

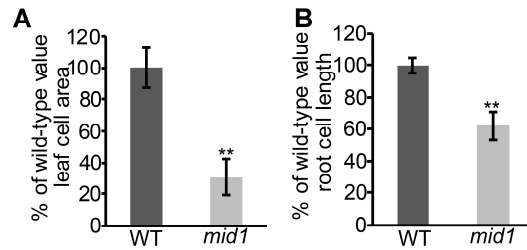
Pentatricopeptide repeat protein MID1 modulates *nad2* intron 1 splicing and *Arabidopsis* development

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² These authors contributed equally to the article.

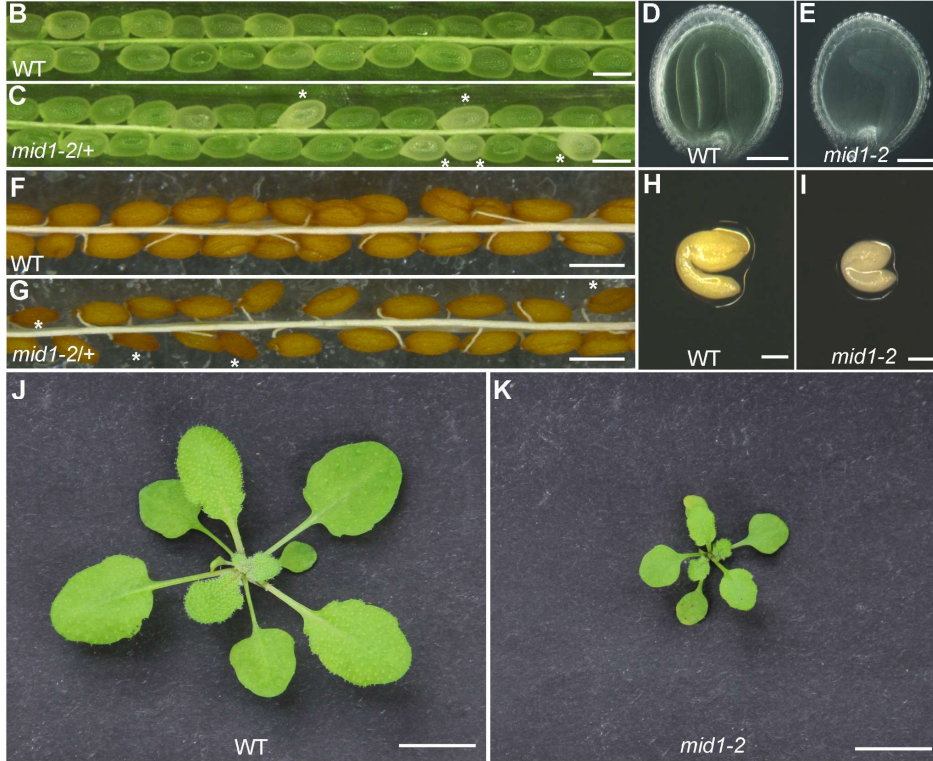
*Corresponding author: wcyang@genetics.ac.cn.



Supplemental Figure 1 The cell expansion deficiency of *mid1*.

(A) The fifth leaf cell area of wild-type and *mid1*. Data are the mean \pm SE, n=100. Student's t tests, **P<0.01. (B) The cell length of wild-type and *mid1* in the root maturation region. Data are the mean \pm SE; n=50. Student's t tests, **P<0.01.

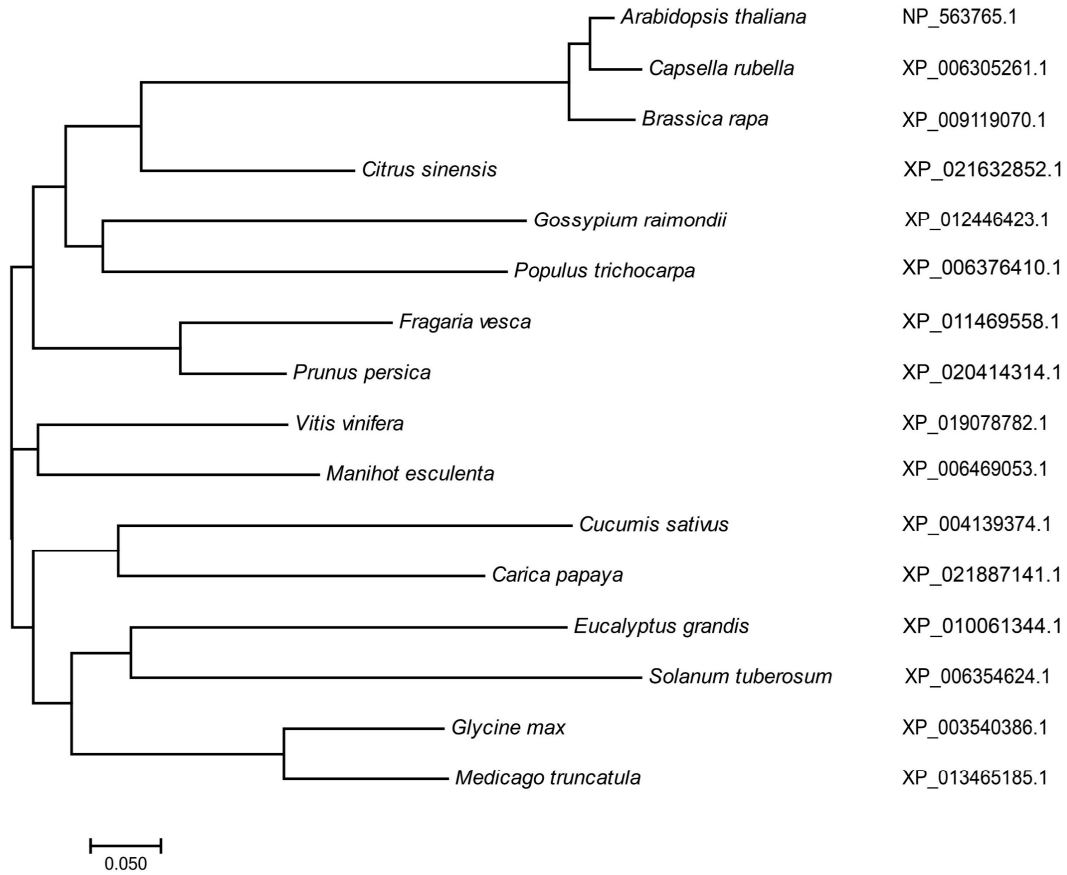
mid1-2 M A I R L T H L R K P L A Y S R S F
 GAT GTC TGC ATT CCG TTT TTC CGG TCA ATC TCG TCC TTT GAA GCG GTT GAA AAG 108bp
 WT D V C I P F F R S I S S F E A V E K
 GAT GTC TGC ATT CCG TTT TTC CGG TCA ATC TCG TCC TTT GAA GCG GTT GAA AAA
mid1-2 D V C I P F F R S I S S F E A V E K
 GCG ATA AAA TGT GCT GTT GAA ACA AAG GAG TAT CTT AGA ATC
 WT A I K C A V E T K E Y L R I -----
mid1-2 GGC GAT AAA ATG TGC TGT TGA AAC AAA GGA GTA TCT TAG AAT
 G D K M C C *



