SUPPLEMENTAL MATERIAL

Control of inflorescence architecture in tomato by BTB/POZ transcriptional regulators

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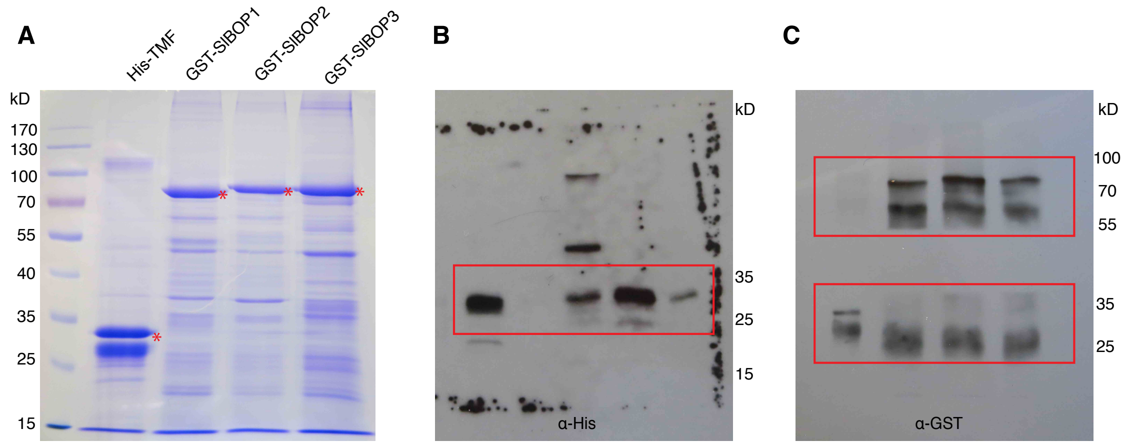
I. Supplemental Figures

II. Supplemental Tables



Supplemental Figure S1. *E.coli*. recombinantly expressed proteins and Western blots for GST-pull down assay. (*A*) Coomassie gel showing purified recombinant expressed His-TMF and GST-SlBOP1/2/3 proteins. (*B, C*) Un-cropped Western blotting images for pull down assay. Red stars note recombinant expressed proteins, Red rectangles indicate the cropped portions for preparing Fig. 1D.

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NPR1        MDTTIDGFADSYEISSTSFVATDNTDSSIVYLAAEQVLTGPDVSALQLLSNSFESVFDSP
AtBOP1      MSNTF----------------------------EESLKSMSLDYLNLLING--------
AtBOP2      -MSNL----------------------------EESLRSLSLDFLNLLING--------
SlBOP1      MSNNP----------------------------EDPLRSLSLDYLNLLING--------
SlBOP2      -MNTL----------------------------EDSLKTLSLDYLNLLING--------
SlBOP3      -MNTL----------------------------EDSLKTLSLDYLNLLING--------
              ..                              *: *   .:. *:** *.
                          BTB/POZ
NPR1        DDFYSDAKLVLSDGREVSFHRCVLSARSSFFKSALAAAKK--------EKDSNNTA----
AtBOP1      -QAFSDVTFSV-EGRLVHAHRCILAARSLFFRKFFCESDPSQ---P--GAEPANQT-GSG
AtBOP2      -QAFSDVTFSV-EGRLVHAHRCILAARSLFFRKFFCGTDSPQ---PVTGIDPTQHG-SVP
SlBOP1      -QAFSDVTFHV-EGHLVHAHRCVLAARSQFFRKFFCGPSS-----P--QSGP-QLG-SVN
SlBOP2      -QAFSDVTFSV-EGRLVHAHRCILAARSLVFRKFFCGPES-----P--GGGP-DPSVGFG
SlBOP3      -QAFSDVTFSV-EGRLIHAHRCILAARSLFFRKFFCGPESASVSGP--RLGPFGVGAGLA
             : :**..: : :*. :  ***:*:*** .*.. :. ..            .

NPR1        ----AVKLELKEIAKDYEVGFDSVVTVLAYVYSSRVRPPPKGV---SECADENCCHVACR
AtBOP1      AR----AAAVGGVIPVNSVGYEVFLLLLQFLYSGQVSIVPHKHEPRSNCGDRGCWHTHCT
AtBOP2      ASPTRGSTAPAGIIPVNSVGYEVFLLLLQFLYSGQVSIVPQKHEPRPNCGERGCWHTHCS
SlBOP1      GPRDTGSPASSVVIPVNSVGYEVFLLMMQFLYSGQVSIVPQKHEPRPNCGERGCWHTHCT
SlBOP2      SPRTSTTSSSQVVIPVNSVGYEVFLLMLQFLYSGQVSIVPQKHEPRPNCGERNCWHTHCT
SlBOP3      SSPRGTTSCSQVVIPVNTVGYEVFLLMLQFLYSGQVSIVPQKHEPRPNCGERNCWHTHCT
                        :     **:: .: :: ::**..*   *:     .:*.: .* *. *

NPR1        PAVDFMLEVLYLAFIFKIPELITLYQRHLLDVVDKVVIEDTLVILKLANICGKACMKLLD
AtBOP1      AAVDLSLDILAAARYFGVEQLALLTQKHLTSMVEKASIEDVMKVLIASR--KQDMHQLWT
AtBOP2      AAVDLALDTLAASRYFGVEQLALLTQKQLASMVEKASIEDVMKVLIASR--KQDMHQLWT
SlBOP1      SAVDLALDTLSAARSFGVEQLALLTQKQLAIMVEKASIEDVMRVLIASR--KQDMNQLWT
SlBOP2      SAVDLALDTLSAARSFGVEQLALLTQKQLTSMVEKTSIEDVMKVLVASR--KQDMPQLWT
SlBOP3      SAVDLALDTLSAARSFGVEQLALLTQKHLISMVEKASIEDVMKVLIASR--KQDMHQLWT
            .***: *:  *  :  * : :*  * *.:*  :*:*. ***.: :*  :.   :   :*

