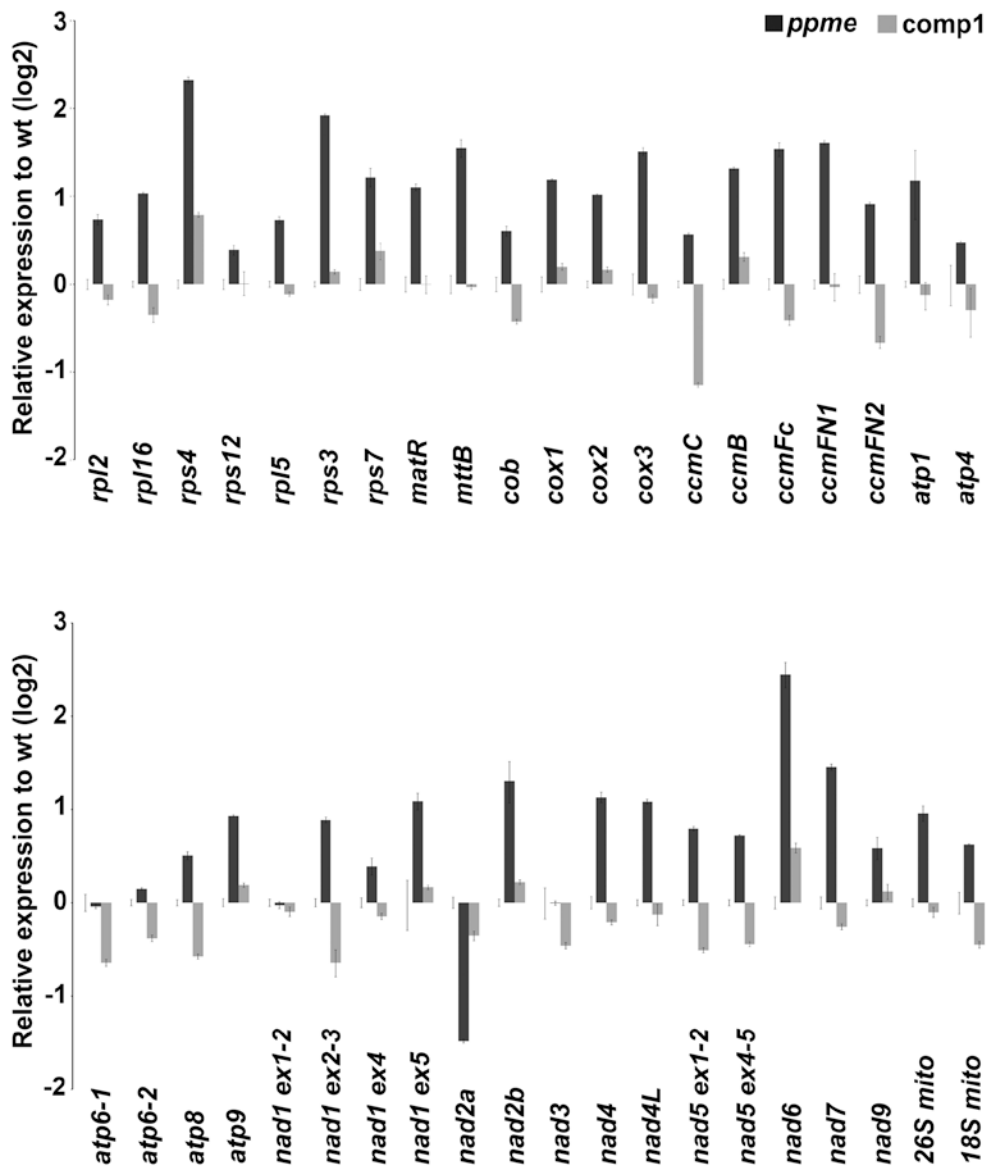