Supplemental Figure 3 Phenotypes of *mid1-2*

(A) CRISPR–Cas9-induced mutation in *mid1-2*. The rectangle marks the target sequence. The red A indicates the nucleoside inserted in *mid1-2* and a premature stop codon was created after six amino acid. The truncated MID1 in *mid1-2* is 42 amino acid in length. **(B)-(C)** Seed set of wild-type and *mid1-2/+* siliques at 9 DPP. Wild-type shows a full seed set while approximately one-quarter of ovules in the *mid1-2/+* silique are abnormal. Asterisks indicate the *mid1-2* ovules. **(D)-(E)** Whole-mounted ovules from silique of *mid1-2/+* plant in **(C)**. **(F)-(G)** Seeds in the mature silique of wild-type and *mid1-2/+*. Compared to the wild-type, about one-quarter of the seeds in *mid1-2/+* display shrunken morphology. Asterisks indicate the *mid1* seeds. **(H)-(I)** Embryos dissected from *mid1-2/+* plant in **(G)**. **(J)** 4-week-old wild-type plant at short day condition. **(K)** 4-week-old *mid1-2* plant at short day condition.

(B), (C), (F), (G), Bars=200 μ m. **(D), (E), (H), (I)**, Bars=50 μ m. **(J), (K)**, Bars=1cm.



Supplemental Figure 4 Phylogenetic analysis of MID1 orthologues

The MID1 orthologues protein sequences of sixteen species are derived from NCBI (<https://www.ncbi.nlm.nih.gov/>). They are aligned to generate the maximum-likelihood phylogenetic tree using MEGA6. The gene locus or GenBank/EMBL accession numbers of these orthologues are listed in the right panel. Branch length represents substitutions per site.

A.thaliana 1 -----M A R L T H R K P L A Y S R F D V C I P F F R S I S - S F E A V E K A I R C A V E T R E Y L R I P E L V V S L K E - P Y Q N S T L F S F L S A F Q R H H R I R V I D E I L L O
C.rubella 1 -----M A R L T H R K P L A Y S R F P D T C I P F F R S I S - S F E A V E K A I R C A V E T R E Y L R I P E L V V S L K E - P Y Q N S M L F S F L S A F H H H H R I R V I D E I L L O
B.rapa 1 -----M A R F P H R K P L A Y S P S R - S I P F S R O V S - S F E A V E K A I R C A V E T R E Y L Q I E R L V V S L K E - P Y Q N S K L F S F L S A F H H H H R I R V I D E I L L O
C.sinensis 1 -----M H G A I S C R S V N R P C I L Q S S L S R S M S - S L R T E F T V R A V D A K M Q C L P E L S G E F E E A C Q N P F S L S F Q R H H R I R V I D E I L L O
C.raimondii 1 -----M A R P R K C H S F M L Y P C S Q F V L V S V S - S L N A V E S V T K A A L S A V Q L P M H V L A L E K - S R I Q N P F S L S F L S L R K R V I D E I L L O
P.trichocarpa 1 -----M T L A K L I S R S L P Y S I L L Q R T L - - S - S H T P E E T L K A A V E C R S Y S K F P D L F D S F K O - S N N I P S F S P L S T F F N L R T Q V I D E I L L O
F.vesca 1 -----M A T V S A K I C R Y L P L N C C V K Y H S I N S T A - - F S H A O E T V R N A V E A K A V Q D I P D L L S F E Q - A C Q N P F S F L S T F F H R M - Q V V O E I L L O
P.persica 1 -----M A T R A A K F C R S F L P L H C R L L O Y C S I Y S I S - S S Q M Q E T I R N A V E A K T Y Q K I P D L L S S A Q - A C Q N P F S F L S F F H N R T Q V I D E I L L O
V.vinifera 1 -----M A T G A T K L C R S F H H Y H S I R O I S S I S H I T - S S Q T L E S I K A A V E S K A V Q K I P D L L S L E E - T C N P N P F S F L S T F S Q N D R T Q V I D E I L L O
M.esculenta 1 -----M L G V T R M C S S P R H H F V L O P L V R S I S I - S - - L E O T R K A V E A R A V Q E I P D L F S Y R G E Y F E N P F S F L S F S Q N D R T Q V I D E I L L O
C.sativus 1 -----M H G R K T S A F L L M H H F Q C Y S S I S I S I - F S Q T Q D S I K A A V E S R S Y K K L D P L F P S L Q E - A C H N P F S F L S T F F H R M Q N D R T Q V I D E I L L O
C.paraya 1 -----M S V P G S S F - - K P F S S F L P L N V C S I S A F H A V E T R A A V S R R V S Q I P D L L S Q S - S G R N P F L P L S F S Q L R R T Q I D E I L L O
E.grandis 1 -----M T G A K Q Y P S R H L S S L V N F S P V R S V S - S L O S E S E K A A H Q A R N V O H I P D L L S S Q D - - E N P R I L S L S F D F P R N R T Q I D E I L L O
S.tuberosum 1 -----M T V A - - - - K P H S - - - - V R P L C R S I S A R M L E S I K A V E D R R V Q I P D L L S S E G - F H R S N P F S F L S T F F E N T S V K I V O I D E I L L O
G.max 1 -----M V M A M H Y R F L C R P I N R C P L G R S V S - S L Q N L E Q A V R A V E A K N Y I K I P E L L S S - D - A C Q I S N P F S F S F S F Q N I Q V I D E I L L O
M.truncatula 1 M L Q Y S I S S R A T R A M Y R S V L H F S I P N Q V P S V R S V S - S P Q N V Q A V R A V E S K N V V R I P D L L T E L S - Q S Q N P F S F L S F F Q N I Q V I D E I L L O