NPR1        RCKEIIVKSNVDMVSLEKSLPEELVKEIID--------------------RRKELGLEV
AtBOP1      TCSYLIAKSGLPQEILAKHLPIELVAKIEELRLKSSMPLRSLMP-------HHHDLTSTL
AtBOP2      TCSHLVAKSGLPPEILAKHLPIDVVTKIEELRLKSSIARRSLMPHN-----HHHDLSVAQ
SlBOP1      TCSHLVAKSGLPPEMLAKHLPIDVVAKIEELRLKSNLARRSLMPHHH----HHLDLSSSA
SlBOP2      TCSHLVAKSGLPPEILAKHLPIDVVAKIEEIRLKTSLARRSLISHH-----HQHDLSSTS
SlBOP3      TCSHLVAKSGLPPEILAKHLPIDVVAKIEDLRLKSSISRRSLIPHHHHNHQHQHQMSSNI
             *. ::.**.:    * * ** ::* :* :                     .. ::
                                            Ankyrin repeat
NPR1        PKVKKHVSNVHKALDSDDIELVKLLLKEDHTNLDDACALHFAVAYCNVKTATDLLKLDLA
AtBOP1      DLEDQKIRRMRRALDSSDVELVKLMVMGEGLNLDESLALIYAVENCSREVVKALLELGAA
AtBOP2      DLEDQKIRRMRRALDSSDVELVKLMVMGEGLNLDESLALHYAVESCSREVVKALLELGAA
SlBOP1      ELEDQKIRRMRRALDSSDVELVKLMVMGEGLNLDESIALHYAVENCSREVVKALLELGAA
SlBOP2      ELEDQKIRRMRRALDSSDVELVKLMVMGEGLNLDESIALHYAVENCSREVVKALLELGAA
SlBOP3      ELEDQKIRRMRRALDSSDVELVKLMVMGEGLNLDESLALHYAVENCSREVVKALLELGAA
               .::: .:..****.*:*****::  :  ***:: ** :**  *. :... **:*. *

NPR1        DVNHRN-PRGYTVLHVAAMRKEPQLILSLLEKGASASEATLEGRTALMIAKQATMAVECN
AtBOP1      DVNYPAGPTGKTALHIAAEMVSPDMVAVLLDHHADPNVQTVDGITPLDILRTLT------
AtBOP2      DVNYPAGPAGKTPLHIAAEMVSPDMVAVLLDHHADPNVRTVGGITPLDILRTLT------
SlBOP1      DVNFPAGPAGKTPLHIAAEMVSPDMVAVLLDHHADPNVRMLDGITPLDILRTLT------
SlBOP2      NVNHPAGPAGKTPLHIASEMVSPDMVAVLLDHHADPNVRTMDGITPLDILQTLT------
SlBOP3      DVNYQAGPSCKSPLHLAAEMVSPDMVAVLLDHHADPNTQTVDGITPLDILRTLT------
            :**.   *   : **:*:   .*:::  **:: *...   : * *.* * .  *

NPR1        NIPEQCKHSLKGRLCVEILEQEDKREQIPRDVPPSFAVAADELKMTLLDLENRVALAQRL
AtBOP1      -----SDFLFKG------------------AIPGLTHIEPNKLRLCL-------------
AtBOP2      -----SDFLFKG------------------AVPGLTHIEPNKLRLCL-------------
SlBOP1      -----SDFLFKG------------------TVPGHVHVEPNKLRLCL-------------
SlBOP2      -----SDFLFKG------------------AIPGLTHIEPNKLRLCL-------------
SlBOP3      -----SDFLFKG------------------AIPGLTHIEPNKLRLCL-------------
                 ... :**                   :*    : .::*.: *

NPR1        FPTEAQAAMEIAEMKGTCEFIVTSLEPDRLTGTKRTSPGVKIAPFRILEEHQSRLKALSK
AtBOP1      ------------ELVQSAALVISREEGNNN---SNDNNTMIYPRM--KDEHTS-------
AtBOP2      ------------ELVQSAAMVISREEGNNSNNQNNDNNTGIYPHM--NEEHNS-------
SlBOP1      ------------ELVQSAAMVISREEGSAN---IDLSSTNIYPPNNMSDDHTS-------
SlBOP2      ------------ELVQSAAMVISREEETTN---NVPSSTAIFQPIN-NEDHGS-------
SlBOP3      ------------ELVQSAAMVISREEGEAN---NNQSSENMYTHI--REDHSS-------
                        *:  :. ::::  *          .           ::* *

NPR1        TVELGKRFFPRCSAVLDQIMNCEDLTQLACGEDDTAEKRLQKKQRYMEIQETLKKAFSED
AtBOP1      ----------------------------------GSSLDSRLV----YLNLGATNR------
AtBOP2      ---------------------GSS-----GGSNNNLDSRLV----YLNLGAGTGQMGPGR
SlBOP1      ---------------------STST----SGTN-NIDSRMV----YLNLGGGVT------
SlBOP2      ---------------------STSNTTNVGGNNLNLDSRMV----YLNLGAGTSIAQQIG
SlBOP3      ---------------------STSS----GNNNLNLDSRMV----YLNLGANVANHHHQM
                                            . . :.*:     *:::

