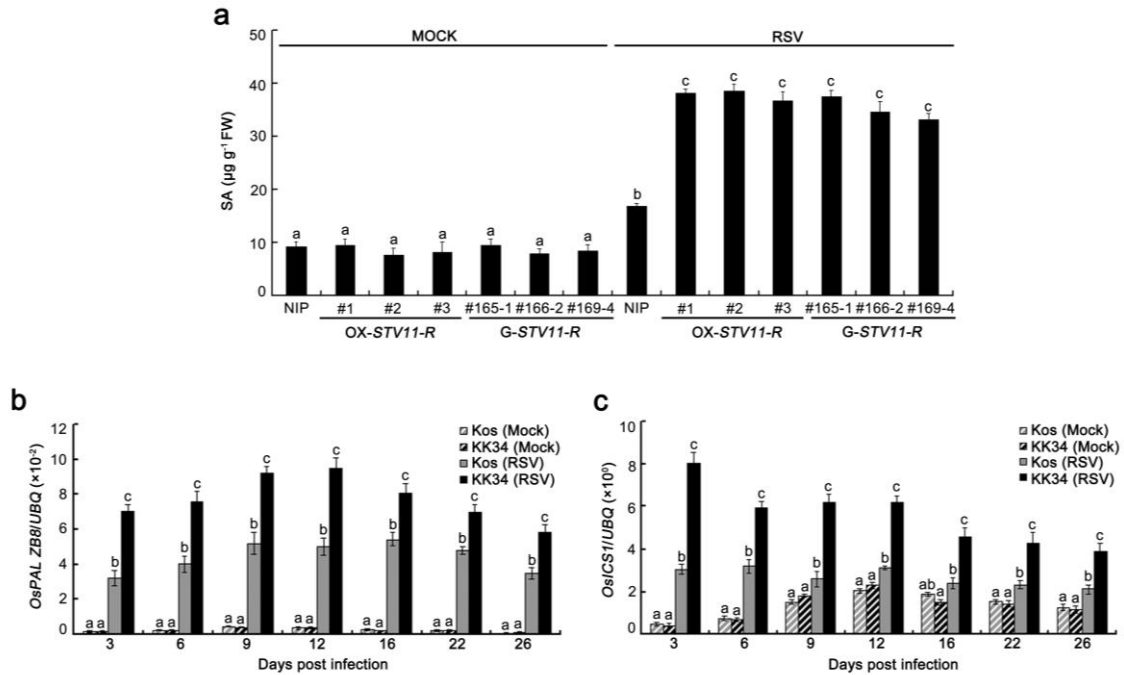
Supplementary Figure 8. Subcellular localization of OsSOT1 in rice leaf sheath protoplasts. **(a)** *p35S-GFP*. **(b)** ER marker mCherry-HDEL co-infected with the *pOsSOT1-GFP*. **(c)** *cis*-Golgi maker GmMan1–mCherry co-infected with *pOsSOT1-GFP*. **(d)** *trans*-Golgi marker ST–mCherry co-infected with *pOsSOT1-GFP*. Protoplasts were visualized 16 h after transfection with plasmids and RSV. Mock, no RSV infection. Scale bar, 5 μm .



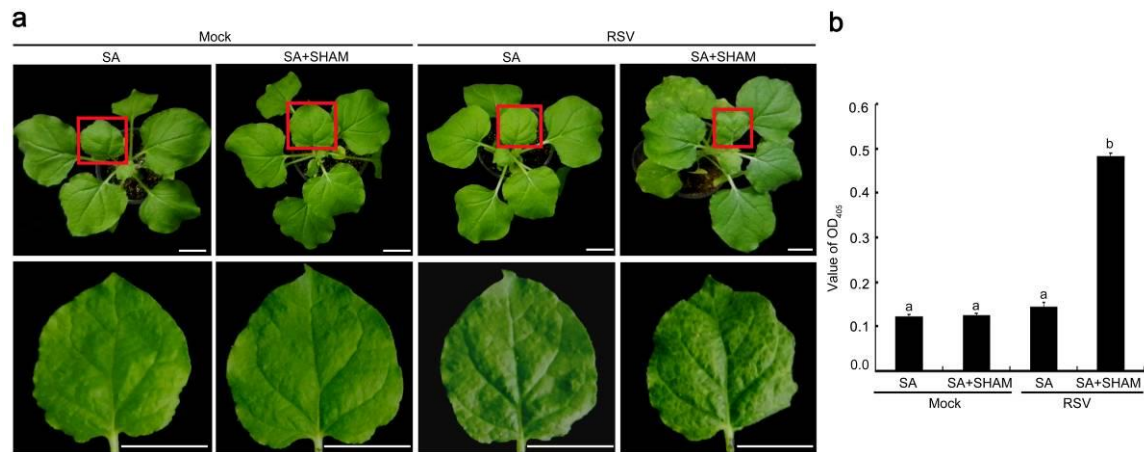
Supplementary Figure 9. OsSOT1 encoded by neither *STV11-R* nor *STV11-S* interacts with the RSV-encoded proteins in yeast two-hybrid assays. RdRp, RNA-dependent RNA polymerase; NS2, sense RSV RNA2; GP, glycoprotein; NS3, sense RSV RNA3; CP, coat protein; SP, disease-specific protein ; MP, movement protein. BK-STV11/AD, vector control; BK-53/AD-T, positive control; BKT7-Lam/AD-T, negative control.



