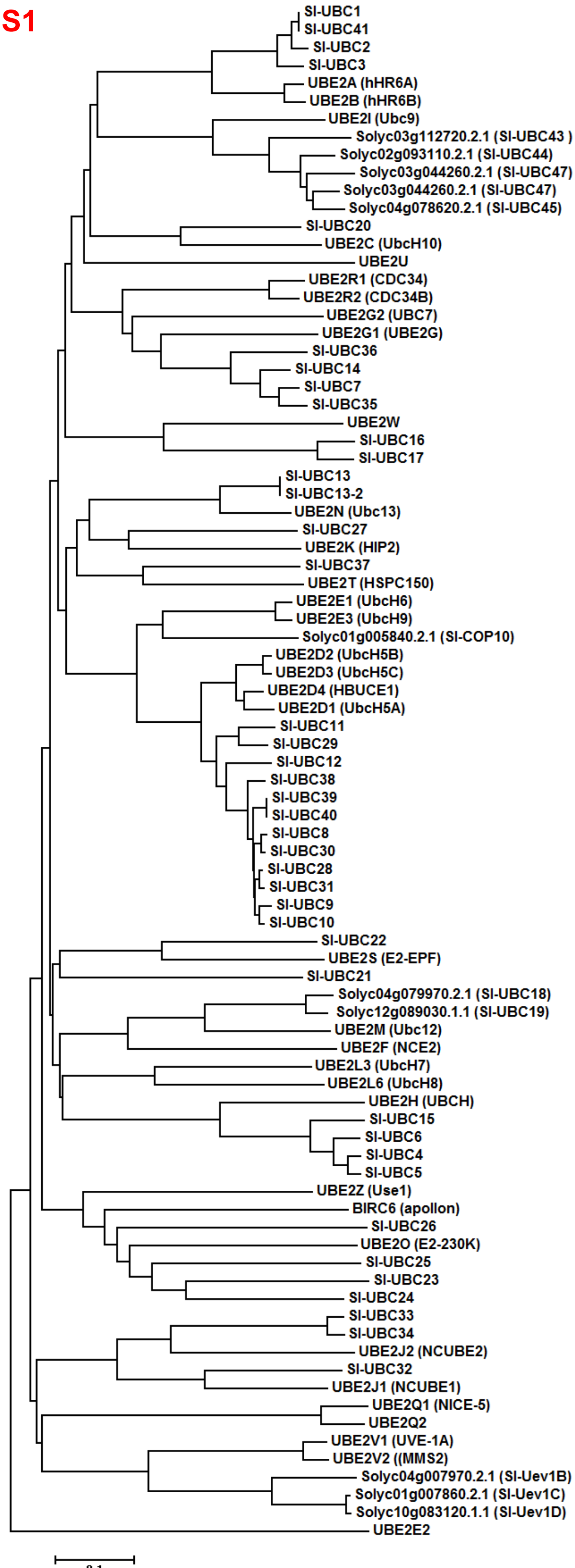
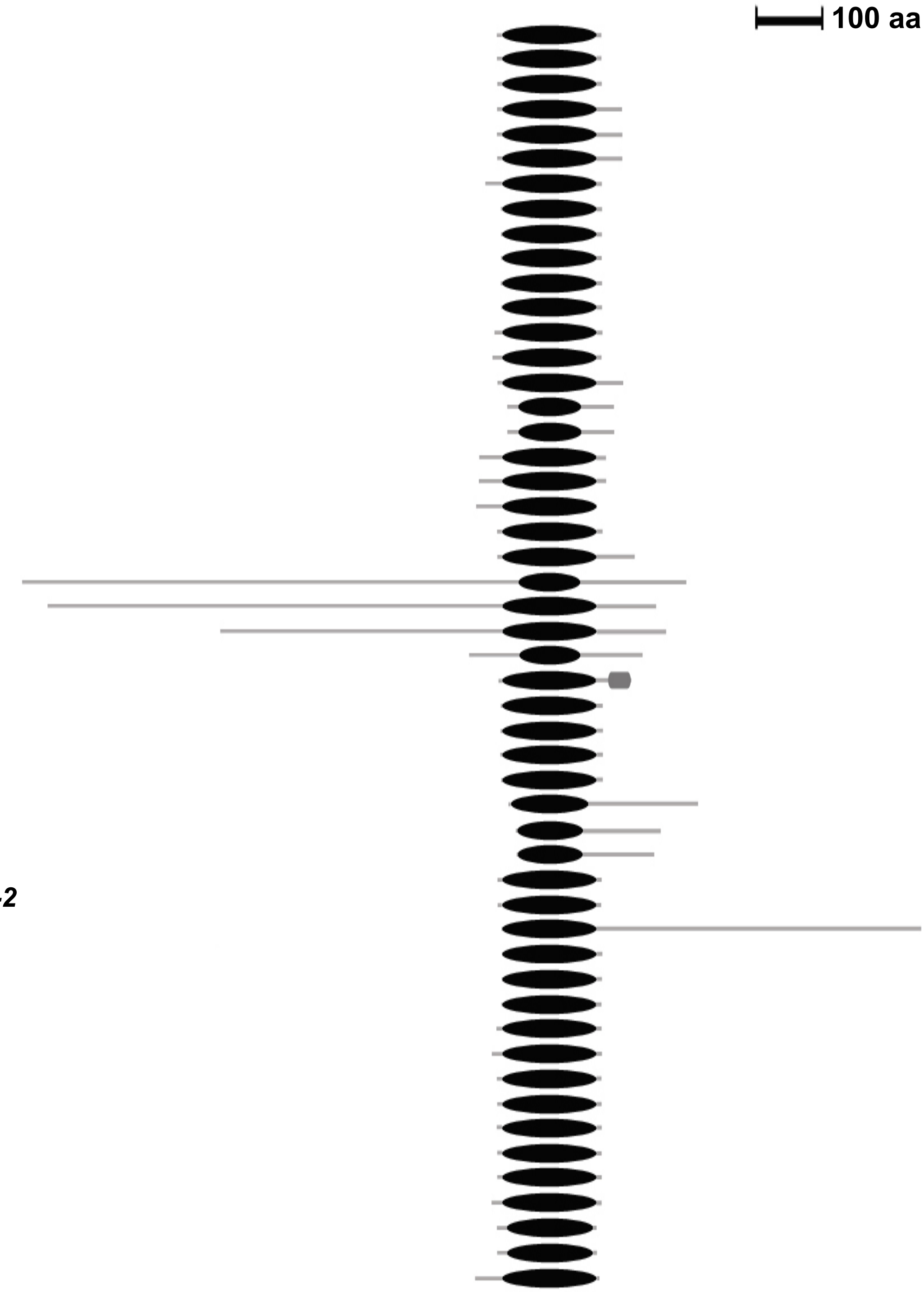
Supplemental Fig. S1



Supplemental Figure S1. Phylogeny of the human and tomato UBC domain-containing proteins. Phylogenetic analysis of the human and tomato UBC domain-containing proteins was performed using the same method and bootstrap trials as described for Figure 1. The phylogenetic tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. Accession numbers of the tomato and human UBC domain-containing proteins are shown in the Supplemental Table I.

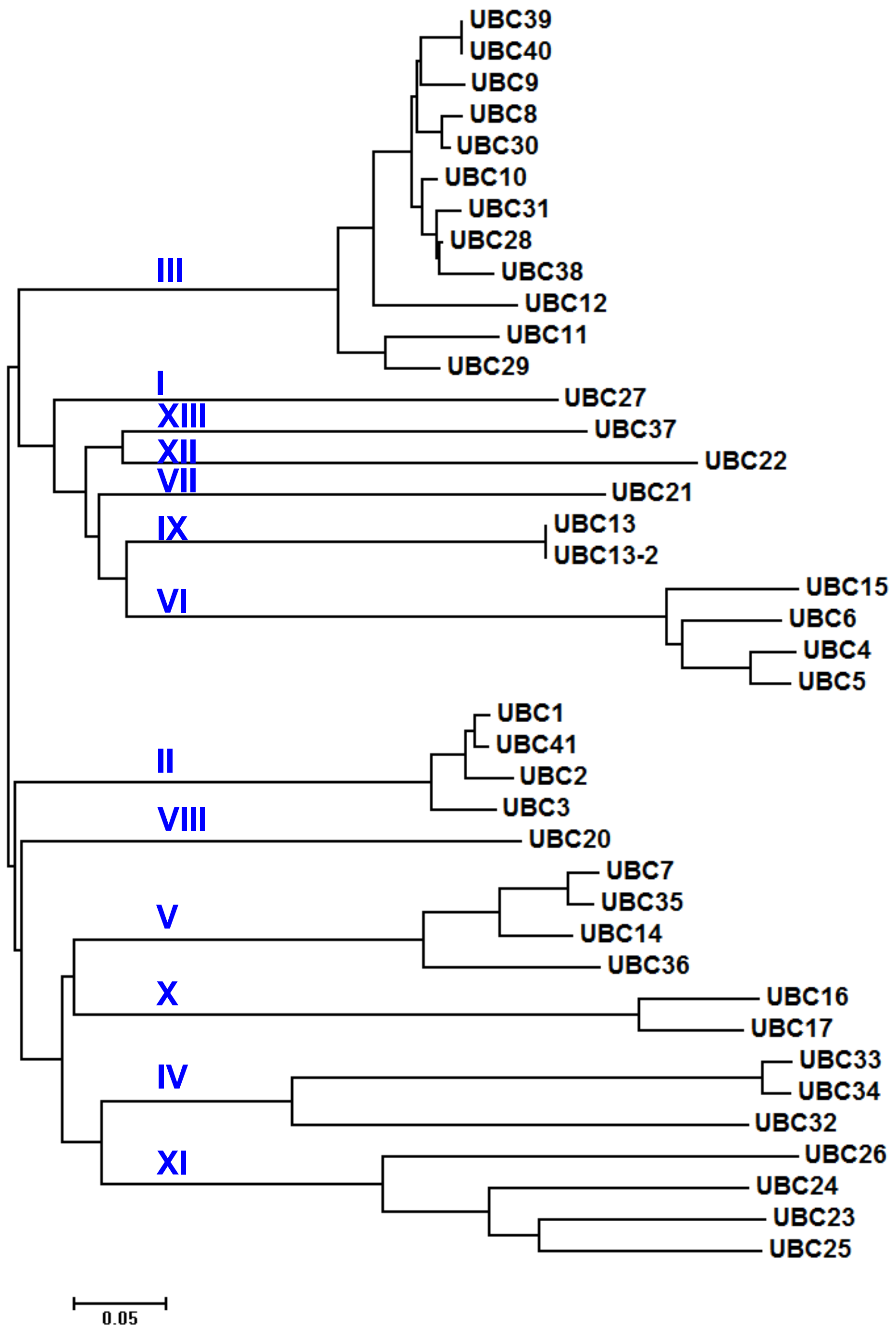
Supplemental Fig. S2

Chromosome locus	Gene name	Domain organization
Solyc06g070980.2.1	*UBC1*	
Solyc03g113100.2.1	*UBC2*	
Solyc02g067420.2.1	*UBC3*	
Solyc10g012240.2.1	*UBC4*	
Solyc01g094810.2.1	*UBC5*	
Solyc08g081270.2.1	UBC6	
Solyc05g054550.2.1	*UBC7*	
Solyc12g056100.1.1	*UBC8*	
Solyc08g008220.2.1	*UBC9*	
Solyc05g050230.2.1	*UBC10*	
Solyc03g033410.2.1	*UBC11*	
Solyc07g066080.2.1	*UBC12*	
Solyc05g054540.2.1	*UBC35*	
Solyc04g011430.2.1	*UBC14*	
Solyc11g071870.1.1	*UBC15*	
Solyc04g080810.2.1	*UBC16*	
Solyc02g084760.2.1	*UBC17*	
Solyc04g079970.2.1	*UBC18*	
Solyc12g089030.1.1	*UBC19*	
Solyc11g065190.1.1	*UBC20*	
Solyc11g071260.1.1	*UBC21*	
Solyc10g081160.1.1	*UBC22*	
Solyc01g111680.2.1	*UBC23*	
Solyc02g078210.2.1	*UBC24*	
Solyc10g007000.2.1	*UBC25*	
Solyc01g079290.1.1	*UBC26*	
Solyc06g072570.2.1	*UBC27*	
Solyc10g011740.2.1	*UBC28*	
Solyc02g083570.2.1	*UBC29*	
Solyc03g007470.2.1	*UBC30*	
Solyc01g095490.2.1	*UBC31*	
Solyc12g099310.1.1	*UBC32*	
Solyc03g123660.2.1	*UBC33*	
Solyc06g063100.2.1	*UBC34*	
Solyc07g062570.2.1	*UBC13*	
Solyc10g007260.2.1	*UBC13-2*	
Solyc07g024070.1.1	*UBC37*	
Solyc08g081950.2.1	*UBC38*	
Solyc06g082600.2.1	*UBC39*	
Solyc06g007510.2.1	*UBC40*	
Solyc02g087750.2.1	*UBC41*	
Solyc09g009720.1.1	*UBC36*	
Solyc03g112720.2.1	*UBC43*	
Solyc02g093110.2.1	*UBC44*	
Solyc04g078620.2.1	*UBC45*	
Solyc12g088680.1.1	*UBC46*	
Solyc03g044260.2.1	*UBC47*	
Solyc04g007970.2.1	*Uev1B*	
Solyc01g007860.2.1	*Uev1C*	
Solyc10g083120.1.1	*Uev1D*	
Solyc01g005840.2.1	*COP10*	



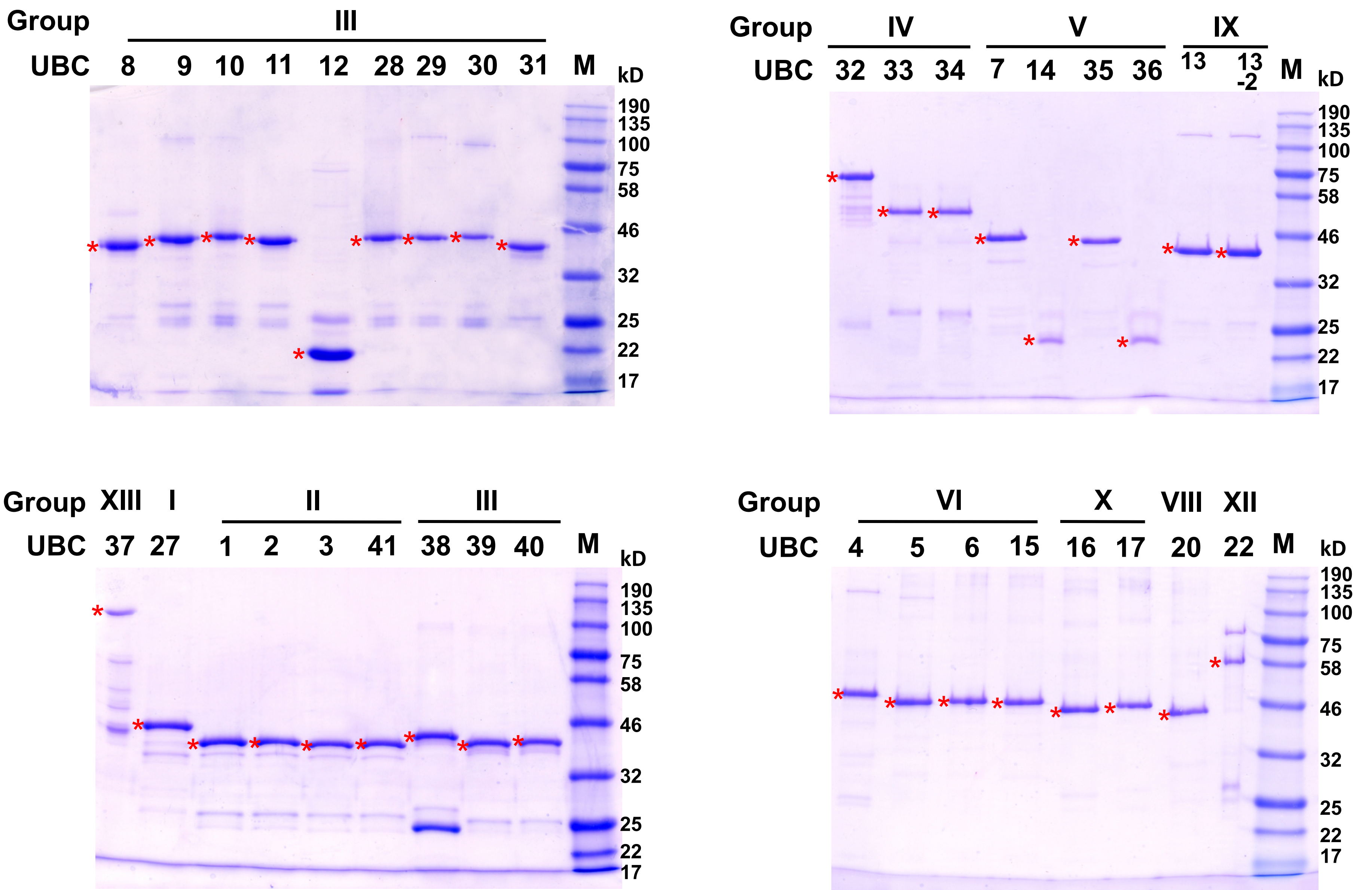
Supplemental Figure S2. Schematic representation of domain organization in the tomato UBC domain-containing proteins. The chromosomal loci and given gene names encoding the UBC domain-containing proteins are shown on the left side. The UBC fold and the extension of the UBC domain-containing proteins are represented as dark ellipse and light-gray line, respectively, both of which are drawn in scale to their length in the number of amino acids. The UBA domain of Sl-UBC27 is indicated as a dark-gray rectangle. The scale bar represents length of protein in amino acids.

