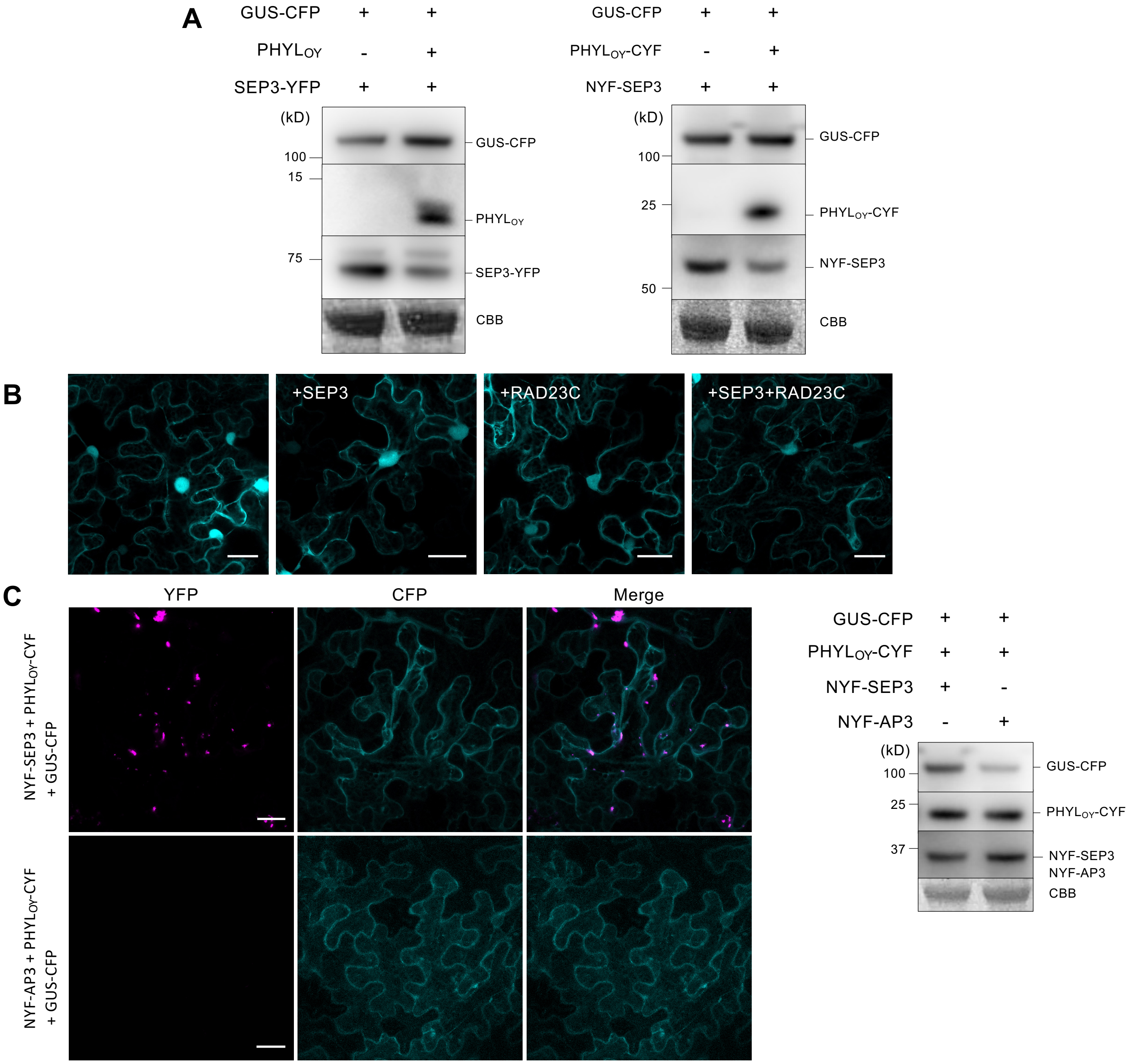
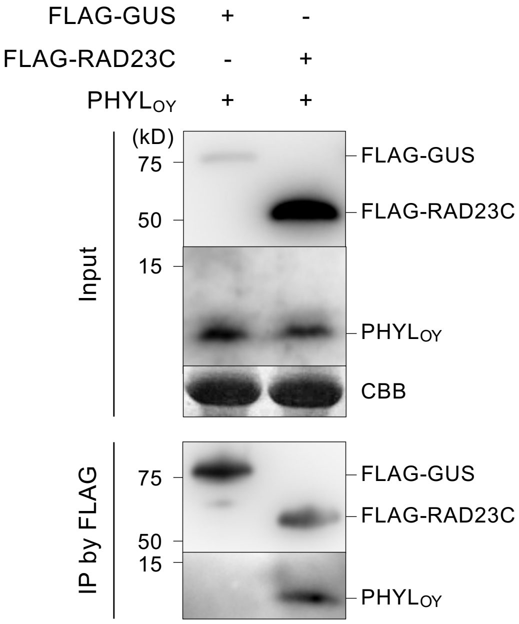


