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Article:

Zhang, H, Hu, Z, Lei, C et al. (2018) A Plant Phytosulfokine Peptide Initiates Auxin-Dependent Immunity through Cytosolic Ca²⁺ Signaling in Tomato. *Plant Cell*, 30 (3). pp. 652-667. ISSN: 1040-4651

<https://doi.org/10.1105/tpc.17.00537>

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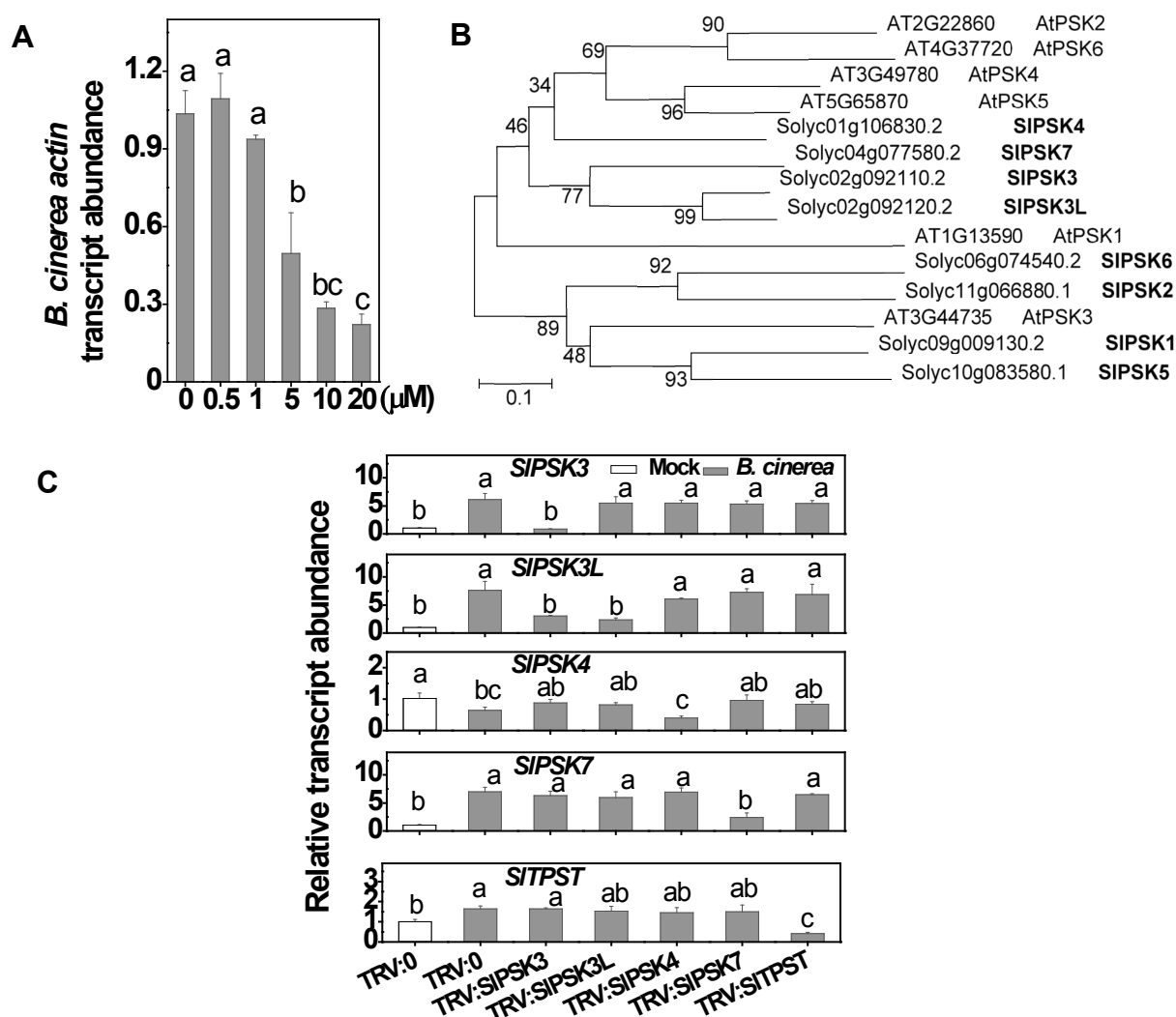
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Supplemental Figure 1



Supplemental Figure 1. The effect of PSK concentration on immunity, and the transcript abundance of PSK biosynthesis-related genes in VIGS tomato plants (supports Figure 1).

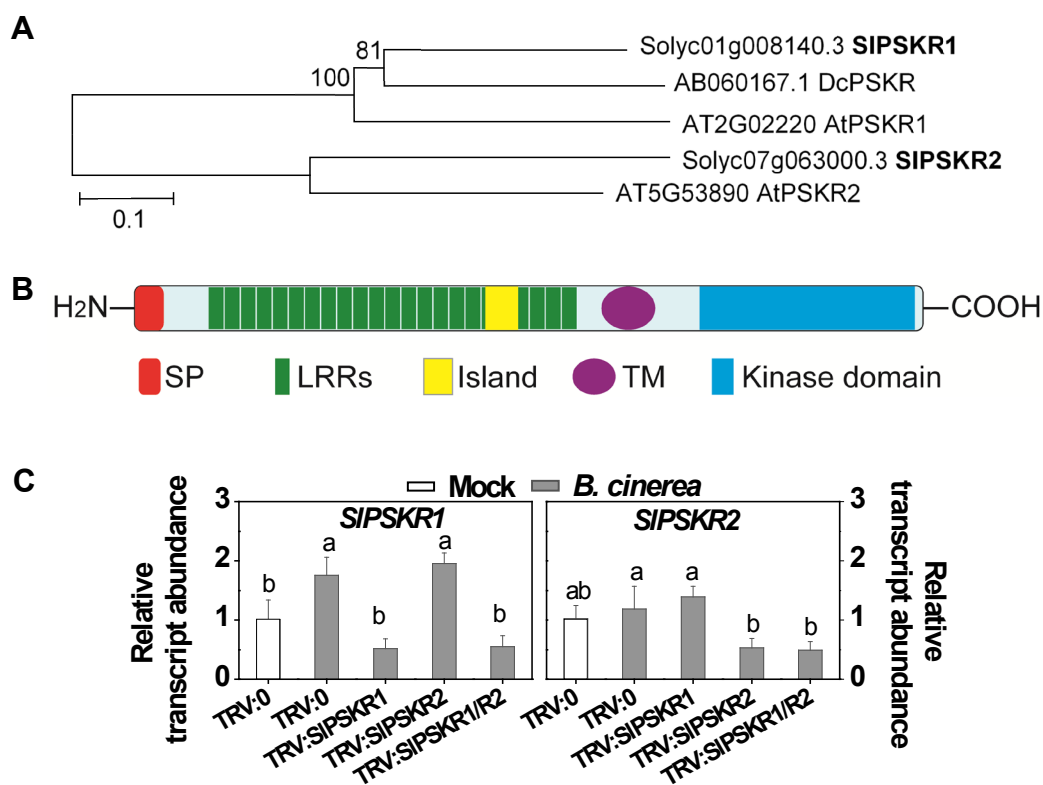
(A) The dose-dependent alleviatory effect of PSK on leaf *B. cinerea* transcript abundance. Four-week-old tomato plants were treated with indicated concentrations of PSK 12 h before *B. cinerea* inoculation, and leaf samples were taken at 1 day post *B. cinerea* inoculation (dpi) for relative leaf *B. cinerea actin* transcript abundance assay.

(B) Phylogenetic analysis of PSK precursor genes from tomato and *Arabidopsis*. Amino acid sequence alignment and tree construction were performed with MEGA program. A consensus neighbor-joining tree was obtained from 1000 bootstrap replicates of aligned sequences. The percentage at branch represents the posterior probabilities of amino acid sequences.

(C) Relative transcript abundance of homologous PSK precursor genes and *SITPST* in VIGS tomato plants. After initial silencing efficiency test 3~4 weeks after *A. tumefaciens* infiltration, tomato plants were subject to *B. cinerea* inoculation, and leaf samples were collected at 1 dpi. The samples are same with those used for *B. cinerea actin* assay in Figure 11. The transcript abundance were expressed as a ratio of the mean levels in TRV:0 control plants, which were defined as 1.

The results in (A and C) are presented as the mean values \pm SD; $n = 3$. Different letters indicate significant differences between treatments ($P < 0.05$, Tukey's test). The experiments in (A) were repeated two times, and experiments in (C) were repeated three times with similar results.