Supplemental Fig. S3



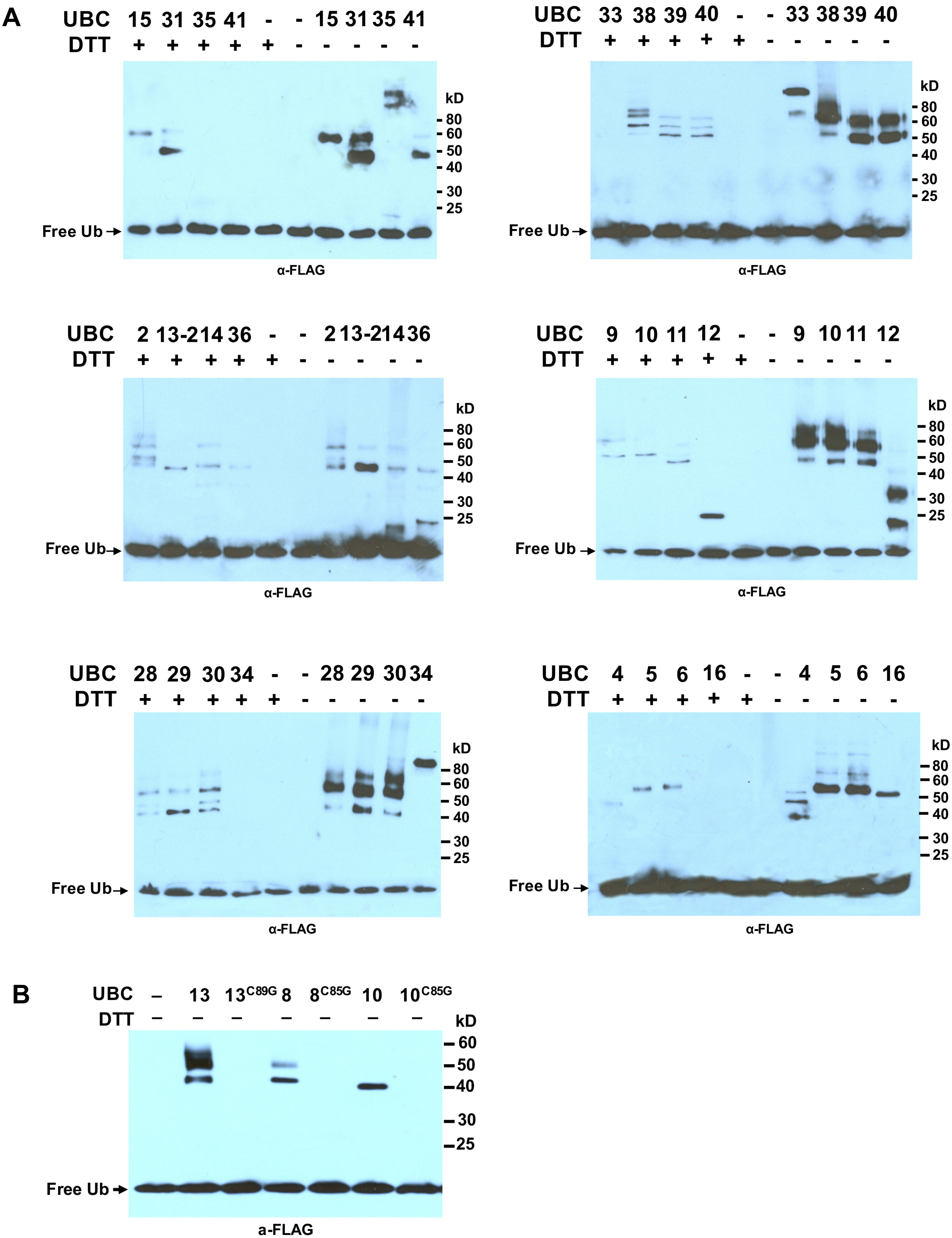
Supplemental Figure S3. The tomato ubiquitin E2 enzymes are classified into thirteen subgroups. Numbering of the groups was based on both the phylogenetic analysis of tomato ubiquitin E2s and the previously reported classification of Arabidopsis ubiquitin E2s (Zhao et al., 2013). Phylogenetic analysis of the forty tomato ubiquitin E2s using the amino acid sequence of core UBC domain was performed using the same method and bootstrap trials as described for Figure 1. The Roman numerals designate the different E2 groups.

Supplemental Fig. S4



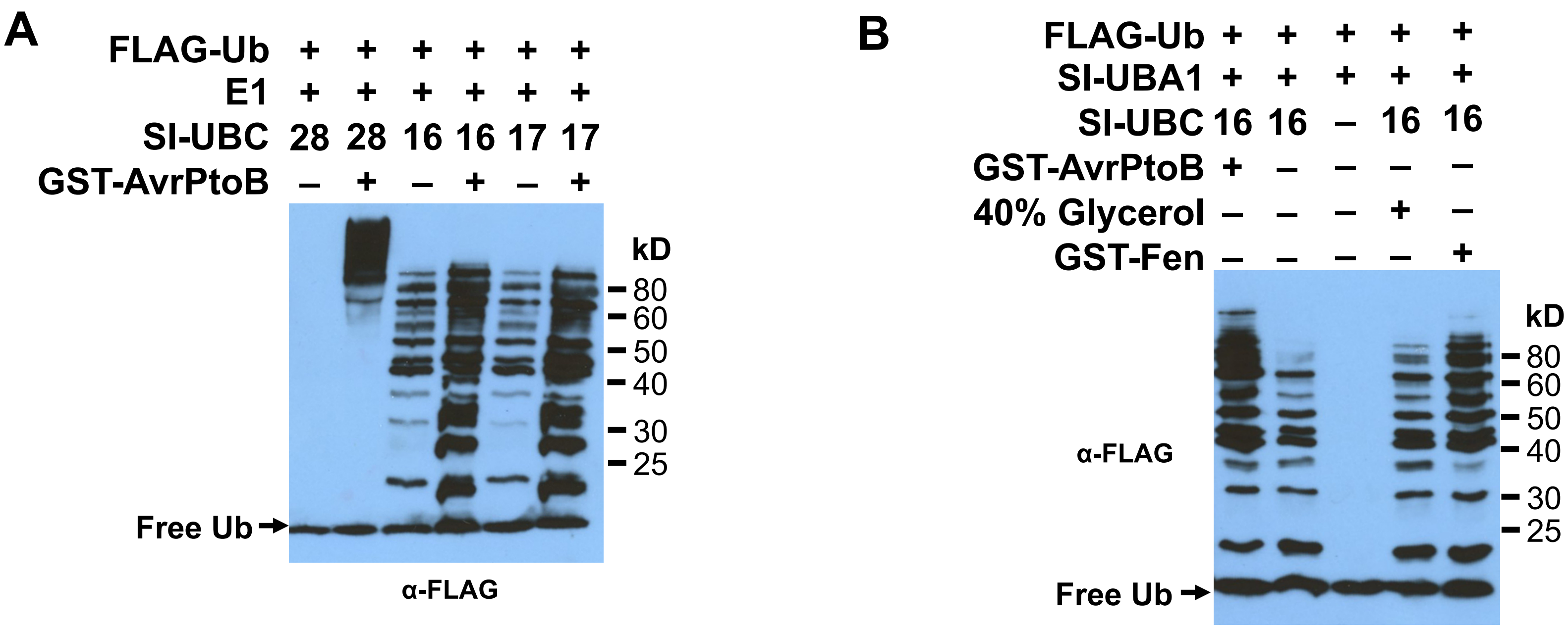
Supplemental Figure S4. Purified tomato E2 proteins as shown by SDS-PAGE. Approximately 3 μg of thirty-five purified E2 proteins were separated by 10% SDS-PAGE and stained with Coomassie Brilliant Blue. The Roman numerals designate the group into which the E2s are classified. M represents the molecular weight markers. The numbers on the right denote the molecular mass of marker proteins in kD. The asterisks denote the band of corresponding purified E2 proteins. Except for UBC12, 14 and 36 that are 6xHis-tagged, all E2s are fused to GST.

Supplemental Fig. S5



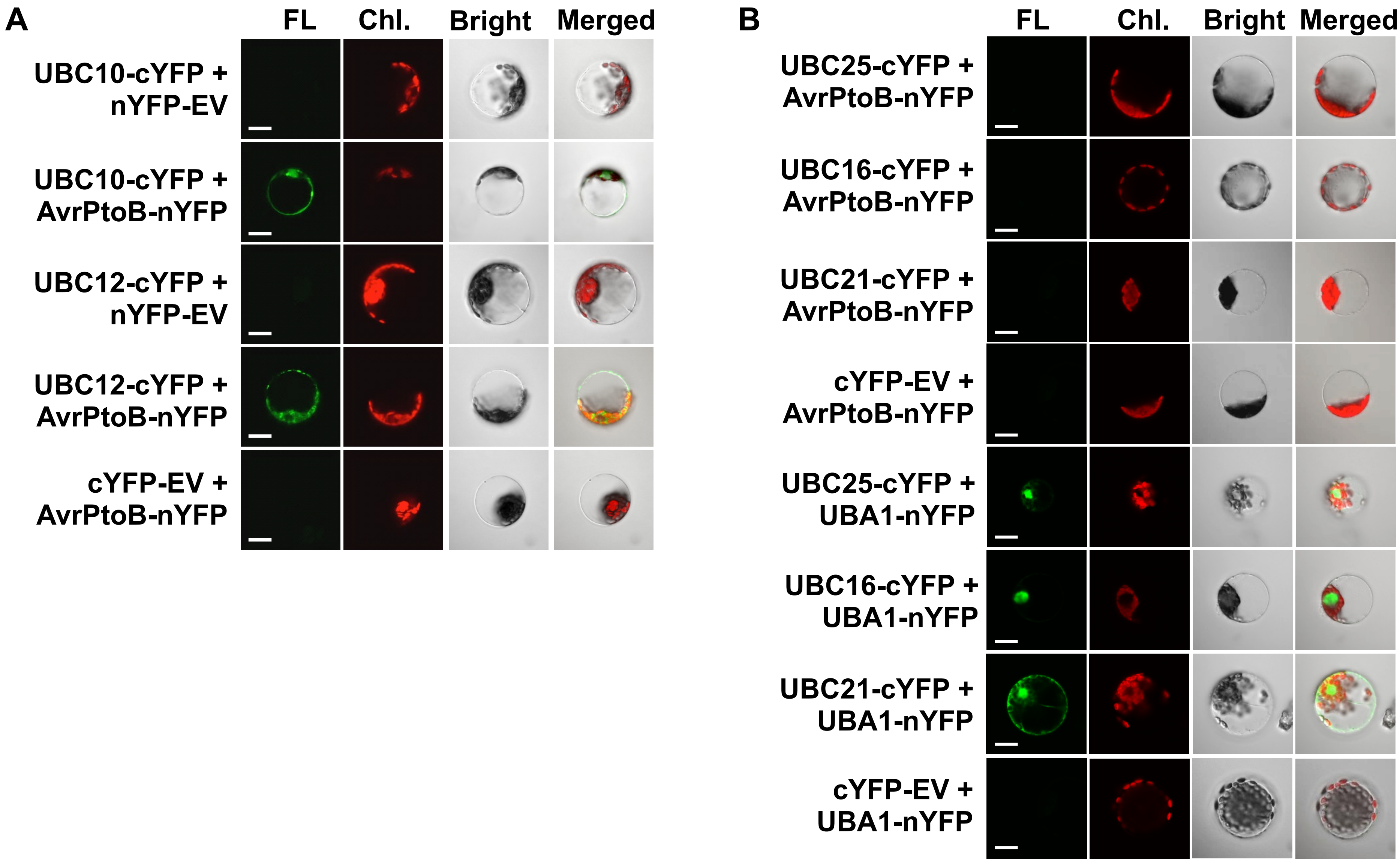
Supplemental Figure S5. Examination of the ubiquitin-conjugating activity of tomato E2s by thioester formation assay. (**A**) Anti-FLAG Western blots were performed following thioester assay of different tomato ubiquitin E2s. The reactions of the assay were terminated by adding SDS sample loading buffer in the presence of 100 mM DTT (DTT +) or 4M Urea (DTT −). The formation of DTT-sensitive ubiquitin adducts by tomato E2s is shown as charged E2. The numbers on the right denote the molecular mass of marker proteins in kD. The experiment was repeated two times with similar results. (**B**) Tomato E2 mutants in which the cysteine residue at the active site mutated lost ubiquitin-conjugating activity. Thioester assay was performed using wild type tomato ubiquitin E2s and E2 mutants. The reactions of the assay were terminated by adding SDS sample loading buffer in the presence of 4M Urea (DTT−). The numbers on the right denote the molecular mass of marker proteins in kD. The experiment was repeated two times with similar results.