Supplementary Figure 10. Structural modeling of OsSOT1. The amino acid substitution (S214T) and the deletion of two amino acids (224A and 225A) are predicted to be in close proximity of the sulphion-binding site.



Supplementary Figure 11. RSV-induced SA accumulation and expression of SA biosynthetic genes. **(a)** SA accumulation is higher in transgenic lines over-expressing *STV11-R* driven by the maize *Ubiquitin-1* gene promoter and transformed with a genomic sequence of *STV11-R* than that in the susceptible Nipponbare (NIP) at 3 dpi. Error bars represent s.e.m., different letters on the top of each column indicate significant differences at $P < 0.01$, based on three replicates by the Student's t -test. **(b, c)** RSV infection induces the expression of SA biosynthetic genes. Mock, the seedlings were infested with RSV-free SBPH. The expression level is shown as the ratio with the rice *Ubiquitin-1* (Os06g0681400). Error bars represent s.e.m.. Different letters on the top of each column indicate significant differences at $P < 0.05$ by the Student's t -test.



Supplementary Figure 12. SA treatment enhances RSV resistance in *N. benthamiana*. (a)

Three week-old *N. benthamiana* plants were sprayed with solutions containing 1 mM SA or a mix of 1 mM SA and 2 mM SHAM twice a day for 5 days before infection with RSV.

Pictures were taken 15 dpi. Mock, *N. benthamiana* plants not infected with RSV. Scale bar, 2 cm.

(b) ELISA assay showing replication of RSV in systemic leaves of *N.*

benthamiana plants 15 dpi. The error bars represent the s.e.m.. Different letters on the top

of each column indicate significant differences at $P < 0.01$, by the Student's *t*-test, based

on 3 replicates.

Supplementary Table 1. Wild rice used in this study

Varieties	Species	Subspecies	Accession No ^a	Origin	Genotype
ruf-KHM1	<i>O. rufipogon</i>	Perennial	106332	Cambodia	R
ruf-KHM2	<i>O. rufipogon</i>	Perennial	89231	Cambodia	R
ruf-IND1	<i>O. rufipogon</i>	Perennial	80506	India	S
ruf-IND2	<i>O. rufipogon</i>	Perennial	106110	India	R
ruf-INA1	<i>O. rufipogon</i>	Perennial	81978	Indonesia	R
ruf-MMR	<i>O. rufipogon</i>	Perennial	80742	Myanmar	R
ruf-PNG1	<i>O. rufipogon</i>	Perennial	106283	Papua New Guinea	R
ruf-PNG2	<i>O. rufipogon</i>	Perennial	106268	Papua New Guinea	R
ruf-CHN1	<i>O. rufipogon</i>	Perennial	81974	Thailand	R'
ruf-CHN2	<i>O. rufipogon</i>	Perennial	DX01	China	S
ruf-CHN3	<i>O. rufipogon</i>	Perennial	TY01	China	S
ruf-CHN4	<i>O. rufipogon</i>	Perennial	HN02	China	S
ruf-CHN5	<i>O. rufipogon</i>	Perennial	HN1	China	S
ruf-CHN6	<i>O. rufipogon</i>	Perennial	WN1	China	R
ruf-CHN7	<i>O. rufipogon</i>	Perennial	WN2	China	R
ruf-CHN8	<i>O. rufipogon</i>	Perennial	ZZ2	China	S
ruf-CHN9	<i>O. rufipogon</i>	Perennial	DX2	China	S
ruf-CHN10	<i>O. rufipogon</i>	Perennial	GZ1	China	S
ruf-CHN11	<i>O. rufipogon</i>	Perennial	GZ2	China	S
ruf-CHN12	<i>O. rufipogon</i>	Perennial	BS2	China	S
ruf-CHN13	<i>O. nivara</i>	Annual	80545	India	R
niv-LA1	<i>O. nivara</i>	Annual	106151	Laos	R
niv-LA2	<i>O. nivara</i>	Annual	106154	Laos	R'
niv-MMR	<i>O. nivara</i>	Annual	80725	Myanmar	R
niv-NPL	<i>O. nivara</i>	Annual	105703	Nepal	R
niv-TH	<i>O. nivara</i>	Annual	105789	Thailand	R
niv-KHM1	<i>O. nivara</i>	Annual	105724	Cambodia	H4
niv-IND1	<i>O. nivara</i>	Annual	81861	India	H5
niv-IND2	<i>O. nivara</i>	Annual	86474	India	H6
niv-IND3	<i>O. nivara</i>	Annual	80559	India	H7