NPR1        NLELGNSSLTDSTSSTSKSTGGKRSNRKLSHRRR---
AtBOP1      DIGDDNSNQREGMNLHHHHH---DPSTMYHHHHH-HF
AtBOP2      DQGDDHNSQREGMSRHHHHHQ--DPSTMYHHHHQHHF
SlBOP1      ----NTSSTHD-----------HPSSMYHHSSH-EY
SlBOP2      CNRMTNQDDHDNSHNKQNRHGEFDPSSMYRPYS----
SlBOP3      ACKMNNNNDHDCSSSHNNQ----NPSTMYHHHHHSQY
                  ..  :             ..
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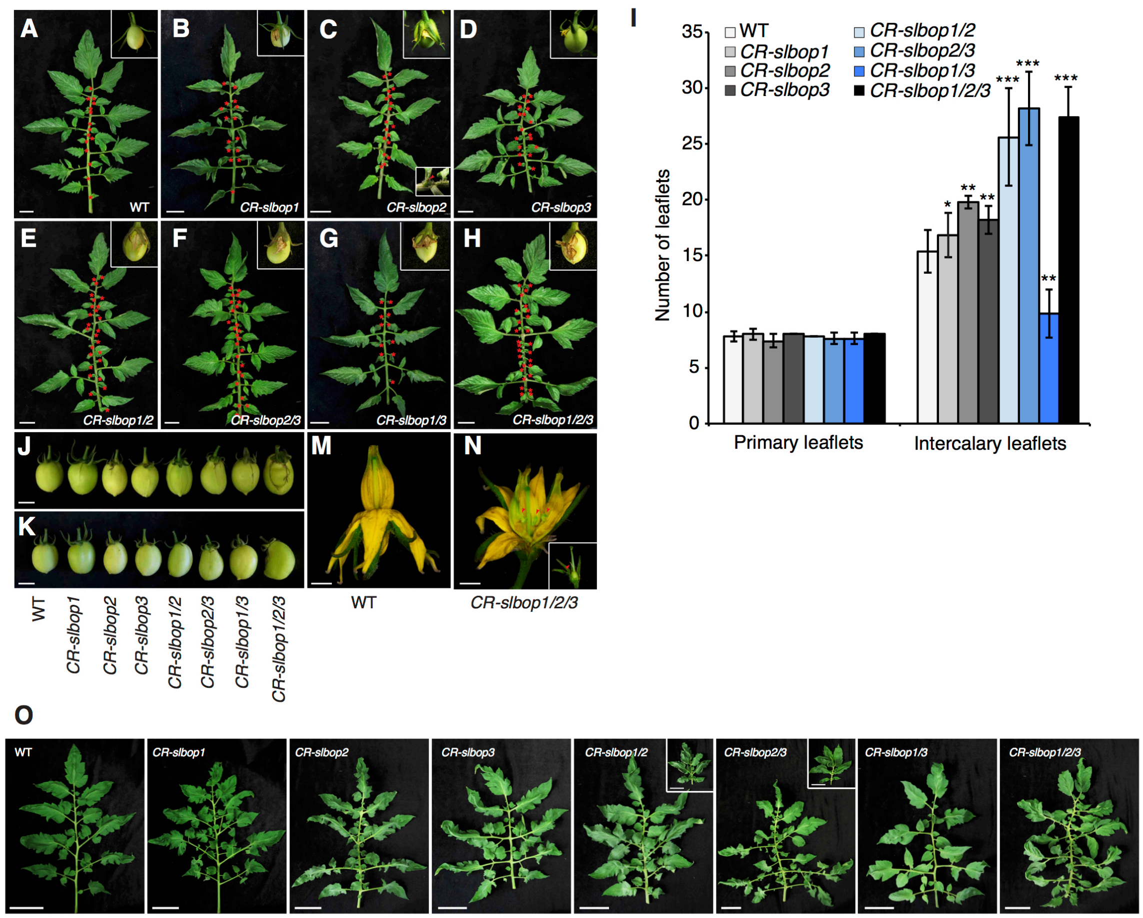
Supplemental Figure S2. Alignment of SlBOP1/2/3 with NPR1 and BOP1/2 proteins from *Arabidopsis* (AtBOP1/2). Single and double lines indicate the BTB/POZ and ankyrin repeat domains, respectively. Blue color highlights the two essential domains and two oxidized cysteine residues in NPR1 that are required for its SA-induced transcriptional regulation, which are absent in SlBOP proteins. Green color and arrow noted the cysteine residue in NPR1 that is critical for its S-nitrosylation and SA-induced oligomerization. Red color highlighted the four conserved cysteine residues in the BTB/POZ domain that are shared among all six BTB/POZ proteins and are important for oligomerization of NPR1. The highly conserved domain marked by the four cysteine residues is labeled by red rectangles.



Supplemental Figure S3. Pleiotropic vegetative and reproductive phenotypes of *CR-slbop* single and higher-order mutant plants**.** (*A-H*) Representative mature leaf from WT (*A*), single mutants of *CR-slbop1* (*B*), *CR-slbop2* (*C*), *CR-slbop3* (*D*), double mutants of *CR-slbop1/2* (*E*), *CR-slbop2/3* (*F*), *CR-slbop1/3* (*G*), and *CR-slbop1/2/3* triple mutants (*H*) showing altered leaf complexity and floral organ abscission defects (insets). Inset in (*C*) shows ectopic shoot generation on the rachis of a *CR-slbop2* leaf. Red asterisks indicate intercalary leaflets and floral abscission defects, respectively. (*I*) Quantification and statistical comparison of leaflets in WT and *CR-slbop* mutants. (*J, K*) Representative fruits from WT and *CR-slbop* mutants showing scars on fruits (*J*) and fruit shape phenotypes (*K*) in *CR-slbop* mutants. (*M, N*) Representative flowers from WT (*M*) and

CR-slbop1/2/3 triple mutants (*N*) showing ectopic twisted stigmas fused with stamens in *CR-slbop1/2/3* triple mutants. Inset shows ectopic stigma fused to the carpels of an ovary, explaining the origin of fruit scarring. (*O*) Representative leaves from single and higher order *CR-slbop* mutants grown under greenhouse conditions, where leaf phenotypes were often enhanced. For example, *CR-slbop1* leaves appeared larger than WT, primarily due to longer petiolules, and *CR-slbop2* leaves developed more intercalary leaflets that were frequently fused along the rachis. Insets show rare examples of more extreme leaves. Data are means (±s.d.); $n = 5$. A two-tailed, two-sample Student's *t* test was performed, and significant differences are represented by black asterisks: *$P < 0.05$, **$P < 0.01$, ***$P < 0.001$. Scale bars, 2 cm (*A-K*), 500 µm (*M, N*), 5 cm (*O*).