**Supplemental Figure 1.** Supporting information for fluorescent microscopy analysis. (Supports Figure 1.)

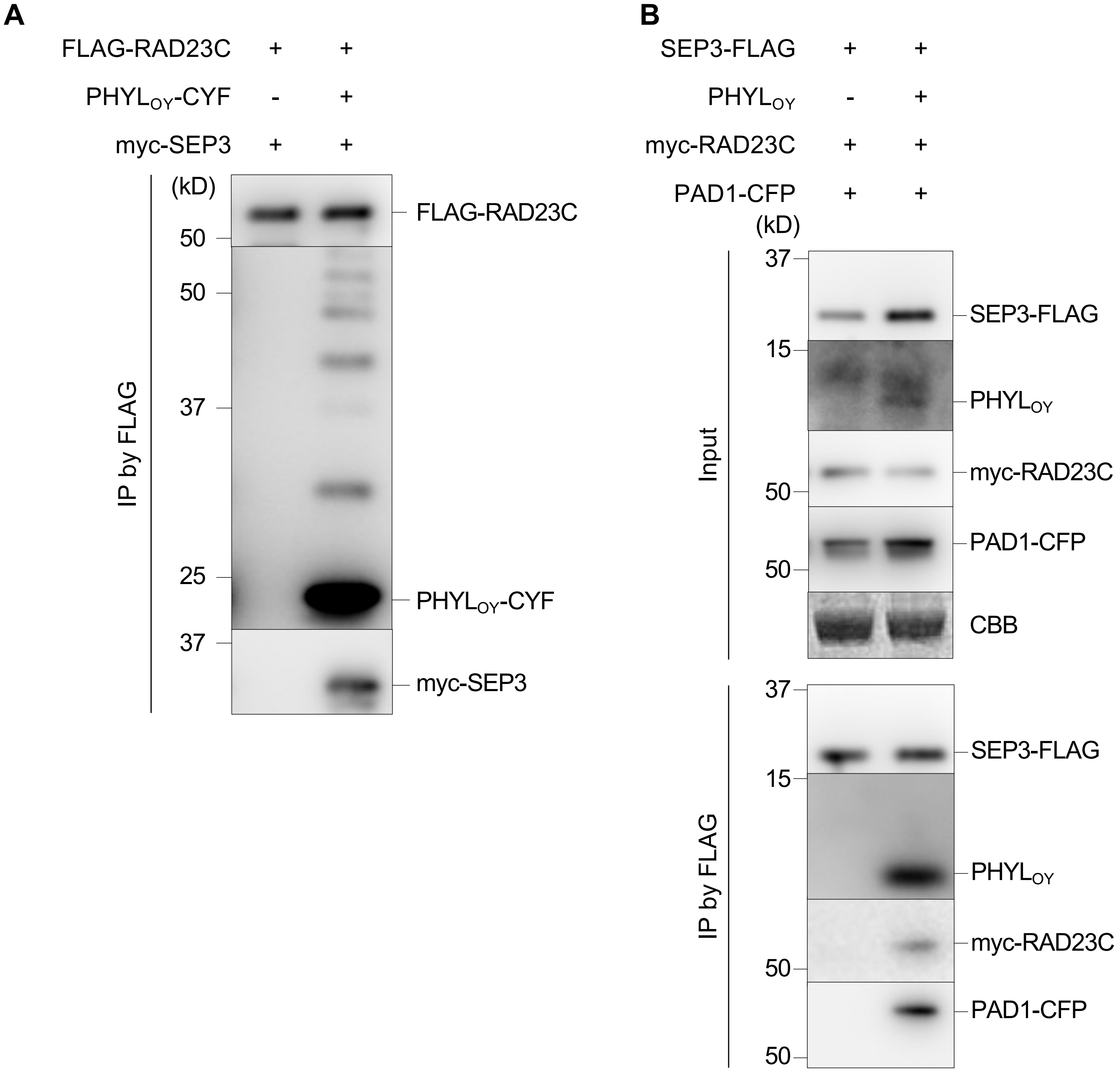
**(A)** Confirmation of moderate SEP3 degradation by PHYL$_{OY}$ and PHYL$_{OY}$-CYF. the expression of PHYL$_{OY}$, SEP3, GUS-CFP, and P19 were mixed at a ratio of 2:4:3:1 and infiltrated into *N. benthamiana* leaves.

**(B)** Localization of PHYL$_{OY}$-CFP in *Nicotiana benthamiana* epidermal cells. *Agrobacterium* cultures (OD$_{600}$ = 1.0) for the expression of PHYL$_{OY}$-CFP, SEP3, RAD23C, and P19 were mixed at a ratio of 2:4:3:1 and infiltrated into *N. benthamiana* leaves.

**(C)** BiFC analysis using NYF-SEP3 or NYF-AP3, PHYL$_{OY}$-CYF, and GUS-CFP. Proteins were expressed as in the case of Figure 1D. Proteins were detected 40 h after infiltration by immunoblot analysis, using a polyclonal anti-GFP or an anti-PHYL$_{OY}$ antibodies. Coomassie Brilliant Blue (CBB) staining is shown as a loading control. Fluorescence was observed 40 h after infiltration. Bars indicate 25 µm.



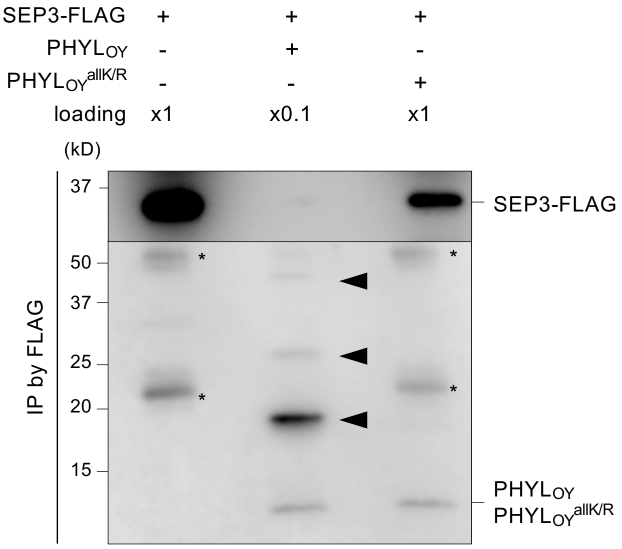
**Supplemental Figure 2.** In planta coimmunoprecipitation assay using FLAG-RAD23C and $\text{PHYL}_{\text{OY}}$. (Supports Figure 2.)
*Agrobacterium* cultures for expression of FLAG-fused proteins ($\text{OD}_{600}$ = 0.5), $\text{PHYL}_{\text{OY}}$ ($\text{OD}_{600}$ = 0.1), and P19 ($\text{OD}_{600}$ = 1.0) were mixed at a ratio of 10:10:1 and infiltrated into *N. benthamiana* leaves. FLAG-GUS was used as a control. The input and immunoprecipitated (IP) proteins (using an anti-FLAG antibody) were detected 36 h after infiltration by immunoblot analysis, using an anti-FLAG or an anti-$\text{PHYL}_{\text{OY}}$ antibody. Coomassie Brilliant Blue (CBB) staining is shown as a loading control.



**Supplemental Figure 3.** In planta coimmunoprecipitation using (A) FLAG-RAD23C, $\text{PHYL}_{\text{OY}}$-CYF, and myc-SEP3 or (B) SEP3-FLAG, $\text{PHYL}_{\text{OY}}$, myc-RAD23C, and PAD1-CFP. (Supports Figure 2.)

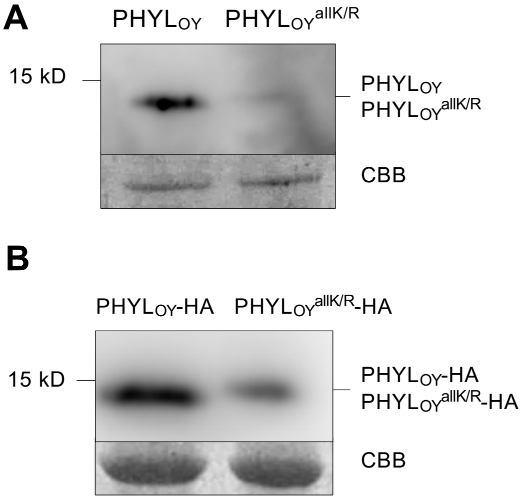
**(A)** Protein expression, immunoprecipitation using an anti-FLAG antibody, and protein detection (immunoprecipitated proteins only) were performed as described in Figure 2A.

**(B)** *Agrobacterium* cultures for expression of SEP3-FLAG ($OD_{600}$ = 1.0), $\text{PHYL}_{\text{OY}}$ ($OD_{600}$ = 0.1), myc-RAD23C($OD_{600}$ = 1.0), PAD1-CFP ($OD_{600}$ = 1.0), and P19 ($OD_{600}$ = 1.0) were mixed at a ratio of 1:1:1:1:0.1 and infiltrated into *N. benthamiana* leaves. Immunoprecipitation using an anti-FLAG antibody, and protein detection were performed as in (A).



