A MADS-box gene *NtSVP* regulates pedicel elongation by directly suppressing a *KNAT1*-like KNOX gene *NtBPL* in tobacco (*Nicotiana tobacum* L.)

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Supplementary figure legends

Supplementary Fig. S1. Protein sequence analysis and tissue-specific expression of *NtSVP*.

(A) Alignment of SVP-like protein sequences . The MADS-box, I domain, K domain and C-terminal domain are marked. Amino acids in black shading and grey shading indicate identical or similar amino acids among the proteins.

(B) An unrooted phylogenetic tree of SVP-clade MADS-box proteins from some species. The scale indicates branch lengths. Accession numbers are as follows: OsMADS22 (Os02g0761000), OsMADS47 (Os03g0186600), OsMADS55 (Os06g0217300), HvBM1 (AJ249142), HvBM10 (EF043040), Brassica campestris (Chinese cabbage) BcSVP (DQ922945), and CaSVP (AFI49342), Eucalyptus grandis EgrSVP (AY263809), NtSTMADS11 (mRNA_51421 in SOL Genomics Network), INCO (CAG27846), JOINTLESS (Solyc11g010570), SVP (At2g22540), AGL24 (At4g24540), Ta-VRT2(DQ022679), SOC1 (At2g45660).

(C) Tissue-specific expression of *NtSVP* in wild-type plants.

Supplementary Fig. S2. Phenotypes of the *NtSVP* transgenic plants.

(A) DNA fragment used for *NtSVP*-RNAi construct.

(B) The morphology of abscission zones in wild-type and *NtSVP*-RNAi transgenic tobacco indicated by white arrows.

(C) The morphology of flower and pedicel in the five developmental stages as described (Zhu *et al.*, 2013).

(D) Quantitative measurement of the pedicel lengths of the WT and two *NtSVP*-RNAi lines from S1 to S5 (N = 10 X 5, 50 pedicels from five individual plants per genotype). Values are means ± SE.

(E) The whole plant morphology of wild-type and *NtSVP* transgenic plants at the reproductive stage.

(F) Quantitative measurement of plant height of WT, *NtSVP*-RNAi and *NtSVP*-OE plants at anthesis stage. (N=5, 5 plants for each genotype). Values are means ± SE.

Supplementary Fig. S3. Protein sequence analysis and tissue-specific expression of *NtBPL*.

(A) Alignment of the NtBPL protein sequence with its homologs in tobacco, tomato and Arabidopsis. KNOX I and KNOX II subdomain, ELK domain, homeobox domain are marked. Amino acids in black shading and grey shading indicate identical or similar amino acids among the proteins.

(B) An unrooted phylogenetic tree of KNOX proteins in tobacco, tomato and Arabidopsis. The scale indicates branch lengths. Accession numbers are as follows: TKN1 (Solyc04g077210.2), TKN2 (Solyc02g081120.2), NTH20 (BAA76904), BP (At4g08150), STM (At1g62360), NTH22 (BAA76905), NTH201 (BAF95776), KNAT2 (At1g70510), KNAT6 (At1g70510), KNAT5 (At4g32040), KNAT7 (At1g62990), KNAT4 (At5g11060), and KNAT3 (At5g25220), ATH1 (At4g32980).

(C) Tissue-specific expression of *NtBPL* in wild-type plants.

Supplementary Fig. S4. Developmental-specific expression of *NtSVP* and *NtBPL* in pedicels of wild-type plants.

Supplementary Fig. S5. Phenotypes of the *NtBPL* transgenic plants.

(A) The whole plant morphology of wild-type and *NtBPL* transgenic plants at the reproductive stage.

(B) Distribution of the angles between the pedicels and the inflorescences in WT, *NtBPL*-OE and *NtBPL*-RNAi plants. N= 10 X 5, 50 pedicels from five plants were measured as a replicate, and three replications were performed. Values are means ± SE.

(C) Longitudinal sections of the pedicels of WT and *NtBPL* transgenic plants at anthesis stage. Asterisks pointed to cortex cells. Bars = 100 μm.

(D) Cell numbers in the longitudinal cortex file of pedicels in WT and *NtBPL* transgenic plants at anthesis (N= 3 X 5, 15 sections from five individual plants per genotype were used). Values are means ± SE.

(E) qRT-PCR detection of *NtSVP* expression in pedicels of WT and *NtBPL* transgenic plants. *NtACTIN9* was used as an internal control.

Supplementary Fig. S6. The promoter sequence of *NtBPL*. The CArG-box and initiation codon were highlighted by black boxes.

Supplementary Fig. S7. Confirmation of microarray data. Four differently expressed genes *NtGRAS1*, *NtEREBP5*, *NtWRKY3*, and *NtSBP2* were randomly selected for qRT-PCR detection compared with those of microarray results. *NtACTIN9* was used as an internal control.

Supplementary Fig. S8. GO enrichment analysis of differentially expressed genes in *NtBPL*-RNAi pedicels and their MapMan classification.

(A) Gene ontology analysis of 427 down-regulated genes in *NtBPL*-RNAi pedicels compared with those in the wild type. Colors indicate significance level of each over-represented terms (FDR ≤ 0.01).

(B) Gene ontology analysis of 230 up-regulated genes in *NtBPL*-RNAi pedicels compared with those in the wild type plant. Colors indicate significance level of each over-represented terms (FDR ≤ 0.01).