**Supplemental Figure 1.** Comparison of mitochondrial splicing efficiency.

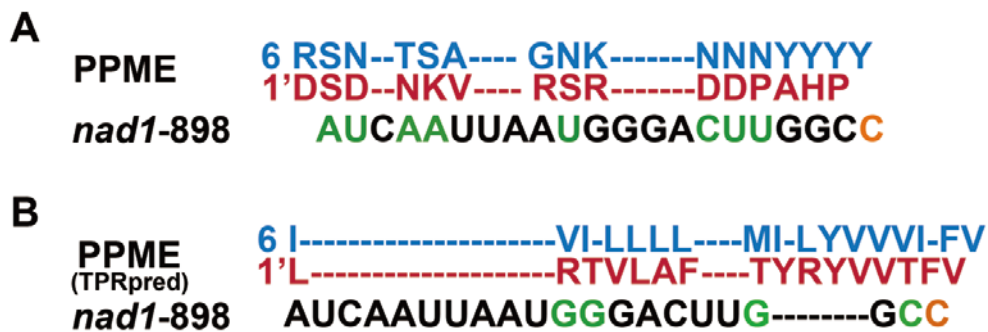
(A) The splicing efficiency of each intron in whole mitochondrial intron containing genes. The transcript levels of exon-exon (Spliced) and intron-exon (Unspliced) of each intron from 14-day-old wild-type, homozygous *ppme*<sup>-/-</sup>, and complementation line seedlings were obtained by qRT-PCR. The ratio of the spliced to unspliced transcripts indicates the splicing efficiency of each intron. The red asterisk indicates that only *nad2* intron 1 displayed obviously lower splicing efficiency.

(B) Detection of individual mitochondrial joined exons after splicing. The primer pairs were designed in the exon near each exon-intron junction, and spliced products were detected by RT-PCR. The orange asterisk indicates the accumulation of spliced *nad2* exon 1-2 after removing *nad2* intron 1, even though the splicing efficiency was lower.



**Supplemental Figure 2.** The transcript abundance of whole mitochondrial genes.

The total RNAs extracted from 14-day-old wild-type, homozygous *ppme*<sup>-/-</sup> and 35S::*PPME-GFP/ppme* complementation line seedlings were used for qRT-PCR to monitor the expression levels of individual mitochondrial genes.



**Supplemental Figure 3:** Predicated PPR combination code between PPME and *nad1-898*.

(A) Analysis of the putative PPR combination code between PPME and *nad1-898*. The combination of the sixth position (6) of each PPR motif and the first position (1') of the following PPR motifs was extracted from 16 PPR motifs of PPME, which was then matched to the -20 upstream region in *nad1-898*. The black labeled nucleotide reveals a mismatched conserved code, and the green labeled nucleotide shows a matched code of the PPR combination between the 6-1' pair for this nucleotide located upstream of *nad1-898*. (B) The 17 PPR motifs predicted by the TPRpred tool showed much lower conservation between PPME and *nad1-898* compared to (A).

