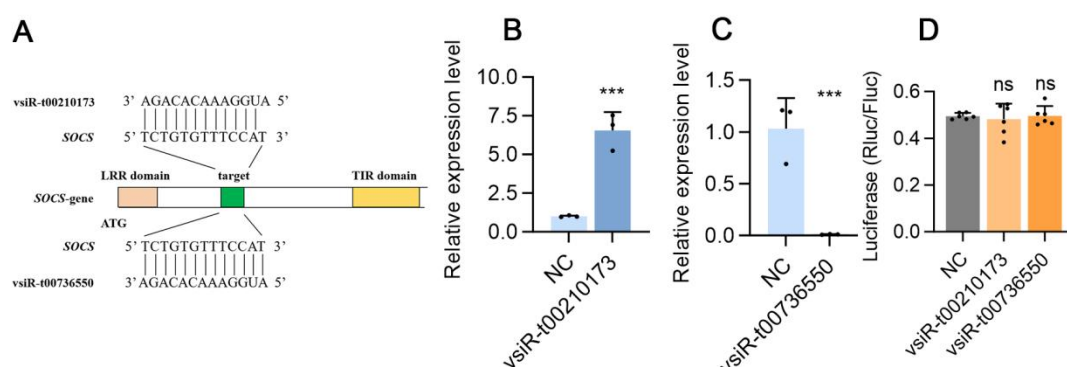
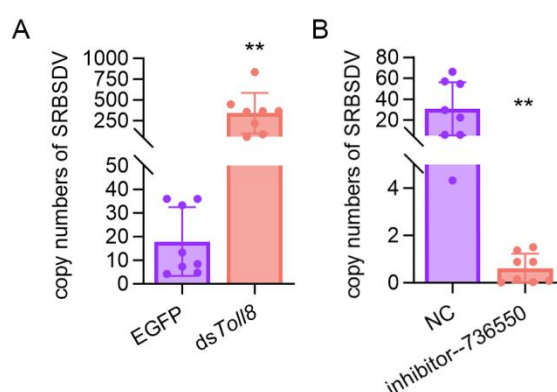




Supplementary Figure 1. Predicted target sites of two vsiRNAs in *SOCS* and their validation. (A) Sequence alignment of two vsiRNAs with their predicted target sites in the CDS of *SOCS*. (B) and (C) The relative expression levels of *SOCS* in *Sogatella furcifera* after injection with the vsiR-t00355379 mimic. Inhibitor-NC was injected as a negative control. (D) Detected luciferase activity in Hek-293T cells. Values were compared by Student's t test. Ns, no significant difference. ***, $P < 0.001$.



Supplementary Figure 2. Quantification of SRBSDV copy number in rice seedlings.

(A) SRBSDV copy number in rice seedlings following feeding by SfToll8-silenced, virus-carrying planthoppers compared to dsEGFP controls. (B) SRBSDV quantification in rice seedlings following feeding by virus-carrying planthoppers injected with inhibitor versus NC treatment.

Supplementary Table 1. Primers used in this study.

Sequence name	Sequence (5' to 3')
Sequences of real-time PCR primers	
<i>SfTPS1</i> -qF	CGGCCTCCATCTACATTCT
<i>SfTPS1</i> -qR	ATTCCTTTCAGCGCCTCCAT
<i>SfTPS2</i> -qF	TGCAAAGGTCTGTGGATCGG
<i>SfTPS2</i> -qR	TGGTGCTTTGTCTTGGGGAT
<i>SfTre1</i> -qF	TTCGAGTTGGCTGACCTCTG
<i>SfTre1</i> -qR	TACCTGGCTTCAGCACATCG
<i>SfTre2</i> -qF	GTACAACGACCAGTCCAGGG
<i>SfTre2</i> -qR	GCCGTCTTCAGTTCTCCGTA
<i>SfGP</i> -qF	TGCCTACACTAACCACACCG
<i>SfGP</i> -qR	CATGTGCCTGGGGAGAATGT