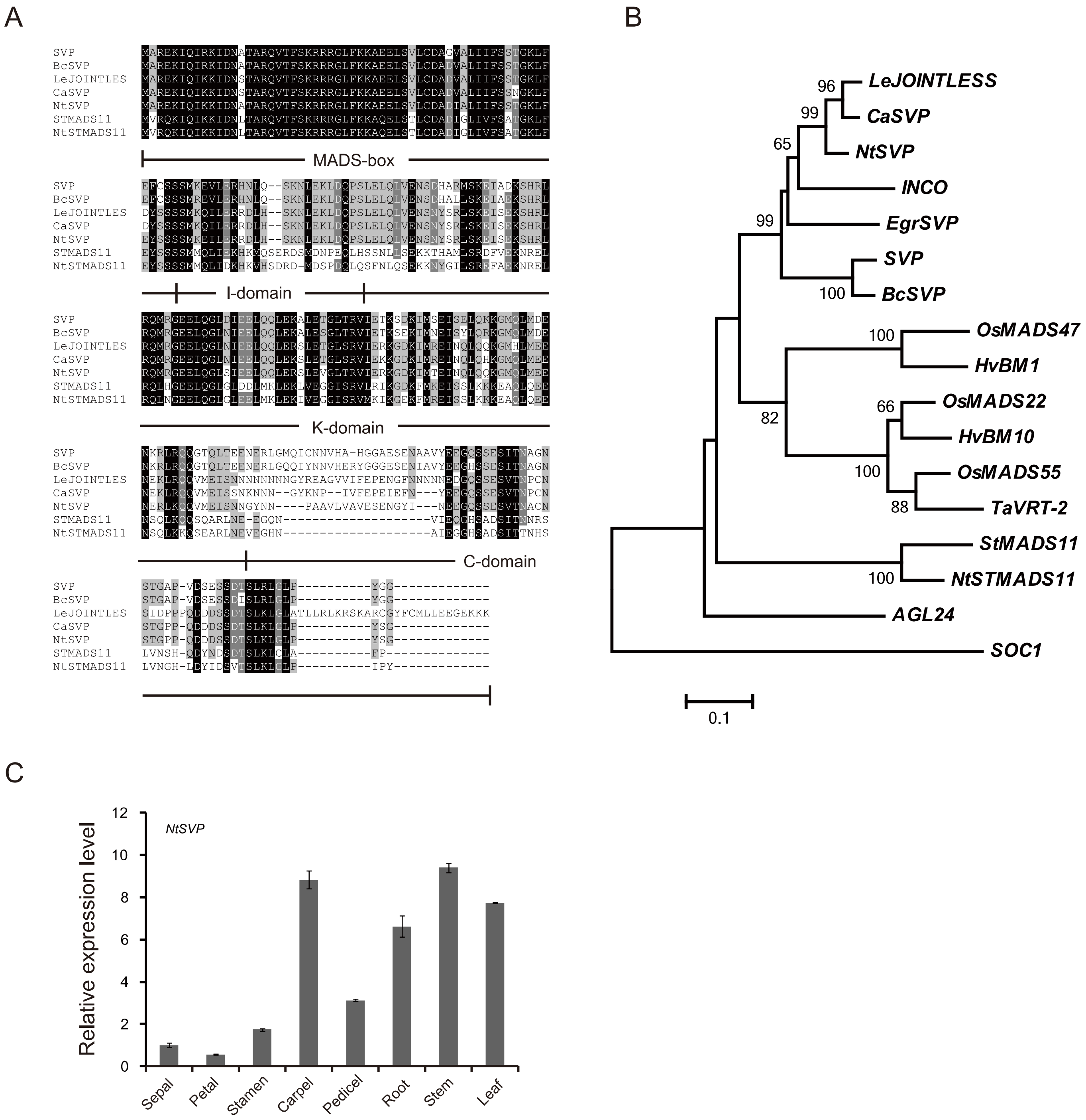
(C) MapMan classification of differentially expressed genes in *NtBPL*-RNAi pedicels.

Supplementary Table S1. Hormone related genes that are differentially expressed due to down-regulation of *NtBPL*.

Supplementary Table S2. Primers used in this work.

Supplementary dataset 1. List of differentially expressed genes between the wild type and *NtBPL*-RNAi pedicels.

Fig. S1



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BcSVP        MAREKIQIRKIDNATARQVTFSKRRRGLFKKAEELSVLCDADVALIIFSSTGKLF
LeJOINTLES   MAREKIQIKKIDNSTARQVTFSKRRRGLFKKAEELSVLCDADVALIIFSSTGKLF
CaSVP        MAREKIQIKKIDNSTARQVTFSKRRRGLFKKAEELSVLCDADVALIIFSSNGKLF
NtSVP        MAREKIQIKKIDNATARQVTFSKRRRGLFKKAEELSVLCDADIALIIFSSTGKLF
STMADS11     MVRQKIQIKKIDNLTARQVTFSKRRRGLFKKAQELSTLCDADIGLIVFSATGKLF
NtSTMADS11   MVRQKIQIKKIDNLTARQVTFSKRRRGLFKKAQELSTLCDADIGLIVFSATGKLF

SVP          EFCSSSMKEVLERHNLQ--SKNLEKLDQPSLELQLVENSDHARMSKEIADKSHRL
BcSVP        EFCSSSMREVLERHNLQ--SKNLEKLDQPSLELQLVENSDHALLSKEIAEKSHRL
LeJOINTLES   DYSSSSMKQILERRDLH--SKNLEKLDQPSLELQLVENSNYSRLSKEISEKSHRL
CaSVP        DYSSSSMKQILERRDLH--SKNLEKLDQPSLELQLVENSNYSRLSKEISEKSHRL
NtSVP        EYSSSSMKEILERRDLH--SKNLEKLDQPSLELQLVENSNYSRLSKEISEKSHRL
STMADS11     EYSSSSMMQLIEKHKMQSERDSMDNPEQLHSSNLLSEKKTHAMLSRDFVEKNREL
NtSTMADS11   EYSSSSMMQLIDKHKVHSDRD-MDSPDQLQSFNLQSEKKNYGILSREFAEKNREL

SVP          RQMRGEELQGLDIEELQQLEKALETGLTRVIETKSDKIMSEISELQKKGMQLMDE
BcSVP        RQMRGEELQGLNIEELQQLEKALESGLTRVIETKSEKIMNEISYLQRKGMQLMDE
LeJOINTLES   RQMRGEELQGLNIEELQQLERSLETGLSRVIERKGDKIMREINQLQQKGMHLMEE
CaSVP        RQMRGEEIQGLNIEELQQLEKSLETGLSRVIEKKGDKIMREINQLQHKGMQLMEE
NtSVP        RQMRGEELQGLSIEELQQLERSLEVGLTRVIERKGDKIMTEINQLQQKGMQLMEE
STMADS11     RQLHGEELQGLGLDDLMKLEKLVEGGISRVLRIKGDKFMKEISSLKKKEAQLQEE
NtSTMADS11   RQLNGEELQGLGLEELMKLEKIVEGGISRVMKIKGEKFMREISSLKKKEAQLQEE

