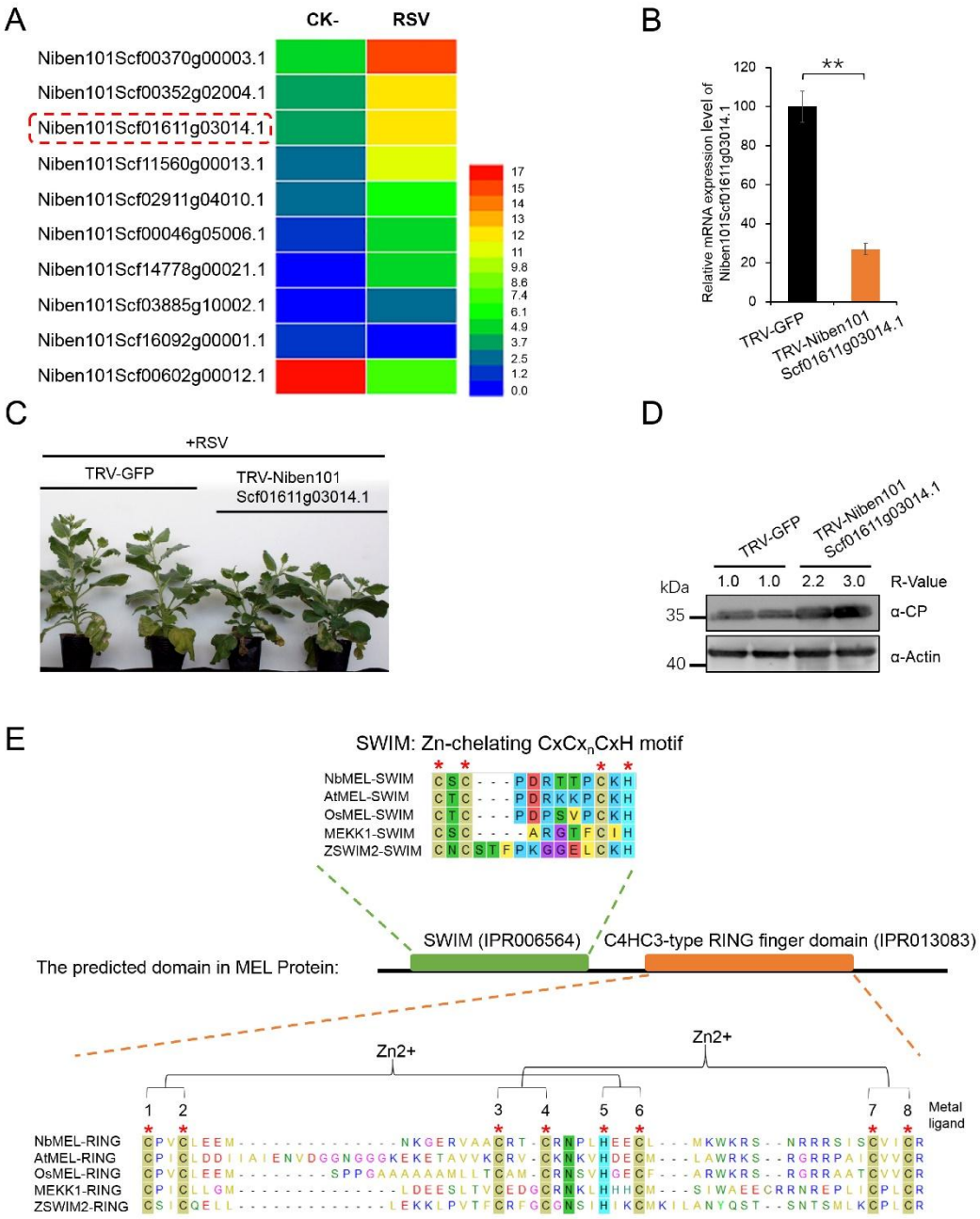
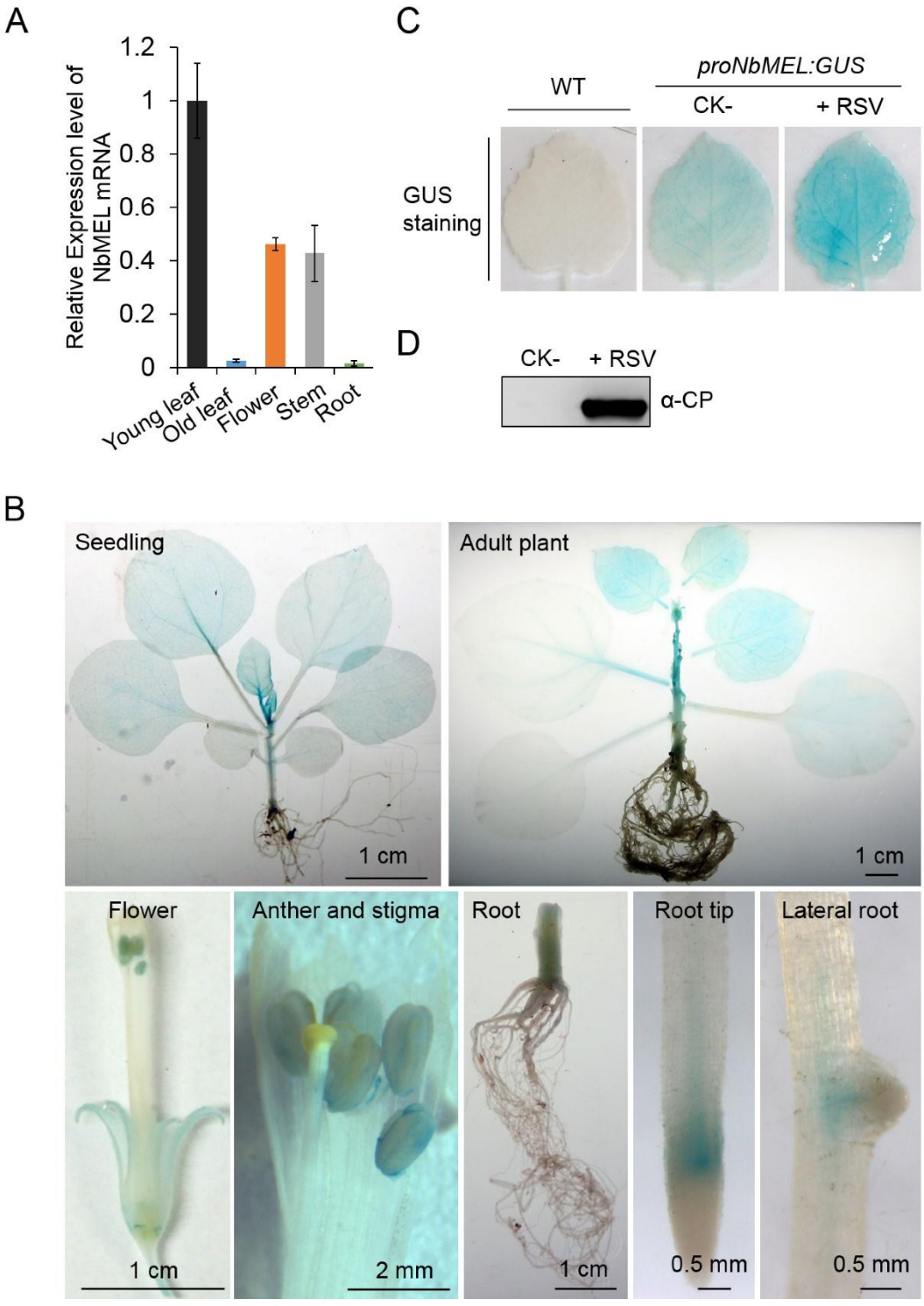


Supplemental Figure S1. NbMEL is a C4HC3 RING type E3 ligase activated by RSV infection and negatively regulates RSV infection (Supports Figure 1).

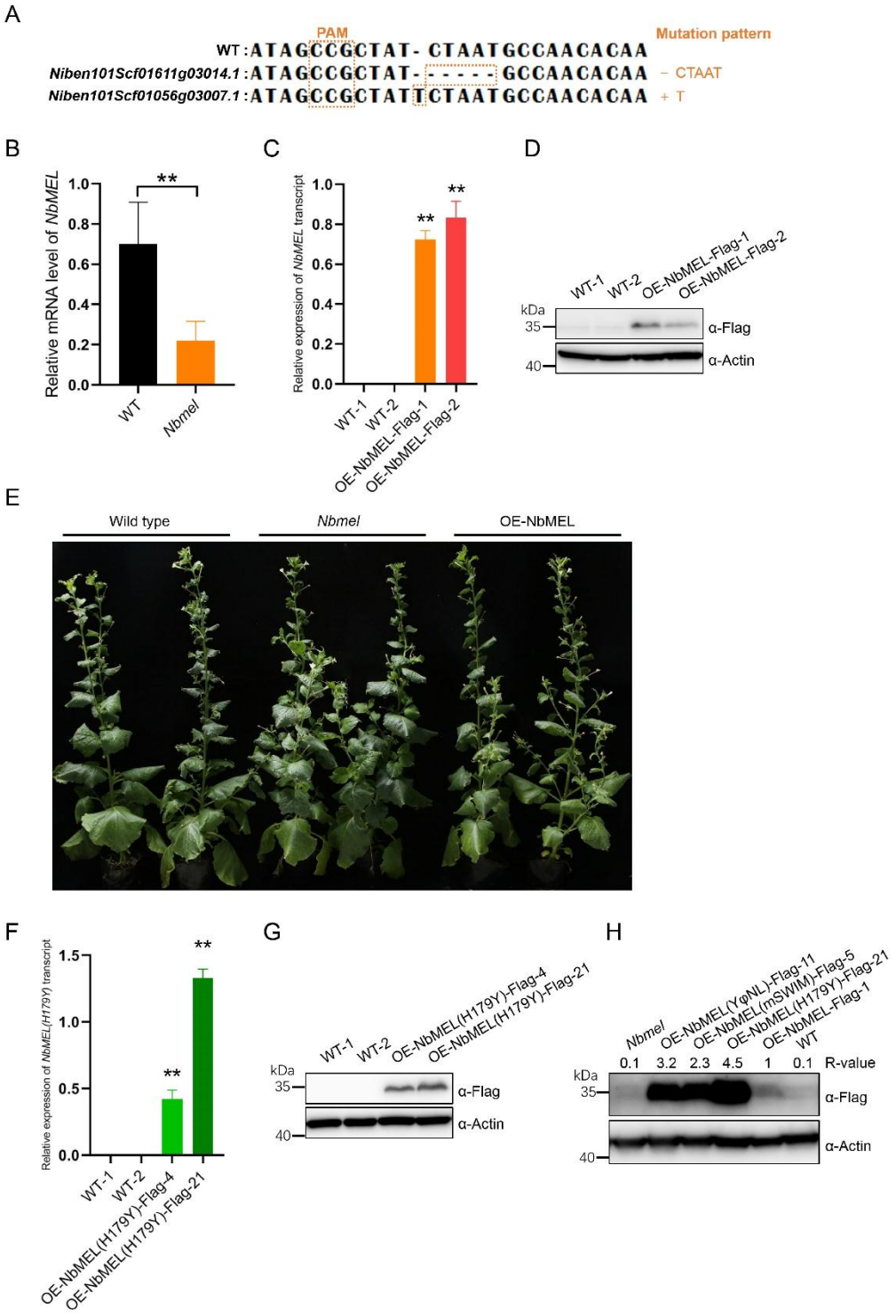
(A) Heat map for ten differentially expressed E3-like ligase transcripts identified by RNA-seq. Relative expression values ranging from 0 to 17 were indicated by color bars. **(B)** Silencing efficiency of Niben101Scf01611g03014.1 detected by RT-qPCR. Data are means ± SD (n=3). Asterisks indicate a statistically significant difference according to Student's *t*-test (two-tailed), **P < 0.01. **(C)**

Silencing of Niben101Scf01611g03014.1 enhances RSV infection symptoms. Photographs of representative symptoms were taken at 20 dpi. **(D)** RSV capsid protein accumulation in Niben101Scf01611g03014.1-silenced and control (TRV-GFP) *N. benthamiana* plants infected by RSV at 20 dpi. The bands in immunoblot are quantified and the relative intensities (R-value) are shown above the band. This experiment was performed three times with similar results. **(E)** Representation of sequence comparison of the SWIM and C4HC3 type RING domain of MELs in *N. benthamiana, Arabidopsis thaliana, Oryza Sativa*, and human ZSWIM2 and MEKK1. Asterisk indicates the conserved amino acid defining the SWIM domain and C4HC3 type RING domain. In the C4HC3 type RING domain, the seven cysteine and one histidine residues that coordinate two Zn^{2+} ions are shown in the bracket.