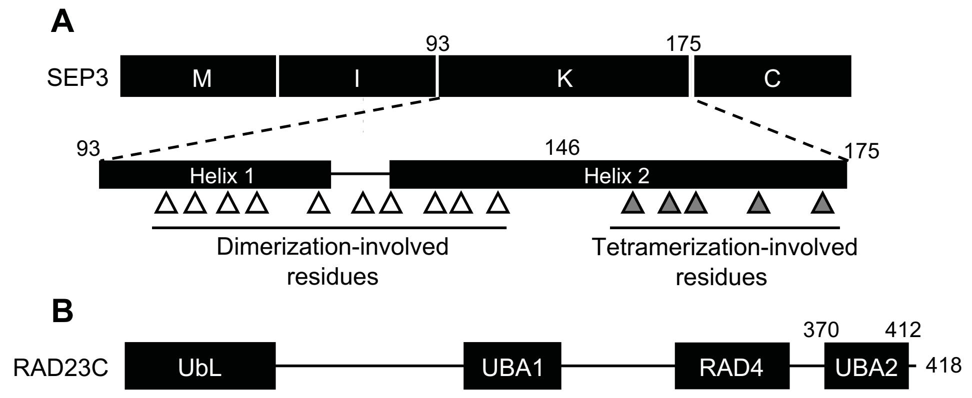
**Supplemental Figure 4.** Comparison of ubiquitination between PHYL$_{OY}$ and PHYL$_{OY}^{allK/R}$. (Supports Figure 3.)

Immunoprecipitation using SEP3-FLAG and PHYL$_{OY}$ or PHYL$_{OY}^{allK/R}$ was performed as in Figure 3A. SEP3-interacting PHYL$_{OY}$ or PHYL$_{OY}^{allK/R}$ was detected by immunoblot analysis using an anti-PHYL$_{OY}$ antibody. Because of the differences of in planta accumulation between PHYL$_{OY}$ and PHYL$_{OY}^{allK/R}$, the loading amount of SEP3-interacting PHYL$_{OY}$ was one-tenth of the amount of PHYL$_{OY}^{allK/R}$ in the experiment. Bands corresponding to ubiquitinated PHYL$_{OY}$ were detected (black arrows) but those to ubiquitinated PHYL$_{OY}^{allK/R}$ were not, indicating that PHYL$_{OY}^{allK/R}$ is not ubiquitinated. Asterisks indicate nonspecific bands, which were observed without PHYL$_{OY}^{allK/R}$ expression.

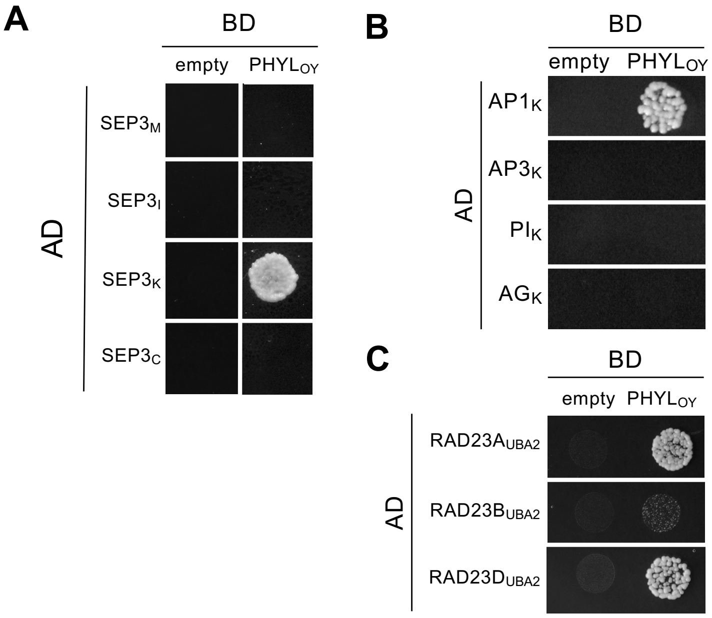


**Supplemental Figure 5.** Comparison of in planta protein accumulation between PHYL$_{OY}$ and PHYL$_{OY}^{allK/R}$ . (Supports Figure 3.)

**(A)**PHYL$_{OY}$ and PHYL$_{OY}^{allK/R}$ or **(B)** PHYL$_{OY}$-HA and PHYL$_{OY}^{allK/R}$-HA were expressed in *N. benthamiana* leaves. Protein detection was performed as described in Figure 3B using an anti-PHYL$_{OY}$ (A) or an anti-HA (B) antibody.



**Supplemental Figure 6.** Protein structure of SEP3 and RAD23C. (Supports Figure 4.)
**(A)** The domains and residues in SEP3 involved in multimerization reported by Puranik *et al*. (2014).
**(B)** Domain organization of RAD23C according to the GenBank reference sequence (AEE73826).