<i>SfTret1</i> -qF	GGCTCAATGGTAGTGGGCTT
<i>SfTret1</i> -qR	AAAGCGCAAAGTGGCATCAG
<i>SfTret1-2</i> -qF	CCAGCGTGCGTACTCCAGCATCT
<i>SfTret1-2</i> -qR	CAGTGCAGGGTCCGAGGTAT
<i>SfHK</i> -qF	ACTGATGTCTTGCGCTTGGA
<i>SfHK</i> -qR	TCTGGCTTCGACTTATCGCC
<i>SfSOCS7</i> -qF	CGACGTGTTGACTTTCGACG
<i>SfSOCS7</i> -qR	TGTGCCGATGATGTCGCTTA
<i>SfToll8</i> -qF	GACACCATAGCTCAAGCGGT
<i>SfToll8</i> -qR	CGCCTATCTCTCAGCACCTG
U6-qF	CTCGCTTCGGCAGCACA
U6-qR	AACGCTTCACGAATTTGCGT
P10-qF	GTCATCTTGTGGAAAGGGTGG
P10-qR	TTTCGCTTACGGACGACTTCT
vsiR-t00210173-RT	GTCGTATCCAGTGCAGGGTCCGAGGTATTTCGCACTGGATACGA CGATATG
vsiR-t00736550-RT	GTCGTATCCAGTGCAGGGTCCGAGGTATTTCGCACTGGATACGA CGATATG
vsiR-t00210173-qF	CGCGCGCGCGAAGGCG
vsiR-t00736550-qF	CGCGCGCGCGCGGGCG
vsiR-R	AGTGCAGGGTCCGAGGTATT

Sequences of RNAi ^a

dsEGFP-T7-F	<u>GGATCCTAATACGACTCACTATAGGG</u> AGGACGACGGCAACTA CAAG
dsEGFP-T7-R	<u>GGATCCTAATACGACTCACTATAGGG</u> GTCCATGCCGAGAGTGA TCC
<i>SfTPS1</i> -T7-F	<u>GGATCCTAATACGACTCACTATAGGG</u> CCCGTTGTGGTGAGAAA TA
<i>SfTPS1</i> -T7-R	<u>GGATCCTAATACGACTCACTATAGGG</u> CAAGGTGGGAATGGAAT G
<i>SfTPS2</i> -T7-F	<u>GGATCCTAATACGACTCACTATAGGG</u> CGCATAGACCGCAACAA C
<i>SfTPS2</i> -T7-R	<u>GGATCCTAATACGACTCACTATAGGG</u> CGCATAGACCGCAACAA C
<i>SfTre1</i> -T7-F	<u>GGATCCTAATACGACTCACTATAGGG</u> TCAAGAGACAGCACAAT GGC
<i>SfTre1</i> -T7-R	<u>GGATCCTAATACGACTCACTATAGGG</u> ACGAAACCGAATCGTTT GAC
<i>SfTre2</i> -T7-F	<u>GGATCCTAATACGACTCACTATAGGG</u> AACATCTCGCCACTTTG GAC
<i>SfTre2</i> -T7-R	<u>GGATCCTAATACGACTCACTATAGGG</u> GAGTTGATGAGGGGTGTG AGG
<i>SfTret1</i> -T7-F	<u>GGATCCTAATACGACTCACTATAGGG</u> TGTTCTCATCCCAGAG ACC

<i>SfTret1</i> -T7-R	<u>GGATCCTAATACGACTCACTATAGGG</u> TTGTGCTCAGATTTTCGT CG
<i>SfTret2</i> -T7-F	<u>GGATCCTAATACGACTCACTATAGGG</u> GCTGGGTGCTGTTATGG ATT
<i>SfTret2</i> -T7-R	<u>GGATCCTAATACGACTCACTATAGGG</u> CCTGCGTAGCAGGTAGG AGG
<i>SfGP</i> -T7-F	<u>GGATCCTAATACGACTCACTATAGGG</u> GCAATGTGGTGAACAAC GAC
<i>SfGP</i> -T7-R	<u>GGATCCTAATACGACTCACTATAGGG</u> CTCCGGGTTTGCATTGT AGT
<i>SfHK</i> -T7-F	<u>GGATCCTAATACGACTCACTATAGGG</u> ACATACGTGCAGGACCT TCC
<i>SfHK</i> -T7-R	<u>GGATCCTAATACGACTCACTATAGGG</u> TCGTATCATTGAGGATG GCA
<i>SfToll8</i> -T7-F	<u>GGATCCTAATACGACTCACTATAGGG</u> ACGCTGGTGACGAATTG CTA
<i>SfToll8</i> -T7-R	<u>GGATCCTAATACGACTCACTATAGGG</u> CATCAGCCAAACCACCA ACG