PPR1

A.thaliana 88 S F V P R P R S L P R I V Y S S L N Y C L O S S D P L L S F A I L Q R L R S G C L P N O T H L L S D A W L E R R - R G S Q S V A D I N E M K L I G Y P D T C N C N Y L V S S L C A V D K
C.rubella 88 S F V P R P R S L P R I V Y S S L N Y C L O S S D P L L S F A I L Q R L R S G C L P N O T H L L S D A W L E R R - R G S Q S V A D I N E M K L I G Y P D T C N C N Y L V S S L C A V D K
B.rapa 86 S F V P R P R S L P R I V Y S S L N Y C L O S S D P L L S F A I L Q R L R S G C L P N O T H L L S D A W L E R R - R G S Q S V E I N E M K L I G Y P D T C N C N Y L V S S L C A V D K
C.sinensis 88 S F T P R P R S R P K L A Y D L L S Y T L Q S D P L P L A L A I L Q R L R S G C V P V Q T H L L S S A W L E R R - C O S S V A D I L L E M S I G Y P D C C N C N Y L V S S L C A V D K
C.raimondii 88 S F S T R P R S R P R I V D L L S Y T L Q S D P L P L A L A I L Q R L R S G C V P A P Q I L L S S A W L E R R - G H S Q P V S D L E M O D I G F C P S M P C N Y L I S S L C A V D Q
P.trichocarpa 86 S I F P R P R R P R I V Y S S L S Y T L O S N L F S L G L A I L Q R L R S G C V P V Q T H L L S S A W L E R R - R E G O S V G D L L E M S I G Y P D C C N C N Y L V S L C N V D Q
F.vesca 86 S I F P R P R S R Q A Y A Y M L S F L Q S S N P L L Q L A I L Q R L R S G C V P V Q T H L L S S A W L E R R - K E S R S V S D L L E M S I G Y P D C C N C N Y L I S S L C A V D Q
P.persica 88 S F T P R P R S R P K A Y C L P L S Y T L Q S D P L P L A L A I L Q R L R S G C V P V Q T H L L S S A W L E R R - N E S S V K L E M S I G Y P D C C N C N Y L I S S L C A V D Q
V.vinifera 88 S F T P R P R S R P K A Y C L P L S Y T L Q S D P L P L A L A I L Q R L R S G C V P V Q T H L L S S A W L E R R - R O S S V N I L L E M S I G Y P D C C N C N Y L I S S L C A V D Q
M.esculenta 86 S I F P L P R P R P Q V Y S C L S Y T L Q S P S P L P L A L A I L Q R L R S G C V P V Q T H L L S S A W L E R R - R O S H V A N I L L E M S I G Y P A D S G C N Y L V S S L C A V D Q
C.sativus 88 S I S I R P R S R S Q P V H G S L P Y T L Q S P S P L P L A L A I L Q R L R S G C V P S P O T H L L S S A W L E R R - S O A K S V A N I L L E M S I G Y P D C C N C N Y L I S S L C S I G E
C.paraya 88 A E F P R P R S R P L A Y S Y L S H L Q A P S P L P L A L A I L Q R L R S G C V P A P Q I L L S S A W L E R R - R O S H S V N I L L E M S I G Y P D C C N C N Y L I S S L C A V D Q
E.grandis 86 S F V P R P R S R P R A Y S C L L Q S Y T L Q S D P L P L A L A I L Q R L R S G C V P V Q A R L L S S A W L E Q L - S O S R S V A D I L L G M R L L I G Y P S D C C N C N Y L V S S L C A V D Q
S.tuberosum 87 S F T T R P R P R P Q A Y S C L L S Y T L Q S S N P L P L A L A I L Q R L R S G C V P V Q T H L L S A W L E R R - S K S Y S V S I L L E M O D I G Y A P D C C N C Y L I S S L C A V D Q
G.max 78 S I F T P R P R S K A O P T Y S M L S Y T L Q S S N P L P L A L A I L Q R L R S G C V P V Q T H L L S S A W L D Q H - C L S H S V A N I L L Q M S I G Y P D C C N C N Y L I S S L C A V D Q
M.truncatula 99 S F T P R P R P R P Q A Y S M L S Y T L Q S S N P L P L A L A I L Q R L R S G C V P V Q T H L L S S A W L D R R - C L S H S V A N I L L Q M S I G Y P D C C T C N H L I S S L C A V R Q