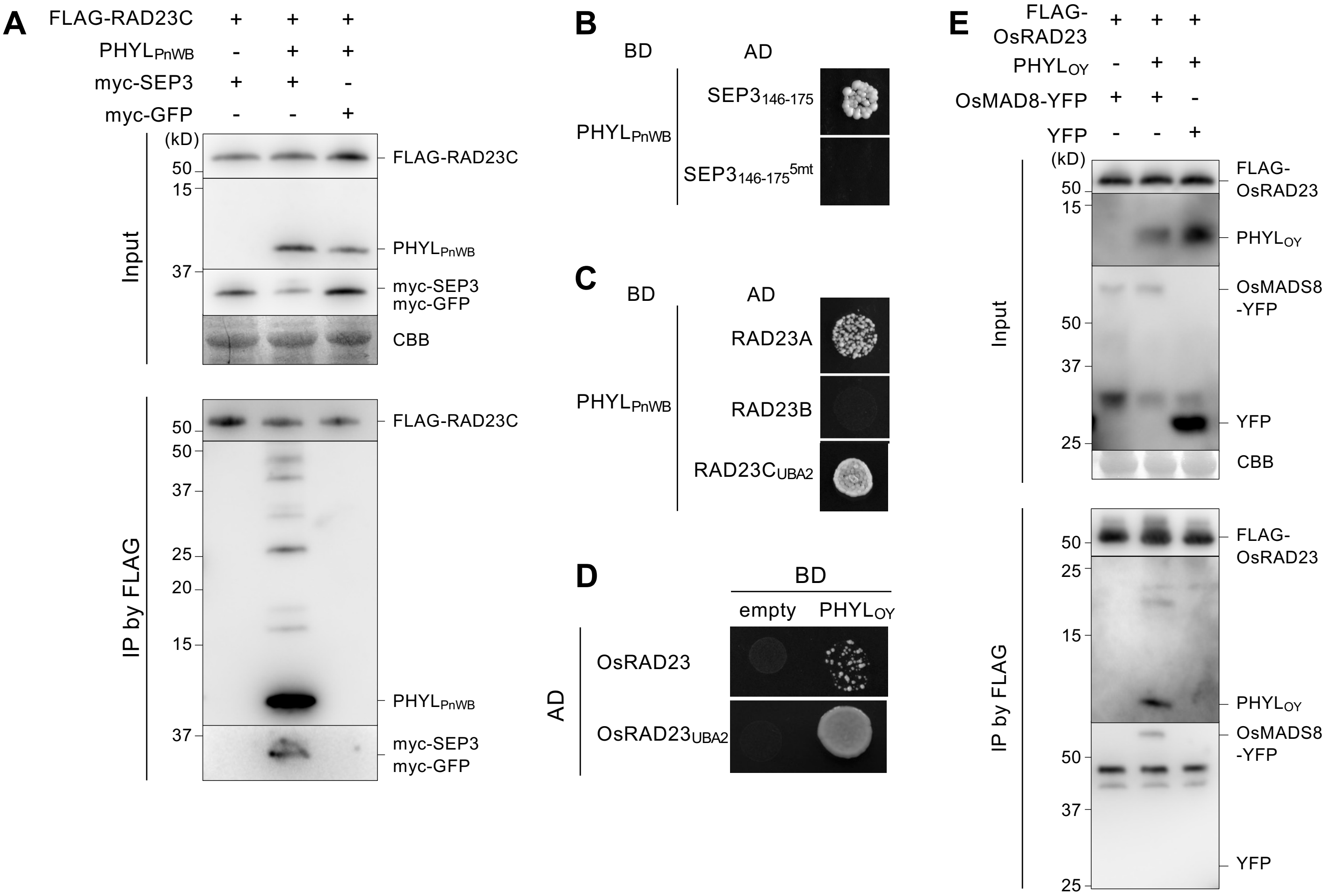


**Supplemental Figure 7.** Y2H assay using PHYL$_{OY}$ and domains in *A. thaliana* MTF or RAD23. (Supports Figure 4.)

**(A)** Interaction of PHYL$_{OY}$ with the M, I, K, and C domains of SEP3.

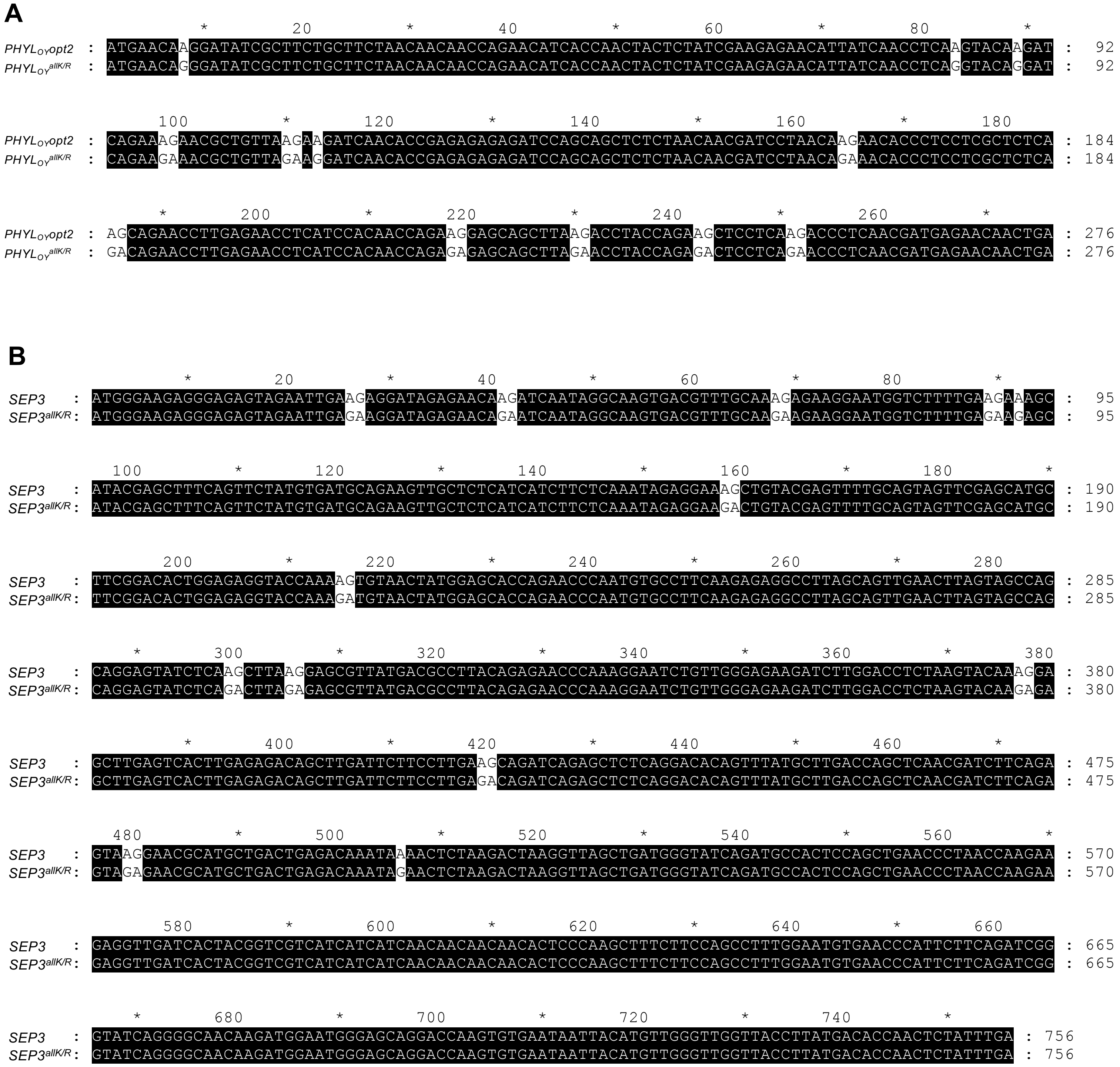
**(B)** Interaction of PHYL$_{OY}$ with the K domains of *Arabidopsis thaliana* A- (AP1), B- (AP3, PI), and C- (AG) class MTFs in yeast cells.

**(C)** Interaction of PHYL$_{OY}$ with the UBA2 domains of *A. thaliana*. Each Y2H assay was performed as described in Figure 4.



**Supplemental Figure 8.** Interactions of the MTF/phyllogen/RAD23 protein complex using different phyllogen or host proteins. (Supports Figure 4.)

