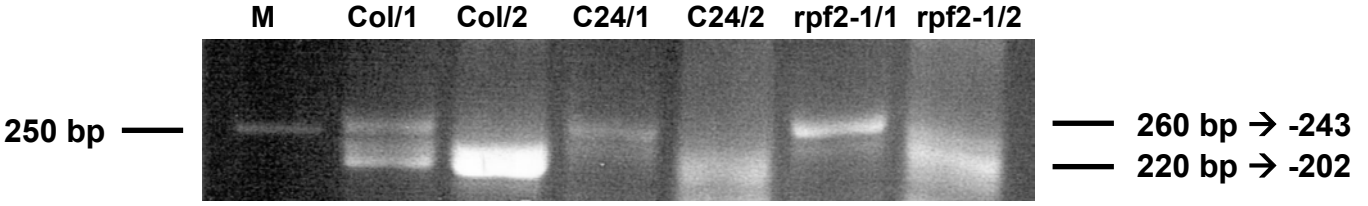
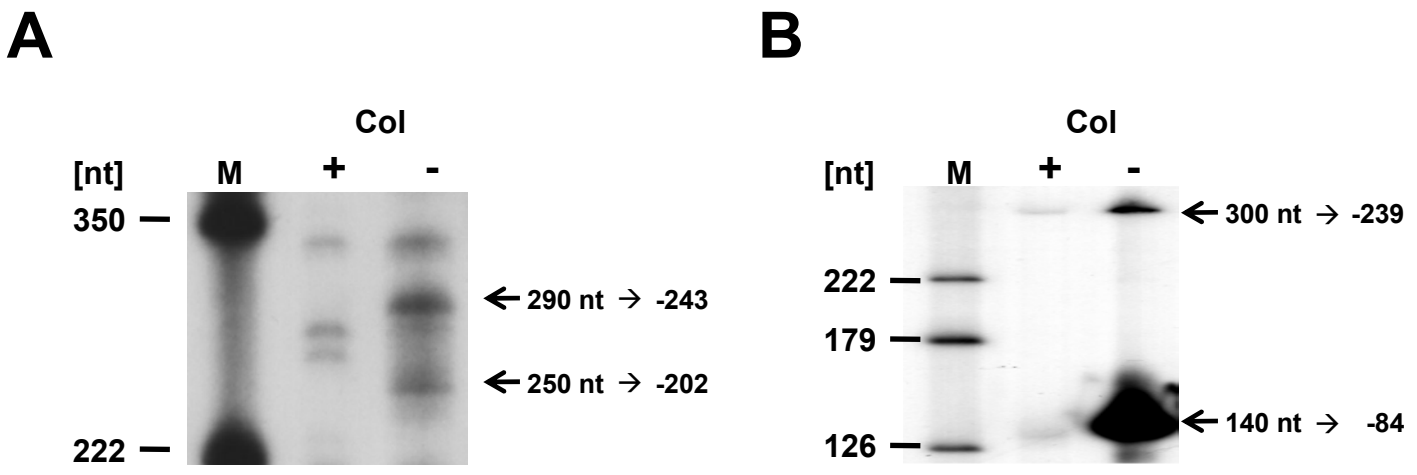
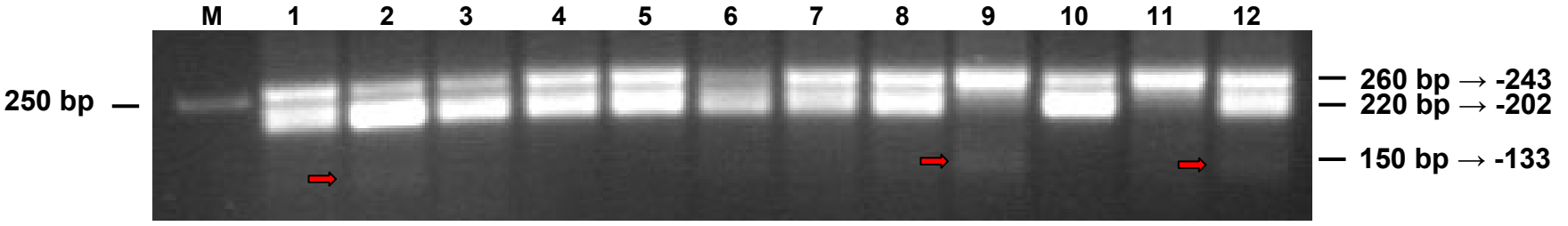


Supplemental Figure S1: Detection of the -202 5' end of the *nad9* mRNA in Col, C24 and *rpf2-1*. CR-RT-PCR was performed with primers Atnad9-3 and Atnad9-7. In Col, 260-bp and 220-bp products indicated the presence of the -243 and the -202 5' ends, respectively. In C24 and *rpf2-1,* the 260-bp products detected the -243 5' end, while no 220-bp product was seen. Products of the first amplification reactions in a size range of about 220 bp were recovered from the gel and used as template for a second PCR analysis under identical conditions. In these reactions 220-bp products were also amplified in C24 and rpf2-1 indicating that minor amounts of the *nad9* transcript with -202 5' end are also present in C24 and *rpf2-1* (lanes Col/2, C24/2 and rpf2-1/2).

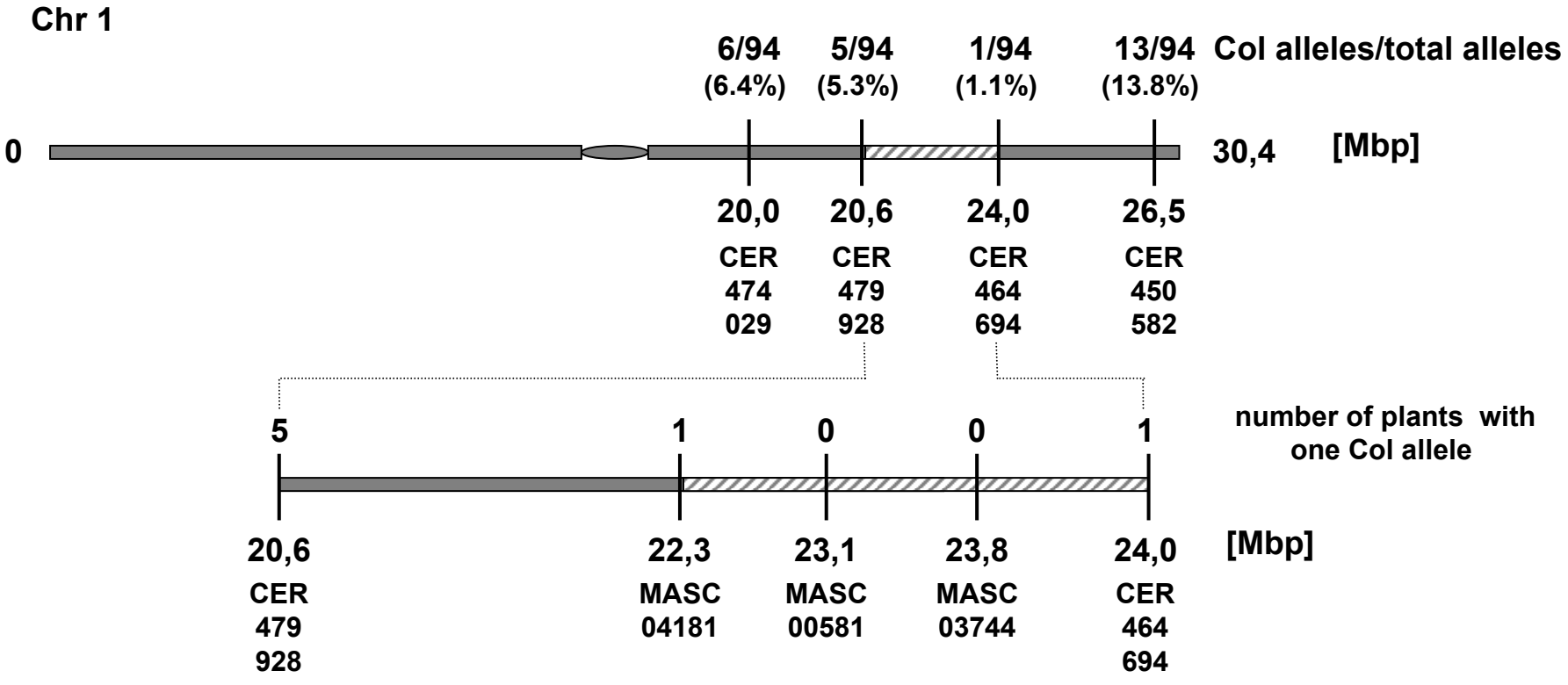


Supplemental Figure S2: Primer extension analysis of *nad9* (A) and *atp9* (B) transcripts from untreated (-) and Terminator™ exonuclease-treated (+) mitochondrial RNA. *nad9* mRNAs with -243 and -202 5' ends were completely degraded by the Terminator™ exonuclease. This demonstrates that these 5' termini derived from posttranscriptional processing. Two extension products of about 270 and 280 nucleotides are barely or not detectable before the treatment of the RNA and are not related to the -243 and -202 5' termini of *nad9* transcripts. In a control experiment a low abundant *atp9* 5' end originating from transcription initiation (-239, Kühn et al., 2005) was still detectable after Terminator™ exonuclease treatment, while the highly abundant mRNA with the processed 5' extremity at position -84 was almost completely digested. Sizes of the primer extension products are given in nucleotides (nt).