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PPR3

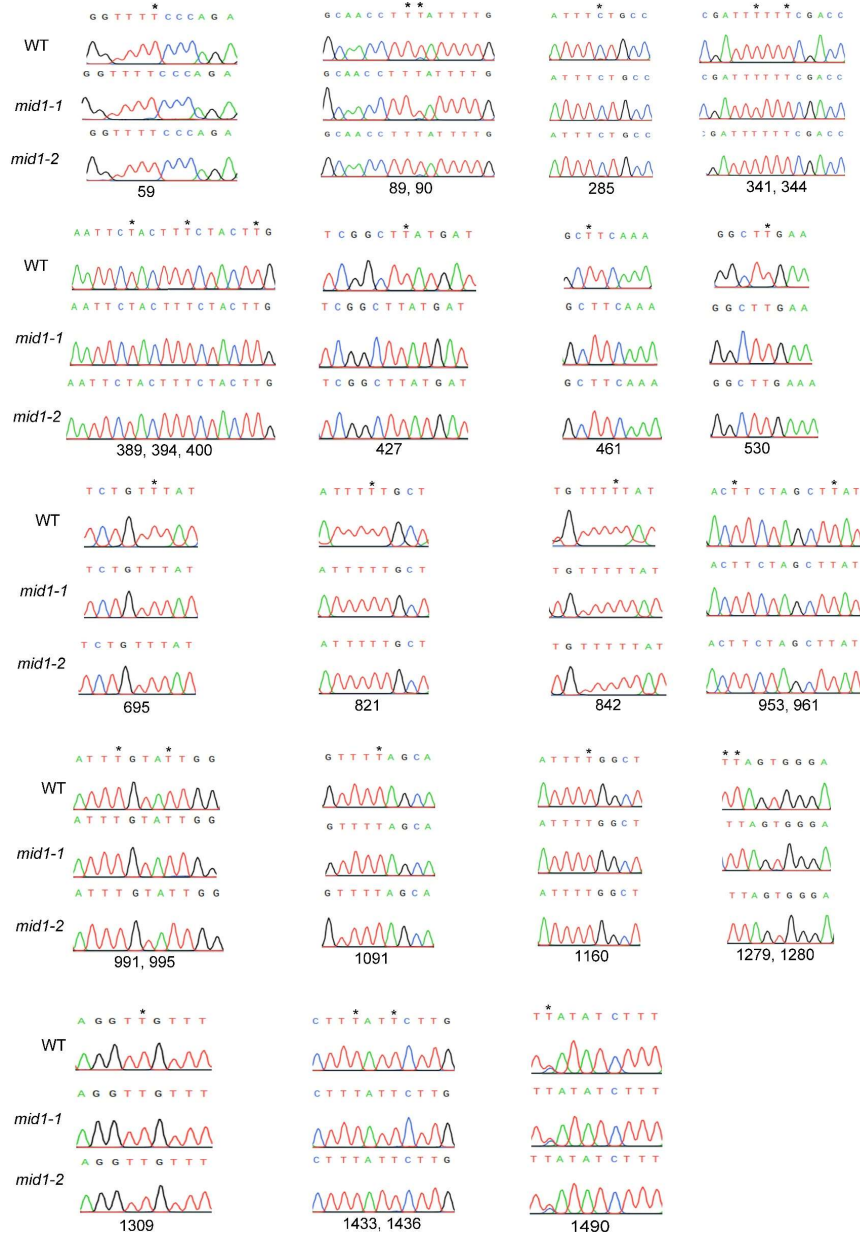
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B.rapa 186 I D E A V R V V E E M S A G C I P D V E S Y G A V I S S N C L A R K T S D V V K I V K E M V S R A G I S P R K G M L T K V A A L R A N R E I W K A I E M I E F V E S R D Y P V F E S Y E L V V E G
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P.trichocarpa 183 I D E A V K L K G M S A G C V P D L E S Y I V I G A M S T A R K L N D A V E M L K E M V I N M G L M P R O G V I V K V A A L R A N R E I W K A I E M I E F L E R K G Q P P G E V V V E G
F.vesca 185 I D E A V K V L K G M S A G C V P D L E S Y I V I G A M C V R R K S E L D M O I K R V E S V G L P R O G V I V K V A A L R A N R E I W R A V E H I E F L E R K D Y P V G F E S Y D L V V E G
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S.tuberosum 177 I D E A V N L K G M S A G C S D L D V G S L I D N I S E L R M S A I I K T I N E M V A F G L S P R E Q L V K A A A L L A N E I R A H I E F L E T N E G V H I G E S Y Q S V I E G
G.max 186 I D E A V R V L K G M S A G C I P D S S Y G A V I G A M C V R R K A K A L D L M O M V O Y Q L P Q G G L V K L L A A L R A N R E I W K A I E M I E F L E R E G N S V G F E S Y E L V I E G
M.truncatula 198 I V E A H D V L K G M S A G C I P D S N S Y G V I G A M C V R R R S D A O D L M O M V A R Y G L P D H G M V R I L S A L R A N R E I W K A I E M I E F L E R E G N S V G F E S Y E L V V E G

PPR4

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C.rubella 287 C L E V R E Y I L A G K V V I M G M T E R G F I P Y I R V R Q K V V E G L A G G E W K L A C V R Q R F A E L R S
B.rapa 286 C L E V R E Y I L A G K V V I M G M T E R G F I P Y I R V R Q K V V E G L A G G E W K L A C V R Q R F A E L R S
C.sinensis 287 C L E C R E Y I L A G K V V I M G M T E R G F I P Y I R V R Q K V V E G L A G G E W K L A C V R Q R F A E L R S
C.raimondii 287 C L E C E Y V L A G K V V I M G M T E R G F I P Y I R V R Q K V V E G L A G G E W K L A C V R Q R F A E L R S
P.trichocarpa 285 C L E C K D F L A R K V V I M G M T E R G F I P Y I R V R Q K V V E G L A G G E W K L A C V R R R F A E L S S
F.vesca 285 C L D S G S N I L A G K V V I M G M T E R G F V P Y I R T R H K V V E R L A G A G E W K L A N A V R Q R F S E L R S
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V.vinifera 287 C L A C E F V L A G K V V I M G M T E R G F I P Y I R V R Q K V V E G L A G G E W K L A C V R Q R F A E L R S
M.esculenta 285 C L E C S E Y L A G K V V I M G M T E R R F I P Y I R V R Q K V V E G L A G G E W K L A C A V R Q R F F E L S
C.sativus 287 C L E C R E Y I L A G K V V I M G M T E R G F I P Y I R V R Q K V V E G L A G G E W L A S A - - - - -
C.paraya 287 C L E C R E F I L A G K V A T E M T D R G F I P Y I R V R Q K V V E G L A S G E W K L A C A V R Q R F A E L R S
E.grandis 285 C L R C C E H V L A G K V V I M G M T A R G F I P Y I D I R Q K V V E G L A A H G E M D I V A R V R Q R F A E L R S
S.tuberosum 277 C L E S R Q F Y L A G R F V E M T K R G F I P Y I R S R Q K V V E G L T S H G E W K L A N A V R Q R F A E L R S
G.max 286 C L E K R E Y V L A K V A T G M T E R G F I P Y I R V R Q K I E G L A S D E W N L A C A V R Q R F A E L R S
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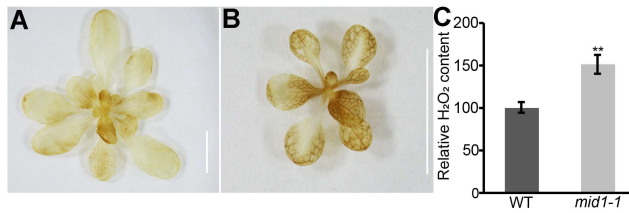
Supplemental Figure 5 Alignment of MID1 orthologues.