SVP          NKRLRQQGTQLTEENERLGMQICNNVHA-HGGAESENAAVYEEGQSSESITNAGN
BcSVP        NKRLRQQGTQLTEENERLGQQIYNNVHERYGGGESENIAVYEEGHSSESITNAGN
LeJOINTLES   NEKLRQQVMEISNNNNNNNGYREAGVVIFEPENGFNNNNNEDGQSSESVTNPCN
CaSVP        NEKLRQQVMEISSNKNNN--GYKNP--IVFEPEIEFN---YEEGQSSESVTNPCN
NtSVP        NERLKQQVMEISNNGYNN----PAAVLVAVESENGYI---NEEGQSSESVTNACN
STMADS11     NSQLKQQSQARLNE-EGQN--------------------VIEQGHSADSITNNRS
NtSTMADS11   NSQLKKQSEARLNEVEGHN--------------------AIEGGHSADSITTNHS

SVP          STGAP-VDSESSDTSLRLGLP----------YGG-------------
BcSVP        STGAP-VDSESSDISLRLGLP----------YGG-------------
LeJOINTLES   SIDPPPQDDDSSDTSLKLGLATLLRLKRSKARCGYFCMLLEEGEKKK
CaSVP        STGPP-QDDDSSDTSLKLGLP----------YSG-------------
NtSVP        STGPP-QDDDSSDTSLKLGLP----------YSG-------------
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NtSTMADS11   LVNGH-LDYIDSVTSLKLGLP----------IPY-------------
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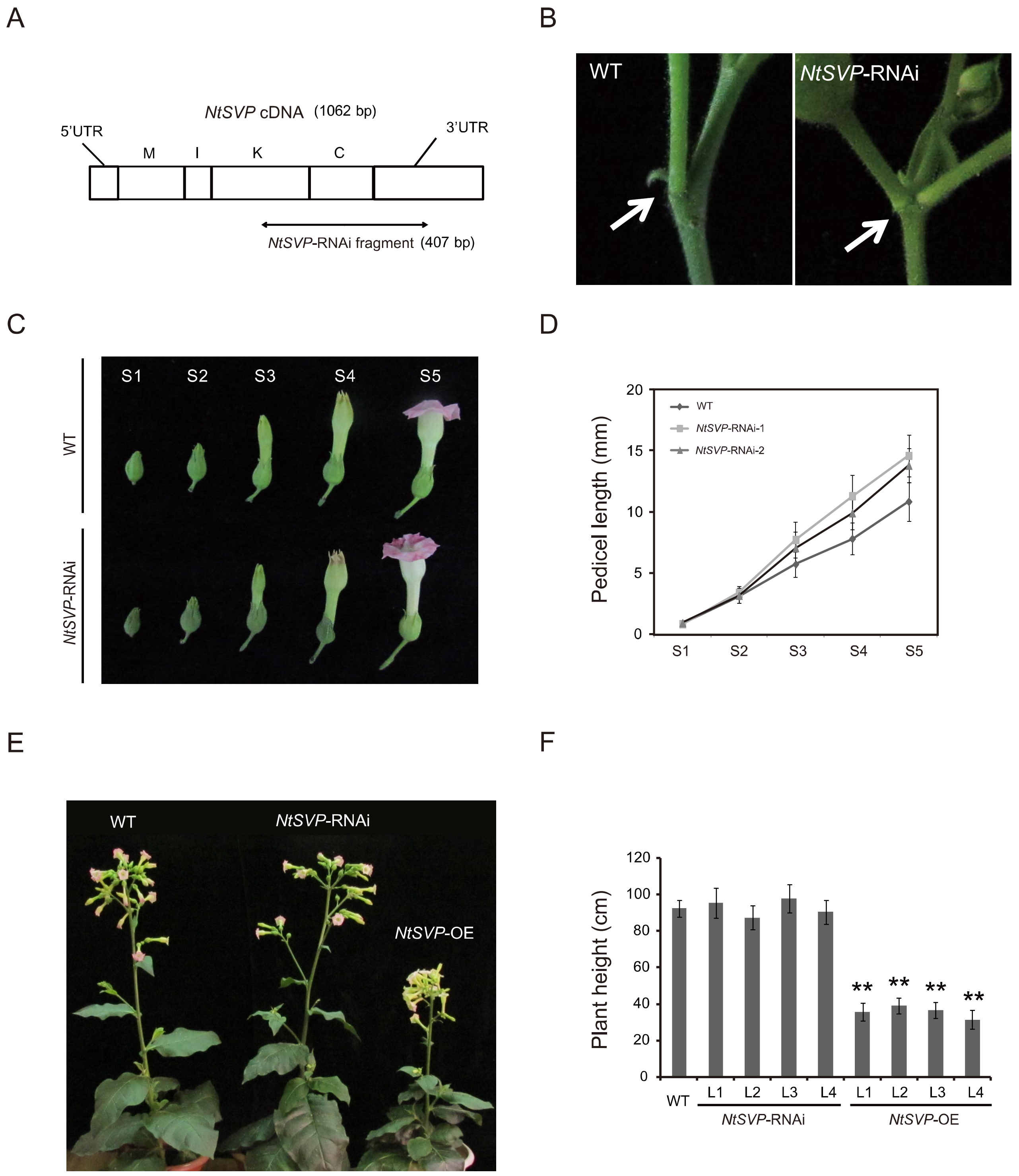
Fig. S2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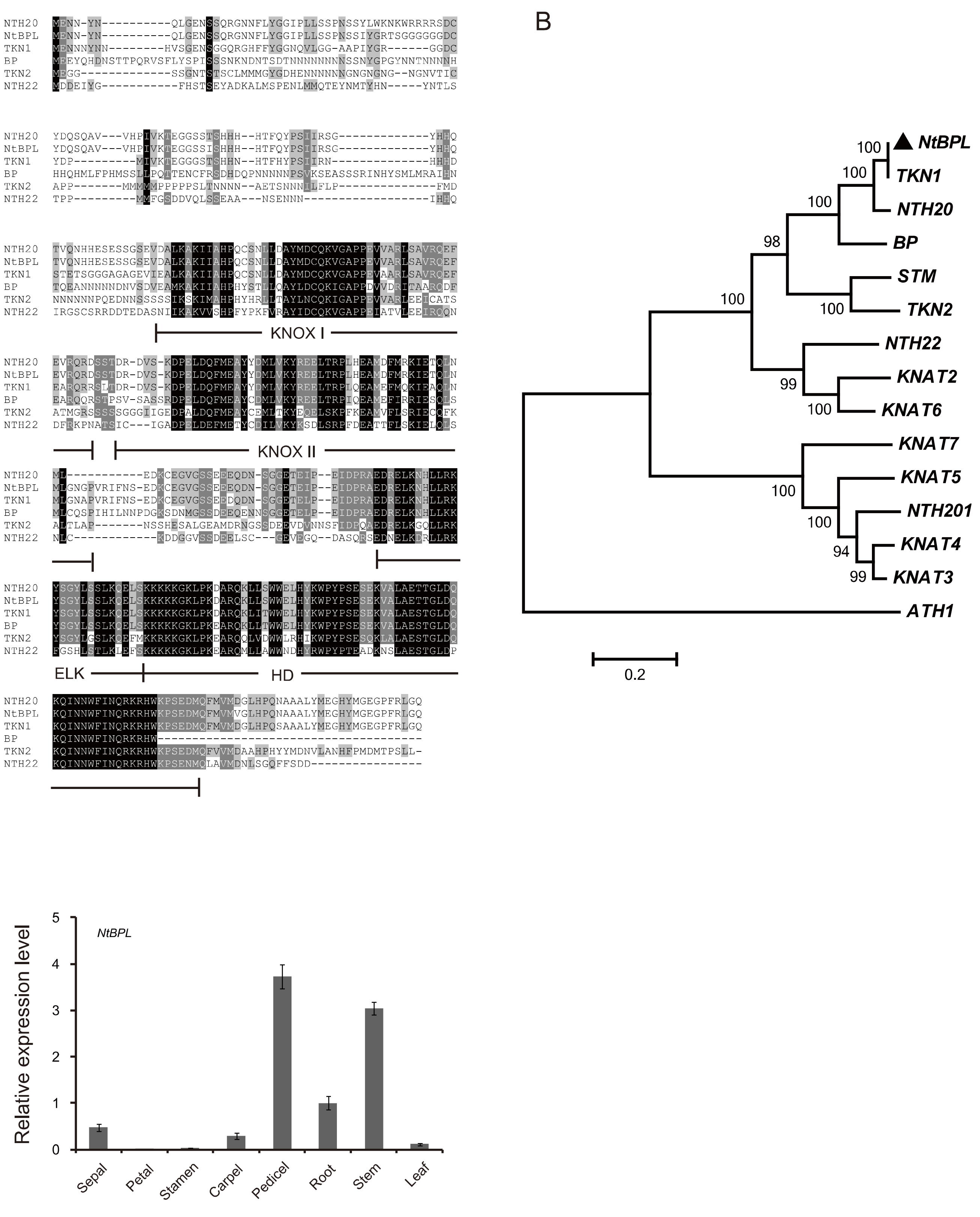
5'UTR
3'UTR
M
I
K
C
NtSVP-RNAi fragment (407 bp)
B
WT
NtSVP-RNAi
C
S1
S2
S3
S4
S5
WT
NtSVP-RNAi
D
Pedicel length (mm)
20
15
10
5
0
WT
NtSVP-RNAi-1
NtSVP-RNAi-2
S1
S2
S3
S4
S5
E
WT
NtSVP-RNAi
NtSVP-OE
F
Plant height (cm)
120
100
80
60
40
20
0
WT
L1
L2
L3
L4
L1
L2
L3
L4
NtSVP-RNAi
NtSVP-OE
**
**
**
**

