

1 cttttaaaaaatcccctccaataatcacctttccctctc
39 tgcacatagaaacttcttcgcttctcgtctcatctcatctcatcc
74 **ATGGCGTCCGATCTCTCAACAAAAGCTAAAGAAGCATAACATCGAC**
M **[A S D L S T K A K E A Y I D**
119 **GATCACTTTGAACTCGCCGTTAACCTGTA**CTCTCAAGCCATTGCT
D H F E L A V N L Y S Q A I A
164 **GTTACTCCTAATAATCCCGAACTTTTCGTTGACCGTGCTCAAGCT**
V T P N N][P E L F V D R A Q A
209 **AATATCAA**ACTCCACA**ACTTCACCGAAGCTGTTACTGATGCAAAC**
N I K L H N F T E A V T D A N
254 **ACGGCGATTGAGTTAGATCCATCAACGGCAAACGCATATATGCGC**
T A I E L D P S T][A N A Y M R
299 **AAGGGTTTGGCCTGTATGGA**ACTTGAAGAGTACCAA**ACTGCGAAG**
K G L A C M E L E E Y Q T A K
344 **GCAGCTCTGGAA**ACTGGT**GCTTCTTTAGCACCAGGAGAATCAAGA**
A A L E T G A S L A P G E] S R
389 **TTC**ACTAGCTTAATCAAAGAATGTGATGAACACATTGCAGGGAAA
F T S L I K E C D E H I A G K
434 **GCTGGAGA**ATTGCCTAAGCATGCAACAGTTGAAACCTCAGCAAGT
A G E L P K H A T V E T S A S
479 **GTTGTCCCTCCTGCTGAATCAAAGTCACTGGATAATGTTGCTGCT**
V V P P A E S K S L D N V A A
524 **GTTACAAAAGATA**CCCAACTGGCTTATAAATCCTGTGAAAGAACA
V T K D T Q L A Y K S C E R T
569 **CCTGCTGTCAAACCAA**AATACAGGCATGAATTCTATCAGAAACCA
P A V **[K P K Y R H E F Y Q K P**
614 **GAGGAGGTGGTGGTA**ACCATATTTGCCAAGGGTATACCTGCCAAG
E E V V V T I F A K G I P A K
659 **AATGTTTCAGTTGACTTTGGCGAACA**AATACTTAGTGTTAGCATT
N V S V D F G E Q I L S V S I
704 **GATATA**CCAGGCGAAGTTGCATACTCTTCCAGCCTAGGTTGTT**C**
D I P G E V A Y S F Q P R L F
749 **GGTAAGATA**ATACCTCAAAAATGCAGATATGAAGTTATGTCTACC
G K I I P Q K C R Y E V M S T
794 **AAATTTGAGATT**CGCCTTGCTAAAGCTGAATCTGTACTACTGGACA
K F E I R L A K A E S V H W T
839 **ACCCTTGAGTATA**CTAGGGATATTGCTGTAGTACAGAGGCCAAAT
T L E] Y T R D I A V V Q R P N
884 **GTGTCATCAGGCAGCTATAAGCCTAGCTACCCTTCCTCTAAATTG**
V S S G S Y K P **[S Y P S S K L**
929 **AGATGCAAGGATTGGGATA**AACTAGAGGCTCAAGTAAAAAGGAG
R C K D W D K L E A Q V K K E
974 **GAAAAAGAAGAAAA**ACTGGATGGAGATGCAGCATTGAACAAATTT
E K E E K L D G D A A L N K F
1019 **TTCCGAGATATTTACAA**AGATGCTGATGAGGATGCAAGAAGAGCT
F R D I Y K D A D E D A R R A
1064 **ATGATGAAATC**ATTTGTGGAATCAAATGGGACTGTTCTGTCCACA
M M K S F V E S N G T V L S T
1109 **AACTGGAAAGAGGTTGGT**ACTAAGAAGGTGGAAGGAAGCCCTCCA
N W K E V G T K K V E G S P P
1154 **GATGGCATGGAGCTGAAGCAATGGGA**ATACTAGaaaatgtagctc
D G M E L K Q W E Y] *
1199 ctctttatcttttgcgaccatttcctgcatttcctttt

Supplemental Figure S1. Kim et al.