1-6: Col x C24 4-1 to 4-6
7-12: C24 x Col 4-1 to 4-6

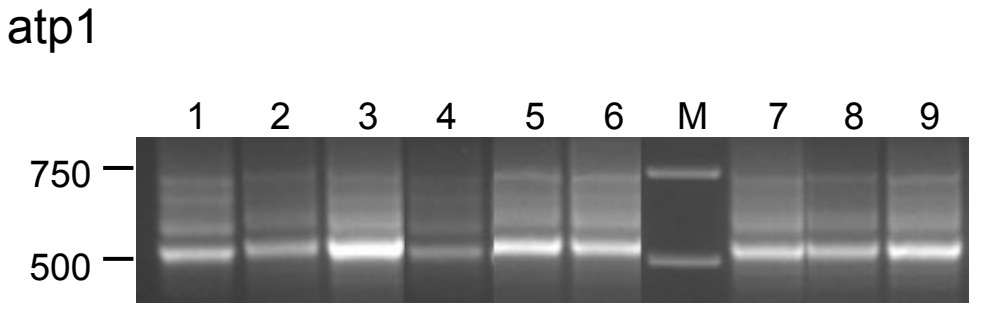
Supplemental Figure S3: Phenotyping of *nad9* mRNA ends in F_2 plants obtained from reciprocal crosses between Col x C24. CR-RT-PCR products amplified from cDNA generated with primer Atnad9-1. PCR products of 260/220 and 150 bp represent mRNAs with 5' ends at -243/-202 and -133, respectively. Primes Atnad9-3 and Atnad9-7 were used for amplification. PCR products were exemplarily shown for 12 plants. Two plants show the recessive C24 phenotype (lanes 9 and 11) i.e. the absence of the 220 bp product after a single round of PCR. Ten plants show the dominant Col phenotype indicated by the 260 and 220-bp products. Red arrows mark the 150-bp product with the -133 5' end, which is inherited independently from the generation of the -202 5' end.



Supplemental Figure S4: Rough mapping of the *RPF2* locus on chromosome 1. 47 of 48 plants showing the recessive C24 *nad9* 5' end phenotype (i.e. undetectable *nad9* -202 5' ends in a single CR-RT-PCR) were used to map the *RPF2* locus. In the first round only markers located on chromosome 1 showed clear co-segregation with this phenotype (upper part of the schema) defining an initial interval of 3.4 Mbp between markers CER479928 and CER464694. Further fine mapping of plants heterozygous for these markers narrowed down this genomic region containing *RPF2* to approximately 1.7 Mbp. For all markers on the other chromosomes an about equal distribution between C24 and Col alleles was found. The defined interval contains 442 protein coding genes ranging from At1g60470 to At1g64620 including 23 PPR genes. Markers are given in Supplemental Table S1.

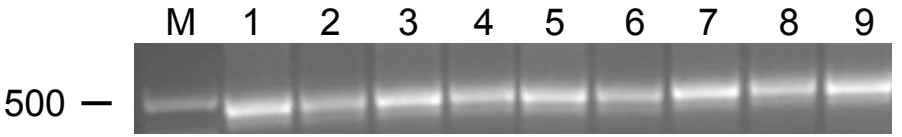
Supplemental Figure S5: CR-RT-PCR analyses of mitochondrial mRNA extremities in PPR T-DNA insertion mutants. Numbering of the mutants and the respective AGI numbers are given below. Oligonucleotides used for cDNA synthesis and PCRs as well as product sizes expected from previous analyses are given in the right margin (Forner et al., 2007; Forner et al., 2008). Oligonucleotide sequences are listed in Supplemental Table 2. Sizes of DNA marker molecules are given in bp.

lane	mutant	gene
1	SALK_061670	(At1g62590)
2	SALK_020638	(At1g63080)
3	SALK_146198	(At1g62670)
4	SALK_139736	(At1g62680)
5	SALK_022264C	(At1g64100)
6	SALK_020230	(At1g63130)
7	SAIL_1282_C03	(At1g63230)
8	SALK_128068	(At1g63070)
9	SALK_087235	(At1g64580)



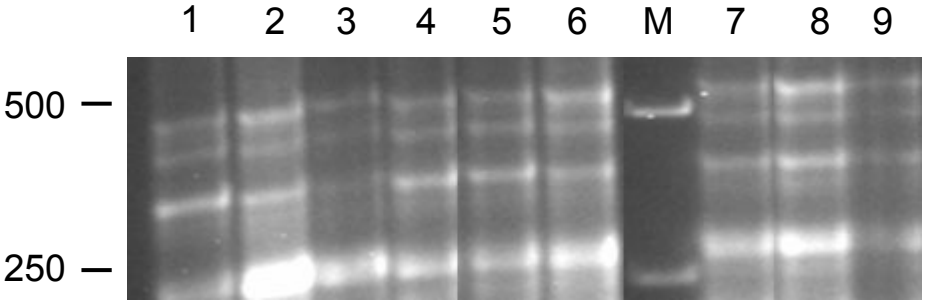
cDNA synthesis: Atatp1-3
PCR: Atatp1-8, Atatp1-9
expected PCR products: 532, 675, 769 bp

atp6-1



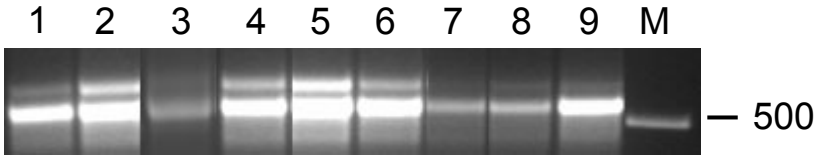
cDNA synthesis: Atatp6-1-NS.R
PCR: Atatp6-3, Atatp6-2
expected PCR product: 459 bp

atp6-2:



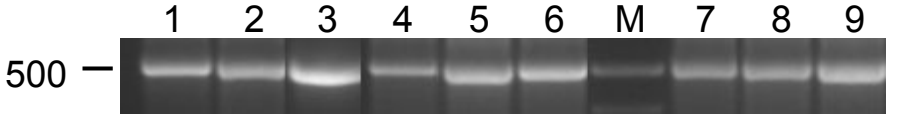
cDNA synthesis: random hexamer primers
PCR: Atatp6-2.Mega.5`, Atatp6.Mega.3'
expected PCR products: 277, 296, 501 bp

atp8 (orfB)



cDNA synthesis: Atatp8-pu2
PCR: Atatp8-1, Atatp8-4
expected PCR products: 528/599 bp

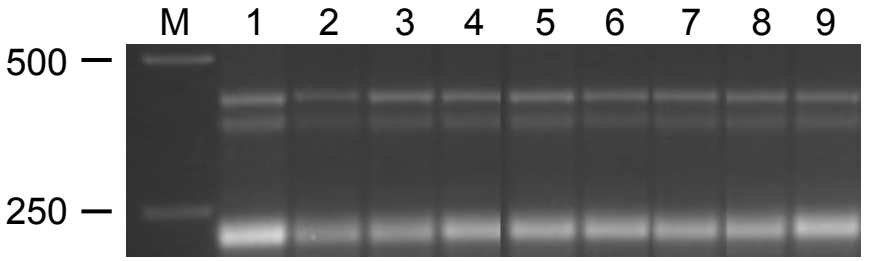
atp9



cDNA synthesis: Atatp9-14
PCR: Atatp9-Mega5`, Atatp9-Mega3`
expected PCR product: 499 bp

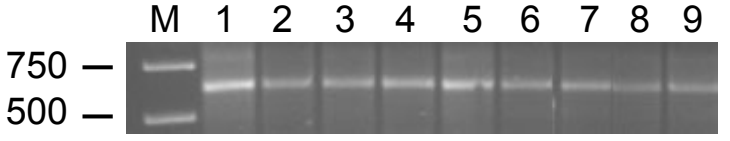
Supplemental Figure S5, continued

ccmB



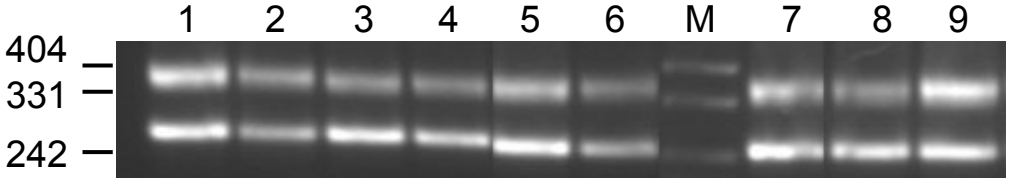
cDNA-Synthese: Atccb2-8
PCR: Atccb2-Mega5‘, Atccb2-Mega3‘
expected PCR products: 190/398 bp

ccmC:



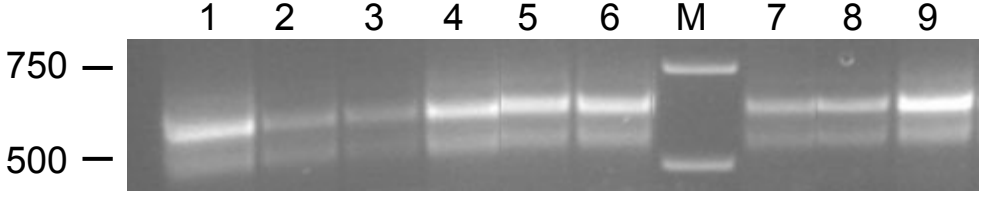
cDNA synthesis: Atccb3-5
PCR: Atccb3-1, Atccb3-3
expected PCR product: 634 bp

$ccmF_C$



cDNA synthesis: Atccb6-2
PCR: Atccb6-1, Atccb6-3
expected PCR products: 249/354 bp

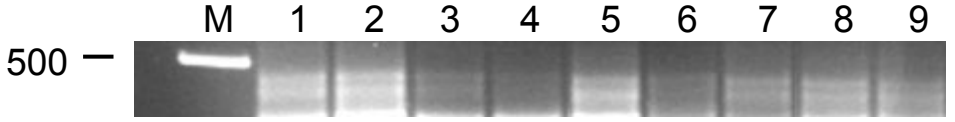
$ccmF_{N1}$



cDNA synthesis: Atccb6n1-1
PCR: Atccb6n1-Mega5‘, Atccb6n1-Mega3‘
expected PCR products: 635/718 bp

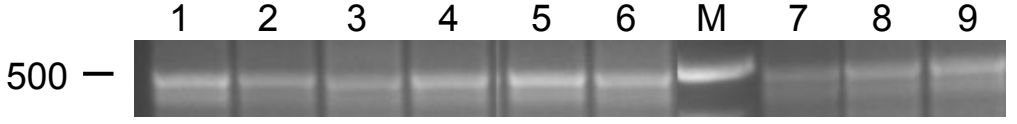
Supplemental Figure S5, continued

$ccmF_{N2}$



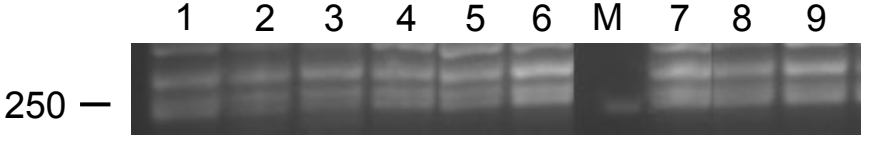
cDNA synthesis: Atccb6n2-1
PCR: Atccb6n2-5, Atccb6n2-6
expected PCR product: 450 bp

cox1



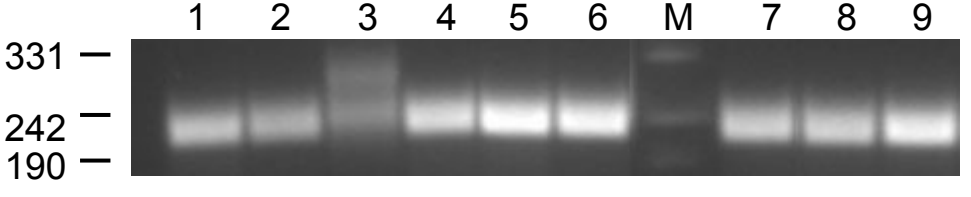
cDNA synthesis: Atcox1-1
PCR: Atcox1-2, Atcox1-4
expected PCR product: 490 bp

cox2



cDNA-Synthese: random hexamer primers
PCR: Atcox2-5, Atcox2-6
expected PCR products: 261/315 bp

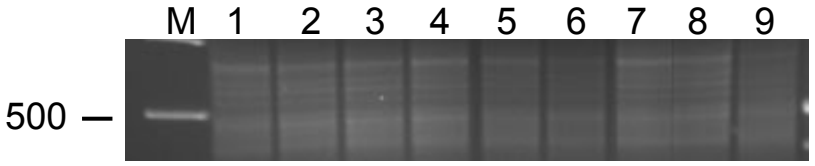
cox3



cDNA synthesis: Atcox3-3'-Primersonde
PCR: Atcox3-Mega5', Atcox3-Mega3'
expected PCR product: 232 bp

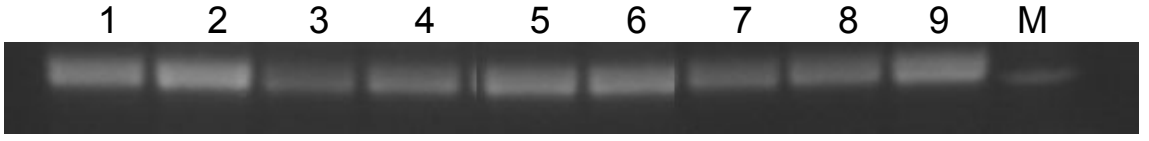
Supplemental Figure S5, continued

nad1



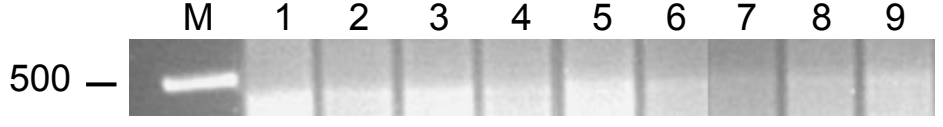
cDNA synthesis: Atnad1a-2
PCR: Atnad1a-Mega5', Atnad1de-Mega3'
expected PCR products: 475, 681, 971 bp

nad2



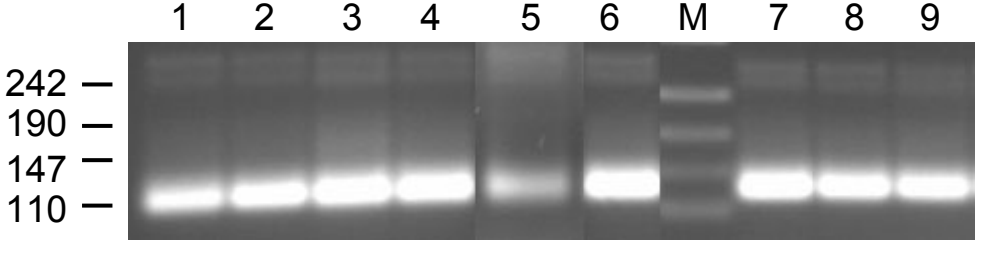
cDNA synthesis: Atnad2ab-1
PCR: Atnad2ab-2, Atnad2cde-3
expected PCR product: 336 bp

nad3/rps12



cDNA synthesis: Atnad3-1
PCR: Atnad3-5, Atrps12-6
expected PCR product: 474 bp

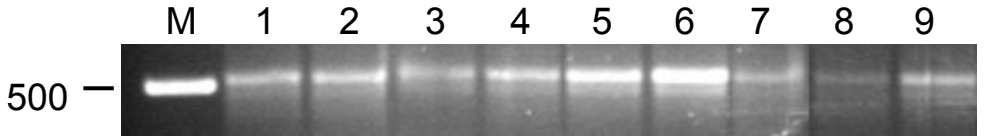
nad4



cDNA synthesis: Atnad4-5
PCR: Atnad4-3, Atnad4-15
expected PCR products: 125, 287 bp

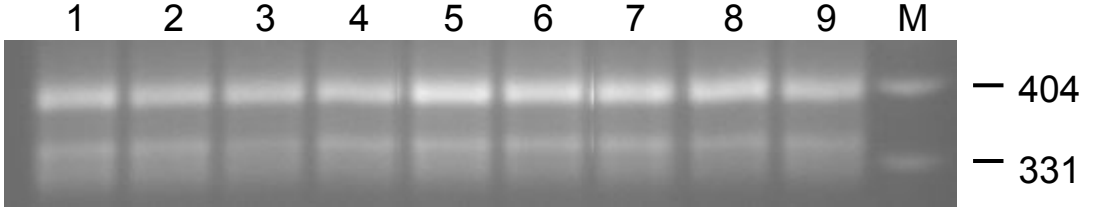
Supplemental Figure S5, continued

nad4L-ORF25



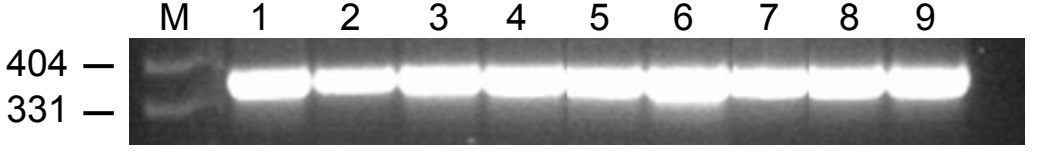
cDNA synthesis: Atnad4L-1
PCR: Atnad4L-2, Atorf25-3
expected PCR products: 514/490 bp