```

A.thaliana : VAVPAPGICGLDGLG--VAVVLERKVMVQCRKGPVVG*FGLLQPADGKRLKEPISPSANFLRRAFAATFMSLVAWAVFPDYGMLSDINIGLLYFA : 112
A.rothii : MRVYIGIARIGIPELLQVAVVLERKVMVQCRKGPVVG*FGLLQPADGKRLKEPISPSANFLRRAFAATFMSLVAWAVFPDYGMLSDINIGLLYFA : 115
A.syrriaca : VAVPAPGICGLDGLG--VAVVLERKVMVQCRKGPVVG*FGLLQPADGKRLKEPISPSANFLRRAFAATFMSLVAWAVFPDYGMLSDINIGLLYFA : 112
A.trichopo : VAVPAPGICGLDGLG--VAVVLERKVMVQCRKGPVVG*FGLLQPADGKRLKEPISPSANFLRRAFAATFMSLVAWAVFPDYGMLSDINIGLLYFA : 112
B.napus : VAVPAPGICGLDGLG--VAVVLERKVMVQCRKGPVVG*FGLLQPADGKRLKEPISPSANFLRRAFAATFMSLVAWAVFPDYGMLSDINIGLLYFA : 112
B.oldhamii : VAVPAPGICGLDGLG--VAVVLERKVMVQCRKGPVVG*FGLLQPADGKRLKEPISPSANFLRRAFAATFMSLVAWAVFPDYGMLSDINIGLLYFA : 112
B.pcmiform : MRVYIGIARIGIPELLQVAVVLERKVMVQCRKGPVVG*FGLLQPADGKRLKEPISPSANFLRRAFAATFMSLVAWAVFPDYGMLSDINIGLLYFA : 115
C.acicular : MRVYIGIARIGIPELLQVAVVLERKVMVQCRKGPVVG*FGLLQPADGKRLKEPISPSANFLRRAFAATFMSLVAWAVFPDYGMLSDINIGLLYFA : 115
C.bailyanu : MRVYIINIIRIGIPELLQVAVVLERKVMVQCRKGPVVG*FGLLQPADGKRLKEPISPSANFLRRAFAATFMSLVAWAVFPDYGMLSDINIGLLYFA : 115
C.globosum : VVWISLAKLQGVVLDGLG--VAVVLERKVMVQCRKGPVVG*FGLLQPADGKRLKEPISPSANFLRRAFAATFMSLVAWAVFPDYGMLSDINIGLLYFA : 112
C.pepo : VAVPAPGICGLDGLG--VAVVLERKVMVQCRKGPVVG*FGLLQPADGKRLKEPISPSANFLRRAFAATFMSLVAWAVFPDYGMLSDINIGLLYFA : 112
I.engelman : MRVYIGVAVRIGIPELLQVAVVLERKVMVQCRKGPVVG*FGLLQPADGKRLKEPISPSANFLRRAFAATFMSLVAWAVFPDYGMLSDINIGLLYFA : 115
L.japonicu : VAVPAPGICGLDGLG--VAVVLERKVMVQCRKGPVVG*FGLLQPADGKRLKEPISPSANFLRRAFAATFMSLVAWAVFPDYGMLSDINIGLLYFA : 112