Supplemental Fig. S6



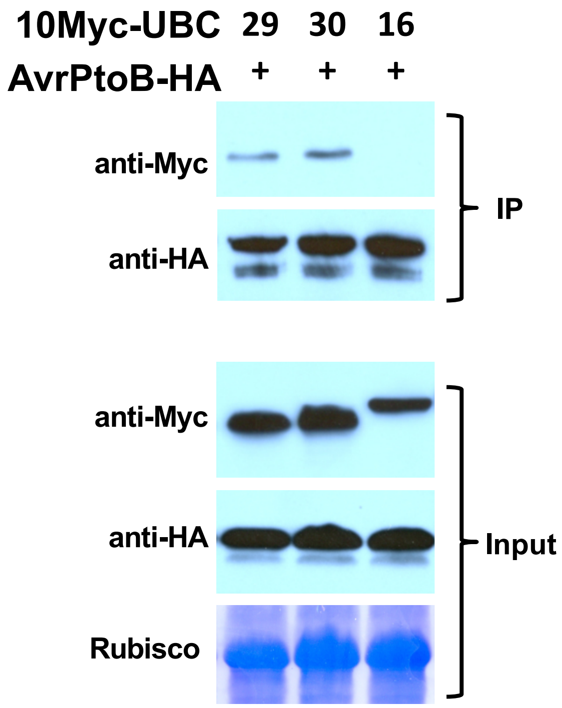
Supplemental Figure S6. AvrPtoB shows no specificity towards the tomato ubiquitin E2 enzymes Sl-UBC16, and 17. (**A**) AvrPtoB shows no specificity towards the tomato E2s Sl-UBC16 and 17 in *in vitro* ubiquitination assay. The E2s Sl-UBC16 and 17 demonstrated auto-ubiquitin-conjugation activity in the absence of an E3 ligase (lane 3 and 5). The presence of AvrPtoB enhanced their conjugation activity but did not alter the pattern of conjugates formed (lane 4 and 6). Sl-UBC28 was included as a control. The numbers on the top mark the lanes/reactions. (**B**) The enhancement of the conjugation activity of Sl-UBC16 by AvrPtoB is non-specific. The presence of a non-E3 ligase protein, GST-Fen also enhanced the auto-ubiquitin-conjugation activity of Sl-UBC16 (lane 5, as compared to lane 2), which is comparable to the effect of AvrPtoB (lane 1). In the absence of Sl-UBC16, no ubiquitin conjugation was observed (lane 3). The numbers on the right denote the molecular mass of marker proteins in kD.

Supplemental Fig. S7



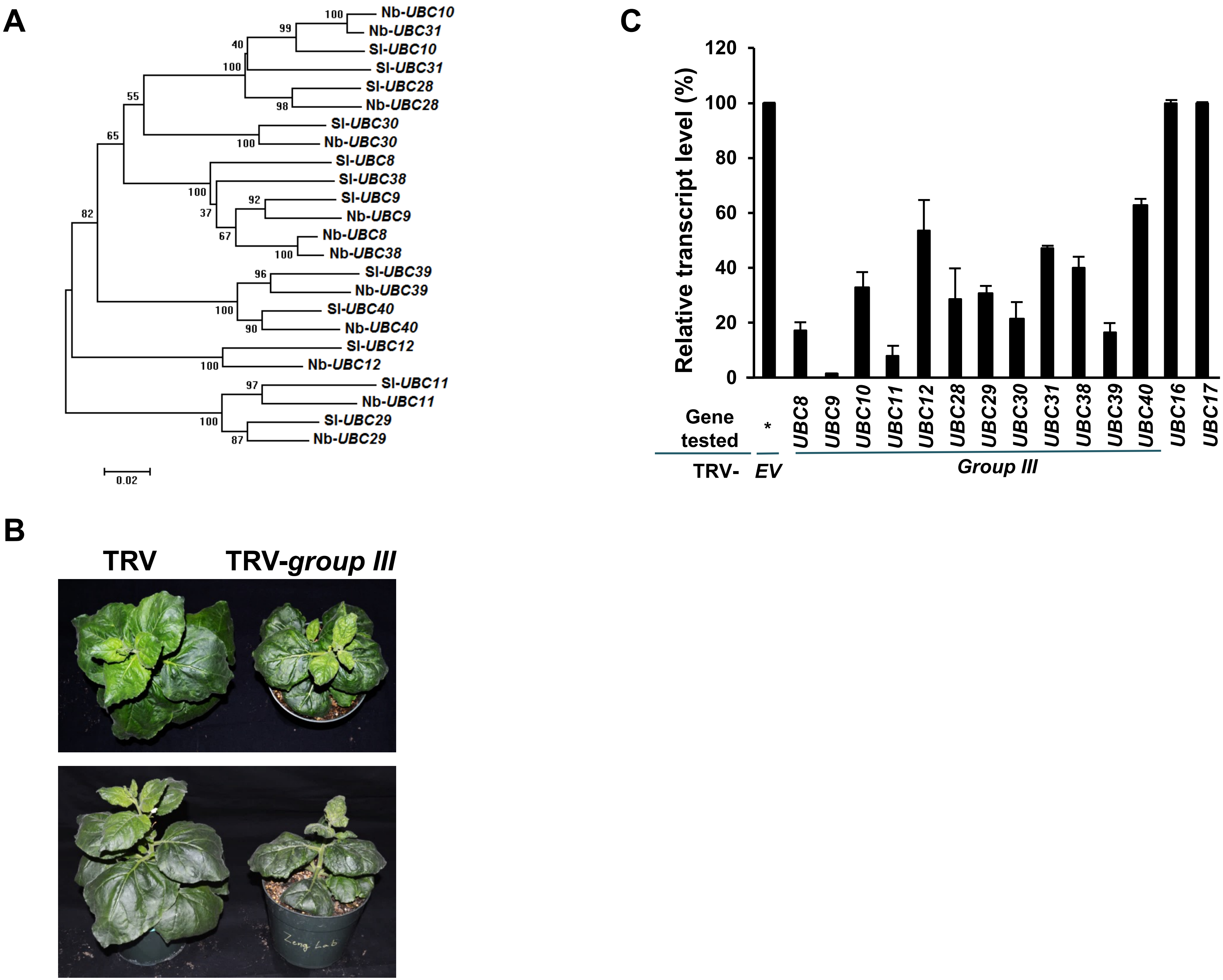
Supplemental Figure S7. AvrPtoB interacts with tomato group III E2 members but not with E2s from other groups in BiFC assays. (**A**) Members of the group III E2s interact with AvrPtoB in *N. benthamiana* protoplasts. (**B**) Members of group VII, X, and XI tomato E2 did not interact with AvrPtoB in the BiFC assay. Tomato ubiquitin E1 enzyme UBA1 was used as positive control. Different construct pairs were transiently co-expressed in protoplasts isolated from *N. benthamiana* leaves. Cells were viewed with a confocal microscope under bright or laser light to detect cells and green fluorescence, respectively. The empty vector expressing N- and C-terminus of YFP (nYFP-EV and cYFP-EV) were used as negative control. EV, empty vector; FL, fluorescence; Chl., chlorophyll autofluorescence; Bright, bright field image. Scale bar = 20 µm.

Supplemental Fig. S8



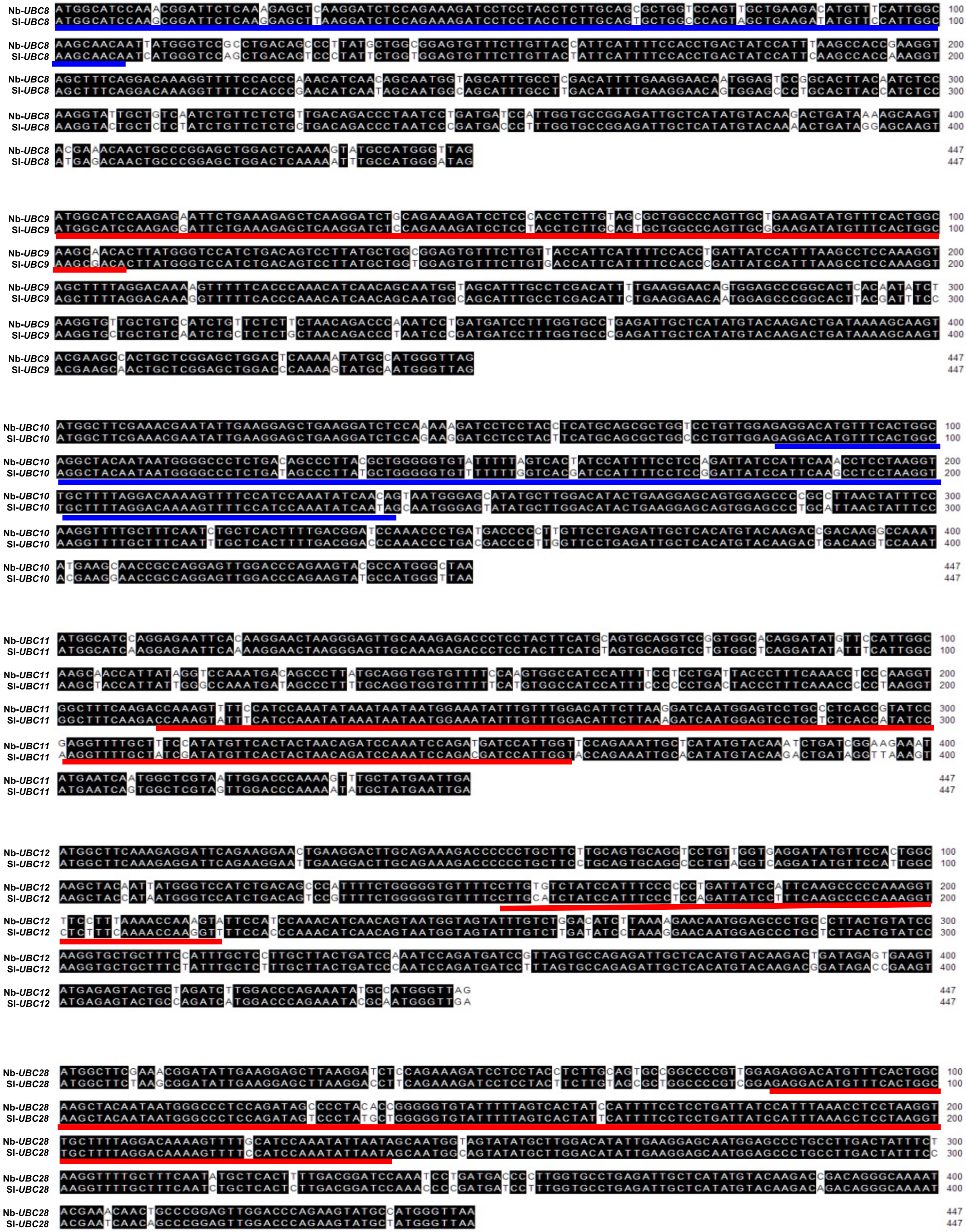
Supplemental Figure S8. Members of Group III E2 interacted with AvrPtoB in co-immunoprecipitation (Co-IP) assay. Group III members Ubc29 and 30 were randomly selected for the assay. AvrPtoB-HA and 10Myc-tagged E2s were transiently co-expressed in *N. benthamiana* leaves. The Co-IP was carried out with an anti-HA antibody (IP: anti-HA). The presence of corresponding proteins (Top panel) and the input (bottom panel) were detected by Western blot using anti-HA antibody for AvrPtoB-HA and anti-Myc antibody for 10Myc-tagged E2s.

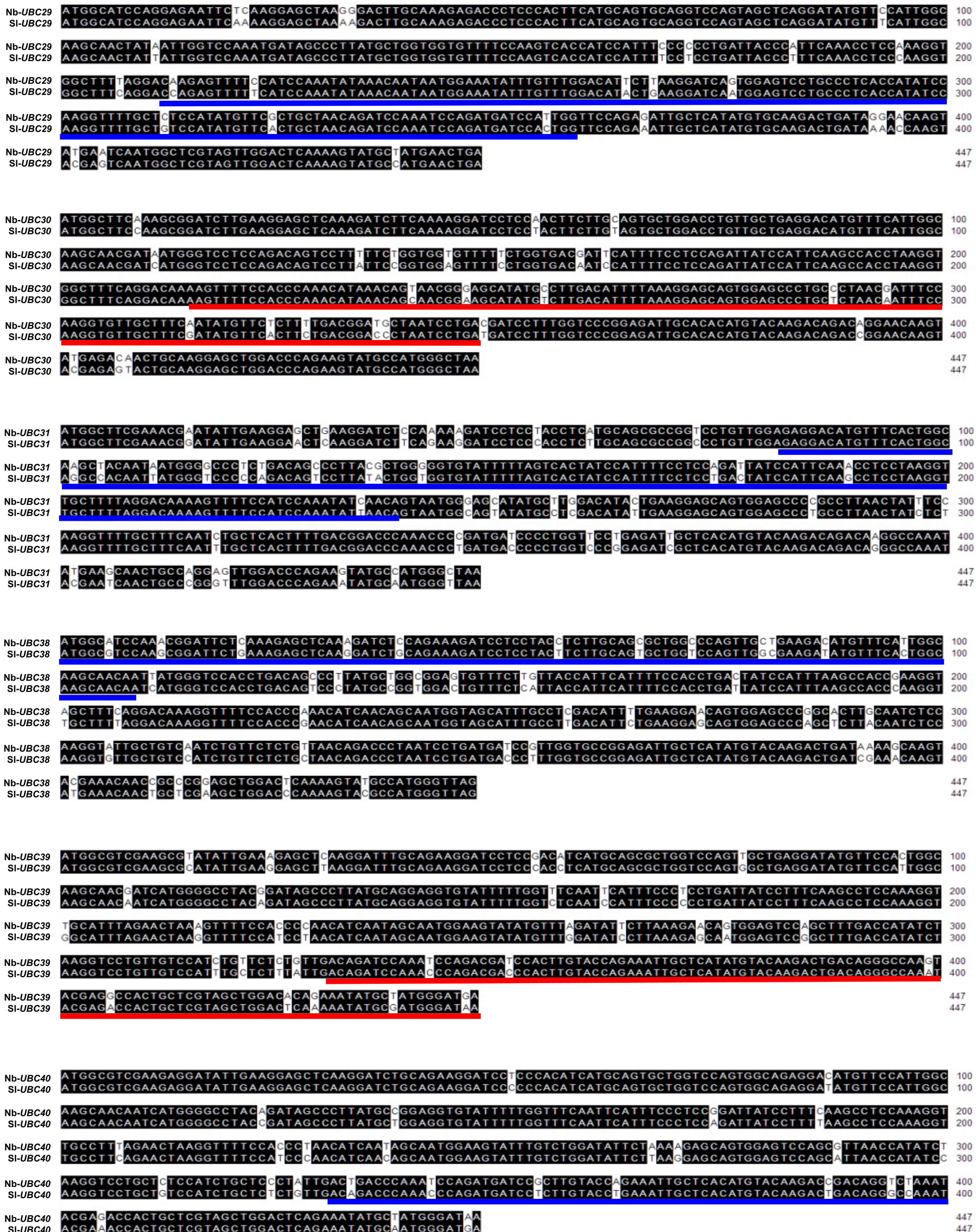
Supplemental Fig. S9



Supplemental Figure S9. Knocking down group III E2 genes in *N. benthamiana* by Virus-Induced Gene Silencing (VIGS). (**A**) The *N. benthamiana* group III E2 genes are highly homologous to their counterparts in tomato. The DNA sequences of *N. benthamiana* and tomato group III E2 genes' open reading frame (ORF) were used to generate the phylogenies. The same method and bootstrap trials as described for Figure 1 were employed for the phylogenetic analysis. The sequence IDs of the *N. benthamiana* ubiquitin E2 genes identified from the Sol Genomics Network database (SGN; http://solgenomics.net/) are shown in Supplemental Table I. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) is shown next to the branches. (**B**) Phenotypes of the *N. benthamiana* plants in which the group III E2 genes are silenced. The non-silenced TRV empty-vector (TRV) was used as a control. Photographs were taken 4 weeks after the approximately 3-week old seedlings were infiltrated with TRV or TRV-*group III* E2 genes constructs. The upper panel shows the top view of the plants while the lower panel shows the side view. (**C**) The group III ubiquitin E2 genes are efficiently and specifically silenced in *N. benthamiana* using the TRV vector. The transcript level of group III E2 genes and closely related E2 genes Nb-*UBC16* and *17* (outside the group III) in non-silenced TRV control (TRV) and group III ubiquitin E2 genes-silenced (TRV-*group III*) *N. benthamiana* plants was examined as described (Mural et al., 2013). Nb-*EF1α* was used as an internal reference for the determination of the amount of cDNA template to be used. Experiments in (**B**) and (**C**) were repeated at least two times with similar results.