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SlBOP1          ATGAGTAATAATCCTGAAGATCCCTTAAGAAGTCTCTCTTTAGATTATCTCAATCTCCTC
SlBOP2          ---ATGAATACTCTTGAAGATTCCTTAAAAACTCTCTCTTTAGATTATCTAAATCTTCTC
SlBOP3          ---ATGAATACTCTTGAAGATTCCTTAAAAACTCTCTCTTTAGATTATCTAAATCTTCTC
                   *  **** ** ******* ****** ** ****************** ***** ***

SlBOP1          ATCAATGGTCAAGCTTTCAGTGATGTTACTTTTCATGTTGAAGGTCATTTAGTCCATGCT
SlBOP2          ATCAATGGTCAAGCTTTTAGTGATGTTACTTTTAGTGTTGAAGGTCGTTTAATACATGCT
SlBOP3          ATCAACGGTCAAGCTTTTAGTGATGTTACTTTTAGTGTTGAAGGTCGTTTAGTACATGCT
                ***** *********** ***************  *********** **** * ******

SlBOP1          CACCGTTGCGTCCTGGCAGCAAGGAGTCAATTCTTCAGAAAATTTTTCTGCGGGCCGAGC
SlBOP2          CATAGATGCATCTTAGCTGCTAGAAGTCTCTTCTTCCGCAAATTCTTCTGCGGGCCGGAG
SlBOP3          CATAGATGCATCTTAGCTGCTAGAAGTCTTGTGTTTAGAAAATTCTTCTGCGGGCCTGAG
                **  * *** ** * ** ** ** ****   * **  * ***** ***********

SlBOP1          TCTCCTCAGTCCGGCCCGCAACTCGGCT---------------------CGGTTAACGGG
SlBOP2          TCAGCATCTGTCTCCGGCCCGCGGTTGGGCCCGTTCGGCGTTGGCGCTGGATTAGCGTCG
SlBOP3          TCGCCTGGTGGCGGTCCAGAC-------------------CCTTCCGTGGCTTTGGAAGC
                **  *      *                                        *

SlBOP1          CCGAGAGATACTGGTTCACCAGCATCATCAGTAGTGATACCGGTGAATTCAGTAGGATAT
SlBOP2          TCGCCGAGGGGCACAACAAGTTGTTCACAAGTAGTAATACCTGTGAACACTGTAGGGTAT
SlBOP3          CCGCGGACTAGTACTACCAGTAGTTCACAGGTAGTAATACCTGTGAACTCGGTAGGGTAT
                 **             *       ***   ***** ***** *****  * ***** ***

SlBOP1          GAGGTGTTTTTATTGATGATGCAGTTTTTATATAGTGGACAAGTATCAATTGTACCGCAA
SlBOP2          GAGGTTTTTTTGTTGATGTTACAATTTTTGTATAGTGGACAAGTTTCAATTGTGCCACAA
SlBOP3          GAGGTTTTTTTGTTGATGTTACAATTTTTGTATAGTGGACAAGTTTCAATTGTGCCACAA
                ***** ***** ****** * ** ***** ************** ******** ** ***

SlBOP1          AAACATGAGCCAAGGCCAAATTGTGGAGAGAGAGGTTGTTGGCATACACATTGCACCTCA
SlBOP2          AAACATGAACCAAGGCCTAATTGTGGTGAAAGAAACTGTTGGCATACACATTGCACATCA
SlBOP3          AAACATGAACCAAGGCCTAATTGTGGTGAAAGAAACTGTTGGCATACACATTGCACATCA
                ******** ******** ******** ** ***   ******************** ***

SlBOP1          GCCGTTGATCTTGCACTTGATACACTCTCAGCCGCTAGATCTTTTGGTGTTGAACAACTT
SlBOP2          GCCGTTGATCTTGCACTGGATACACTCTCAGCCGCTAGATCTTTTGGAGTTGAACAACTT
SlBOP3          GCCGTTGATCTTGCACTTGATACACTCTCAGCCGCTAGATCTTTTGGTGTTGAACAACTT
                ***************** ***************************** ************

SlBOP1          GCTTTGCTCACTCAGAAGCAATTGGCAATCATGGTAGAAAAAGCTTCAATTGAGGATGTG
SlBOP2          GCTTTGCTTACTCAGAAGCATTTGATAAGCATGGTGGAAAAAGCTTCAATTGAGGATGTG
SlBOP3          GCTTTGCTTACTCAGAAGCAATTGACAAGCATGGTAGAGAAAACTTCAATTGAGGATGTG
                ******** *********** ***  ** ****** ** *** *****************

SlBOP1          ATGAGAGTTCTAATAGCATCAAGGAAGCAAGACATGAATCAACTATGGACTACGTGTTCA
SlBOP2          ATGAAAGTTTTAATAGCTTCAAGAAAACAAGACATGCATCAACTTTGGACTACTTGTTCT
SlBOP3          ATGAAAGTTTTAGTTGCTTCAAGAAAACAAGACATGCCTCAACTTTGGACTACTTGTTCT
                **** **** ** * ** ***** ** *********  ****** ******** *****