M.pinnata : VAVPAPGICGLDGLG--VAVVLERKVMVQCRKGPVVG*FGLLQPADGKRLKEPISPSANFLRRAFAATFMSLVAWAVFPDYGMLSDINIGLLYFA : 112
N.tabacum : VAVPAPGICGLDGLG--VAVVLERKVMVQCRKGPVVG*FGLLQPADGKRLKEPISPSANFLRRAFAATFMSLVAWAVFPDYGMLSDINIGLLYFA : 112
O.berteroa : VAVPAPGICGLDGLG--VAVVLERKVMVQCRKGPVVG*FGLLQPADGKRLKEPISPSANFLRRAFAATFMSLVAWAVFPDYGMLSDINIGLLYFA : 112
C.stellatu : MRVYIGIARIGIPELLQVAVVLERKVMVQCRKGPVVG*FGLLQPADGKRLKEPISPSANFLRRAFAATFMSLVAWAVFPDYGMLSDINIGLLYFA : 115
P.cyniseta : MRVYIGIARIGIPELLQVAVVLERKVMVQCRKGPVVG*FGLLQPADGKRLKEPISPSANFLRRAFAATFMSLVAWAVFPDYGMLSDINIGLLYFA : 115
P.patens : MRVYIGIARIGIPELLQVAVVLERKVMVQCRKGPVVG*FGLLQPADGKRLKEPISPSANFLRRAFAATFMSLVAWAVFPDYGMLSDINIGLLYFA : 115
S.conica : VAVPAPGICGLDGLG--VAVVLERKVMVQCRKGPVVG*FGLLQPADGKRLKEPISPSANFLRRAFAATFMSLVAWAVFPDYGMLSDINIGLLYFA : 112
S.latifoli : VAVPAPGICGLDGLG--VAVVLERKVMVQCRKGPVVG*FGLLQPADGKRLKEPISPSANFLRRAFAATFMSLVAWAVFPDYGMLSDINIGLLYFA : 112
S.noctiflo : VAVPAPGICGLDGLG--VAVVLERKVMVQCRKGPVVG*FGLLQPADGKRLKEPISPSANFLRRAFAATFMSLVAWAVFPDYGMLSDINIGLLYFA : 112
S.palustre : MRVYIGIARIGIPELLQVAVVLERKVMVQCRKGPVVG*FGLLQPADGKRLKEPISPSANFLRRAFAATFMSLVAWAVFPDYGMLSDINIGLLYFA : 115
T.fuegianu : MRVYIGIARIGIPELLQVAVVLERKVMVQCRKGPVVG*FGLLQPADGKRLKEPISPSANFLRRAFAATFMSLVAWAVFPDYGMLSDINIGLLYFA : 115
T.pellucid : MRVYIGIARIGIPELLQVAVVLERKVMVQCRKGPVVG*FGLLQPADGKRLKEPISPSANFLRRAFAATFMSLVAWAVFPDYGMLSDINIGLLYFA : 115
U.hutchins : MRVYIGIARIGIPELLQVAVVLERKVMVQCRKGPVVG*FGLLQPADGKRLKEPISPSANFLRRAFAATFMSLVAWAVFPDYGMLSDINIGLLYFA : 115
H.sapiens : M---FMANMLLVEVLA---MAMIMLPERKIIQVYCRKGPVVG*YGLLQPADGKRLKEPISPSANFLRRAFAATFMSLVAWAVFPDYGMLSDINIGLLYFA : 107
M 6 66 66 6AF16LaERR66a 6QCRKGPVVG 5GLLQPADG KRLKEP6 Ps3an f6 MAP tfm6s16awav6PfdygmVsl1n16G6L56fa

```

```