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(-----TPR domain-----
CaSGT1 ----MASDLSTKAKEAYIDDFELAVNLYSQAIAVTFNNPELFDRAQANIKLHNFTEAV 56
NtSGT1 ----MASDLETRAKEAFIDDFELAVDLYTQAIAMTPKNAELFADRAQANIKLNYFTEAV 56
CaSgt1b ----MASDLETRAKEAFIDDFELAVDLYTQAISSLSPKNPELFDRAQANIKLNYFTEAV 56
OsSgt1  MATAAASDLESKAKAAAFVDDDFELAAELYTQAIETASAPATAELYADRAQAHIKLGNYTEAV 60
AtSGT1a ----MAKELADKAKEAFVDDDFDVAVDLYSKAIDLDPNCAEFFADRAQAYIKLESFTEAV 56
AtSGT1b ----MAKELAEKAKEAFVDDDFDVAVDLYSKAIDLDPNCAEFFADRAQANIKLIDNFTEAV 56

-----)

CaSGT1 TDANTAIELDPSTANAYMRKGLACMELEEYQTAKAALETGASLAPGESRFTSLIKECDEH 116
NtSGT1 VDANKAIELDPSMSKAYLRKGLACMKLEEYQTAKAALETGASLAPAESRFTKLIKECDEH 116
CaSgt1b VDANKAIELDPYMSKAYLRKGLACMKLEEYQTAKAALETGASLAPGESRFTKLMKECDES 116
OsSgt1  ADANKAIELDPSMHKAYLRKGAACIRLEEYQTAKAALELGYSFASGDSRFTRLMKECDEH 120
AtSGT1a ADANKAIELDPSLTKAYLRKGTACMKLEEYRTAKTALEKASITPSESKEFKKLIDECNFL 116
AtSGT1b VDANKAIELEPTLAKAYLRKGTACMKLEEYSTAKAALEKASVAPNEPKFKKMIDECDLR 116