The conserved PPR domains are indicated by black line on the top.



Supplemental Figure 6 *nad2* editing status in wild-type and *mid1* mutants.

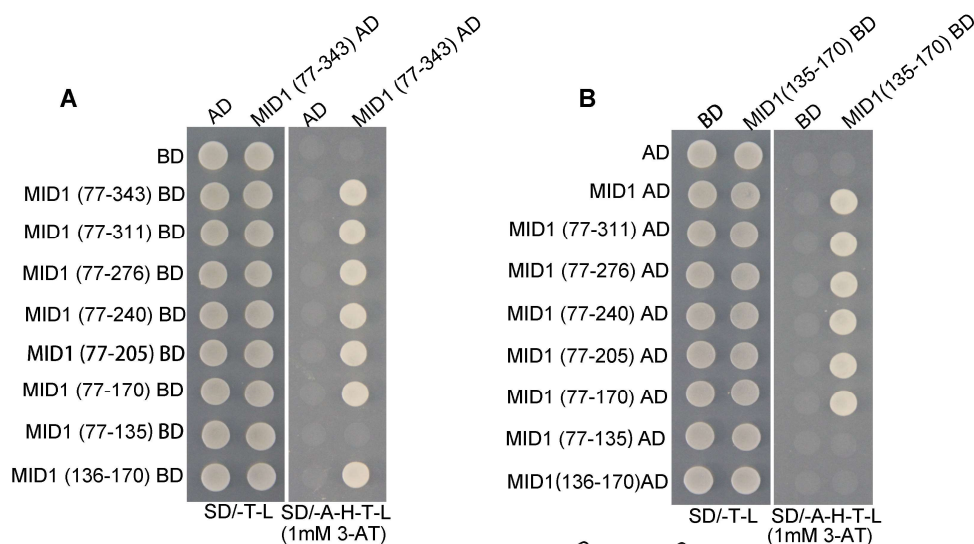
The asterisks indicate the editing sites. The number under the sequence map marks the position of each editing site.



Supplemental Figure 7 Measurement of H₂O₂ content in *mid1*

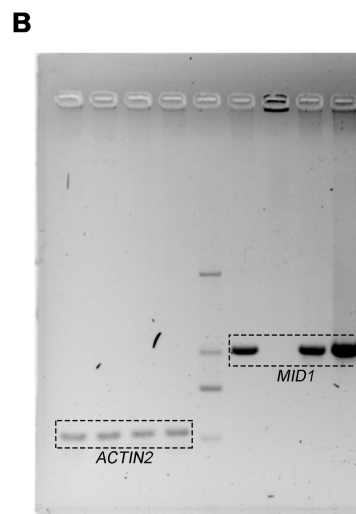
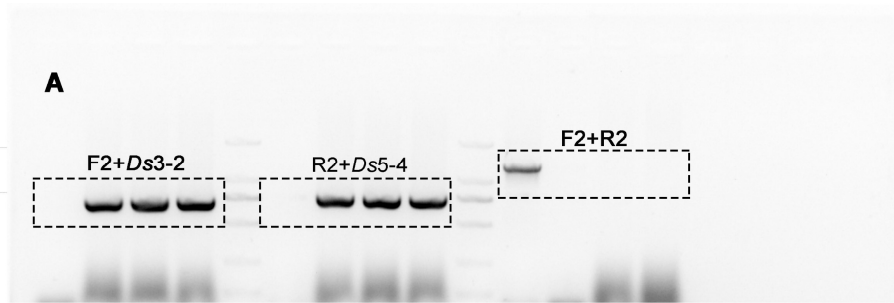
DAB staining detection of H₂O₂ in 4-week-old wild-type (A) and *mid1-1* plant (B). Bars=1 cm.

(C) Quantitative assay of H₂O₂ content in (A) and (B), Student's t tests, **P<0.01.