A.thaliana : SSSLVYGLLFRSNSVAIFGALRSAAQVSEYVSLIILITLQVGSNSIVMCKIWECPFFVVMFFISCLAETNRPFDLPEAEELVAGYNVEYSMCGEAL : 227
A.rothii : SSSLVYGLLFRSNSVAIFGALRSAAQVSEYVSLIILITLQVGSNSIVMCKIWECPFFVVMFFISCLAETNRPFDLPEAEELVAGYNVEYSMCGEAL : 230
A.syrriaca : SSSLVYGLLFRSNSVAIFGALRSAAQVSEYVSLIILITLQVGSNSIVMCKIWECPFFVVMFFISCLAETNRPFDLPEAEELVAGYNVEYSMCGEAL : 227
A.trichopo : SSSLVYGLLFRSNSVAIFGALRSAAQVSEYVSLIILITLQVGSNSIVMCKIWECPFFVVMFFISCLAETNRPFDLPEAEELVAGYNVEYSMCGEAL : 227
B.napus : SSSLVYGLLFRSNSVAIFGALRSAAQVSEYVSLIILITLQVGSNSIVMCKIWECPFFVVMFFISCLAETNRPFDLPEAEELVAGYNVEYSMCGEAL : 227
B.oldhamii : SSSLVYGLLFRSNSVAIFGALRSAAQVSEYVSLIILITLQVGSNSIVMCKIWECPFFVVMFFISCLAETNRPFDLPEAEELVAGYNVEYSMCGEAL : 227
B.pcmiform : SSSLVYGLLFRSNSVAIFGALRSAAQVSEYVSLIILITLQVGSNSIVMCKIWECPFFVVMFFISCLAETNRPFDLPEAEELVAGYNVEYSMCGEAL : 230
C.acicular : SSSLVYGLLFRSNSVAIFGALRSAAQVSEYVSLIILITLQVGSNSIVMCKIWECPFFVVMFFISCLAETNRPFDLPEAEELVAGYNVEYSMCGEAL : 230
C.bailyanu : SSSLVYGLLFRSNSVAIFGALRSAAQVSEYVSLIILITLQVGSNSIVMCKIWECPFFVVMFFISCLAETNRPFDLPEAEELVAGYNVEYSMCGEAL : 230
C.globosum : SSSLVYGLLFRSNSVAIFGALRSAAQVSEYVSLIILITLQVGSNSIVMCKIWECPFFVVMFFISCLAETNRPFDLPEAEELVAGYNVEYSMCGEAL : 227
C.pepo : SSSLVYGLLFRSNSVAIFGALRSAAQVSEYVSLIILITLQVGSNSIVMCKIWECPFFVVMFFISCLAETNRPFDLPEAEELVAGYNVEYSMCGEAL : 230
I.engelman : SSSLVYGLLFRSNSVAIFGALRSAAQVSEYVSLIILITLQVGSNSIVMCKIWECPFFVVMFFISCLAETNRPFDLPEAEELVAGYNVEYSMCGEAL : 230
L.japonicu : SSSLVYGLLFRSNSVAIFGALRSAAQVSEYVSLIILITLQVGSNSIVMCKIWECPFFVVMFFISCLAETNRPFDLPEAEELVAGYNVEYSMCGEAL : 227
M.pinnata : SSSLVYGLLFRSNSVAIFGALRSAAQVSEYVSLIILITLQVGSNSIVMCKIWECPFFVVMFFISCLAETNRPFDLPEAEELVAGYNVEYSMCGEAL : 227
N.tabacum : SSSLVYGLLFRSNSVAIFGALRSAAQVSEYVSLIILITLQVGSNSIVMCKIWECPFFVVMFFISCLAETNRPFDLPEAEELVAGYNVEYSMCGEAL : 227
O.berteroa : SSSLVYGLLFRSNSVAIFGALRSAAQVSEYVSLIILITLQVGSNSIVMCKIWECPFFVVMFFISCLAETNRPFDLPEAEELVAGYNVEYSMCGEAL : 227