Fig. S3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TKN1 MENNNYNN--------HVSGENSGGQRGHFFYGGNQVLGG-AAPIYGR------GGDC
BP MEEYQHDNSTTPQRVSFLYSPISSSNKNDNTSDTNNNNNNNNSSNYGPGYNNTNNNNH
TKN2 MEGG-------------SSGNTSTSCLMMMGYGDHENNNNNNGNGNGNG--NGNVTIC
NTH22 MDDEIYG-----------FHSTSEYADKALMSPENLMMQTEYNMTYHN-----YNTLS
NTH20 YDQSQAV---VHPIVKTEGGSSTSHHH--HTFQYPSIIRSG-------------YHHQ
NtBPL YDQSQAV---VHPIVKTEGGSSISHHH--HTFQYPSIIRSG-------------YHHQ
TKN1 YDP---------MIVKTEGGGSTSHHN--HTFHYPSIIRN--------------HHHD
BP HHQHMLFPHMSSLLPQTTENCFRSDHDQPNNNNNPSVKSEASSSRINHYSMLMRAIHN
TKN2 APP-------MMMMMPPPPPSLTNNNN--AETSNNNILFLP--------------FMD
NTH22 TPP---------MMFGSDDVQLSSEAA---NSENNN------------------IHHQ
NTH20 TVQNHHESESSGSEVDALKAKIIAHPQCSNLLDAYMDCQKVGAPPEVVARLSAVRQEF
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TKN1 STETSGGGAGAGEVIEALKAKIIAHPQCSNLLDAYMDCQKVGAPPEVAARLSAVRQEF
BP TQEANNNNNDNVSDVEAMKAKIIAHPHYSTLLQAYLDCQKIGAPPDVVDRITAARQDF
TKN2 NNNNNNPQEDNNSSSSSIKSKIMAHPHYHRLLTAYLNCQKIGAPPEVVARLEEICATS
NTH22 IRGSCSRRDDTEDASNIIKAKVVSHPFYPKFVRAYIDCQKVGAPPEIATVLEEIRQQN
KNOX I
NTH20 EVRQRDSSTDR-DVS-KDPELDQFMEAYYDMLVKYREELTRPLHEAMDFMRKIETQLN
NtBPL EVRQRDSSTDR-DVS-KDPELDQFMEAYYDMLVKYREELTRPLHEAMDFMRKIETQLN
TKN1 EARQRRSLTDR-DVS-KDPELDQFMEAYYDMLVKYREELTRPLQEAMEFMQKIEAQLN
BP EARQQRSTPSV-SASSRDPELDQFMEAYCDMLVKYREELTRPIQEAMEFIRRIESQLS
TKN2 ATMGRSSSSSGGGIIGEDPALDQFMEAYCEMLTKYEQELSKPFKEAMVFLSRIECQFK
NTH22 DFRKPNATSIC---IGADPELDEFMETYCDILVKYKSDLSRPFDEATTFLSKIELQLS
KNOX II
NTH20 ML-----------EDKCEGVGSSEEEQDN-SGGETEIP--EIDPRAEDRELKNHLLRK
NtBPL MLGNGPVRIFNS-EDKCEGVGSSEEEQDN-SGGETEIP--EIDPRAEDRELKNHLLRK
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ELK
HD
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NtBPL KQINNWFINQRKRHWKPSEDMQFMVMVGLHPQNAAALYMEGHYMGEGPFRLGQ
TKN1 KQINNWFINQRKRHWKPSEDMQFMVMDGLHPQSAAALYMEGHYMGEGPFRLGQ
BP KQINNWFINQRKRHW--------------------------------------
TKN2 KQINNWFINQRKRHWKPSEDMQFVVMDAAHPHYYMDNVLANHFPMDMTPSLL-
NTH22 KQINNWFINQRKRHWKPSENMQLAVMDNLSGQFFSDD----------------
B
▲ NtBPL
TKN1
NTH20
BP
STM
TKN2
NTH22
KNAT2
KNAT6
KNAT7
KNAT5
NTH201
KNAT4
KNAT3
ATH1
100
100
100
98
100
100
99
100
100
100
94
99
0.2
C
NtBPL
Relative expression level
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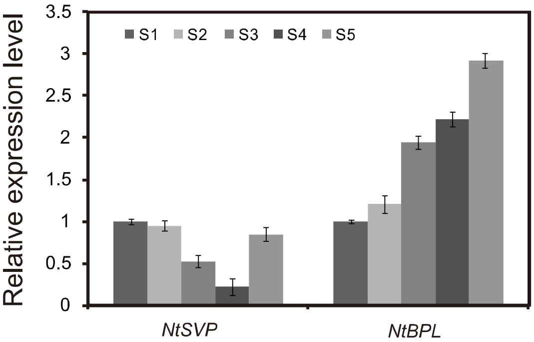
2
3
4
5
Sepal
Petal
Stamen
Carpel
Pedicel
Root
Stem
Leaf

