Supplementary material

Figure S1. Alignment of SERK proteins

Amino acid sequence alignment of deduced *N. attenuata* NaBAK1, NaSERK1 (partial), *N. benthamiana* NbSERK3/BAK1 (partial), and other SERK proteins. NCBI (GenBank) accession numbers of *SERK* genes and SERK proteins included in this alignment are: *N. attenuata*: *NaBAK1* (HM639279), *NaSERK1* (HM639280); *N. benthamiana*: *NbSERK3/BAK1* (CK291393); *Arabidopsis thaliana*: AtSERK1 (NP_177328), AtSERK2 (NP_174683), AtSERK3 (NP_567920), AtSERK4 (NP_178999), AtSERK5 (NP_179000); *Solanum tuberosum*: StSERK1 (ABO14172); *Medicago truncatula*: MtSERK1 (AAN64294); *Oryza sativa*: OsSERK1 (BAD86793); *Zea mays*: ZmSERK1 (CAC37638); ZmSERK2 (CAC37639). Amino acids in white background are different from the consensus sequence.

Figure S2. Morphology of EV and NaBAK1-VIGS plants

N. attenuata plants were inoculated with *Agrobacterium* carrying pTV00 empty vector or pTV-NaBAK1 to generate EV and *NaBAK1*-silenced (NaBAK1-VIGS) plants, respectively. (A) Plants at early elongation stage. (B) Plants at flowering stage.

Figure S3. NaBAK1 positively regulates the W+OS- and W+W-induced accumulation of jasmonic acid (JA) and JA-isoleucine (JA-Ile).

Leaves of EV and NaBAK1-VIGS plants were wounded with a pattern wheel and 20 µl of water (W+W) or *M. sexta* oral secretions (W+OS) were immediately applied to each leaf. Individual leaves from 5 replicate plants were harvested at the indicated times. Asterisks represent significantly different levels between EV and NaBAK1-VIGS plants at indicated times (unpaired *t*-test; *, $p < 0.05$; **, $p < 0.01$; ***, $p < 0.001$; N = 5). (A) Mean (± SE) JA concentrations in EV and NaBAK1-VIGS plants. (B) Mean (± SE) JA-Ile concentrations in EV and NaBAK1-VIGS plants.

Figure S4. EV and NaBAK1-VIGS plants have the same levels of SA and ethylene production after W+OS induction.

Leaves of EV and NaBAK1-VIGS plants were wounded with a pattern wheel and 20 µl of water (W+W), *M. sexta* oral secretions (W+OS), or FAC A solution (W+FAC) were immediately applied to each leaf. Individual leaves from 5 replicate plants were harvested after 1.5 h. Asterisks represent significantly different levels between EV and NaBAK1-VIGS plants at indicated times (unpaired *t*-test; *, $p < 0.05$; **, $p < 0.01$; ***, $p < 0.001$; N = 5). (A) Mean SA concentrations (± SE) in EV and NaBAK1-VIGS plants. Leaves of EV and NaBAK1-VIGS plants were wounded with a pattern wheel and treated with 20 µl of *M. sexta* OS (W+OS). (B) Ethylene emission (± SE) was measured using a photoacoustic spectrometer 5 h after W+OS treatment (N = 5).

Figure S5. Transcript accumulation of JA biosynthetic genes in EV and NaBAK1-VIGS plants

Mean transcript levels (± SE) of *NaLOX3* (A), *NaAOS* (B), *NaAOC* (C), *NaOPR3* (D), and *NaACX1* (E) were measured with qPCR. Asterisks represent significantly different levels between EV and NaBAK1-VIGS plants at indicated times (unpaired *t*-test; *, $p < 0.05$; **, $p < 0.01$; ***, $p < 0.001$; N = 5).

Figure S6. EV and NaBAK1-VIGS plants have similar levels of DTGs in response to W+OS and MeJA treatment

(A) Leaves from EV and NaBAK1-VIGS plants were left untreated (control) or wounded with a pattern wheel and 20 µl of *M. sexta* oral secretions were immediately applied to each leaf (W+OS). Samples were harvested three days after treatment, and DTG content were determined.

(B) EV and NaBAK1-VIGS leaves were treated with 20 µl of lanolin or lanolin containing MeJA (7.5 µg µl^{-1}). Samples were harvested three days after treatment, and DTG content were determined. Error bars represent standard errors; different letters indicate significant differences (two-way ANOVA, Fisher's PLSD test; $p < 0.05$; N = 5).