SlBOP1          CATTTGGTTGCAAAATCAGGTCTTCCACCCGAAATGTTGGCCAAACACCTCCCCATTGAT
SlBOP2          CATTTGGTTGCTAAATCAGGTCTCCCACCTGAAATCCTAGCCAAACACCTCCCTATTGAT
SlBOP3          CATTTGGTTGCAAAATCAGGCCTTCCACCTGAAATCCTAGCAAAACACCTTCCCATCGAC
                *********** ******** ** ***** *****  * ** ******** ** ** **

SlBOP1          GTTGTAGCCAAAATTGAAGAACTACGCCTCAAATCCAACCTAGCACGTCGATCCTTAATG
SlBOP2          GTTGTTGCCAAAATCGAAGACCTTCGTCTCAAATCCTCTATATCGAGAAGATCTTTAATC
SlBOP3          GTTGTCGCGAAAATCGAGGAAATTCGCCTAAAAACTTCATTAGCGCGAAGATCCTTGATC
                ***** ** ***** ** **  * ** ** *** *     ** *  *  **** ** **

SlBOP1          CCACATCATCATCACCACCTCGA------------CCTCAGCTCTTCAGCTGAGCTCGAG
SlBOP2          CCTCATCATCATCACAACCATCAACATCAACATCAAATGTCCTCGAACATTGAGCTCGAG
SlBOP3          TCTCACCATCACCAGCACGAC---------------CTAAGTTCGACCTCGGAGCTCGAG
                 * ** ***** **  **                   *    **       *********

SlBOP1          GACCAAAAAATCCGTAGGATGAGACGAGCCCTTGACTCATCGGACGTTGAACTTGT
SlBOP2          GACCAGAAGATCCGACGAATGAGACGAGCGCTCGATTCGTCGGACGTGGAATTAGT
SlBOP3          GACCAAAAGATCCGACGAATGAGACGAGCCCTAGACTCATCCGACGTGGAATTGGT
                ***** ** *****  * *********** ** ** ** ** ***** *** * **
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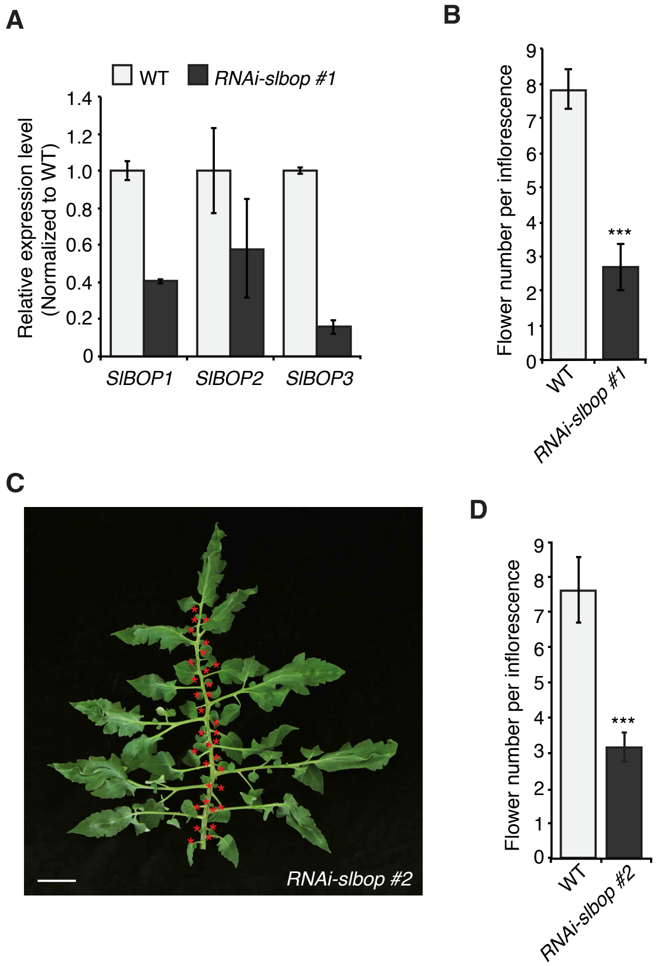
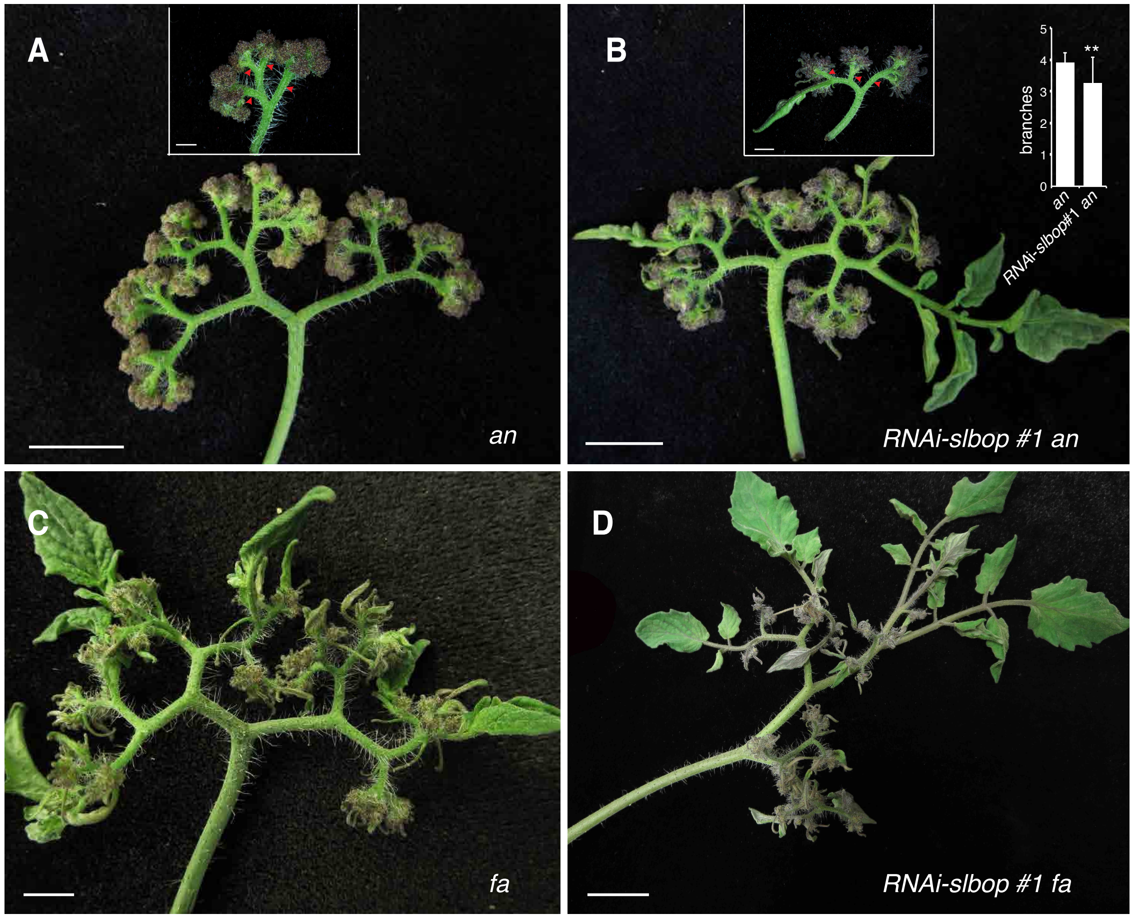
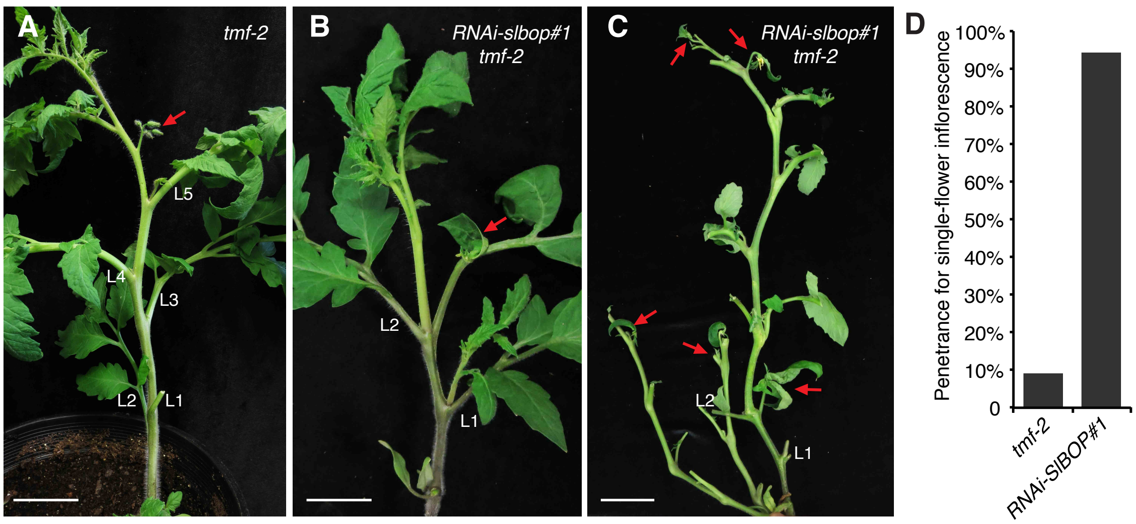
Supplemental Figure S4. Alignment of *SlBOP1, 2, 3* coding sequences used for generating the hairpin RNAi construct to knockdown *SlBOP1*, *2* and *3* transcript levels in *RNAi-slbop* plants. Note the stretches of nucleotide consensus among all three genes, indicated by red stars.