Supplemental Figure 2



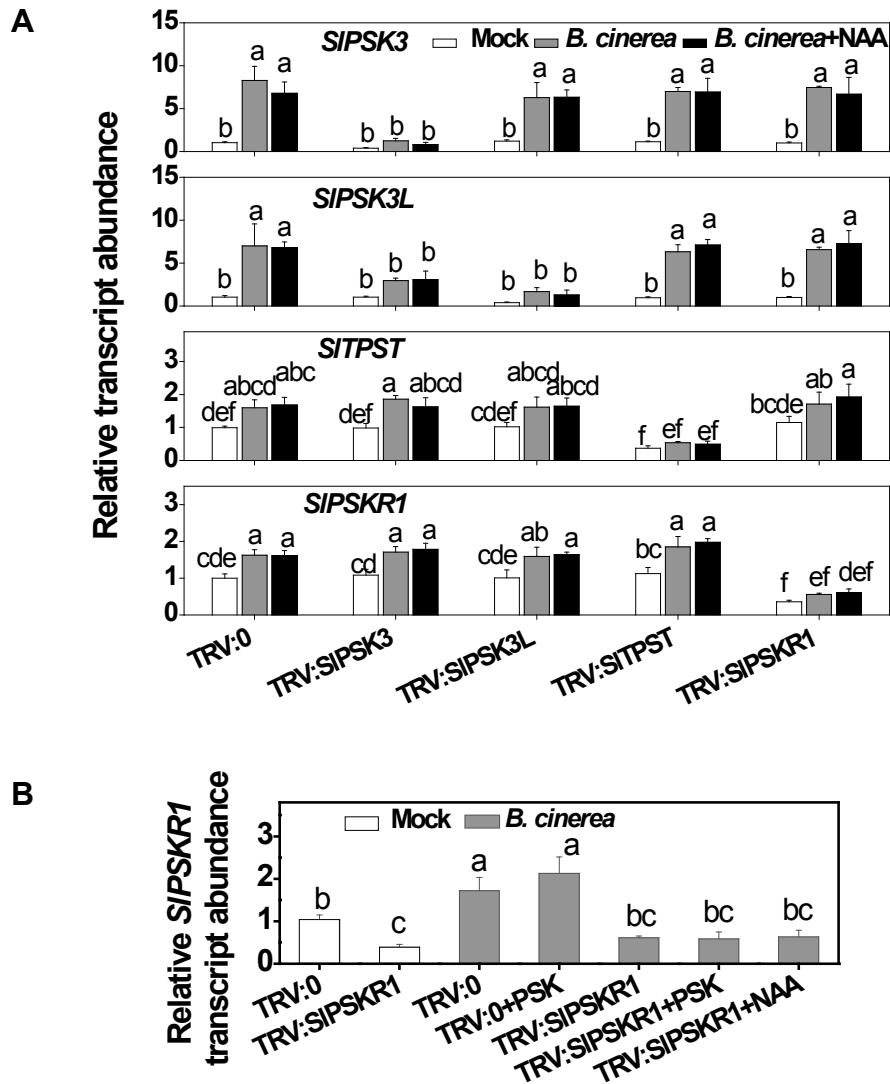
Supplemental Figure 2. Analysis of PSK receptor sequences, and the transcript abundance of *SIPSKR*s in VIGS tomato plants (supports Figure 2).

(A) Phylogenetic analysis of PSK receptors from tomato, *Arabidopsis* and *Daucus carota*. Amino acid sequence alignment and tree construction were performed with MEGA program. A consensus neighbor-joining tree was obtained from 1000 bootstrap replicates of aligned sequences. The percentage at branch represents the posterior probabilities of amino acid sequences.

(B) Schematic of *SIPSKR1/R2* protein. The diagram shows the signal peptide (SP), extracellular leucine-rich repeats (LRRs), an island domain, a transmembrane domain (TM), and a cytoplasmic Ser/Thr kinase domain.

(C) Relative transcript abundance of *SIPSKR*s in VIGS tomato plants. After initial silencing efficiency test 3~4 weeks after *A. tumefaciens* infiltration, tomato plants were subject to *B. cinerea* inoculation, and leaf samples were collected at 1 dpi. The samples are same with those used for *B. cinerea* actin assay in Figure 2F. The transcript abundance were expressed as a ratio of the mean levels in TRV:0 control plants, which were defined as 1. The results are presented as the mean values \pm SD; $n = 3$. Different letters indicate significant differences between treatments ($P < 0.05$, Tukey's test). The experiments were repeated two times with similar results.

Supplemental Figure 3



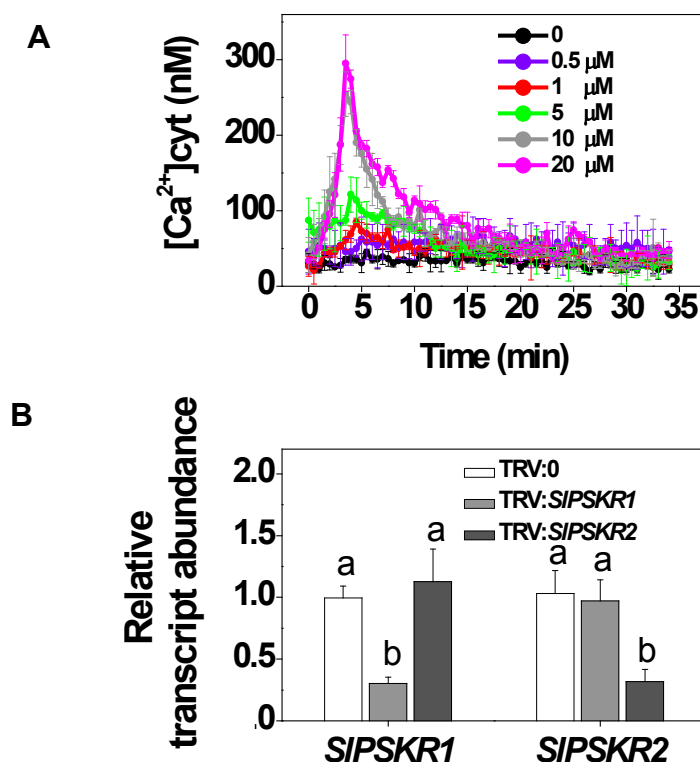
Supplemental Figure 3. The transcript abundance of PSK signaling-related genes in VIGS tomato plants (supports Figure 4).

(A) Relative transcript abundance of *SIPSK3*, *SIPSK3L*, *SITPST*, and *SIPSKR1* in VIGS tomato plants.

(B) Relative transcript abundance of *SIPSKR1* in VIGS tomato plants.

After initial silencing efficiency test 3~4 weeks after *A. tumefaciens* infiltration, tomato plants were subject to pharmacological treatment and *B. cinerea* inoculation, and leaf samples were collected at 1 dpi. The samples in (A) are same with those used for *B. cinerea* actin assay in Figure 4B. The samples in (B) are same with those used for Figure 4D. The transcript abundance were expressed as a ratio of the mean levels in TRV:0 control plants, which were defined as 1. The results are presented as the mean values \pm SD; $n = 3$. Different letters indicate significant differences between treatments ($P < 0.05$, Tukey's test). The experiments in (A) were repeated three times, and experiments in (B) were repeated two times with similar results.

Supplemental Figure 4



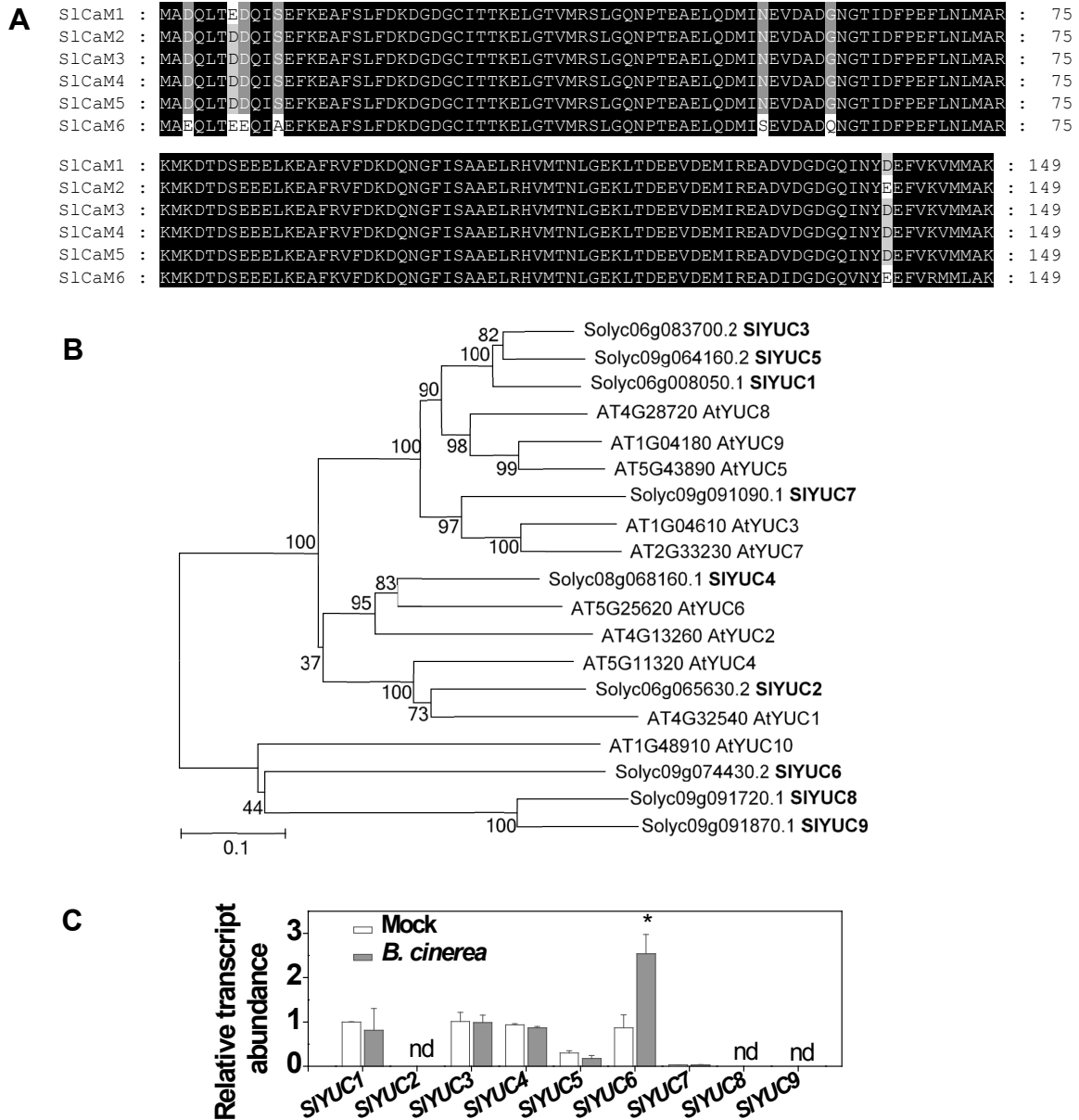
Supplemental Figure 4. The effect of PSK concentration on cytosolic Ca^{2+} levels, and the transcript abundance of *SIPSKRs* in VIGS tomato plants (supports Figure 5).