^a The germplasms from Chinese Crop Germplasm Bank.

Supplementary Table 2. Correlation between *STVII* alleles and RSV resistance

Varieties	Genotype	Phenotype	Polymorphic nucleotide								
			150	161	640	670	671	672	673	674	675
KK34	R	R	G	C	T	-	-	-	-	-	-
Kasalath	R	R	G	C	T	-	-	-	-	-	-
IR36	R	R	G	C	T	-	-	-	-	-	-
N22	R	R	G	C	T	-	-	-	-	-	-
Habataki	R	R	G	C	T	-	-	-	-	-	-
Nanjing11	R	R	G	C	T	-	-	-	-	-	-
Lianjing4	R	R	G	C	T	-	-	-	-	-	-
Xudao3	R	R	G	C	T	-	-	-	-	-	-
Yangdao8	R	R	G	C	T	-	-	-	-	-	-
Xiaoxiangdao	R	R	G	C	T	-	-	-	-	-	-
Magu	R	R	G	C	T	-	-	-	-	-	-
Zaozaohe	R	R	G	C	T	-	-	-	-	-	-
Shilixiang	R	R	G	C	T	-	-	-	-	-	-
Guangchangai	R	R	G	C	T	-	-	-	-	-	-
Sihuisanchaoqi	R	R	G	C	T	-	-	-	-	-	-
Qiyuexian	R	R	G	C	T	-	-	-	-	-	-
Teqing	R	R	G	C	T	-	-	-	-	-	-
Qiuqianbai	R	R	G	C	T	-	-	-	-	-	-
Zhendao88	R	R	G	C	T	-	-	-	-	-	-
Lianjing3	R	R	G	C	T	-	-	-	-	-	-
Nanjing44	R	R	G	C	T	-	-	-	-	-	-
Yangjing4227	R	R	G	C	T	-	-	-	-	-	-
Zhendao10	R	R	G	C	T	-	-	-	-	-	-
Yangjing9538	R	R	G	C	T	-	-	-	-	-	-
Akenohoshi	R	R	G	C	T	-	-	-	-	-	-
Norin 300	R	R	G	C	T	-	-	-	-	-	-
Laijing	R	R	G	C	T	-	-	-	-	-	-
Shuiyuan251	R	R	G	C	T	-	-	-	-	-	-
T1	R	R	G	C	T	-	-	-	-	-	-
BJ 1	R	R	G	C	T	-	-	-	-	-	-
Padi Boenor	R	R	G	C	T	-	-	-	-	-	-
Gie 57	R	R	G	C	T	-	-	-	-	-	-
RTS13	R	R	G	C	T	-	-	-	-	-	-
Tam Cau-10A	R	R	G	C	T	-	-	-	-	-	-
SAMPONG P 9	R	R	G	C	T	-	-	-	-	-	-
DV85	R	R	G	C	T	-	-	-	-	-	-
Dhala Shaitta	R	R	G	C	T	-	-	-	-	-	-
DV1	R	R	G	C	T	-	-	-	-	-	-