C.stellatu : SSSLVYGLLFRSNSVAIFGALRSAAQVSEYVSLIILITLQVGSNSIVMCKIWECPFFVVMFFISCLAETNRPFDLPEAEELVAGYNVEYSMCGEAL : 230
P.cyniseta : SSSLVYGLLFRSNSVAIFGALRSAAQVSEYVSLIILITLQVGSNSIVMCKIWECPFFVVMFFISCLAETNRPFDLPEAEELVAGYNVEYSMCGEAL : 230
P.patens : SSSLVYGLLFRSNSVAIFGALRSAAQVSEYVSLIILITLQVGSNSIVMCKIWECPFFVVMFFISCLAETNRPFDLPEAEELVAGYNVEYSMCGEAL : 230
S.conica : SSSLVYGLLFRSNSVAIFGALRSAAQVSEYVSLIILITLQVGSNSIVMCKIWECPFFVVMFFISCLAETNRPFDLPEAEELVAGYNVEYSMCGEAL : 227
S.latifoli : SSSLVYGLLFRSNSVAIFGALRSAAQVSEYVSLIILITLQVGSNSIVMCKIWECPFFVVMFFISCLAETNRPFDLPEAEELVAGYNVEYSMCGEAL : 227
S.noctiflo : SSSLVYGLLFRSNSVAIFGALRSAAQVSEYVSLIILITLQVGSNSIVMCKIWECPFFVVMFFISCLAETNRPFDLPEAEELVAGYNVEYSMCGEAL : 227
S.palustre : SSSLVYGLLFRSNSVAIFGALRSAAQVSEYVSLIILITLQVGSNSIVMCKIWECPFFVVMFFISCLAETNRPFDLPEAEELVAGYNVEYSMCGEAL : 230
T.fuegianu : SSSLVYGLLFRSNSVAIFGALRSAAQVSEYVSLIILITLQVGSNSIVMCKIWECPFFVVMFFISCLAETNRPFDLPEAEELVAGYNVEYSMCGEAL : 230
T.pellucid : SSSLVYGLLFRSNSVAIFGALRSAAQVSEYVSLIILITLQVGSNSIVMCKIWECPFFVVMFFISCLAETNRPFDLPEAEELVAGYNVEYSMCGEAL : 230
U.hutchins : SSSLVYGLLFRSNSVAIFGALRSAAQVSEYVSLIILITLQVGSNSIVMCKIWECPFFVVMFFISCLAETNRPFDLPEAEELVAGYNVEYSMCGEAL : 230
H.sapiens : ISSLgVYg16 agwSNSkYf GALRsaAc6sYEV36g6Vl6cvGScN Se66 aqkq6Wf P15P6 6M5FIScLAETNRaPFDLPEaEaELVaGNS6EYs6mgfAL

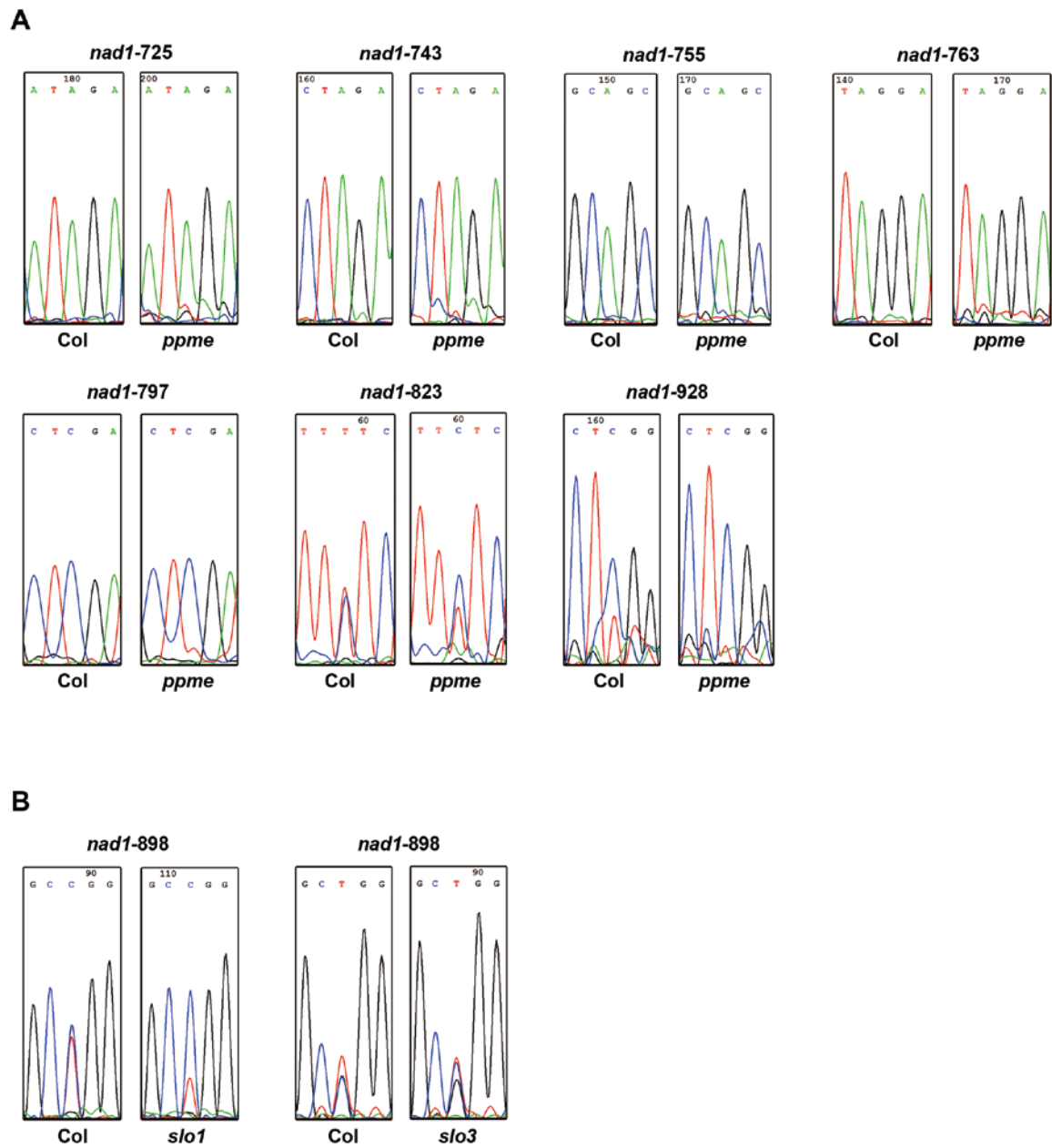
```

```

A.thaliana : FFLGEYANNILMSGLTFLFLGWLPIILDPIKPKIPGSIWFSIKVLEFLFYIIVVRAAPPYRYDLMGLGWRFLPLSLAVVVSQGLVITQQLP--- : 325
A.rothii : FFLGEYANNILMSGLTFLFLGWLPIILDPIKPKIPGSIWFSIKVLEFLFYIIVVRAAPPYRYDLMGLGWRFLPLSLAVVVSQGLVITQQLP--- : 328
A.syrriaca : FFLGEYANNILMSGLTFLFLGWLPIILDPIKPKIPGSIWFSIKVLEFLFYIIVVRAAPPYRYDLMGLGWRFLPLSLAVVVSQGLVITQQLP--- : 325
A.trichopo : FFLGEYANNILMSGLTFLFLGWLPIILDPIKPKIPGSIWFSIKVLEFLFYIIVVRAAPPYRYDLMGLGWRFLPLSLAVVVSQGLVITQQLP--- : 325