Fig. S4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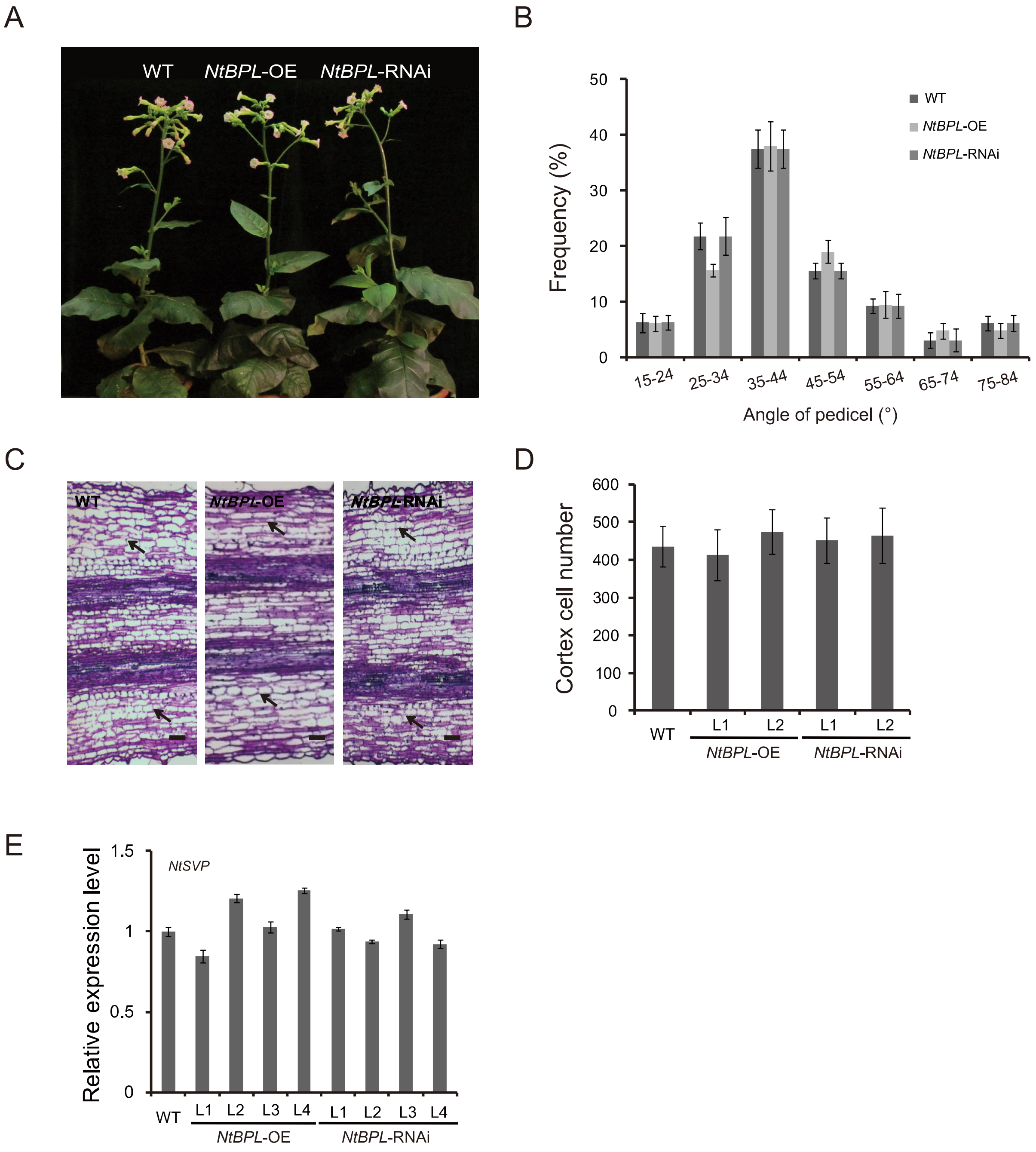
3
2.5
2
1.5
1
0.5
0
S1
S2
S3
S4
S5
NtSVP
NtBPL