A
Relative Expression level of NbMEL mRNA
1.2
1
0.8
0.6
0.4
0.2
0
Young leaf
Old leaf
Flower
Stem
Root
C
WT
proNbMEL:GUS
CK-
+ RSV
GUS staining
D
CK-
+ RSV
α-CP
B
Seedling
1 cm
Adult plant
1 cm
Flower
1 cm
Anther and stigma
2 mm
Root
1 cm
Root tip
0.5 mm
Lateral root
0.5 mm

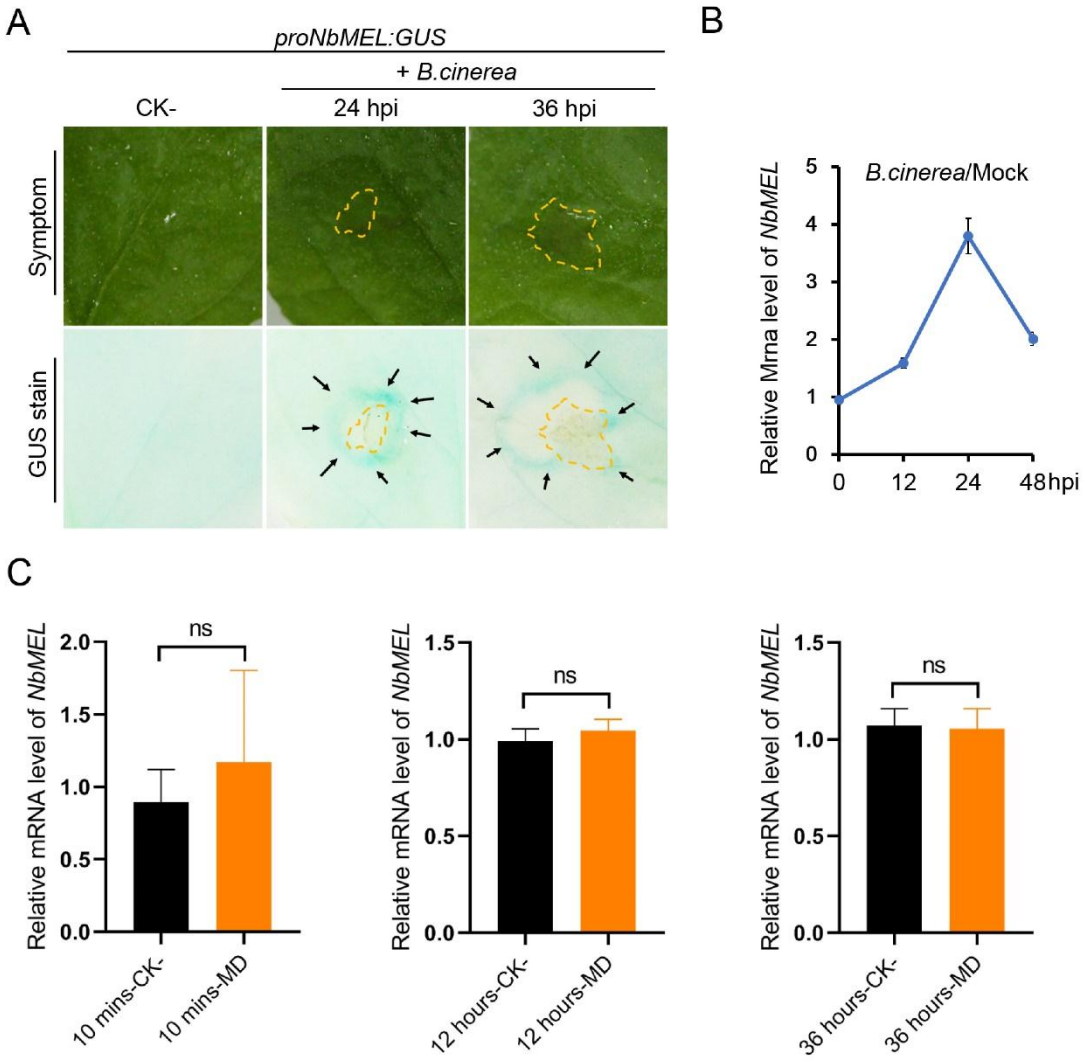
Supplemental Figure S2. Transcript expression and promoter activity assay of *NbMEL* in different *N. benthamiana* plant tissues (Supports Figure 1).

(A) Expression of *NbMEL* in different organs as detected by RT-qPCR. Data are means ± SD (n=3). **(B)** Histochemical GUS staining of various tissues from *proNbMEL:GUS* transgenic *N. benthamiana* plants. **(C)** Histochemical GUS staining of systemic leaves of *proMEL:GUS* transgenic *N. benthamiana* plants in response to RSV infection at 10 dpi. **(D)** Immunoblot detection of RSV capsid protein accumulation in respective systemic leaves of *proMEL:GUS* transgenic *N. benthamiana* plants in (C). All the experiments were performed three times with similar results.


A
PAM
Mutation pattern
WT : ATAGCCGCTAT- CTAATGCCAACACAA
Niben101Scf01611g03014.1 : ATAGCCGCTAT- - - - - GCCAACACAA – CTAAT
Niben101Scf01056g03007.1 : ATAGCCGCTATTCTAATGCCAACACAA + T
B
Relative mRNA level of NbMEL
WT
Nbmel
C
Relative expression of NbMEL transcript
WT-1
WT-2
OE-NbMEL-Flag-1
OE-NbMEL-Flag-2
D
kDa
35
40
α-Flag
α-Actin
E
Wild type
Nbmel
OE-NbMEL
F
Relative expression of NbMEL(H179Y) transcript
OE-NbMEL(H179Y)-Flag-4
OE-NbMEL(H179Y)-Flag-21
G
H
Nbmel
OE-NbMEL(YqNL)-Flag-11
OE-NbMEL(mSWIM)-Flag-5
OE-NbMEL(H179Y)-Flag-21
OE-NbMEL-Flag-1
WT
0.1 3.2 2.3 4.5 1 0.1 R-value

Supplemental Figure S3. Analysis of transcript, protein and growth phenotype of transgenic *N. benthamiana* plants overexpressing *NbMEL* or its mutants (Supports Figure 1 and Figure 2).

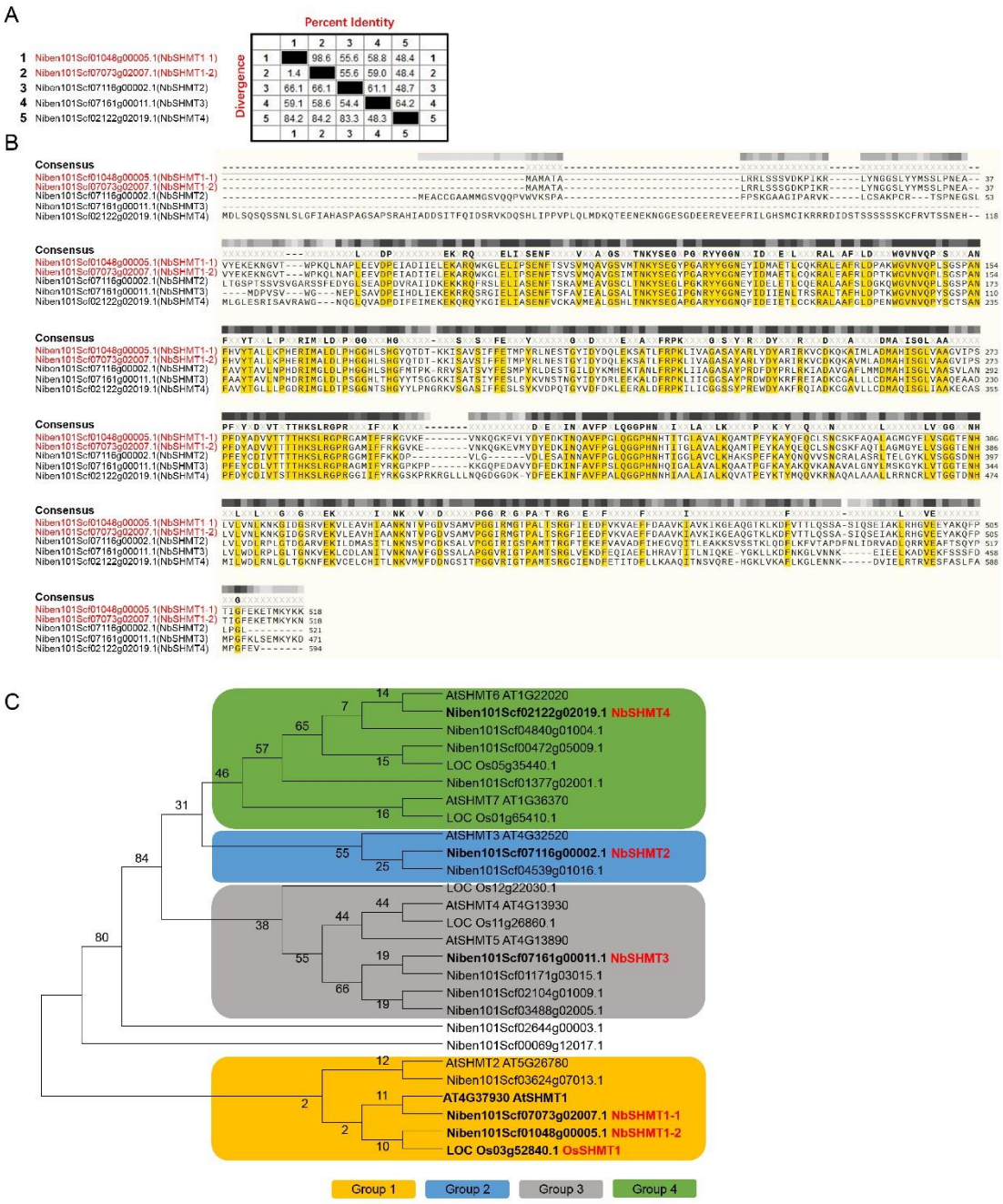
(A) Mutation pattern of *Nbmel N. benthamiana* plants detected by Sanger sequencing. PAM sequence of the target sequence is labeled by the red dashed box. The mutation pattern is annotated behind the sequence. **(B)** Relative mRNA level of *NbMEL* in *Nbmel N. benthamiana* plants as detected by RT-qPCR. Data are means ± SD (n=3). Asterisks indicate a statistically significant difference according to Student's *t*-test (two-tailed), **p < 0.01. **(C)** Relative mRNA level of *NbMEL* in *NbMEL* overexpression transgenic *N. benthamiana* plants as detected by RT-qPCR. Data are means ± SD (n=3). **(D)** NbMEL-Flag accumulation in *NbMEL* overexpression transgenic *N. benthamiana* plants detected by immunoblotting using the Flag antibody. Actin was used as a loading control. **(E)** Phenotype comparison of *NbMEL* overexpression (OE-NbMEL), *NbMEL* knockout (*Nbmel*) and wild-type *N. benthamiana* plants. **(F)** Relative mRNA level of *NbMEL(H179Y)* in *NbMEL(H179Y)*-Flag overexpression transgenic *N. benthamiana* plants as detected by RT-qPCR. Data are means ± SD (n=3). **(G)** NbMEL(H179Y)-Flag accumulation in transgenic *N. benthamiana* plants overexpressing *NbMEL(H179Y)-Flag* detected by immunoblotting using the Flag antibody. Actin was used as a loading control. **(H)** Accumulation comparison of Flag-tagged NbMEL and its mutants in respective overexpression transgenic *N. benthamiana* plants. Proteins were detected by immunoblotting using the Flag antibody. Actin was used as a loading control. All experiments were performed three times with similar results.



Supplemental Figure S4. Analysis of *NbMEL* promoter or transcript in response to *B. cinerea* infection or mechanical damage (MD) (Supports Figure 2).

(A) Histochemical GUS staining of *proNbMEL:GUS* transgenic *N. benthamiana* plants in response to *B. cinerea* conidial inoculation. Yellow dashed lines indicate the symptom boundary of *B. cinerea* infection site. Black arrows indicate GUS staining result showing *NbMEL* promoter is activated surrounding the *B. cinerea* infection site. **(B)** Relative mRNA levels of *NbMEL* at 0, 24, 36, and 48 hours post inoculation of *B. cinerea* conidia as detected by RT-qPCR. Data are means ± SD (n=3). **(C)** Relative mRNA levels of *NbMEL* in *N. benthamiana* leaves under mechanical damage (MD) at 10 minutes, 12 hours, and 36 hours post needling treatment as detected by RT-qPCR. Data are

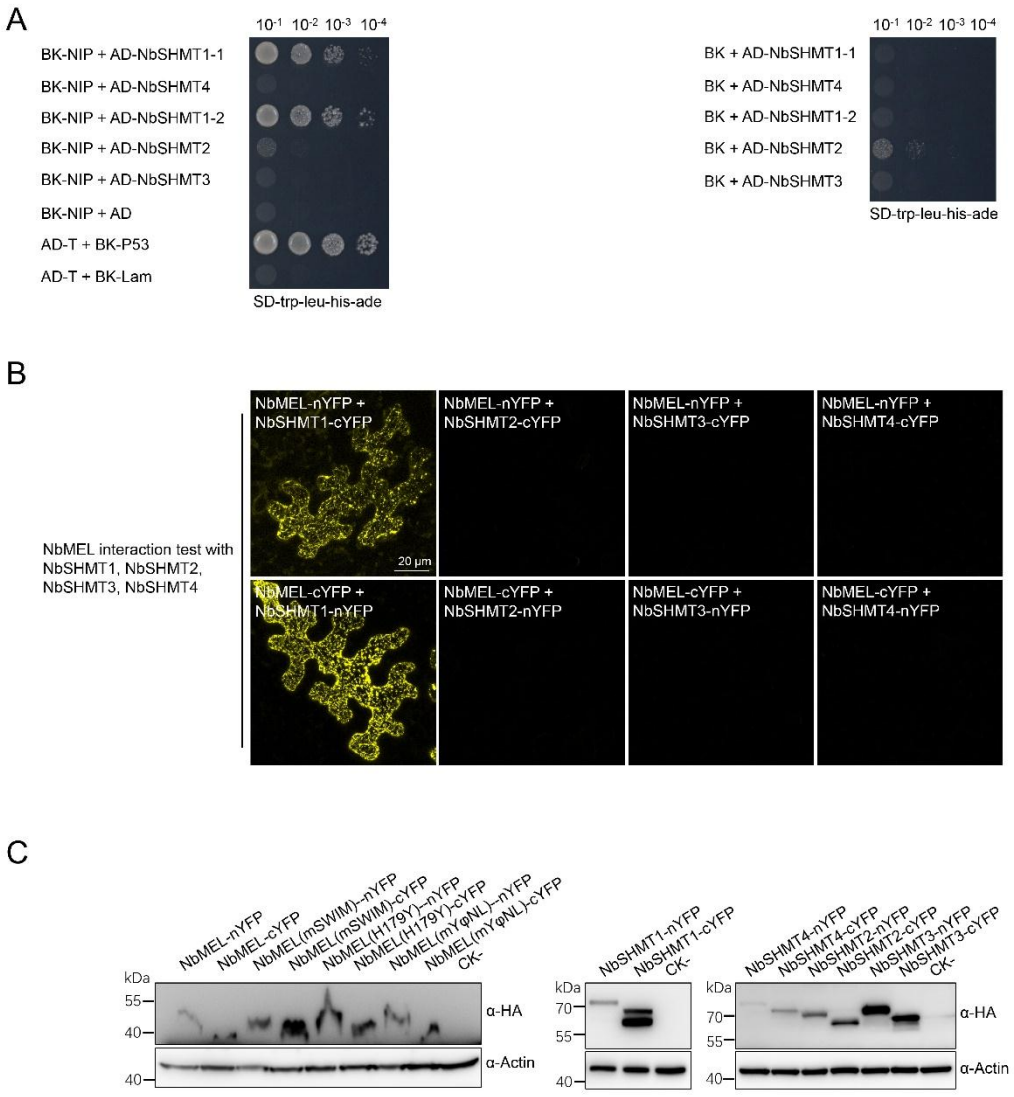
means ± SD (n=3). “ns” indicates no statistically significant difference according to Student’s *t*-test (two-tailed) ($p > 0.05$). All experiments were performed three times with similar results.