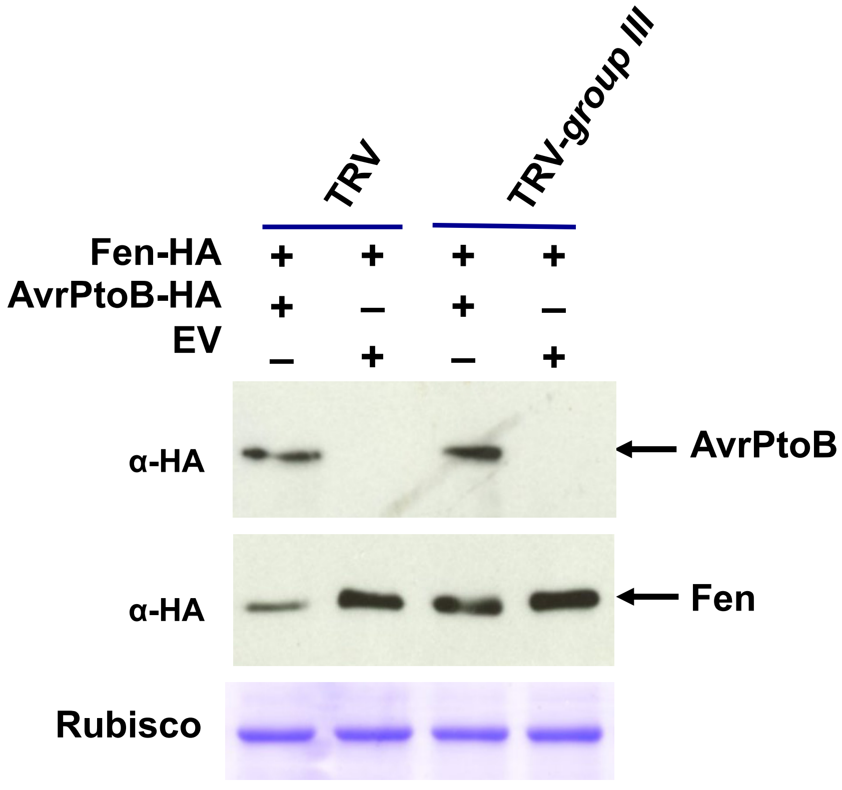
Supplemental Fig S10




Nb-UBC29
Sl-UBC29
Nb-UBC30
Sl-UBC30
Nb-UBC31
Sl-UBC31
Nb-UBC38
Sl-UBC38
Nb-UBC39
Sl-UBC39
Nb-UBC40
Sl-UBC40
100
200
300
400
447

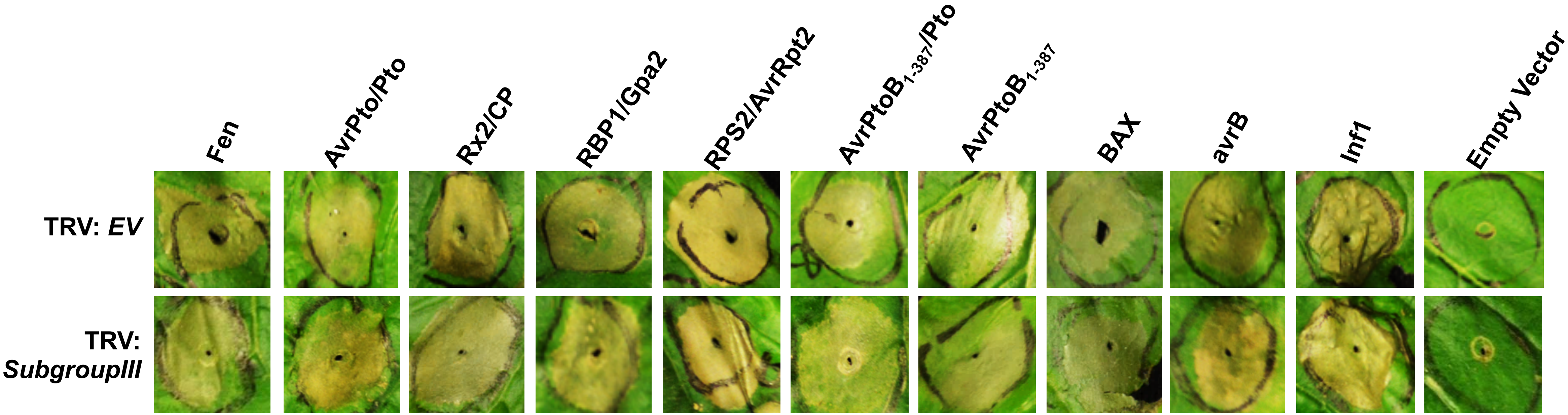
Supplemental Figure S10. Homologs of the group III E2 genes from *N. benthamiana* share high nucleotide sequence identity to their counterpart of tomato. The group III E2 genes from *N. benthamiana* were searched using the BLAST algorithm (Camacho et al., 2009) against the Sol Genomics Network (SGN, http://solgenomics.net) database with the counterparts from tomato as the queries. The Clustal X algorithm (Larkin et al., 2007) was used for the sequence alignment. The sequences underlined red were the fragments used for building the TRV-*group III* VIGS construct. The DNA fragment from Nb-*UBC9* was designed for silencing Nb-*UBC8*, *9* and *38*; the DNA fragment from Nb-*UBC28* was designed for silencing Nb-*UBC10*, *28* and *31*; the fragment from Nb-*UBC11* for silencing Nb-*UBC11* and *29*; and the fragment from Nb-*UBC39* for silencing Nb-*UBC39* and *40*. The blue-underlined were sequences that are putatively targeted in VIGS by the red-underlined sequence of the corresponding gene from the same clade in the phylogenetic tree (Figure S6A).

Supplemental Fig. S11



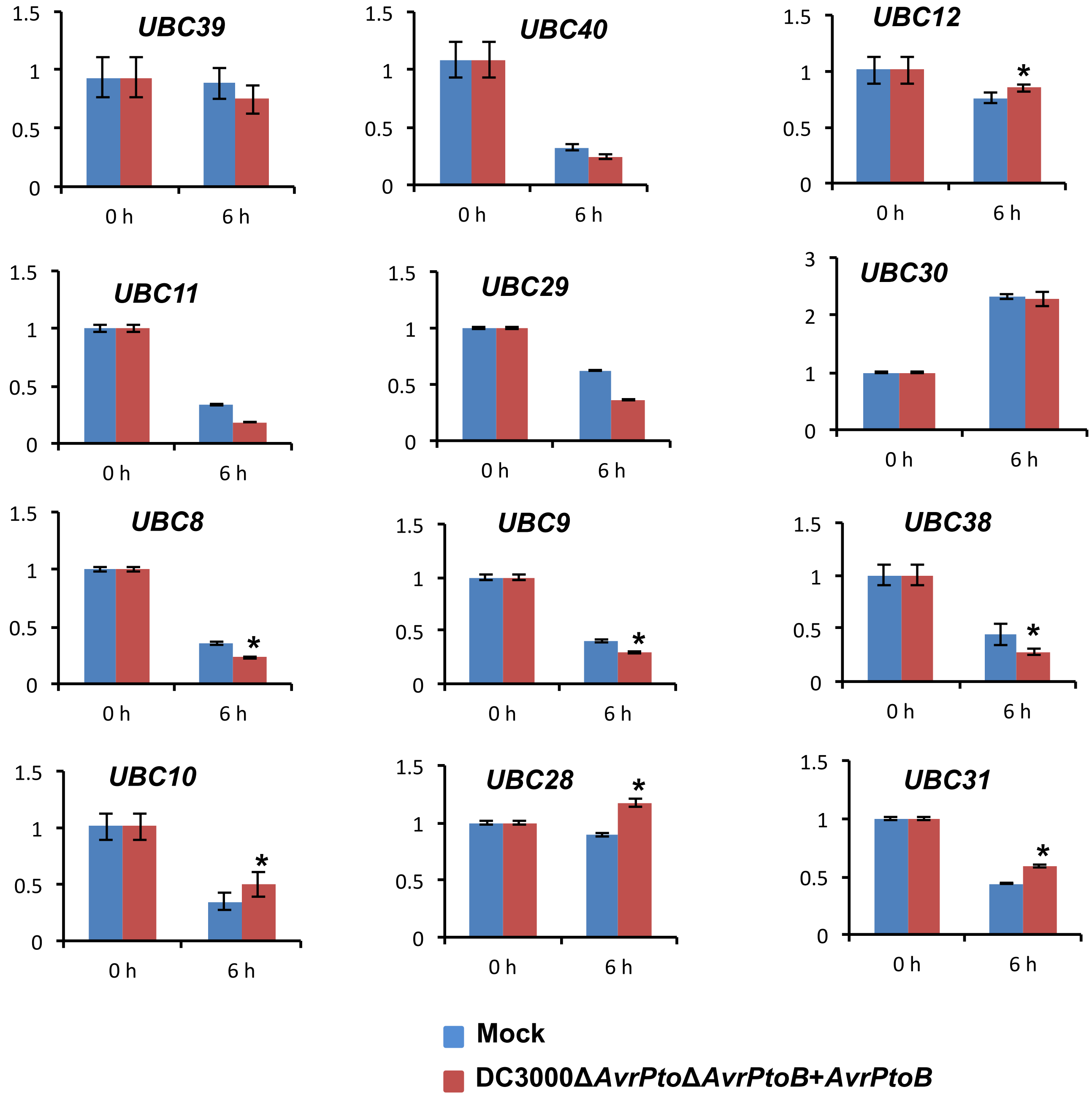
Supplemental Figure S11. Silencing group III E2 genes diminished AvrPtoB-promoted degradation of Fen in *N. benthamiana* protoplasts. AvrPtoB-HA and Fen-HA were transiently co-expressed in protoplasts isolated from leaves of group III E2 genes-silenced (TRV-*group III*) and non-silenced TRV control (TRV) *N. benthamiana* plants. Protoplasts were harvested and lysed at 21 h after the protoplasts were transfected with DNA carrying corresponding genes to isolate total proteins. Western blot was performed using anti-HA antibody for detecting Fen-HA and AvrPtoB-HA. Staining of ribulose 1, 5-bisphosphate carboxylase–oxygenase (Rubisco) subunits by Coomassie blue demonstrated equal loading. Marker minus (-) denotes the corresponding gene was not transfected into the protoplasts. The experiment was repeated two times with similar results.

Supplemental Fig S12



Supplemental Figure S12. Silencing group III E2 genes does not influence multiple ETI elicitors-triggered programmed cell death (PCD). *Agrobacterium*-mediated transient expression of Fen, AvrPto/Pto, Rx2/CP, RBP1/Gpa2, RPS2/AvrRpt2, AvrPtoB1-387/Pto, AvrPtoB1-387, BAX, avrB and Inf1 were performed in group III ubiquitin E2 genes-silenced (TRV-*group III*) and non-silenced TRV control (TRV) *N. benthamiana* plants as described (Mural et al., 2013). *Agrobacterium*-mediated transient expression of empty vector (EV) was performed as the control. At least three spots of infiltration were performed for each elicitor or EV on four different plants with typical result being shown. Photographs were taken on day four after infiltration. The experiment was repeated at least two times with similar results.

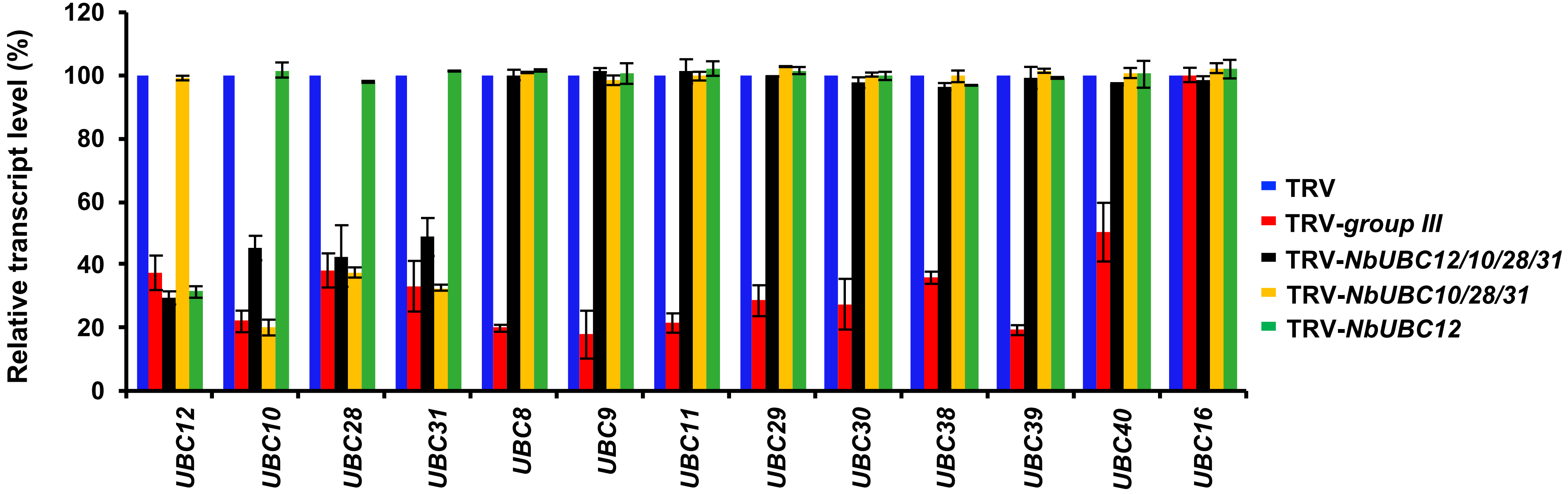
Supplemental Fig S13



Supplemental Figure S13. Effect of AvrPtoB on the expression of group III E2 genes. Real time PCR analysis of the transcript level of group III E2 genes in *Pst*- or mock-treated tomato plants. Tomato RG-pto11 plants were inoculated with *Pst* strain DC3000*ΔavrPtoΔavrPtoB* expressing AvrPtoB or mock (10 mM $MgCl_2$). Samples were collected at 0 and 6 h post inoculation. The Y-axis depicts the relative expression of the gene being tested. The experiment was performed using three technical repeats in each of the three biological replicates. Asterisks denote significant difference ($P<0.05$) in the expression of the E2 gene on the plants inoculated with *Pst* strain DC3000*ΔavrPtoΔavrPtoB* expressing AvrPtoB compared with mock inoculation.