(=====
CaSGT1 IAGKAGELPKHATVETSASVPPAESKSLDNVAAVTKDTQLAYKSCERTPAVKPKYRHEF 176
NtSGT1 IAEEAGELPNQSVDKTSGNVVAPPASESLDNVAVAPKDAQPTVNLSYQGSAAAPKYRHEF 176
CaSgt1b IAEEAGELPNISLEKPSANAVASSASESLDNVAIAPRDPQSTVTLSHQESAAAPKYRHEF 176
OsSgt1  IAEEELTEVP---VKKAEDGAAAPSVASFVE-----EKDDAANMNDTPPMVEVKPKYRHDF 172
AtSGT1a ITEEEKDLVQVPVSTLPSSVTAPPVS-----ELDVTPT-----AK--YRHEY 156
AtSGT1b IAEEEKDLVQPMPPSLPSSSTTPLAT-----EADAPPVPIPAAPAKPMEYRHEF 164

=====CS domain=====
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NtSGT1 YQKPEEVVVVTFIFAKGIPAKNVVDFGEQILSVSIDIPEGEVAYSFQPRLFCKIIPQKCRYE 236
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OsSgt1  YNSATEVVLTFIFAKGVPAENVVDFGEQMLSVSIEVPGEEPYHFQPRLFCKIIPKESRYQ 232
AtSGT1a YQKPEEVVVVTFIFAKGIPKQNVNIDFGEQILSVVIEVPGEDAYYLQPRLFCKIIPDKCKYE 216
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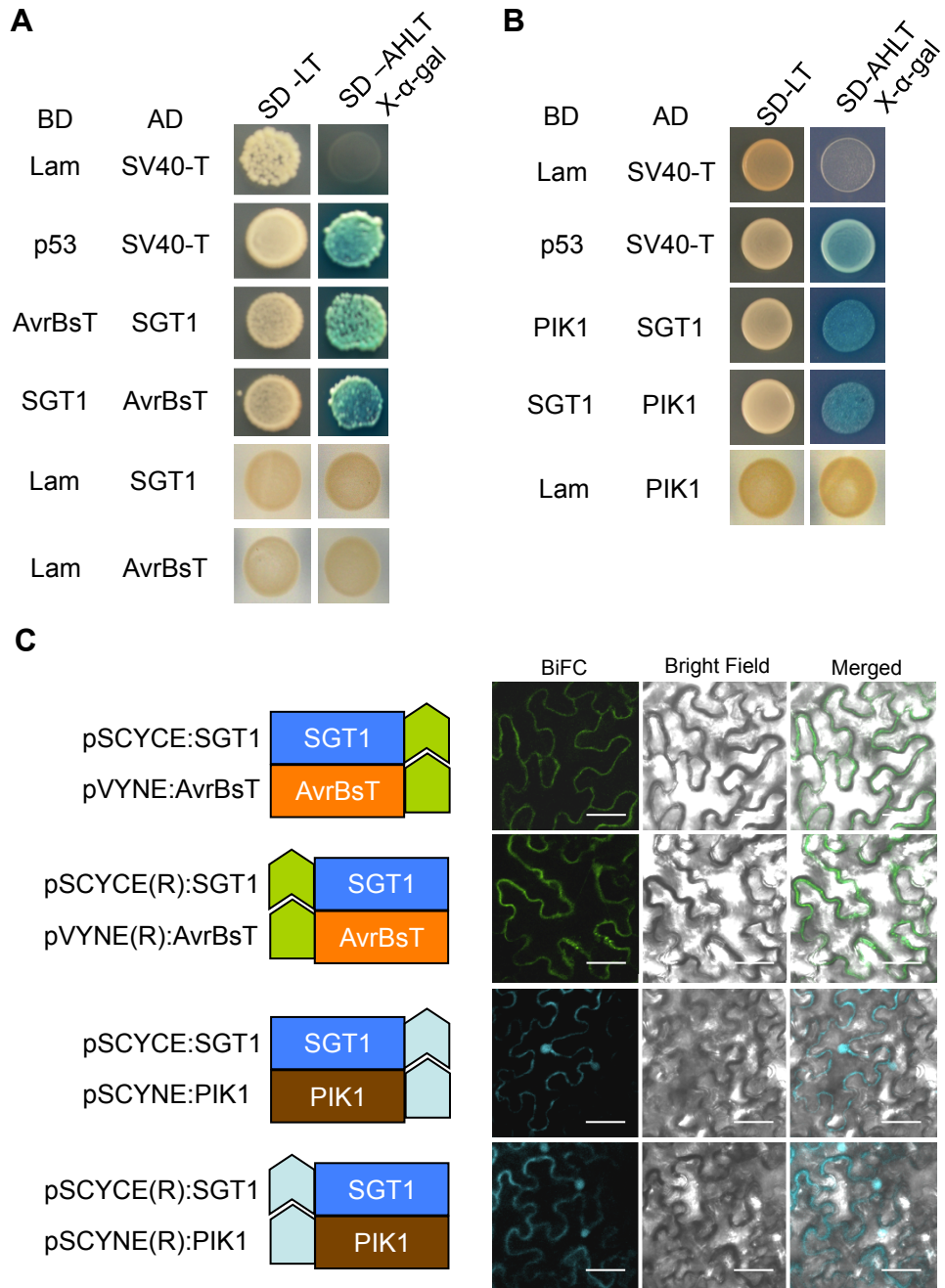