nad5



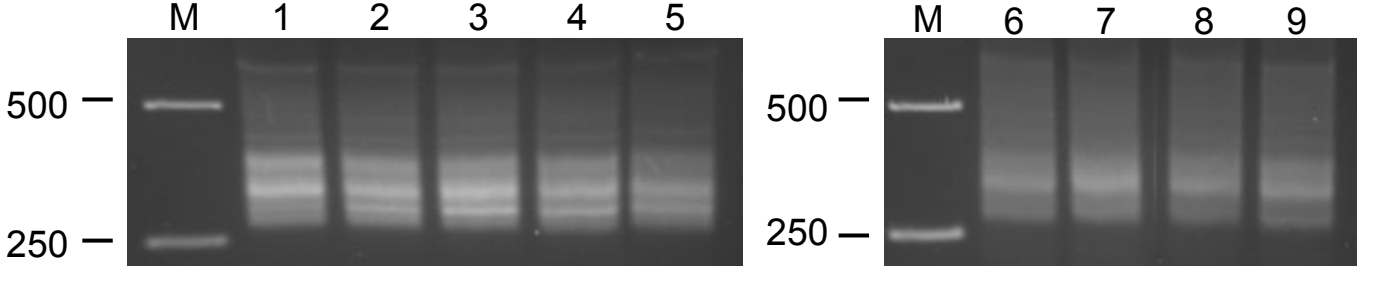
cDNA synthesis: Atnad5ab-1
PCR: Atnad5ab-2, Atnad5de-4
expected PCR products: 357, 408 bp

nad6



cDNA synthesis: Atnad6-1
PCR: Atnad6-2, Atnad6-4
expected PCR product:363 bp

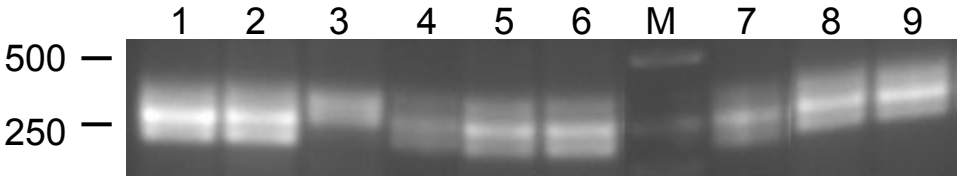
nad7



cDNA synthesis: Atnad7-2
PCR: Atnad7-7, Atnad7-8
expected PCR products:
338, 379, 645 bp

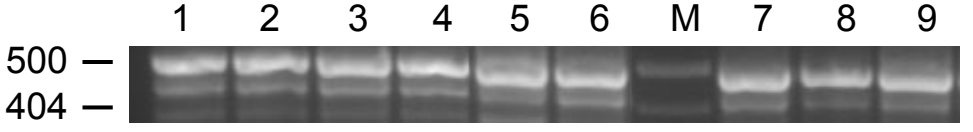
Supplemental Figure S5, continued

nad9



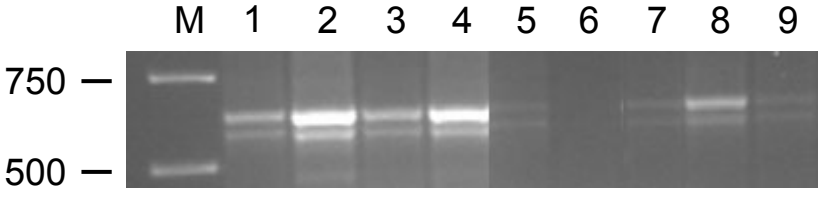
cDNA-Synthese: Atnad9-1
PCR: Atnad9-3, Atnad9-7
expected PCR products: 217, 258 bp

rpl2-orfx



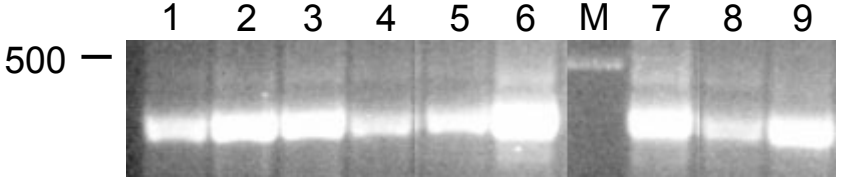
cDNA synthesis: Atrpl2-3
PCR: Atrpl2-2, Atorfx-3
expected PCR product: 429 bp

rpl5/cob



cDNA synthesis: Atrpl5-1
PCR: Atrpl5-5, Atcob-3
expected PCR products: 584/637 bp

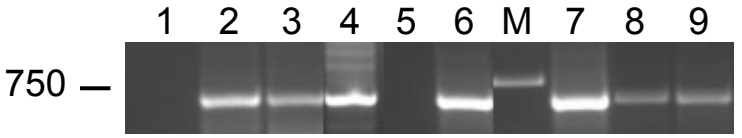
rps3-rpl16



cDNA-Synthese: Atrps3-1
PCR: Atrps3-2, Atrpl16-3
expected PCR products: 400 bp

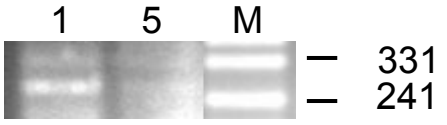
Supplemental Figure S5, continued

rps4



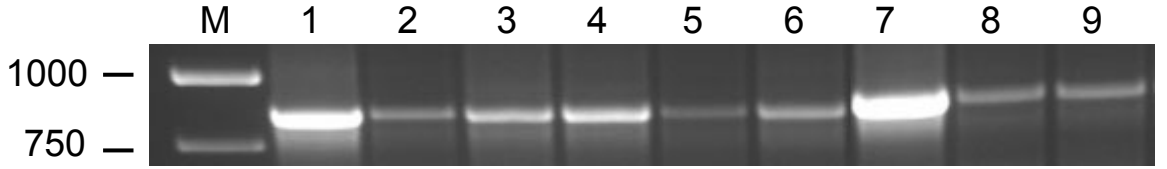
cDNA synthesis: random hexamer primers
PCR: Atrps4-2, Atrps4-4
expected PCR product: 678 bp

products obtained after PCR analysis with different primers:



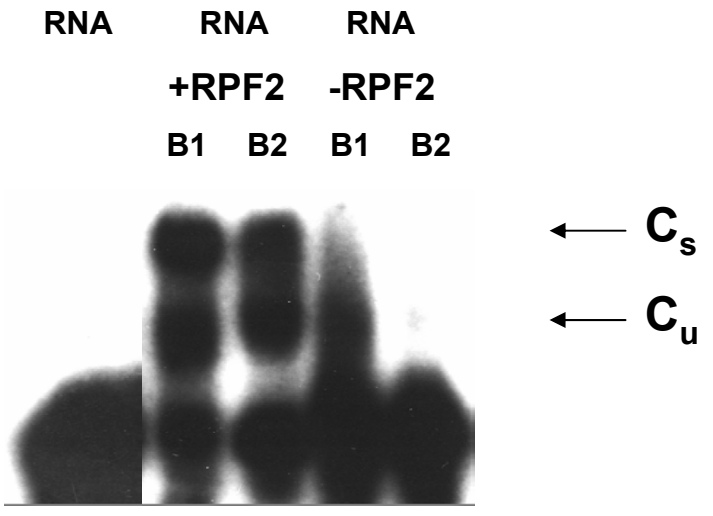
PCR (repetition): Atrps4-2/ Atrps4-6
expected PCR product after repetition: 265 bp