B.napus : FFLGEYANNILMSGLTFLFLGWLPIILDPIKPKIPGSIWFSIKVLEFLFYIIVVRAAPPYRYDLMGLGWRFLPLSLAVVVSQGLVITQQLP--- : 325
B.oldhamii : FFLGEYANNILMSGLTFLFLGWLPIILDPIKPKIPGSIWFSIKVLEFLFYIIVVRAAPPYRYDLMGLGWRFLPLSLAVVVSQGLVITQQLP--- : 325
B.pcmiform : FFLGEYANNILMSGLTFLFLGWLPIILDPIKPKIPGSIWFSIKVLEFLFYIIVVRAAPPYRYDLMGLGWRFLPLSLAVVVSQGLVITQQLP--- : 327
C.acicular : FFLGEYANNILMSGLTFLFLGWLPIILDPIKPKIPGSIWFSIKVLEFLFYIIVVRAAPPYRYDLMGLGWRFLPLSLAVVVSQGLVITQQLP--- : 328
C.bailyanu : FFLGEYANNILMSGLTFLFLGWLPIILDPIKPKIPGSIWFSIKVLEFLFYIIVVRAAPPYRYDLMGLGWRFLPLSLAVVVSQGLVITQQLP--- : 328
C.globosum : FFLGEYANNILMSGLTFLFLGWLPIILDPIKPKIPGSIWFSIKVLEFLFYIIVVRAAPPYRYDLMGLGWRFLPLSLAVVVSQGLVITQQLP--- : 325
C.pepo : FFLGEYANNILMSGLTFLFLGWLPIILDPIKPKIPGSIWFSIKVLEFLFYIIVVRAAPPYRYDLMGLGWRFLPLSLAVVVSQGLVITQQLP--- : 325
I.engelman : FFLGEYANNILMSGLTFLFLGWLPIILDPIKPKIPGSIWFSIKVLEFLFYIIVVRAAPPYRYDLMGLGWRFLPLSLAVVVSQGLVITQQLP--- : 328
L.japonicu : FFLGEYANNILMSGLTFLFLGWLPIILDPIKPKIPGSIWFSIKVLEFLFYIIVVRAAPPYRYDLMGLGWRFLPLSLAVVVSQGLVITQQLP--- : 325
M.pinnata : FFLGEYANNILMSGLTFLFLGWLPIILDPIKPKIPGSIWFSIKVLEFLFYIIVVRAAPPYRYDLMGLGWRFLPLSLAVVVSQGLVITQQLP--- : 325
N.tabacum : FFLGEYANNILMSGLTFLFLGWLPIILDPIKPKIPGSIWFSIKVLEFLFYIIVVRAAPPYRYDLMGLGWRFLPLSLAVVVSQGLVITQQLP--- : 325
O.berteroa : FFLGEYANNILMSGLTFLFLGWLPIILDPIKPKIPGSIWFSIKVLEFLFYIIVVRAAPPYRYDLMGLGWRFLPLSLAVVVSQGLVITQQLP--- : 325
C.stellatu : FFLGEYANNILMSGLTFLFLGWLPIILDPIKPKIPGSIWFSIKVLEFLFYIIVVRAAPPYRYDLMGLGWRFLPLSLAVVVSQGLVITQQLP--- : 328
P.cyniseta : FFLGEYANNILMSGLTFLFLGWLPIILDPIKPKIPGSIWFSIKVLEFLFYIIVVRAAPPYRYDLMGLGWRFLPLSLAVVVSQGLVITQQLP--- : 328
P.patens : FFLGEYANNILMSGLTFLFLGWLPIILDPIKPKIPGSIWFSIKVLEFLFYIIVVRAAPPYRYDLMGLGWRFLPLSLAVVVSQGLVITQQLP--- : 328