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OsSgt1  VLSTKVEIRLAKAEQITWTSLDYDKKPKAVPQKIIPPAESAQRPSYPSSKSK-KDWDKLE 291
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*****SGS domain*****
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OsSgt1  AEVKKEEKEEKLEGDAALNKFFRDIYSDAEDMRRAMKSEFVESNGTVLSTNWKDVGSKK 351
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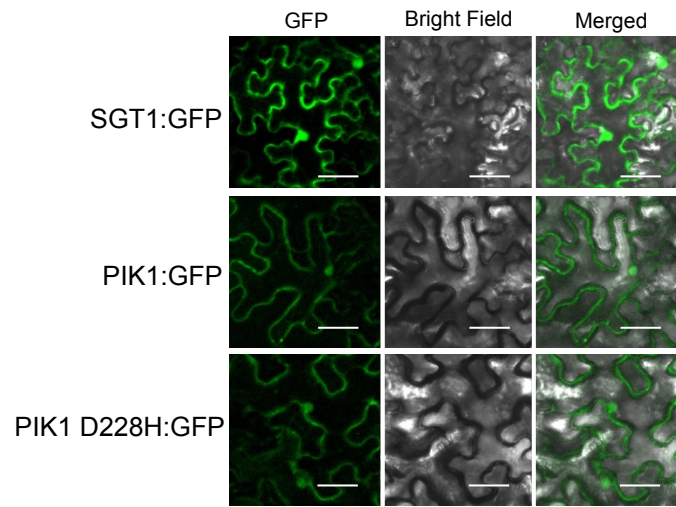
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CaSGT1 VEGSPPDGMELKQWEY 370
NtSGT1 VEGSPPDGMELKKWEI 370 (79%)
CaSgt1b VEGSPPDGMELKKWEI 370 (77%)
OsSgt1  VEGSPPDGMELKKWEY 367 (64%)
AtSGT1a IESTPPDGMELKKWEI 350 (63%)
AtSGT1b VESTPPDGMELKKWEY 358 (62%)

```

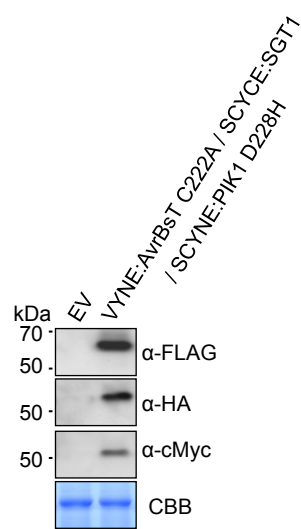
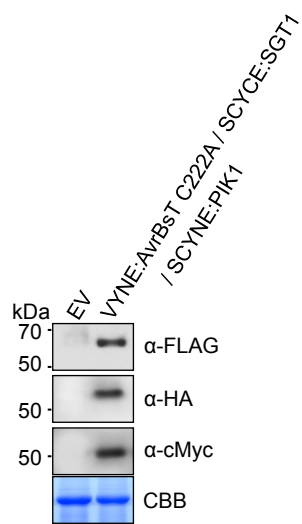
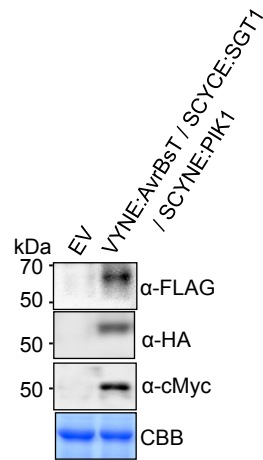
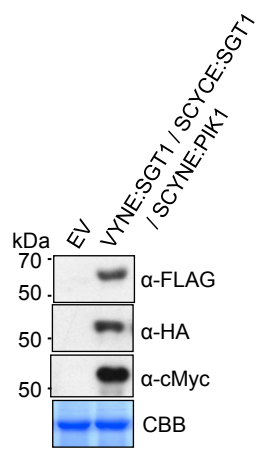
Supplemental Figure S2. Kim et al..



Supplemental Figure S3. Kim et al.

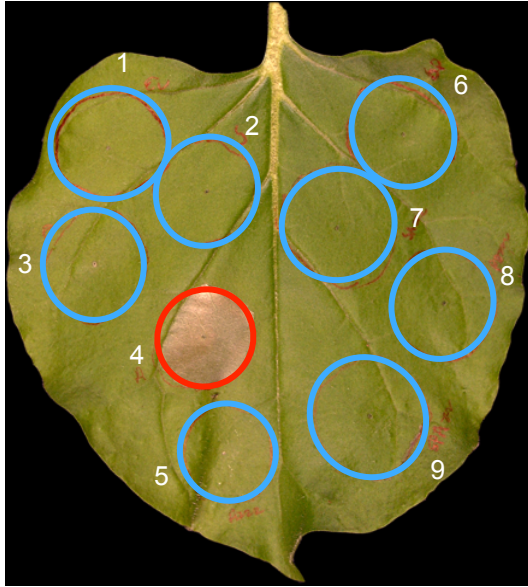


Supplemental Figure S4. Kim et al.