(A) The dose-dependent effect of PSK on cytosolic Ca^{2+} elevation in leaves of aequorin-expressing tomato plants. The signals shown at 0.5-min intervals are the mean values \pm SD generated from 8 leaf discs per treatment.

(B) Relative transcript abundance of *SIPSKR1* and *SIPSKR2* in VIGS tomato plants. Approximately three weeks after *A. tumefaciens* infiltration, each plant was taken with an uppermost expanded leaflet for target gene silencing efficiency analysis by qRT-PCR. Five plants with efficient silencing from each TRV: *SIPSKR1* and TRV: *SIPSKR2* group were selected and transcript abundance of target genes are shown as the mean values \pm SD ($n = 5$). These selected plants were further used for cytosolic Ca^{2+} assay in Figure 5B, and leaf discs samples for cytosolic Ca^{2+} assay were taken from the corresponding opposite leaflet for the silencing efficiency assay. The transcript abundance were expressed as a ratio of the mean levels in TRV:0 control plants, which were defined as 1. Different letters indicate significant differences between treatments ($P < 0.05$, Tukey's test).

The experiments in **(A)** were repeated two times, and experiments in **(B)** were repeated three times with similar results.

Supplemental Figure 5



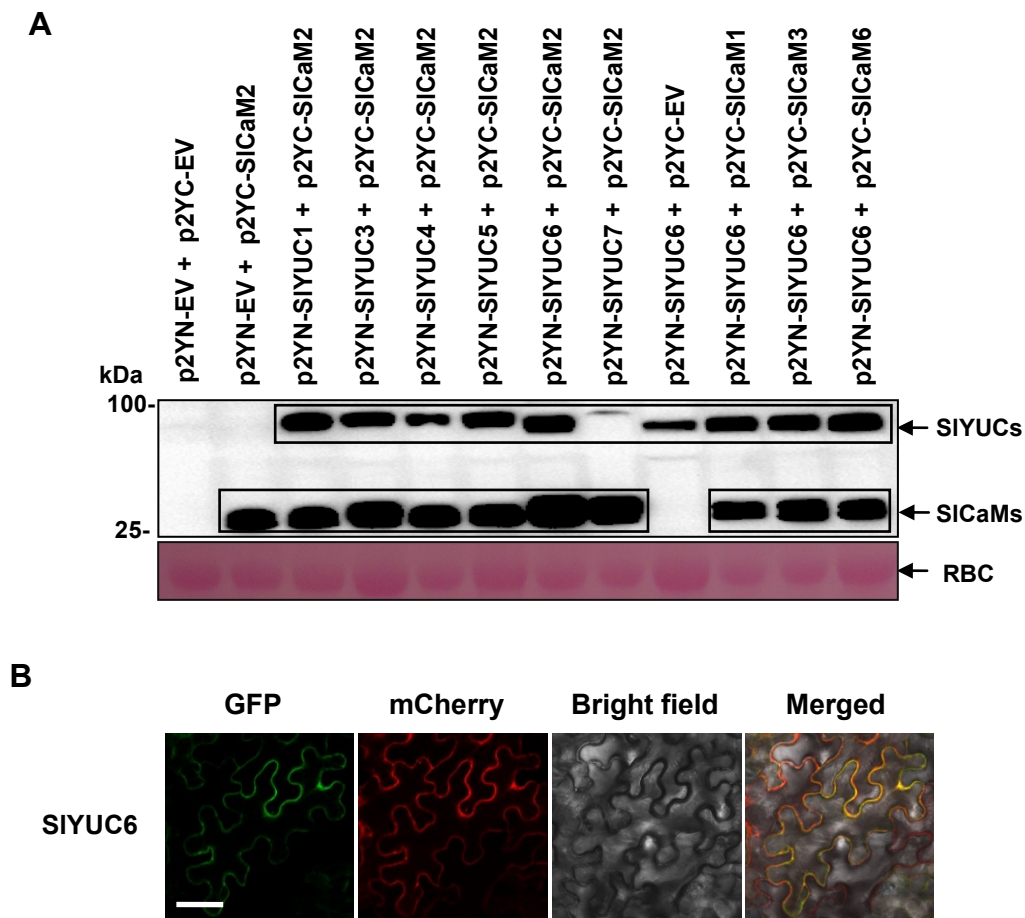
Supplemental Figure 5. Analysis of tomato CaM and YUC homologs (supports Figure 6).

(A) Amino acid sequence alignments of tomato CaM homologs with Clustal X program.

(B) Phylogenetic analysis of YUCs from tomato and *Arabidopsis*. Amino acid sequence alignment and tree construction were performed with MEGA program. A consensus neighbor-joining tree was obtained from 1000 bootstrap replicates of aligned sequences. The percentage at branch represents the posterior probabilities of amino acid sequences.

(C) Effects of *B. cinerea* inoculation on the relative transcript abundance of *SIYUCs* in leaves at 0.5 dpi. The transcript abundance of *SIYUC1* in mock-inoculated condition were defined as 1. The results are presented as the mean values \pm SD; $n = 3$. nd, not detected. The asterisk indicates a significant effect of *B. cinerea* inoculation with tomato plants. The experiments were repeated two times with similar results.

Supplemental Figure 6



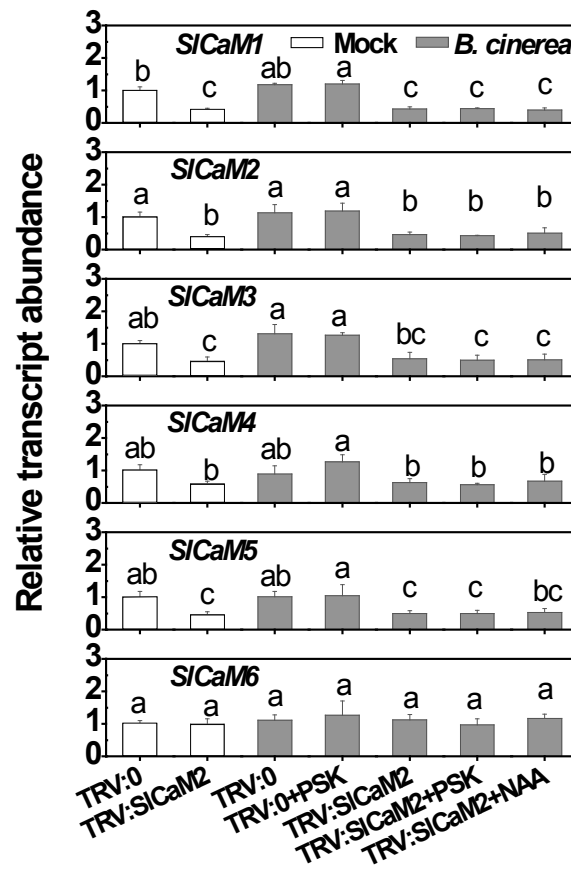
Supplemental Figure 6. Co-expression of SICaMs and SIYUCs in *N. benthamiana* leaves (supports Figure 6).

(A) Co-expression of p2YC-SICaMs and p2YN-SIYUCs proteins were detected by immunoblot analysis with an anti-HA antibody. Samples of infiltrated areas were collected from *N. benthamiana* leaves after 48 h *A. tumefaciens* infiltration. Rubisco (RBC) was stained with Ponceau for protein loading control (bottom). The black boxes indicate specific SIYUCs and SICaMs bands.

(B) SIYUC6 localizes to plasma membrane. SIYUC6-GFP and FLS2-mCherry (marker for plasma membrane localization) plasmids were transiently co-expressed into *N. benthamiana* leaves. The GFP and mCherry signals were visualized under confocal microscopy after 48 h infiltration. Scale bar = 50 μ m.

The experiments were repeated two times with similar results.

Supplemental Figure 7



Supplemental Figure 7. Effects of *SICaM2* silencing on the transcript abundance of *SICaM* homologs in tomato plants (supports Figure 7).

After initial silencing efficiency test 3~4 weeks after *A. tumefaciens* infiltration, tomato plants were subject to *B. cinerea* inoculation, and leaf samples were collected at 1 dpi. The samples are same with those used for *B. cinerea actin* assay in Figure 7C. The transcript abundance were expressed as a ratio of the mean levels in TRV:0 control plants, which were defined as 1. The results are presented as the mean values \pm SD; $n = 3$. Different letters indicate significant differences between treatments ($P < 0.05$, Tukey's test). The experiments were repeated three times with similar results.

Supplemental Data Set 1. Nucleotide sequence alignments based on mRNA region of tomato PSK homologs (supports Figures 1 and 4; Supplemental Figures 1 and 3).