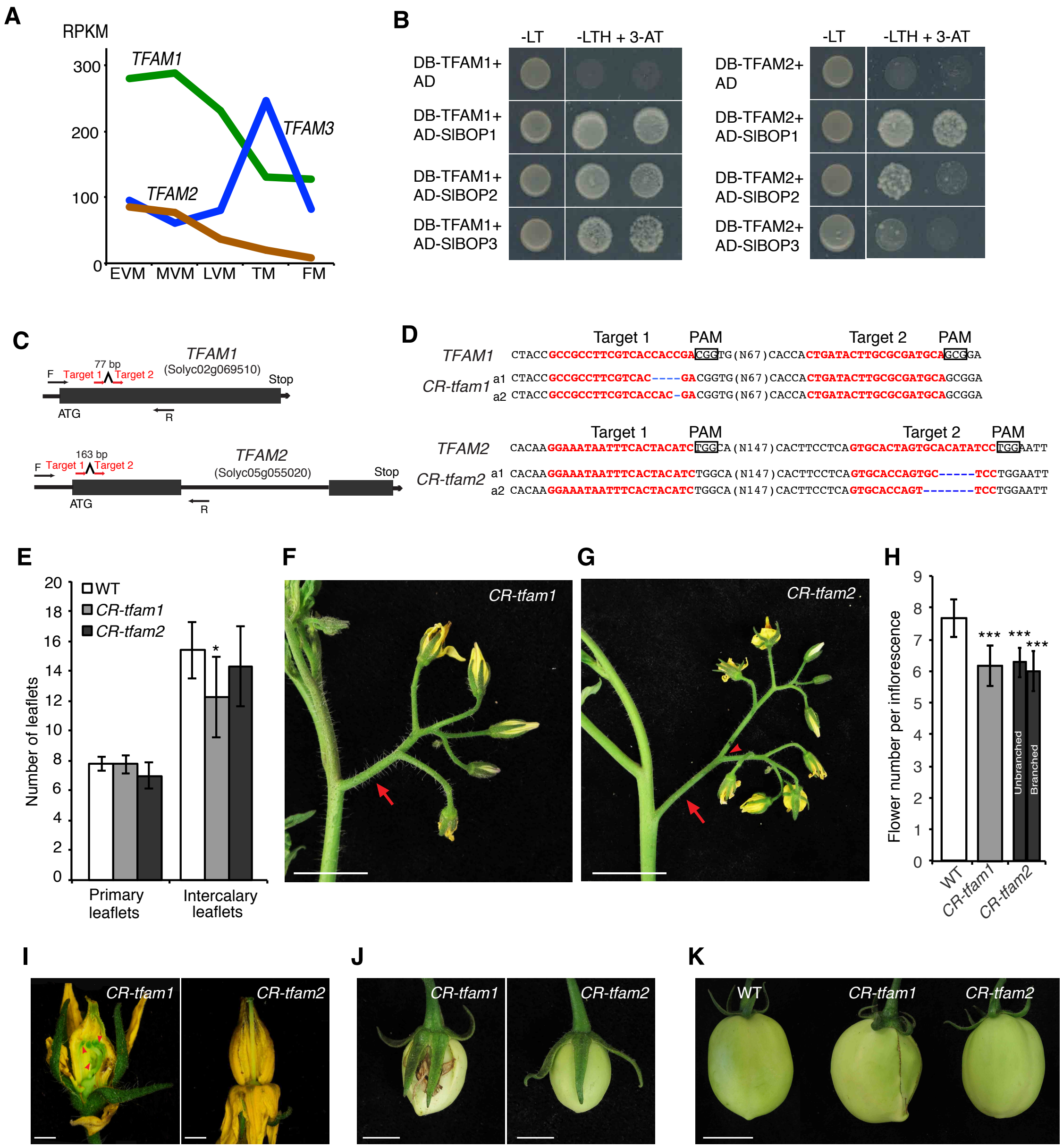
Supplemental Figure S5. Molecular and phenotypic analysis of *RNAi-slbop* plants. (*A*) qRT-PCR showing transcriptional knock-down of *SlBOP1*, *2* and *3* at the TM stage of *RNAi-slbop #1* used for genetic analyses shown in Figure 6. (*B*) Quantification and comparison of flowers per inflorescence in WT and *RNAi-slbop #1* plants. (*C*) Representative mature leaf from *RNAi-slbop #2* plants. (*D*) Quantification of flower number per inflorescence from an additional *RNAi-slbop* transgenic line. Data are means *(±s.d.)*; n = 3 (*A*), 12 (*B, D*). A two-tailed, two-sample Student's t test was performed, and significant differences are represented by black asterisks: ***$P < 0.001$. Scale bar, 5 cm.