Supplemental Figure S5. Sequence comparison and phylogenetic tree of SHMT homologs from *N. benthamiana*, *O. sativa* and *Arabidopsis* (Supports Figure 3).

(A) Amino acid sequence identity between five *N. benthamiana* SHMT homologs (NbSHMT1-1, NbSHMT1-2, NbSHMT2, NbSHMT3, and NbSHMT4) by MegAlign software. Red box denotes two alleles of NbSHMT1. **(B)** Comparison of the amino acid sequence of five *N. benthamiana* SHMT

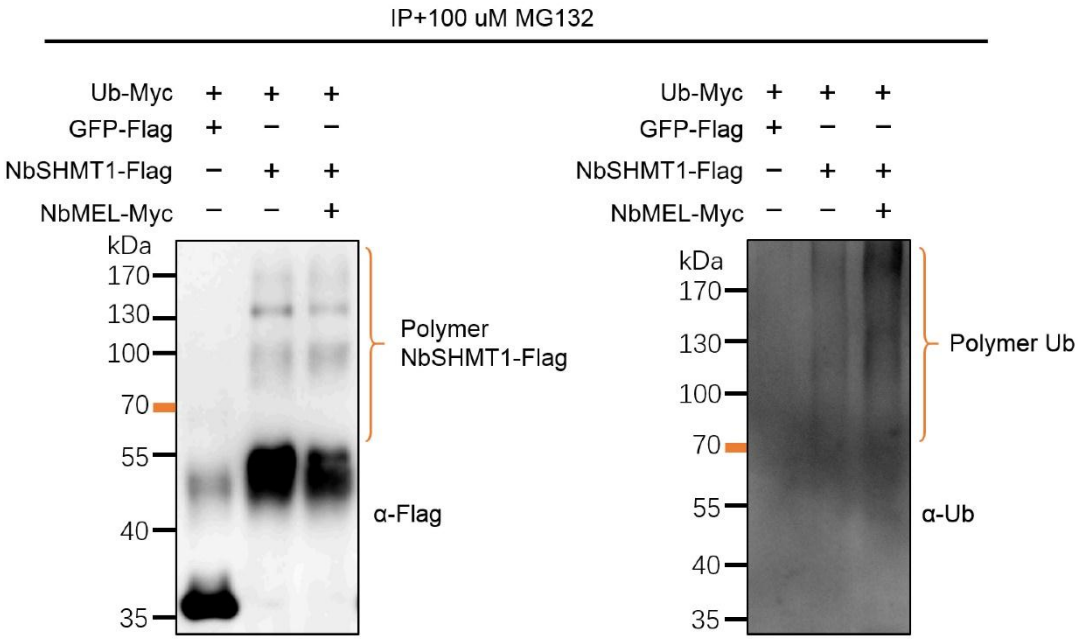
homologs (NbSHMT1-1, NbSHMT1-2, NbSHMT2, NbSHMT3, and NbSHMT4) by MUSCLE. **(C)** Phylogenetic tree of all SHMT homologs from *N. benthamiana, A. thaliana* and *O. Sativa*. Phylogenetic tree was constructed by the Maximum Likelihood method. The bootstrap consensus tree inferred from 1000 replicates is taken to represent the evolutionary history of the taxa analyzed.



Supplemental Figure S6. NbMEL interacts with NbSHMT1 (Supports Figure 3).

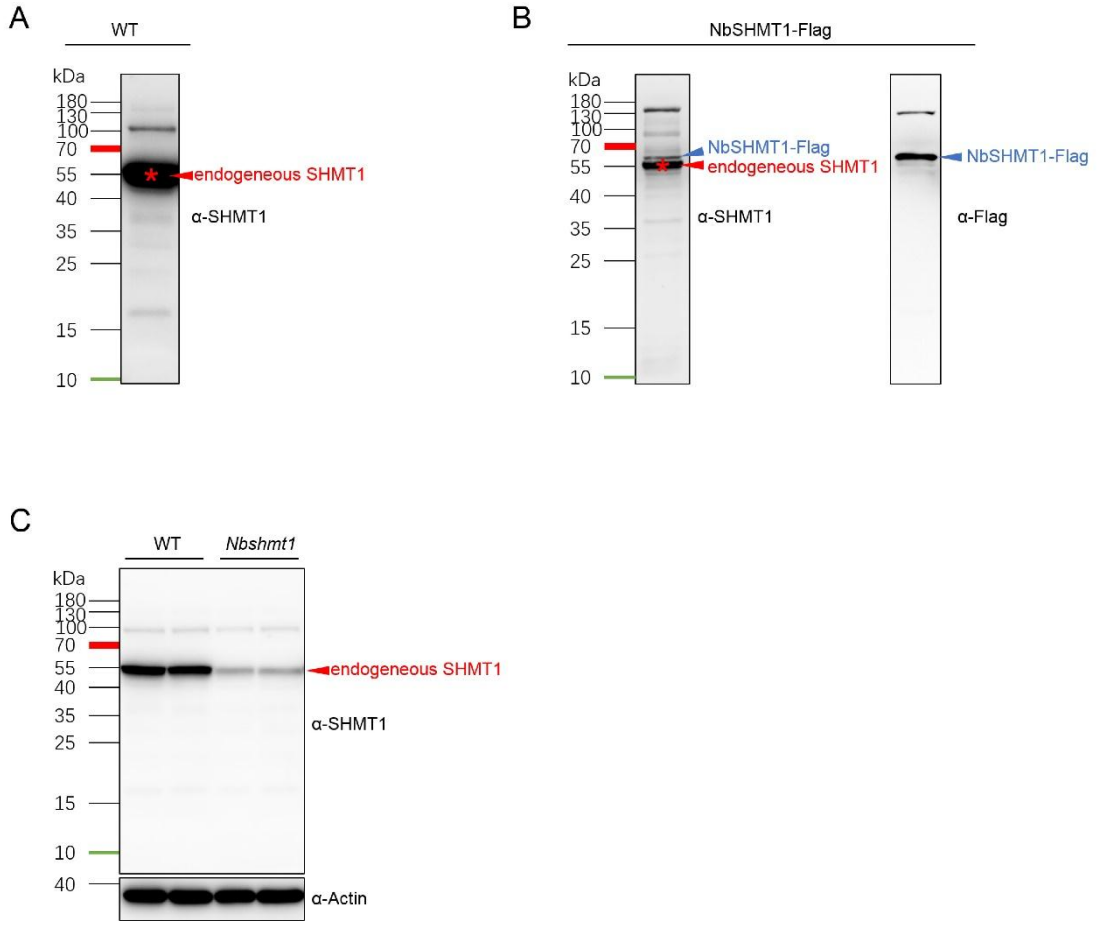
(A) Interaction test between NbMEL and five *N. benthamiana* SHMT homologs (NbSHMT1-1, NbSHMT1-2, NbSHMT2, NbSHMT3, and NbSHMT4) by Y2H. Serial dilutions of yeast cells co-transfected with two recombination vectors were plated on SD-Trp-Leu-His-Ade medium. Yeast cells co-transfected with pGADT7-T and pGBKT7-p53 or with pGADT7-T and pGBKT7-Lam were used as positive and negative controls, respectively. **(B)** Interaction test between NbMEL and five *N. benthamiana* SHMT homologs (NbSHMT1-1, NbSHMT1-2, NbSHMT2, NbSHMT3, and NbSHMT4) by BiFC. Confocal images were taken at 48 hpi. Bars: 20 μm. **(C)** Detection of the expressions of all vectors used in

BiFC by immunoblotting. Actin was used as a loading control. All experiments were performed three times with similar results.



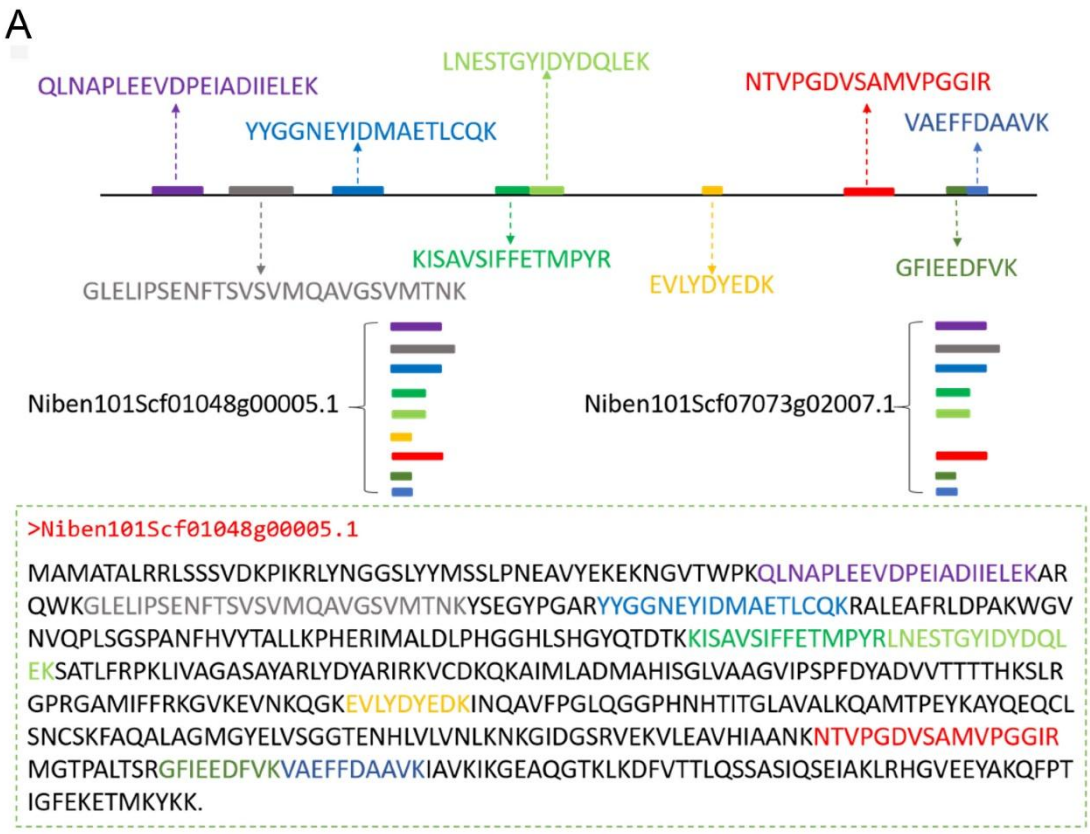
Supplemental Figure S7. NbSHMT1 is ubiquitinated by NbMEL (Supports Figure 3).

NbMEL enhances NbSHMT1 ubiquitination *in vivo*. NbSHMT1-Flag and Ub-Myc, or NbMEL-Myc, NbSHMT1-Flag, and Ub-Myc, were co-expressed by agroinfiltration in *N. benthamiana* leaves, then 100 uM MG132 was pre-infiltrated into leaves 4 hours before total protein extraction. Total proteins were extracted and NbSHMT1-Flag was immunoprecipitated (IP) using anti-Flag beads. The poly-ubiquitination of NbSHMT1-Flag was detected with the anti-Flag (left) and anti-Ub antibody (right). Orange brackets denote ubiquitinated NbSHMT1 bands. This experiment was performed three times with similar results.



Supplemental Figure S8. Specificity of SHMT1 antibody (Supports Figure 3 and Figure 4).