Figure S7. *M. sexta* has similar growth rates on EV and NaBAK1-VIGS plants

Each EV and NaBAK1-VIGS plant was infested with one *M. sexta* neonate. The larval mass was subsequently recorded on day 6, 8, and 11 (N = 25).

```
MtSERK1       -----MEET--KFCALAFICAFFLLLLHPLWLVSANMEGDALHNLRTNLQD---PNNVLQ 50
OsSERk1       -----MAAHR---WAVWAVLLLRLLVP--AARVLANMEGDALHSLRTNLVD---PNNVLQ 47
ZmSERK1       -----MAASL---RWWWSAVVFSVVVG--VIPVVANTEGDALYSLRQSLKD---NNNVLQ 47
StSERK1       -----MVKVMEKDAVVVSLVVWLILVVHHLKLIYANMEGDALHSLRVNLQD---PNNVLQ 52
NaSERK1       ------------------------------------------------------------ 0
AtSERK1       -----MES----SYVVFILLSLILLPNHSLWLASANLEGDALHTLRVTLVD---PNNVLQ 48
AtSERK2       -----MGRKKFEAFGFVCLISLLLLFN-SLWLASSNMEGDALHSLRANLVD---PNNVLQ 51
ZmSERK2       -----MAASASAGRWWAVVLAVAVLLG--PGQVVANTEGDALYSLRQSLKD---ANNVLQ 50
AtSERK3/BAK1  -----MERRLMIPCFFWLILVLDLVLR-----VSGNAEGDALSALKNSLAD---PNKVLQ 47
NaSERK3/BAK1  -----MDQWILG--ILGFVSAFLCLIGLLLVPVSANIEGDALNALKTNLAD---PNNVLQ 50
NbSERK3/BAK1  ------------------------------------------------------------ 0
AtSERK4/BKK1  MTSSKMEQRSLL-CFLYLLLLFNFTLR-----VAGNAEGDALTQLKNSLSSGDPANNVLQ 54
AtSERK5       -----MEHGSSR-GFIWLILFLDFVSR-----VTGKTQVDALIALRSSLSSGDHTNNILQ 49

MtSERK1       SWDPTLVNPCTWFHVTCNNDNSVIRVDLGNAALSGTLVPQLGQLKNLQYLELYSNNITGP 110
OsSERk1       SWDPTLVNPCTWFHVTCNNDNSVIRVDLGNAALSGTLVPQLGQLKNLQYLELYSNNISGT 107
ZmSERK1       SWDPTLVNPCTWFHVTCNPDNSVIRLDLGNAQLSGPLVPQLGQLKNMQYLELYSNNISGP 107
StSERK1       SWDPTLVNPCTWFHVTCNNDNSVIRVDLGNAALSGLLVPQLGLLKNLQYLELYSNNISGL 112
NaSERK1       ------------------------------------------------------------ 0
AtSERK1       SWDPTLVNPCTWFHVTCNNENSVIRVDLGNAELSGHLVPELGVLKNLQYLELYSNNITGP 108
AtSERK2       SWDPTLVNPCTWFHVTCNNENSVIRVDLGNADLSGQLVPQLGQLKNLQYLELYSNNITGP 111
ZmSERK2       SWDPTLVNPCTWFHVTCNNDNSVIRVDLGNAQLSGVLVPQLGQLKNLQYLELYSNNISGT 110
AtSERK3/BAK1  SWDATLVTPCTWFHVTCNSDNSVTRVDLGNANLSGQLVMQLGQLPNLQYLELYSNNITGT 107
NaSERK3/BAK1  SWDPTLVNPCTWFHVTCNSENSVTRVDLGNANLSGQLVPQLGQLPNLQYLELYSNNISGR 110
NbSERK3/BAK1  ------------------------------------------------------------ 0
AtSERK4/BKK1  SWDATLVTPCTWFHVTCNPENKVTRVDLGNAKLSGKLVPELGQLLNLQYLELYSNNITGE 114
AtSERK5       SWNATHVTPCSWFHVTCNTENSVTRLDLGSANLSGELVPQLAQLPNLQYLELFNNNITGE 109

MtSERK1       IPSDLGNLTNLVSLDLYLNRFNGPIPDSLGKLSKLRFLRLNNNSLMGPIPMSLTNISALQ 170
OsSERk1       IPSELGNLTNLVSLDLYLNNFTGPIPDSLGNLLKLRFLRLNNNSLSGSIPKSLTAITALQ 167
ZmSERK1       IPPELGNLTNLVSLDLYLNNFTGGIPDTLGQLSKLRFLRLNNNSLSGQIPKTLTNINTLQ 167
StSERK1       IPSDLGNLTNLVSLDLYLNNFVGPIPDSLGKLSKLRFLRLNNNSLTGNIPMSLTNISSLQ 172
NaSERK1       ------------------------------------------------------------ 0
AtSERK1       IPSNLGNLTNLVSLDLYLNSFSGPIPESLGKLSKLRFLRLNNNSLTGSIPMSLTNITTLQ 168
AtSERK2       VPSDLGNLTNLVSLDLYLNSFTGPIPDSLGKLFKLRFLRLNNNSLTGPIPMSLTNIMTLQ 171
ZmSERK2       IPPELGNLTNLVSLDLYMNNFSGNIPDSLGNLVKLRFLRLNNNSLVGPIPVSLTNISTLQ 170
AtSERK3/BAK1  IPEQLGNLTELVSLDLYLNNLSGPIPSTLGRLKKLRFLRLNNNSLSGEIPRSLTAVLTLQ 167
NaSERK3/BAK1  IPFELGNLTNLVSLDLYLNRLNGPIPDTLGKLQKLRFLRLNNNSLNGRIPMLLTTVISLQ 170
NbSERK3/BAK1  ------------------------------------------------------------ 0
AtSERK4/BKK1  IPEELGDLVELVSLDLYANSISGPIPSSLGKLGKLRFLRLNNNSLSGEIPMTLTSVQ-LQ 173
AtSERK5       IPEELGDLMELVSLDLFANNISGPIPSSLGKLGKLRFLRLYNNSLSGEIPRSLTALP-LD 168
```

```
MtSERK1        VLDLSNNQLSGVVPDNGSFSLFTPISFANNLNLCGPVTGHPCPGSPPFSPPPPFVPPPPI 230
OsSERk1        VLDLSNNNLSGEVPSTGSFSLFTPISFANNPSLCGPGTTKPCPGAPPFSPPPPYNPPTPV 227
ZmSERK1        VLDLSNNNLSGGVPSSGSFSLFTPISFANNPNLCGPGTTKPCPGAPPFSPPPPYNPPAP- 226
StSERK1        VLDLSNNRLSGVVPDNGSFSLFTPISFANNLDLCGPVTGRPCPGSPPFSPPPPFVPPPPI 232
NaSERK1        ------------------------------------------------------------ 0
AtSERK1        VLDLSNNRLSGSVPDNGSFSLFTPISFANNLDLCGPVTSHPCPGSPPFSPPPPFIQPPPV 228
AtSERK2        VLDLSNNRLSGSVPDNGSFSLFTPISFANNLDLCGPVTSRPCPGSPPFSPPPPFIPPPIV 231
ZmSERK2        VLDLSNNNLSGQVPSTGSFSLFTPISFANNPNLCGPGTSKPCPGAPPFSPPPPFNPPSPP 230
AtSERK3/BAK1   VLDLSNNPLTGDIPVNGSFSLFTPISFANTKLTP-------LP-----ASPPPPISPTPP 215
NaSERK3/BAK1   VLDLSNNNLTGPVPVNGSFSLFTPISFANNP-----------LDIPPAAPPPPISPTPTS 219
NbSERK3/BAK1   ------------------------------------------------------------ 0
AtSERK4/BKK1   VLDISNNRLSGDIPVNGSFSLFTPISFANNSLTD-------LP-----EPPPTSTSPTPP 221
AtSERK5        VLDISNNRLSGDIPVNGSFSQFTSMSFANNKLR----------------PRPASPSPS-- 210

MtSERK1        SAPGSGGATGAIAGGVAAGAALLFAAPAIAFAWWRRRKPQEFFFDVPAEEDPEVHLGQLK 290
OsSERk1        QSPGSSSSTGAIAGGVAAGAALLFAIPAIGFAWYRRRKPQEHFFDVPAEEDPEVHLGQLK 287
ZmSERK1        TSSKGVSSTGAVAGGVAAGTALLIAVPAIGYALWRRRKPEEQFFDVPAEEDPEVHLGQLK 286
StSERK1        SAPGGNGATGAIAGGVAAGAALLFAAPAIAFAWWRRRKPQEYFFDVPAEEDPEVHLGQLK 292
NaSERK1        ------------------------------------------------------------ 0
