
Article:

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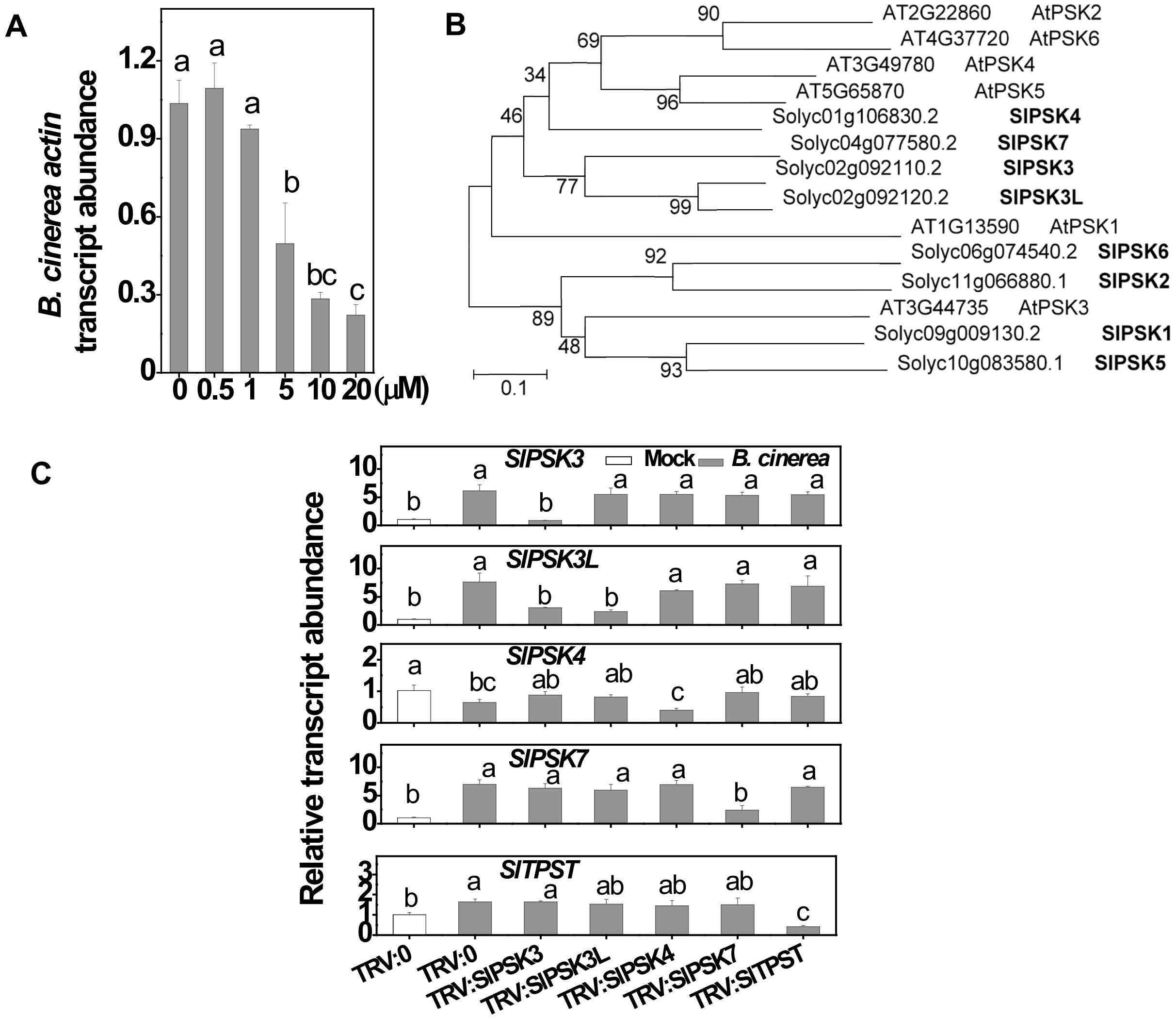
Supplemental Figure 1



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).

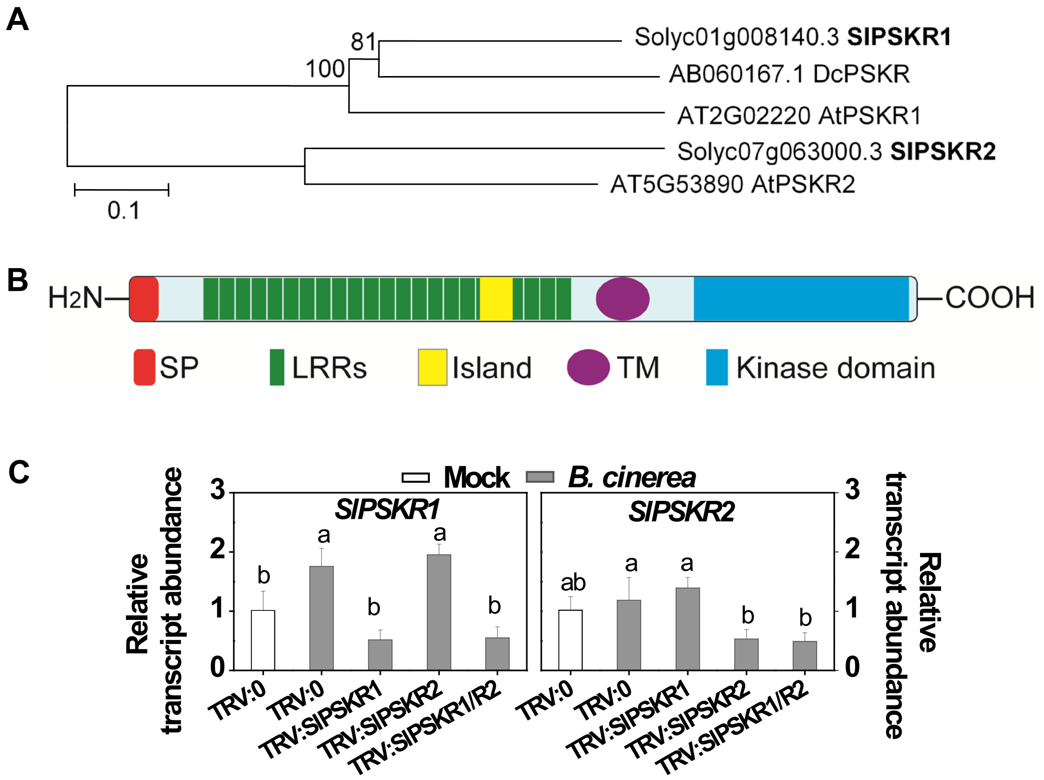
(A) The dose-dependent alleviatory effect of PSK on leaf *B. cinerea* transcript abundance. Four-week-old tomato plants were treated with indicated concentrations of PSK 12 h before *B. cinerea* inoculation, and leaf samples were taken at 1 day post *B. cinerea* inoculation (dpi) for relative leaf *B.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



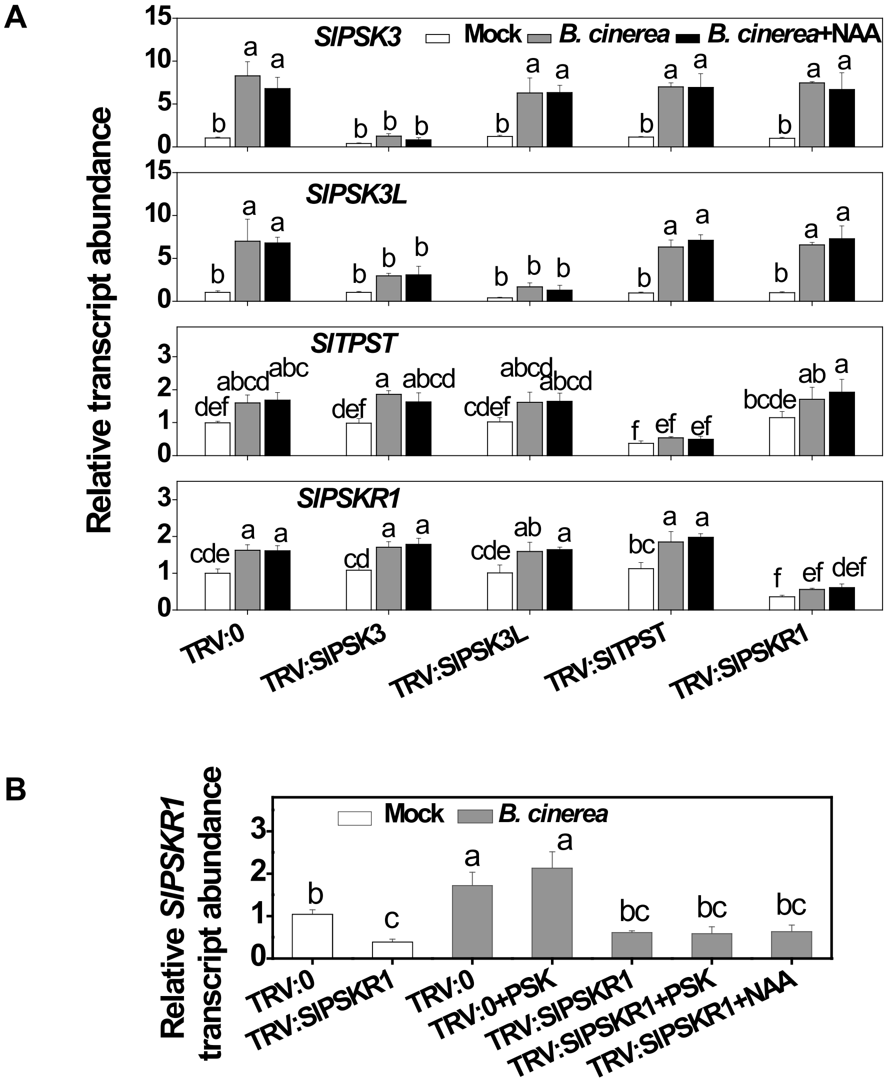
Supplemental Figure 2. Analysis of PSK receptor sequences, and the transcript abundance of *SlPSKRs* in VIGS tomato plants (supports Figure 2).