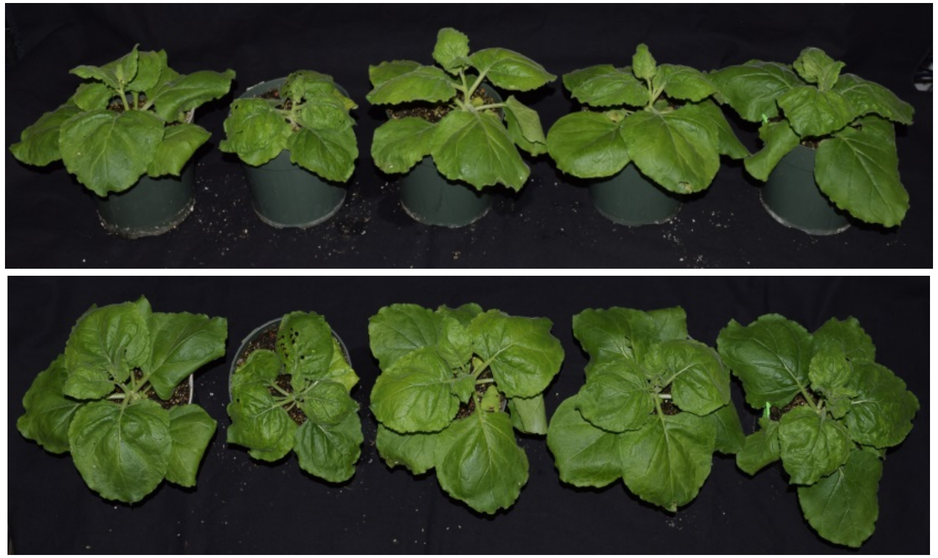
Supplemental Fig S14

A



B

1 2 3 4 5

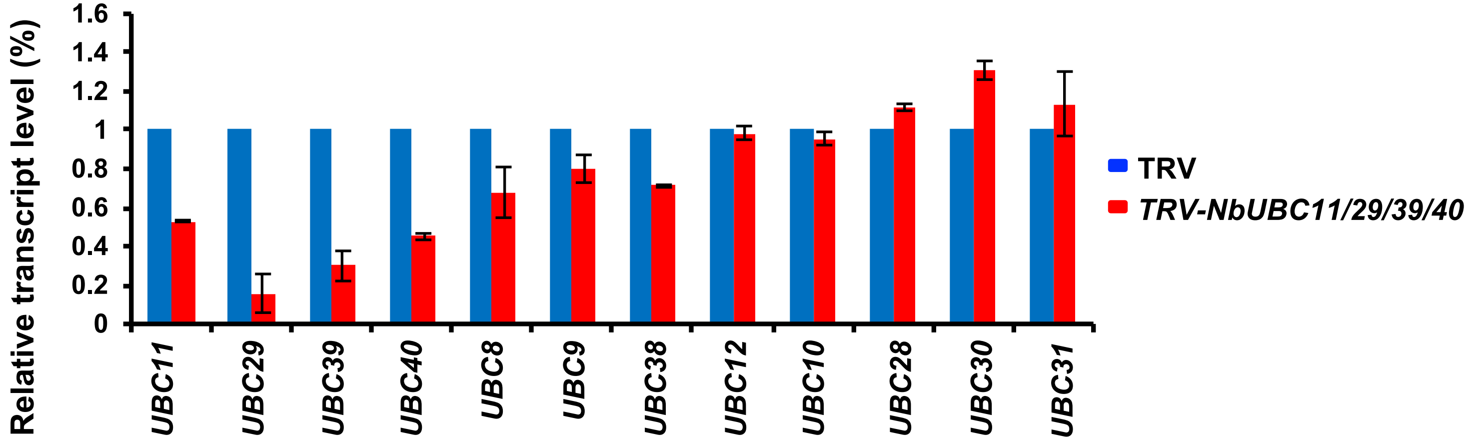


1. TRV
2. TRV-*group III*
3. TRV-*NbUBC12*
4. TRV-*NbUBC10/28/31*
5. TRV-*NbUBC12/10/28/31*

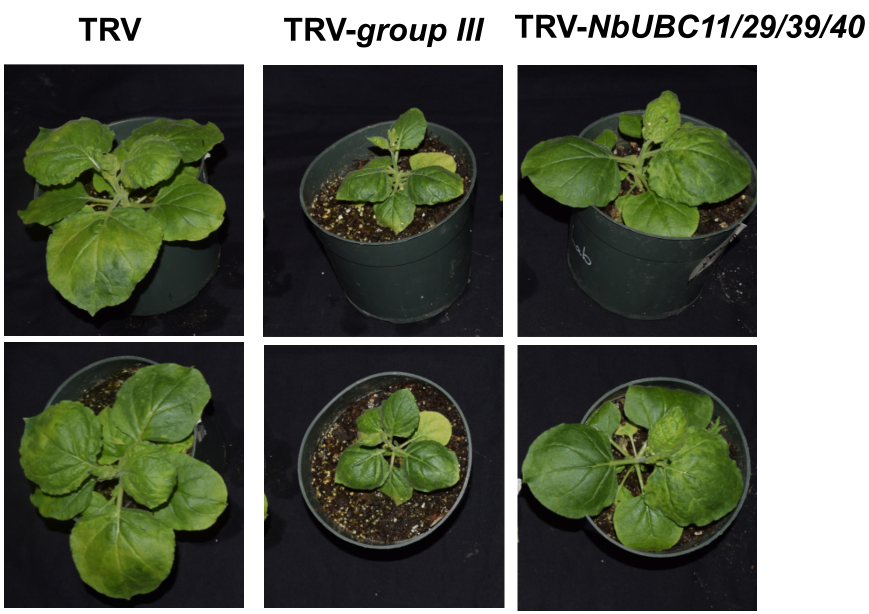
Supplemental Figure S14. Specific silencing of E2 genes Nb-*UBC12* alone, Nb-*UBC10*, *28* and *31* together, or Nb-*UBC10*, *12, 28* and *31* together in *N. benthamiana* by Virus-Induced Gene Silencing. (**A**) Nb-*UBC10*, *12*, *28* and *31* genes were specifically and efficiently silenced in *N. benthamiana* by TRV-based VIGS. The transcript level of group III E2 genes and a closely-related E2 gene outside the group III, Nb-*UBC16* in various VIGS-treated *N. benthamiana* plants was examined as described (Mural et al., 2013). Nb-*EF1α* was used as an internal reference for the determination of the amount of cDNA template to be used. The experiment was repeated three times with similar results. (**B**) Phenotypes of the *N. benthamiana* plants in which Nb-*UBC12* alone, three E2 genes Nb-*UBC10*, *28* and *31*, or Nb-*UBC10, 12*, *28* and *31* were specifically silenced. The non-silenced TRV-infected plant and *group III*-silenced plant were included as control. Photographs were taken 4 weeks after the ~ 3-week-old seedlings were infiltrated with TRV vector-based VIGS constructs. The upper panel shows the side view of the plants while the lower panel shows the top view.

Supplemental Fig S15

A

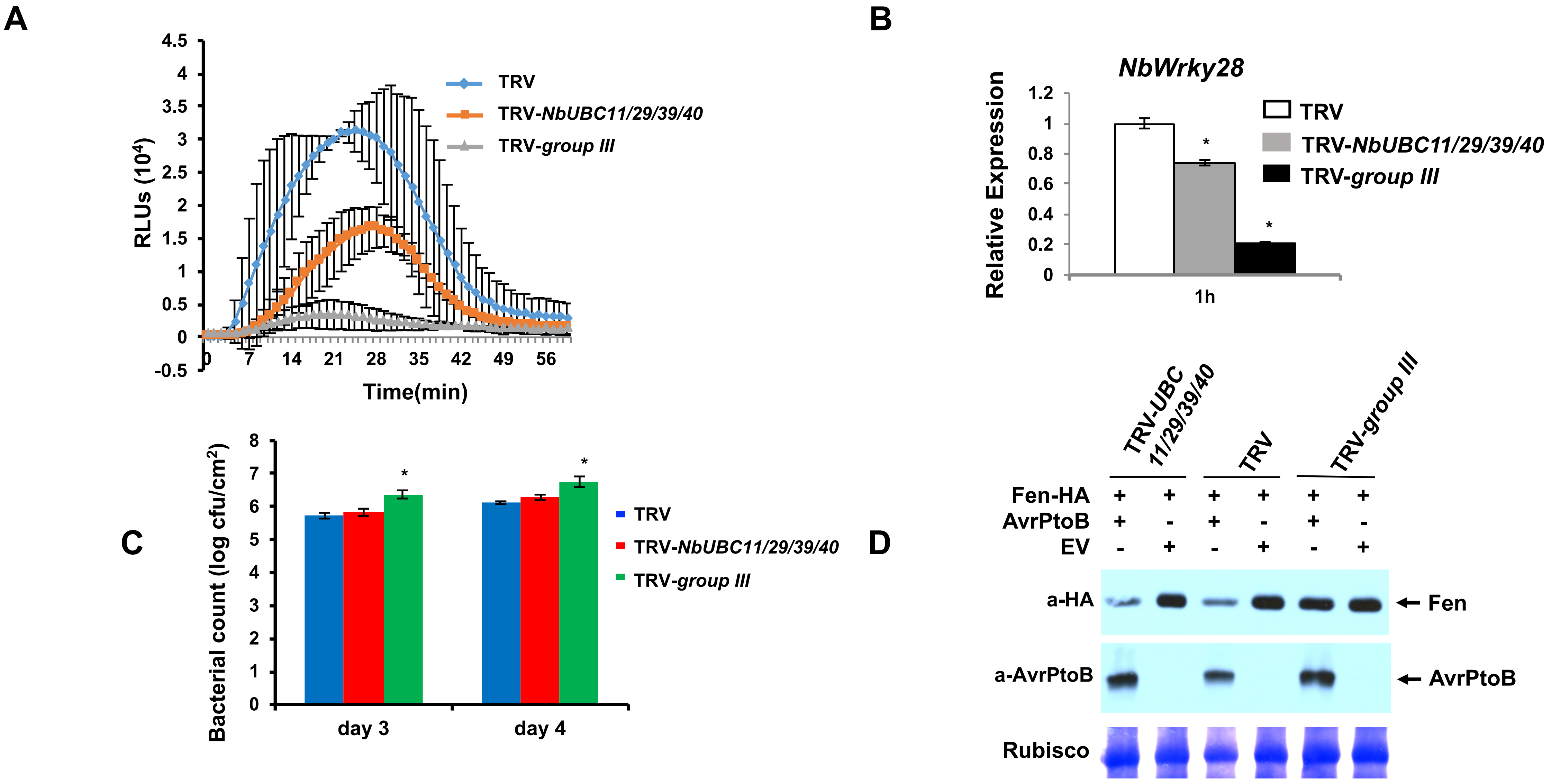


B



Supplemental Figure S15. Specific silencing of E2 genes Nb-*UBC11, 29, 39 and 40* together in *N. benthamiana* by Virus-Induced Gene Silencing. (**A**) Nb-*UBC11*, *29*, *39* and *40* genes were efficiently silenced in *N. benthamiana* by TRV-based VIGS. The Nb-*UBC8*, *9* and *38* were also very slightly knocked down in the plants. The transcript level of group III E2 genes in VIGS-treated *N. benthamiana* plants was examined as described (Mural et al., 2013). Nb-*EF1α* was used as an internal reference for the determination of the amount of cDNA template to be used. The experiment was repeated three times with similar results. (**B**) Phenotypes of the *N. benthamiana* plants in which Nb-*UBC11*, *29, 39* and *40* were silenced. The non-silenced TRV-infected plant and *group III*-silenced plant were included as control. Photographs were taken 4 weeks after the ~ 3-week-old seedlings were infiltrated with TRV vector-based VIGS constructs. The upper panel shows the side view of the plants while the lower panel shows the top view.

Supplemental Fig S16



Supplemental Figure S16. UBC11, 29, 39 and 40 of group III play a more important role in PTI. (A) Silencing the E2 genes *UBC11*, *29, 39* and *40* resulted in reduced ROS production induced by flg22 in a chemiluminescence assay. The diminishment of ROS on the *UBC11*/*29*/*39*/*40*-silenced plants was to a less extent than that on the group III-knocked down plants. **(B)** Knocking down the E2 genes *UBC11*, *29, 39* and *40* down-regulates the induction of PTI reporter gene *Wrky28* by flg22. The expression of *N. benthamiana* PTI marker gene *Wrky28* was performed as described in Figure 6. The experiment was performed with three technical repeats in each of the three biological replicates. Error bars indicate standard deviation. Asterisks mark significant reduction of the expression of *Wrky28*in group III E2 genes-silenced and *UBC11*/*29*/*39*/*40*-silenced plants compared to non-silenced TRV control plants ($P < 0.05$). **(C)** Bacterial populations of the *Pst* strain DC3000*ΔhopQ1-1* on leaves of various VIGS-treated plants. Experiments were performed as described in Figure 8D and repeated three times with similar results. Asterisks indicate significantly increased bacterial growth on *group III*-silenced plants compared to the non-silenced control plants based on the one-way ANOVA ($P < 0.01$). **(D)** No effect on the degradation of Fen caused by AvrPtoB was observed on *N. benthamiana* plants in which the expression of Nb-*UBC11*, *29*, *39* and *40* was knocked down. The experiment was performed as shown in Figure 5B and was repeated two times with similar results.

Supplemental Table I. List of UBC domain-containing proteins from tomato, Arabidopsis, *N. benthamiana*, and human.

Supplemental Table II. List of primers used in this study.

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Larkin, M.A., Blackshields, G., Brown, N.P., Chenna, R., McGettigan, P.A., McWilliam, H., Valentin, F., Wallace, I.M., Wilm, A., Lopez, R., Thompson, J.D., Gibson, T.J., and Higgins, D.G. (2007). Clustal W and Clustal X version 2.0. Bioinformatics **23,** 2947-2948.

Mural, R.V., Liu, Y., Rosebrock, T.R., Brady, J.J., Hamera, S., Connor, R.A., Martin, G.B., and Zeng, L. (2013). The tomato Fni3 lysine-63-specific ubiquitin-conjugating enzyme and SUV ubiquitin E2 variant positively regulate plant immunity. Plant Cell **25,** 3615-3631.

Zhao, Q., Tian, M., Li, Q., Cui, F., Liu, L., Yin, B., and Xie, Q. (2013). A plant-specific in vitro ubiquitination analysis system. Plant J **74,** 524-533.