AtSERK1        STPSGYGITGAIAGGVAAGAALLFAAPAIAFAWWRRRKPLDIFFDVPAEEDPEVHLGQLK 288
AtSERK2        PTPGGYSATGAIAGGVAAGAALLFAAPALAFAWWRRRKPQEFFFDVPAEEDPEVHLGQLK 291
ZmSERK2        TQSTGASSTGAIAGGVAAGAALVFAVPAIAFAMWRRRKPEEHFFDVPAEEDPEVHLGQLK 290
AtSERK3/BAK1   SPAGSNRITGAIAGGVAAGAALLFAVPAIALAWWRRKKPQDHFFDVPAEEDPEVHLGQLK 275
NaSERK3/BAK1   SSGVGNSATGAIAGGVAAGAALLFAAPAILLAWWRRRKPQDHFFDVPAEEDPEVHLGQLK 279
NbSERK3/BAK1   ------------------------------------------------------------ 0
AtSERK4/BKK1   PPSGG-QMTAAIAGGVAAGAALLFAVPAIAFAWWLRRKPQDHFFDVPAEEDPEVHLGQLK 280
AtSERK5        -PSG---TSAAIVVGVAAGAALLFAL-----AWWLRRKLQGHFLDVPAEEDPEVYLGQFK 261

MtSERK1        RFSLRELQVATDTFSNKNILGRGGFGKVYKGRLADGSLVAVKRLKEERTPGGELQFQTEV 350
OsSERk1        RFSLRELQVATDTFSNKNILGRGGFGKVYKGRLADGSLVAVKRLKEERTPGGELQFQTEV 347
ZmSERK1        RFSLRELQVATDNFNNRNVLGRGGFGKVYKGRLTDGSLVAVKRLKEERTPGGELQFQTEV 346
StSERK1        RFSLRELQVATDSFSNKNILGRGGFGKVYKGRLADGSLVAVKRLKEERTPGGELQFQTEV 352
NaSERK1        ------------------------------------------------------------ 0
AtSERK1        RFSLRELQVASDGFSNKNILGRGGFGKVYKGRLADGTLVAVKRLKEERTPGGELQFQTEV 348
AtSERK2        RFSLRELQVATDSFSNKNILGRGGFGKVYKGRLADGTLVAVKRLKEERTPGGELQFQTEV 351
ZmSERK2        KFSLRELQVATDNFSNKNILGRGGFGKVYKGRLADGSLVAVKRLKEERTPGGELQFQTEV 350
AtSERK3/BAK1   RFSLRELQVASDNFSNKNILGRGGFGKVYKGRLADGTLVAVKRLKEERTQGGELQFQTEV 335
NaSERK3/BAK1   RFSLRELQVATDNFSNKNILVEEDLARVYKGRLADGSLVAVKRLKEERTQGGELQFQTEV 339
NbSERK3/BAK1   ------------------------------------------------------------ 0
AtSERK4/BKK1   RFTLRELLVATDNFSNKNVLGRGGFGKVYKGRLADGNLVAVKRLKEERTKGGELQFQTEV 340
AtSERK5        RFSLRELLVATEKFSKRNVLGKGRFGILYKGRLADDTLVAVKRLNEERTKGGELQFQTEV 321
```

```
MtSERK1       EMISMAVHRNLLRLRGFCMTPTERLLVYPYMANGSVASCLRERPPHQEPLDWPTRKRIAL 410
OsSERk1       EMISMAVHRNLLRLRGFCMTPTERLLVYPYMANGSVASRLRERPPSEPPLDWRTRRRIAL 407
ZmSERK1       ELISMAVHRNLLRLRGFCMTPTERLLVYPYMANGSVASRLRERAPNEPPLEWETRARIAL 406
StSERK1       EMISMAVHRNLLRLRGFCMTPTERLLVYPYMANGSVASCLRERPPSEPPLXWPXRKRIAL 412
NaSERK1       --------------------------------NGSVASCLRERPPSEPPLDWPTRKRIAL 28
AtSERK1       EMISMAVHRNLLRLRGFCMTPTERLLVYPYMANGSVASCLRERPPSQPPLDWPTRKRIAL 408
AtSERK2       EMISMAVHRNLLRLRGFCMTPTERLLVYPYMANGSVASCLRERPPSQLPLAWSIRQQIAL 411
ZmSERK2       EMISMAVHKNLLRLRGFCMTPTERLLVYPYMANGSVASRLRERQPSEPPLSWEPRRRIAL 410
AtSERK3/BAK1  EMISMAVHRNLLRLRGFCMTPTERLLVYPYMANGSVASCLRERPESQPPLDWPKRQRIAL 395
NaSERK3/BAK1  EMISMAVHRNLLRLLGFCMTATERLLVYPYMSNGSVASRLRERPESDPPLEWSIRKRIAL 399
NbSERK3/BAK1  ------------------------------------------------------------ 0
AtSERK4/BKK1  EMISMAVHRNLLRLRGFCMTPTERLLVYPYMANGSVASCLRERPEGNPALDWPKRKHIAL 400
AtSERK5       EMISMAVHRNLLRLRGFCMTPTERLLVYPYMANGSVASCLRERPEGNPALDWPKRKHIAL 381

MtSERK1       GSARGLSYLHDHCDPKIIHRDVKAANILLDEEFEAVVGDFGLAKLMDYKDTHVTTAVRGT 470
OsSERk1       GSARGLSYLHDHCDPKIIHRDVKAANILLDEDFEAVVGDFGLAKLMDYKDTHVTTAVRGT 467
ZmSERK1       GSARGLSYLHDHCDPKIIHRDVKAANILLDEDFEAVVGDFGLAKLMDYKDTHVTTAVRGT 466
StSERK1       GSARGLSYLHDHCDPKIIHRDVKAANILLDEEFEAVVGDFGLAKLMDYKDTHVTTAVRGT 472
NaSERK1       GSARGLSYLHDHCDPKIIHRDVKAANILLDEEFEAVVGDFGLAKLMDYKDTHVTTAVRGT 88
AtSERK1       GSARGLSYLHDHCDPKIIHRDVKAANILLDEEFEAVVGDFGLAKLMDYKDTHVTTAVRGT 468
AtSERK2       GSARGLSYLHDHCDPKIIHRDVKAANILLDEEFEAVVGDFGLARLMDYKDTHVTTAVRGT 471
ZmSERK2       GSARGLSYLHDHCDPKIIHRDVKAANILLDEDFEAVVGDFGLAKLMDYKDTHVTTAVRGT 470
AtSERK3/BAK1  GSARGLAYLHDHCDPKIIHRDVKAANILLDEEFEAVVGDFGLAKLMDYKDTHVTTAVRGT 455
NaSERK3/BAK1  GSARGLAYLHDHCDPKIIHRDVKAANILLDEEYEAVVGDFGLAKLMDYKDTHVTTAVRGT 459
NbSERK3/BAK1  ------------------------------------------------------------ 0
AtSERK4/BKK1  GSARGLAYLHDHCDQKIIHRDVKAANILLDEEFEAVVGDFGLAKLMNYNDSHVTTAVRGT 460
AtSERK5       GSARGLAYLHDHCDQKIIHLDVKAANILLDEEFEAVVGDFGLAKLMNYNDSHVTTAVRGT 441

MtSERK1       IGHIAPEYLSTGKSSEKTDVFGYGIMLLELITGQRAFDLARLANDDDVMLLDWVKGLLKE 530
OsSERk1       IGHIAPEYLSTGKSSEKTDVFGYGIMLLELITGQRAFDLARLANDDDVMLLDWVKGLLKE 527
ZmSERK1       IGHIAPEYLSTGKSSEKTDVFGYGIMLLELITGQRAFDLARLANDDDVMLLDWVKALLKE 526
StSERK1       IGHIAPEYLSTGKSSEKTDVFGYGIMLLELITGQRAFDLARLANDDDVMLLDWVKGLLKE 532
NaSERK1       IGHIAPEYLSTGKSSEKTDVFGYGIMLLELITGQRAFDLARLANDDDVMLLDWVKGLLKE 148
AtSERK1       IGHIAPEYLSTGKSSEKTDVFGYGIMLLELITGQRAFDLARLANDDDVMLLDWVKGLLKE 528
AtSERK2       IGHIAPEYLSTGKSSEKTDVFGYGIMLLELITGQRAFDLARLANDDDVMLLDWVKGLLKE 531
ZmSERK2       IGHIAPEYLSTGKSSEKTDVFGYGIMLLELITGQRAFDLARLANDDDVMLLDWVKGLLKE 530
AtSERK3/BAK1  IGHIAPEYLSTGKSSEKTDVFGYGVMLLELITGQRAFDLARLANDDDVMLLDWVKGLLKE 515
NaSERK3/BAK1  IGHIAPEYLSTGKSSEKTDVFGYGVMLLELITGQRAFDLARLANDDDVMLLDWVKGLLKD 519
NbSERK3/BAK1  -------------------VFGYGVMLLELITGQRAFDLARLANDDDVMLLDWVKGLLKD 41
AtSERK4/BKK1  IGHIAPEYLSTGKSSEKTDVFGYGVMLLELITGQKAFDLARLANDDDIMLLDWVKEVLKE 520
AtSERK5       IGHIAPEYLSTGKSSEKTDVFGYGVMLLELITGQKAFDLARLANDDDIMLLDWVKEVLKE 501
```