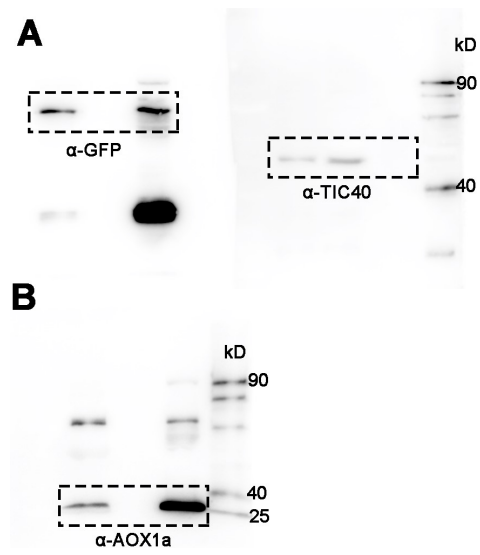


Supplemental Figure 8 Identification of Domains Necessary for MID1 Homodimer

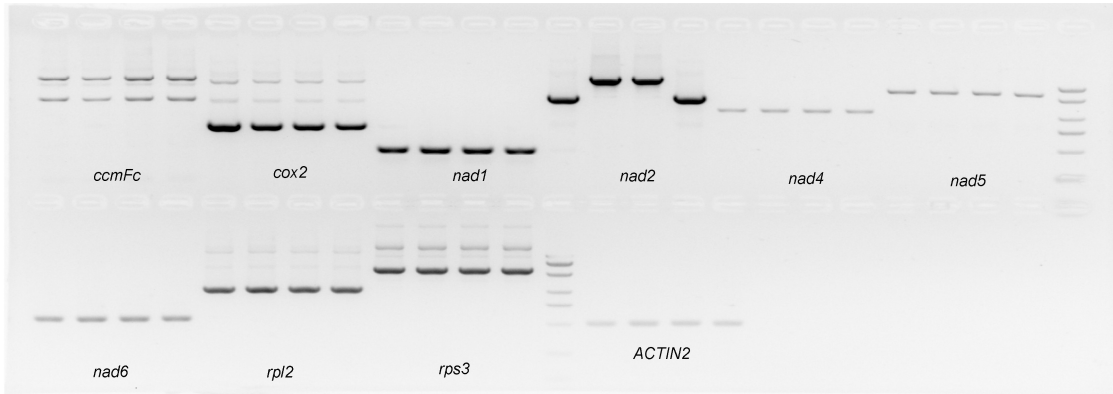
(A) Identification of domains directly mediating the physical interaction during MID1 homodimer formation. 1mM 3-AT was added to inhibit the autoactivation. **(B)** Identification of domains that can facilitate the formation of MID1 homodimer. 1mM 3-AT was added to inhibit the autoactivation.



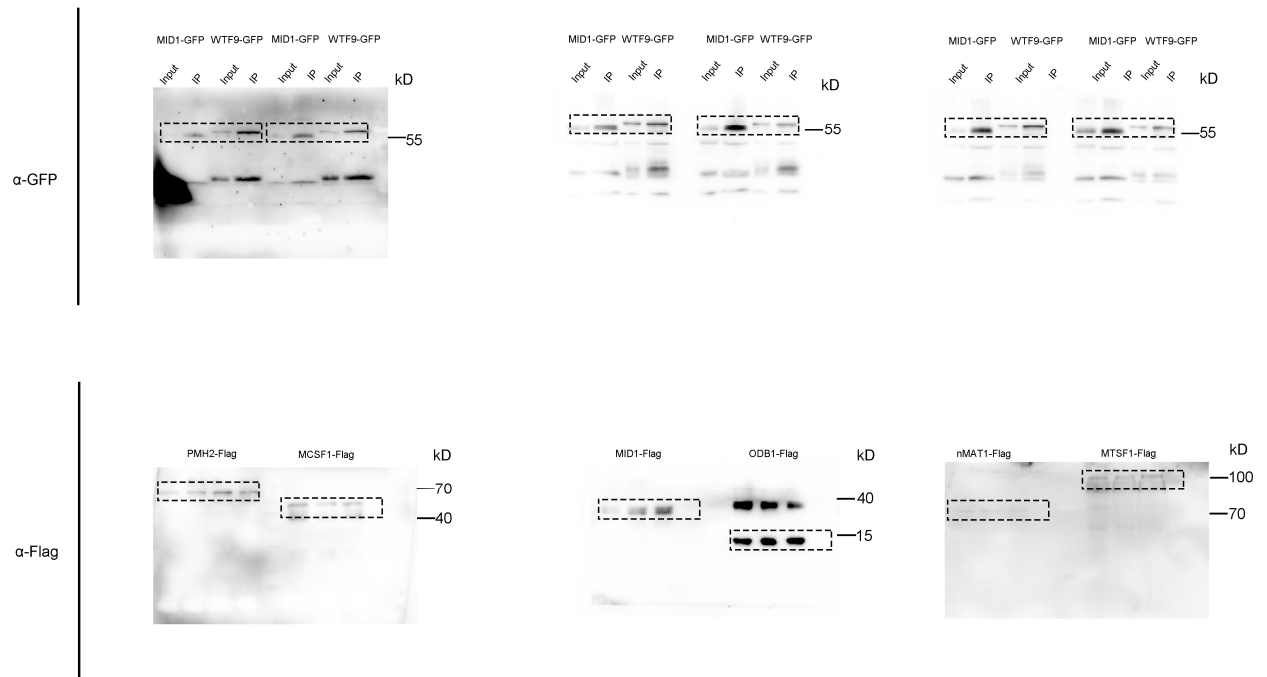
Supplemental Figure 9 Uncropped image of Figure 3C



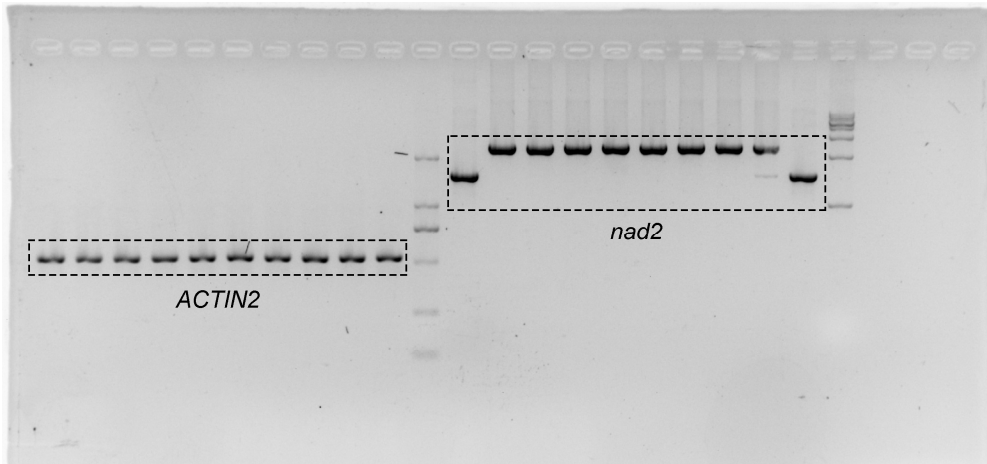
Supplemental Figure 10 Uncropped image of Figure 4D