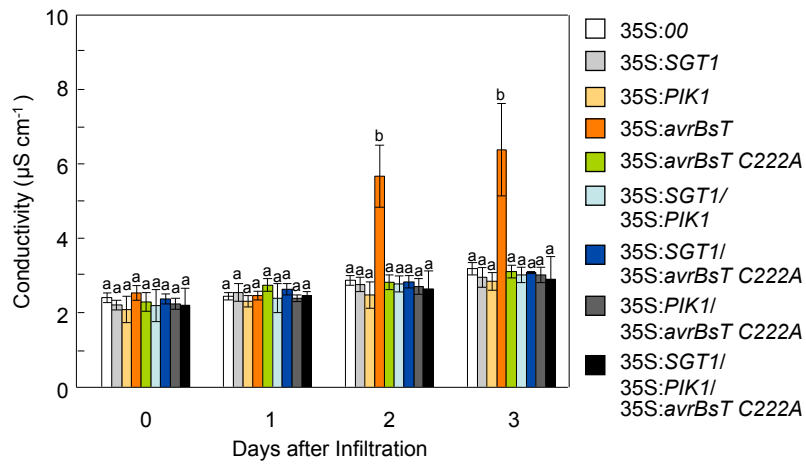
Supplemental Figure S5. Kim et al.

A

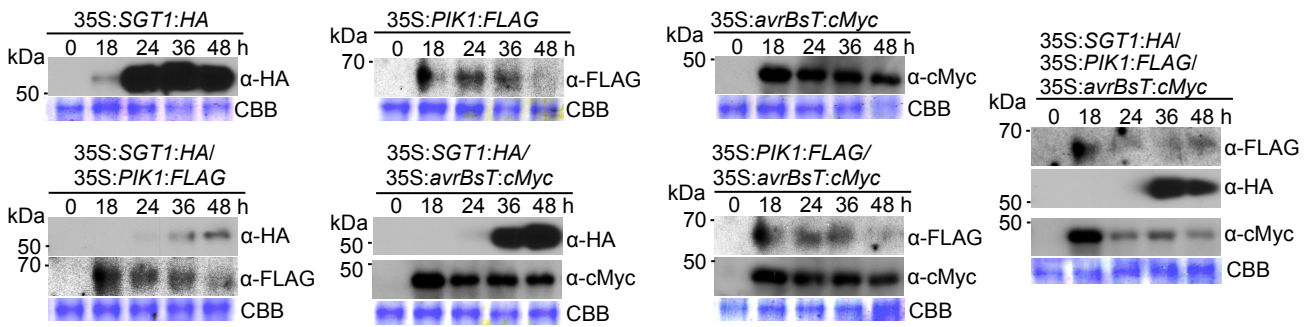
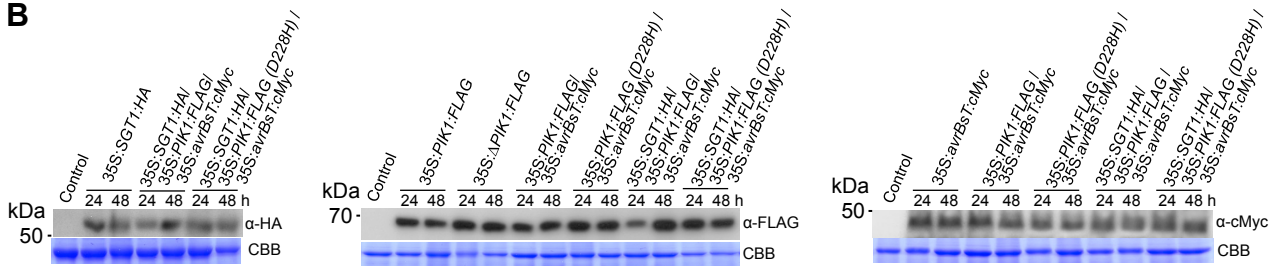


1. 35S:00
2. 35S:SGT1
3. 35S:PIK1
4. 35S:avrBsT
5. 35S:avrBsT C222A