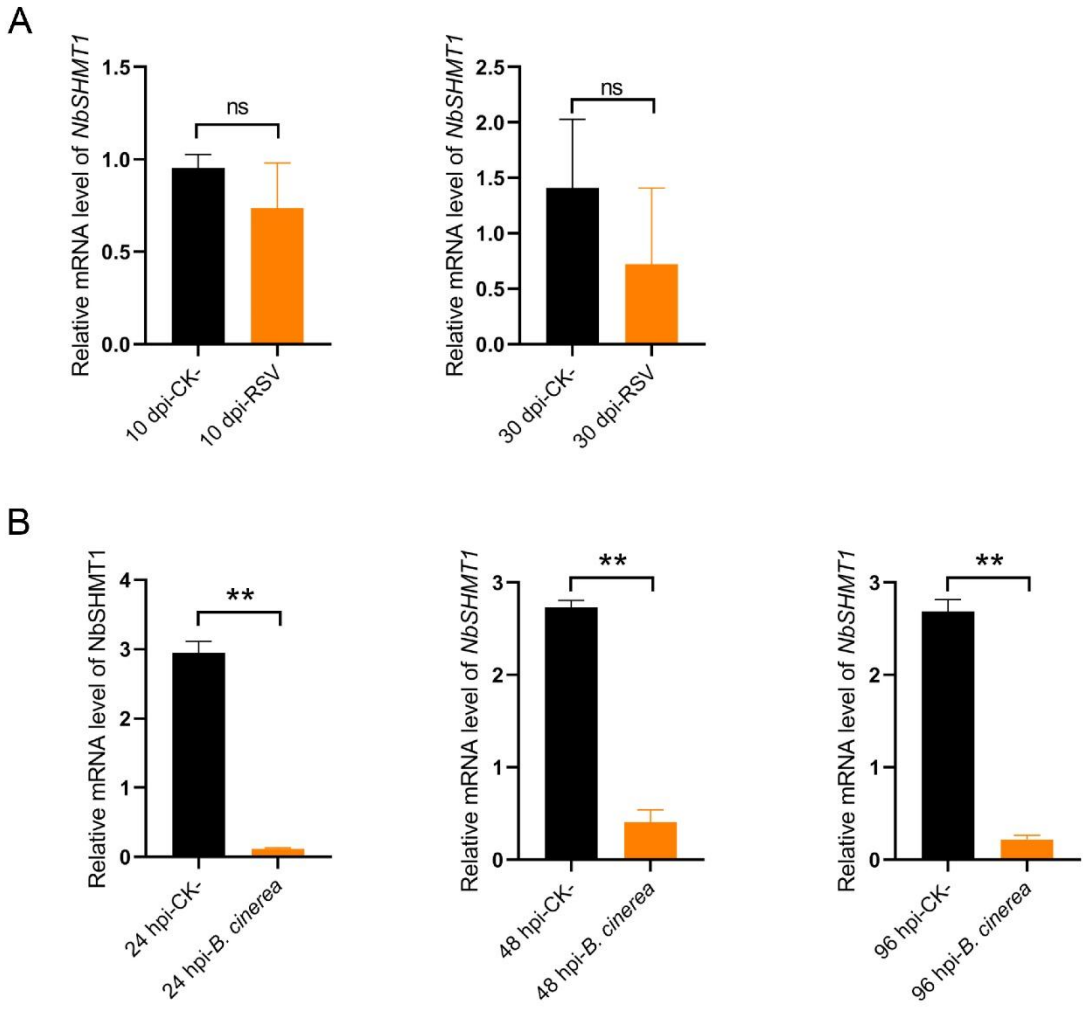
(A) Detection of endogenous NbSHMT1 in *N. benthamiana* by immunoblotting using the SHMT1 antibody. Red star indicates the endogenous SHMT1 band. **(B)** Detection of NbSHMT1-Flag expressed in *N. benthamiana* leaves by agroinfiltration by immunoblotting using SHMT1 antibody or Flag antibody. Blue triangle marks the NbSHMT1-Flag band, red star indicates the endogenous SHMT1 band. **(C)** Detection of endogenous NbSHMT1 in wild-type or *Nbshmt1 N. benthamiana* by immunoblotting using SHMT1 antibody. Red triangle marks the endogenous SHMT1 band. All experiments were performed three times with similar results.



Supplemental Figure S9. NbSHMT1 protein down-regulated in response to RSV infection quantified by iTRAQ (Supports Figure 4).

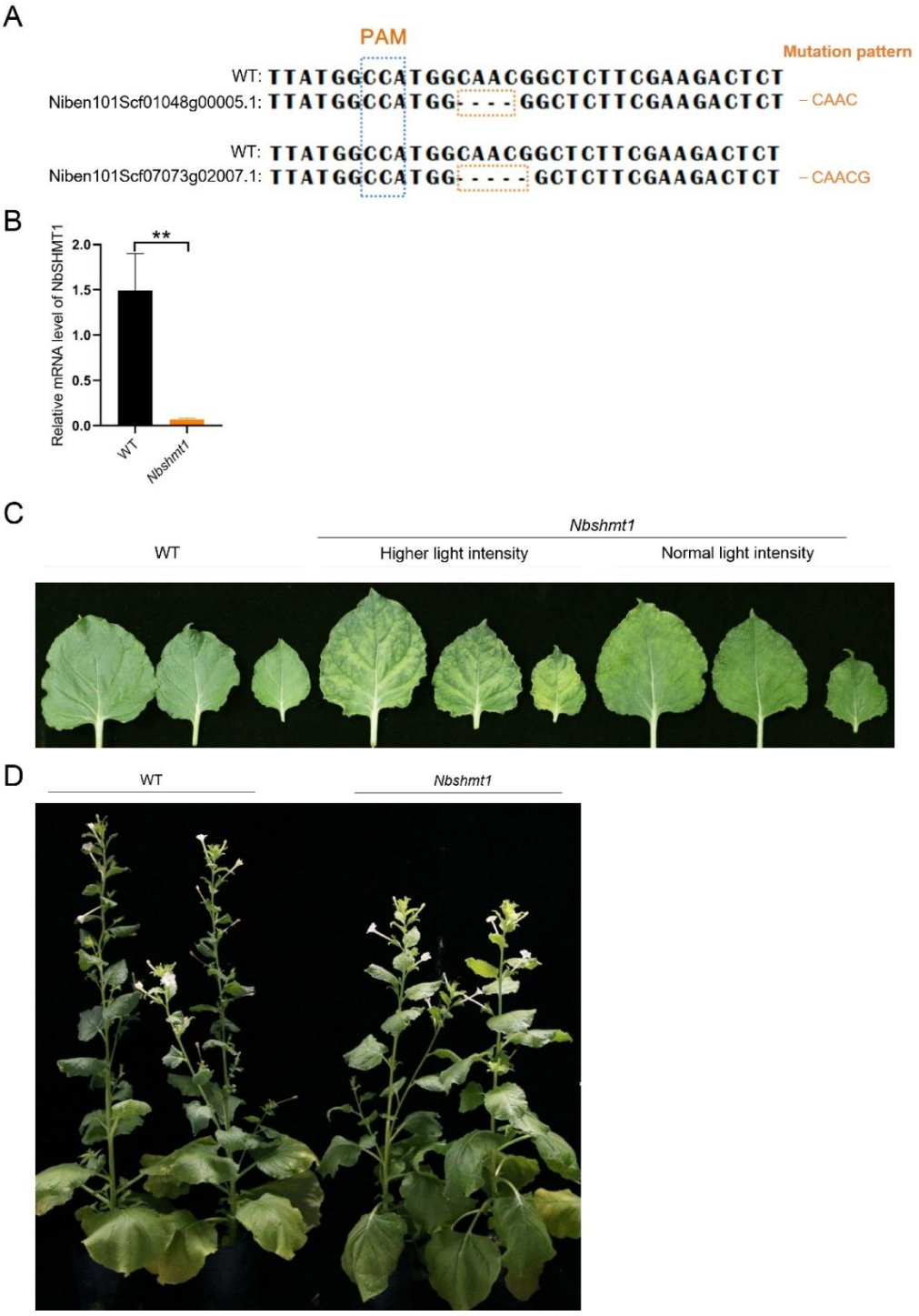
(A) Eight peptides of NbSHMT1 identified by iTRAQ were used for NbSHMT1 protein accumulation quantitative analysis. Eight peptides of NbSHMT1 were marked by eight colors. **(B)** NbSHMT1 protein accumulation showed

down-regulated in *N. benthamiana* plants in response to RSV infection at 10- or 30-dpi as detected by iTRAQ. Asterisks indicate a statistically significant difference according to Student's *t*-test (two-tailed), *0.01<P < 0.05.



Supplemental Figure S10. Relative mRNA levels of *NbSHMT1* in response to RSV or *B. cinerea* infection (Supports Figure 4).

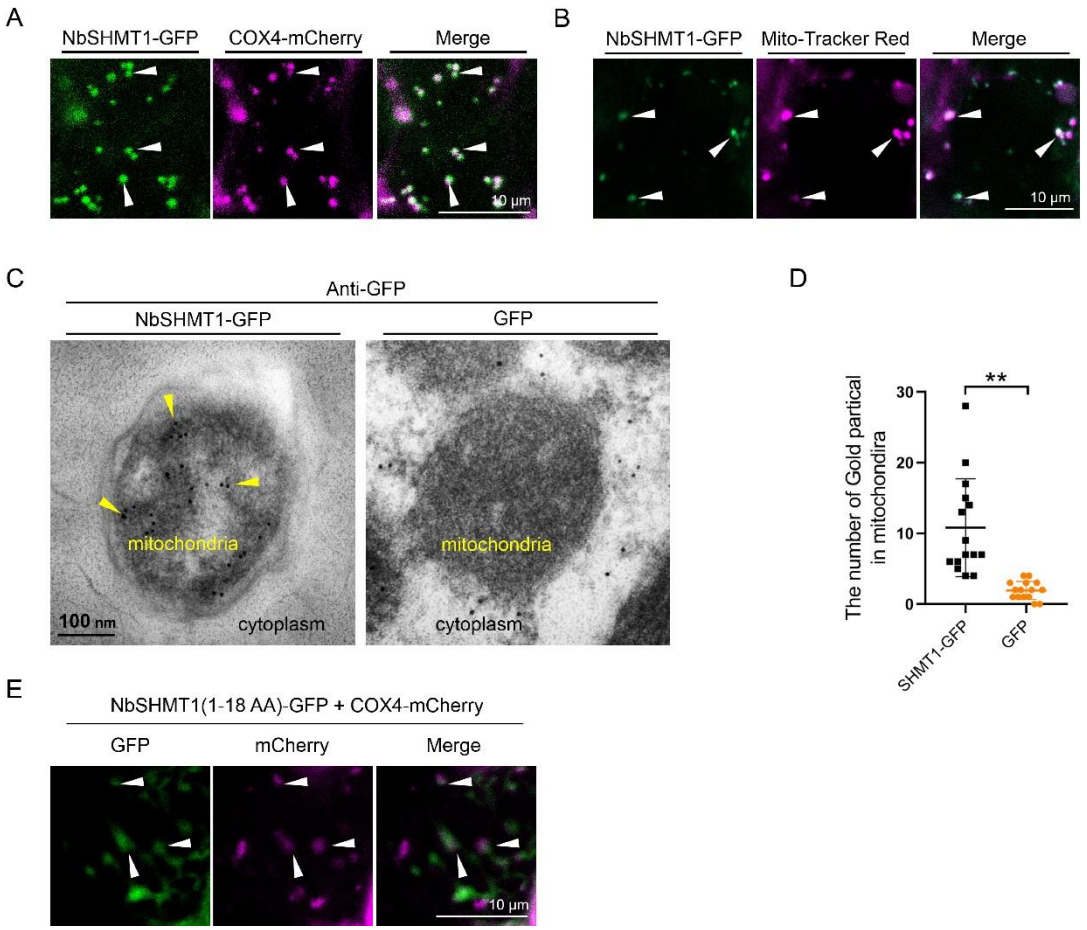
(A) Relative mRNA levels of *NbSHMT1* in response to RSV infection at 10-dpi and 30-dpi as detected by RT-qPCR. Data are means ± SD (n=3). "ns" indicates no statistically significant difference according to Student's *t*-test (two-tailed) ($p>0.05$). **(B)** Relative mRNA levels of *NbSHMT1* in response to *B. cinerea* infection at 24-hpi, 48-hpi and 96-hpi as detected by RT-qPCR. Data are means ± SD (n=3). Asterisks indicate a statistically significant difference according to Student's *t*-test (two-tailed), **$P < 0.01$. All experiments were performed three times with similar results.



Supplemental Figure S11. *NbSHMT1* knock-out and overexpression in *N. benthamiana* (Supports Figure 4).

(A) Mutation pattern of *Nbshmt1 N. benthamiana* plants detected by Sanger sequencing. PAM sequence of the target sequence is labeled by the blue dashed box. The mutation pattern is annotated behind the sequence. **(B)**

Relative mRNA level of *NbSHMT1* in *Nbshmt1 N. benthamiana* plants as detected by RT-qPCR. Data are means ± SD (n=3). Asterisks indicate a statistically significant difference according to Student's *t*-test (two-tailed), ** $p < 0.01$. **(C)** Phenotype of *NbSHMT1* knock out (*Nbshmt1*) *N. benthamiana* leaves compared to wild type (WT) *N. benthamiana* leaves under normal growth conditions and high light intensity growth conditions. **(D)** Plant developmental phenotype of *NbSHMT1* knock out (*Nbshmt1*) *N. benthamiana* plants compared to WT *N. benthamiana* plants under normal growth condition (26°C, 16/8 h day/night).