Supplemental Figure 11 Uncropped image of Figure 5B



Supplemental Figure 12 Uncropped image of Figure 6B



Supplemental Figure 13 Uncropped image of Figure 7C

Primers for Y2H assay

Primer name	Primer sequence (5'-3')
MID1 BD 77aa forward	ATCTCAGAGGAGGACCTGCATCATAGAATCAGAGTCATTGACG
MID1 BD 136aa forward	ATCTCAGAGGAGGACCTGCATCAGACTCATCTCCTTCTCTCT
MID1 BD 135aa reverse	GAATTCGGCCTCCATGGCCATAGGGTTAGGTAGACAGCCAGAACG
MID1 BD 170aa reverse	GAATTCGGCCTCCATGGCCATATCAGGACTGTATCCAATC
MID1 BD 205aa reverse	GAATTCGGCCTCCATGGCCATATCAGGAATACAGCCAGCTGCAC
MID1 BD 240aa reverse	GAATTCGGCCTCCATGGCCATTGGAGAGATCCCAGCTTTGCTCA
MID1 BD 276aa reverse	GAATTCGGCCTCCATGGCCATCTCCACAGGGTAATCCCGAC
MID1 BD 311aa reverse	GAATTCGGCCTCCATGGCCATATACGGTATGAACCCTC
MID1 BD 343aa reverse	GAATTCGGCCTCCATGGCCATAGACCTCAGTTCAGAAACCCTTTG
nMAT1 BD 90aa forward	ATCTCAGAGGAGGACCTGCATTGGGTCTTAGCTTATCAACGAAC
nMAT1 BD 711aa reverse	GAATTCGGCCTCCATGGCCATTGTTTGTGAGTCTAATTTCTGCAACC
MCSF1 BD 28aa forward	ATCTCAGAGGAGGACCTGCATTCACGACTCCGAGACCTTTACA
MCSF1 BD 405aa reverse	GAATTCGGCCTCCATGGCCATGGTTGTCTCGTCAGGAGAATCT
MTSF1 BD 43aa forward	ATCTCAGAGGAGGACCTGCATTCCACTCCTCCGCCGATGACAT
MTSF1 BD 997aa reverse	GAATTCGGCCTCCATGGCCATAGTCCCATCAGATGTTTTCTTTTC
ODB1 BD 47aa forward	ATCTCAGAGGAGGACCTGCATACTTCAGGAATCAGTAGACCACTC
ODB1 BD 176aa reverse	GAATTCGGCCTCCATGGCCATCAAAGCATCCTCGTGATAAAGATG
PMH2 BD 26aa forward	ATCTCAGAGGAGGACCTGCATAAATACTGTTCTGTTTCACAACCTGGC
PMH2 BD 616aa forward	GAATTCGGCCTCCATGGCCATGTAAGATCTTTTCCCATCATTTGATC
MID1 AD 77aa forward	GACGTACCAGATTACGCTCATCATAGAATCAGAGTCATTGACG
MID1 AD 136aa forward	GACGTACCAGATTACGCTCATCAGACTCATCTCCTTCTCTCT
MID1 AD 135aa reverse	TTCCTGACTGGCCTCCATGGCCATAGGGTTAGGTAGACAGCCAGAACG
MID1 AD 170aa reverse	TTCCTGACTGGCCTCCATGGCCATATCAGGACTGTATCCAATC
MID1 AD 205aa reverse	TTCCTGACTGGCCTCCATGGCCATATCAGGAATACAGCCAGCTGCAC
MID1 AD 240aa reverse	TTCCTGACTGGCCTCCATGGCCATTGGAGAGATCCCAGCTTTGCTCA
MID1 AD 276aa reverse	TTCCTGACTGGCCTCCATGGCCATCTCCACAGGGTAATCCCGAC
MID1 AD 311aa reverse	TTCCTGACTGGCCTCCATGGCCATATACGGTATGAACCCTC
MID1 AD 343aa reverse	TTCCTGACTGGCCTCCATGGCCATAGACCTCAGTTCAGAAACCCTTTG
nMAT1 AD 90aa forward	GACGTACCAGATTACGCTCATTGGGTCTTAGCTTATCAACGAAC
nMAT1 AD 711aa reverse	TTCCTGACTGGCCTCCATGGCCATTGTTTGTGAGTCTAATTTCTGCAACC
MCSF1 AD 28aa forward	GACGTACCAGATTACGCTCATTCCACTCCGAGACCTTTACA
MCSF1 AD 405aa reverse	TTCCTGACTGGCCTCCATGGCCATGGTTGTCTCGTCAGGAGAATCT
MTSF1 AD 43aa forward	GACGTACCAGATTACGCTCATTCCACTCCTCCGCCGATGACAT
MTSF1 AD 997aa reverse	TTCCTGACTGGCCTCCATGGCCATAGTCCCATCAGATGTTTTCTTTTC
ODB1 AD 47aa forward	GACGTACCAGATTACGCTCATACTTCAGGAATCAGTAGACCACTC
ODB1 AD 176aa reverse	TTCCTGACTGGCCTCCATGGCCATCAAAGCATCCTCGTGATAAAGATG
PMH2 AD 26aa forward	GACGTACCAGATTACGCTCATAAATACTGTTCTGTTTCACAACCTGGC
PMH2 AD 616aa forward	TTCCTGACTGGCCTCCATGGCCATGTAAGATCTTTTCCCATCATTTGATC
MID1 GFP forward	ATCGAATTCCTGCAGCCCCGGGATGGCAATTCGCTTGACGCATC
MID1(90aa) GFP reverse	CACCATTCTAGAACTAGTAACAAAACCTTTGGAGGATTTTCGTC
MID1 GFP reverse	CACCATTCTAGAACTAGTAGACCTCAGTTCAGAAACCCTTTG
WTF9 forward	ATCGAATTCCTGCAGCCCCGGGATGCTCTCTATTTCGCCCATGCCAA