S.conica : FFLGEYANNILMSGLTFLFLGWLPIILDPIKPKIPGSIWFSIKVLEFLFYIIVVRAAPPYRYDLMGLGWRFLPLSLAVVVSQGLVITQQLP--- : 325
S.latifoli : FFLGEYANNILMSGLTFLFLGWLPIILDPIKPKIPGSIWFSIKVLEFLFYIIVVRAAPPYRYDLMGLGWRFLPLSLAVVVSQGLVITQQLP--- : 325
S.noctiflo : FFLGEYANNILMSGLTFLFLGWLPIILDPIKPKIPGSIWFSIKVLEFLFYIIVVRAAPPYRYDLMGLGWRFLPLSLAVVVSQGLVITQQLP--- : 325
S.palustre : FFLGEYANNILMSGLTFLFLGWLPIILDPIKPKIPGSIWFSIKVLEFLFYIIVVRAAPPYRYDLMGLGWRFLPLSLAVVVSQGLVITQQLP--- : 328
T.fuegianu : FFLGEYANNILMSGLTFLFLGWLPIILDPIKPKIPGSIWFSIKVLEFLFYIIVVRAAPPYRYDLMGLGWRFLPLSLAVVVSQGLVITQQLP--- : 328
T.pellucid : FFLGEYANNILMSGLTFLFLGWLPIILDPIKPKIPGSIWFSIKVLEFLFYIIVVRAAPPYRYDLMGLGWRFLPLSLAVVVSQGLVITQQLP--- : 328
U.hutchins : FFLGEYANNILMSGLTFLFLGWLPIILDPIKPKIPGSIWFSIKVLEFLFYIIVVRAAPPYRYDLMGLGWRFLPLSLAVVVSQGLVITQQLP--- : 328
H.sapiens : FFLGEYANNILMSGLTFLFLGWLPIILDPIKPKIPGSIWFSIKVLEFLFYIIVVRAAPPYRYDLMGLGWRFLPLSLAVVVSQGLVITQQLP--- : 318
ff gEYAN6I6MS LcT1 FLGwlp 1 p ipg 5fs Kv6 flf 56W6Raa5Pr5RYDqLM LgWKvFLPL3LAW66 vsg6l f w6p

```

**Supplemental Figure 4.** Protein alignment mitochondrial NAD1 among different species. NAD1 is highly conserved among all tested species. Protein sequence alignment of Arabidopsis mitochondrial NAD1 and its homologs in different species was generated using CLUSTALW and GeneDoc software. The black, gray, and white regions indicate identical, highly conserved, and lack of conserved amino acids, respectively.



**Figure S5.** RNA editing efficiency of the *nad1* editing sites in *ppme* and *slo* mutants.

(A) The raw sequence data for each editing site near the *nad1-898* editing site. The middle C/T and G/A nucleotides of each panel indicate the editing efficiency of each editing site.  
 (B) RNA editing efficiency of *nad1-898* in the *slo1* and *slo3* mutants.