**(A)** to **(C)** Interaction of PHYL$_{\text{PnWB}}$ with *Arabidopsis* proteins. **(A)** In planta immunoprecipitation using FLAG-RAD23C, PHYL$_{\text{PnWB}}$, and myc-SEP3. **(B)** to **(C)** Y2H assay using PHYL$_{\text{PnWB}}$ and partial region of SEP3 (B) or *A. thaliana* RAD23 homologs (C). **(D)** to **(E)** Interaction of PHYL$_{\text{OY}}$ with rice proteins. **(D)** Y2H assay using PHYL$_{\text{OY}}$ and OsRAD23 or its UBA2 domain. **(E)** In planta immunoprecipitation using SEP3 and RAD23 homologs of rice with PHYL$_{\text{OY}}$. Y2H and immunoprecipitation experiments were performed as described in Figures 4 and 2A, respectively.



```
A
                          *        20         *        40         *        60         *        80         *
PHYLOYopt2  : ATGAACAAGGATATCGCTTCTGCTTCTAACAACAACCAGAACATCACCAACTACTCTATCGAAGAGAACATTATCAACCTCAAGTACAAGAT :  92
PHYLOYallK/R: ATGAACAGGGATATCGCTTCTGCTTCTAACAACAACCAGAACATCACCAACTACTCTATCGAAGAGAACATTATCAACCTCAGGTACAGGAT :  92

                     100         *       120         *       140         *       160         *       180
PHYLOYopt2  : CAGAAAGAACGCTGTTAAGAAGATCAACACCGAGAGAGAGATCCAGCAGCTCTCTAACAACGATCCTAACAAGAACACCCTCCTCGCTCTCA : 184
PHYLOYallK/R: CAGAAGAAACGCTGTTAGAAGGATCAACACCGAGAGAGAGATCCAGCAGCTCTCTAACAACGATCCTAACAGAAACACCCTCCTCGCTCTCA : 184

                       *       200         *       220         *       240         *       260         *
PHYLOYopt2  : AGCAGAACCTTGAGAACCTCATCCACAACCAGAAGGAGCAGCTTAAGACCTACCAGAAGCTCCTCAAGACCCTCAACGATGAGAACAACTGA : 276
PHYLOYallK/R: GACAGAACCTTGAGAACCTCATCCACAACCAGAGAGAGCAGCTTAGAACCTACCAGAGACTCCTCAGAACCCTCAACGATGAGAACAACTGA : 276

B
                      *        20         *        40         *        60         *        80         *
SEP3     : ATGGGAAGAGGGAGAGTAGAATTGAAGAGGATAGAGAACAAGATCAATAGGCAAGTGACGTTTGCAAAGAGAAGGAATGGTCTTTTGAAGAAAAGC :  95
SEP3allK/R: ATGGGAAGAGGGAGAGTAGAATTGAGAAGGATAGAGAACAGAATCAATAGGCAAGTGACGTTTGCAAGAAGAAGGAATGGTCTTTTGAGAAGAGC :  95

             100         *       120         *       140         *       160         *       180         *
SEP3     : ATACGAGCTTTCAGTTCTATGTGATGCAGAAGTTGCTCTCATCATCTTCTCAAATAGAGGAAAGCTGTACGAGTTTTGCAGTAGTTCGAGCATGC : 190
SEP3allK/R: ATACGAGCTTTCAGTTCTATGTGATGCAGAAGTTGCTCTCATCATCTTCTCAAATAGAGGAAGACTGTACGAGTTTTGCAGTAGTTCGAGCATGC : 190

                   200         *       220         *       240         *       260         *       280
SEP3     : TTCGGACACTGGAGAGGTACCAAAAGTGTAACTATGGAGCACCAGAACCCAATGTGCCTTCAAGAGAGGCCTTAGCAGTTGAACTTAGTAGCCAG : 285
SEP3allK/R: TTCGGACACTGGAGAGGTACCAAAGATGTAACTATGGAGCACCAGAACCCAATGTGCCTTCAAGAGAGGCCTTAGCAGTTGAACTTAGTAGCCAG : 285

               *       300         *       320         *       340         *       360         *       380
SEP3     : CAGGAGTATCTCAAGCTTAAGGAGCGTTATGACGCCTTACAGAGAACCCAAAGGAATCTGTTGGGAGAAGATCTTGGACCTCTAAGTACAAAGGA : 380
SEP3allK/R: CAGGAGTATCTCAGACTTAGAGAGCGTTATGACGCCTTACAGAGAACCCAAAGGAATCTGTTGGGAGAAGATCTTGGACCTCTAAGTACAAGAGA : 380

                      *       400         *       420         *       440         *       460         *
SEP3     : GCTTGAGTCACTTGAGAGACAGCTTGATTCTTCCTTGAAGCAGATCAGAGCTCTCAGGACACAGTTTATGCTTGACCAGCTCAACGATCTTCAGA : 475
SEP3allK/R: GCTTGAGTCACTTGAGAGACAGCTTGATTCTTCCTTGAGACAGATCAGAGCTCTCAGGACACAGTTTATGCTTGACCAGCTCAACGATCTTCAGA : 475

             480         *       500         *       520         *       540         *       560         *
SEP3     : GTAAGGAACGCATGCTGACTGAGACAAATAAAACTCTAAGACTAAGGTTAGCTGATGGGTATCAGATGCCACTCCAGCTGAACCCTAACCAAGAA : 570
SEP3allK/R: GTAGAGAACGCATGCTGACTGAGACAAATAGAACTCTAAGACTAAGGTTAGCTGATGGGTATCAGATGCCACTCCAGCTGAACCCTAACCAAGAA : 570

                   580         *       600         *       620         *       640         *       660