MtSERK1 KKLEMLVDPDLKTNYIEAAEVEQLIQVALLCTQGSPMDRPKMSDVVRMLEGDGLAERWDEW 590
OsSERk1 KRLEMLVDPDLQSNYIDVEVESLIQVALLCTQGSPTERPKMAEVVRMLEGDGLAERWEEW 587
ZmSERK1 KKLEQLVDPDLQGRYVDQEVESLIQVALLCTQGSPMERPKMSEVARMLEGDGLAERWEQW 586
StSERK1 KKLEMLVDPDLQNKYVEAEVEQLIQVALLCTQSNPMDRPKMSEVVRMLEGDGLAERWDEW 592
NaSERK1 KKLEMLVDPDLQNKYVEAEVEQLIQVALLCTQSSPMDRPKMSEVVRMLEGDGLAERWDEW 208
AtSERK1 KKLEMLVDPDLQTNYEERELEQVIQVALLCTQGSPMERPKMSEVVRMLEGDGLAEKWDEW 588
AtSERK2 KKLEMLVDPDLQSNYTEAEVEQLIQVALLCTQSSPMERPKMSEVVRMLEGDGLAEKWDEW 591
ZmSERK2 KKVEMLVDPDLQKAYEEVEVESLIQVALLCTQGSPLDRPKMSEVVRMLEGDGLAERWDEW 590
AtSERK3/BAK1 KKLEALVDVDLQGNYKDEEVEQLIQVALLCTQSSPMERPKMSEVVRMLEGDGLAERWEEW 575
NaSERK3/BAK1 KKYETLVDADLQGNYEEEEVEQLIRVALLCTGSSPMERPKMSEVVRMLEGDGLAERWEEW 579
NbSERK3/BAK1 KKYETLVDADLQGNYEEEEVEQLIRVALLCTGSSPLERPKMSEVVRMLDGDGLAERWEEW 101
AtSERK4/BKK1 KKLESLVDAELEGKYVETEVEQLIQMALLCTQSSAMERPKMSEVVRMLEGDGLAERWEEW 580
AtSERK5 KKLESLVDAELEGKYVETEVEQLIQMALLCTQSSAMERPKMSEVVRMLEGDGLAERWEEW 561
MtSERK1 QKGEVLRQEVELAPHPNS--DWIV-DSTENLHAVELSGPR 627
OsSERk1 QKIEVVRQEVELGPHRNS--EWIV-DSTDNLHAVELSGPR 624
ZmSERK1 QKVEVMRQEAELAPRHN---DWIV-DSTYNLRAVELSGPR 622
StSERK1 QKVEVLRQEVELAPHPGS--DWLV-DSTENLHAVELSGPR 629
NaSERK1 QKVEVLRQEVELAPHPGS--DWIV-DSTENLHAVELSGPR 245
AtSERK1 QKVEILREEIDLSPNPNS--DWIL-DSTYNLHAVELSGPR 625
AtSERK2 QKVEVLRQEVELSSHPTS--DWIL-DSTDNLHAMELSGPR 628
ZmSERK2 QKVEVVRQEAESAPLRN---DWIV-DSTYNLRAVELSGPR 626
AtSERK3/BAK1 QKEEMFRQDFNYPTHHPAVSGWIIGDSTSQIENEYPSGPR 615
NaSERK3/BAK1 QKEEMVRQDYP-AHHPHT--DWIIADSTYNLRPDELSGPR 616
NbSERK3/BAK1 QKEEMVRQDYP-AHHPHT--DWIIADSTYNIRPDELSGPR 138
AtSERK4/BKK1 QKEEMPIHDFNYQAYPHAGTDWLIPYSNSLIENDYPSGPR 620
AtSERK5 QKEEMPIHDFNYQAYPHAGTDWLIPYSNSLIENDYPSGPR 601