Varieties	Genotype	Phenotype	Polymorphic nucleotide								
Shundetanghe	R'	R	G	T	T	-	-	-	-	-	-
Wenxiangnuo	R'	R	G	T	T	-	-	-	-	-	-
Haolai	R'	R	G	T	T	-	-	-	-	-	-
CO 18	R'	R	G	T	T	-	-	-	-	-	-
Taducan	R'	R	G	T	T	-	-	-	-	-	-
Khao Dawk Mali 105	R'	R	G	T	T	-	-	-	-	-	-
TD25	R'	R	G	T	T	-	-	-	-	-	-
Patnai 23	S	R	T	C	A	G	C	G	G	C	G
JC92	S	R	T	C	A	G	C	G	G	C	G
Longtefu	S	S	T	C	A	G	C	G	G	C	G
Guangluai	S	S	T	C	A	G	C	G	G	C	G
Koshihikari	S	S	T	C	A	G	C	G	G	C	G
Nipponbare	S	S	T	C	A	G	C	G	G	C	G
Neken2	S	S	T	C	A	G	C	G	G	C	G
Akihikari	S	S	T	C	A	G	C	G	G	C	G
Balilla	S	S	T	C	A	G	C	G	G	C	G
USSR5	S	S	T	C	A	G	C	G	G	C	G
Wuyujing3	S	S	T	C	A	G	C	G	G	C	G
Dongdao	S	S	T	C	A	G	C	G	G	C	G
Dajinxian	S	S	T	C	A	G	C	G	G	C	G
Lucaihao	S	S	T	C	A	G	C	G	G	C	G
Zaohuangdao	S	S	T	C	A	G	C	G	G	C	G
Sanbaili	S	S	T	C	A	G	C	G	G	C	G
Jinnanfeng	S	S	T	C	A	G	C	G	G	C	G
Wufujing	S	S	T	C	A	G	C	G	G	C	G
Wyunjing8	S	S	T	C	A	G	C	G	G	C	G
Wuxiangjing1	S	S	T	C	A	G	C	G	G	C	G
Xiushui48	S	S	T	C	A	G	C	G	G	C	G
Nanjing35	S	S	T	C	A	G	C	G	G	C	G
Wyunjing7	S	S	T	C	A	G	C	G	G	C	G
Changnongjing1	S	S	T	C	A	G	C	G	G	C	G
Wuxiangjing14	S	S	T	C	A	G	C	G	G	C	G
Baipixiaodao	S	S	T	C	A	G	C	G	G	C	G
Mudanjing2	S	S	T	C	A	G	C	G	G	C	G
			$R=0.95$	$R=0.05$	$R=0.95, P=2.2 \times 10^{-16}$						
			$P=2.2 \times 10^{-16}$	$P=0.65$							

Supplementary Table 3. Cultivars derived from Modan or Kanto 72

Cultivars	Genotype	Phenotype [#]	Resistance donor parent	Subspecies	Origin
Modan	R	R	-	indica	India
Kanto 72	R	R	-	indica	Japan
Asanohikari	R	R	Modan	japonica	Japan
Chugoku 31	R	R	Modan	japonica	Japan
Aichi97	R	R	Modan	japonica	Japan
Chugoku 40	R	R	Kanto 72	japonica	Japan
Norin 300	R	R	Modan	japonica	Japan
Norin 24	R	R	Modan	japonica	Japan
Zhendao88	R	R	Modan	japonica	China
Nanjing44	R	R	Modan	japonica	China
Yangjing4227	R	R	Modan	japonica	China
Zhendao10	R	R	Modan	japonica	China
Xudao3	R	R	Modan	japonica	China
Lianjing4	R	R	Modan	japonica	China
Yangjing9538	R	R	Modan	japonica	China

[#] The criteria for phenotyping RSV resistance were described by Zhang et al. 2011⁸.

Supplementary Table 4. List of the primers used for vectors construction and sequence and gene expression.