(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 SlPSKR1/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 *SlPSKRs* 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 ± 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



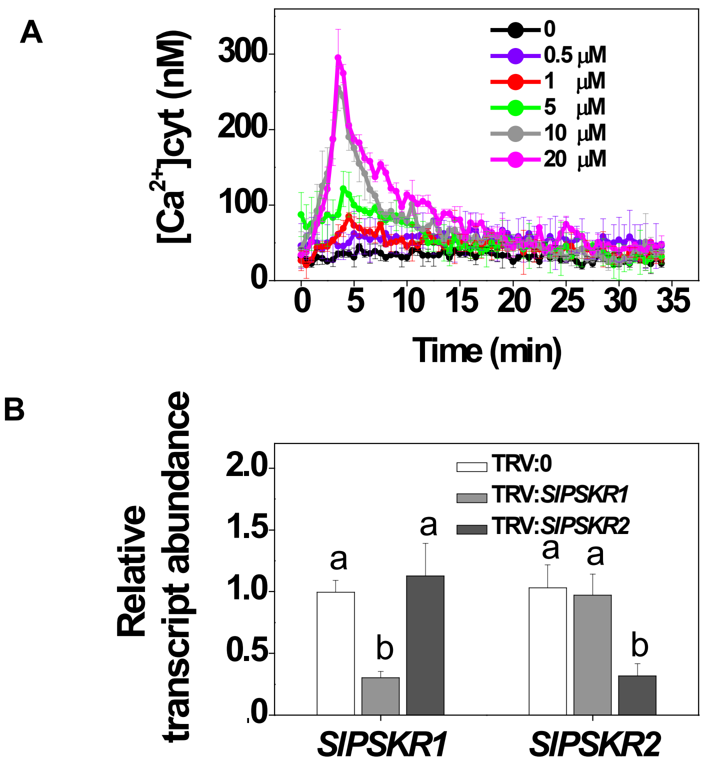
Supplemental Figure 3. The transcript abundance of PSK signaling-related genes in VIGS tomato plants (supports Figure 4).

(A) Relative transcript abundance of *SlPSK3*, *SlPSK3L*, *SlTPST*, and *SlPSKR1* in VIGS tomato plants.

(B) Relative transcript abundance of *SlPSKR1* in VIGS tomato plants.

After initial silencing efficiency test 3~4 weeks after *A. tumefaciens* infiltration, tomato plants were subject to pharmalogical 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 ± 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



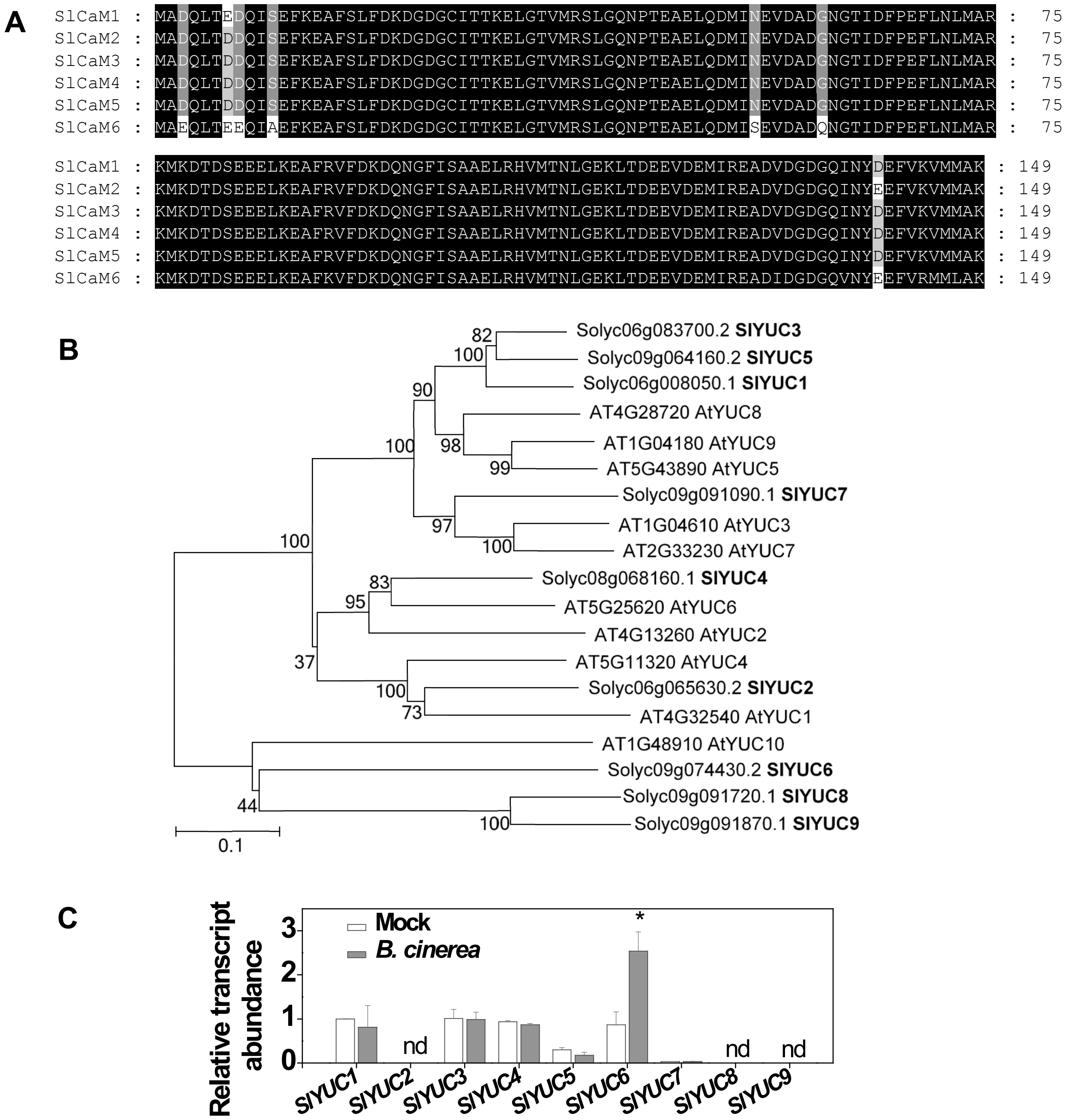
Supplemental Figure 4. The effect of PSK concentration on cytosolic Ca^{2+} levels, and the transcript abundance of *SlPSKRs* in VIGS tomato plants (supports Figure 5).

(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 ± SD generated from 8 leaf discs per treatment.

(B) Relative transcript abundance of *SlPSKR1* and *SlPSKR2* 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: *SlPSKR1* and TRV: *SlPSKR2* group were selected and transcript abundance of target genes are shown as the mean values ± 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



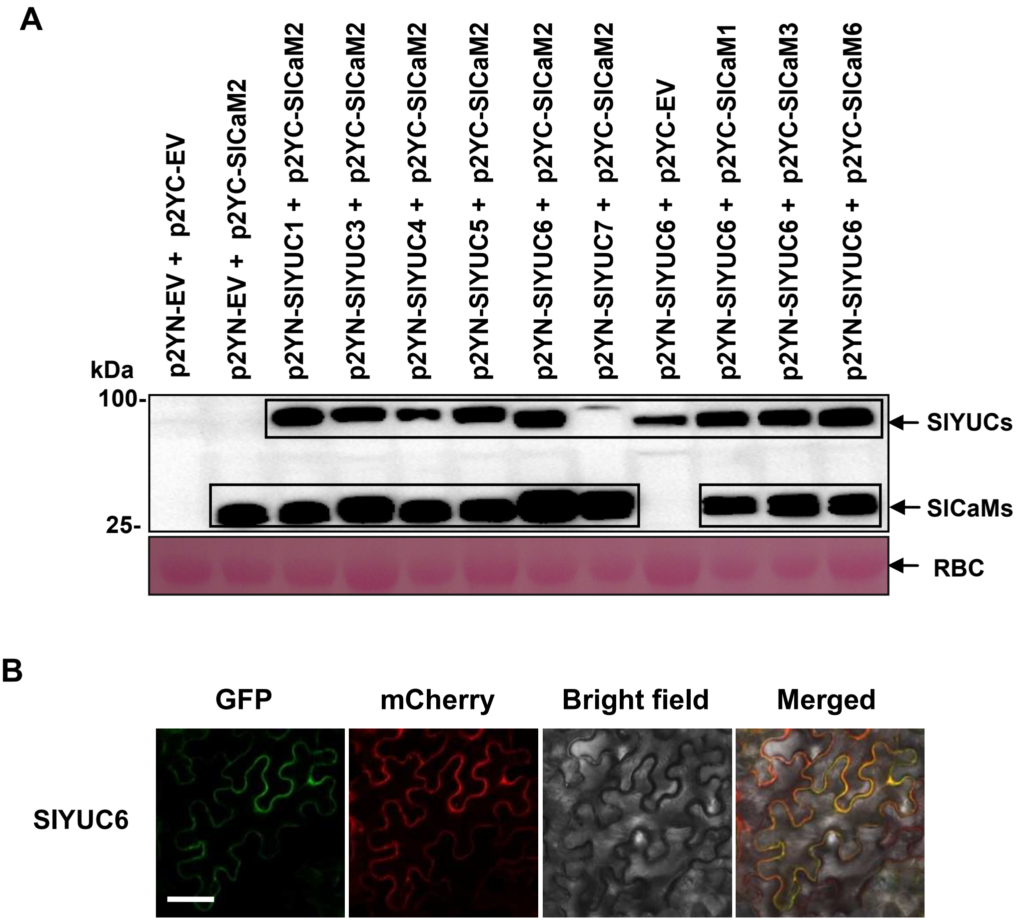
Supplemental Figure 5. Analysis of tomato CaM and YUC homologs (supports Figure 6).