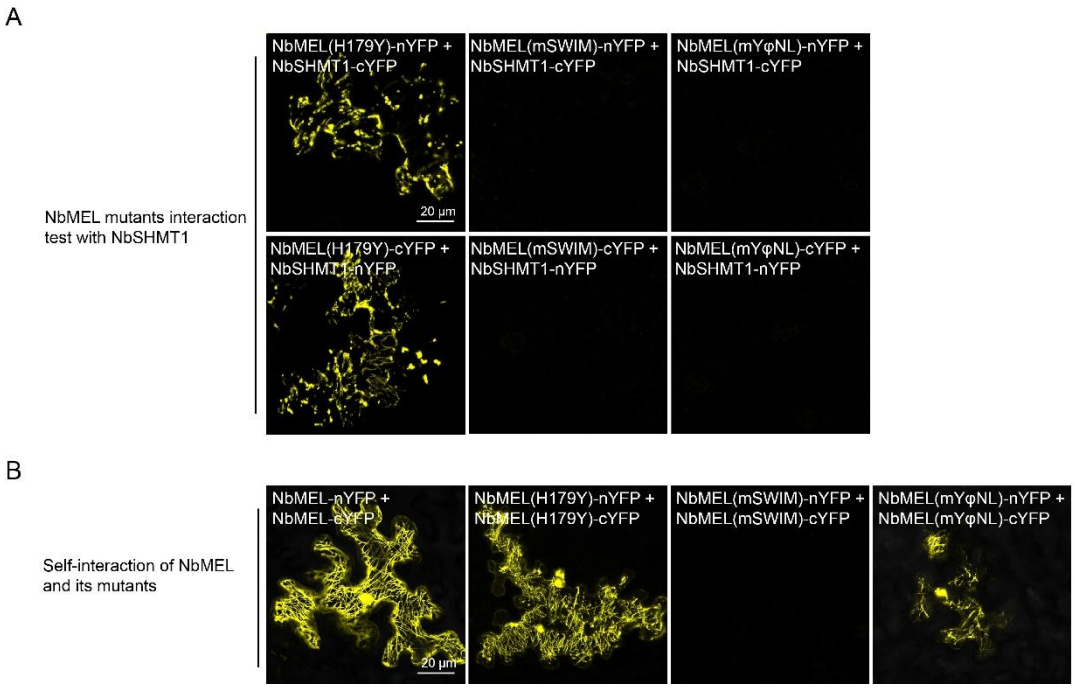
Supplemental Figure S12. NbSHMT1 localizes in mitochondria (Supports Figure 4).

(A, B) NbSHMT1-GFP co-localize with the mitochondrial marker COX4-mCherry (A) or Mito-Tracker Red stained mitochondria (B) in *N. benthamiana* epidermal cells, white triangles indicate co-localization between NbSHMT1-GFP and mitochondria. Bar: 10 μm. **(C)** Immunogold electron microscopy observation of NbSHMT1-GFP in *N. benthamiana* leaves. GFP signal was labeled using anti-GFP as primary antibody and 10 nm colloidal gold particle-conjugated secondary antibody was used to localize the GFP primary antibody. Gold particles are indicated by yellow triangles. Bar: 100 μm. **(D)** Comparison of gold particles number in mitochondria between NbSHMT1-GFP and GFP expressed *N. benthamiana* cells. Data are means ± SD (n=15). Asterisks mark significant differences according to two-tailed Student's *t*-test; *P < 0.05; **P < 0.01. **(E)** Confocal images of *N. benthamiana* epidermal cells co-expression of NbSHMT1(1-18 AA)-GFP with mitochondrial marker

COX4-mCherry by agroinfiltration. White arrows indicate co-localization of NbSHMT1(1-18 AA)-GFP with COX4-mCherry. Bar: 20 μm. These experiments were performed three times with similar results.

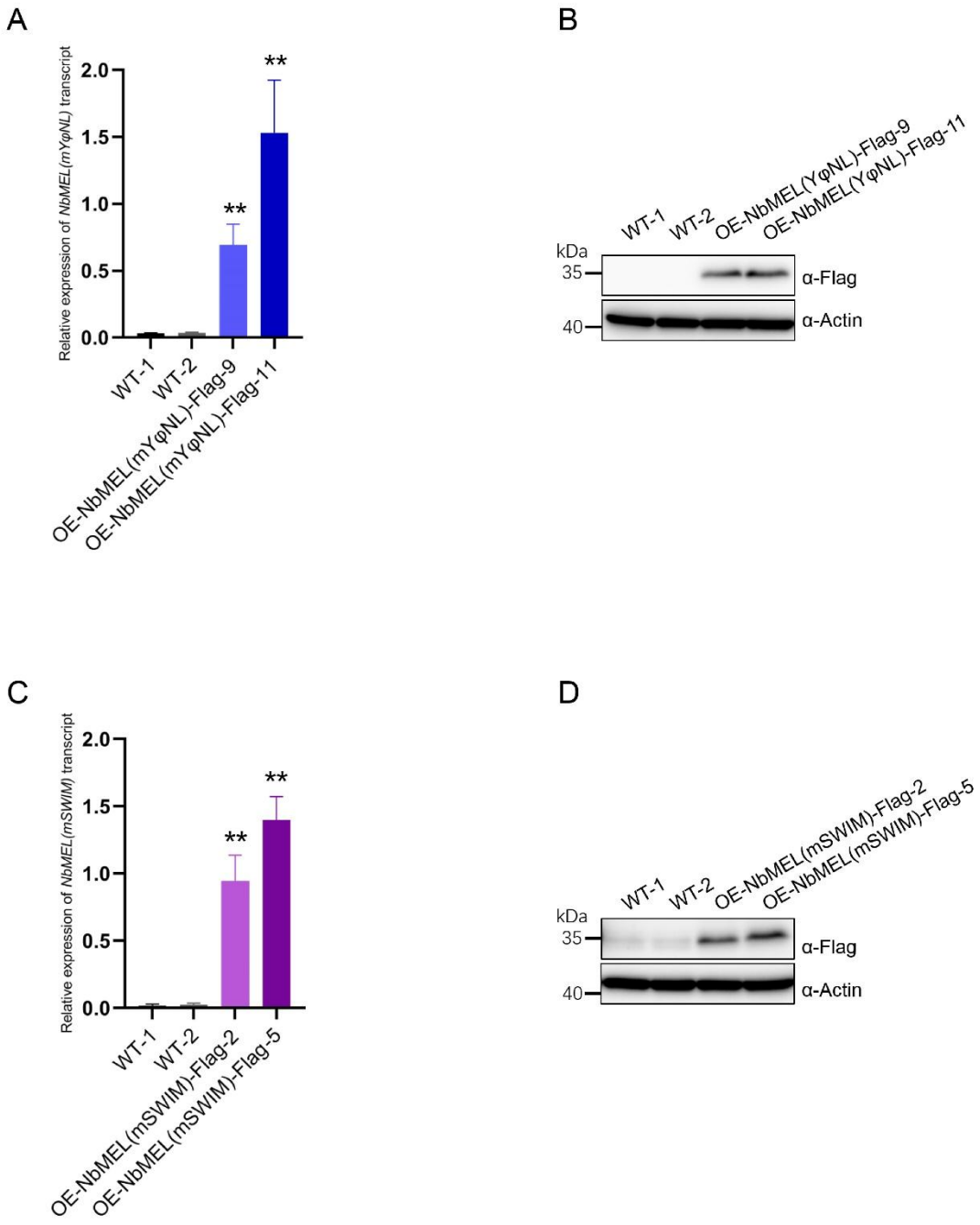
Supplemental Figure S13. VDAC1 (Voltage-dependent anion-selective channel protein 1-5) accumulation in OE-NbMEL and *Nbshmt1 N. benthamiana* plant leaves (Supports Figure 4).

(A) Comparison of VDAC1 accumulation in *Nbshmt1* and wild-type (WT) *N. benthamiana* plant leaves. **(B)** Comparison of VDAC1 accumulation in OE-NbMEL and WT *N. benthamiana* plant leaves. Actin was used as a loading control. The bands in immunoblots are quantified and the relative intensities (R-value) are shown above the band. All experiments were performed three times with similar results.



Supplemental Figure S14. BiFC assay to test the self-interaction of NbMEL or its mutants, and the interaction between NbMEL mutants and NbSHMT1 (Supports Figure 5).

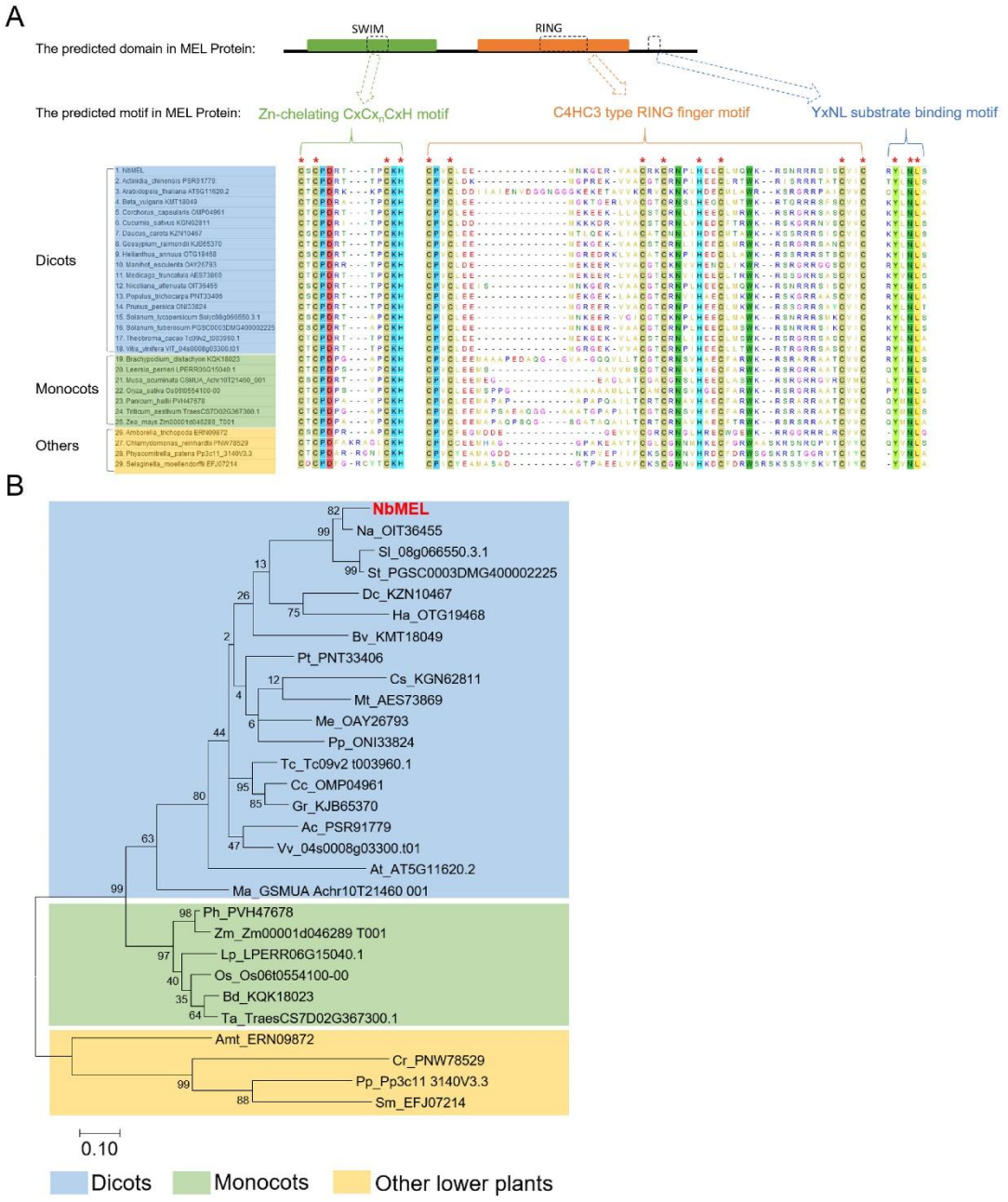
(A) Interaction test between NbMEL mutants and NbSHMT1 by BiFC. Confocal images were taken at 48 hpi. Bars: 20 μm. **(B)** Self-interaction test of NbMEL and its mutants by BiFC. Confocal images were taken at 48 hpi. Bars: 20 μm.



Supplemental Figure S15. Analysis of transcript, protein expression of transgenic *N. benthamiana* plants overexpressing *NbMEL(mYφNL)* or *NbMEL(mSWIM)* (Supports Figure 5).

(A) Relative mRNA level of *NbMEL(mYφNL)* in *NbMEL(mYφNL)-Flag* overexpression transgenic *N. benthamiana* plants as detected by RT-qPCR. Data are means ± SD (n=3). **(B)** NbMEL(mYφNL)-Flag accumulation in *NbMEL(mYφNL)-Flag* overexpression transgenic *N. benthamiana* plants

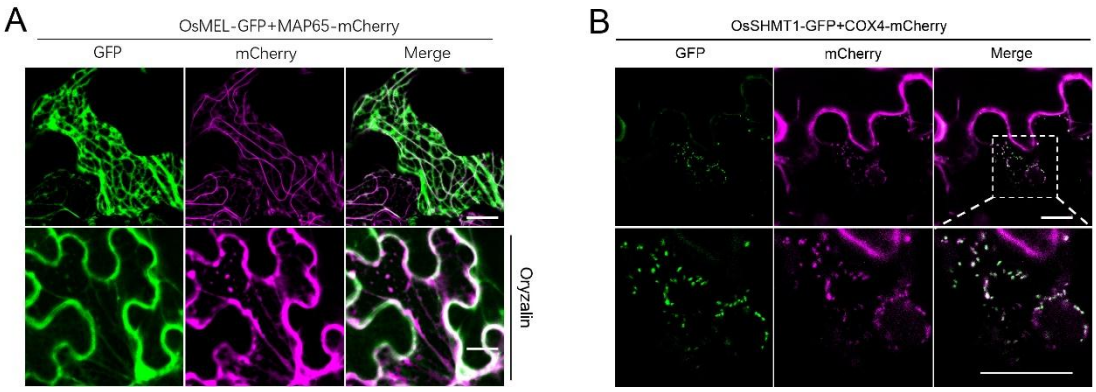
detected by immunoblotting using Flag antibody. Actin was used as the loading control. **(C)** Relative mRNA level of *NbMEL(mSWIM)* in *NbMEL(mSWIM)-Flag* overexpression transgenic *N. benthamiana* plants as detected by RT-qPCR. Data are means ± SD (n=3). **(D)** NbMEL(mSWIM)-Flag accumulation in *NbMEL(mSWIM)-Flag* overexpression transgenic *N. benthamiana* plants detected by immunoblotting using Flag antibody. Actin was used as the loading control. All experiments were performed three times with similar results.