SEP3     : GAGGTTGATCACTACGGTCGTCATCATCATCAACAACAACAACACTCCCAAGCTTTCTTCCAGCCTTTGGAATGTGAACCCATTCTTCAGATCGG : 665
SEP3allK/R: GAGGTTGATCACTACGGTCGTCATCATCATCAACAACAACAACACTCCCAAGCTTTCTTCCAGCCTTTGGAATGTGAACCCATTCTTCAGATCGG : 665

               *       680         *       700         *       720         *       740         *
SEP3     : GTATCAGGGGCAACAAGATGGAATGGGAGCAGGACCAAGTGTGAATAATTACATGTTGGGTTGGTTACCTTATGACACCAACTCTATTTGA : 756
SEP3allK/R: GTATCAGGGGCAACAAGATGGAATGGGAGCAGGACCAAGTGTGAATAATTACATGTTGGGTTGGTTACCTTATGACACCAACTCTATTTGA : 756
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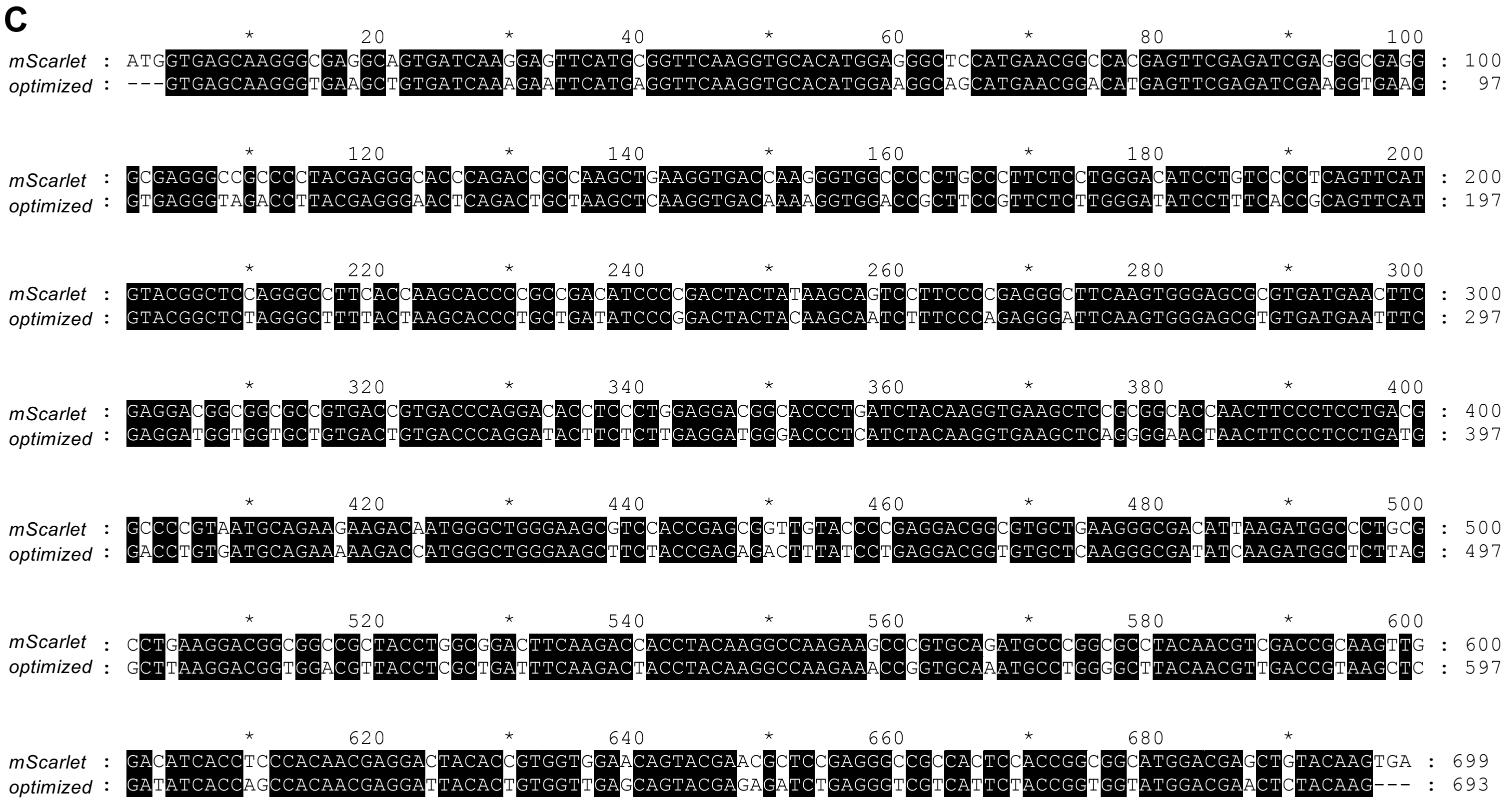
**Supplemental Figure 9.** Modified nucleotide sequences cloned in the study. (Supports Figures 1 to 4.)

Sequences of **(A)** *PHYL*$_{OY}$$^{allK/R}$, **(B)** *SEP3*$^{allK/R}$, and **(C)** plant codon-optimized *mScarlet* are shown with the reference sequences (*PHYL*$_{OY}$*opt2*, *SEP3*, and *mScarlet*, respectively). Identical nucleotides are indicated by black boxes.



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                       *        20         *        40         *        60         *        80         *       100
mScarlet  : ATGGTGAGCAAGGGCGAGGCAGTGATCAAGGAGTTCATGCGGTTCAAGGTGCACATGGAGGGCTCCATGAACGGCCACGAGTTCGAGATCGAGGGCGAGG : 100
optimized : ---GTGAGCAAGGGTGAAGCTGTGATCAAAGAATTCATGAGGTTCAAGGTGCACATGGAAGGCAGCATGAACGGACATGAGTTCGAGATCGAAGGTGAAG :  97

                       *       120         *       140         *       160         *       180         *       200
mScarlet  : GCGAGGGCCGCCCCTACGAGGGCACCCAGACCGCCAAGCTGAAGGTGACCAAGGGTGGCCCCCTGCCCTTCTCCTGGGACATCCTGTCCCCTCAGTTCAT : 200
optimized : GTGAGGGTAGACCTTACGAGGGAACTCAGACTGCTAAGCTCAAGGTGACAAAAGGTGGACCGCTTCCGTTCTCTTGGGATATCCTTTCACCGCAGTTCAT : 197

                       *       220         *       240         *       260         *       280         *       300
mScarlet  : GTACGGCTCCAGGGCCTTCACCAAGCACCCCGCCGACATCCCCGACTACTATAAGCAGTCCTTCCCCGAGGGCTTCAAGTGGGAGCGCGTGATGAACTTC : 300
optimized : GTACGGCTCTAGGGCTTTTACTAAGCACCCTGCTGATATCCCGGACTACTACAAGCAATCTTTCCCAGAGGGATTCAAGTGGGAGCGTGTGATGAATTTC : 297

                       *       320         *       340         *       360         *       380         *       400
mScarlet  : GAGGACGGCGGCGCCGTGACCGTGACCCAGGACACCTCCCTGGAGGACGGCACCCTGATCTACAAGGTGAAGCTCCGCGGCACCAACTTCCCTCCTGACG : 400
optimized : GAGGATGGTGGTGCTGTGACTGTGACCCAGGATACTTCTCTTGAGGATGGGACCCTCATCTACAAGGTGAAGCTCAGGGGAACTAACTTCCCTCCTGATG : 397

                       *       420         *       440         *       460         *       480         *       500
mScarlet  : GCCCCGTAATGCAGAAGAAGACAATGGGCTGGGAAGCGTCCACCGAGCGGTTGTACCCCGAGGACGGCGTGCTGAAGGGCGACATTAAGATGGCCCTGCG : 500
optimized : GACCTGTGATGCAGAAAAAGACCATGGGCTGGGAAGCTTCTACCGAGAGACTTTATCCTGAGGACGGTGTGCTCAAGGGCGATATCAAGATGGCTCTTAG : 497

                       *       520         *       540         *       560         *       580         *       600
mScarlet  : CCTGAAGGACGGCGGCCGCTACCTGGCGGACTTCAAGACCACCTACAAGGCCAAGAAGCCCGTGCAGATGCCCGGCGCCTACAACGTCGACCGCAAGTTG : 600
optimized : GCTTAAGGACGGTGGACGTTACCTCGCTGATTTCAAGACTACCTACAAGGCCAAGAAACCGGTGCAAATGCCTGGGGCTTACAACGTTGACCGTAAGCTC : 597

                       *       620         *       640         *       660         *       680         *
mScarlet  : GACATCACCTCCCACAACGAGGACTACACCGTGGTGGAACAGTACGAACGCTCCGAGGGCCGCCACTCCACCGGCGGCATGGACGAGCTGTACAAGTGA : 699
optimized : GATATCACCAGCCACAACGAGGATTACACTGTGGTTGAGCAGTACGAGAGATCTGAGGGTCGTCATTCTACCGGTGGTATGGACGAACTCTACAAG--- : 693
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**Supplemental Figure 9, continued.**

**Supplemental Table 1.** Primers used in this study.

| Primer name | Sequence (5'→3') | Targets | Purpose |