Figure S1

A

B

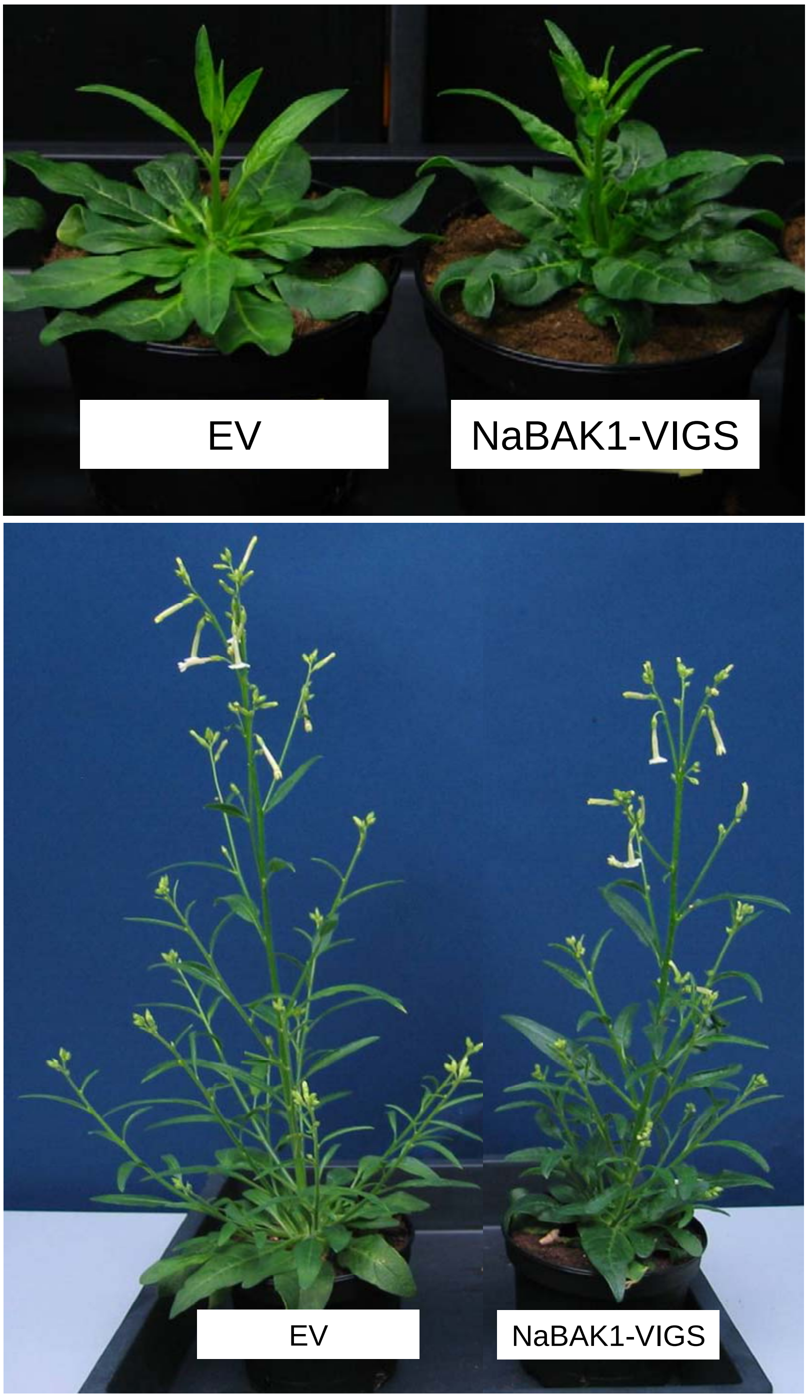


Figure S2

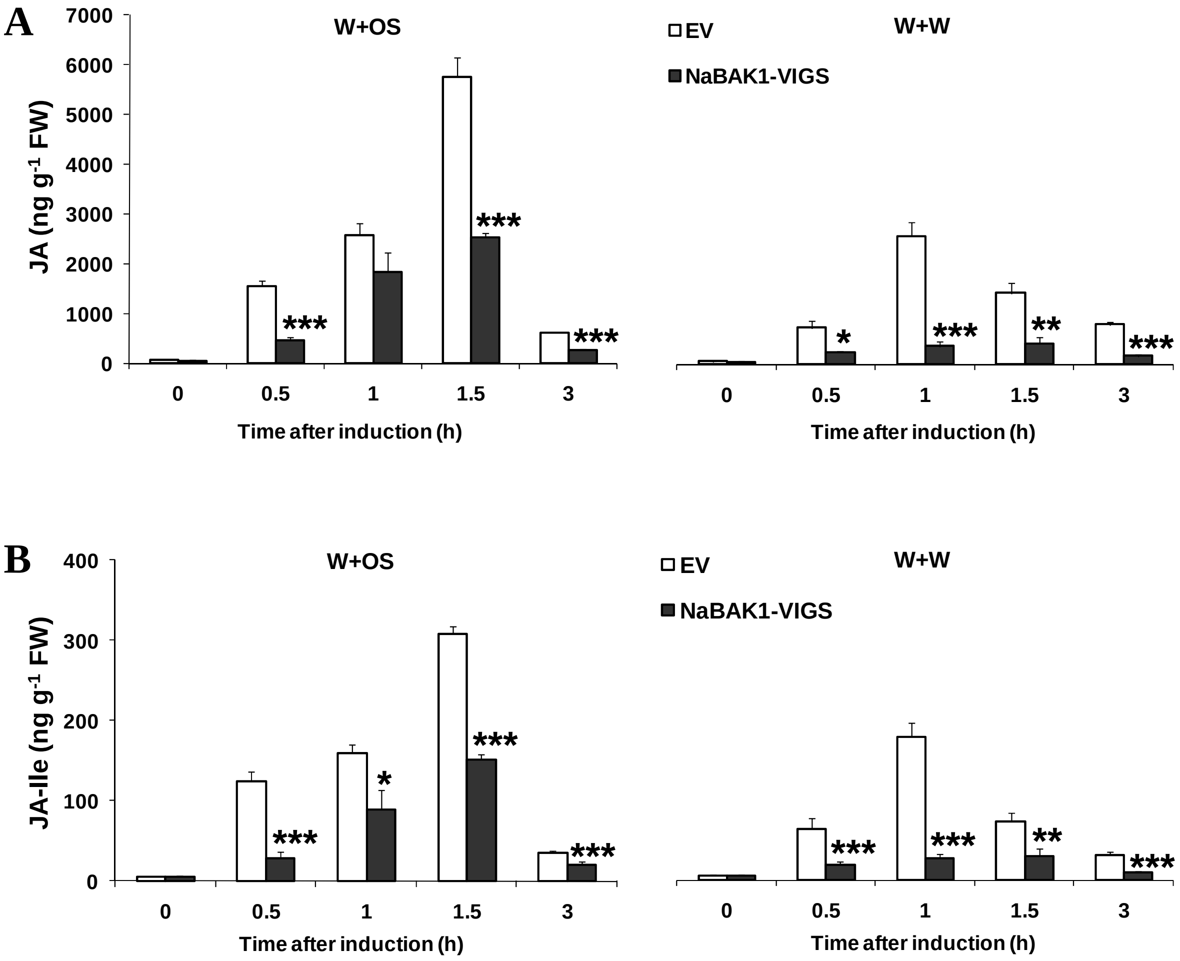

A
B
W+OS
W+W
EV
NaBAK1-VIGS
JA (ng g-1 FW)
JA-Ile (ng g-1 FW)
Time after induction (h)
0
0.5
1
1.5
3
7000
6000
5000
4000
3000
2000
1000
400
300
200
100
***
**
*