Supplemental Table I List of UBC domain-containing proteins from tomato, Arabidopsis, *N. benthamiana*, and human

Arabidopsis UBCs

NCBI Accession number of genes	**Accession number of proteins**	**Gene locus**	**Protein name**
NM_101307.4	NP_563951.1	AT1G14400	AtUBC1
NM_126331.3	NP_565289.1	AT2G02760	AtUBC2
NM_125648.3	NP_568956.1	AT5G62540	AtUBC3
NM_123499.4	NP_568589.1	AT5G41340	AtUBC4
NM_105055.2	NP_564817.2	AT1G63800	AtUBC5
NM_130166.3	NP_566062.1	AT2G46030	AtUBC6
NM_125320.1	NP_568902.1	AT5G59300	AtUBC7
NM_180783.1	NP_851114.1	AT5G41700	AtUBC8
NM_118934.2	NP_567791.1	AT4G27960	AtUBC9
NM_124709.2	NP_568788.1	AT5G53300	AtUBC10
NM_111703.3	NP_566331.1	AT3G08690	AtUBC11
NM_111704.1	NP_566332.1	AT3G08700	AtUBC12
NM_114513.5	NP_566884.1	AT3G46460	AtUBC13
NM_115396.3	NP_567020.1	AT3G55380	AtUBC14
NM_103582.3	NP_564493.1	AT1G45050	AtUBC15
NM_106198.4	NP_565110.1	AT1G75440	AtUBC16
NM_119804.2	NP_568004.1	AT4G36410	AtUBC17
NM_123665.5	NP_568619.1	AT5G42990	AtUBC18
NM_112897.3	NP_566653.1	AT3G20060	AtUBC19
NM_103932.3	NP_564572.1	AT1G50490	AtUBC20
NM_122477.2	NP_568476.1	AT5G25760	AtUBC21/PEX4
NM_120590.2	NP_568148.1	AT5G05080	AtUBC22
NM_127245.2	NP_179284.1	AT2G16920	AtUBC23
NM_179887.2	NP_850218.1	AT2G33770	AtUBC24/PHO2
NM_112402.2	NP_188154.1	AT3G15355	AtUBC25
NM_104180.1	NP_175710.1	AT1G53020	AtUBC26
NM_124465.5	NP_199900.1	AT5G50870	AtUBC27
NM_105097.8	NP_564828.1	AT1G64230	AtUBC28
NM_127226.2	NP_565391.1	AT4G27960	AtUBC29
NM_124997.3	NP_568835.1	AT5G56150	AtUBC30
NM_103322.2	NP_564472.1	AT1G36340	AtUBC31
NM_112576.2	NP_566563.1	AT3G17000	AtUBC32
NM_124425.3	NP_199854	AT5G50430	AtUBC33
NM_001084085.1	NP_001077554.1	AT1G17280	AtUBC34
NM_106535.3	NP_565192.1	AT1G78870	AtUBC35
NM_101550.3	NP_564011.1	AT1G16890	AtUBC36
NM_113362.1	NP_566751.1	AT3G24515	AtUBC37
NM_001160817.1	NP_001154289.1	AT4G36800	AtRCE1
NM_127416.3	NP_565440.1	AT2G18600	AtRCE2/AtUB12L
NM_112075.2	NP_566423.1	AT3G12400	AtELC

NM_121389.2	NP_196890.1	AT5G13860	AtELCL(ELC-Like)
NM_115649.2	NP_191346.1	AT3G57870	AtSCE1
NM_102517.4.	NP_564289.1	AT1G27530	AtUfc1
NM_128839.2	NP_565754.1	AT2G32790	AtUBCD/E
NM_112201.4	NP_566459.2	AT3G13550	AtCOP10
NM_180353.2	NP_850684.1	AT3G52560	AtUEV1D
NM_105734.3	NP_564994.1	AT1G70660	AtUEV1B
NM_129165.3	NP_565834	AT2G36060	AtUEV1C
NM_102175.3	NP_564191	AT1G23260	AtUEV1A

Tomato UBCs

Chromosome loci	**Gene name**
Solyc08g081270.2.1	SlUBC 6
Solyc05g054550.2.1	SlUBC 7
Solyc12g056100.1.1	SlUBC 8
Solyc08g008220.2.1	SlUBC 9
Solyc05g050230.2.1	SlUBC 10
Solyc03g033410.2.1	SlUBC 11
Solyc07g066080.2.1	SlUBC 12
Solyc07g062570.2.1	SlUBC 13
Solyc10g007260.2.1	SlUBC 13-2
Solyc04g011430.2.1	SlUBC 14
Solyc11g071870.1.1	SlUBC 15
Solyc04g080810.2.1	SlUBC 16
Solyc02g084760.2.1	SlUBC 17
Solyc04g079970.2.1	SlUBC 18
Solyc12g089030.1.1	SlUBC 19
Solyc11g065190.1.1	SlUBC 20
Solyc11g071260.1.1	SlUBC 21
Solyc10g081160.1.1	SlUBC 22
Solyc01g111680.2.1	SlUBC 23
Solyc02g078210.2.1	SlUBC 24
Solyc10g007000.2.1	SlUBC 25
Solyc01g079290.1.1	SlUBC 26
Solyc06g072570.2.1	SlUBC 27
Solyc10g011740.2.1	SlUBC 28
Solyc02g083570.2.1	SlUBC 29
Solyc03g007470.2.1	SlUBC 30
Solyc01g095490.2.1	SlUBC 31
Solyc12g099310.1.1	SlUBC 32
Solyc03g123660.2.1	SlUBC 33
Solyc06g063100.2.1	SlUBC 34
Solyc05g054540.2.1	SlUBC 35
Solyc09g009720.1.1	SlUBC 36
Solyc07g024070.1.1	SlUBC 37
Solyc08g081950.2.1	SlUBC 38

Solyc06g082600.2.1	SlUBC 39
Solyc06g007510.2.1	SlUBC 40
Solyc02g087750.2.1	SlUBC 41
Solyc03g112720.2.1	SlUBC 43
Solyc02g093110.2.1	SlUBC 44
Solyc04g078620.2.1	SlUBC 45
Solyc12g088680.1.1	SlUBC 46
Solyc03g044260.2.1	SlUBC 47
Solyc01g005840.2.1	SlCOP 10
Solyc04g007970.2.1	SlUEV1B
Solyc01g007860.2.1	SlUEV1C
Solyc10g083120.1.1	SlUEV1D

N. benthamina ubiquitin E2s

Sequence ID in sol genomics network (http://solgenomics.net/)	**Gene name**
Niben101Scf05166g02005.1	*NbUBC1*
Niben101Scf03194g01006.1	*NbUBC2*
Niben101Scf02253g03005.1	*NbUBC3*
Niben101Scf05118g08003.1	*NbUBC4*
Niben101Scf07327g02015.1	*NbUBC5*
Niben101Scf04988g01009.1	*NbUBC6*
Niben101Scf06359g00012.1	*NbUBC7*
Niben101Scf06668g00002.1	*NbUBC8*
Niben101Scf12932g00011.1	*NbUBC9*
Niben101Scf19214g00010.1	*NbUBC10*
Niben101Scf01664g02017.1	*NbUBC11*
Niben101Scf05528g01009.1	*NbUBC12*
Niben101Scf01002g13002.1	*NbUBC13*
Niben101Scf00398g00015.1	*NbUBC13-2*
Niben101Scf00449g06005.1	*NbUBC14*
Niben101Scf03817g13003.1	*NbUBC15*
Niben101Scf01701g12001.1	*NbUBC16*
Niben101Scf05764g03007.1	*NbUBC17*
Niben101Scf12320g03008.1	*NbUBC20*
Niben101Scf00961g02009.1	*NbUBC21*
Niben101Scf16833g00005.1	*NbUBC22*
Niben101Scf01718g01006.1	*NbUBC23*
Niben101Scf04899g03004.1	*NbUBC24*
Niben101Scf02507g04024.1	*NbUBC25*
Niben101Scf06412g04011.1	*NbUBC26*
Niben101Scf03886g02005.1	*NbUBC27*
Niben101Scf00470g04003.1	*NbUBC28*
Niben101Scf01664g02017.1	*NbUBC29*
Niben101Scf08278g00004.1	*NbUBC30*

Niben101Scf05584g02011.1	*NbUBC31*
Niben101Scf02111g11001.1	*NbUBC32*
Niben101Scf00240g02004.1	*NbUBC33*
Niben101Scf00870g02009.1	*NbUBC34*
Niben101Scf06359g00012.1	*NbUBC35*
Niben101Scf09492g00008.1	*NbUBC36*
Niben101Scf00936g00004.1	*NbUBC37*
Niben101Scf04673g02005.1	*NbUBC38*
Niben101Scf00262g04002.1	*NbUBC39*
Niben101Scf04436g07003.1	*NbUBC40*
Niben101Scf01326g08022.1	*NbUBC41*

Human ubiquitin E2s

NCBI Accession number of proteins	Protein name
P49459.2	UBE2A(hHR6A)
CAG28562.1	UBE2B(hHR6B)
CAG33269.1	UBE2C(UbcH10)
NP_003329.1	UBE2D1(UbcH5A)
P62837.1	UBE2D2(UbcH5B)
CAG33197.1	UBE2D3(UbcH5C)
Q9Y2X8.1	UBE2D4(HBUCE1)
NP_003332.1	UBE2E1(UbcH6)
CCQ43860.1	UBE2E2
NP_872619.1	UBE2E3(UbcH9)
Q5U203.2	UBE2F(NCE2)
NP_003333.1	UBE2G1(UBE2G)
NP_003334.2	UBE2G2(UBC7)
NP_003335.1	UBE2H(UBCH)
NP_919237.1	UBE2I(Ubc9)
NP_057105.2	UBE2J1(NCUBE1)
NP_919296.1	UBE2J2(NCUBE2)
NP_005330.1	UBE2K(HIP2)
CAG30492.1	UBE2L3(UbcH7)
CAG33407.1	UBE2L6(UbcH8)
NP_003960.1	UBE2M(Ubc12)
NP_003339.1	UBE2N(Ubc13)
NP_071349.3	UBE2O(E2-230K)
Q7Z7E8.1	UBE2Q1(NICE-5)
NP_775740.1	UBE2Q2
P49427.2	UBE2R1(CDC34)
Q6ZWZ2.1	UBE2R2(CDC34B)
Q16763.2	UBE2S(E2-EPF)
Q9NPD8.1	UBE2T(HSPC150)
NP_689702.1	UBE2U
NP_001244322.1	UBE2V1(UVE-1A)

Q15819.4	UBE2V2(MMS2)
AAH10900.1	UBE2W
Q9H832.2	UBE2Z(Use1)
Q9NR09.2	BIRC6(apollon)

Supplemental Table II List of primers used in this study

Name	Sequence(5'-3')	purpose
Sl-UBC8-EcoRI-F	ACGGATCCATGGCATCCAAGCGGATTC	Sl-*UBC8* in the pGEX-4T-1 vector
Sl-UBC8-XhoI-R	CGCTCGAGCTATCCCATGGCAAATTTTTG	Sl-*UBC8* in the pGEX-4T-1 vector
Sl-UBC14-GW-F	CACCATGGCTTCACAAGCTAGTC	Sl-*UBC14* ORF gateway cloning in pDEST17 vector
Sl-UBC14-GW-R	TTCTCGAGCTACATTTCTTGTGACCGTC	Sl-*UBC14* ORF gateway cloning in pDEST17 vector
Sl-UBC31-EcoRI-F	TAGAATTCATGGCTTCGAAACGGATATT	Sl-*UBC31* in the pGEX-4T-1 vector
Sl-UBC31-XhoI-R	TTCTCGAGTTAACCCATTGCATATTTCTGG	Sl-*UBC31* in the pGEX-4T-1 vector
Sl-UBC39-EcoRI-F	AGGAATTCATGGCGTCGAAGCGCATAT	Sl-*UBC39* in the pGEX-4T-1 vector
Sl-UBC39-XhoI-R	TGCTCGAGTTATCCCATCGCATATTTTTGA	Sl-*UBC39* in the pGEX-4T-1 vector
Sl-UBC40-EcoRI-F	TTGAATTCATGGCGTCGAAGAGGATATT	Sl-*UBC40* in the pGEX-4T-1 vector
Sl-UBC40-XhoI-R	AACTCGAGTCATCCCATTGCATATTTCTGA	Sl-*UBC40* in the pGEX-4T-1 vector
Sl-UBC36-F-GW	CACCATGGCTTCTTCACAAGCCG	Sl-*UBC36* ORF gateway cloning in pDEST17 vector
Sl-UBC36-R	CGCTCGAGTCACAACATCTCTTGTGATTTC	Sl-*UBC36* ORF gateway cloning in pDEST17 vector
Sl-UBC3-EcoRI-F	AGGAATTCATGTCGACACCGGCGAAG	Sl-*UBC3* in the pGEX-4T-1 vector
Sl-UBC3-XhoI-R	CGCTCGAGTCAGTCTGCTGTCCAGCTT	Sl-*UBC3* in the pGEX-4T-1 vector
Sl-UBC5-EcoRI-F	TAGGATCCATGTCTTCTCCAAGCAAACG	Sl-*UBC5* in the pGEX-4T-1 vector
Sl-UBC5-XhoI-R	TGCTCGAGTCATGGATCAACAGGGCCT	Sl-*UBC5* in the pGEX-4T-1 vector
Sl-UBC6-EcoRI-F	CAGAATTCATGTCTTCCCCTAGCAAACG	Sl-*UBC6* in the pGEX-4T-1 vector
Sl-UBC6-XhoI-R	TGCTCGAGTTAGGGATCTGCTTTTCCAG	Sl-*UBC6* in the pGEX-4T-1 vector
Sl-UBC12-F-GW	CACCATGGCTTCAAAGAGGATTCAG	Sl-*UBC12* ORF gateway cloning in pDEST17 vector
Sl-UBC12-R	CGCTCGAGTCAACCCATTGCGTATTTCT	Sl-*UBC12* ORF gateway cloning in pDEST17 vector
Sl-UBC16-BamHI-F	GAGGATCCATGACTAGTGCTTCTGCTTC	Sl-*UBC16* in the pGEX-4T-1 vector
Sl-UBC16-XhoI-R	CACTCGAGCTACACTTTATCGTCATGGAA	Sl-*UBC16* in the pGEX-4T-1 vector
Sl-UBC17-BamHI-F	AAGGATCCATGTCGGCCTCCTCTGCC	Sl-*UBC17* in the pGEX-4T-1 vector
Sl-UBC17-XhoI-R	TGCTCGAGTCACACCTTATCATCATGGAA	Sl-*UBC17* in the pGEX-4T-1 vector
Sl-UBC20-BamHI-F	GTGGATCCATGGCGACAATGAACAGTGG	Sl-*UBC20* in the pGEX-4T-1 vector
Sl-UBC20-XhoI-R	CGCTCGAGCTACACACTAGGCTTGTATAG	Sl-*UBC20* in the pGEX-4T-1 vector
Sl-UBC27-BamHI-F	GAGGATCCATGGTGGACTTGGCTAGGG	Sl-*UBC27* in the pGEX-4T-1 vector
Sl-UBC27-XhoI-R	CGCTCGAGTTAGCTGGACAACAGCTTTTC	Sl-*UBC27* in the pGEX-4T-1 vector
Sl-UBC32-BamHI-F	GTGGATCCATGGCGGAAGACAAGTATAAT	Sl-*UBC32* in the pGEX-4T-1 vector
Sl-UBC32-XhoI-R	CGCTCGAGTTACGATTCATCCATAAAGACA	Sl-*UBC32* in the pGEX-4T-1 vector
Sl-UBC1-EcoRI-F	CGGAATTCATGTCGACTCCAGCT	Sl-*UBC1* in the pGEX-4T-1 vector
Sl-UBC1-XhoI-R	AACTCGAGTCAGTCAGCAGTCCA	Sl-*UBC1* in the pGEX-4T-1 vector
Sl-UBC2-EcoRI-F	CGGAATTCATGTCAACTCCTTCA	Sl-*UBC2* in the pGEX-4T-1 vector
Sl-UBC2-XhoI-R	AACTCGAGTCAGTCTGCAGTCCA	Sl-*UBC2* in the pGEX-4T-1 vector
SlUbc7-GW-F	CACCATGGCTTCAACTTCTCCTTC	Sl-*UBC7* ORF gateway cloning in pDEST15 vector
SlUbc7-GW-R	TTACATCATTTCTTGAGACCG	Sl-*UBC7* ORF gateway cloning in pDEST15 vector
Sl-UBC15-EcoRI-F	CGGAATTCATGTCTTCTCCAAGC	Sl-*UBC15* in the pGEX-4T-1 vector
Sl-UBC15-XhoI-R	AACTCGAGTCAAGGATCAGCATG	Sl-*UBC15* in the pGEX-4T-1 vector
Sl-UBC21-EcoRI-F	CGGAATTCATGCAGGCTTCAAGG	Sl-*UBC21* in the pGEX-4T-1 vector
Sl-UBC21-XhoI-R	AACTCGAGTTAGCCCTTCTTGGG	Sl-*UBC21* in the pGEX-4T-1 vector
Sl-UBC22-EcoRI-F	CGGAATTCATGGCAACTAATGAA	Sl-*UBC22* in the pGEX-4T-1 vector
Sl-UBC22-XhoI-R	CGCTCGAGTTATAATCTCTTCAA	Sl-*UBC22* in the pGEX-4T-1 vector
Sl-UBC41-EcoRI-F	CGGAATTCATGTCGACGCCGGCT	Sl-*UBC41* in the pGEX-4T-1 vector
Sl-UBC41-XhoI-R	AACTCGAGTCAGTCCGCCGTCCA	Sl-*UBC41* in the pGEX-4T-1 vector
Sl-UBC10-ORF-F	CACCATGGCTTCGAAACGAATATTGAA	Sl-*UBC10* ORF gateway cloning in pDEST15 vector
Sl-UBC10-ORF-R	TTAACCCATGGCATACTTCTG	Sl-*UBC10* ORF gateway cloning in pDEST15 vector
Sl-UBC35-ORF-F	CACCATGGCTTCAGCTTCTCCTTC	Sl-*UBC35* ORF gateway cloning in pDEST15 vector
Sl-UBC35-ORF-R	TTACGTCATTTCTTGGGACCG	Sl-*UBC35* ORF gateway cloning in pDEST15 vector
Sl-UBC26-ORF-F	CACCATGGATGAGGCAAACAAGAAC	Sl-*UBC26* ORF gateway cloning in pDEST15 vector
Sl-UBC26-ORF-R	TTAACTAACCCTTGGCTGTTTGA	Sl-*UBC26* ORF gateway cloning in pDEST15 vector
Sl-UBC25-ORF-F	CACCATGGAGACTCATAAACAAGTAG	Sl-*UBC25* ORF gateway cloning in pDEST15 vector
Sl-UBC25-ORF-R	GCTACTCAGTCCCATTCTGT	Sl-*UBC25* ORF gateway cloning in pDEST15 vector
Sl-UBC28-ORF-F	CACCATGGCTTCTAAGCGGATATTG	Sl-*UBC28* ORF gateway cloning in pDEST15 vector
Sl-UBC28-ORF-R	TTAACCCATAGCATACTTCTG	Sl-*UBC28* ORF gateway cloning in pDEST15 vector
Sl-UBC33-ORF-F	CACCATGGCAGAAAAAGCATGTGTAA	Sl-*UBC33* ORF gateway cloning in pDEST15 vector
Sl-UBC33-ORF-R	TCAAAGCTGAAGCAGAGGCA	Sl-*UBC33* ORF gateway cloning in pDEST15 vector
Sl-UBC13-ORF-F	CGGAATTCATGGCTAACAGC	Sl-*UBC13* in the pGEX-4T-1 vector
Sl-UBC13-ORF-R	CCGCTCGAGTCATGCACCACTAG	Sl-*UBC13* in the pGEX-4T-1 vector
Sl-UBC13-2-ORF-F	CGGAATTCATGGCTAACAGC	Sl-*UBC13-2* in the pGEX-4T-1 vector
Sl-UBC13-2-ORF-R	CCGCTCGAGTCATGCACCACTAG	Sl-*UBC13-2* in the pGEX-4T-1 vector
Sl-UBC4-GW-F	CACCATGTCTTCCCCAAGCAAAAG	Sl-*UBC4* ORF gateway cloning in pDEST15 vector