6. 35S:SGT1/
35S:PIK1
7. 35S:SGT1/
35S:avrBsT C222A
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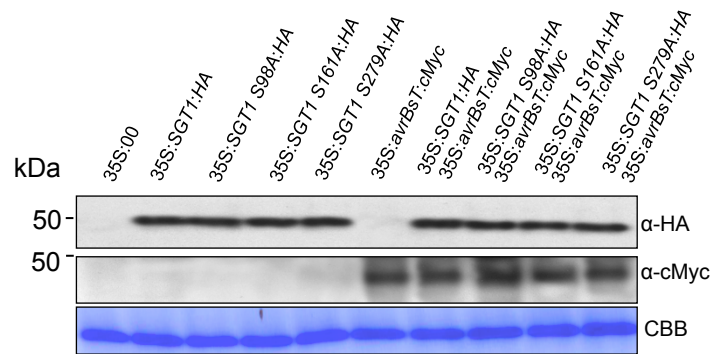
B



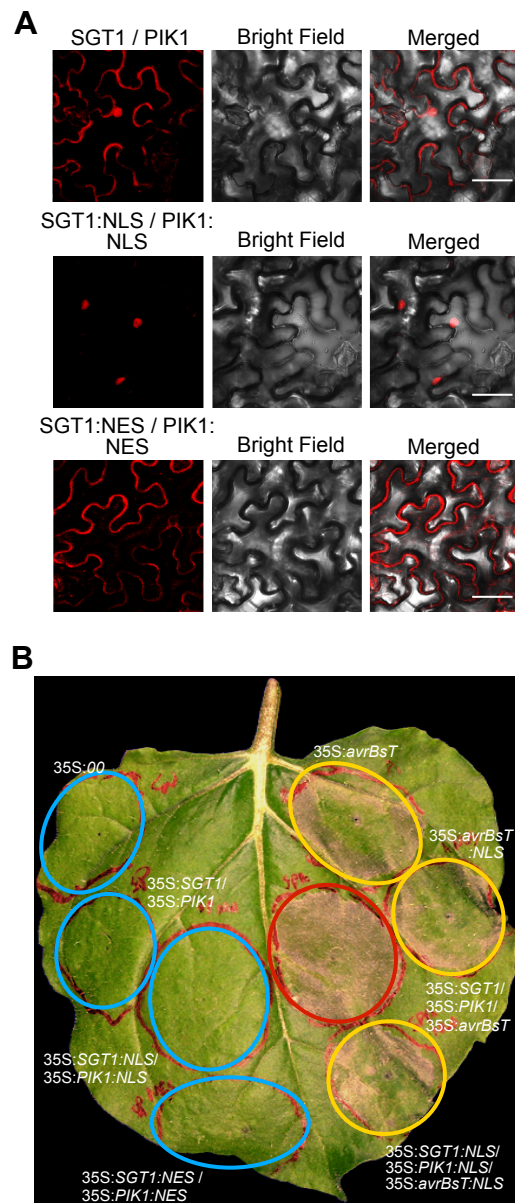
Supplemental Figure S6. Kim et al.