Fig. S5


A
WT
NtBPL-OE
NtBPL-RNAi
B
Frequency (%)
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40
30
20
10
0
WT
NtBPL-OE
NtBPL-RNAi
15-24
25-34
35-44
45-54
55-64
65-74
75-84
Angle of pedicel (°)
C
WT
NtBPL-OE
NtBPL-RNAi
D
Cortex cell number
600
500
400
300
200
100
0
WT
L1
L2
L1
L2
NtBPL-OE
NtBPL-RNAi
E
Relative expression level
1.5
1
0.5
0
NtSVP
WT
L1
L2
L3
L4
L1
L2
L3
L4
NtBPL-OE
NtBPL-RNAi

Fig. S6

GGCCTACTAA TAGGGGGCGA TTGAGCTGCC CTTAGCTTCG CTTCTTCTAT CAATTCCTTG

CCATCATCCT CTTTGATAAT GTAAACAATT GAACCAATTT ATATAACTCA ATTTTTCTAT

CAATTATAAG AAACTAACTT TTCCAAGGTA GTGAAATAAA TAATCAATAG AAAAAGAAAG

CArG-box

ACCTCACAAA AGGAAAAAGA AAATGAAAAG GGCTTCCCAT GGAAGTAATA GGAAAAGCAA

AAGAATACAA AAAGAAAGAG AAAGTTAAAA GATCTAACTA ACTAACTCTA TATATATACA

TATATATATA TTGAATAAAA TAATTATGCT TTCTTTATAA TTGAGTGGTT TTCTCTGCAT

AGGATTATAG GGGGTATAGT TAAACTAAAG ACTAATATTT TCCAATACAT TTCCTTATTC

TTCAACGTAA GAACGTCTTG TCATCTACGA AGCCGCTACC AGGAGCGGCC ACTAGCTTAC

CCCTTCCCTT CCTTTCCTTT CCTTTTTTCT TTGTTCACAG CCACTATCTT CTATGTTGTC

AAGATAAGTT CATTCCAAAA CTTCTTCAGT ACAACTTCAT CTCCTTGGCC TCCTTAACCA

GACAACACTA GTAAAAATAT CCAATTATTA TTATTTTTTG TGTGTGTTTC TTTTACCAAA

TAAAGAAGAG ATCTCGAAGA GTTAAATGAA CTTTCCCCCT ATAGTTGTGT TAGTTTGACG

AATAATAAGT ATTCTAGACT TTGTTTAGGG TTTCATCTAG TTCTCAACTG TTTATCCACA

TCTTTGATTT AGGGTTGCCG ATCTTCATAT ATTTTTTTTA CCATATCTTG TTAGGGTAAT

TATCTAGAAA GGGCAGCTTG GCGTAATCAT GGTCATAGCT GTTTCCTGTG TGAATTGTTA

TCCGCTCACA ATTCCACACA ACATACGAGC CGGAAGCATA AAGTGTAAAG CCTGGGGTGC

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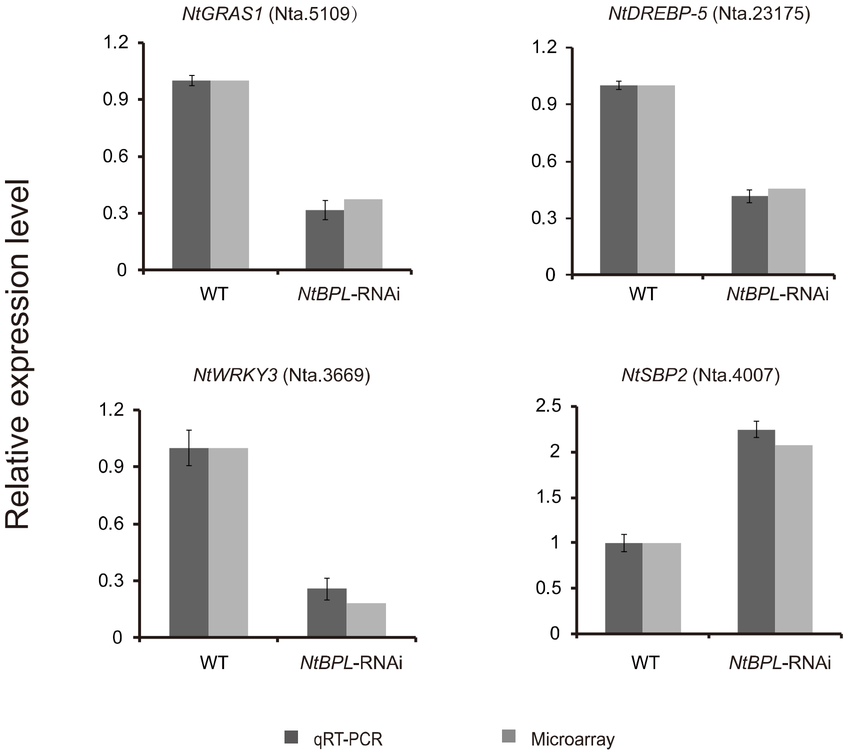
Initiation Codon