Sl-UBC4-GW-R	TTATGGATCAACAGGTCCTG	Sl-*UBC4* ORF gateway cloning in pDEST15 vector
Sl-UBC7-GW-F	CACCATGGCTTCAACTTCTCCTTC	Sl-*UBC7* ORF gateway cloning in pDEST15 vector
Sl-UBC7-GW-R	TTACATCATTTCTTGAGACCG	Sl-*UBC7* ORF gateway cloning in pDEST15 vector
Sl-UBC9-GW-F	CACCATGGCATCCAAGAGGATTCT	Sl-*UBC9* ORF gateway cloning in pDEST15 vector
Sl-UBC9-GW-R	CTAACCCATTGCATACTTTTG	Sl-*UBC9* ORF gateway cloning in pDEST15 vector
Sl-UBC11-GW-F	CACCATGGCATCAAGGAGAATTCAA	Sl-*UBC11* ORF gateway cloning in pDEST15 vector
Sl-UBC11-GW-R	TCAATTCATAGCATATTTTTGGG	Sl-*UBC11* ORF gateway cloning in pDEST15 vector
Sl-UBC23-GW-1F	CACCATGGATGAGTCTGAGTCTAC	Sl-*UBC23* ORF gateway cloning in pDEST15 vector
Sl-UBC23-GW-1R	TCCTGCCAAGCAACATCAAC	Sl-*UBC23* ORF gateway cloning in pDEST15 vector
Sl-UBC23-GW-2F	AGATCCGCAAAGTTGTGGTT	Sl-*UBC23* ORF gateway cloning in pDEST15 vector
Sl-UBC23-GW-2R	GCAGCAGGTAGCCTTGGA	Sl-*UBC23* ORF gateway cloning in pDEST15 vector
Sl-UBC23-GW-3F	GATTCATGGTCCCAAAGGTC	Sl-*UBC23* ORF gateway cloning in pDEST15 vector
Sl-UBC23-GW23-3R	CTACAATTGGTGGAGATGTTG	Sl-*UBC23* ORF gateway cloning in pDEST15 vector
Sl-UBC24-GW-1F	CACCATGGATACATCTCTAAGTGAC	Sl-*UBC24* ORF gateway cloning in pDEST15 vector
Sl-UBC24-GW-1R	GCCAACAATAATACCGATACA	Sl-*UBC24* ORF gateway cloning in pDEST15 vector
Sl-UBC24-GW-2F	CTGTTTAGGTGATGCGGTTT	Sl-*UBC24* ORF gateway cloning in pDEST15 vector
Sl-UBC24-GW-2R	TTAATCGGACAACTGACTGC	Sl-*UBC24* ORF gateway cloning in pDEST15 vector
Sl-UBC29-GW-F	CACCATGGCATCCAGGAGAATTCA	Sl-*UBC29* ORF gateway cloning in pDEST15 vector
Sl-UBC29-GW-R	TCAGTTCATGGCATACTTTTG	Sl-*UBC29* ORF gateway cloning in pDEST15 vector
Sl-UBC30-GW-F	CACCATGGCTTCCAAGCGGATCT	Sl-*UBC30* ORF gateway cloning in pDEST15 vector
Sl-UBC30-GW-R	TTAGCCCATGGCATACTTCT	Sl-*UBC30* ORF gateway cloning in pDEST15 vector
Sl-UBC34-GW-F	CACCATGGCAGAAAAGGCATGTGT	Sl-*UBC34* ORF gateway cloning in pDEST15 vector
Sl-UBC34-GW-R	TCAAAGCTGAAGTAGCGGCA	Sl-*UBC34* ORF gateway cloning in pDEST15 vector
Sl-UBC37-GW-1F	CACCATGGCTCAAGAGGCGCGG	Sl-*UBC37* ORF gateway cloning in pDEST15 vector
Sl-UBC37-GW-1R	TGAAATCGGTTGACTGAAGC	Sl-*UBC37* ORF gateway cloning in pDEST15 vector
Sl-UBC37-GW-2F	CAGGCTATAAGCAATTCAGG	Sl-*UBC37* ORF gateway cloning in pDEST15 vector
Sl-UBC37-GW-2R	TCAAGATATTGGATAAAAAGATTG	Sl-*UBC37* ORF gateway cloning in pDEST15 vector
Sl-UBC38new-GW-F	CACCATGGCGTCCAAGCGGATTCT	Sl-*UBC38* ORF gateway cloning in pDEST15 vector
Sl-UBC38-GW-R	CTAACCCATGGCGTACTTTT	Sl-*UBC38* ORF gateway cloning in pDEST15 vector
Nb-UBC9-GW-F	CACCATGGCATCCAAGAGGATTCT	Group III VIGS fragment Nb-*UBC9* cloning
Nb-UBC9-VIGS-R	TGTAGCCTGCCAGTGAAACAT	Group III VIGS fragment Nb-*UBC9* cloning
Nb-UBC28-VIGS-F	GAAGATATGTTTCACTGGCA	Group III VIGS fragment Nb-*UBC28* cloning
Nb-UBC28-VIGS-R	TATTTATATTTGGATGGAAAACTTTTG	Group III VIGS fragment Nb-*UBC28* cloning
Nb-UBC11-VIGS-F	CAAAAGTATTTCCATCCAAATATA	Group III VIGS fragment Nb-*UBC11* cloning
Nb-UBC11-VIGS-R	TCGTCTGGATTTGGATCTGT	Group III VIGS fragment Nb-*UBC11* cloning
Nb-UBC39-VIGS-F	ACAGATCCAAACCCAGACGA	Group III VIGS fragment Nb-*UBC39* cloning
Nb-UBC39-R	TGCTCGAGTTATCCCATCGCATATTTTTGA	Group III VIGS fragment Nb-*UBC39* cloning
Nb-UBC12-VIGS-F	ATGGGATAACTCGAGCATCTATCCATTTCC	Group III VIGS fragment Nb-*UBC12* cloning
Nb-UBC12-VIGS-R	TGCTGTTTATGTTTGGGTGG	Group III VIGS fragment Nb-*UBC12* cloning
Nb-UBC30-VIGS-F	GGTTTTCCACCCAAACATAAACAGCA	Group III VIGS fragment Nb-*UBC30* cloning
Nb-UBC30-VIGS-R	GATTAGGGTCCGTCAGAAGTG	Group III VIGS fragment Nb-*UBC30* cloning
Nb-UBC12VIGS-G-F	CACCAGTATTTGTCTGGACATCTTAAAAG	VIGS fragment cloning forsilencing Nb-*UBC12* alone or the four E2 genes Nb-*UBC12* , *10* , *28* and *31*.
Nb-UBC12VIGS-G-R	AAGCAAAACCTTGGTGAGCAGCACCTTGGATACAGT	VIGS fragment cloning forsilencing Nb-*UBC12* alone or the four E2 genes Nb-*UBC12* , *10* , *28* and *31*.
Nb-UBC10VIGS-G-F	CACCAAGGTTTTGCTTTCAATCTGC	VIGS fragment cloning for silencing the three E2 genes Nb-*UBC10, 28* and *31* or the four E2 genes Nb-*UBC12* , *10* , *28* and *31*.
Nb-UBC10VIGS-G-R	TTATTGTAGCTTGGTGGCAATCTCAGGAACAAGGGG	VIGS fragment cloning for silencing the three E2 genes Nb-*UBC10, 28* and *31* or the four E2 genes Nb-*UBC12* , *10* , *28* and *31*.
Nb-UBC28VIGS-G-F	CACCAAGCTACAATAATGGGCCC	VIGS fragment cloning for silencing the three E2 genes Nb-*UBC10, 28* and *31* or the four E2 genes Nb-*UBC12* , *10* , *28* and *31*.
Nb-UBC28VIGS-G-R	AATGGATAGTGACTAAAAATAC	VIGS fragment cloning for silencing the three E2 genes Nb-*UBC10, 28* and *31* or the four E2 genes Nb-*UBC12* , *10* , *28* and *31*.
Nb-UBC11VIGS-F	CACCGACAGCCCTTATGCAGGTGG	VIGS fragment cloning for silencing the three E2 genes Nb-*UBC11, 29, 39 and 40.*
Nb-UBC11VIGS-R	GAATTCTCCTCAGGAGGAAAATGGATGGCC	VIGS fragment cloning for silencing the three E2 genes Nb-*UBC11, 29, 39 and 40.*
Nb-UBC29VIGS-F	TTTCCTCCTGAGGAGAATTCTCAAGGAGC	VIGS fragment cloning for silencing the three E2 genes Nb-*UBC11, 29, 39 and 40.*
Nb-UBC29VIGS-R	CTACTGGACCTGCACTGCATGAAG	VIGS fragment cloning for silencing the three E2 genes Nb-*UBC11, 29, 39 and 40.*