rps7

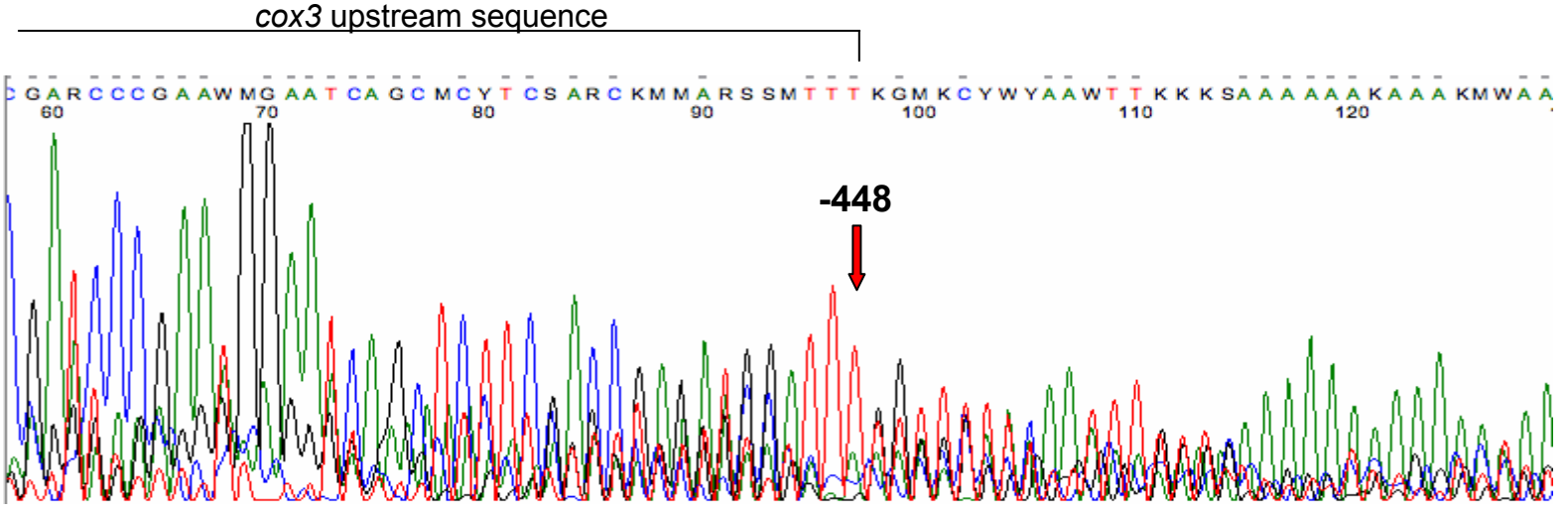


cDNA synthesis: Atrps7-2
PCR: Atrps7-7, Atrps7-8
expected PCR product: 863 bp

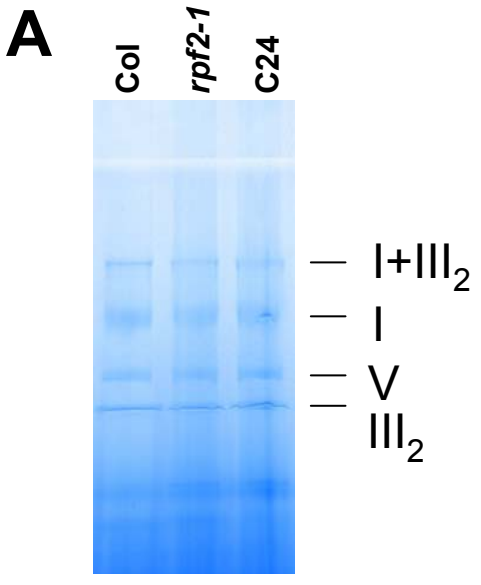
Supplemental Figure S5, continued

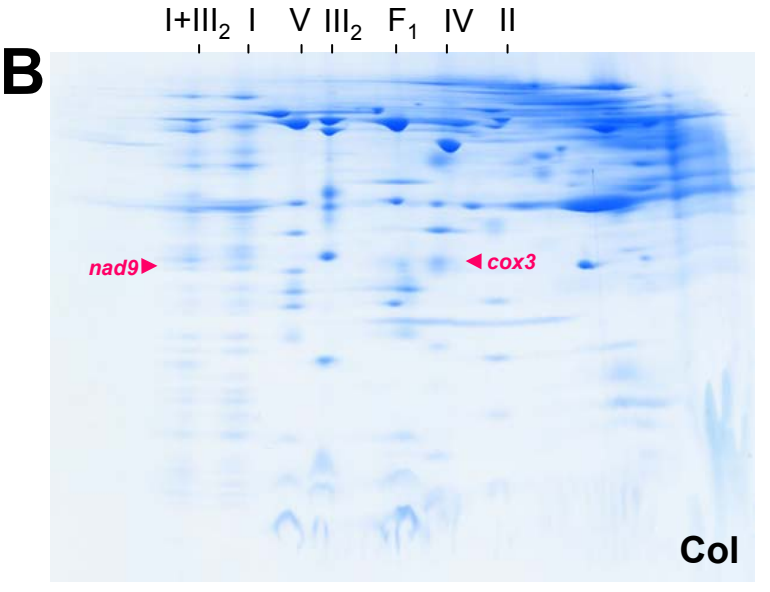


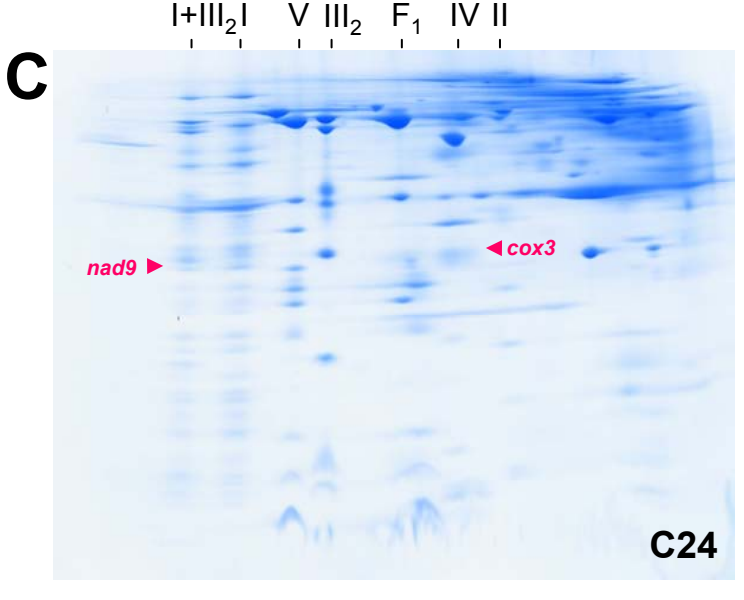
Supplemental Figure S6. Electrophoretic mobility shift assays (EMSA) performed with recombinant RPF2 and a synthetic *nad9* RNA (RNA) covering the -202 5' ends (-296 to –124). The formation of a specific complex (C_s) was observed in two different buffer systems (+RPF2, B1 and B2). This complex was not seen in binding reactions performed with a control lysate obtained from *E. coli* expressing an empty pET32a vector (-RPF2). This result confirmed that the formation of C_s was specific for RPF2, while a smaller complex C_u was also formed in the control reactions.

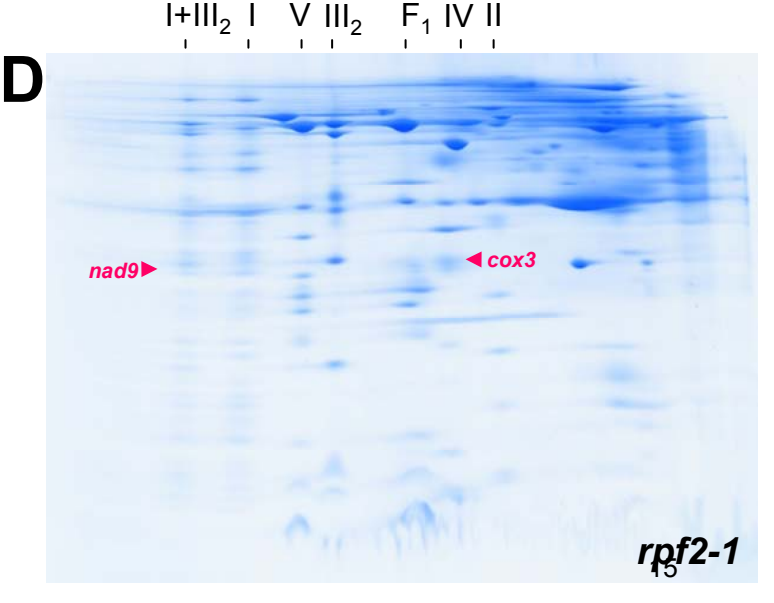


Supplemental Figure S7: Sequence analysis of the 300-bp PCR product obtained in the CR-RT-PCR analysis of *cox3* mRNAs with oligonucleotides Atcox3-Mega3' and Atcox3-Mega5'. Sequencing was done with primer Atcox3-Mega5'. Position -448, indicated by an vertical red arrow, is the last nucleotide position, which corresponds the *cox3* upstream sequence. This marks the 5' end of the *cox3* precursor RNA.