(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 *SlYUCs* in leaves at 0.5 dpi. The transcript abundance of *SlYUC1* in mock-inoculated condition were defined as 1. The results are presented as the mean values ± 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



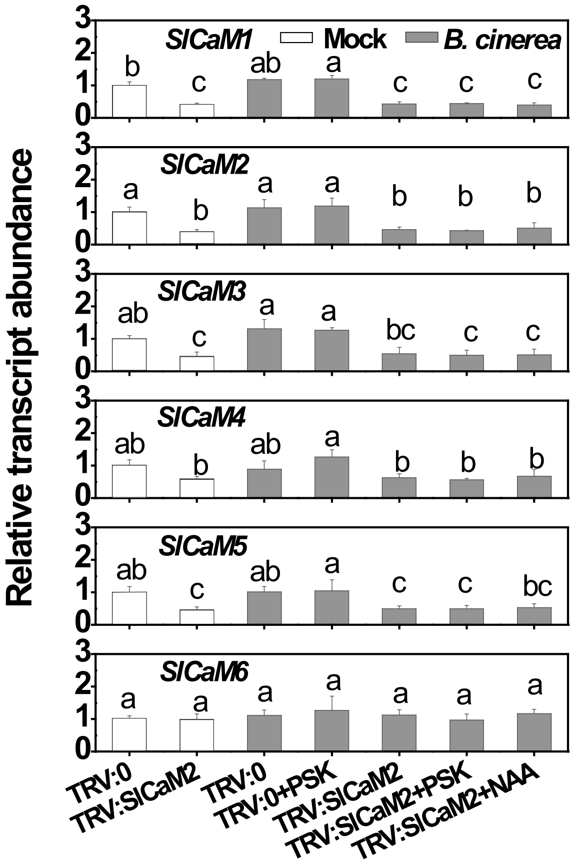
Supplemental Figure 6. Co-expression of SlCaMs and SlYUCs in *N. benthamiana* leaves (supports Figure 6).

(A) Co-expression of p2YC-SlCAMs and p2YN-SlYUCs 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 SlYUCs and SlCaMs bands.

(B) SlYUC6 localizes to plasma membrane. SlYUC6-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 µm.

The experiments were repeated two times with similar results.

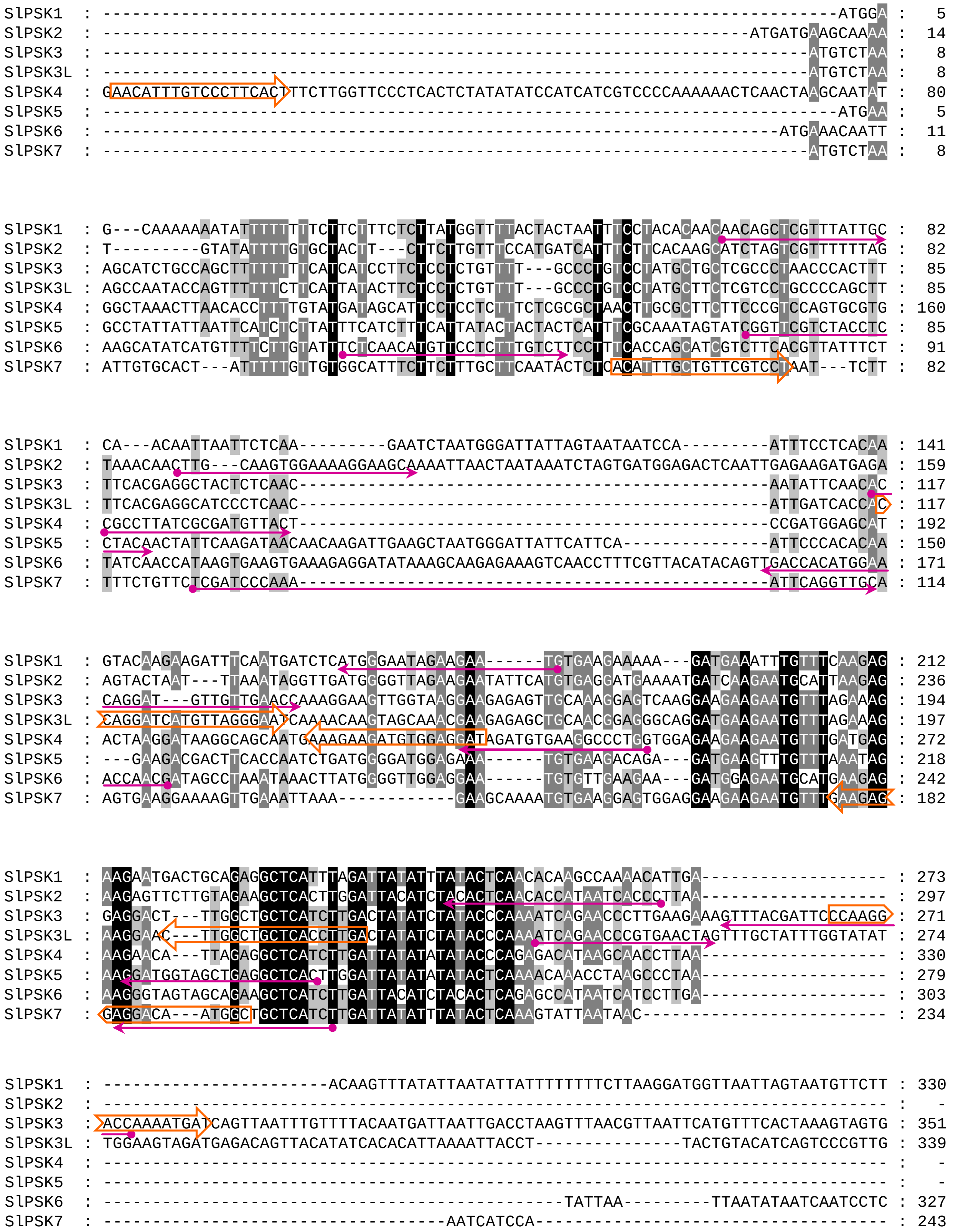
Supplemental Figure 7



Supplemental Figure 7. Effects of *SlCaM2* silencing on the transcript abundance of *SlCaM* 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 ± 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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SlPSK2  : ------------------------------------------------------------------ATGATGAAGCAAAA :  14
SlPSK3  : ------------------------------------------------------------------------ATGTCTAA :   8
SlPSK3L : ------------------------------------------------------------------------ATGTCTAA :   8
SlPSK4  : GAACATTTGTCCCTTCACTTTCTTGGTTCCCTCACTCTATATATCCATCATCGTCCCCAAAAAACTCAACTAAGCAATAT :  80
SlPSK5  : ---------------------------------------------------------------------------ATGAA :   5
SlPSK6  : ---------------------------------------------------------------------ATGAAACAATT :  11
SlPSK7  : ------------------------------------------------------------------------ATGTCTAA :   8

SlPSK1  : G---CAAAAAAATATTTTTTTCTTCTTTCTCTTATGGTTTTACTACTAATTTCCTACACAACAACAGCTCGTTTATTGC :  82
SlPSK2  : T---------GTATATTTTGTGCTACTT---CTTCTTGTTTCCATGATCATTTCTTCACAAGCATCTAGTCGTTTTTTAG :  82
SlPSK3  : AGCATCTGCCAGCTTTTTTTTCATCATCCTTCTCCTCTGTTTT---GCCCTGTCCTATGCTGCTCGCCCTAACCCACTTT :  85
SlPSK3L : AGCCAATACCAGTTTTTTCTTCATTATACTTCTCCTCTGTTTT---GCCCTGTCCTATGCTTCTCGTCCTGCCCCAGCTT :  85
SlPSK4  : GGCTAAACTTAACACCTTTTGTATGATAGCATTCCTCCTCTTTCTCGCGCTAACTTGCGCTTCTTCCCGTCCAGTGCGTG : 160
SlPSK5  : GCCTATTATTAATTCATCTCTTATTTCATCTTTCATTATACTACTACTCATTTCGCAAATAGTATCGGTTCGTCTACCTC :  85
SlPSK6  : AAGCATATCATGTTTTCTTGTATTTCTCAACATGTTCCTCTTTGTCTTCCTTTCACCAGCATCGTCTTCACGTTATTTCT :  91
SlPSK7  : ATTGTGCACT---ATTTTTGTTGTGGCATTTCTTCTTTGCTTCAATACTCTCACATTTGCTGTTCGTCCTAAT---TCTT :  82

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SlPSK3L : TTCACGAGGCATCCCTCAAC------------------------------------------------ATTGATCACCAC : 117
SlPSK4  : CGCCTTATCGCGATGTTACT------------------------------------------------CCGATGGAGCAT : 192
SlPSK5  : CTACAACTATTCAAGATAACAACAAGATTGAAGCTAATGGGATTATTCATTCA---------------ATTCCCACACAA : 150
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SlPSK7  : TTTCTGTTCTCGATCCCAAA------------------------------------------------ATTCAGGTTGCA : 114