Sequences of expression plasmid construction

<i>SfTre1</i> -Tar1-F	TTCTAGGCGATCGCTCGAGTTCGAGTTGGCTGACCTCTG
<i>SfTre1</i> -Tar1-R	TTTTATTGCGGCCAGCGGCCGCACCATTTGGTACCTGGCTT
<i>SfTre1</i> -Tar2-F	ATTCTAGGCGATCGCTCGAGGAATTCATGTATTGGATGAG
<i>SfTre1</i> -Tar2-R	TATTGCGGCCAGCGGCCGCAGGTCTGGGACTTCTAGAATA
<i>SfTre1</i> -Tar1-MUT-F	ACTTCAAGGGATTCCCTTCTCATACTTAACGTTTCGAGAAGT
<i>SfTre1</i> -Tar1-MUT-R	ACGTTAAGTATGAGAAGGGAATCCCTTGAAGTTGGACTTGAT
<i>SfTre1</i> -Tar2-MUT-F	GTGTCAGTGCGTAAACCGTTTCCACACGCAACCTTGGCGAGAT T
<i>SfTre1</i> -Tar2-MUT-R	GGTTGCGTGTGGAAACGGTTTACGCACTGACACCATTTTGAA C
<i>SfToll8</i> -F	TAATTCTAGGCGATCGCTCGAGGGAGTACGTGTGTCGCCG
<i>SfToll8</i> -R	TATTTTATTGCGGCCAGCGGCCGCTGGTAGCGTAGCGCTG
<i>SfToll8</i> -MUT-F	CGCCGCGGCATTATGGTTGAGTGTGGGGCGTTGGTGG
<i>SfToll8</i> -MUT-R	CCCACACTCAACCATAATGCCGCGGCGACACACGTAC
<i>SfSOCS</i> -F	TAATTCTAGGCGATCGCTCGAGGGAGTACGTGTGTCGCCG
<i>SfSOCS</i> -R	TATTTTATTGCGGCCAGCGGCCGCATAACAAAAAATGTG

^a The underlined portion represents the T7 sequence.

Supplementary Table 2. Potential off- target analysis of dsRNA sequences.

Gene ID	Score	E-Value	Align-length
	e	e	h
Sfur000494.1 (Tre1)	706	0.0	409
Sfur007891.1	48.2	4e-05	51

Sfur001856.1	33.7	0.89	18
Sfur004603.1	31.9	3.1	17
Sfur012498.1	31.9	3.1	20
Sfur012498.2	31.9	3.1	20

Gene ID	Score	E-Value	Align-length
Sfur002384.1 (TPS1)	854	0.0	473
Sfur013759.1	93.3	1e-18	165
Sfur001991.1	37.4	0.086	30
Sfur002919.1	31.9	3.6	20
Sfur002548.1	31.9	3.6	20
Sfur009629.1	31.9	3.6	17

Gene ID	Score	E-Value	Align-length
Sfur013759.1 (TPS2)	829	0.0	459
Sfur002027.1	82.4	2e-15	208
Sfur006025.1	35.6	0.29	34
Sfur006406.2	35.6	0.29	34
Sfur006406.1	35.6	0.29	34
Sfur001545.2	33.7	1.0	33

Gene ID	Score	E-Value	Align-length
Sfur012294.1 (Tret1-2)	863	0.0	478
Sfur012962.1	35.6	0.30	54
Sfur007748.1	33.7	1.1	38
Sfur000914.1	33.7	1.1	23
Sfur004924.1	31.9	3.7	22
Sfur004924.2	31.9	3.7	22