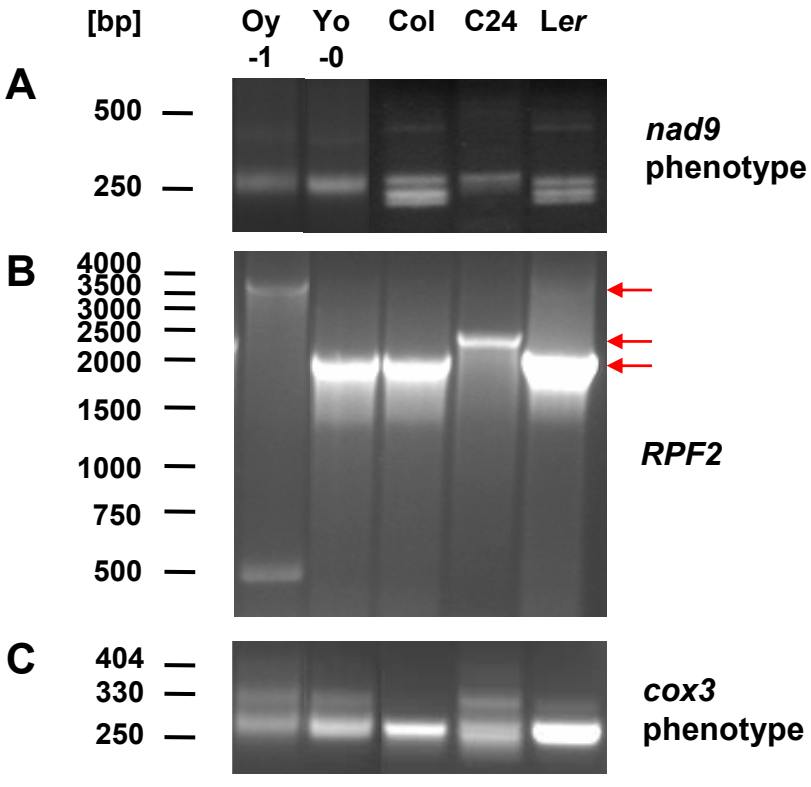

A
Col
rpf2-1
C24
I+III2
I
V
III2


B
I+III2 I V III2 F1 IV II
nad9
cox3
Col

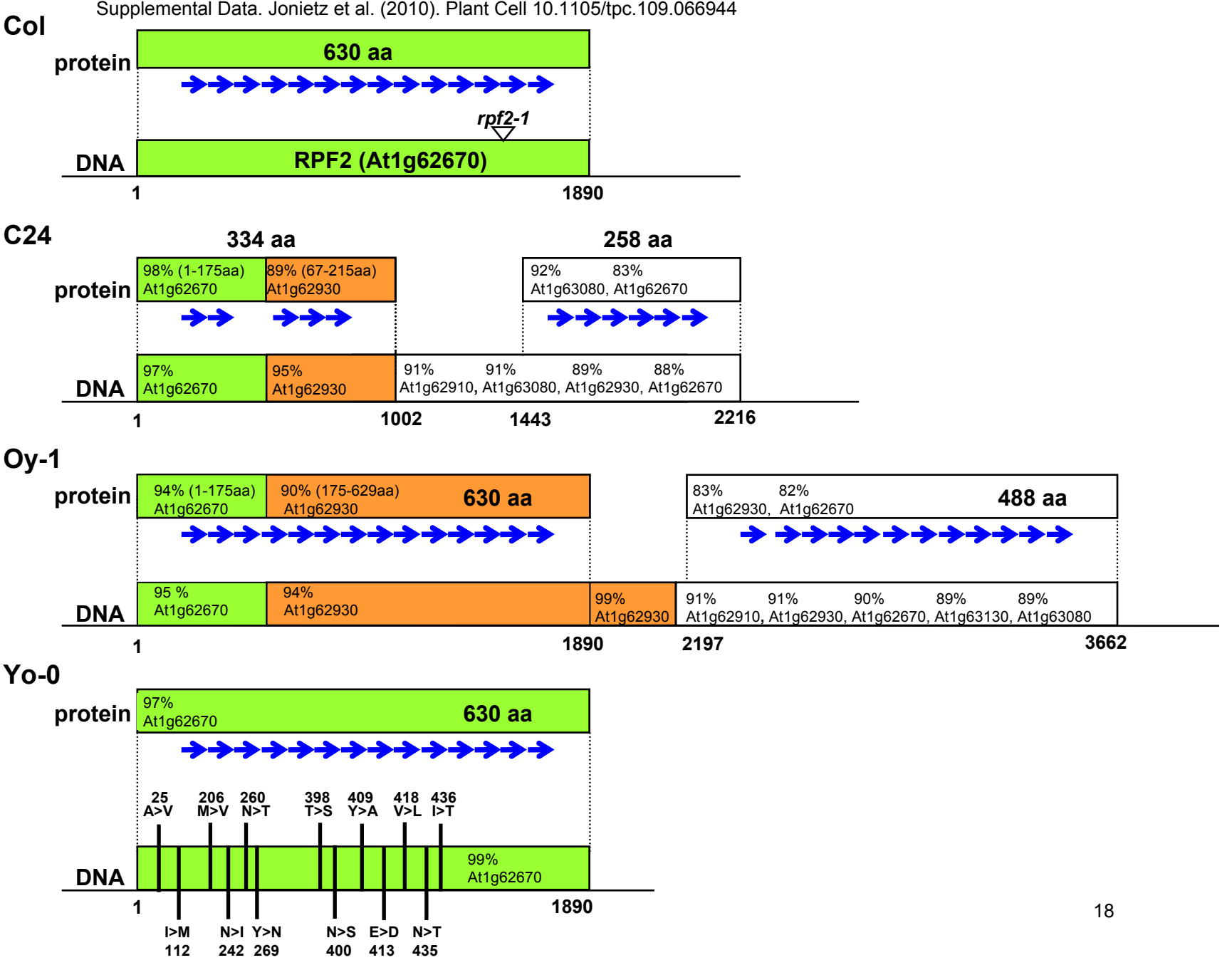

C
I+III2 I V III2 F1 IV II
nad9
cox3
C24


D
I+III2 I V III2 F1 IV II
nad9
cox3
rpf2-1

Supplemental Figure S8: Blue native (BN)/SDS polyacrylamide gel electrophoresis (PAGE) of mitochondrial protein from *Arabidopsis*. (A) About 1.0 mg of mitochondrial protein isolated from cell suspension cultures from accession Columbia (Col), from *rpf2-1* and from C24 were separated by blue native PAGE in the first dimension. (B to D) Lanes from the first dimension were cut from the gel and proteins subsequently separated by SDS PAGE in the second dimension. A comparison between the protein patterns from the different lines (B to D) did not reveal any differences in the abundance of *nad9* and *cox3* polypeptides (indicated by red arrow heads). Thus altered 5' processing of the corresponding mRNAs has no influence on the steady levels of these polypeptides. This result is consistent with the immunodetection analysis of the *nad9* protein (Fig. 5). Positions of different respiratory chain complexes are indicated.



Supplemental Figure S9: Correlation of *nad9* and *cox3* mRNA 5'end phenotypes with the *RPF2* genotype. Accessions Oystese-1 (Oy-1) and Yosemite-0 (Yo-0) showing the C24 *nad9* 5' end phenotype (A, absence of -202 5' ends) were analyzed in respect to the *RPF2* genotype (B) and the *cox3* 5' end phenotype (C). Both accessions showed major *cox3* 5' ends at -380 and one or two additional *cox3* 5' ends at -448 or -540. PCR products of 3.7, 2.4 and 2.0 kb (red arrows) indicated three *RPF2* genotypes defective in *nad9* and *cox3* processing. The PCR product from Yo-0 had the same size as the corresponding product from Col DNA (2.0 kb), while a 2.4 kb-product was obtained from C24. A PCR product of approximately 3.7 kb was amplified from Oy-1. Sequence analyses confirmed that these products were amplified from *RPF2* (see also Supplemental Figure 10 and 11). Nucleotide sequences are available in the data base.

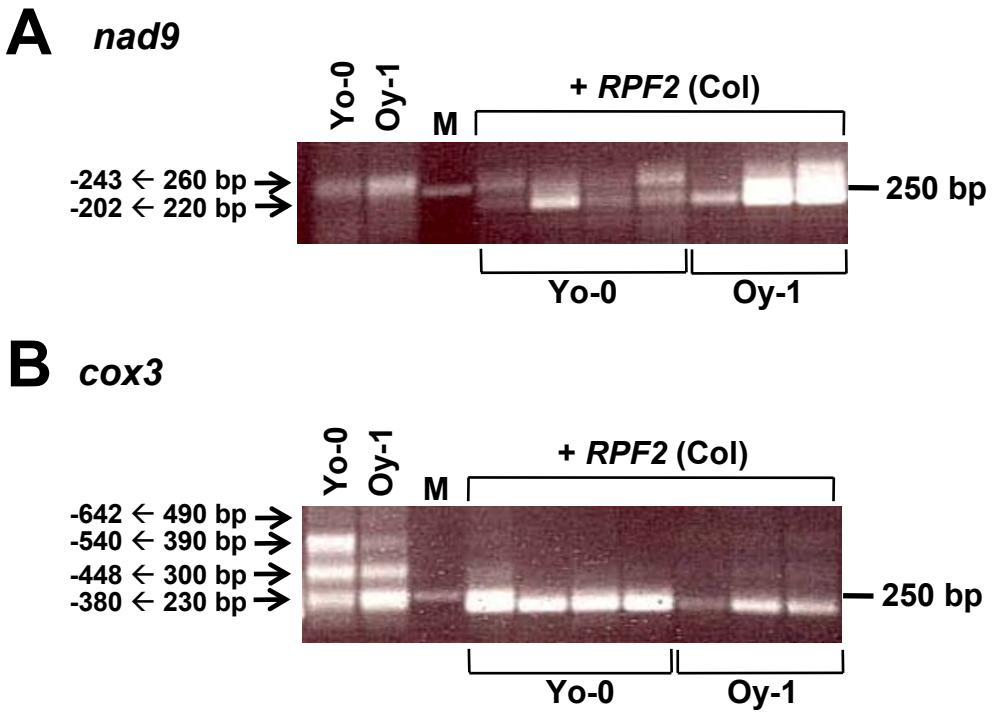

Col
protein
630 aa
rpf2-1
DNA
RPF2 (At1g62670)
1
1890
C24
334 aa
258 aa
protein
98% (1-175aa)
At1g62670
89% (67-215aa)
At1g62930
92%
83%
At1g63080, At1g62670
DNA
97%
At1g62670
95%
At1g62930
91%
91%
89%
88%
At1g62910, At1g63080, At1g62930, At1g62670
1
1002
1443
2216
Oy-1
protein
94% (1-175aa)
At1g62670
90% (175-629aa)
At1g62930
630 aa
83%
82%
At1g62930, At1g62670
488 aa
DNA
95 %
At1g62670
94%
At1g62930
99%
At1g62930
91%
91%
90%
89%
89%
At1g62910, At1g62930, At1g62670, At1g63130, At1g63080
1
1890
2197
3662
Yo-0
protein
97%
At1g62670
630 aa
25
A>V
206
M>V
260
N>T
398
T>S
409
Y>A
418
V>L
436
I>T
DNA
99%
At1g62670
1
1890
I>M
112
N>I
242
Y>N
269
N>S
400
E>D
413
N>T
435

Supplemental Figure S10: *RPF2* (At1g62670) alleles in accessions Col, C24, Oy-1 and Yo-0. Nucleotide and amino acid sequence identities between *RPF2* from these accessions and different RF-like PPR genes from Col are given. The C-terminal parts of the *RPF2* alleles from C24 and Oy-1 correspond to different parts of At1g62930 (C24: 67-215; Oy-1: 175-630). Green boxes indicate highest similarity to RPF2 (At1g62670), orange boxes represent regions with highest similarity to At1g62930 and white boxes stand for highest similarities to various RF-like PPR genes. Amino acid identities that are different between the *RFP2* alleles from Col and Yo-0 are indicated (Col > Yo-0), Their approximate positions are indicated by black vertical lines. Lengths of the proteins are given in amino acids (aa). Numbering refers to the first and last nucleotide position of the reading frame (without stop codon) and is given with respect to the ATG (A = +1) of the first reading frame. The T-DNA insertion in *rpf2-1* is indicated by a triangle. PPR repeats are given as blue arrows.