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SlPSK4  : ACTAAGGATAAGGCAGCAATGAAAGAAGATGTGGAGGATAGATGTGAAGGCCCTGGTGGAGAAGAAGAATGTTTGATGAG : 272
SlPSK5  : ---GAAGACGACTTCACCAATCTGATGGGGATGGAGAAA------TGTGAAGACAGA---GATGAAGTTTGTTTAAATAG : 218
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SlPSK6  : AAGGGTAGTAGCAGAAGCTCATCTTGATTACATCTACACTCAGAGCCATAATCATCCTTGA------------------- : 303
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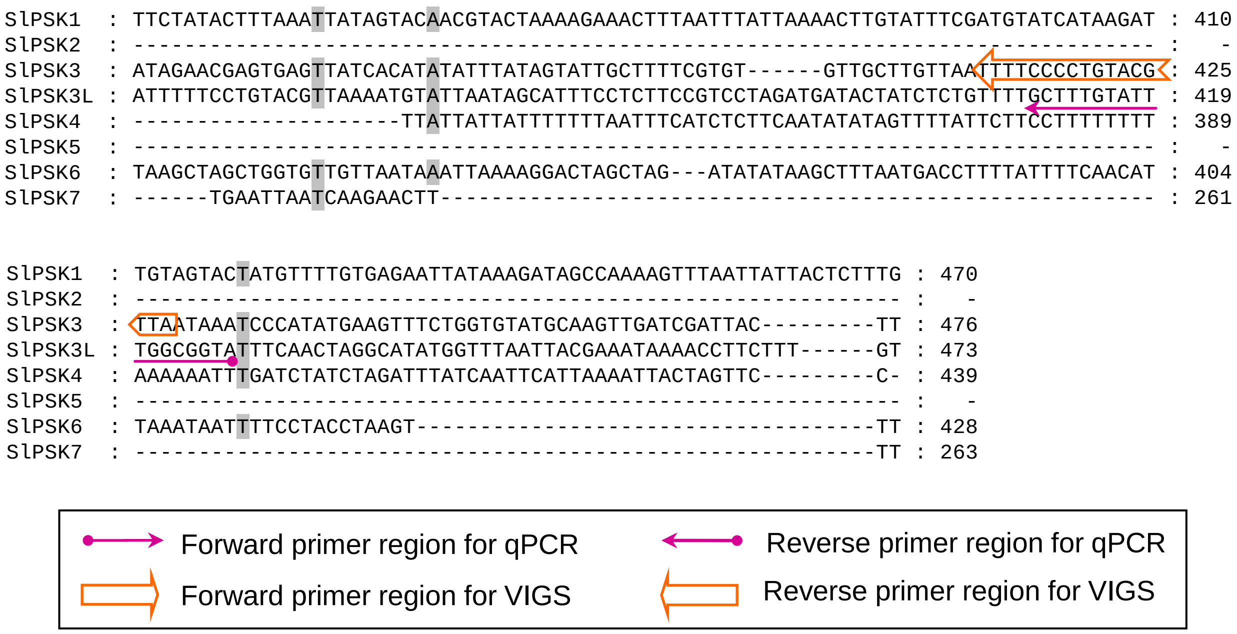
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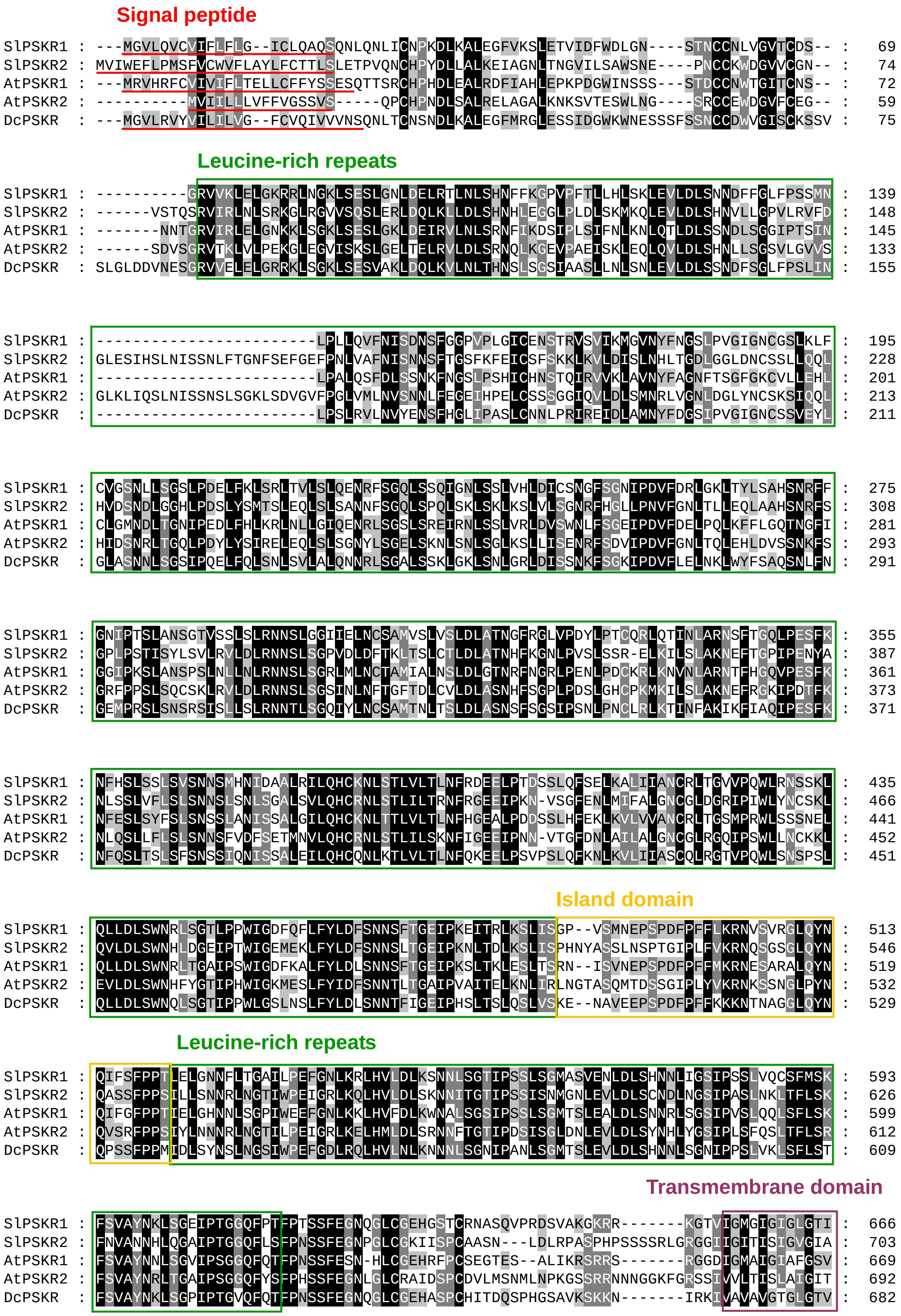
SlPSK5 : -- : -
SlPSK6 : TAAATAATTTTCCTACCTAAGT------------------------------------TT : 428
SlPSK7 : --TT : 263
Forward primer region for qPCR
Reverse primer region for qPCR
Forward primer region for VIGS
Reverse primer region for VIGS

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).



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DcPSKR  : ---MGVLRVYVILILVG--FCVQIVVVNSQNLTCNSNDLKALEGFMRGLESSIDGWKWNESSSFSSNCCDWVGISCKSSV :   75

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SlPSKR2 : QVLDLSWNHLDGEIPTWIGEMEKLFYLDFSNNSLTGEIPKNLTDLKSLISPHNYASSLNSPTGIPLFVKRNQSGSGLQYN :  546
AtPSKR1 : QLLDLSWNRLTGAIPSWIGDFKALFYLDLSNNSFTGEIPKSLTKLESLTSRN--ISVNEPSPDFPFFMKRNESARALQYN :  519
AtPSKR2 : EVLDLSWNHFYGTIPHWIGKMESLFYIDFSNNTLTGAIPVAITELKNLIRLNGTASQMTDSSGIPLYVKRNKSSNGLPYN :  532
DcPSKR  : QLLDLSWNQLSGTIPPWLGSLNSLFYLDLSNNTFIGEIPHSLTSLQSLVSKE--NAVEEPSPDFPFFKKKNTNAGGLQYN :  529

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AtPSKR2 : QVSRFPPSIYLNNNRLNGTILPEIGRLKELHMLDLSRNNFTGTIPDSISGLDNLEVLDLSYNHLYGSIPLSFQSLTFLSR :  612
DcPSKR  : QPSSFPPMIDLSYNSLNGSIWPEFGDLRQLHVLNLKNNNLSGNIPANLSGMTSLEVLDLSHNNLSGNIPPSLVKLSFLST :  609