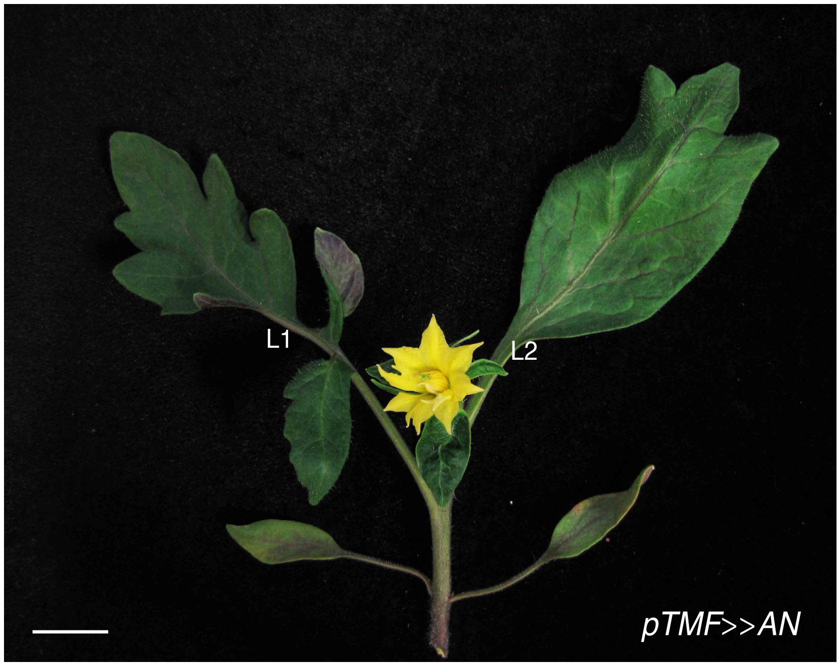
Supplemental Figure S6. Inflorescence phenotypes of *RNAi-slbop an* and *RNAi-slbop fa* mutant plants. (*A, B*) A representative inflorescence for *an* mutant (*A*) and *RNAi-slbop an* mutant plants (*B*). *RNAi-slbop an* plants branch less frequently than *an* mutants, as measured by the first branches, and thus SIMs, produced during early inflorescence development (insets and bar graph). (*C, D*) A highly branched leafy inflorescence from *fa* mutant (*C*) and *RNAi-slbop fa* mutant plants (*D*). Data are means (±s.d.); $n = 21$. A two-tailed, two-sample Student's t test was performed, and significant differences are represented by black asterisks: $^{**}P < 0.01$. Scale bars, 2 cm.