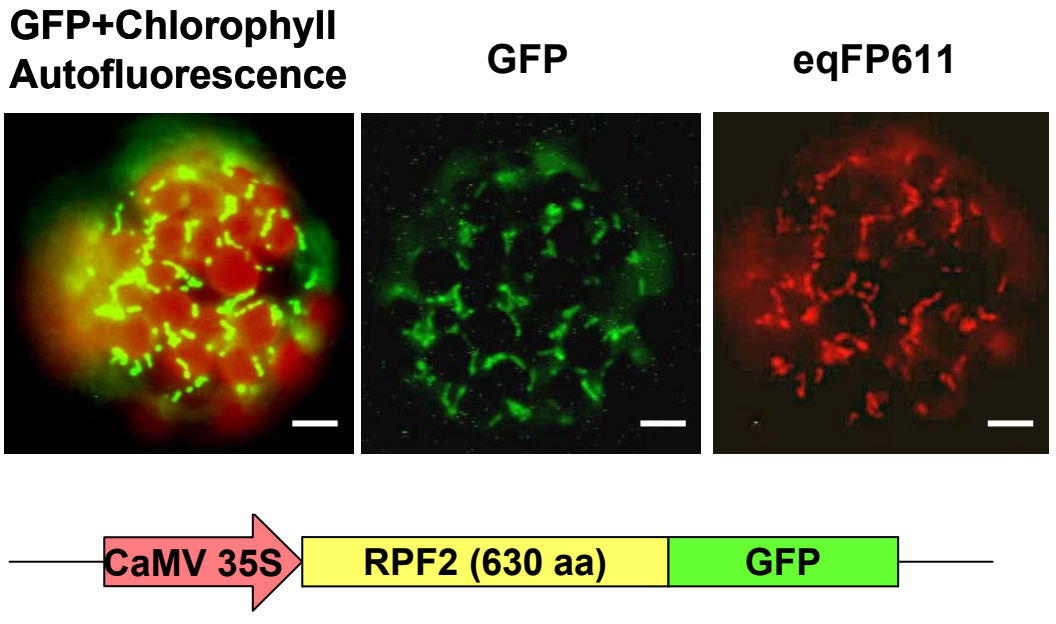
```
Col 62670       MRISFAIASTAKRFVHRSLVVRGNAATVSPSFSFFWRRAFSGKTSYDYREKLSRNGLSEL 60
Yo-0 62670      MRISFAIASTAKRFVHRSLVVRGNVATVSPSFSFFWRRAFSGKTSYDYREKLSRNGLSEL 60
Oy-1 62670      MRISFAIASTAKRFVHRSLVVRGNAATVSPSLSFFWRRAFSGKTSYDYREKLSRNGLSEL 60
Col 62930       MTSCVHLGIVASQSKKMSLAKR-FAQLRKASPLFSLRGVYFSAASYDYREKLSRNVLLDL 59
C24 62670N      MRISFAIASTAKRFVHRSLVVRGNAATVSPSLSFFWRRAFSGKTSYDYREKLSRNGLSEL 60
C24 62670C      ------------------------------------------------------------

                                                                        →
Col 62670       KLDDAVALFGEMVKSRPFPSIIEFSKLLSAIAKMNKFDVVISLGEQMQNLGIPHNHYTYS 120
Yo-0 62670      KLDDAVALFGEMVKSRPFPSIIEFSKLLSAIAKMNKFDVVISLGEQMQNLGMPHNHYTYS 120
Oy-1 62670      KLDDAVALFGEMVKSRPFPSIIEFSKLLSAIAKMNKFDVVISLGEQMQNLGIPHNHYTYS 120
Col 62930       KLDDAVDLFGEMVQSRPLPSIVEFNKLLSAIAKMNKFDLVISLGERMQNLRISYDLYSYN 119
C24 62670N      KLDDAVALFGEMVKSRPFPSIIEFSKLLSAIAKMNKFDVVISLGEQMQNLGIPHNHYTYS 120
C24 62670C      -------LFGEMVQSRPLPSIVEFNKLLSAIAKMNKFDLVISLGERMQNLRISYDLYSYN 228

                                        →
Col 62670       ILINCFCRRSQLPLALAVLGKMMKLGYEPNIVTLSSLLNGYCHSKRISEAVALVDQMFVT 180
Yo-0 62670      ILINCFCRRSQLPLALAVLGKMMKLGYEPNIVTLSSLLNGYCHSKRISEAVALVDQMFVT 180
Oy-1 62670      ILLNCFCRRSQLPLALAVLGKMMKLGYEPDIVTLSSLLNGYCHGKRISEAVALVDQMVEM 180
Col 62930       ILINCFCRRSQLPLALAVLGKMMKLGYEPDIVTLSSLLNGYCHGKRISEAVALVDQMFVM 179
C24 62670N      ILLNCFCRRSQLPLALAVLGKMMKLGYEPNIVTLSSLLNGYCHGKRISEAVALVD----- 175
C24 62670C      ILINCFCRRSQLPLALAVLGKMMKLGYEPDIVTLNSLLNGFCHGNRISDAVALVDQMVEM 288

                  →                                 →
Col 62670       GYQPNTVTFNTLIHGLFLHNKASEAMALIDRMVAKGCQPDLVTYGVVVNGLCKRGDTDLA 240
Yo-0 62670      GYQPNTVTFNTLIHGLFLHNKASEAVALIDRMVAKGCQPDLVTYGVVVNGLCKRGDTDLA 240
Oy-1 62670      GYKPDTVTFNTLIHGLFLHNKASEAVALIDRMVARGCQPDLFTYGTVVNGLCKRGDIDLA 240
Col 62930       EYQPNTVTFNTLIHGLFLHNKASEAVALIDRMVARGCQPDLFTYGTVVNGLCKRGDIDLA 239
C24 62670N      ------------------------------------------------------------
C24 62670C      GYKPDTVTFNTLIHGLFLHNKASEAVALMIEWLPEGVNQIWLLMEW-------------- 334

                            →                                 →
Col 62670       FNLLNKMEQGKLEPGVLIYNTIIDGLCKYKHMDDALNLFKEMETKGIRPNVVTYSSLISC 300
Yo-0 62670      FILLNKMEQGKLEPGVLIYTTIIDGLCKNKHMDDALNLFKEMETKGIRPNVVTYSSLISC 300
Oy-1 62670      LSLLKKMEKGKIEANVVIYNTIIDGLCKYKHMDDAFDLFNKMETKGIKPDVFTYNSLISC 300
Col 62930       LSLLKKMEKGKIEADVVIYTTIIDALCNYKNVNDALNLFTEMDNKGIRPNVVTYNSLIRC 299
C24 62670N      ------------------------------------------------------------
C24 62670C      ------------------------------------------------------------

                                        →
Col 62670       LCNYGRWSDASRLLSDMIERKINPDVFTTFSALIDAFVKEGKLVEAEKLYDEMVKRSIDPS 360
Yo-0 62670      LCNYGRWSDASRLLSDMIERKINPDVFTTFSALIDAFVKEGKLVEAEKLYDEMVKRSIDPS 360
Oy-1 62670      LCNYGRWSDASRLLSDMIERKINPNVVTFNSLIDAFAKEGKLIEAEKLFDEMIQRSIDPN 360
Col 62930       LCNYGRWSDASRLLSDMIERKINPNVVTFSALIDAFVKEGKLVEAEKLYDEMIKRSIDPD 359
C24 62670N      ------------------------------------------------------------
C24 62670C      ------------------------------------------------------------
```

```
                  →                                                →
Col 62670         IVTYSSLINGFCMHDRLDEAKQMFEFMVSKHCFPDVVTYNTLIKGFCKYKRVEEGMEVFR 420
Yo-0 62670        IVTYSSLINGFCMHDRLDEAKQMFEFMVSKHCFPDVVSYSTLIKGFCKAKRVDEGMELFR 420
Oy-1 62670        IVTYNSLINGFCMHDRLDEAQQIFTLMVSKDCLPDVVTYNTLIKGFCKAKRVEEGMELFR 420
Col 62930         IFTYSSLINGFCMHDRLDEAKHMFELMISKDCFPNVVTYNTLIKGFCKAKRVEEGMELFR 419
C24 62670N        ------------------------------------------------------------
C24 62670C        ------------------------------------------------------------

                                  →                                          →
Col 62670         EMSQRGLVGNTVTYNILIQGLFQAGDCDMAQEIFKEMVSDGVPPNIMTYNTLLDGLCKNG 480
Yo-0 62670        EMSQRGLVGNTVTYTTLIQGLFQAGDCDMAQEIFKEMVSDGVPPNIMTYNTLLDGLCKNG 480
Oy-1 62670        EMSQRGLVGNTVTYNTLIQGLFQAGDCDMAQKIFKKMVSDGVPPDIITYSILLDGLCKYG 480
Col 62930         EMSQRGLVGNTVTYNTLIQGLFQAGDCDMAQKIFKKMVSDGVPPDIITYSILLDGLCKYG 479
C24 62670N        ------------------------------------------------------------
C24 62670C        ------------------------------------------------------------

                                        →                                    →
Col 62670         KLEKAMVVFEYLQRSKMEPTIYTYNIMIEGMCKAGKVEDGWDLFCNLSLKGVKPDVVAYN 540
Yo-0 62670        KLEKAMVVFEYLQRSKMEPTIYTYNIMIEGMCKAGKVEDGWDLFCNLSLKGVKPDVVAYN 540
Oy-1 62670        KLEKALVVFEYLQKSKMEPNIYTYNIMIEGMCKAGKVEDGWDLFCSLSLKGVKPNVIIYT 540
Col 62930         KLEKALVVFEYLQKSKMEPDIYTYNIMIEGMCKAGKVEDGWDLFCSLSLKGVKPNVIIYT 539
C24 62670N        ------------------------------------------------------------
C24 62670C        ------------------------------------------------------------

                                              →
Col 62670         TMISGFCRKGSKEEADALFKEMKEDGTLPNSGCYNTLIRARLRDGDREASAELIKEMRSC 600
Yo-0 62670        TMISGFCRKGSKEEADALFKEMKEDGTLPNSGCYNTLIRARLRDGDREASAELIKEMRSC 600
Oy-1 62670        TMISGFCRKGLKEEADALFREMKEDGTLPDSGCYNTLIRARLRDGDKAASAELIKEMRSC 600
Col 62930         TMISGFCRKGLKEEADALFREMKEDGTLPNSGTYNTLIRARLRDGDKAASAELIKEMRSC 599
C24 62670N        ------------------------------------------------------------
C24 62670C        ------------------------------------------------------------


Col 62670         GFAGDASTIGLVTNMLHDGRLDKSFLDMLS 630
Yo-0 62670        GFAGDASTIGLVTNMLHDGRLDKSFLDMLS 630
Oy-1 62670        GFVGDASTISMVINMLHDGRLEKSYLEMLS 630
Col 62930         GFVGDASTISMVINMLHDGRLEKSYLEMLS 629
C24 62670N        -------------------------------
C24 62670C        -------------------------------
```