Supplementary Table 3. Prediction of vsiRNAs for the target gene *SfTre1*

vsiRNA ID	Sequence	miRanda (Total Energy/ kcal/mol)	RNAhybrid (Total Energy) kcal/mol	Pita (Total Energy) kcal/mol	Target Start-end
vsiR-t00545797	UUGGUCUGUGUUUCCAUAUCCA	-25.58	-30.0	-18.47	1772-1793
vsiR-t00296090	AAAUUGGUCUGUGUUUCCAUA	-25.62	-30.0	-18.07	1045-1065
vsiR-t00175432	CAAAUUGGUCUGUGUUUCCAUA	-26.44	-30.0	-16.90	1045-1066
vsiR-t00200545	UUGGUCUGUGUUUCCAUAUCC	-25.58	-30.0	-16.77	1773-1793
vsiR-t00210173	AAUUGGUCUGUGUUUCCAUAUC	-26.04	-30.0	-16.74	1043-1064
vsiR-t00757450	CAAAUUGGUCUGUGUUUCCAUA	-25.25	-30.0	-16.20	1046-1066
vsiR-t00116261	AUUGGUCUGUGUUUCCAUAUC	-25.01	-30.0	-16.03	-10431063
vsiR-t00736550	UUGGUCUGUGUUUCCAUAUC	-25.58	-30.0	-15.28	1774-1793 1043-1062

Supplementary Table 4. Target of vsiR-t00736550 in *Sogatella furcifera*

Target_Gene	Target sequence	Description	Score	vsiRNA_ start-end	Target Start-end
Sfur002206.1	TGGTCTGTGTTTCCA	Probable helicase with zinc finger domain	28.3	2-16	3635-3649
Sfur012994.1	GGTCTGTGTTTCCAT	Xanthine dehydrogenase	28.3	3-17	2578-2592
Sfur007624.1	TTGGTCTGTGTTT	Kinetochore-associated protein 1	24.7	1-13	2989-3001
Sfur006749.1	GGTCTGTGTTTCC	Probable E3 ubiquitin-protein ligase HERC1	24.7	3-15	11346- 11358
Sfur000974.4	TCTGTGTTTCCAT	Phosphorylase superfamily	24.7	5-17	4104-4116
Sfur000455.1	TTGGTCTGTGTTTCCAT ATC	Trypsin I-P1	24.7	1-20	14-32
Sfur010857.1	GGTCTGTGTTTCCATAT C	RNA-binding protein 12	24.7	3-20	3071-3088
Sfur010755.1	TCTGTGTTTCCAT	Suppressor of cytokine signaling 7	24.7	5-17	3850-3862
Sfur001948.1	TCTGTGTTTCCAT	Serine/threonine-protein kinase SMG1	24.7	5-17	15880- 15892
Sfur002310.1	TCTGTGTTTCCATATC	Voltage-dependent calcium channel type D subunit alpha-1	24.7	5-20	2737-2752
Sfur002218.5	GTCTGTGTTTCCATAT	Proton-coupled amino acid transporter 4	24.7	4-19	187-202
Sfur011600.13	ATTGGTCTGTGTTTCCA	Tight junction protein ZO-1	24.7	1-16	1060-1075
Sfur003482.1	GGTCTGTGTTTCCATAT C	TRNA (uracil-O(2)-)-methyltransferase	24.7	3-20	238-255
Sfur012801.3	TCTGTGTTTCCATATC	Ras-related C3 botulinum toxin substrate 1	24.7	5-20	5060-5075
Sfur012812.3	TCTGTGTTTCCAT	Remodeling and spacing factor 1	24.7	5-17	13419- 13431
Sfur007526.4	TTGGTCTGTGTTTCCAT	Phosphatidylinositol 4-phosphate 5-kinase type-1 alpha	22.9	1-17	10769- 10785
Sfur007777.1	TTGGTCTGTGTTTCCAT ATC	Plexin-A4	22.9	1-20	5472-5492