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S1PSK1 : -----ATGGA : 5
S1PSK2 : -----ATGATGAGCAAAA : 14
S1PSK3 : -----ATGTCTAA : 8
S1PSK3L : -----ATGTCTAA : 8
S1PSK4 : GAAACATTGTCCCTTCACTTCTTGGTTCCTCACTCTATATATCCATCATCGTCCCCAAAACTCAACTAAGCAATAT : 80
S1PSK5 : -----ATGAA : 5
S1PSK6 : -----ATGAAACAATT : 11
S1PSK7 : -----ATGTCTAA : 8

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S1PSK1 : G---CAAAAAATATTTTTTTCCTTCCTTCTCTTATGGTTTACTACTAATTTCTTACACAACAACAGCTCGTTTATTGC : 82
S1PSK2 : T-----GTATATTTTGTGCTACTT---CTTCTTGTTCCATGATCATTTCTTACACAAGCATCTAGTCTTTTTTAG : 82
S1PSK3 : AGCATCTGCCAGCTTTTTTTCATCATCCTTCTCTCTGTTTT---GCCCTGTCCATGCTGCTCGCCCTAACCCACTTT : 85
S1PSK3L : AGCCAATACCAGTTTTTCTTCACTTACTTCTCCTCTGTTTT---GCCCTGTCCATGCTGCTCGCTTCCCCAGCTT : 85
S1PSK4 : GGCTAAACTTAACACCTTTTGTATGAAAGCATTCCTCCTCTTCTCGCGCTAACTTGCCTTCTTCCCGTCCAGTGGTG : 160
S1PSK5 : GCCTATTATTAATTCATCTCTTATTTTCACTTTCATATACACTACTCATTTCGCAATAGTATCGGTTCTGTTACTCTC : 85
S1PSK6 : AAGCATATCATGTTTTCTTGTATTTTCAACATGTTCCCTCTTGTCTTCTTCCACAGCATGTCTTCACTTATTCT : 91
S1PSK7 : ATTGTCACT---ATTTTTGTGTGGCATTCTTCTTGTCTCAACTACTCTCACAATTGCTGTCTCGTCTAAT---TCTT : 82

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S1PSK1 : CA---ACAATTAATCTCAA-----GAATCTAATGGGATTATTAGTAATAATCCA-----ATTTCCTCACAA : 141
S1PSK2 : TAAACAATTG---CAAGTGGAAAAGGAAGCAAAATTAATAATAAATCTAGTGATGGAGACTCAATTGAGAAGATGAGA : 159
S1PSK3 : TTCACGAGGCTACTCTCAAC-----AATATCAACAC : 117
S1PSK3L : TTCACGAGGCATCCCTCAAC-----ATTGATCACCAAC : 117
S1PSK4 : CGCCTTATCGCGATGTTACT-----CCGATGGAGCAT : 192
S1PSK5 : CTACAACTATTCAAGATAACAACAAGATTGAAGCTAATGGGATTATTCATTCA-----ATTCACACACAA : 150
S1PSK6 : TATCAACCAATAAGTGAAGTGAAGAGGATATAAAGCAAGAGAAAGTCAACCTTTCGTTACATACAGTTGACCACATGGAA : 171
S1PSK7 : TTTCTGTTCTCGATCCCAA-----ATTGAGTTGCA : 114

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S1PSK1 : GTACAGAAAGATTTCATGTACTCTATGCGAATAGAAAGAA-----TCTGAAACAAAA---GATGAATTTGTTTCAAGAG : 212
S1PSK2 : AGTACTAAT---TTAAATAGGTTGATGGGGTTAGAAAGAAATATTCACTGAGGATGAAAATGATCAAGAATGCATTAAGAG : 236
S1PSK3 : CAGGAT---GTTGTGAACCAAGGAAGTTGGTAAGGAAGAGAGTTGCAAGGAGTCAAGGAAGAAGATGTTTAGAAG : 194
S1PSK3L : CAGGATCATGTTAGGGAATCAAACAAGTAGCAAAAGAAAGAGAGCTGCAACGGAGGGCAGGATGAAGAATGTTTAGAAG : 197
S1PSK4 : ACTAAGGATAAGGCAGCAATGAAAGAAAGATGCGAGATAGATGTGAAGGCCCTGTTGGAGAAAGAAATGTTTAGAGAG : 272
S1PSK5 : ---GAAGACGACTTACCAATCTGATGGGGATGGAGAAA-----TCTGAAACACAGA---GATGAATTTGTTTAAATAG : 218
S1PSK6 : ACCAAGCATAGCCTAAATAAACTTATGGGGTTGGAGGAA-----TCTGTTCAAGAA---GATGGAGAATGCATGAAGAG : 242
S1PSK7 : AGTGAAGGAAAAGTTGAAATAAA-----GAAGCAAAACTGAAAGGAGTGGAGGAAGAAGAATGTTTGAAGAG : 182

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S1PSK1 : AAGAATGACTGCAGAGGCTCAATTTAGATTATATTTAFACTCAACACAAGCCAAAACATTGA----- : 273
S1PSK2 : AAGAGTTCTTGTAGAGCTCACTTGGATTACATCTACACTCAACACCATAATCACCCCTTAA----- : 297
S1PSK3 : GAGGACT---TTGGCTGCTCATCTTGACTATATCTATACCCAAAATCAGAACCCCTGAAGAAAGTTTACGATTCCCAAGG : 271
S1PSK3L : AAGGAAC---TTGGCTGCTCACCTTGACTATATCTATACCCAAAATCAGAACCCCTGAAGAAAGTTTGTATTGTTGATAT : 274
S1PSK4 : AAGAAC---TTAGAGGCTCATCTTGAATTATATATATACCAGAGACATAAGCAACCTTAA----- : 330
S1PSK5 : AAGGATGGTAGCTGAGGCTCACTTGGATTATATATAACTCAAAAACAACCTAAGCCCTAA----- : 279
S1PSK6 : AAGGGTAGTAGCAGAGCTCATCTTGAATTACATCTACACTCAGAGCCATAATCATCTTGA----- : 303
S1PSK7 : GAGGACA---ATGGCTGCTCATCTTGAATTATTTAFACTCAAAGTATTAATAAC----- : 234

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S1PSK1 : -----ACAAGTTTATATTAATATATTTTTTTTTTCTAAGGATGGTTAATTAGTAATGTTCTT : 330
S1PSK2 : ----- : -
S1PSK3 : ACCAAAATGATCAGTTAATTTGTTTTACAATGATTAATTGACCTAAGTTTAAAGTTAATTCATGTTTCACTAAAGTAGTG : 351
S1PSK3L : TGAAGTAGATGAGACAGTTACATATCACACATTAATAATACCT-----TACTGTACATCAGTCCCGTTG : 339
S1PSK4 : ----- : -
S1PSK5 : ----- : -
S1PSK6 : -----TATTAA-----TTAATATAATCAATCCTC : 327
S1PSK7 : -----AATCATCCA----- : 243

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S1PSK1 : TTCTATACTTTAAATATATAGTACAACGCTACTAAAAGAACTTTAATTTATTAAAACCTGTATTTTCGATGTATCATAAGAT : 410
 S1PSK2 : ----- : -
 S1PSK3 : ATAGAACGAGTGAGTTATCACATATATTTATAGTATTGCTTTTCGTGT-----GTTGCTTGTTAAATTTCCCTGTACG : 425
 S1PSK3L : ATTTTCCTGTACGTTAAAATGTATTAATAGCATTTCCTCTCCGTCCTAGATGATACTATCTCTGTTTTCCTTTGTATT : 419
 S1PSK4 : -----TTATTATTATTTTTTAATTCATCTCTTCAATATATAGTTTATCTTCTTTTTTTT : 389
 S1PSK5 : ----- : -
 S1PSK6 : TAAGCTAGCTGGTGTGTTAATAAATAAAAGGACTAGCTAG---ATATATAAGCTTTAATGACCTTTTATTTCAACAT : 404
 S1PSK7 : -----TGAATTAATCAAGAACTT----- : 261

S1PSK1 : TGTAGTACTATGTTTTGTGAGAATTATAAAGATAGCCAAAAGTTTAATTATTACTCTTTG : 470
 S1PSK2 : ----- : -
 S1PSK3 : TTAATAAAATCCCATATGAAGTTTCTGGTGTATGCAAGTTGATCGATTAC-----TT : 476
 S1PSK3L : TGGCGGTATTTCAACTAGGCATATGGTTAATTACGAAATAAAACCTTCTTT-----GT : 473
 S1PSK4 : AAAAAATTTGATCTATCTAGATTTATCAATTCATTAATAAATTACTAGTTC-----C- : 439
 S1PSK5 : ----- : -
 S1PSK6 : TAAATAATTTCCCTACCTAAGT-----TT : 428
 S1PSK7 : -----TT : 263



Supplemental Data Set 2. Amino acid sequence alignments of PSKR homologs from tomato, *Arabidopsis* and *Daucus carota* (supports Figure 2 and Supplemental Figure 2). The conserved domains were predicted by SMART (<http://smart.embl-heidelberg.de>).

Signal peptide

SlPSKR1 : ---MGVLRVYVILILVGV--FCVQIVVNSQNLTCNSNDLKALEGFMRLGLESSIDGWKWNSSSFSSNCCDVGITCKSSV : 69
 SlPSKR2 : MVIWEFLPMSFVWCWVFLAYLFCITLISLETPVQNCHEPYDILLALKEIAGNLTVGVILSAWSNE----PNCCNKNDGVVCGN-- : 74
 AtPSKR1 : ---MRVHRFCVIVIFITTELLCFFYSSESQTTSRCHPHDLEALRDFIAHLEPKPDGWINSSS---SDCCNWTGITCNS-- : 72
 AtPSKR2 : -----MVTILLVFFVGVSSVS-----QPCHPNDLSALRELALGNKNSVTESWLVNG---SRCCDWDGVFCEG-- : 59
 DcPSKR : ---MGVLRVYVILILVGV--FCVQIVVNSQNLTCNSNDLKALEGFMRLGLESSIDGWKWNSSSFSSNCCDVGITCKSSV : 75