Supplemental Figure S16. MEL is highly conserved in the plant kingdom (Supports Figure 5, Figure 6).

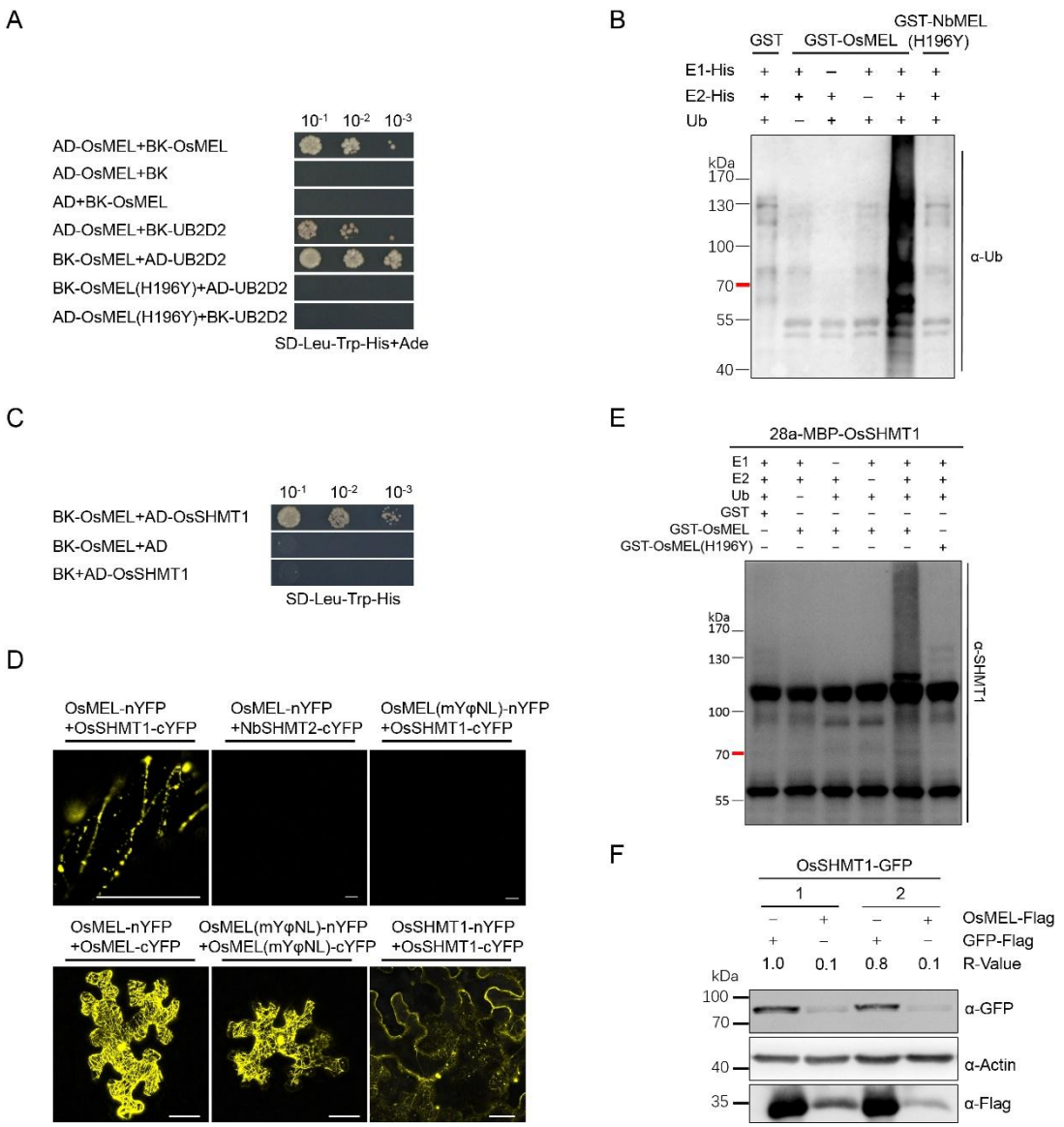
(A) Multiple sequence alignment of 28 MEL homologs from dicot, monocot, algae, and fern in the plant kingdom. Red asterisks indicate the highly conserved residues in the SWIM domain, C4HC3-type RING domain, and YφNL motif. **(B)** Phylogenetic tree of 28 MEL homologs from dicot, monocot, algae, and fern in the plant kingdom. Phylogenetic tree was constructed by the Maximum Likelihood method. The bootstrap consensus tree inferred from 1000

replicates is taken to represent the evolutionary history of the taxa analyzed. The evolutionary history was inferred by using the Maximum Likelihood method and JTT matrix-based model. The tree with the highest log likelihood is shown. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. All positions containing gaps and missing data were eliminated (complete deletion option). Evolutionary analyses were conducted in MEGA 7.



Supplemental Figure S17. Subcellular localization of OsMEL and OsSHMT1 (Supports Figure 6).

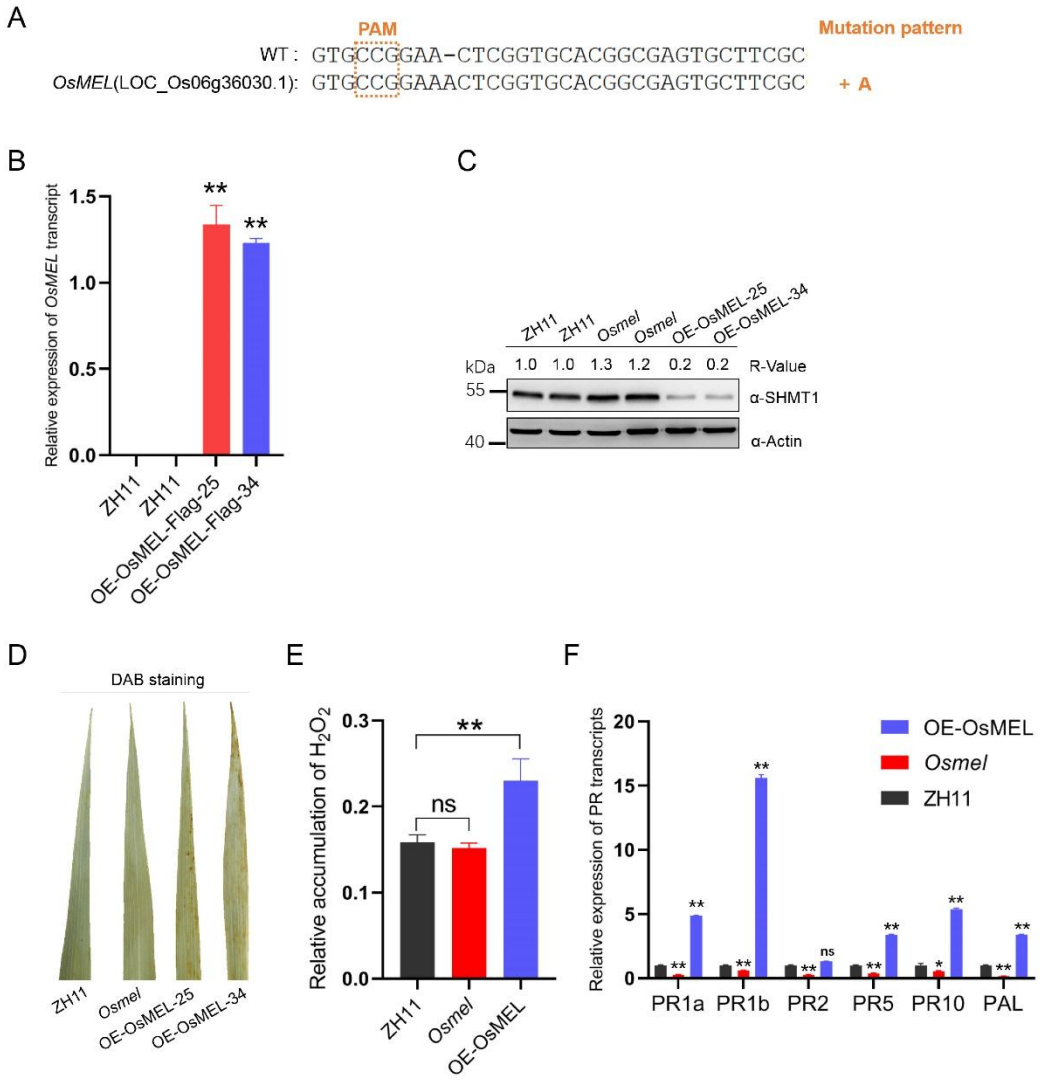
(A) OsMEL-GFP co-localized with the microtubule-associated protein 65 (MAP65-mCherry) in *N. benthamiana* epidermal cells. Bar: 20 μm. **(B)** OsSHMT1-GFP co-localized with COX4-mCherry in mitochondria. Bar: 20 μm. Confocal images were taken at 48 hpi. All experiments were performed three times with similar results.



Supplemental Figure S18. OsMEL is an E3 ligase that interacts, ubiquitinates and promotes degradation of OsSHMT1 (Supports Figure 6).

(A) Yeast two hybrid assay showed OsMEL interacts with E2 ubiquitin-conjugating enzyme UB2D2 and its ubiquitin ligase inactive mutant OsMEL(H196Y) lost the interaction ability. **(B)** *In vitro* ubiquitination assay showed OsMEL self-ubiquitination and its ubiquitin ligase inactive mutant OsMEL(H196Y) lost self-ubiquitination ability. GST-tagged OsMEL and its ubiquitin ligase inactive mutant OsMEL(H196Y) were assayed for self-ubiquitination in the presence of E1, human E2(UB2D2), and Ub. GST was used as a negative control. An anti-ubiquitin antibody was used to detect

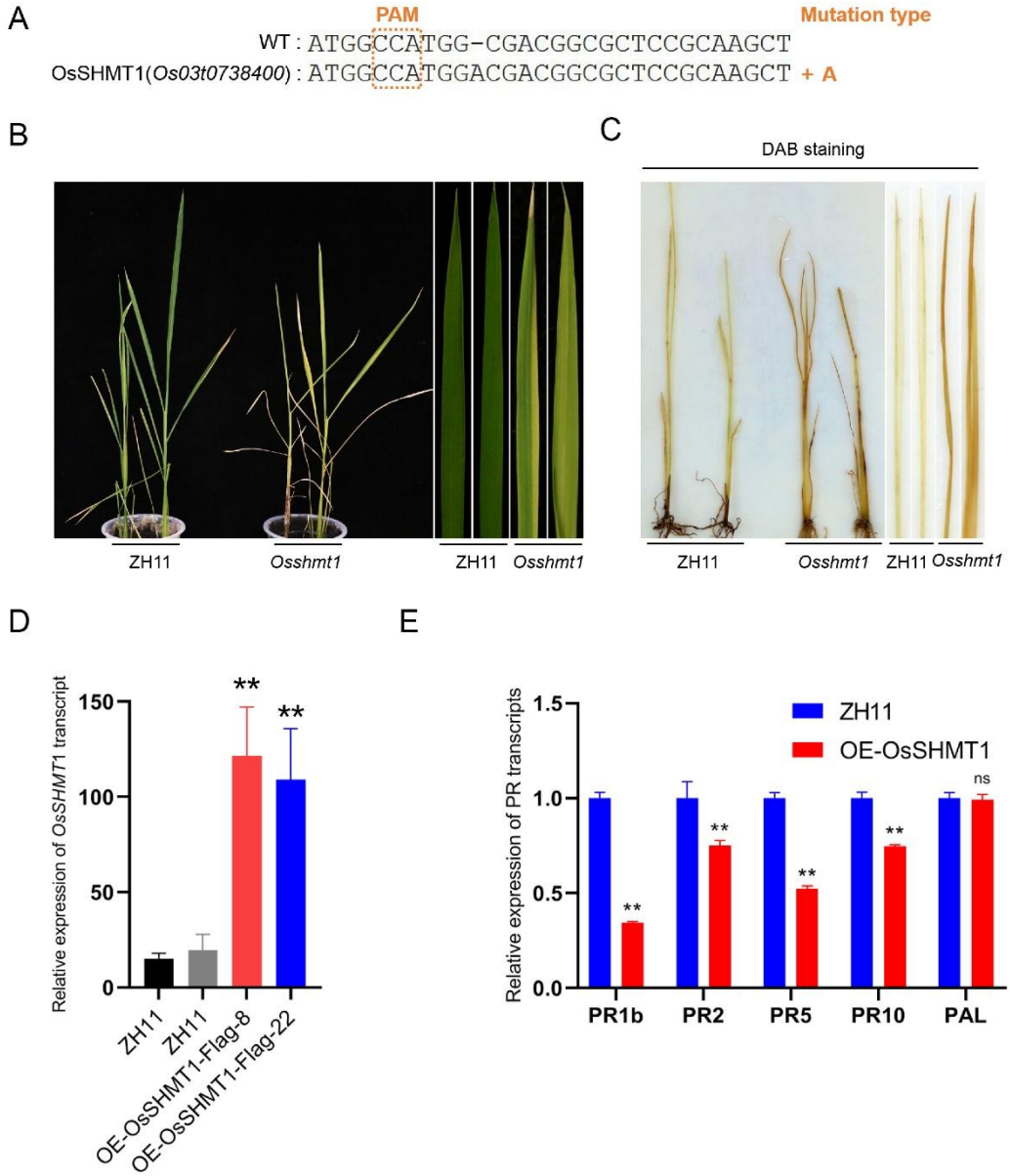
ubiquitination. **(C)** OsMEL interacts with OsSHMT1 in yeast two hybrid assay. **(D)** Bimolecular-fluorescence complementation assay showing OsMEL-OsSHMT1 interaction. Self-interaction of OsMEL, OsMEL(mYφNL) and OsSHMT1 were used as controls, indicating all vectors used in BiFC had expressed *in vivo*. Confocal images were taken at 48 hpi. Bars: 20 μm. **(E)** *In vitro* ubiquitination assay. NbSHMT1 was ubiquitinated by OsMEL *in vitro*, but not its ubiquitin ligase–inactive mutant OsMEL(H196Y). Ubiquitination of MBP-NbSHMT1 was detected by immunoblotting using SHMT1 antibody. **(F)** Accumulation of OsSHMT1-GFP in *N. benthamiana* leaves co-expressed with OsMEL or GFP (control). Actin was used as the loading control. The bands in immunoblot were quantified, and the relative intensities (R-value) are shown above each band. All experiments were performed three times with similar results.