SlPSKR1 : FSVAYNKLSGEIPTGGQFPTFPTSSFEGNQGLCGEHGSTCRNASQVPRDSVAKGKRR-------KGTVIGMGIGIGLGTI :  666
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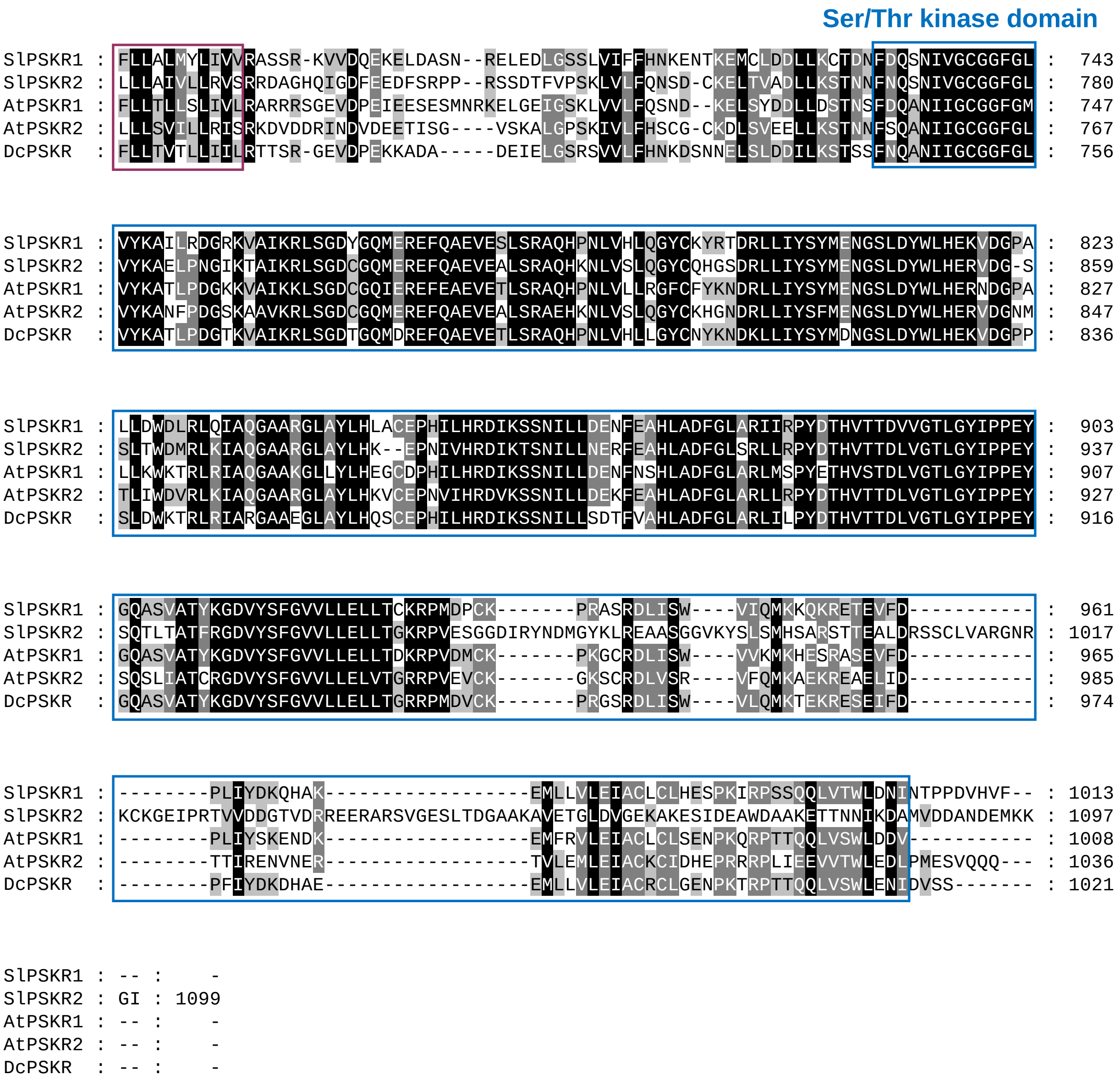

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AtPSKR1 : FLLTLLSLIVLRARRRSGEVDPEIEESESMNRKELGEIGSKLVVLFQSND--KELSYDDLLDSTNSFDQANIIGCGGFGM :  747
AtPSKR2 : LLLSVILLRISRKDVDDRINDVDEETISG----VSKALGPSKIVLFHSCG-CKDLSVEELLKSTNNFSQANIIGCGGFGL :  767
DcPSKR  : FLLTVTLLIILRTTSR-GEVDPEKKADA-----DEIELGSRSVVLFHNKDSNNELSLDDILKSTSSFNQANIIGCGGFGL :  756

SlPSKR1 : VYKAILRDGRKVAIKRLSGDYGQMEREFQAEVESLSRAQHPNLVHLQGYCKYRTDRLLIYSYMENGSLDYWLHEKVDGPA :  823
SlPSKR2 : VYKAELPNGIKTAIKRLSGDCGQMEREFQAEVEALSRAQHKNLVSLQGYCQHGSDRLLIYSYMENGSLDYWLHERVDG-S :  859
AtPSKR1 : VYKATLPDGKKVAIKKLSGDCGQIEREFEAEVETLSRAQHPNLVLLRGFCFYKNDRLLIYSYMENGSLDYWLHERNDGPA :  827
AtPSKR2 : VYKANFPDGSKAAVKRLSGDCGQMEREFQAEVEALSRAEHKNLVSLQGYCKHGNDRLLIYSFMENGSLDYWLHERVDGNM :  847
DcPSKR  : VYKATLPDGTKVAIKRLSGDTGQMDREFQAEVETLSRAQHPNLVHLLGYCNYKNDKLLIYSYMDNGSLDYWLHEKVDGPP :  836

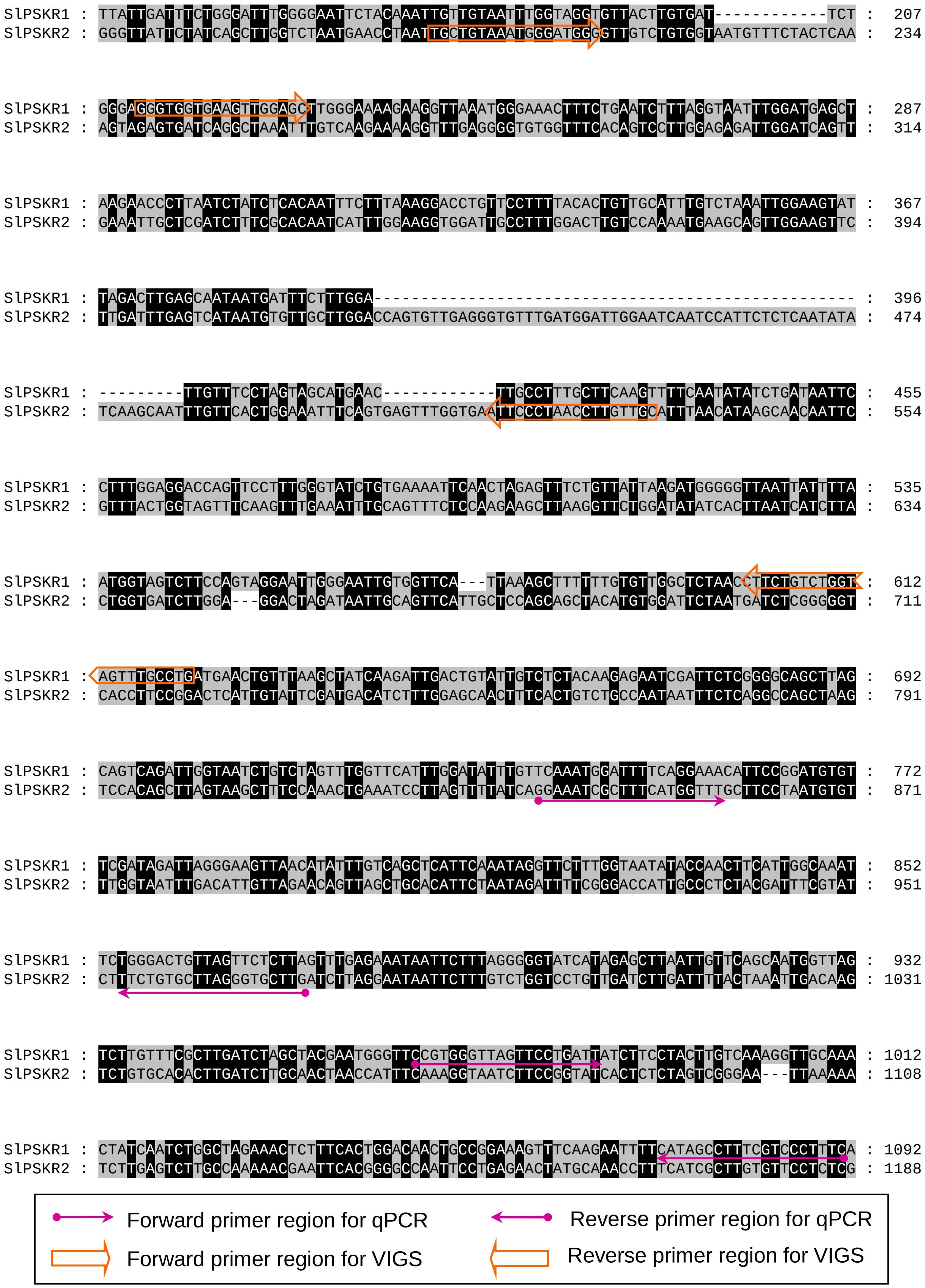
SlPSKR1 : LLDWDLRLQIAQGAARGLAYLHLACEPHILHRDIKSSNILLDENFEAHLADFGLARIIRPYDTHVTTDVVGTLGYIPPEY :  903
SlPSKR2 : SLTWDMRLKIAQGAARGLAYLHK--EPNIVHRDIKTSNILLNERFEAHLADFGLSRLLRPYDTHVTTDLVGTLGYIPPEY :  937
AtPSKR1 : LLKWKTRLRIAQGAAKGLLYLHEGCDPHILHRDIKSSNILLDENFNSHLADFGLARLMSPYETHVSTDLVGTLGYIPPEY :  907
AtPSKR2 : TLIWDVRLKIAQGAARGLAYLHKVCEPNVIHRDVKSSNILLDEKFEAHLADFGLARLLRPYDTHVTTDLVGTLGYIPPEY :  927
DcPSKR  : SLDWKTRLRIARGAAEGLAYLHQSCEPHILHRDIKSSNILLSDTFVAHLADFGLARLILPYDTHVTTDLVGTLGYIPPEY :  916