Supplemental Figure S7. *RNAi-slbop* enhances a weak allele of *tmf*. (*A*) Representative primary shoot of the weak *tmf-2* mutation that flowers early, but shows normal multi-flowered primary inflorescences. *(B)* Introducing *RNAi-slbop* into the *tmf-2* background by crossing results in earlier flowering compared to *tmf-2* alone, and nearly full penetrance for single-flower primary inflorescences that also exhibit enhanced leaf-like sepals. (*C*) A whole plant view of *RNAi-slbop tmf-2* plants showing enhanced early flowering and single-flower inflorescences in both primary and side shoots showing leaf-like sepals. Red arrows indicate inflorescences. Leaves were removed to show inflorescences. (*D*) Quantification and comparison of the penetrance for the single-flower primary inflorescence phenotype in *tmf-2* and *RNAi-slbop tmf-2* plants. L: leaf. Scale bars: 2.5 cm (*A*, *B*), 5 cm (*C*).



Supplemental Figure S8. CRISPR/Cas9-generated null mutations in *TFAM1* and *2* result in phenotypes that match multiple defects of *slbop* single mutants. (*A*) Normalized RNA-seq read counts for *TFAM1, 2,* and *3* in five stages of primary shoot meristem maturation showing dynamic expression of *TFAM1* and *TFAM2*, similar to *TMF* and *SlBOP1* and *2* (Fig.3). (*B*) Yeast two-hybrid assays showing SlBOP1, 2, and 3 interact with TFAM1 and TFAM2. (*C*) Schematics illustrating two sgRNAs (red arrows) targeting *TFAM1* and *TFAM2*. Black arrows represent PCR genotyping primers. (*D*) Sequences from homozygous T1 transgenic progeny plants lacking the *Cas9* transgene showing out-of-frame deletions (blue dashed lines) for *CR-tfam1* and 2*,* resulting in two independent null loss-of-function alleles (a1, a2). Red font highlights sgRNA targets, and black boxes indicate PAM sequences. (*E*) Quantification and statistical comparison of leaflets in WT and *CR-tfam1* and *2* mutants. (*F, G*) Representative inflorescences (red arrow) from *CR-tfam1* (*F*) and *CR-tfam2* mutants (*G*). Red arrowhead in (*G*) indicates a single branching event often observed in *CR-tfam2* mutants, similar to *CR-slbop2* mutants (Figure 4D). (*H*) Quantification and statistical comparison of flowers per inflorescence in WT and *CR-tfam1* and *2* mutants. Note that flower number for *CR-tfam2* plants was quantified as the flowers on each inflorescence branch from branched inflorescences, and from unbranched inflorescences separately. (*I*) Representative flowers from *CR-tfam1* (left), *CR-tfam2* (right) mutants showing ectopic twisted stigmas fused with stamens (arrowheads) in *CR-tfam1*. (*J, K*) Representative fruits from *CR-tfam1 and 2* showing floral organ abscission defects (*J*), scars on fruits, and altered fruit shape (*K*) in *CR-tfam1*, similar to *CR-slbop* single mutants (Supplemental Fig. S3). Scale bars, 2 cm (*F, G, K*), 500 μm (*I, J*). Data are means (±s.d.); n = 5-11 (*E*); n= 11-21 (*H*). A two-tailed, two-sample Student's t test was performed, and significant differences represented by black asterisks: *$P < 0.05$, ***$P < 0.001$.



Supplemental Figure S9. Driving expression of the flower specification gene *AN* in the earliest stage of meristem maturation using *TMF* promoter (Transactivation, LhG4, OP system) results in single-flower primary inflorescence after producing only two leaves. Scale bars, 2 cm.

	Guide RNA sequences		Genotyping primers	
Gene	**Target 1**	**Target 2**	**Forward**	**Reverse**
SlBOP1	ATTGGGCCGAGCTCTCCTCAGTC	ATTGTGATACCGGTGAATTCAGT	CACAAGACAAAACACCAACCA	GCTCATGTTTTTGCGGTACA
SlBOP2	ATTGGCCCGCGGTTGGGCCCGTT	ATTGTAATACCTGTGAACACTGT	GCCACTAACCTTTCTCCTATTG	GGCTGATGTGCAATGTGTATG
SlBOP3	ATTGGGCCTGAGTCGCCTGGTGG	ATTGGTAGTAATACCTGTGAACT	CACAAAATCATCTTCCACTATGTGA	TGCAATGTGTATGCCAACAG
TFAM1	ATTGCCGCCTTCGTCACCACCGA	ATTCTGATACTTGCGCGATGCA	AAAGTAACACAGCCATGTTAGACG	GCCGAAAAACGGACAATTAC
TFAM2	ATTGGAAATAATTTCACTACATC	ATTGTGCACTAGTGCACATATCC	TTTCCTCCCTATTTCAAGAATCA	TCCTTCAAAAATTACCACTTTATCC

Supplemental Table S1. Single guide RNA (sgRNA) sequences and genotyping primers of *CR-slbops* and *CR-tfams*.

Primer name	Primer Sequence 5' to 3'
SlBOP1-F	TGGCATCACTCCATTGGACA
SlBOP1-R	GATCAATGTTTGCGCTCCCT
SlBOP2-F	GGGTGAAGCGAATAACAATCAA
SlBOP2-R	TGCATGCCATTTGATGATGATG
SlBOP3-F	TCTTCCACCGCGATATTCCA
SlBOP3-R	TTCGTCATTCTGTTGCACCC
FA-F	CACTGCCTTGATGAGGATGC
FA-R	TCAGAATGGCACAGCTGTCG
AN-F	GAGCCTTGTTGAAGGGAATG
AN-R	CCTTGTCCATTCTCCACTTC
SlSEP3-F	CGGCAAACAACTCAAACTCA
SlSEP3-R	TGATAGGAAAACCATTGAGCA
FUL-F	AGAAAGCGCTCCAAGAACAA
FUL-R	CCGATCCATCTCTGTTCATTCC
S-F	TTCAACTGTTTCTCCTCTTGCT
S-R	CCTATCCCAACCTCAAAAGC

Supplemental Table S2. qRT-PCR primers used in this study.