Supplemental Figure S19. The phenotype of *OsMEL* overexpression (OE-OsMEL-25/34) and knockout (*Osmel*) *Oryzae sativa* plants (Supports Figure 6).

(A) Mutation pattern of *Osmel O. sativa* detected by Sanger sequencing. PAM sequence of the target sequence is labeled by orange dashed box. The mutation pattern is annotated behind the sequence. **(B)** Relative mRNA level of *OsMEL* in OE-OsMEL and wild type ZH11 *O. sativa* plants as detected by RT-qPCR. Data are means ± SD (n=3). Asterisks indicate a statistically significant difference according to Student's *t*-test (two-tailed); **P < 0.01. **(C)** Endogenous OsSHMT1 protein accumulation in OE-OsMEL, *Osmel*, and ZH11 (wild type) *O. sativa* plants. Actin was used as the loading control. The bands in immunoblot were quantified, and the relative intensities (R-value) are shown

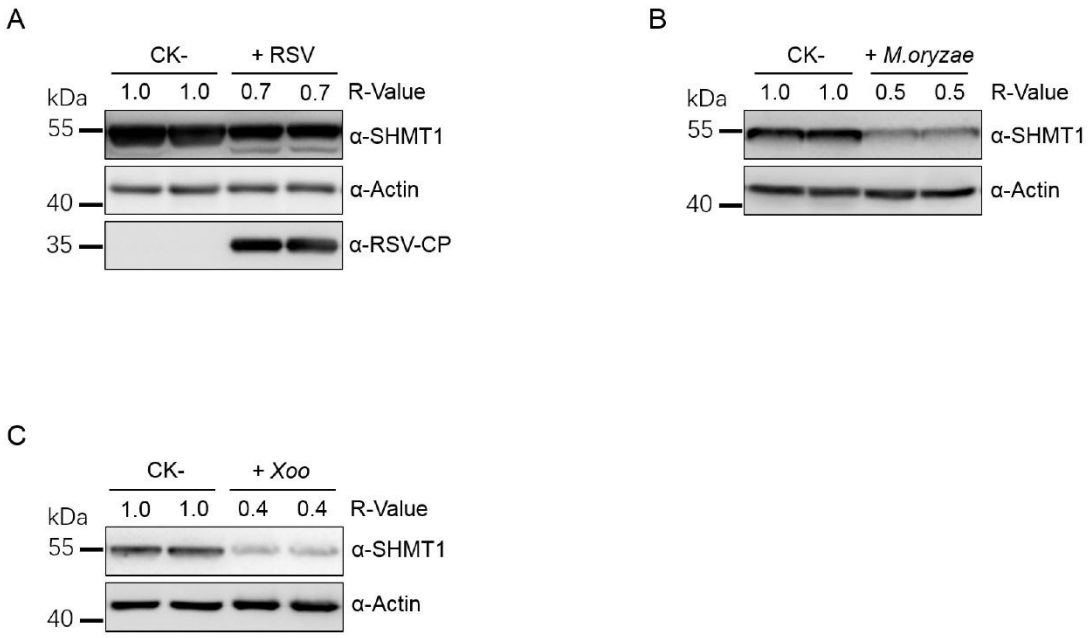
above the bands. **(D)** DAB staining in OE-OsMEL, *Osme*l, and wild type ZH11 *O. sativa* leaves. **(E)** Relative H_2O_2 accumulation in OE-OsMEL, *Osme*l, and wild-type ZH11 *O. sativa* plant leaves were measured by Amplex red. Data are means ± SD (n=8). Asterisks indicate a statistically significant difference according to Student's *t*-test (two-tailed); **P < 0.01; ns, no statistically significant difference (p > 0.05). **(F)** RT-qPCR detection of the relative expression level of defense-related genes in OE-OsMEL, *Osme*l, and wild-type ZH11 *O. sativa* plants. Data are means ± SD (n=3). Asterisks indicate a statistically significant difference according to Student's *t*-test (two-tailed); *P < 0.05; **P < 0.01; ns, no statistically significant difference (p > 0.05). All experiments were performed three times with similar results.



Supplemental Figure S20. The phenotype of OsSHMT1 overexpression (OE-OsSHMT-8/22) and knockout (*Osshmt1*) *O. sativa* plants (Supports Figure 6).

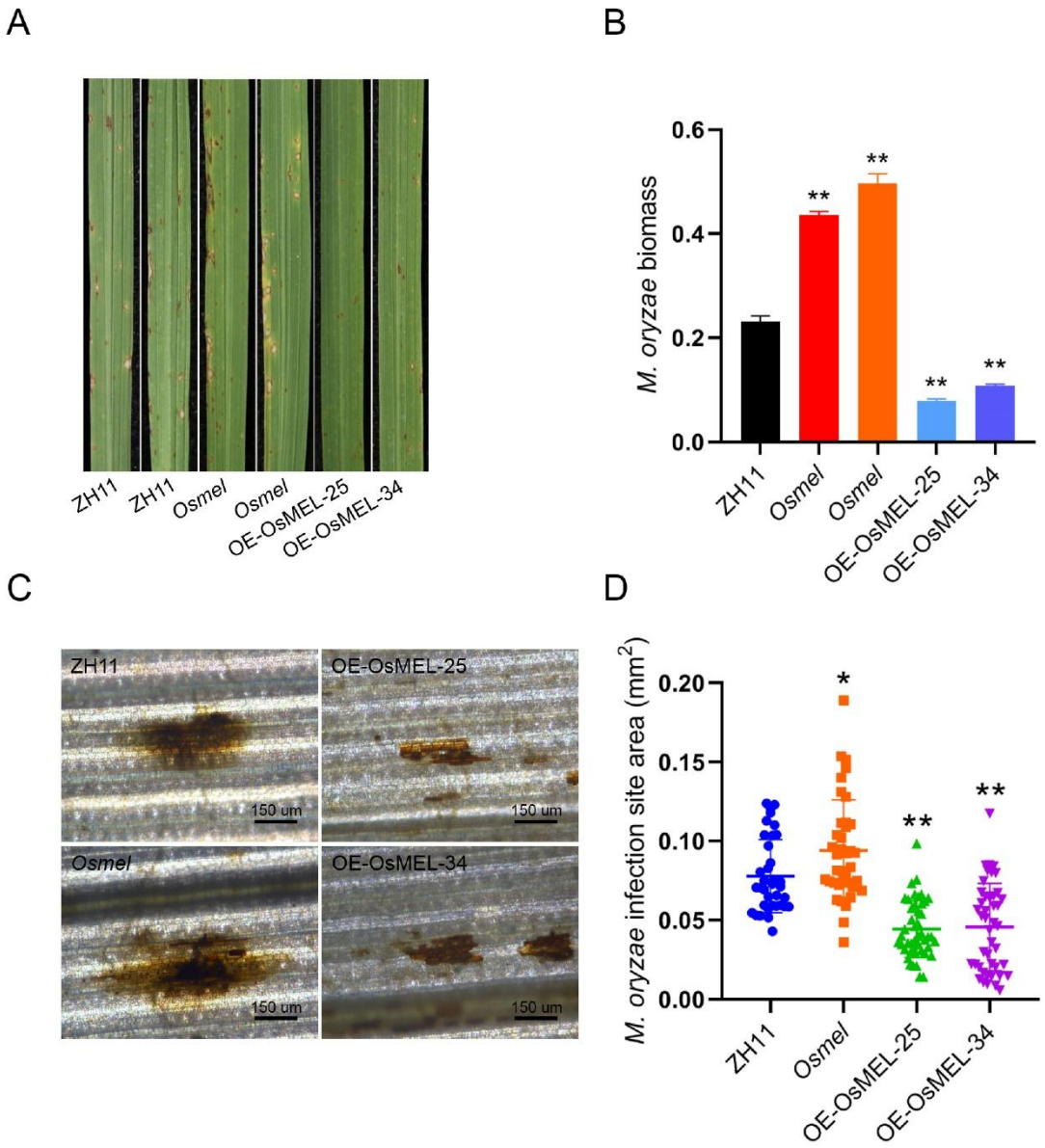
(A) Mutation pattern of *Osshmt1 O. sativa* detected by Sanger sequencing. PAM sequence of target sequence is labeled by orange dashed box. The mutation pattern is annotated behind the sequence. **(B)** Phenotype of *Osshmt1 O. sativa* plants, showing severe leaf chlorosis and plant lethality. **(C)** DAB staining in *Osshmt1* and wild-type ZH11 *O. sativa* plants, showing high H_2O_2 accumulation in *Osshmt1 O. sativa* plants. **(D)** Relative expression level of

OsSHMT1 in OE-OsSHMT1 and wild type ZH11 *O. sativa* plants as detected by RT-qPCR. Data are means ± SD (n=3). Asterisks indicate a statistically significant difference according to Student's *t*-test (two-tailed); **P < 0.01. **(E)** Relative expression level of defense-related genes in OE-OsSHMT1 plants and ZH11 *O. sativa* plants as detected by RT-qPCR. Data are means ± SD (n=3). Asterisks indicate a statistically significant difference according to Student's *t*-test (two-tailed); **P < 0.01; ns, no statistically significant difference (p > 0.05). All experiments were performed three times with similar results.



Supplemental Figure S21. Comparison of endogenous OsSHMT1 accumulation in RSV (A), *M. oryzae* (B), or *Xoo* (C)-infected *O. sativa* plants with mock (CK-) *O. sativa* plants (Supports Figure 6).

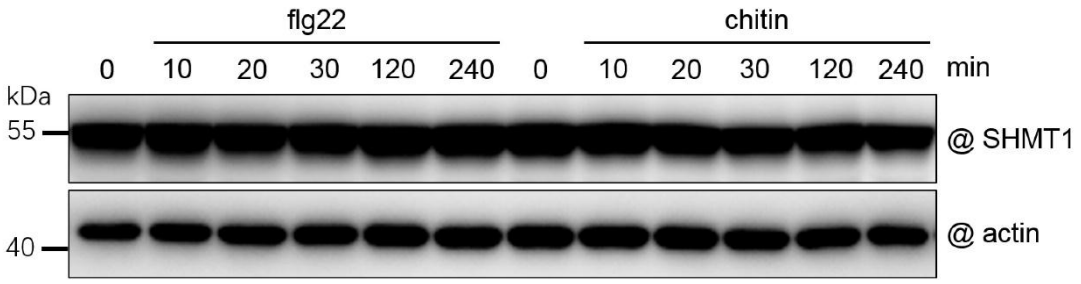
The bands in immunoblot were quantified, and the relative intensities (R-value) are shown above the band. All experiments were performed three times with similar results.



Supplemental Figure S22. OsMEL positively regulates *O. sativa* plants resistance to *M. oryzae* (Supports Figure 6).

(A, B) *M. oryzae* infection symptoms (A) and biomass (B) in OE-OsMEL, *Osmel*, and wild type ZH11 *O. sativa* plants inoculated with *M. oryzae* conidia by spray. Lesions were photographed at 5 dpi. *M. oryzae* biomass was detected by RT-qPCR. Data are means ± SD (n=3). Asterisks indicate a statistically significant difference according to Student's *t*-test (two-tailed), **P < 0.01. **(C, D)** DAB staining (C) and lesion measurement (D) of *M. oryzae* infection sites in OE-OsMEL, *Osmel*, and wild-type ZH11 *O. sativa* plants inoculated with *M.*

*oryza*e conidia by spray. Lesions were photographed at 3 dpi. Data are means ± SD, n=37. Asterisks indicate a statistically significant difference according to Student's *t*-test (two-tailed); *0.01<P < 0.05; **P < 0.01. All experiments were performed three times with similar results.



Supplemental Figure S23. NbSHMT1 protein accumulation assay under flg22 or chitin treatment (Supports Figure 4).

NbSHMT1 protein accumulations at 10, 20, 30, 120, 240 minutes post flg22 or chitin treatment. Actin was used as the loading control. This experiment was performed three times with similar results.

Supplemental Table S1. Primers used in this work.