Leucine-rich repeats

SlPSKR1 : -----GRVVKLEELGKRRRLNGKLSSESLGNLDELRTLNLSHNFVKGPVFFTLHLHLSKLEVLDSLNNDFFLGFPSSM : 139
 SlPSKR2 : -----VSTQSRVIRLNLNRKGLRGVVSOSLERLDQLKLLDLSHNHLEGLPLDLDSKMKOLEVLDSLHNVLLGPVLRVFD : 148
 AtPSKR1 : -----NNTGRVIRLELGNKLSGKLSSESLGKLEIRVNLNRNFITKDSIPLSIFNLKNLQTLDSLNNDSLGGIPTSI : 145
 AtPSKR2 : -----SDVSGRVTKLVLPKGLGELVLSKSLGELTELRLVLDLSRNQKGEVPAETSKLEQLQVLDLSHNLSSGVLGVV : 133
 DcPSKR : SLGLDDVNESGRVVELELGRRLSGKLSSEVAKLDQLKVLNLTNLSLGSIAASLNLNSLEVLDLSSNDFSGLFPPLIN : 155

SlPSKR1 : -----LPLLOVFNISDNISFGGVPVPLGICENSTRVSVIKMGVNYFNGSLPVGIGNCGSLKLF : 195
 SlPSKR2 : GLESIHSLNISSNLTGNFSEFGFENLVAFNISNNSFTGFSFKFEICSFKKLKVLDSLNLHLEGLDGLDNCSSLLOQL : 228
 AtPSKR1 : -----LPALQSEFDLSSNKFNSTPSHICHNSIQIRVVKLAVNYFAGNFTSFGFKCVLLEHL : 201
 AtPSKR2 : GLKLIQSLNISSNLSGKLSVDGVVPLGLVMLNVSNLFEGETHPELCSSSGGIIQVLDLSMNRVGNLDGLYNCSKSIQQL : 213
 DcPSKR : -----LPSLRVNLVYENSFHLPLASLCCNNLPIREIDLAMNYFDGSLPVGIGNCGSSVEYL : 211

SlPSKR1 : CVGSNLLSGSLPDELFLKLSRLTVLSLQENRFSGQLSSQIGNLSSLVHLDLCSNGFSGNIPDVDFRGLKLTLSAHSNRFF : 275
 SlPSKR2 : HVDSDNLDGGLHLPDSLYSMTSLQSLSANFSGQLSPQLSKLSKLSVLVSGNRFHGLLPNVFGNLTLLEQLAAHSNRFS : 308
 AtPSKR1 : CLGMNDLIGNIPEDLFHLKRNLLGIQENRISGSLREIRNLSSLVRLDVSWNLFSGEIPDVDFELPQLKFFLQGTNGFTI : 281
 AtPSKR2 : HTDSNRLTGQLPDYLYSTRELEQLSLSGNYLSEGLSKNLSNLGKLSLLISENRFSDVLPDVFGNLTQLEHLDVSSNKF : 293
 DcPSKR : GLASNLLSGSIPQELFQLSNLSVLAQNNRLSGALSSKLGRLSRLGRLDLSNKFSGKIPDVDFELNKLWYFSAQSNLFN : 291

SlPSKR1 : GNLPTSLANSGLVSSLSLRNNSLGGITELNCSAMVSLVSLDLATNGFRGLVDPDYLETQRLQTLNLRNNSFTGOLPESFK : 355
 SlPSKR2 : GPLPSTISYLSVDRVLDLRNNSLGGVLDLDFTKLISLCTLDLATNHFKNLPLVLSLR-ELKILSLAKNEFTGPIPENYA : 387
 AtPSKR1 : GGLPKSLANSPLNLLNLRNNSLGRMLNCTAMIALNSLDLGTNRFRNGRLPENLEDCKRLKNVNLARNTFHCQVPESEFK : 361
 AtPSKR2 : GRFPPLSQCSKDRVLDLRNNSLGSINLNEFTGFTDLCVLDLASNHFSGPLPDSLGHCPKMKILSLAKNEFRCKIPDIFK : 373
 DcPSKR : GEMPRSLNSRSLISLSLRNNTLSGQTYLNCAMINLTLSDLASNFSGSLPSNLENCLRLKTNFAKIRFIAQIPESFK : 371

SlPSKR1 : NFHSLSLISVSNNSMHNIDARLRILQHCKNLSTLVLTLLNFRDEEELPTDSSLQFSELKALITIANCRITGVVPOWLRNSSK : 435
 SlPSKR2 : NLSLVLFLSLSNNSLNSLGSALSVLQHCNRLSTLILTRNFRGEEIPKN-VSGFENLMIFALGNCGLDGRIPWLYNCSKL : 466
 AtPSKR1 : NFESLSYFSLNSLSSLANISSALGILQHCKNLSTLVLTLLNFRHGEALPDDSSLHFELKLVVANCRLTGSMPRWLSSSNE : 441
 AtPSKR2 : NLQSLFLSLSNNSFVDFSETMNVLQHCNRLSTLILSKNFIGEEIPNN-VTGFNLAIALGNCGLRGQIPSWLLNCKKL : 452
 DcPSKR : NFQSLTSLSFSNSSIQNLSSALEILQHCQNLKTLVLTLLNFRQEEELSVPSLQFKNLKVLTIASCOLRGTVPQWLSNPSL : 451

Island domain

SlPSKR1 : QLLDLSWNRLSGTLPPIWIGDFQFLFYLDFSNNSFTGIPKBITRLKSLISGP--VSMNEPSPDFPFFLKRNVSVRGLQYN : 513
 SlPSKR2 : QVLDLSWNHLDGEIPTWIGEMEKLFYLDFSNNSLTGIPKNLTDLKSLISPHNYASSLNSPTGIPFLVKRNOSSGGLQYN : 546
 AtPSKR1 : QLLDLSWNRLTGAIPSNWIGDFKALFYLDLSNNSFTGIPKSLTKLESLSRN--ISVNEPSPDFPFMKNRESARALQYN : 519
 AtPSKR2 : EVLDLSWNHFYGTIPHWIGKMSLFYIDFSNNTLTGAIPVAITELKLNLRNGTASQMTDSSGIPLYVKRKNSSNGLPYN : 532
 DcPSKR : QLLDLSWNQLSGTIPPLWGLSLSLFYLDLSNNTFIGEIPHSLSLSLQSLVSKS--NAVEEPSPDFPFFKKNNTNAGLQYN : 529

Leucine-rich repeats

SlPSKR1 : QIFSFPPITLGLGNFLLTGAILEFEGNLKRLHVLDDLKSNNSLGTIPSSLSGMAVENLDLSHNNLIGSIPSSLVQCSFMSK : 593
 SlPSKR2 : QASSFPPIILLSSNRLNGTIWPEIIGRLKQLHVLDDLKSNNTGTIPSSISNMGNLEVLDSLQNDLNGSIPASLNKLTFLSK : 626
 AtPSKR1 : QIFGFPPITLGLGNLSCPIWEEFEGNLKRLHVLDDLKSNNSLGTIPSSLSGMAVENLDLSHNNLIGSIPSSLVQCSFMSK : 599
 AtPSKR2 : QVSRFPPIILLSSNRLNGTIWPEIIGRLKELHMLDDLKSNNTGTIPDPSISGNLLEVLDSLHNNLIGSIPSSLVQCSFMSK : 612
 DcPSKR : QPSSFPPIIDLSSNRLNGSIWPEFEGDLRQLHVLNLLKSNNSLGTIPANLSGNTSLEVLDSLHNNLIGSIPSSLVQCSFMSK : 609

Transmembrane domain

SlPSKR1 : FSVAYNKLSGEIPVGGQFPTFTSSFEQNLGCGEHCSTCRNASQVPRDSVAKGKRR-----KGTVIEMGIGIGLGTI : 666
 SlPSKR2 : FNVANNHLOCAIPTGGQFLSFPNSSFEQNLGCGEHCSTCRNASQVPRDSVAKGKRR-----KGTVIEMGIGIGLGTI : 703
 AtPSKR1 : FSVAYNKLSGVIPSQGFQTFPNSSEFENLHCGEHRFPCSEGTE--ALIKRSRRS-----RGGDICAIGIAFGSV : 669
 AtPSKR2 : FSVAYNRLTGAIPSGGFYSFPNSSFEQNLGCGEHCSTCRNASQVPRDSVAKGKRR-----KGTVIEMGIGIGLGTI : 692
 DcPSKR : FSVAYNKLSGEIPVGGQFPTFTSSFEQNLGCGEHCSTCRNASQVPRDSVAKGKRR-----KGTVIEMGIGIGLGTI : 682

Ser/Thr kinase domain

SlPSKR1 : FLLALVYLIIVVASSR-KVVVDQEKELDASN--RELEDLGSSLVIFFHNKENTKEMCLDDLLKCTDNFDQSNIVGCGGFGL : 743
 SlPSKR2 : LLLAIVLLRVSRRDAGHQIGDFEEDFSRPP--RSSDTFVPSKLVVLFQNSD-CKELTVADLLKSTNNEFNQSNIVGCGGFGL : 780
 AtPSKR1 : FLLTLVSLIVLRARRRSGEVDPEIEESESNNRKELGELGSKLVVLFQNSD--KELSYDDLDDSTNSFDQANIIGCGFGM : 747
 AtPSKR2 : LLLSVLLLRISRKVDDDRINDVDEETISG----VSKALGPSKIVLFHSCG-CKDLSVEELLKSTNNEFNQANIIGCGGFGL : 767
 DcPSKR : FLLTVTLVLLIILRTTSR-GEVDPEKKADA-----DEIELGSRSVVLFHNKDSNNELSLDDILKSTSSFQANIIGCGGFGL : 756