|---|---|---|---|
| PHYL1_ver2_mnsF | CCTCAACGATGAGAACAACTATCTAGACCCAGC | PHYL$_{OY}$ | deletion of stop codon |
| PHYL1_ver2_mnsR | GCTGGGTCTAGATAGTTGTTCTCATCGTTGAGG | PHYL$_{OY}$ | deletion of stop codon |
| Phyl1-pColdF | GGGAATTCCATATGATGAATAAGGATATTGCTTCTG | PHYL$_{OY}$ | cloning (pCOLD I) |
| Phyl1-pColdR | CTAGTCTAGACTATCAATTATTTTCATCATTAAGAGTC | PHYL$_{OY}$ | cloning (pCOLD I) |
| PHYL1opt2_to_ALSVver2_R | TCCCCCGGGGTTGTTCTCATCGTTGAGGG | PHYL$_{OY}$ | cloning (ALSV vector) |
| KallR_to_ALSVver2_F | CCGCTCGAGATGAACAGGGATATCGCTTC | PHYL$_{OY}^{allK/R}$ | cloning (ALSV vector) |
| Phyl1opt2_ALSVver2_F | CCGCTCGAGATGAACAAGGATATCGCTTC | PHYL$_{OY}$,<br>PHYL$_{OY}^{allK/R}$ | cloning (ALSV vector) |
| PHYL_to_pENTA_F | AAGGAACCAATTCAGTCATGAACA | PHYL$_{OY}$,<br>PHYL$_{OY}^{allK/R}$ | HA-tag fusion |
| PHYL1_G8_HA_R | TGGGTATCCACCTCCACCTCCACCTCCACCGTTGTTCTCATCGTTGAG | PHYL$_{OY}$,<br>PHYL$_{OY}^{allK/R}$ | HA-tag fusion |
| EcoRI_NdeI_PnWB_F | GGGAATTCCATATGGATCCTAAGCTCCCTGAG | PHYL$_{PnWB}$ | cloning (pCOLD I) |
| XhoI_PnWB_R | CCGCTCGAGTCAGTTCTTCTCATCGTTG | PHYL$_{PnWB}$ | cloning (pCOLD I) |
| Rad23A_to_pGADT7_F | ACCAGATTACGCTCATATGAAGCTCACTGTTAAGACTCTCAAGG | RAD23A | cloning (pGADT7) |
| Rad23A_to_pGADT7_R | TGCCCACCCGGGTGGAATCAGTCTTCAAAATCTGCTG | RAD23A | cloning (pGADT7) |
| Rad23B_to_pGADT7_F | ACCAGATTACGCTCATATGAAGCTCACCGTTAAAACTCTCAAGG | RAD23B | cloning (pGADT7) |
| Rad23B_to_pGADT7_R | TGCCCACCCGGGTGGAATCAGTCTTCAAAGTCACCTGAG | RAD23B | cloning (pGADT7) |
| pENTA_Rad23C_mnsF | GCATGAATTCGAGGAATATCTAGACCCAGCTT | RAD23C | deletion of stop codon |
| pENTA_Rad23C_mnsR | AAGCTGGGTCTAGATATTCCTCGAATTCATGC | RAD23C | deletion of stop codon |
| Rad23C_G8_R | TCCACCTCCACCTCCACCTCCACCTTCCTCGAATTCATGCATGTGATC | RAD23C | cloning (pMAL-c5X) |
| 23C_to_pMAL_F2 | ATCGAGGGAAGGATTTCACATATGAAGATATTTGTGAAAACTCTCAAG | RAD23C | cloning (pMAL-c5X) |
| Rad23C_to_pGADT7_F | ACCAGATTACGCTCATATGAAGATATTTGTGAAAACTCTC | RAD23C$_{UbL}$ | cloning (pGADT7) |
| UbL_R | TGCCCACCCGGGTGGAATCATTTACTCTTGTTCATCATAATGAC | RAD23C$_{UbL}$ | cloning (pGADT7) |
| UBA1_F | ACCAGATTACGCTCATATGCTAGCCGCTGGAAGTAATTTAGAGAG | RAD23C$_{UbA1}$ | cloning (pGADT7) |
| UBA1_R | TGCCCACCCGGGTGGAATCAAGGGATCCCAGTATAAAGATATTC | RAD23C$_{UbA1}$ | cloning (pGADT7) |
| Rad4_F | ACCAGATTACGCTCATATGCTTGACTTCTTGCGCAACAGCCAAC | RAD23C$_{RAD4}$ | cloning (pGADT7) |
| Rad4_R | TGCCCACCCGGGTGGAATCATCCTTCAACGGGTTCATTGATTAAG | RAD23C$_{RAD4}$ | cloning (pGADT7) |
| UBA2_F | ACCAGATTACGCTCATATGGTCACACATGAGGAACGTGAAGCCA | RAD23C$_{UBA2}$ | cloning (pGADT7) |
| UBA2_R | TGCCCACCCGGGTGGAATCAGTGATCTAGAAGATAGTTTGCAGC | RAD23C$_{UBA2}$ | cloning (pGADT7) |
| UBA2_to_pENTA_F | AAGGAACCAATTCAGTCATGGTCACACATGAGGAACGTGA | RAD23C$_{UBA2}$ | cloning (pENTA) |
| Rad23D_to_pGADT7_F | ACCAGATTACGCTCATATGAAGATTTTCGTGAAGACTCTC | RAD23D | cloning (pGADT7) |
| Rad23D_to_pGADT7_R | TGCCCACCCGGGTGGAATTATTGATCTTCAAACTCATGCATGTG | RAD23D | cloning (pGADT7) |
| OsRAD23_to_pGADT7_F | ACCAGATTACGCTCATATGAAGATATCCGTGAAGACACTCAAGG | OsRAD23 | cloning (pGADT7) |
| OsRAD23_to_pGADT7_R | TGCCCACCCGGGTGGAATTATGGTGGCCCCTCGTCGTCGA | OsRAD23 | cloning (pGADT7) |
| OsRAD23_to_pENTA_F | AAGGAACCAATTCAGTCATGAAGATATCCGTGAAGACACTCAAGG | OsRAD23 | cloning (pENTA) |
| OsRAD23_to_pENTA_R | AAGCTGGGTCTAGATTTATGGTGGCCCCTCGTCGTCGA | OsRAD23 | cloning (pENTA) |
| OsRAD23_UBA2__to_pGADT7_F | ACCAGATTACGCTCATATGGTTACTCCAGAGGAGAATGAAGC | OsRAD23$_{UBA2}$ | cloning (pGADT7) |
| OsRAD23_UBA2__to_pGADT7_R | TGCCCACCCGGGTGGAATCAGTGATCTAGGAGATAGTTTGC | OsRAD23$_{UBA2}$ | cloning (pGADT7) |
| pAD-AP1-k-F | GTACCAGATTACGCTCATATGAACTGGTCGATGGAGTATAAC | AP1 (K domain) | cloning (pGADT7) |