A**B**

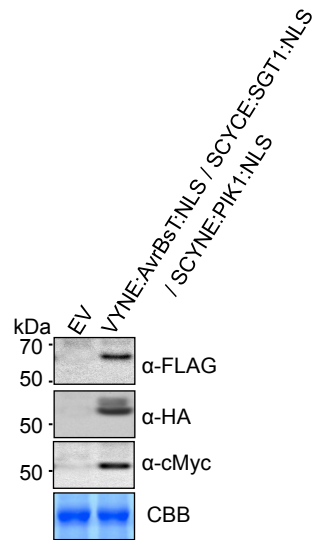
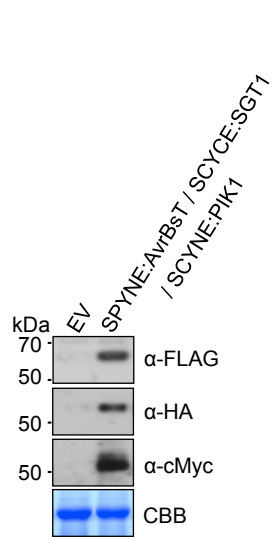
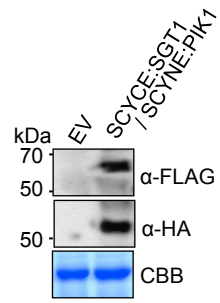
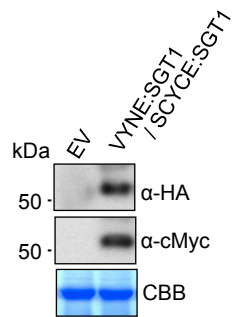
Supplemental Figure S7. Kim et al.



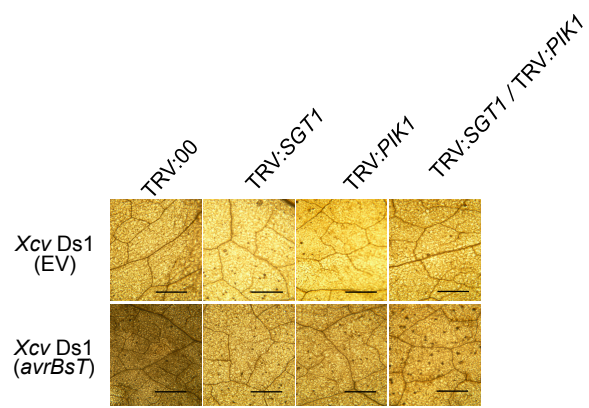
Supplemental Figure S8. Kim et al.



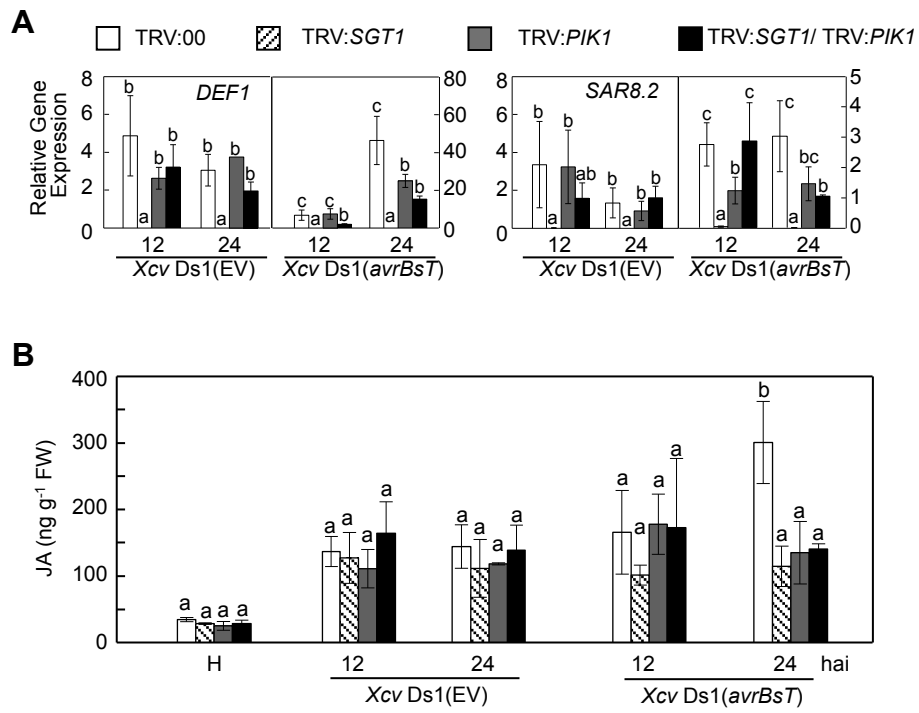
Supplemental Figure S9. Kim et al.



Supplemental Figure S10. Kim et al.



Supplemental Figure S11. Kim et al.



Supplemental Figure S12. Kim et al.