SlPSKR1 : VYKAITLRDGRKVAIKRLSGDYGQMEREFQAEVEALSRAQHPNLVHLLQGYCKYRTDRLLIYSYMENGLDYLWHEKVDGPA : 823
 SlPSKR2 : VYKAELENGIKTAIKRLSGDCGQMEREFQAEVEALSRAQHKNLVSLOGYCYQHGSRRLLIYSYMENGLDYLWHERVDG-S : 859
 AtPSKR1 : VYKATLPDGGKVAIKRLSGDCGQIEREFQAEVEALSRAQHPNLVLLRGFYKNDRLIYSYMENGLDYLWHERNDGPA : 827
 AtPSKR2 : VYKANFEDGSKAAVKRLSGDCGQMEREFQAEVEALSRAEHKNLVSLOGYCKHGNDRLLIYSYMENGLDYLWHERVDGNM : 847
 DcPSKR : VYKATLPDGTKVAIKRLSGDTGQMDREFQAEVEALSRAQHPNLVHLLGYCNYKNDKLLIYSYMDNGSLDYLWHEKVDGPP : 836

SlPSKR1 : LLDWDLRQLTAQGAARGLAYLHLACEPHILHRDIKSSNILLDENFEAHLADFGLARIRPYDTHVTTDVLVGTGLGYIPPEY : 903
 SlPSKR2 : SLTWDMLRKLIAQGAARGLAYLHK--EPNIVHRDIKSSNILLNERFEAHLADFGLSRLLRPYDTHVTTDLVGTGLGYIPPEY : 937
 AtPSKR1 : LLKWKTRLRIAQGAARGLAYLHLEGDPEHILHRDIKSSNILLDENFNESHADFGLARLMSPYETHVSTDLVGTGLGYIPPEY : 907
 AtPSKR2 : TLIWDLRKLIAQGAARGLAYLHKVCEPNVIHRDIKSSNILLDEKFEAHLADFGLARLLRPYDTHVTTDLVGTGLGYIPPEY : 927
 DcPSKR : SLDWKTRLRIARGAARGLAYLHQSCPEHILHRDIKSSNILLSDFVAHLADFGLARLLIPYDTHVTTDLVGTGLGYIPPEY : 916

SlPSKR1 : GQASVATYKGDVYSFGVVLELLTCKRPMDPCK-----PRASRDLSW---VIQMKKQKRETEVFD----- : 961
 SlPSKR2 : SQTLTATFRGDVYSFGVVLELLTCKRPVESGGDIRYNDMGYKLRQAASGGVKYSLSMHSAKSTTEALDRSSCLVARGNR : 1017
 AtPSKR1 : GQASVATYKGDVYSFGVVLELLTCKRPVDMCK-----PKGCRDLISW---VVKMKHESRASEVFD----- : 965
 AtPSKR2 : SQSLIATCRGDVYSFGVVLELVTGRRPVEVCK-----GKSCRDLVSR---VFQMKAEKREAELEID----- : 985
 DcPSKR : GQASVATYKGDVYSFGVVLELLTCKRPMDPCK-----PRGSRDLISW---VLOMKTEKRESELEFD----- : 974

SlPSKR1 : -----PLIYDKQHAKE-----EMLLVLEIACLCLHESPKIRPSSQQLVTVLWLDNINTPPDVHVF-- : 1013
 SlPSKR2 : KCKGEIPRTVDDGTVDREERARSVGESLTDGAAKAVETGLDVGEKAKESIDEAWDAAKETNNIKDAMVDDANDEMKK : 1097
 AtPSKR1 : -----PLIYSKENDK-----EMFRVLEIACLCLSENPKQRPTTQQLVSWLDDV----- : 1008
 AtPSKR2 : -----TTIRENVNER-----TVLEMLEIACKCIDHEPRRRPLIEEVVTVLELDLPMESVQQQ-- : 1036
 DcPSKR : -----PFIYDKDHAE-----EMLLVLEIACRCLGENPKTRPTTQQLVSWLBNIDVSS----- : 1021

SlPSKR1 : -- : -
 SlPSKR2 : GI : 1099
 AtPSKR1 : -- : -
 AtPSKR2 : -- : -
 DcPSKR : -- : -

Supplemental Data Set 3. Nucleotide sequence alignments based on mRNA region of tomato *PSKR* homologs (supports Figure 2 and Supplemental Figure 2).

S1PSKR1 : TTATTGATTTCTGGGATTGGGAATCTACA AATGTTGTAATTTGGTAGGTGTTACTTGTGAT-----TCT : 207
S1PSKR2 : GGGTTATTCTATCAGCTTGGCTAATGAACCTAAATGCTGTAAATGGGATGGGTTTGTCTGTGGTAAATGTTTCTACTCAA : 234

S1PSKR1 : GGGAGGCTGGTCAAGTTGGAGCTTGGGAAAAGAAGTTAAATGGGAACTTTCTGAATCTTTAGGTAATTTGGATGAGCT : 287
S1PSKR2 : AGTAGAGTGATCAGGCTAAATTTGTCAAGAAAAGTTTGAAGGGTGGTTTCACAGTCTTGCAGAGATTGGATCAGTT : 314

S1PSKR1 : AAGAACCCTTAATCTATCTCACAAATTTCTTTAAAGGACCTGTTCTTTTACACTGTTGCAATTGTCTAAATTTGGAAGTAT : 367
S1PSKR2 : GAAATTGCTCGATCTTTCGCACAATCATTTGGAAGTGGATTGCTTTTGGACTTGTCCAAAATGAAGCAGTTGGAAGTTC : 394

S1PSKR1 : TAGACTTGAGCAATAATGATTTCTTTGGA----- : 396
S1PSKR2 : TTGATTGAGTGATAATGTGTTGCTTGGACCAGTGTGAGGGTGTGATGGATTGGAATCAATCCATTCTCTCAATATA : 474

S1PSKR1 : -----TTGTTTCTAGTAGCATGAAC-----TTGCCTTGGCTTCAAGTTTTC AATATATCTGATAATTC : 455
S1PSKR2 : TCAAGCAATTTGTTCACTGGAAATTTCAAGTGGTTTGGTGAATTCCTTACCTTGTTCATTAAACATAAGCAACAATTC : 554

S1PSKR1 : CTTTGGAGGACCAGTTCCTTTGGGTATCTGTGAAAATTCAACTAGAGTTTCTGTTATTAAGATGGGGTTAATTTATTTTA : 535
S1PSKR2 : GTTACTGGTAGTTTCAAGTTTGAATTTGCAGTTTCTCAAGAGCTTAAGGTTCTGGATATATCACTTAAATCATCTTA : 634

S1PSKR1 : ATGGTAGTCTTCCAGTAGGAATTTGGCAATTGTGTTCA---TTAAAGCTTTTGTGTTGGCTCTAACCTTCTGTCTGGT : 612
S1PSKR2 : CTGGTGATCTTGGG---GGACTAGATAATTGCAGTTCATTGCTCCAGCAGCTACATGTGCATTCTAAATGATCTCGGGGTT : 711

S1PSKR1 : AGTTTGCCTGATGAACGTGTTTAAGCTATCAAGATTGACTGTATTGTCTCTACAAGAGAATCGATTCTCGGGCAGCTTAG : 692
S1PSKR2 : CACCTTCCGGACTCATGTATTTCGATGACATCTTTGGAGCAACTTTCACCTGCTGCCAATAATTTCTCAGGCAGCTAAG : 791

S1PSKR1 : CAGTCAGATTGTAATCTGTCTAGTTTGGTTCATTTGGATATTTGTTCAATGGAATTTTCAGGAAACATTCGGATGTGT : 772
S1PSKR2 : TCCACAGCTTAGTAACTTTCCAAACTGAAATCCTTAGTTTATCAGGAAATCGCTTTCATGTTTGGCTTCCATTAATGTGT : 871

S1PSKR1 : TCGATAGATTAGGGAAGTTAACATAATTTGTGAGCTCATTCAAAATAGGTTCTTTGGTAATATACCAACTTCATTTGGCAAA : 852
S1PSKR2 : TTGGTAATTTGACATTGTTAGAACAGTTAGCTGCAATTCTAATAGATTTTCGGGACCATTGCCCTCTACGATTTCTGTAT : 951

S1PSKR1 : TCTGGGACTGTTAGTTCTCTTAGTTTGGAGAAATAATCTTTAGGGGGTATCATAGAGCTTAATTGTTTCAGCAATGGTTAG : 932
S1PSKR2 : CTTTCTGTGCTTAGGGTCTTGTATCTTAGCAATAATCTTTGCTGGTCTGTGATCTTGATTTTACTAAATTTGACAAG : 1031

S1PSKR1 : TCTTGTTCGCTTGATCTAGCTACGAATGGGTTCCGTGGGTTAGTTCCCTGATTTATCTTCTACTTGTCAAAGGTTGCAAAA : 1012
S1PSKR2 : TCTGTGCACACTTGATCTTGCAACTAACCATTTCAAAGGTAATCTCCGCTATCACTCTCTAGTCCGGGAA---TTAAAAA : 1108

S1PSKR1 : CTATCAATCTGCTAGAACTCTTTCCTGGACAACTGCCGGAAAGTTTCAAGAAATTTTCATAGCCTTTCGTCCCTTCA : 1092
S1PSKR2 : TCTTGAATCTTGCAAAACGAATTCACGGGGCCAACTTCTGAGAACTATGCAACCTTTCATGCTTGTGTTCCTCTCG : 1188



Supplemental Data Set 4. Nucleotide sequence alignments based on mRNA region of tomato *CaM* homologs (supports Figure 7 and Supplemental Figure 7).