| pAD_AP1_K_R | ATGCCCACCCGGGTGGAATTCTTAGATCTGTTTAGAAAGCAT | AP1 (K domain) | cloning (pGADT7) |
| pENTA-AP3F | AAGGAACCAATTCAGTCATGGCGAGAGGGAAGATCCAG | AP3 | cloning (pENTA) |
| pENTA-AP3R2 | CTCGAGTGCGGCCGCGAATTTTATTCAAGAAGATGGAAGG | AP3 | cloning (pENTA) |
| pAD-AP3-k-F | GTACCAGATTACGCTCATATGCGAATGCAAGAAACCAAGAGG | AP3 (K domain) | cloning (pGADT7) |
| pAD_AP3_K_R | ATGCCCACCCGGGTGGAATTCTTACAGCTCATGTATGAG | AP3 (K domain) | cloning (pGADT7) |
| pAD-PI-k-F | GTACCAGATTACGCTCATATGAACCTTAGCAATGAGATTG | PI (K domain) | cloning (pGADT7) |
| pAD_PI_K_R | ATGCCCACCCGGGTGGAATTCTTACAGCTGGAAAGTGAG | PI (K domain) | cloning (pGADT7) |
| pAD_AG_K_F | GTACCAGATTACGCTCATATGTATTATCAACAAGAATCA | AG (K domain) | cloning (pGADT7) |
| pAD_AG_K_R | ATGCCCACCCGGGTGGAATTCTTATATCTTTGCACGAAGAAT | AG (K domain) | cloning (pGADT7) |
| SEP3_inverse_R | GCTGATGGGTATCAGATGCCA | SEP3 | construction of SEP3$^{5mt}$ |

## Supplemental Table 1, continued.

| Primer name | Sequence (5'→3') | Targets | Purpose |
|---|---|---|---|
| 30aa5mt_to_SEP3_F | GCAGATCAGAGCTCTCAGGACACAGTTTGCTCTTG | SEP3 | construction of SEP3$^{5mt}$ |
| 30aa5mt_to_SEP3_R | TGGCATCTGATACCCATCAGCTAACCTTAGTCTAGCAG | SEP3 | construction of SEP3$^{5mt}$ |
| SEP3_inverse_for30aacloning_F | CTGTGTCCTGAGAGCTCTGATCTGC | SEP3 | construction of SEP3$^{5mt}$ |
| SEP3_to_pENTA_F | AAGGAACCAATTCAGTCATGGGAAGAGGGAGAGTAG | SEP3 | HA- or FLAG-tag fusion |
| SEP3_G8_R | TCCACCTCCACCTCCACCTCCACCAATAGAGTTGGTGTCATAAGG | SEP3 | HA- or FLAG-tag fusion |
| SEP3-ADF | ACCAGATTACGCTCAAATGGGAAGAGGGAGAGTAGA | SEP3 (M domain) | cloning (pGADT7) |
| SEP3-AD177R | ATGCCCACCCGGGTGGTCAACTGCAAAACTCGTACAGCT | SEP3 (M domain) | cloning (pGADT7) |
| SEP3-AD178F | ACCAGATTACGCTCAAAGTTCGAGCATGCTTCGGAC | SEP3 (I domain) | cloning (pGADT7) |
| SEP3-AD276R | ATGCCCACCCGGGTGGTCAAAGTTCAACTGCTAAGGCCT | SEP3 (I domain) | cloning (pGADT7) |
| SEP3-AD277F | ACCAGATTACGCTCAAAGTAGCCAGCAGGAGTATCT | SEP3 (K domain) | cloning (pGADT7) |
| SEP3-AD525R | ATGCCCACCCGGGTGGTCATAACCTTAGTCTTAGAGTTTT | SEP3 (K domain) | cloning (pGADT7) |
| pAD_SEP3_146F | GTACCAGATTACGCTCATATGAGGACACAGTTTATGCTT | SEP3 (K domain) | cloning (pGADT7) |
| pAD_SEP3_145R | ATGCCCACCCGGGTGGAATTCTTAGAGAGCTCTGATCTGCTT | SEP3 (K domain) | cloning (pGADT7) |
| pGEX_SEP3_K_F | CGCGGATCCAGTAGCCAGCAGGAGTATC | SEP3 (K domain) | cloning (pGEX-4T-1) |
| pGEX_SEP3_K_R | CCCTCGAGGAATTCTCATAACCTTAGTCTTAGAGTT | SEP3 (K domain) | cloning (pGEX-4T-1) |
| pAD_SEP3_5mt_F | GTACCAGATTACGCTCATATGAGGACACAGTTTGCTCTTGAC | SEP3$^{5mt}$ | cloning (pGADT7) |
| pAD_SEP3_5mt_R | ATGCCCACCCGGGTGGAATTCTTATAACCTTAGTCTAGC | SEP3$^{5mt}$ | cloning (pGADT7) |
| SEP3-AD526F | ACCAGATTACGCTCAAGCTGATGGGTATCAGATGCC | SEP3 (C domain) | cloning (pGADT7) |
| SEP3-ADR | ATGCCCACCCGGGTGGCCTCAAATAGAGTTGGTGTCAT | SEP3 (C domain) | cloning (pGADT7) |
| AtPAD1-F1 | AAGGAACCAATTCAGTCATGGCGAGATACGATCGAGCAATCACTG | PAD1 | cloning (pENTA) |
| AtPAD1-R1 | AAGCTGGGTCTAGATATGTTTCCTTCGCAGGGCCTTTC | PAD1 | cloning (pENTA) |
| pENTA_to_pGADT7_R | TGCCCACCCGGGTGGAAGTACAAGAAAGCTGGGTCTAGAT | genes cloned in pENTA | cloning (pGADT7) |
| pENTA_R | GACTGAATTGGTTCCTTTAAAGCCTGC | pENTA | FLAG- or HA-tag fusion |
| G8-Flag-pENTA_F | GGAGGTGGAGGTGGAGGTGGAGACTACAAGGACGACGATGACAAGTGAATCTAGACCCAGCTT | pENTA | FLAG-tag fusion |
| G7-HA-pENTA_F | GGAGGTGGAGGTGGAGGTGGATACCCATACGATGTTCCAGATTACGCTTGAATCTAGACCCAGCTT | pENTA | HA-tag fusion |
| G8_Flag_pMALX_F | GGAGGTGGAGGTGGAGGTGGAGACTACAAGGACGACGATGACAAGTGATCCGAATTCCCTGCAGG | pMAL-C5X | FLAG-tag fusion |
| pMALX_R | CATATGTGAAATCCTTCCCTCGA | pMAL-C5X | FLAG-tag fusion |
| M13R-pCAM2338F | GTCATAGCTGTTTCCTGACTATCAGTGTTTGACAGGA | pCAMBIA1301 | cloning (ALSV vector) |
| M13F-pCAM8718 | ACTGGCCGTCGTTTTACTTCGGCGTTAATTCAGTACA | pCAMBIA1301 | cloning (ALSV vector) |