Description	Primer name	Accession/Locus ID	Forward primer sequence (5'-3')	Reverse primer sequence (5'-3')	Recombinanat site	Reference
Vector construction	UBI- <i>STV11-R</i>	LOC_Os11g30910	TTGGTACCAGTCCAGAGAGGCAGAGG	TTGGATCCAGCTTGACACATGCGATC	-	This study
	G- <i>STV11-R</i>	LOC_Os11g30910	ccatgattacgaattcCATCACACAAAGAAGAGAC	taccgagctcgaattcTAGATACTAGCTTGACACA	<i>EcoR</i> I	This study
	p35S- <i>STV11-R (S)</i>	LOC_Os11g30910	TTGGTACCAGTCCAGAGAGGCAGAGG	TTGGATCCAGCTTGACACATGCGATC	-	This study
	pOs <i>SOT1</i> -GFP	LOC_Os11g30910	ATGGCCCCAACCTCCAGC	TTCGGAGTCGCCGGCAG	-	This study
	GEX- <i>STV11</i>	LOC_Os11g30910	CGCGGATCCATGGCCCCAACCTCCAGC	ATAAGAATGCGGCCGCTCATTTCGGAGTCGCCGGCAG	-	This study
Sequence	Se- <i>STV11</i>	LOC_Os11g30910	TGAGCGACAATACTCCAGA	AAGATAGATACTAGCTTGACACAT	-	This study
	S30899	LOC_Os11g30899	AAGTAACCAAGAACTTGGAACG	CAGCCTCTTTATCCCCTCAC	-	This study
	S30920-1	LOC_Os11g30920	GTGCCCTTCATTCCCTT	GCTCCTTTGGGTGGGTT	-	This study
	S30920-2	LOC_Os11g30920	ATAGGAACCCACCCAAAG	TCACAGACCCACCATTCA	-	This study
	S30930-1	LOC_Os11g30930	TGCCTCACTTCAGTCCTT	TGCTCCGAATGTTGTTC	-	This study
	S30930-2	LOC_Os11g30930	TAGAAACAACATTCGGAGCA	TCAACGGGCAGAGCAAGG	-	This study
	S30930-3	LOC_Os11g30930	GGGTGAACATTTACAGGC	GATGGAGGGACACGAACT	-	This study
	S30930-4	LOC_Os11g30930	GCAGTTCGTGTCCCTCCA	ACGGCGATTCTCCCTTGA	-	This study
	S30940-1	LOC_Os11g30940	CCATGACGCCAAGTGATCT	GCTAACCACGGTGCCAGAC	-	This study
	S30940-2	LOC_Os11g30940	GCATTGCTTAGTCTAACGC	TGTTTAGTACTTGAGCCTCG	-	This study
	S30950-1	LOC_Os11g30950	CATGTATGCGACGCCTCAT	CAGTCTAACTCACCCACTTCTT	-	This study
	S30960-1	LOC_Os11g30960	CACGAAGAAAAGCAAAGCG	GACAATGACGACGATGAGG	-	This study
	S30960-2	LOC_Os11g30960	ATGTTCTCATACTTGCCACC	TTCTCACTGGCGTAGTAGGAT	-	This study
	S30960-3	LOC_Os11g30960	ATTAGTTCTGGCGGATGTCTG	GGCTACTGAGCGGTGGTT	-	This study
	Gene expression	qRT- <i>STV11 (P1)</i>	LOC_Os11g30910	GCAATACGGCGGCTACT	GATGGCGAAGGTGGACT	-
qRT- <i>STV11 (P2)</i>		LOC_Os11g30910	ACATCCCCTACTCCCTCTCG	TGGTCGTTGTGACACCCTTC	-	This study

Continued

Description	Primer name	Accession/Locus ID	Forward primer sequence (5'-3')	Reverse primer sequence (5'-3')	Recombinant site	Reference
	899-P1	LOC_Os11g30899	GCGATGACAGCTGAGAC	CATCTACCAGCGATGGA	-	This study
	899-P2	LOC_Os11g30899	TGGCGATGACAGCTGAGACC	GTCGGCTACGGATCCACCTC	-	This study
	920-P1	LOC_Os11g30920	AGAAGGGCATCTACAACG	CACGAGGCGAATATCAAG	-	This study
	920-P2	LOC_Os11g30920	CTTCTTTGCCTCACTTCA	TAGCCTCTCTTTGTTCAT	-	This study
	930-P1	LOC_Os11g30930	TGGGTTCTGGGGTTTCT	ATTCAGTCTCGGGCACA	-	This study
	930-P2	LOC_Os11g30930	TGACAGCGATCTATGGTTG	AATCTCTTGCCTAAGCCTC	-	This study
	940-P1	LOC_Os11g30940	GAAGGTTCCGCGAAGGAGA	ACCCCATTTGTTGCCAGTC	-	This study
	940-P2	LOC_Os11g30940	AAGGAGATAATGCCAGGAA	ACGCACATAGTATCGCTTG	-	This study
	950-P1	LOC_Os11g30950	CTGTGGGGTTGGGTGTTA	ACGACCTTGTGTCTTTCT	-	This study
	950-P2	LOC_Os11g30950	CCAGCCAAAACCCCAATA	ACGGCCCAGAAGACACAGT	-	This study
	960-P1	LOC_Os11g30960	ACGACATCCGCCAGAACT	TTGTCAACCCTTCCCATT	-	This study
	960-P2	LOC_Os11g30960	TCTATGTTTCGATTGTCC	TTCATACTCAATATCCGA	-	This study
qRT- <i>Ubiquitin-1</i>		Os06g0681400	GTGGTGGCCAGTAAGTCCTC	GGACACAATGATTAGGGATCA	-	3
qRT- <i>RSVCP</i>		X53563.1	CTAGTCATCTGCACCTTCT	CCATGCCAGAGGGTAAGAAG	-	This study
qRT- <i>OsPAL ZB8</i>		Os02g0626100	CTCGCCGTCCACTCCTTG	GCTCGGCTGCGTATTCCT	-	4
qRT- <i>OsICS1</i>		Os09g0361500	TATGGTGCTATCCGCTTCGAT	CGAGAACCGAGCTCTCTTCAA	-	5

Supplementary References

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