SlPSKR1 : GQASVATYKGDVYSFGVVLLELLTCKRPMDPCK-------PRASRDLISW----VIQMKKQKRETEVFD----------- :  961
SlPSKR2 : SQTLTATFRGDVYSFGVVLLELLTGKRPVESGGDIRYNDMGYKLREAASGGVKYSLSMHSARSTTEALDRSSCLVARGNR : 1017
AtPSKR1 : GQASVATYKGDVYSFGVVLLELLTDKRPVDMCK-------PKGCRDLISW----VVKMKHESRASEVFD----------- :  965
AtPSKR2 : SQSLIATCRGDVYSFGVVLLELVTGRRPVEVCK-------GKSCRDLVSR----VFQMKAEKREAELID----------- :  985
DcPSKR  : GQASVATYKGDVYSFGVVLLELLTGRRPMDVCK-------PRGSRDLISW----VLQMKTEKRESEIFD----------- :  974

SlPSKR1 : --------PLIYDKQHAK-----------------EMLLVLEIACLCLHESPKIRPSSQQLVTWLDNINTPPDVHVF-- : 1013
SlPSKR2 : KCKGEIPRTVVDDGTVDRREERARSVGESLTDGAAKAVETGLDVGEKAKESIDEAWDAAKETTNNIKDAMVDDANDEMKK : 1097
AtPSKR1 : --------PLIYSKENDK-----------------EMFRVLEIACLCLSENPKQRPTTQQLVSWLDDV----------- : 1008
AtPSKR2 : --------TTIRENVNER-----------------TVLEMLEIACKCIDHEPRRRPLIEEVVTWLEDLPMESVQQQ--- : 1036
DcPSKR  : --------PFIYDKDHAE-----------------EMLLVLEIACRCLGENPKTRPTTQQLVSWLENIDVSS------- : 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).



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SlPSKR1 : TTATTGATTTCTGGGATTTGGGGAATTCTACAAATTGTTGTAATTTGGTAGGTGTTACTTGTGAT------------TCT :  207
SlPSKR2 : GGGTTATTCTATCAGCTTGGTCTAATGAACCTAATTGCTGTAAATGGGATGGGGTTGTCTGTGGTAATGTTTCTACTCAA :  234

SlPSKR1 : GGGAGGGTGGTGAAGTTGGAGCTTGGGAAAAGAAGGTTAAATGGGAAACTTTCTGAATCTTTAGGTAATTTGGATGAGCT :  287
SlPSKR2 : AGTAGAGTGATCAGGCTAAATTTGTCAAGAAAAGGTTTGAGGGGTGTGGTTTCACAGTCCTTGGAGAGATTGGATCAGTT :  314

SlPSKR1 : AAGAACCCTTAATCTATCTCACAATTTCTTTAAAGGACCTGTTCCTTTTACACTGTTGCATTTGTCTAAATTGGAAGTAT :  367
SlPSKR2 : GAAATTGCTCGATCTTTCGCACAATCATTTGGAAGGTGGATTGCCTTTGGACTTGTCCAAAATGAAGCAGTTGGAAGTTC :  394

SlPSKR1 : TAGACTTGAGCAATAATGATTTCTTTGGA--------------------------------------------------- :  396
SlPSKR2 : TTGATTTGAGTCATAATGTGTTGCTTGGACCAGTGTTGAGGGTGTTTGATGGATTGGAATCAATCCATTCTCTCAATATA :  474

SlPSKR1 : ---------TTGTTTCCTAGTAGCATGAAC------------TTGCCTTTGCTTCAAGTTTTCAATATATCTGATAATTC :  455
SlPSKR2 : TCAAGCAATTTGTTCACTGGAAATTTCAGTGAGTTTGGTGAATTCCCTAACCTTGTTGCATTTAACATAAGCAACAATTC :  554

SlPSKR1 : CTTTGGAGGACCAGTTCCTTTGGGTATCTGTGAAAATTCAACTAGAGTTTCTGTTATTAAGATGGGGGTTAATTATTTTA :  535
SlPSKR2 : GTTTACTGGTAGTTTCAAGTTTGAAATTTGCAGTTTCTCCAAGAAGCTTAAGGTTCTGGATATATCACTTAATCATCTTA :  634

SlPSKR1 : ATGGTAGTCTTCCAGTAGGAATTGGGAATTGTGGTTCA---TTAAAGCTTTTTTGTGTTGGCTCTAACCTTCTGTCTGGT :  612
SlPSKR2 : CTGGTGATCTTGGA---GGACTAGATAATTGCAGTTCATTGCTCCAGCAGCTACATGTGGATTCTAATGATCTCGGGGGT :  711

SlPSKR1 : AGTTTGCCTGATGAACTGTTTAAGCTATCAAGATTGACTGTATTGTCTCTACAAGAGAATCGATTCTCGGGGCAGCTTAG :  692
SlPSKR2 : CACCTTCCGGACTCATTGTATTCGATGACATCTTTGGAGCAACTTTCACTGTCTGCCAATAATTTCTCAGGCCAGCTAAG :  791

SlPSKR1 : CAGTCAGATTGGTAATCTGTCTAGTTTGGTTCATTTGGATATTTGTTCAAATGGATTTTCAGGAAACATTCCGGATGTGT :  772
SlPSKR2 : TCCACAGCTTAGTAAGCTTTCCAAACTGAAATCCTTAGTTTTATCAGGAAATCGCTTTCATGGTTTGCTTCCTAATGTGT :  871

SlPSKR1 : TCGATAGATTAGGGAAGTTAACATATTTGTCAGCTCATTCAAATAGGTTCTTTGGTAATATACCAACTTCATTGGCAAAT :  852
SlPSKR2 : TTGGTAATTTGACATTGTTAGAACAGTTAGCTGCACATTCTAATAGATTTTCGGGACCATTGCCCTCTACGATTTCGTAT :  951

SlPSKR1 : TCTGGGACTGTTAGTTCTCTTAGTTTGAGAAATAATTCTTTAGGGGGTATCATAGAGCTTAATTGTTCAGCAATGGTTAG :  932
SlPSKR2 : CTTTCTGTGCTTAGGGTGCTTGATCTTAGGAATAATTCTTTGTCTGGTCCTGTTGATCTTGATTTTACTAAATTGACAAG : 1031

SlPSKR1 : TCTTGTTTCGCTTGATCTAGCTACGAATGGGTTCCGTGGGTTAGTTCCTGATTATCTTCCTACTTGTCAAAGGTTGCAAA : 1012
SlPSKR2 : TCTGTGCACACTTGATCTTGCAACTAACCATTTCAAAGGTAATCTTCCGGTATCACTCTCTAGTCGGGAA---TTAAAAA : 1108