Nb-UBC39VIGS-F	CACCTTATGCAGGAGGTGTATT	VIGS fragment cloning for silencing the three E2 genes Nb-*UBC11, 29, 39 and 40.*
Nb-UBC39VIGS-R	TCCAGACAAAATCAGGAGGGAAATGAATTG	VIGS fragment cloning for silencing the three E2 genes Nb-*UBC11, 29, 39 and 40.*
Nb-UBC40VIGS-F	CTCCTGATTTTGTCTGGATATTCTAAAAGAG	VIGS fragment cloning for silencing the three E2 genes Nb-*UBC11, 29, 39 and 40.*
Nb-UBC40VIGS-R	AAGGGCTGTCGGTGGATTTGGGTCAGTCAATAGGGAG	VIGS fragment cloning for silencing the three E2 genes Nb-*UBC11, 29, 39 and 40.*
Sl-06-ube1-1F	CACCATGCTTCCTAGAAAGAGAC	Sl-*UBA1* ORF gateway cloning in pDEST15 vector
Sl-06-ube1-1R	GAATGCCAAATGTAGCAGAGG	Sl-*UBA1* ORF gateway cloning in pDEST15 vector
Sl-06-ube1-2F	AACGAACTTTGGTCCCTATG	Sl-*UBA1* ORF gateway cloning in pDEST15 vector
Sl-06-ube1-2R	CATTCACTTCGGCTGGTGT	Sl-*UBA1* ORF gateway cloning in pDEST15 vector
Sl-06-ube1-3F	CCAATGTGCACTTTGCATTC	Sl-*UBA1* ORF gateway cloning in pDEST15 vector
Sl-06-ube1-3R	GATTACCAAGAAAATTCAACGGA	Sl-*UBA1* ORF gateway cloning in pDEST15 vector
Sl-UBC10-XhoI-KpnI-F	GGCTCGAGGTACCATGGCTTCGAAACGAATATTG	Sl-*UBC10* ORF cloning for constrcucting pA7-nYFP-Sl-*UBC10 and* pSPYCE(M)-*SlUBC10*
Sl-UBC10-StuI-PstI-R	GGAGGCCTGCAGACCCATGGCATACTTCTGGG	Sl-*UBC10* ORF cloning for constrcucting pA7-nYFP-Sl-*UBC10* and pSPYCE(M)-*SlUBC10*
Sl-UBC12-KpnI-XhoI-F	GGTACCCTCGAGATGGCTTCAAAGAGGATTCAG	Sl-*UBC12* ORF cloning for constrcucting pA7-nYFP-Sl-*UBC12* and pSPYCE(M)-*SlUBC12*
Sl-UBC12-PstI-R	GGGCTGCAGACCCATTGCGTATTTCTGGG	Sl-*UBC12* ORF cloning for constrcucting pA7-nYFP-Sl-*UBC12* and pSPYCE(M)-*SlUBC12*
Sl-UBC25-XhoI-F	CACCTCGAGATGGAGACTCATAAACAAGTAG	Sl-*UBC25* ORF cloning for constrcucting pA7-nYFP-Sl-*UBC25*
Sl-UBC25-SmaI-R	CCCGGGCTCAGTCCCATTCTGTGTC	Sl-*UBC25* ORF cloning for constrcucting pA7-nYFP-Sl-*UBC25*
Sl-UBC21-XhoI-F	CACCTCGAGATGCAGGCTTCAAGGGCAAGAC	Sl-*UBC21* ORF cloning for constrcucting pA7-nYFP-Sl-*UBC21*
Sl-UBC21-SmaI-R	CCCGGGGCCCTTCTTGGGCATTGC	Sl-*UBC21* ORF cloning for constrcucting pA7-nYFP-Sl-*UBC21*
Sl-UBC16-XhoI-F	CACCTCGAGATGACTAGTGCTTCTGCTTCATC	Sl-*UBC16* ORF cloning for constrcucting pA7-nYFP-Sl-*UBC16* and pSPYCE(M)-*SlUBC16*
Sl-UBC16-SmaI-R	CCCGGGCACTTTATCGTCATGGAACC	Sl-*UBC16* ORF cloning for constrcucting pA7-nYFP-Sl-*UBC16* and pSPYCE(M)-*SlUBC16*
Sl-UBA1-XhoI-F	CACCTCGAGATGCTTCCTAGAAAGAGACCGG	Sl-*UBA1* ORF cloning for constrcucting pA7-cYFP-Sl-*UBA1*
Sl-UBA1-SmaI-R	CCCGGGACGGAAGTATACAGACACCAG	Sl-*UBA1* ORF cloning for constrcucting pA7-cYFP-Sl-*UBA1*
AvrptoB-XhoI-KpnI-F	GGCTCGAGGTACCATGGCGGGTATCAATAGAGC	*AvrPtoB* ORF cloning for constrcucting pA7-cYFP-*AvrPtoB* and pBTEX-nYFP-*AvrPtoB*
AvrptoB-StuI-PstI-R	GGAGGCCTGCAGGGGGACTATTCTAAAAGCAT	*AvrPtoB* ORF cloning for constrcucting pA7-cYFP-*AvrPtoB* and pBTEX-nYFP-*AvrPtoB*
Nb-EF1a-F	AGCCTGGTATGGTTGTGACTTTTG	RT-PCR for reference gene Nb-*EF1a*
Nb-EF1a-R	CATGGGCTTGGTGGGAATC	RT-PCR for reference gene Nb-*EF1a*
Nb-UBC8-RT-F	CACCATGGCATCCAAACGGATTCTCAAAG	RT-PCR for Nb-*UBC8*
Nb-UBC8-RT-R	AGCCCCTCCAGAGATGGTCACT	RT-PCR for Nb-*UBC8*
Nb-UBC9-RT-F	CACCATGGCATCCAAGAGAATTCTGAAAG	RT-PCR for Nb-*UBC9*
Nb-UBC9-RT-R	CCAAATATTTGTGTTTCAGCAACTAACCC	RT-PCR for Nb-*UBC9*
Nb-UBC10-RT-F	CACCATGGCTTCGAAACGAATATTGAA	RT-PCR for Nb-*UBC10*
Nb-UBC10-RT-R	CCGCCATAGGCAATATTTAGCCCA	RT-PCR for Nb-*UBC10*
Nb-UBC11-RT-F	CACCATGGCATCCAGGAGAATTCA	RT-PCR for Nb-*UBC11*
Nb-UBC11-RT-R	CAACTCAATTCATAGCAAACTTTTGG	RT-PCR for Nb-*UBC11*
Nb-UBC12-RT-F	TCTTACTGTATCCAAGGTGCTGCT	RT-PCR for Nb-*UBC12*
Nb-UBC12-RT-R	CCAAATGTTTTCATCCCATGGCATAT	RT-PCR for Nb-*UBC12*
Nb-UBC28-RT-F	TAGAATTCATGGCTTCGAAACGGATATT	RT-PCR for Nb-*UBC28*
Nb-UBC28-RT-R	CATGGGTTAAACCGTTACCTATGG	RT-PCR for Nb-*UBC28*
Nb-UBC29-RT-F	CACCATGGCATCCAGGAGAATTCA	RT-PCR for Nb-*UBC29*
Nb-UBC29-RT-R	CTTCATGTCTTCAGACTCAGTTCATA	RT-PCR for Nb-*UBC29*
Nb-UBC30-RT-F	CACCATGGCTTCCAAGCGGATCT	RT-PCR for Nb-*UBC30*
Nb-UBC30-RT-R	TTAGCCCATGGCATACTTCT	RT-PCR for Nb-*UBC30*
Nb-UBC31-RT-F	CACCATGGCTTCGAAACGAATATTGAA	RT-PCR for Nb-*UBC31*
Nb-UBC31-RT-R	GCCGCCATAGGCAATAGTTAGCCC	RT-PCR for Nb-*UBC31*
Nb-UBC38-RT-F	ACGGATCCATGGCATCCAAGCGGATTC	RT-PCR for Nb-*UBC38*
Nb-UBC38-RT-R	CTAACCCATGGCGTACTTTT	RT-PCR for Nb-*UBC38*
Nb-UBC39-RT-F	AGGAATTCATGGCGTCGAAGCGCATAT	RT-PCR for Nb-*UBC39*
Nb-UBC39-RT-R	GGACACTTTCCGCATCATCCCATA	RT-PCR for Nb-*UBC39*
Nb-UBC40-RT-F	TTGAATTCATGGCGTCGAAGAGGATATT	RT-PCR for Nb-*UBC40*
Nb-UBC40-RT-R	TCATTCACCACAAGCACAATAAGA	RT-PCR for Nb-*UBC40*
Nb-UBC16-RT-F	GGGCACCAGGAACTCTGTAT	RT-PCR for Nb-*UBC16*

Nb-UBC16-RT-R	TGGTATGGGAGTTGGAGTCA	RT-PCR for Nb-*UBC16*
Nb-UBC17-RT-F	TGGGTGATTGAAGTGATTGGG	RT-PCR for Nb-*UBC17*
Nb-UBC17-RT-R	TCAAGGGTCAGAAGGACACC	RT-PCR for Nb-*UBC17*
Sl-EF1a-RT-F	TCCAAAGATGGTCAGACCCGTGAA	Real-time PCR for reference gene Sl-*EF1a*
Sl-EF1a-RT-R	ATACCTAGCCTTGGAGTACTTGGG	Real-time PCR for reference gene Sl-*EF1a*
Sl-UBC8-RT-F	CATTTTGAAGGAACAGTGGAGC	Real-time PCR for Sl-*UBC8*
Sl-UBC8-RT-R	CTCCGGGCAGTTGTCTCATAC	Real-time PCR for Sl-*UBC8*
Sl-UBC9-RT-F	TTCCAAGGTGCTGCTGTCAATC	Real-time PCR for Sl-*UBC9*
Sl-UBC9-RT-R	ATGGGTCTGAGCAGCAACTAAC	Real-time PCR for Sl-*UBC9*
Sl-UBC10-RT-F	TGCTGGGGGTGTTTTTTTGGTC	Real-time PCR for Sl-*UBC10*
Sl-UBC10-RT-R	AAGGGGTCGTCAGGGTTTGGGT	Real-time PCR for Sl-*UBC10*
Sl-UBC11-RT-F	AGGTCCTGTGGCTCAGGATATA	Real-time PCR for Sl-*UBC11*
Sl-UBC11-RT-R	CTTAGGGGGTTTGAAAGGGTAG	Real-time PCR for Sl-*UBC11*
Sl-UBC12-RT-F	TCTTACTGTATCCAAGGTGCTGCT	Real-time PCR for Sl-*UBC12*
Sl-UBC12-RT-R	GTGTTCAACCCATTGCGTATTTCT	Real-time PCR for Sl-*UBC12*
Sl-UBC28-RT-F	TACAAGACAGACAGGGCAAAATA	Real-time PCR for Sl-*UBC28*
Sl-UBC28-RT-R	GGGAAGGTAGAGGACAGAGAGAC	Real-time PCR for Sl-*UBC28*
Sl-UBC29-RT-F	CATGCAGTGCAGGTCCAGTAGC	Real-time PCR for Sl-*UBC29*
Sl-UBC29-RT-R	CTTGGGAGGTTTGAAAGGGTAA	Real-time PCR for Sl-*UBC29*
Sl-UBC30-RT-F	AGTCCTTATTCCGGTGGAGTTT	Real-time PCR for Sl-*UBC30*
Sl-UBC30-RT-R	CTTCCGTTGCTGTTTATGTTTG	Real-time PCR for Sl-*UBC30*
Sl-UBC31-RT-F	AGGTTTTGCTTTCAATTTGCTC	Real-time PCR for Sl-*UBC31*
Sl-UBC31-RT-R	GGCAGTTGATTCGTATTTGGC	Real-time PCR for Sl-*UBC31*
Sl-UBC38-RT-F	TCCTACTTCTTGCAGTGCTGGT	Real-time PCR for Sl-*UBC38*
Sl-UBC38-RT-R	CATTGCTGTTGATGTTCGGGTG	Real-time PCR for Sl-*UBC38*
Sl-UBC39-RT-F	TTTCCCCCCTGATTATCCTTTC	Real-time PCR for Sl-*UBC39*
Sl-UBC39-RT-R	GTGGTCTCGTATTTGGCCCTGT	Real-time PCR for Sl-*UBC39*
Sl-UBC40-RT-F	CCCTTATGCTGGAGGTGTATT	Real-time PCR for Sl-*UBC40*
Sl-UBC40-RT-R	ATCATCTGGGTTTGGGTCTGT	Real-time PCR for Sl-*UBC40*
Nb-EF1a-F	TACTGGTGGTTTTGAAGCTG	Real-time PCR for reference gene Nb-*EF1a*
Nb-EF1a-R	ATACCTAGCCTTGGAGTACTTGGG	Real-time PCR for reference gene Nb-*EF1a*
Nb-Wrky28-F	GCATTCATGACAAAGAGTGAGGTT	Real-time PCR for Nb-*Wrky28*
Nb-Wrky28-R	GACATTTTTGACTTGTGCACCTAT	Real-time PCR for Nb-*Wrky28*
Nb-Pti5-F	CCTCCAAGTTTGAGCTCAGATAGT	Real-time PCR for Nb-*Pti5*
Nb-Pti5-R	CCAAGAAATTCTCCATGTACTCTGTC	Real-time PCR for Nb-*Pti5*
Nb-Acre31-F	GAGAAACTGGGATTGCCTGAAGGA	Real-time PCR for Nb-*Acre31*
Nb-Acre31-R	AACTTGGCCATCGTGATCTTGGTC	Real-time PCR for Nb-*Acre31*
Nb-Gras2-F	TCATGAGGCGTTACTCGGAGCATT	Real-time PCR for Nb-*Gras2*
Nb-Gras2-R	TACCTAGCACCAAGCAGATGCAGA	Real-time PCR for Nb-*Gras2*
AvrPtoB307-smaI-R	CCCGGGTACATGTCTTTCAAGGGCCGTG	*AvrPtoB* ORF cloning for constrcucting pSPYNE173-*AvrPtoB1-307*
Sl-UBC8-XhoI-F	CACCCTCGAGATGGCATCCAAGCGGATTCTC	Sl-*UBC8* ORF cloning for constrcucting pSPYCE(M)-*SlUBC8*
Sl-UBC8-SmaI-R	CCCGGGTCCCATGGCAAATTTTTGAGTC	Sl-*UBC8* ORF cloning for constrcucting pSPYCE(M)-*SlUBC8*
Sl-UBC9-XhoI-F	CACCCTCGAGATGGCATCCAAGAGGATTCTG	Sl-*UBC9* ORF cloning for constrcucting pSPYCE(M)-*SlUBC9*
Sl-UBC9-SmaI-R	CCCGGGACCCATTGCATACTTTTGGG	Sl-*UBC9* ORF cloning for constrcucting pSPYCE(M)-*SlUBC9*
Sl-UBC11-XhoI-F	CACCCTCGAGATGGCATCAAGGAGAATTCAAA	Sl-*UBC11* ORF cloning for constrcucting pSPYCE(M)-*SlUBC11*
Sl-UBC11-SmaI-R	CCCGGGATTCATAGCATATTTTTGGGTC	Sl-*UBC11* ORF cloning for constrcucting pSPYCE(M)-*SlUBC11*
Sl-UBC28-XhoI-F	CACCCTCGAGATGGCTTCTAAGCGGATATTG	Sl-*UBC28* ORF cloning for constrcucting pSPYCE(M)-*SlUBC28*
Sl-UBC28-SmaI-R	CCCGGGACCCATAGCATACTTCTGGG	Sl-*UBC28* ORF cloning for constrcucting pSPYCE(M)-*SlUBC28*
Sl-UBC29-XhoI-F	CACCCTCGAGATGGCATCCAGGAGAATTCAAAAG	Sl-*UBC29* ORF cloning for constrcucting pSPYCE(M)-*SlUBC29*
Sl-UBC29-SmaI-R	CCCGGGGTTCATGGCATACTTTTGAG	Sl-*UBC29* ORF cloning for constrcucting pSPYCE(M)-*SlUBC29*
Sl-UBC30-XhoI-F	ggtaccctcgagATGGCTTCCAAGCGGATC	Sl-*UBC30* ORF cloning for constrcucting pSPYCE(M)-*SlUBC30*
Sl-UBC30-SmaI-R	GGGctgcagGCCCATGGCATACTTCTGGG	Sl-*UBC30* ORF cloning for constrcucting pSPYCE(M)-*SlUBC30*
Sl-UBC31-XhoI-F	CACCCTCGAGATGGCTTCGAAACGGATATTG	Sl-*UBC31* ORF cloning for constrcucting pSPYCE(M)-*SlUBC31*

Sl-UBC31-SmaI-R	CCCGGGACCCATTGCATATTTCTGGG	Sl-*UBC31* ORF cloning for constrcucting pSPYCE(M)-*SlUBC31*
Sl-UBC38-XhoI-F	CACCCTCGAGATGGCGTCCAAGCGGATTCTG	Sl-*UBC38* ORF cloning for constrcucting pSPYCE(M)-*SlUBC38*
Sl-UBC38-SmaI-R	CCCGGGACCCATGGCGTACTTTTGGG	Sl-*UBC38* ORF cloning for constrcucting pSPYCE(M)-*SlUBC38*
Sl-UBC39-XhoI-F	CACCCTCGAGATGGCGTCGAAGCGCATATTG	Sl-*UBC39* ORF cloning for constrcucting pSPYCE(M)-*SlUBC39*
Sl-UBC39-SmaI-R	CCCGGGTCCCATCGCATATTTTTGAG	Sl-*UBC39* ORF cloning for constrcucting pSPYCE(M)-*SlUBC39*
Sl-UBC40-XhoI-F	CACCCTCGAGATGGCGTCGAAGAGGATATTG	Sl-*UBC40* ORF cloning for constrcucting pSPYCE(M)-*SlUBC40*
Sl-UBC40-SmaI-R	CCCGGGTCCCATTGCATATTTCTGAG	Sl-*UBC40* ORF cloning for constrcucting pSPYCE(M)-*SlUBC40*
SlUBC8C85G-F	GGCAGCATTgGCCTTGACATT	Sl-*UBC8C85G* ORF gateway cloning in pDEST15 vector
SlUBC8C85G-R	AATGTCAAGGCcAATGCTGCC	Sl-*UBC10C85G* ORF gateway cloning in pDEST15 vector
SlUBC10C85G-F	CAATGGGAGTATAgGCTTGGAC	Sl-*UBC10C85G* ORF gateway cloning in pDEST15 vector
SlUBC10C85G-R	CAGTATGTCCAAGCcTATACTC	Sl-*UBC10C85G* ORF gateway cloning in pDEST15 vector