S1CaM1 : ATGGCGGATCAGCTCACCGAAGATCAGATCTCTGAGTTCAAGGAAGCTTTTCTTTTTCGACAAAGACGGGATGGTTG : 80
 S1CaM2 : ATGGCGGATCAGCTCACCGGATGACCAGATCTCTGAGTTCAAAGAGGCTTTTCTTTTTCGACAAAGACGGGATGGTTG : 80
 S1CaM3 : ATGGCAGATCAGCTCACCGATGATCAGATCTCTGAGTTCAAAGGAGGCTTTTCTTTTTCGACAAAGACGGGATGGTTG : 80
 S1CaM4 : ATGGCGGATCAGCTCACCGATCAGATCTCTGAGTTCAAAGGAAGCTTTTCTTTTTCGACAAAGGATGGGATGGTTG : 80
 S1CaM5 : ATGGCGGATCAGCTTACAGATGATCAGATCTCTGAGTTCAAAGGAAGCTTTTCTTTTTCGACAAAGATGGGATGGTTG : 80
 S1CaM6 : ATGGCAGAGCAGCTCACGGAGGAGCAGATGCTGAGTTCAAAGGAAGCTTTTCTTTTTCGACAAAGGATGGGATGGCTG : 80

S1CaM1 : TATCACAACAAAGGAACCTTGGAAACGTAATGCGGTCATTGGGGCAGAAACCAACCGAGGCTGAGCTTCAAGAATGATCA : 160
 S1CaM2 : CATCACGACTAAGGAGCTTGGGACTGTGATGAGGTCGTTGGGACAGAAACCTACTGAAAGCTGAGCTCCAGGACATGATAA : 160
 S1CaM3 : CATTACAACAAAGGAGCTTGGGACTGTGATGAGGTCGTTGGGACAGAAACCAACTGAAGCTGAGCTCCAGGACATGATAA : 160
 S1CaM4 : TATCACAACAAAGGAGCTTGGAAACGTAATGCGGTCATTGGGGCAGAAACCAACTGAGGCTGAGCTTCAAGAATGATCA : 160
 S1CaM5 : CATCACGACTAAGGAGCTTGGAAACGTAATGCGGTCGTTGGGACAGAAACCAACTGAGGCTGAGCTTCAAGAATGATCA : 160
 S1CaM6 : TATTACTACAAAGGAGCTTGGAAACGTAATGAGATCACTTGGTCAGAAATCCCACTGAAAGCTGAACTACAGGATATGATCA : 160

S1CaM1 : ATGAAGTTGATGCTGATGGAATGGGACCATGATTTCCAGAGTTCCTTAAACCTGATGGCTCGCAAGATGAAGGACACT : 240
 S1CaM2 : ACGAGTGGATGCAAGATGGTAATGGAACCATCGACTTCCAGAGTTCCTTAAACCTTATGGCCAGGAAGATGAAGGATACT : 240
 S1CaM3 : ATGAAGTGGATGCTGATGGTAATGGAACCATCGACTTCCCGAGTTCCTTAAACCTCATGGCCAGGAAGATGAAGGATACA : 240
 S1CaM4 : ATGAAGTTGATGCTGATGGAATGGGACCATGACTTCCCGAGTTCCTTAAACCTGATGGCTCGCAAGATGAAGGACACT : 240
 S1CaM5 : ATGAAGTTGATGCTGATGGAATGGAACCATGACTTCCCGAGTTCCTTAAACCTGATGGCTCGCAAGATGAAGGACACT : 240
 S1CaM6 : GTGAAGTTGATGCTGATCAGAATGGAACCATGATTTCCAGAGTTCCTTGAATCTGATGGCAGGGAAGATGAAGGACACT : 240

S1CaM1 : GATTCGAGGAGGAGCTCAAGGAAGCTTTTCAAGATGTTTGACAAGGATCAGAATGGATTCATCTCCGGAGCTGAGCTTCG : 320
 S1CaM2 : GACTTCGAGGAGGAGCTTGAAGAGGCATTCAAGATGTTTGACAAGGATCAAAATGGCTTCATCTCCGGTCTGAGCTTCG : 320
 S1CaM3 : GACTTCGAGGAGGAGCTAAAGGAGGCATTCAAGATGTTTGACAAGGATCAGAATGGGTTTCATCTCTGCTGCTGAGCTCCG : 320
 S1CaM4 : GATTCGAGGAGGAGCTCAAGGAAGCTTTTCAAGATGTTTGACAAGGATCAGAATGGATTCATCTCTGCTGCTGAGCTTCG : 320
 S1CaM5 : GATTCGAGGAGGAGCTGAAGGAAGCTTTTCCGGTCTTTGACAAGGATCAGAATGGATTCATTCCTGCAAGCTGAGCTACG : 320
 S1CaM6 : GATTCGAGGAAGGACTCAAGGAGGCTTTTCAAGTTCCTTGAATAAGATCAGAATGGCTTTATTCCTGCAAGCTGAGCTTCG : 320

S1CaM1 : TCATGTGATGACAAACCTAGGCGAAGAGCTTACTGATGAAGAGGTTGATGAGATGATTCGTTGAAAGCTGATGTGGATGGTTG : 400
 S1CaM2 : TCATGTGATGACTAACCTTGGAGAGAAGCTTACTGATGAAGAAGTTCGATGAGATGATTCGTTGAAAGCTGATGTGGATGGTTG : 400
 S1CaM3 : TCATGTGATGACTAACCTTGGTGAAGAAGCTTACTGATGAAGAAGTTGATGAAATGATCAGAGAGGCTGATGTGGATGGCTG : 400
 S1CaM4 : CCATGTGATGACTAACCTAGGTGAGAAGCTTACAGATGAAGAAGTTGATGAGATGATTCGTTGAAAGCTGATGTGGATGGTTG : 400
 S1CaM5 : CCATGTGATGACAAACCTAGGCGAAGAGCTTACAGATGAAGAAGTTGACGAGATGATTCGTTGAAAGCTGATGTGGATGGTTG : 400
 S1CaM6 : TCATGTGATGACAAACCTTGGAGAGAAGCTGACTGATGAAGAAGTTGATGAGATGATTCGAGAGGCGAGATATTGATGGTTG : 400

S1CaM1 : ATGGGCAGATCAACTACGACGAGTTTGGTCAAGGTTATGATGGCCAAGTGA : 450
 S1CaM2 : ATGGACAAATCAACTATGAGGAGTTTGGTCAAGGTCATGATGGCCAAGTAA : 450
 S1CaM3 : ATGGACAAATCAACTACGATGAGTTTGGTCAAGGTCATGATGGCCAAGTGA : 450
 S1CaM4 : ATGGACAGATCAACTATGACGAGTTTGGTCAAGGTCATGATGGCCAAGTGA : 450
 S1CaM5 : ATGGACAGATCAACTATGACGAGTTTGGTCAAGGTCATGATGGCCAAGTGA : 450
 S1CaM6 : ATGGACAAGTTAATTATGACGAGTTTGGTCCGTATGATGCTTGGCCAAGTGA : 450



Supplemental Data Set 5. Primers used in this study.

Gene	Annotation	Accession No.	Primer pairs	Assay
<i>SIPSK1</i>	putative phytosulfokine	Solyc09g009130.2	F: 5'- AACAGCTCGTTTATTGC -3' R: 5'- CATTCTTCTATTCCCAT -3'	qPCR
<i>SIPSK2</i>	putative phytosulfokines 2	Solyc11g066880.1	F: 5'- CTTGCAAGTGAAAAGGAAGCA -3' R: 5'- GGGTGATTATGGTGTGAGTGT-3'	qPCR
<i>SIPSK3</i>	putative phytosulfokines 3	Solyc02g092110.2	F: 5'-TCCcccgggCCAAGGACCAAATGAT -3' R: 5'-CGCggatccTAACGTACAGGGGAAAA -3'	VIGS
			F: 5'-ACCAGGATGTTGTTGAACC -3' R: 5'-GGTCCTTGGGAATCGTAAAC -3'	qPCR
<i>SIPSK3L</i>	phytosulfokines 3 like	Solyc02g092120.2	F: 5'- TCCcccgggCCAGGATCATGTTAGGGAAT -3' R: 5'- CGCggatccTCAAGGTGAGCAGCCAAG -3'	VIGS
			F: 5'- ATCAGAACCCGTGAACTA -3' R: 5'- TACCGCCAAATACAAAGC -3'	qPCR
<i>SIPSK4</i>	putative phytosulfokines 4	Solyc01g106830.2	F: 5'-TCCcccgggAACATTTGTCCCTTCACT-3' R: 5'-CGCggatccATCCTCCACATCTTT-3'	VIGS
			F: 5'-CGCCTTATCGCGATGTTAC -3' R: 5'-CCAGGGCCTTCACATCTATC -3'	qPCR
<i>SIPSK5</i>	putative phytosulfokines 5	Solyc10g083580.1	F: 5'- CGGTTCTGTCTACCTCCTACA -3' R: 5'- GTGAGCCTCAGCTACCATCC -3'	qPCR
<i>SIPSK6</i>	putative phytosulfokines 6	Solyc06g074540.2	F: 5'- TCTCAACATGTTCTTTGTCT -3' R: 5'- CGTTGGTTTCCATGTGGTCA -3'	qPCR
<i>SIPSK7</i>	putative phytosulfokines	Solyc04g077580.2	F: 5'-TCCcccgggACATTTGCTGTTTCGTCCT-3' R: 5'-CGCggatccGCCATTGTCCTCCTCTTC -3'	VIGS