SlPSKR1 : CTATCAATCTGGCTAGAAACTCTTTCACTGGACAACTGCCGGAAAGTTTCAAGAATTTTCATAGCCTTTCGTCCCTTTCA : 1092
SlPSKR2 : TCTTGAGTCTTGCCAAAAACGAATTCACGGGGCCAATTCCTGAGAACTATGCAAACCTTTCATCGCTTGTGTTCCTCTCG : 1188
```
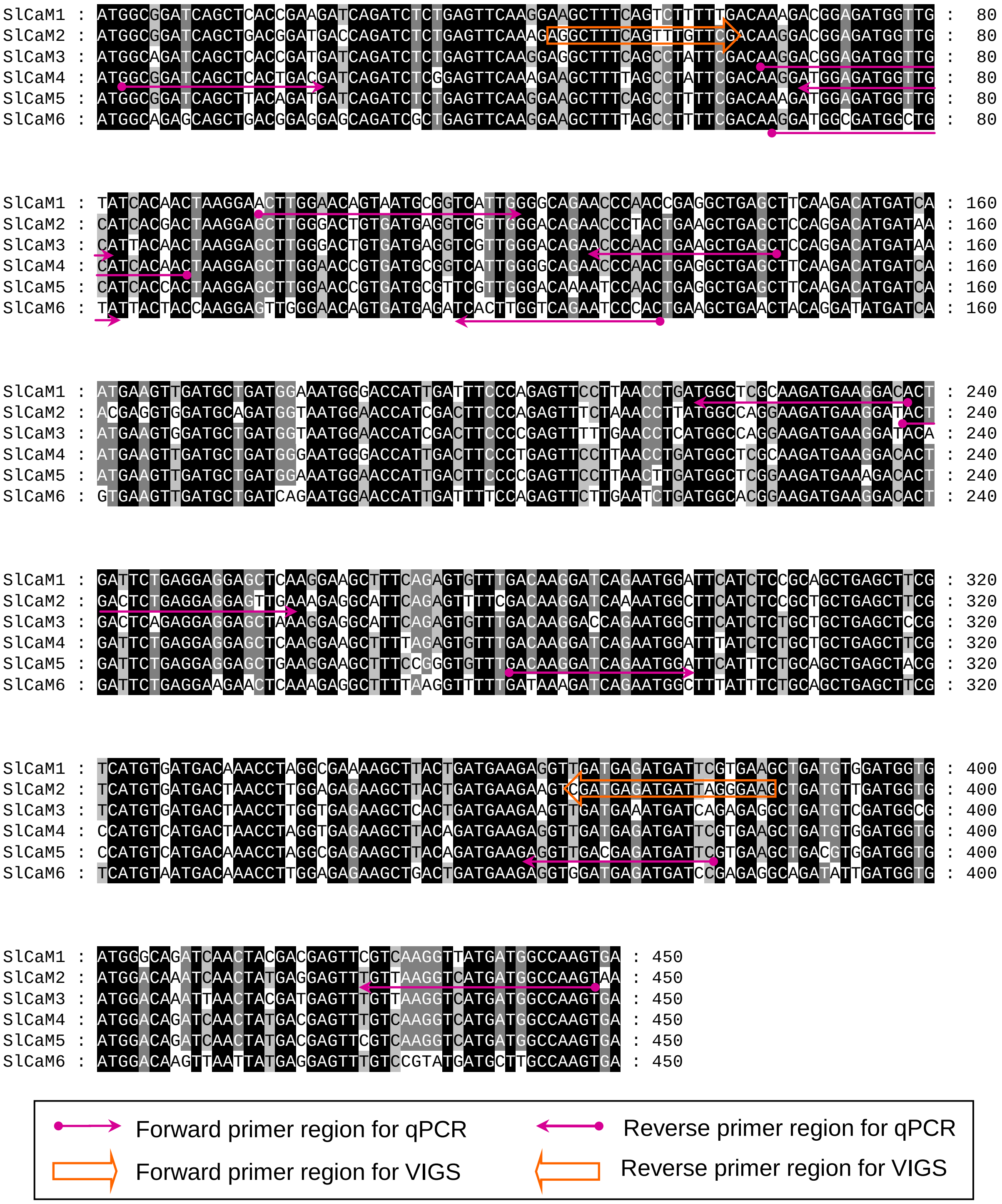

Supplemental Data Set 4. Nucleotide sequence alignments based on mRNA region of tomato *CaM* homologs (supports Figure 7 and Supplemental Figure 7).



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SlCaM1 : ATGGCGGATCAGCTCACCGAAGATCAGATCTCTGAGTTCAAGGAAGCTTTCAGTCTTTTTGACAAAGACGGAGATGGTTG :  80
SlCaM2 : ATGGCGGATCAGCTGACGGATGACCAGATCTCTGAGTTCAAAGAGGCTTTCAGTTTGTTCGACAAGGACGGAGATGGTTG :  80
SlCaM3 : ATGGCAGATCAGCTCACCGATGATCAGATCTCTGAGTTCAAGGAGGCTTTCAGCCTATTCGACAAGGACGGAGATGGTTG :  80
SlCaM4 : ATGGCGGATCAGCTCACTGACGATCAGATCTCGGAGTTCAAAGAAGCTTTTAGCCTATTCGACAAGGATGGAGATGGTTG :  80
SlCaM5 : ATGGCGGATCAGCTTACAGATGATCAGATCTCTGAGTTCAAGGAAGCTTTCAGCCTTTTCGACAAAGATGGAGATGGTTG :  80
SlCaM6 : ATGGCAGAGCAGCTGACGGAGGAGCAGATCGCTGAGTTCAAGGAAGCTTTTAGCCTTTTCGACAAGGATGGCGATGGCTG :  80


SlCaM1 : TATCACAACTAAGGAACTTGGAACAGTAATGCGGTCATTGGGGCAGAACCCAACCGAGGCTGAGCTTCAAGACATGATCA : 160
SlCaM2 : CATCACGACTAAGGAGCTTGGGACTGTGATGAGGTCGTTGGGACAGAACCCTACTGAAGCTGAGCTCCAGGACATGATAA : 160
SlCaM3 : CATTACAACTAAGGAGCTTGGGACTGTGATGAGGTCGTTGGGACAGAACCCAACTGAAGCTGAGCTCCAGGACATGATAA : 160
SlCaM4 : CATCACAACTAAGGAGCTTGGAACCGTGATGCGGTCATTGGGGCAGAACCCAACTGAGGCTGAGCTTCAAGACATGATCA : 160
SlCaM5 : CATCACCACTAAGGAGCTTGGAACCGTGATGCGTTCGTTGGGACAAAATCCAACTGAGGCTGAGCTTCAAGACATGATCA : 160
SlCaM6 : TATTACTACCAAGGAGTTGGGAACAGTGATGAGATCACTTGGTCAGAATCCCACTGAAGCTGAACTACAGGATATGATCA : 160


SlCaM1 : ATGAAGTTGATGCTGATGGAAATGGGACCATTGATTTCCCAGAGTTCCTTAACCTGATGGCTCGCAAGATGAAGGACACT : 240
SlCaM2 : ACGAGGTGGATGCAGATGGTAATGGAACCATCGACTTCCCAGAGTTTCTAAACCTTATGGCCAGGAAGATGAAGGATACT : 240
SlCaM3 : ATGAAGTGGATGCTGATGGTAATGGAACCATCGACTTCCCCGAGTTTTTGAACCTCATGGCCAGGAAGATGAAGGATACA : 240
SlCaM4 : ATGAAGTTGATGCTGATGGGAATGGGACCATTGACTTCCCTGAGTTCCTTAACCTGATGGCTCGCAAGATGAAGGACACT : 240
SlCaM5 : ATGAAGTTGATGCTGATGGAAATGGAACCATTGACTTCCCCGAGTTCCTTAACTTGATGGCTCGGAAGATGAAAGACACT : 240
SlCaM6 : GTGAAGTTGATGCTGATCAGAATGGAACCATTGATTTTCCAGAGTTCTTGAATCTGATGGCACGGAAGATGAAGGACACT : 240


SlCaM1 : GATTCTGAGGAGGAGCTCAAGGAAGCTTTCAGAGTGTTTGACAAGGATCAGAATGGATTCATCTCCGCAGCTGAGCTTCG : 320
SlCaM2 : GACTCTGAGGAGGAGTTGAAAGAGGCATTCAGAGTTTTCGACAAGGATCAAAATGGCTTCATCTCCGCTGCTGAGCTTCG : 320
SlCaM3 : GACTCAGAGGAGGAGCTAAAGGAGGCATTCAGAGTGTTTGACAAGGACCAGAATGGGTTCATCTCTGCTGCTGAGCTCCG : 320
SlCaM4 : GATTCTGAGGAGGAGCTCAAGGAAGCTTTTAGAGTGTTTGACAAGGATCAGAATGGATTTATCTCTGCTGCTGAGCTTCG : 320
SlCaM5 : GATTCTGAGGAGGAGCTGAAGGAAGCTTTCCGGGTGTTTGACAAGGATCAGAATGGATTCATTTCTGCAGCTGAGCTACG : 320
SlCaM6 : GATTCTGAGGAAGAACTCAAAGAGGCTTTTAAGGTTTTTGATAAAGATCAGAATGGCTTTATTTCTGCAGCTGAGCTTCG : 320


SlCaM1 : TCATGTGATGACAAACCTAGGCGAAAAGCTTACTGATGAAGAGGTTGATGAGATGATTCGTGAAGCTGATGTGGATGGTG : 400
SlCaM2 : TCATGTGATGACTAACCTTGGAGAGAAGCTTACTGATGAAGAAGTCGATGAGATGATTAGGGAAGCTGATGTTGATGGTG : 400
SlCaM3 : TCATGTGATGACTAACCTTGGTGAGAAGCTCACTGATGAAGAAGTTGATGAAATGATCAGAGAGGCTGATGTCGATGGCG : 400
SlCaM4 : CCATGTCATGACTAACCTAGGTGAGAAGCTTACAGATGAAGAGGTTGATGAGATGATTCGTGAAGCTGATGTGGATGGTG : 400
SlCaM5 : CCATGTCATGACAAACCTAGGCGAGAAGCTTACAGATGAAGAGGTTGACGAGATGATTCGTGAAGCTGACGTGGATGGTG : 400
SlCaM6 : TCATGTAATGACAAACCTTGGAGAGAAGCTGACTGATGAAGAGGTGGATGAGATGATCCGAGAGGCAGATATTGATGGTG : 400


SlCaM1 : ATGGGCAGATCAACTACGACGAGTTCGTCAAGGTTATGATGGCCAAGTGA : 450
SlCaM2 : ATGGACAAATCAACTATGAGGAGTTTGTTAAGGTCATGATGGCCAAGTAA : 450
SlCaM3 : ATGGACAAATTAACTACGATGAGTTTGTTAAGGTCATGATGGCCAAGTGA : 450
SlCaM4 : ATGGACAGATCAACTATGACGAGTTTGTCAAGGTCATGATGGCCAAGTGA : 450
SlCaM5 : ATGGACAGATCAACTATGACGAGTTCGTCAAGGTCATGATGGCCAAGTGA : 450
SlCaM6 : ATGGACAAGTTAATTATGAGGAGTTTGTCCGTATGATGCTTGCCAAGTGA : 450
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Supplemental Data Set 5. Primers used in this study.

Gene	Annotation	Accession No.	Primer pairs	Assay
SlPSK1	putative phytosulfokine	Solyc09g009130.2	F: 5’- AACAGCTCGTTTATTGC -3’ R: 5’- CATTCTTCTATTCCCAT -3’	qPCR
SlPSK2	putative phytosulfokines 2	Solyc11g066880.1	F: 5’- CTTGCAAGTGGAAAAGGAAGCA -3’ R: 5’- GGGTGATTATGGTGTTGAGTGT-3’	qPCR
SlPSK3	putative phytosulfokines 3	Solyc02g092110.2	F: 5’-TCCcccgggCCAAGGACCAAAATGAT -3’ R: 5’-CGCggatccTAACGTACAGGGGAAAA -3’	VIGS
			F: 5’-ACCAGGATGTTGTTGAACC -3’ R: 5’-GGTCCTTGGGAATCGTAAAC -3’	qPCR
SlPSK3L	phytosulfokines 3 like	Solyc02g092120.2	F: 5’- TCCcccgggCCAGGATCATGTTAGGGAAT -3’ R: 5’- CGCggatccTCAAGGTGAGCAGCCAAG -3’	VIGS
			F: 5’- ATCAGAACCCGTGAACTA -3’ R: 5’- TACCGCCAAATACAAAGC -3’	qPCR
SlPSK4	putative phytosulfokines 4	Solyc01g106830.2	F: 5’-TCCcccgggAACATTTGTCCCTTCACT-3’ R: 5’-CGCggatccATCCTCCACATCTTCTTT-3’	VIGS
			F: 5’-CGCCTTATCGCGATGTTAC -3’ R: 5’-CCAGGGCCTTCACATCTATC -3’	qPCR
SlPSK5	putative phytosulfokines 5	Solyc10g083580.1	F: 5’- CGGTTCGTCTACCTCCTACA -3’ R: 5’- GTGAGCCTCAGCTACCATCC -3’	qPCR