Primers for protoplast transformation

	WTF9 reverse	CACCATTCTAGAACTAGTGCCTTCAAAATCCAAATCCAAATC	
	nMAT1 Flag forward	TCTCTCGAGGTCGACGGTATCGAATGAAAAGACTGACATATCCATTGAG	
	nMAT1 Flag reverse	TTCTGCAGGAATTTCGATATCTGTTTGTGAGTCTAATTTCTGCAACC	
	MCSF1 Flag forward	TCTCTCGAGGTCGACGGTATCGAATGTTCTTGATTTCGTCTCTCCCGC	
	MCSF1 Flag reverse	TTCTGCAGGAATTTCGATATCGGTTGTCTCGTCAGGAGAATCT	
	MTSF1 Flag forward	TCTCTCGAGGTCGACGGTATCGAATGAACAAAACAGTCGTAAGATGTC	
	MTSF1 Flag reverse	TTCTGCAGGAATTTCGATATCAGTCCCATCAGATGTTTTCTTTTC	
	ODB1 Flag forward	TCTCTCGAGGTCGACGGTATCGAATGGCGGGGTTAGGGTTA	
	ODB1 Flag reverse	TTCTGCAGGAATTTCGATATCCAAAGCATCCTCGTGATAAAGATG	
	PMH2 Flag forward	TCTCTCGAGGTCGACGGTATCGAATGATCACTACAGTGCTACGACG	
	PMH2 Flag reverse	TTCTGCAGGAATTTCGATATCGTAAGATCTTTTCCCATCATTTGATC	
Primers for genetic complementation	MID1 forward	GGGGGACTCTAGAGGATCCCCATGGCAATTCGCTTGACGCATC	
	MID1 135aa reverse	CTCGCCCTTGCTCACGGTACCCAGGGTTAGGTAGACAGCCAGAACG	
	MID1 170aa reverse	CTCGCCCTTGCTCACGGTACCCATCAGGACTGTATCCAATC	
	MID1 205aa reverse	CTCGCCCTTGCTCACGGTACCCATCAGGAATACAGCCAGCTGCAC	
	MID1 240aa reverse	CTCGCCCTTGCTCACGGTACCCTGGAGAGATCCCAGCTTTGCTCA	
	MID1 276aa reverse	CTCGCCCTTGCTCACGGTACCCCTCCACAGGGTAATCCCCGAC	
	MID1 311aa reverse	CTCGCCCTTGCTCACGGTACCCATACGGTATGAACCCTC	
	MID1 343aa reverse	CTCGCCCTTGCTCACGGTACCCAGACCTCAGTTCAGAAACCCTTG	
	MID1 Δ (101-135aa) inter reverse	GAGAGAAGGAGATGAGTCTGAATCTTGGGCAGTGAACGA	
	MID1 Δ (101-135aa) inter forward	TCGTTCACTGCCAAGATTCAGACTCATCTCCTTCTCTC	
	MID1 Δ (136-170aa) inter reverse	AAGTAATTGCAGGTTCCAGTAGGGTTAGGTAGACAGCCAG	
	MID1 Δ (136-170aa) inter forward	CTGGCTGTCTACCTAACCTACTGGAACCTGCAATTACTT	
	MID1Pro forward	CAGTGCCAAGCTTGCATGCCGTAATAATGTTTGACGG	
	MID1Pro reverse	TGCGTCAAGCGAATTGCCATTTCTATTCTCAGAGACCTG	
	MID1 CDS forward	CAGGTCTCTGAGAATAGGAAATGGCAATTCGCTTGACGCA	
	MID1 Flag reverse	GTCGACAGGCCTTTCGAAAGACCTCAGTTCAGAAACCC	
	MID1 GUS reverse	TTCGAGCTCGGTACCCGGGGATCCAGACCTCAGTTCAGAAACCC	
	Primers for RT-PCR	F1	ATGGCAATTCGCTTGACGCATCT
		R1	CTAAGACCTCAGTTCAGAAACCC
		F2	CCGGATTATTCCTCCTGGGATTAG
R2		CCAGGATCGTAACTGCAGCTATTC	
ACTIN2 RT forward		ATCCTTCCTGATATCGAC	
ACTIN2 RT reverse		GAGAAGATGACTCAGATC	
<i>ccmFc</i> forward		ATTTTTATGGTCGTGCCTTGTGGCA	
<i>ccmFc</i> reverse		TGAACTCCACGGAACCTTCTCGATT	
<i>cox2</i> forward		CCTCACAATTTCTCCTTGTGATGC	
<i>cox2</i> reverse		TTCCCCGGTTTGGGGGATTAAT	
<i>rp12</i> forward		TGAGACCAGGGAGAGCAAGAGC	
<i>rp12</i> reverse		ACAGTGAATAAGGGCTTAGGATGG	
<i>rps3</i> forward		ATGGCACGAAAAGGAAATCCG	
<i>rps3</i> reverse		TCGTACGTTTCGGATATAGCAC	

Primers for RT-PCR analysis of *nad* transcripts are from [des Francs-Small et al. , 2014](#)

Primers for qRT-PCR

MID1 qRT forward
MID1 qRT reverse
ACTIN2 qRT forward
ACTIN2 qRT reverse

TTTTTCCGGTCAATCTCGTC
GCAGTGAACGAGGTCTCACA
ACACTGTGCCAATCTACGAGGGTT
ACAATTTCCCGCTCTGCTGTTGTG

Primers for luciferase complementation assay

MID1-NLuc forward
MID1-NLuc reverse
WTF9-NLuc forward
WTF9-NLuc reverse
CLuc-MID1 forward
CLuc-MID1 reverse
CLuc-MTSF1 forward
CLuc-MTSF1 reverse

AGAACACGGGGGACGAGCTCGGTACCATGCATAGAATCAGAGTCATTGACG
AGTCCATTTGTTGGATCCCGGGTACCAGACCTCAGTTCAGAAACCCTTTGTC
AGAACACGGGGGACGAGCTCGGTACCATGCACCTTCTTAAGGAAGTTTCCTTCAA
AGTCCATTTGTTGGATCCCGGGTACCGCCTTCAAAATCCAAATCCAAATCT
TCTCGTACGCGTCCCGGGGCGGTACCCATAGAATCAGAGTCATTGACG
AGTCCATTTGTTGGATCCCGGGTACCCTAAGACCTCAGTTCAGAAACCCT
TCTCGTACGCGTCCCGGGGCGGTACCTCCACTCCTCCGCCGGATGACATGT
AGTCCATTTGTTGGATCCCGGGTACCCTAAGTCCCATCAGATGTTTTTC