Gene	Annotation	Accession No.	Primer pairs	Assay
			F: 5'- TCGATCCCAAATTCAGGTTGC -3' R: 5'- AGATGAGCAGCCATTGTCCT -3'	qPCR
<i>SITPST</i>	protein-tyrosine sulfotransferase	Solyc11g069520.1	F: 5'-CCGgaattcGGGCGTCTTCTTCACTCG -3' R: 5'-CGCg gatccGGAACCTGGCTGCTACCT -3'	VIGS
			F: 5'-CGTGGAAGTATTTGGTCCCT -3' R: 5'-CGTGTAGAGGCATCACCATC -3'	qPCR
<i>SIPSKR1</i>	receptor like kinase	Solyc01g008140.3	F: 5'-TGCTctagaGGGTGGTGAAGTTGGAGC -3' R: 5'-CGCg gatccCAGGCAAACCTACCAGACAGAAG -3'	VIGS
			F: 5'-CCGTGGGTTAGTTCCTGATT -3' R: 5'-GAAAGGGACGAAAGGCTATG -3'	qPCR
			F: 5'-GCGg gatccAATCTCCAGAACTTGATATG -3' R: 5'-GCGg tgcacTCAAGTTCCTTTGCGCCTCTTTCC-3'	truncated protein (23-653 aa) expression for SPR
			F: 5'- TCCcccgggGAATGGGTGTGTTGCAAGTTTG -3' R: 5'- CATGccatggAAAACACATGAACATCAGGTG -3'	GFP Fluorescence
<i>SIPSKR2</i>	receptor like kinase	Solyc07g063000.3	F: 5'- CgagctcTGCTGTAATGGGATGGG -3' R: 5'- TCCcccgggGCAACAAGGTTAGGGAAT -3'	VIGS
			F: 5'-GGAAATCGCTTTTCATGGTTT -3' R: 5'-CAAGCACCCCTAAGCACAGAA -3'	qPCR
			F: 5'-GCGg gatccGAAACCCCAGTTCAAACCTG -3'	truncated protein (28-689 aa)

Gene	Annotation	Accession No.	Primer pairs	Assay
			R: 5'-GCGgtcgacTCAACCTCGGCCAAGCCTACTAC -3'	expression for SPR
			F: 5'- TCCcccgggGAATGGTGAATTTGGGAGTTTCTGCC -3'	GFP
			R: 5'- CGCggatccCCTCTCCTTTACACTTGCGATTG -3'	Fluorescence
<i>SIPR1b</i>	pathogenesis-related protein 1b	Solyc00g174340.1	F: 5'-ATCTCATTGTTACTCACTTGTC -3' R: 5'-AACGTGCCCCGACCA -3'	qPCR
<i>SICO11</i>	coronatine-insensitive 1	Solyc05g052620.2	F: 5'-GGATGCTTCTGGGATACGTT -3' R: 5'-TGGATGCTCCGAGACTACAG -3'	qPCR
<i>SIERF1</i>	ethylene-responsive factor 1	Solyc05g051200.1	F: 5'-ATTGGAGTTAGAAAGAGGCCAT -3' R: 5'-CTCATTGATAATGCGGCTTG -3'	qPCR
<i>SIARF5</i>	auxin response factor 5	Solyc04g081240.2	F: 5'-CACGTGTGCGGACATATACA -3' R: 5'-TCGAGTGTCATTCAGAAGCC -3'	qPCR
<i>SIACTIN</i>	actin	Solyc03g078400.2	F: 5'-TGGTCGGAATGGGACAGAAG -3' R: 5'-CTCAGTCAGGAGAACAGGGT -3'	qPCR
<i>SICaM1</i>	calmodulin 1	Solyc01g008950.2	F: 5'-ACTTGGAACAGTAATGCGGTCATTG -3' R: 5'-TGTCCTTCATCTTGCGAGCCA -3'	qPCR
			F: 5'- CCTtaattaaCATGGCGGATCAGCTCACCGAA -3' R: 5'- CTAGactagtCTTGGCCATCATAACCTTGACG -3'	BiFC-cYFP
<i>SICaM2</i>	calmodulin 2	Solyc10g081170.1	F: 5'- CGCggatccAGGCTTTCAGTTTGTTCG -3' R: 5'- CCGgaattcCTTCCCTAATCATCTCATCG -3'	VIGS
			F: 5'- ACTGACTCTGAGGAGGAGTTGA -3' R: 5'- ACTTGGCCATCATGACCTTAACA -3'	qPCR
			F: 5'- TTggcgcgccATGGCGGATCAGCTGACGGA -3'	Co-IP

Gene	Annotation	Accession No.	Primer pairs	Assay
			R: 5'- CGGggtaccCTTGGCCATCATGACCTTAAC -3'	
			F: 5'- CCTtaattaaCATGGCGGATCAGCTGACGGA -3'	BiFC-cYFP
			R: 5'- CTAGactagtCTTGGCCATCATGACCTTAAC -3'	
<i>SlCaM3</i>	calmodulin 3	Solyc10g077010.1	F: 5'- AAGGACGGAGATGGTTGC -3'	qPCR
			R: 5'- GCTCAGCTTCAGTTGGGT -3'	
			F: 5'- CCTtaattaaCATGGCAGATCAGCTCACCGATG -3'	BiFC-cYFP
			R: 5'- CTAGactagtCTTGGCCATCATGACCTTAAC -3'	
<i>SlCaM4</i>	calmodulin 4	Solyc11g072240.1	F: 5'-GGCGGATCAGCTCACTGAC -3'	qPCR
			R: 5'- GTTGTGATGCAACCATCTCCAT -3'	
<i>SlCaM5</i>	calmodulin 5	Solyc12g099990.1	F: 5'- GACAAGGATCAGAATGGA -3'	qPCR
			R: 5'- GAATCATCTCGTCAACCT -3'	
<i>SlCaM6</i>	calmodulin 6	Solyc03g098050.2	F: 5'- AGGATGGCGATGGCTGTA -3'	qPCR
			R: 5'- GTGGGATTCTGACCAAGTGA -3'	
			F: 5'- CCTtaattaaCATGGCAGAGCAGCTGACGGAG -3'	BiFC-cYFP
			R: 5'- CTAGactagtCTTGGCAAGCATCATACGGAC -3'	
<i>SlYUC1</i>	monooxygenase	Solyc06g008050.2	F: 5'- TGGACATTGGTGCATTGGAA -3'	qPCR
			R: 5'- AGCCAGTAGCAAGAAGAACAGA -3'	
			F: 5'- CCTtaattaaCATGGCTAGCTTCAATGACCAT -3'	BiFC-nYFP
			R: 5'- TTggcgcgccCCAAGGTTGAAATTTTTTTTGC -3'	
<i>SlYUC2</i>	monooxygenase	Solyc06g065630.2	F: 5'- AAATGCAGAGGCAGTTAT -3'	qPCR
			R: 5'- ATGAGGAATGGCGTTATG -3'	

Gene	Annotation	Accession No.	Primer pairs	Assay
			F: 5'- CCttaattaaCATGGGTTGTTGTAAAGAGG -3' R: 5'- TTggcgcgccCAAACATATGCCTTGGTTATC -3'	BiFC-nYFP
<i>SIYUC3</i>	monooxygenase	Solyc06g083700.2	F: 5'- TGGCCCTGTAATTGTTGGTG -3' R: 5'- GCCACAGTGATGCGATACAG -3'	qPCR
			F: 5'- CCttaattaaCATGTTTACCTTCTCATCAGAAC -3' R: 5'- TTggcgcgccCAAAGTTGAGATGCATCTTC -3'	BiFC-nYFP
<i>SIYUC4</i>	monooxygenase	Solyc08g068160.1	F: 5'- CCttaattaaCATGGATTCTTATTTGAAAGA -3' R: 5'- TTggcgcgccCTTGAAAATATTGATGAATGT-3'	BiFC-nYFP
			F: 5'- CGTCCCGACTCGGATTAGAT -3' R: 5'- GCGTTCCAACGTCAAGTACA -3'	qPCR
<i>SIYUC5</i>	monooxygenase	Solyc09g064160.2	F: 5'-ATGGCTTGTCGTTGCTACTG -3' R: 5'-CAACCAACGACCACCACTTT -3'	qPCR
			F: 5'- CCttaattaaCATGTTTGTAGTTTTTCAGATAACG -3' R: 5'-TTggcgcgccCAAAGTTGAGATGCAACGTCTG -3'	BiFC-nYFP
<i>SIYUC6</i>	monooxygenase	Solyc09g074430.2	F: 5'- CCttaattaaCATGGCAACATTTGATAATC -3' R: 5'- CGGactagtTTCAGAGAGCAGAGAGTTG -3'	BiFC-nYFP
			F: 5'- TTggcgcgccATGGCAACATTTGATAATC -3' R: 5'-CGGggtaccTTCAGAGAGCAGAGAGTTG -3	Co-IP
			F: 5'- CgagctcATGGCAACATTTGATAATC -3' R: 5'- CGCggatccTTCAGAGAGCAGAGAGTTG -3'	GFP

Gene	Annotation	Accession No.	Primer pairs	Assay
			F: 5'- TGGCAACATTTGATAATCATGTAGA -3' R: 5'- TGCAGATGTAGCAAGACCAC -3'	qPCR
<i>SIYUC7</i>	monoxygenase	Solyc09g091090.1	F: 5'- CCttaattaaCATGAATCAATATTGTAATAG -3' R: 5'- TTggcgcgccCGAAGGAAGATAACTTGTTTCTT -3'	BiFC-nYFP
			F: 5'- GAGTCGGTCCACTCTGCTAA -3' R: 5'- TCCTTCGAATTCGGGCACTA -3'	qPCR
<i>SIYUC8</i>	monoxygenase	Solyc09g091720.1	F: 5'- GGGAGATGGTGTACATGGCAA -3' R: 5'- AATGGGCCTTCTTCTGGTTGT -3'	qPCR
<i>SIYUC9</i>	monoxygenase	Solyc09g091870.1	F: 5'-GGCTCTACGCTGCTGGATTT -3' R: 5'-TTGTCTCCTCTGACAGACTT -3'	qPCR
<i>B. cinerea actin</i>	<i>B. cinerea actin</i>	XM_001553318.1 (NCBI)	F: 5'-GGTAACATTGTTATGTCTGG -3' R: 5'-CTTGACCTTCATCGACG -3'	qPCR