Fig. S7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0.6
0.3
0
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NtBPL-RNAi
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1.2
0.9
0.6
0.3
0
WT
NtBPL-RNAi
NtWRKY3 (Nta.3669)
1.2
0.9
0.6
0.3
0
WT
NtBPL-RNAi
NtSBP2 (Nta.4007)
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1
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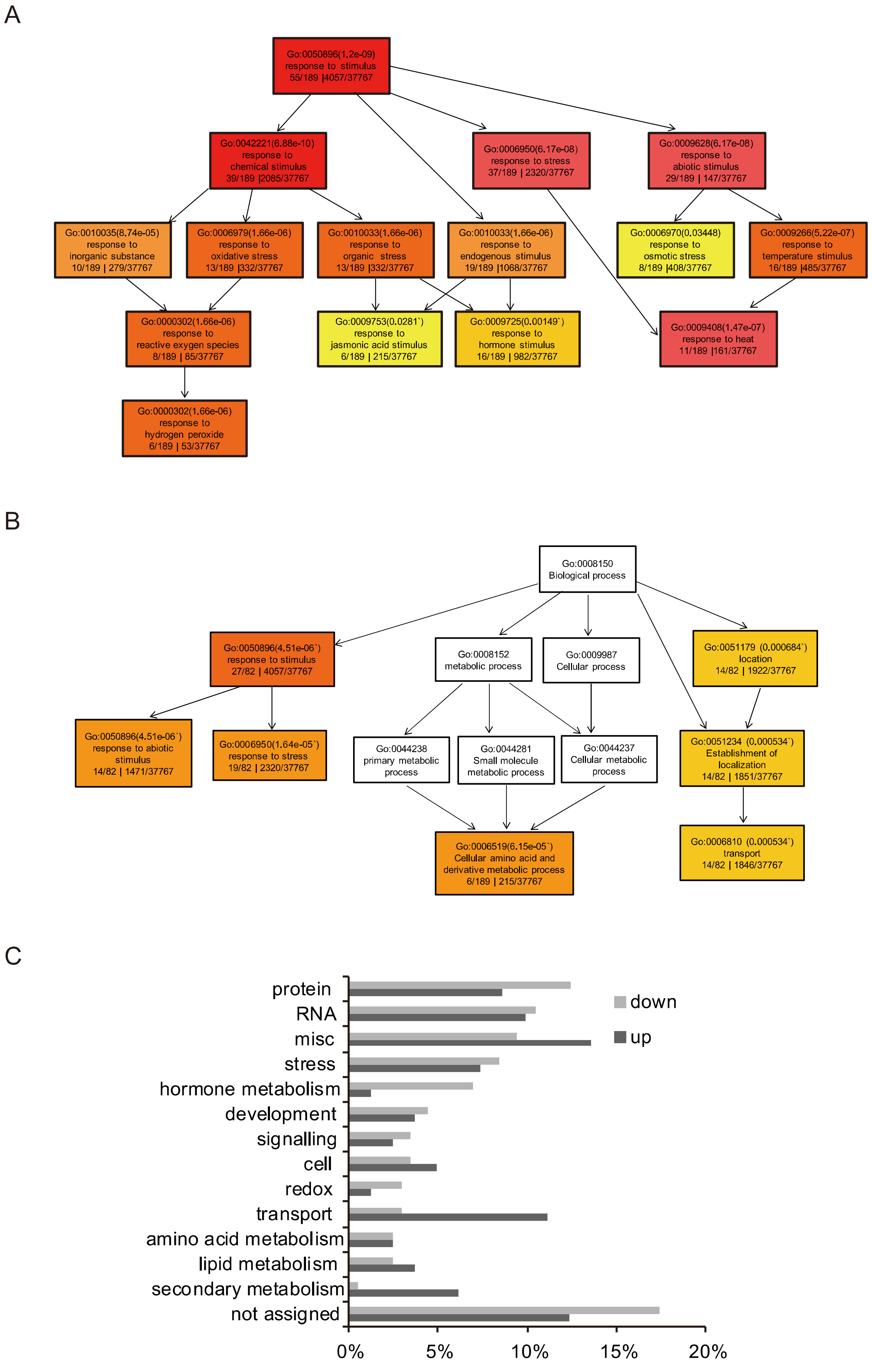
qRT-PCR
Microarray

Fig. S8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Go:0044281 Small molecule metabolic process
Go:0044237 Cellular metabolic process
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Go:0006519(6.15e-05`) Cellular amino acid and derivative metabolic process 6/189 | 215/37767
Go:0006810 (0.000534`) transport 14/82 | 1846/37767
C
protein
RNA
misc
stress
hormone metabolism
development
signalling
cell
redox
transport
amino acid metabolism
lipid metabolism
secondary metabolism
not assigned
0%
5%
10%
15%
20%
down
up

Supplementary Table S1. Hormone related genes that are differentially expressed due to down-regulation of *NtBPL* .

	Arabidopsis homologs	Description	Foldchange	UniGene ID
Up regulated				
auxin.induced-regulated-responsive-activated	at5g54510	GH3.6, DFL1 | DFL1 (DWARF IN LIGHT 1)	2.3	Nta.23121
gibberelin.induced-regulated-responsive-activated	at3g02885	GASA5	6.01	Nta.8147
Down regulated				
auxin.induced-regulated-responsive-activated	at2g45210	Auxin-responsive protein-related	0.24	Nta.3096
auxin.induced-regulated-responsive-activated	at5g35735	Auxin-responsive family protein	0.297	Nta.8872
auxin.induced-regulated-responsive-activated	at4g27450	Unknown protein	0.42	Nta.801
brassinosteroid.synthesis-degradation.BRs.metabolic regulation	at2g26710	BAS1, CYP734A1, CYP72B1	0.48	Nta.15867
ethylene.synthesis-degradation.1-aminocyclopropane-1-carboxylate synthase	at5g65800	ACS5, CIN5, ETO2, ATACS5	0.35	Nta.14789
ethylene.synthesis-degradation.1-aminocyclopropane-1-carboxylate oxidase	at2g19590	ACO1	0.15	Nta.12328
gibberelin.synthesis-degradation.copalyl diphosphate synthase	at4g02780	GA1, ABC33, ATCPS1	0.22	Nta.4073
gibberelin.synthesis-degradation.ent-kaurene synthase	at1g79460	GA2, KS, ATKS	0.38	Nta.23734
gibberelin.synthesis-degradation.ent-kaurenoic acid hydroxylase/oxygenase	at1g05160	CYP88A3, ATKAO1, KAO1	0.47	Nta.4075
gibberelin.synthesis-degradation.GA3 oxidase	at1g15550	GA4, ATGA3OX1, GA3OX1	0.33	Nta.3870
gibberelin.synthesis-degradation.GA3 oxidase	at1g80340	GA4H, ATGA3OX2, GA3OX2	0.18	Nta.9957
gibberelin.induced-regulated-responsive-activated	at2g14900	GASA7	0.23	Nta.3268