Sfur014910.1	TGGTCTGTGTTT	Toll-like receptor Toll	22.9	2-13	427-438
Sfur001067.1	TGGTCTGTGTTTCCATA TC	Probable chitinase 10	22.9	2-20	4867-4885
Sfur006710.1	TGTGTTTCCATA	RNA-binding protein MEX3B	22.9	7-18	9537-9548

Supplementary Table 5. Target of vsiR-t00210173 in *Sogatella furcifera*

Target_Gene	Target sequence	Description	Score	vsiRNA_ start-end	Target Start-end
Sfur002206.1	TGGTCTGTGTTTCCA	Probable helicase with zinc finger domain	28.3	4-18	3635-3649
Sfur012994.1	GGTCTGTGTTTCCAT	Xanthine dehydrogenase	28.3	5-19	2578-2592
Sfur007907.1	AATTGGTCTGTGTTTC CAT	Ankyrin repeat domain-containing protein 50	26.5	1-19	5-23
Sfur000494.1	AATTGGTCTGTGTTTC CAT	Trehalase	26.5	1-19	788-806
Sfur011600.13	ATTGGTCTGTGTTTCC A	Tight junction protein ZO-1	24.7	2-18	1059-1075
Sfur007526.4	ATTGGTCTGTGTTTCC AT	Phosphatidylinositol 4-phosphate 5-kinase type-1 alpha	24.7	2-19	10769- 10786
Sfur007624.1	TTGGTCTGTGTTT	Kinetochore-associated protein 1	24.7	3-15	2989-3001
Sfur010755.1	TCTGTGTTTCCAT	Suppressor of cytokine signaling 7	24.7	5-17	3850-3862
Sfur001948.1	TCTGTGTTTCCAT	Serine/threonine-protein kinase SMG1	24.7	7-19	15880- 15892
Sfur011342.1	ATTGGTCTGTGTT	Glucose dehydrogenase [FAD, quinone]	24.7	2-14	392-404
Sfur003482.1	GGTCTGTGTTTCCATA TC	Probable tRNA (uracil - O (2-) -methyltransferase	24.7	5-22	238-255
Sfur011600.13	ATTGGTCTGTGTTTCC A	Tight junction protein ZO-1	24.7	2-18	1059-1075
Sfur003482.1	GGTCTGTGTTTCCATA TC	TRNA (uracil-O(2)-)-methyltransferase	24.7	5-22	238-255
Sfur012801.3	TCTGTGTTTCCATATC	Ras-related C3 botulinum toxin substrate 1	24.7	7-22	5050-5075
Sfur012812.3	TCTGTGTTTCCAT	Remodeling and spacing factor 1	24.7	5-17	13419- 13431
Sfur012601.1	TGTGTTTCCATAT	Phosphoinositide 3-kinase adapter protein 1	24.7	9-21	3179-3191
Sfur001067.1	TGGTCTGTGTTTCCAT ATC	Probable chitinase 10	24.7	2-20	4865-4884
Sfur006749.1	GGTCTGTGTTTCC	Probable E3 ubiquitin-protein ligase HERC1	24.7	5-17	11346- 11358

Figure 1A.

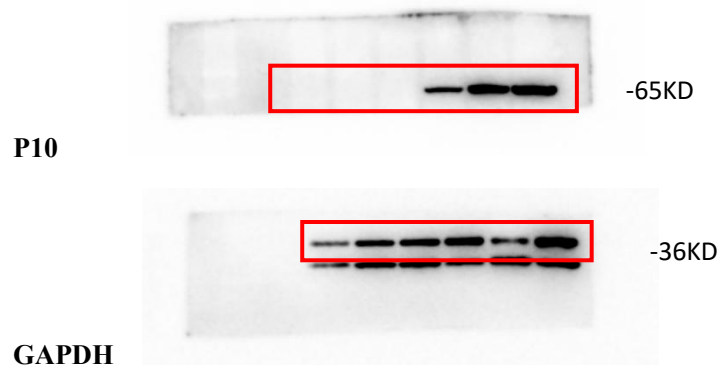


Figure 6F and Figure 6H.