Figure S3

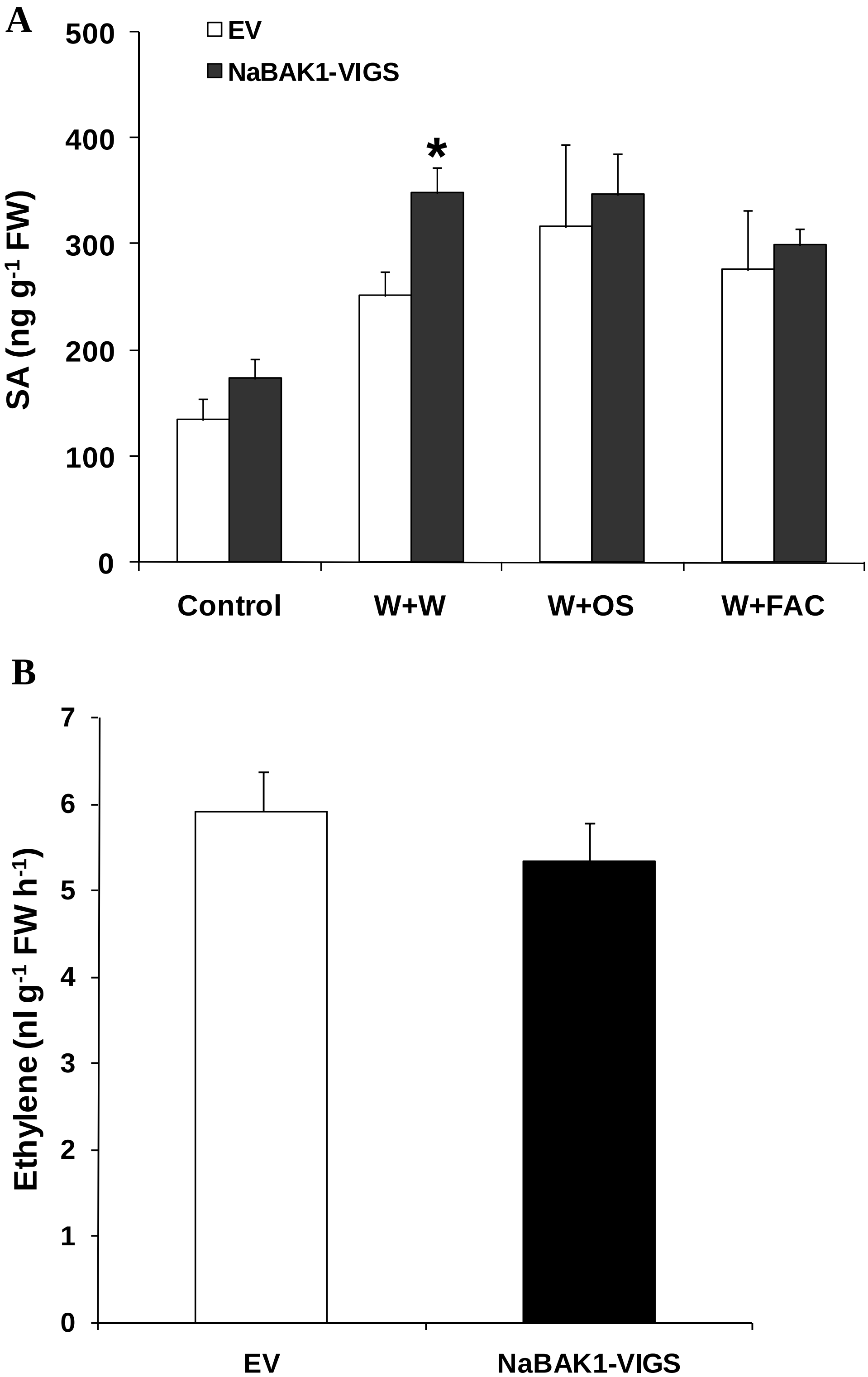
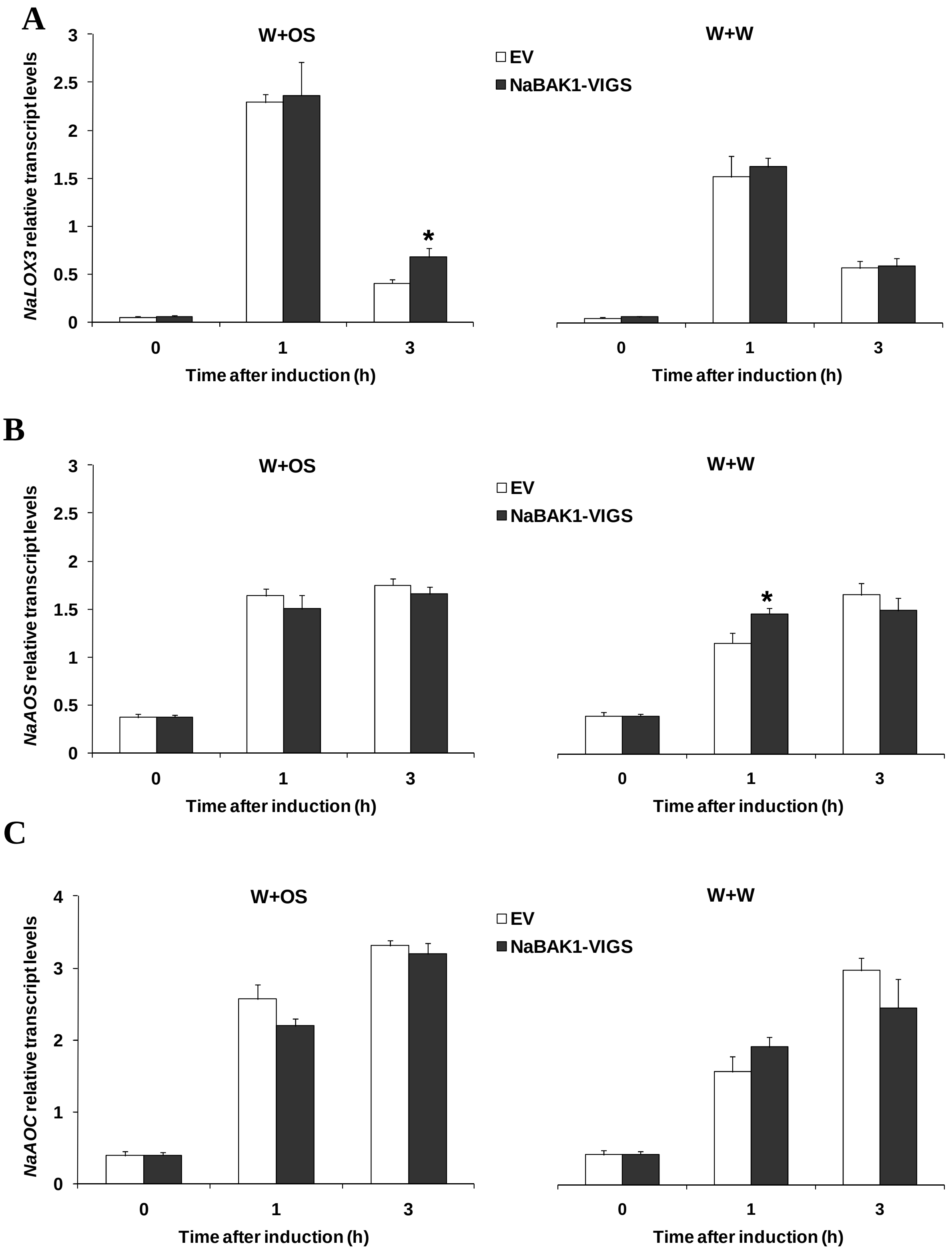