Supplementary Table S2. Primers used in this work

	Sequence (5'-3')
For transgenic plants	
NtSVP RNAi-F	GTCATAGAGA GAAAG
NtSVP RNAi-R	GCCAAACATG AATCTGA
NtSVP OE-F	CGATGAGCTCATGGCTAGAGAGAAAATT
NtSVP OE-R	CGTAGGTACCTCAACCTGAGTAGGGCAG
For RACE	
NtSVP gstWR	TTTCTCTCTATGACGCGGGTCAATCCAG
NtSVP -F1	TCCAATAATGGATACAACAACCCAG
NtSVP -F2	GCAGCAGTATTAGTAGCAGTTGAAT
Gene Racer 5' primer	CGACTGGAGCACGAGGACACTGA
For TAIL-PCR	
NtBPL -SP1	CCGCTTGTTCTTCCATAAATAG
NtBPL -SP2	TATGGGATGTACCACTGCTTG
NtBPL -SP3	GATGAGTTCTCCCCCAGTTGAT
For real-time PCR	
NtACTIN9 -F	CTATTCTCCGCTTTGGACTTGGCA
NtACTIN9 -F	AGGACCTCAGGACAACGGAAACG
NtSVP -F	TGTGATGCTGATGTTGCTCTC
NtSTMADS11 -F	AGAGCTGCAAGGACTTGGCTT
NtSTMADS11 -R	TGATGGAGTCTGCGGAATGTC
NTH20- Fw	TACAATCAACTGGGGGAGAAC
NTH20 -Rv	CTACGAATAATCGAAGGGTA
NTH22 -F	AGTTTGGGAGTCACCTAAGTAC
NTH22 -R	AGCTAACTGCATATTCTCTGAC
NtSVP -R	GTTCTTCTCCCCTCATTTGTC
NtBPL -F	AGCAGTGGTACATCCCATAGT
NtBPL -R	CTCACTTCAAACTCTTGCCGT
NtCPS- F	TCAAAGAGAAGATGGATCTTGGG
NtCPS- R	AGGTGAAATCTGATCCTTGTTATC
NtKS -F	GTCATGGGCCAAGAATGGTG
NtKS-R	CGCTGAAAATATGATGCCCAC
NtKAO -F	TGGGGATGGTATAACCATTAATCAT
NtKAO -R	TGAATCTTCTGGTCATATTACAATG
NtGA3ox1 -F	GCCTTTTTTCGCTTCCAATGC
NtGA3ox1 -R	GCTTTTCCATTTCCCTTTCGT
NtGA3ox2 -F	GAGGAAGCTGGAAAACGACTT
NtGA3ox2 -R	AGCATCAGCCACATCAGTCTT
NtAS1- F	AGAGGAGCAGCGTCTTGTTAT
NtAS1- R	GACACTCCGCTCTTTCACAAT
NtAS2- F	TCTACCGTGGCTGATCCATAC
NtAS2- R	AGAAACCTCGAACCATCCTTG
NtER- F	AAACAGCTGGAACTGCTGAAC
NtER- R	CGCACATCAAAATACCACAGG
NtCRM- F	CTGTTCAGGCTAATGTGGTAT
NtCRM -R	GGGATGATGGACAAACAAGAG
NtYUCC5 -F	AGTTTCTCAGATAACGATTTCTTTGC
NtYUCC5 -R	GTCTCTTTGTAGGGTACTCAGGGTAG
For yeast one hybrid	
NtSVP -F	aagcagtggtatcaacgcagagtggccattatggcccATGGCTAGAGAGAAAATTCAGATCA
NtSVP -R	AGATCTCCGGCTCCGCCGGCTGTACACCTGAGTAGGGCAGCCCCAACTTG
CArG-box	GAGCTCGCAATTAAAAGACGCTATTAAAAGACGCTATTAAAAGACCTCGA
CArG-box(m)	GAGCTCGCAAGGAAAAGACGCTATTAAAAGACGCTATTAAAAGACCTCG
Probes for EMSA	
mu-pro*NtBPL* (+)	actcaatttttctatGGATGCATCCaaactaacttttcca
mu-pro*NtBPL* (-)	TGGAAAAGTTAGTTTGGATGCATCCATAGAAAAATTGAGT
wt-pro*NtBPL* (+)	ACTCAATTTT TCTATCAATT ATAAGAAACT AACTTTTCCA
wt-pro*NtBPL* (-)	TGGAAAAGTTAGTTTCTTATAATTGATAGAAAAATTGAGT
BamHI-*NtSVP* Fw	CGAggatccATGGCTAGAGAGAAAATTCAG
XhoII-*NtSVP* Rv	CGCctcgagACCTGAGTAGGGCAGCCC
For dual-luciferase assay	
Sal I-pro*NtBPL* -Fw	cacGTCGACgcttcgcttcttctatcaattc
Bam HI-pro*NtBPL* -Rv	cgcGGATCCTAATTACCCTAACAAGATATGGT
m1CArG-R	TACCTTGGAAAAGTTAGTTTATTATAATTTATAGAAAAATTGAG
m1CArG-F	ACTCAATTTTTCTATAAATTATAATAAACTAACTTTTCCAAGGT
m2CArG-R	ACCTTGGAAAAGTTAGTTTATTAGCATTTATAGAAAAATTGAGT
m2CArG-F	ACTCAATTTTTCTATAAATGCTAATAAACTAACTTTTCCAAGGT