TRV-based VIGS	
TRV-NbMEL-F	TGCTCTAGAGGAATCGGTCGCGTCTAGTT
TRV-NbMEL-R	CGCGGATCCGAATACACGTGTCGTCGATTGAG
NbMEL promoter assay	
NbMEL-Promoter-F	catgattacgaattcccatggACGGTCTTTTCCTTGCGATCA
NbMEL-Promoter-R	tctagaggatccccgggtaccACTTTTGGAAAGTCGCAATATTTTT
GFP/Flag/Myc-tagged plasmid used for transiently expression or transformation	
NbMEL-GFP-F	gagaacacgggggacgagctcATGGAATCCATCGCATCTAGTTC
NbMEL-GFP-R	gctcaccatgtcgactctagaATTCCCACAGTAGCTGTGCTGAT
OsMEL-GFP-F	gagaacacgggggacgagctcATGGAGCCCGTGACGGCG
OsMEL-GFP-R	gctcaccatgtcgactctagaCCCGGCGCACAGTCCCCC
NbSHMT1-GFP-F	acgggggacgagctcggtaccATGGCCATGGCAACGGCT
NbSHMT1-GFP-R	gctcaccatgtcgactctagaTTTTTTGTACTTCATGGTTTCCTTCT
NbMEL-Flag/Myc-F	acgggggacgagctcggtaccATGGAATCCATCGCATCTAGTTC
NbMEL-Flag-R	gtggtccttatagtcgtcgacATTCCCACAGTAGCTGTGCTGAT
NbMEL-Myc-R	gagtttctgctccatgtcgacATTCCCACAGTAGCTGTGCTGAT
NbSHMT-Flag/Myc-F	acgggggacgagctcggtaccATGGCCATGGCAACGGCT
NbSHMT-Flag-R	gtggtccttatagtcgtcgacTTTTTTGTACTTCATGGTTTCCTTCT
NbSHMT-Myc-R	gagtttctgctccatgtcgacTTTTTTGTACTTCATGGTTTCCTTCT
OsMEL-Flag/Myc/GFP-F	acgggggacgagctcggtaccATGGAGCCCGTGACGGCG
OsMEL-Flag-R	gtggtccttatagtcgtcgacCCCGGCGCACAGTCCCCC
OsMEL-Myc-R	gagtttctgctccatgtcgacCCCGGCGCACAGTCCCCC
OsSHM1-Flag/Myc/GFP-F	acgggggacgagctcggtaccATGGCCATGGCGACGGCG
OsSHM1-Flag-R	gtggtccttatagtcgtcgacGTTCTTGTACTTCATGGTTTCTTTCTCA
OsSHM1-Myc-R	gagtttctgctccatgtcgacGTTCTTGTACTTCATGGTTTCTTTCTCA
OsSHM1-GFP-R	gcccttgctcaccatgtcgacGTTCTTGTACTTCATGGTTTCTTTCTCA
GFP-Flag-F	acgggggacgagctcggtaccATGGTGAGCAAGGGCGAGG
GFP-Flag-R	gtggtccttatagtcgtcgacCTTGTACAGCTCGTCCATGCC
Yeast two hybrid assays	
AD-NbMEL-F	gccatggaggccagtgaattcATGGAATCCATCGCATCTAGTTC
AD-NbMEL-R	atgcccacccgggtggaattcCTAATTCCCACAGTAGCTGTGCTG
BD-NbMEL-F	atggccatggaggccgaattcATGGAATCCATCGCATCTAGTTC
BD-NbMEL-R	tcgacggatccccgggaattcCTAATTCCCACAGTAGCTGTGCTG

BK-NbMEL(1-90AA)-R	tcgacggatccccgggaattcTCAACCCAAAACGCGAATG
BK-NbMEL(1-140AA)-R	tcgacggatccccgggaattcTCATCGTTCCTTAAAAAACGTCTCGT
BK-NbMEL(1-206AA)-R	tcgacggatccccgggaattcTCAATCTCTCCACCTTGCCCTGC
BK-NbMEL(207-229AA)-R	tcgacggatccccgggaattcTCACATGTCATTATCGCCGC
BK-NbMEL(91-242AA)-F	atggccatggaggccgaattcATGGTCTCCATCGACGACACG
BK-NbMEL(141-242AA)-F	atggccatggaggccgaattcATGCCAAAAAGTTCGCCGTTGAG
BK-NbMEL(207-242AA)-F	atggccatggaggccgaattcATGAGAGCTGAGCAAGAAGCTGA
PM-NbMEL-H179Y-F	CCATTAtacGAAGAATGTTTGATGCAATGGAAG
PM-NbMEL-H179Y-R	CATTCTTCgtaTAATGGATTTCTACATTTCCGACATG
PM-NbMEL(YφNL)-F	GAGGgctgcggctgctTCTGCTTATATGGGCGGC
PM-NbMEL(YφNL)-R	AagcagccgcagcCCTCTCAGCTTCTTGCTCAGCT
PM-NbMEL(mSWIM)-F	cctgatcgaaccaccccagccaaagccATCCTCTTCGTCCTCATTCGC
PM-NbMEL(mSWIM)-R	tggggtggttcgatcaggggcgctggcTGATGGGGTTGTGGAGAGGTT
AD-OsMEL-F	gccatggaggccagtgaattcATGGAGCCCGTGACGGCG
AD-OsMEL-R	atgcccacccgggtggaattcCTACCCGGCGCACAGTCC
BD-OsMEL-F	atggccatggaggccgaattcATGGAGCCCGTGACGGCG
BD-OsMEL-R	tcgacggatccccgggaattcCTACCCGGCGCACAGTCC
PM-OsMEL(H196Y)-F	AACTCGGTGtacGGCGAGTGCTTCGCGCGGTG
PM-OsMEL(H196Y)-R	TCGCCgtaCACCGAGTTCCGGCACATCGCGCA
AD-UB2D2-F	gccatggaggccagtgaattcATGGCTCTGAAGAGAATCCACAA
AD-UB2D2-R	atgcccacccgggtggaattcCCTATCTTTATTTGTAGAGGTTATCCAATA
BK-UB2D2-F	atggccatggaggccgaattcATGGCTCTGAAGAGAATCCACAA
BK-UB2D2-R	tcgacggatccccgggaattcCCTATCTTTATTTGTAGAGGTTATCCAATA
AD-NbSHMT1-F	gccatggaggccagtgaattcATGGCCATGGCAACGGCT
AD-NbSHMT1-R	atgcccacccgggtggaattcTCATTTTTTGTACTTCATGGTTTCCT
BD-NbSHMT1-F	atggccatggaggccgaattcATGGCCATGGCAACGGCT
BD-NbSHMT1-R	tcgacggatccccgggaattcTCATTTTTTGTACTTCATGGTTTCCT
BiFC assays	
2YN/2YC-NbMEL-F	atttacgaacgatagttaattaaATGGAATCCATCGCATCTAGTTC
2YN/2YC-NbMEL-R	acctcctccactagtggcgcgccCATTCCCACAGTAGCTGTGCTG
2YN/2YC-OsMEL-F	atttacgaacgatagttaattaaATGGAGCCCGTGACGGCG
2YN/2YC-OsMEL-R	acctcctccactagtggcgcgccCCCCGGCGCACAGTCCCC
2YN/2YC-NbSHMT1-F	atttacgaacgatagttaattaaATGGCCATGGCAACGGCT
2YN/2YC-NbSHMT1-R	acctcctccactagtggcgcgccCTTTTTTGTACTTCATGGTTTCCTTC

2YN/2YC-OsSHMT1-F	atttacgaacgatagttaattaaATGGCCATGGCGACGGCG
2YN/2YC-OsSHMT1-R	acctcctccactagtggcgcgccCGTTCTTGTACTTCATGGTTTC
In vitro assays	
GST-NbMEL-F	gatctggttccgcgtggatccATGGAATCCATCGCATCTAGTTC
GST-NbMEL-R	gatgcggccgctcgagtcgacCTAATTCCCACAGTAGCTGTGCTG
GST-NbSHMT1-F	gatctggttccgcgtggatccATGGCCATGGCAACGGCT
GST-NbSHMT1-R	gatgcggccgctcgagtcgacTCATTTTTTGTACTTCATGGTTTCCT
28a-UB2D2-F	cagcaaatgggtcgcggatccATGGCTCTGAAGAGAATCCACAA
28a-UB2D2-R	tgcggccgcaagcttgtcgacCATCGCATACTTCTGAGTCCATTC
28a-NbMEL-F	cagcaaatgggtcgcggatccATGGAATCCATCGCATCTAGTTC
28a-NbMEL-R	tgcggccgcaagcttgtcgacATTCCCACAGTAGCTGTGCTGAT
28a-NbMEL-MBP-F	tatcggaattaattcggatccGATGGAATCCATCGCATCTAGTT
28a-NbMEL-MBP-R	tgcggccgcaagcttgtcgacATTCCCACAGTAGCTGTGCTGAT
28a-NbSHMT1-MBP-F	tatcggaattaattcggatccGATGGCCATGGCAACGGC
28a-NbSHMT1-MBP-R	tgcggccgcaagcttgtcgacTTTTTTGTACTTCATGGTTTCCTTCT
GST-OsMEL-F	gatctggttccgcgtggatccATGGAGCCCGTGACGGCG
GST-OsMEL-R	gatgcggccgctcgagtcgacCTACCCGGCGCACAGTCC
MBP-28a-OsSHMT1-F	atcggaattaattcggatccGATGGCCATGGCGACGGC
MBP-28a-OsSHMT1-R	gcggccgcaagcttgtcgacGTTCTTGTACTTCATGGTTTC
NbMEL/OsMEL/OsSHMT1 CRISPR/Cas9-based knock-out transformation assays	
BGK01-KA-NbMEL-Up	TGATTGCTGTGTTGGCATTAGATGG
BGK01-KA-NbMEL-Low	AAACCCATCTAATGCCAACACAGCA
BGK01-KA-NbSHMT1-Up	TGATTGCTTCGAAGAGCCGTTGCCA
BGK01-KA-NbSHMT1-Low	AAACTGGCAACGGCTCTTCGAAGCA
DNA-NbMEL-1611-F	TTCCTACAAAACATACCAAAAC
DNA-NbMEL-1611-R	AAATTAGGCTACGAAAGAGAAT
DNA-NbMEL-1056-F	TTCCCTACAAAACATACATACC
DNA-NbMEL-1056-R	GATATTAGAGTAGACAAGAGTTCCT
DNA-NbSHMT1-1048-F	CCACCCAAAAATAACTCATTAC
DNA-NbSHMT1-1048-R	CATGGTACTGGAGTGATTTAAAT
DNA-NbSHMT1-7073-F	CACCCAAAACACAAGTCATT
DNA-NbSHMT1-7073-R	ATACTTCTTTGTAACGGGTGC
BGK03-OsMEL-UP	TGTGTGCTGCGGCTGCTGCACCGCG
BGK03-OsMEL-LOW	AAACCGCGGTGCAGCAGCCGCAGCA

BGK03-OsSHMT1-UP	TGTGTGGGTCTGGAGCTCATCCCGT
BGK03-OsSHMT1-LOW	AAACACGGGATGAGCTCCAGACCCA
DNA-OsSHMT1-F	ATCCCGAGATCGCCGACATCAT
DNA-OsSHMT1-R	TATTCGTTTCCACCGTAGTATCTCGC
DNA-OsMEL-F	AAGCACATCCTCTTCGTCCTCCTC
DNA-OsMEL-R	TGAATAACTGAAGTAGCAAGGTCAGCCT
RT-qPCR	
RT-NbMEL-F1	CACATCCTCTTCGTCCTCATTC
RT-NbMEL-R1	CTTAAAAAACGTCTCGTGAAATCT
RT-NbSHMT1-F1	TGGCGGCTCTCTCTATTACATG
RT-NbSHMT1-R1	TCCACTGGCGTGCTTTCTC
RT-NbPR1-F	AGGTGTGTGGACACTATACTCAAGTG
RT-NbPR1-R	CACATATAACGTGAAATGGACGC
RT-NbPR2-F	GGAGATTATTGTATCTGAAAGTGGATG
RT-NbPR2-R	TCCTTCCTTATTATTTTCATCAAATATG
RT-NbPR4-F	TCAGAAATATGGCTGGACTGCTT
RT-NbPR4-R	TTGTGTCCAATTGGTTAAAGACGT
RT-NbPR5-F	TACATTCACATGTTCTAATGCCAATT
RT-NbPR5-R	GACCCTGATTCAGTACCTGGAAGT
RT-NbWRKY33-F	AGCTACGCTATGAATAAACCTCCAT
RT-NbWRKY33-R	AACTTGAACTTCCAGAGCTCTGTAAC
RT-NbACTIN-F	CAATCCAGACACTGTACTTTCTCTC
RT-NbACTIN-R	AAGCTGCAGGTATCCATGAGACTA
RT-OsUBQ5-F	ACCACTTCGACCGCACTACT
RT-OsUBQ5-R	ACGCCTAAGCCTGCTGGTT
RT-OsMEL-F	AACGTGTACACGGTGACGC
RT-OsMELR	CGACCACAGCTGGTGGAAC
RT-OsPR1b-F	TACGCCAGCCAGAGGAGC
RT-OsPR1b-R	GCCGAACCCCAGAAGAGG
RT-OsPR2-F	GCGTTGCTTCCGTTTTAACACT
RT-OsPR2-R	TTCTTGGGAAGTAGATGCGCAT
RT-OsPR5-F	CAACAGCAACTACCAAGTCGTCTT
RT-OsPR5-R	CAAGGTGTCGTTTTATTCATCAAC
RT-OsPR10-F	GTCCGGGCACCATCTACACC

RT-OsPR10-R	CAAGCTTCGTCTCCGTCGAGT
RT-OsPAL1-F	CTACAACAACGGGCTGACCT
RT-OsPAL1-R	TCTGGACATGGTTGGTGATG
***M. oryzae* biomass assay**	
MoPOT2-F	ACGACCCGTCTTTACTTATTTGG
MoPOT2-R	AAGTAGCGTTGGTTTTGTTGGAT
OsUb-F	TTCTGGTCCTTCCACTTTCAG
OsUb-R	ACGATTGATTTAACCAGTCCATGA