A
500
400
300
200
100
0
EV
NaBAK1-VIGS
*
SA (ng g-1 FW)
Control
W+W
W+OS
W+FAC
B
7
6
5
4
3
2
1
0
Ethylene (nl g-1 FW h-1)
EV
NaBAK1-VIGS

Figure S4


A
W+OS
W+W
EV
NaBAK1-VIGS
NaLOX3 relative transcript levels
0
0.5
1
1.5
2
2.5
3
*
0
1
3
Time after induction (h)
B
W+OS
W+W
EV
NaBAK1-VIGS
NaAOS relative transcript levels
0
0.5
1
1.5
2
2.5
3
*
0
1
3
Time after induction (h)
C
W+OS
W+W
EV
NaBAK1-VIGS
NaAOC relative transcript levels
0
1
2
3
4
0
1
3
Time after induction (h)

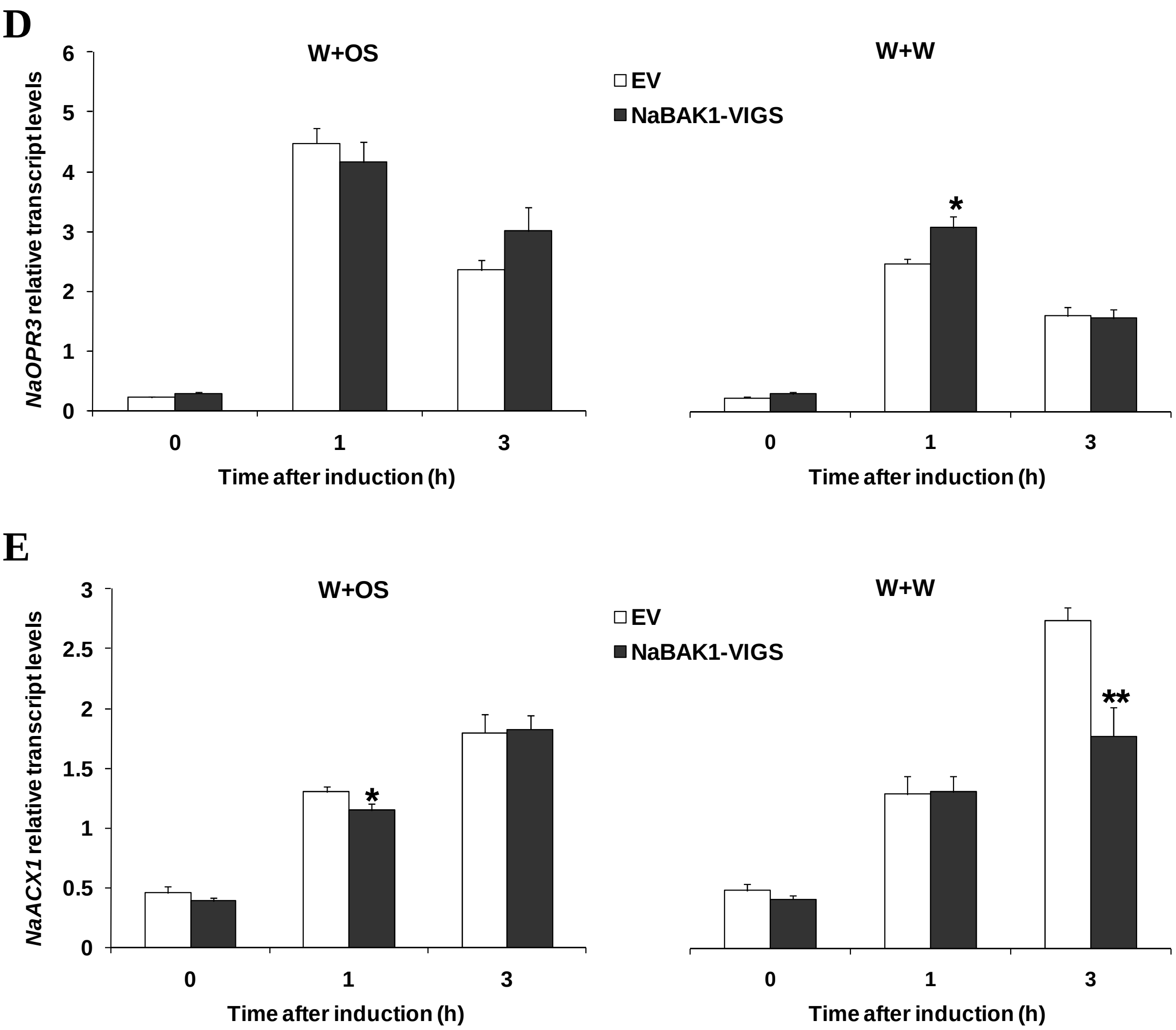

D
W+OS
W+W
EV
NaBAK1-VIGS
NaOPR3 relative transcript levels
6
5
4
3
2
1
0
*
Time after induction (h)
E
NaACX1 relative transcript levels
3
2.5
2
1.5
1
0.5
0
*
**
Time after induction (h)