SlPSK6	putative phytosulfokines 6	Solyc06g074540.2	F: 5’- TCTCAACATGTTCCTCTTTGTCT -3’ R: 5’- CGTTGGTTTCCATGTGGTCA -3’	qPCR
SlPSK7	putative phytosulfokines	Solyc04g077580.2	F: 5’-TCCcccgggACATTTGCTGTTCGTCCT-3’ R: 5’-CGCggatccGCCATTGTCCTCCTCTTC -3’	VIGS

Gene	**Annotation**	**Accession No.**	**Primer pairs**	**Assay**
			F: 5’- TCGATCCCAAAATTCAGGTTGC -3’ R: 5’- AGATGAGCAGCCATTGTCCT -3’	qPCR
SlTPST	protein-tyrosine sulfotransferase	Solyc11g069520.1	F: 5’-CCGgaattcGGGCGTCTTCTTCACTCG -3’ R: 5’-CGCggatccGGAACCTGGCTGCTACCT -3’	VIGS
			F: 5’-CGTGGAAGTATTTGGTCCCT -3’ R: 5’-CGTGTAGAGGCATCACCATC -3’	qPCR
SlPSKR1	receptor like kinase	Solyc01g008140.3	F: 5’-TGCtctagaGGGTGGTGAAGTTGGAGC -3’ R: 5’-CGCggatccCAGGCAAACTACCAGACAGAAG -3’	VIGS
			F: 5’-CCGTGGGTTAGTTCCTGATT -3’ R: 5’-GAAAGGGACGAAAGGCTATG -3’	qPCR
			F: 5’-GCGggatccAATCTCCAGAACTTGATATG -3’ R: 5’-GCGgtcgacTCAAGTTCCTTTGCGCCTCTTTCC-3’	truncated protein (23-653 aa) expression for SPR
			F: 5’- TCCcccgggGAATGGGTGTGTTGCAAGTTTG -3’ R: 5’- CATGccatggAAAACACATGAACATCAGGTG -3’	GFP Fluorescence
SlPSKR2	receptor like kinase	Solyc07g063000.3	F: 5’- CgagctcTGCTGTAAATGGGATGGG -3’ R: 5’- TCCcccgggGCAACAAGGTTAGGGAAT -3’	VIGS
			F: 5’-GGAAATCGCTTTCATGGTTT -3’ R: 5’-CAAGCACCCTAAGCACAGAA -3’	qPCR
			F: 5’-GCGggatccGAAACCCCAGTTCAAAACTG -3’	truncated protein (28-689 aa)

Gene	**Annotation**	**Accession No.**	**Primer pairs**	**Assay**
			R: 5’-GCGgtcgacTCAACCTCGGCCAAGCCTACTAC -3’	expression for SPR
			F: 5’- TCCcccgggGAATGGTGATTTGGGAGTTTCTGCC -3’ R: 5’- CGCggatccCCTCTCCTTTACACTTGCGATTG -3’	GFP Fluorescence
SlPR1b	pathogenesis-related protein 1b	Solyc00g174340.1	F: 5’-ATCTCATTGTTACTCACTTGTC -3’ R: 5’-AACGTGCCCGACCA -3’	qPCR
SlCOI1	coronatine-insensitive 1	Solyc05g052620.2	F: 5’-GGATGCTTCTGGGATACGTT -3’ R: 5’-TGGATGCTCCGAGACTACAG -3’	qPCR
SlERF1	ethylene-responsive factor 1	Solyc05g051200.1	F: 5’-ATTGGAGTTAGAAAGAGGCCAT -3’ R: 5’-CTCATTGATAATGCGGCTTG -3’	qPCR
SlARF5	auxin response factor 5	Solyc04g081240.2	F: 5’-CACGTGTGCGGACATATACA -3’ R: 5’-TCGAGTGTCATTCAGAAGCC -3’	qPCR
SlACTIN	actin	Solyc03g078400.2	F: 5’-TGGTCGGAATGGGACAGAAG -3’ R: 5’-CTCAGTCAGGAGAACAGGGT -3’	qPCR
SlCaM1	calmodulin 1	Solyc01g008950.2	F: 5’-ACTTGGAACAGTAATGCGGTCATTG -3’ R: 5’-TGTCCTTCATCTTGCGAGCCA -3’	qPCR
			F: 5’- CCttaattaaCATGGCGGATCAGCTCACCGAA -3’ R: 5’- CTAGactagtCTTGGCCATCATAACCTTGACG -3’	BiFC-cYFP
SlCaM2	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’ R: 5’- CTAGactagtCTTGGCCATCATGACCTTAAC -3’	BiFC-cYFP
SlCaM3	calmodulin 3	Solyc10g077010.1	F: 5’- AAGGACGGAGATGGTTGC -3’ R: 5’- GCTCAGCTTCAGTTGGGT -3’	qPCR
			F: 5’- CCttaattaaCATGGCAGATCAGCTCACCGATG -3’ R: 5’- CTAGactagtCTTGGCCATCATGACCTTAAC -3’	BiFC-cYFP
SlCaM4	calmodulin 4	Solyc11g072240.1	F: 5’-GGCGGATCAGCTCACTGAC -3’ R: 5’- GTTGTGATGCAACCATCTCCAT -3’	qPCR
SlCaM5	calmodulin 5	Solyc12g099990.1	F: 5’- GACAAGGATCAGAATGGA -3’ R: 5’- GAATCATCTCGTCAACCT -3’	qPCR
SlCaM6	calmodulin 6	Solyc03g098050.2	F: 5’- AGGATGGCGATGGCTGTA -3’ R: 5’- GTGGGATTCTGACCAAGTGA -3’	qPCR
			F: 5’- CCttaattaaCATGGCAGAGCAGCTGACGGAG -3’ R: 5’- CTAGactagtCTTGGCAAGCATCATACGGAC -3’	BiFC-cYFP
SlYUC1	monooxygenase	Solyc06g008050.2	F: 5’- TGGACATTGGTGCATTGGAA -3’ R: 5’- AGCCAGTAGCAAGAAGAACAGA -3’	qPCR
			F: 5’- CCttaattaaCATGGCTAGCTTCAATGACCAT -3’ R: 5’- TTggcgcgccCCAAGGTTGAAATTTTTTTTGC -3’	BiFC-nYFP
SlYUC2	monooxygenase	Solyc06g065630.2	F: 5’- AAATGCAGAGGCAGTTAT -3’ R: 5’- ATGAGGAATGGCGTTATG -3’	qPCR

Gene	Annotation	Accession No.	Primer pairs	Assay
			F: 5’- CCttaattaaCATGGGTTGTTGTAAAGAGG -3’ R: 5’- TTggcgcgccCAAAACATATGCCTTGGTTATC -3’	BiFC-nYFP
SlYUC3	monooxygenase	Solyc06g083700.2	F: 5’- TGGCCCTGTAATTGTTGGTG -3’ R: 5’- GCCACAGTGATGCGATACAG -3’	qPCR
			F: 5’- CCttaattaaCATGTTTACCTTCTCATCAGAAC -3’ R: 5’- TTggcgcgccCAAAAGTTGAGATGCATCTTC -3’	BiFC-nYFP
SlYUC4	monooxygenase	Solyc08g068160.1	F: 5’- CCttaattaaCATGGATTCTTATTTGAAAGA -3’ R: 5’- TTggcgcgccCTTGAAAATATTGATGAATGT-3’	BiFC-nYFP
			F: 5’- CGTCCCGACTCGGATTAGAT -3’ F: 5’- GCGTTCCAACGTCAAGTACA -3’	qPCR
SlYUC5	monooxygenase	Solyc09g064160.2	F: 5’-ATGGCTTGTCGTTGCTACTG -3’ R: 5’-CAACCAACGACCACCACTTT -3’	qPCR
			F: 5’- CCttaattaaCATGTTTAGTTTTTCAGATAACG -3’ R: 5’-TTggcgcgccCAAAGGTTGAGATGCAACGTCTG -3’	BiFC-nYFP
SlYUC6	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’	qPCR
			R: 5’- TGCAGATGTAGCAAGACCAC -3’	
SlYUC7	monooxygenase	Solyc09g091090.1	F: 5’- CCttaattaaCATGAATCAATATTGTAATAG -3’	
			R: 5’- TTggcgcgccCGAAGGAAGATAACTTGTTTCTT -3’	BiFC-nYFP
			F: 5’- GAGTCGGTCCACTCTGCTAA -3’	qPCR
			R: 5’- TCCTTCGAATTCGGGCACTA -3’	
SlYUC8	monooxygenase	Solyc09g091720.1	F: 5’- GGGAGATGGTGTACATGGCAA -3’	qPCR
			R: 5’- AATGGGCCTTCTTCTGGTTGT -3’	
SlYUC9	monooxygenase	Solyc09g091870.1	F: 5’-GGCTCTACGCTGCTGGATTT -3’	qPCR
			R: 5’-TTGTCTCCTCTGACAGACTT -3’	
B. cinerea actin	*B. cinerea actin*	XM_001553318.1 (NCBI)	F: 5’-GGTAACATTGTTATGTCTGG -3’	qPCR
			R: 5’-CTTGACCTTCATCGACG -3’	