Figure S5

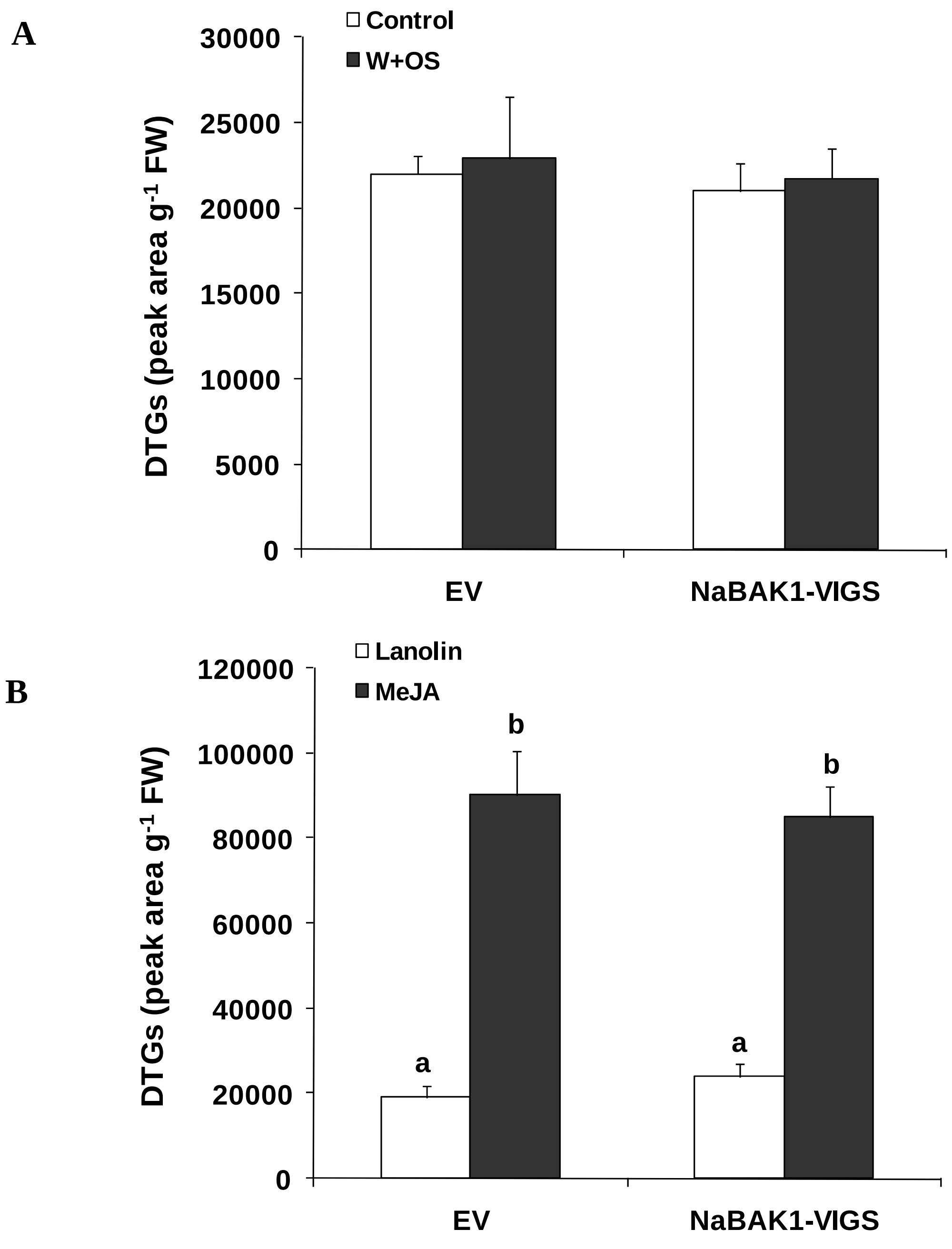

A
Control
W+OS
DTGs (peak area g-1 FW)
30000
25000
20000
15000
10000
5000
0
EV
NaBAK1-VIGS
B
Lanolin
MeJA
120000
100000
80000
60000
40000
20000
0
b
b
a
a
EV
NaBAK1-VIGS

Figure S6

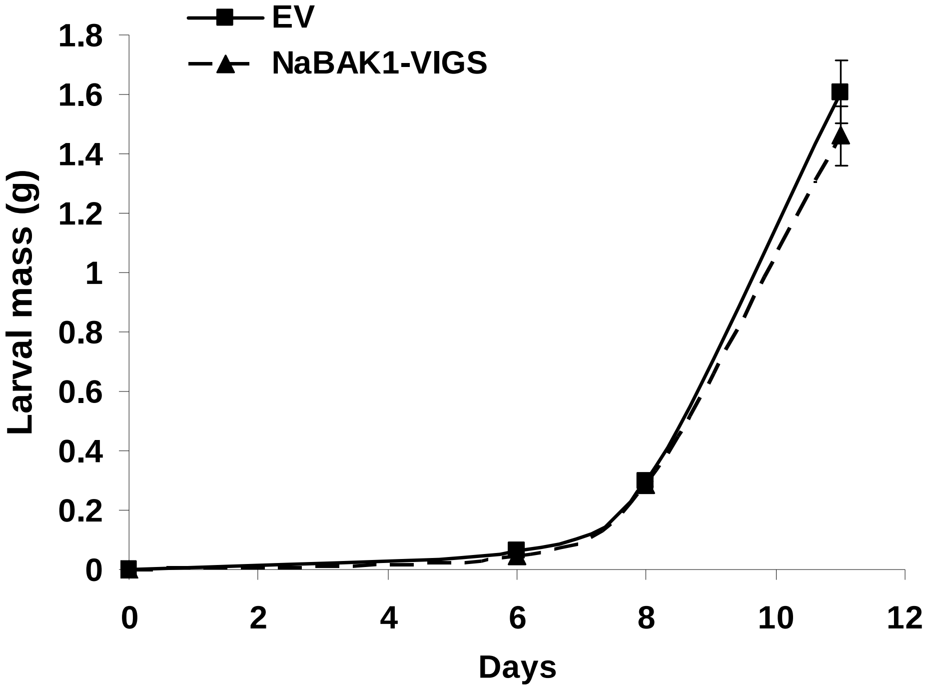

EV
NaBAK1-VIGS
Larval mass (g)
1.8
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
0
2
4
6
8
10
12
Days

Figure S7

Table S1 Primers used for cloning of NaBAK1 and NaSERK1, and preparation of pTV-NaBAK1 construct

Genes	***Primer (5'-3')****
NaBAK1-1	ATGGATCAATGGATATTGGGGATC
NaBAK1-2	GAACACCCACTATCTGATACATCCAG
NaSERK1-1	AATGGAAGTGTTGCATCGTGCCTG
NaSERK1-2	CGCCTATGTTCAACTTGTCAGGGCATAG
NaBAK1-VIGS-BamHI	ACGT**GGATCC**AAGTGGAGTCTGCGATAATCC
NaBAK1-VIGS-SalI	ACGT**GTCGAC**GATTGGGTCAAGGGACTTC

* Nucleotides underlined are *Bam*H I and *Sal* I sites

Table S2 Primer sequences used for quantitative real-time PCR (SYBR Green analysis)

Genes	***Forward Primer (5'-3')***	***Reverse Primer (5'-3')***
NaActin2	GGTCGTACCACCGGTATTGTG	GTCAAGACGGAGAATGGCATG
NaBAK1	TTAAGTCTTTATATTTGTATGTCAGGAA	AAAAGAAAATACATTTGTGCTTCCAC
NaSERK1	GAACTCTAATTTTGTTGATCTTGAAAGTT	ATATAGCCACTACGCCTATGTTC
NaLOX3	GGCAGTGAAATTCAAAGTAAGAGC	CCCAAAATTTGAATCCACAACA
NaAOS	GACGGCAAGAGTTTTCCCAC	TAACCGCCGGTGAGTTCAGT
NaAOC	AACTACCTAACCCTCTCATTTCTCA	AAGCGAAGATAGGCAGGGC
NaOPR3	AATGGAGTTGGAGTTTGTTT	AGGTGGTTGAAGCAGTCGTT
NaACX1	GAATGTCTGTTGCTTGTGCTCA	TACCGCAAAGCACCTCCAG
NaTD	TAAGGCATTTGATGGGAGGC	TCTCCCTGTTCACGATAATGGAA
NaJAR4	ATGCCAGTCGGTCTAACTGAA	TGCCATTGTGGAATCCTTTTAT
NaJAR6	TGGAGTAAACGTTAACCCGAAA	AGAATTTGCTTGCTCAATGCCA