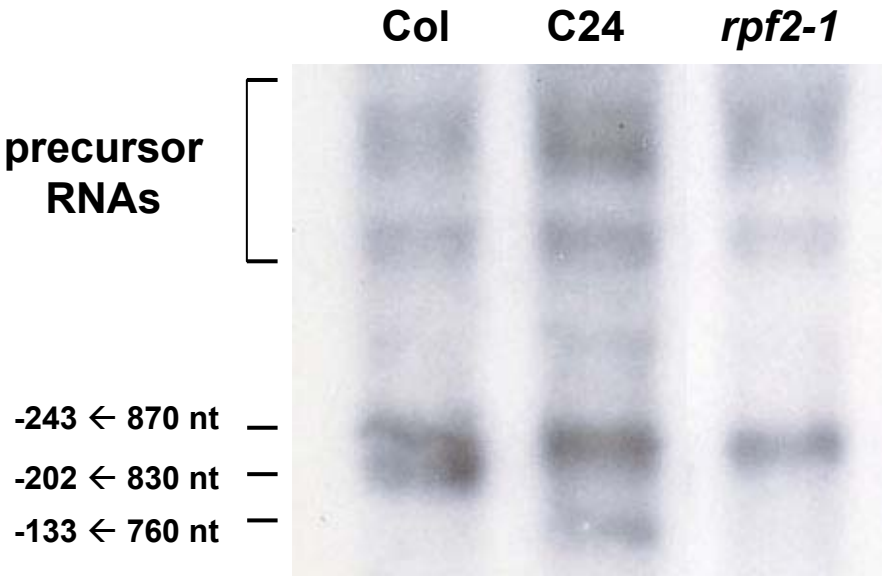
Supplemental Figure S11: Alignment of amino acid sequence deduced from the *RPF2* alleles (62670) from accessions Col, Yo-0, Oy-1 and C24 and from the At1g62930 gene (62930) from Col. Amino acid identities differing between the distinct *RPF2* alleles are highlighted in blue, amino acid residues that are different between At1g62930 and RPF2 are given in red. Blue arrows above the sequences mark the starts of PPR repeats.



Supplemental Figure S12: Complementation studies of *Arabidopsis* accessions Yosemite-0 (Yo-0) and Oystese-1 (Oy-1). The introduction of the Col *RPF2* gene (+*RPF2*) into these accessions resulted in the generation of *nad9* -202 5' ends (A) and in efficient processing of *cox3* mRNAs (B). These results together with the incapability of the *RPF2* alleles from Oy-1 and Yo-0 to restore the *nad9* and *cox3* mRNA processing phenotypes in *rpf2-1* plants (data not shown) demonstrate that these alleles are defective in 5' processing of these mitochondrial mRNAs.



Supplemental Figure S13: RPF2 is a mitochondrial protein. A fusion protein consisting of the complete RPF2 (630 amino acids) and the green fluorescent protein (GFP) is transiently expressed in transgenic tobacco protoplasts. Fluorescence of GFP and chlorophyll, GFP alone and the red fluorescence protein from the sea anemone *Entacmaea quadricolor* (eqFP611) are visualized through different filter sets. eqFP611 C-terminally fused to the N-terminal part of the mitochondrial isovaleryl-CoA dehydrogenase has been previously established as mitochondrial marker in transgenic tobacco (Forner and Binder, 2007). The fluorescence pattern is typical for a localization of the RFP2:GFP fusion protein in mitochondria, as shown in Fig. 6. No fluorescence of the full-length RFP2:GFP is found in chloroplasts. Bars = 10 μm.



Supplemental Figure S14: Northern blot analysis of *nad9* transcripts in Col, C24 and *rpf2-1* plants. The lack of the 830-nucleotide mRNA with the -202 5' ends in C24 and *rpf2-1* is not accompanied by an increase in larger precursor RNAs.

Supplemental Table S1:

Genetic markers used for mapping of the *RPF2* locus in *Arabidopsis*

Marker	Chromosome	PCR product length Col/C24 [bp]	location on chromosomes	percentage of C24 alleles in F2 hybrids [%]
CER479928	1	190/170	20,610,106 to 20,610,048	94.7
CER449403	2	230/187	1,830,693 to 1,830,736	56.4
CER458621	2	206/160	5,395,955 to 5,395,990	57.4
CER449629	2	559/499	12,664,598 to 12,664,665	59.6
CER464947	3	347/300	3,108,758 to 3,108,804	45
CER470109	3	183/150	22,754,153 to 22,754,187	50
CER460528	4	279/140	5,742,442 to 5,742,487	44.7
CER456657	5	633/535	5,938,730 to 5,938,828	55.3
CER464694	1	238/207	24,013,992 to 24,014,023	98.9
CER474029	1	230/200	20,018,769 to 20,018,799	93.6
CER450582	1	226/194	26,464,219 to 26,464,250	88.3
MASC04181	1	SNP T →C	22,279,931	1
MASC00581	1	SNP A →G	23,053,433	0
MASC03744	1	SNP A →G	23,824,203	0

Oligonucleotide sequences are given in Supplemental Table S2.

Supplemental Table S2:

Oligonucleotide sequences

Oligonucleotide	**Sequence (5' to 3')**
Atnad9-1	agagggatcatcaactccgc
Atnad9-2	cttgggtaaagtctcccaac
Atnad9-3	cgattttgctagtccttggg
Atnad9-7	ttggtccaaccaagaaaggc
Atnad9-NS.H	atggataaccaattcattttc
Atnad9-NS.R	ttatccgtcgctacgctg
Atnad9-EMSA.H	ggtcgagttaagtaaagactggttacc
Atnad9-EMSA.R	taatacgactcactataggggcgagtcgtctagggcatc
Atatp9-2	ttgcaccttctaacatctcg
Atcox3-2	gagtgaacccgaaataggcc
Atcox3-23	gatctatcgagtaaccaggaaagag
Le-cox3-HindIII.H	atataagctttccataggcttggccctag
Le-cox3-HindIII.R	ctaagaagcttcgaataccctttaccaag
Atcox3-3‘Primersonde	cgactttggtatgatgtcct
Atcox3-Mega3‘	cacataaatgaaggaatcgaagagattatggcag
Atcox3-Mega5‘	aacggagacaccaattaaggaacgcac
Atcox3-5'-Primersonde	gattgaatctcagaggcattc
Atcox3-3'-Primersonde	cgactttggtatgatgtcct
At1g62670.H	ggttgaattttacagagcttccgaatcagagagc
At1g62670.R	gatatggtttgctcgactattctctcgactcaagg
At1g62670-Kompl.H	atgcagtcgagcggcgcgccttgtaattgttactgtgtttgtgcatttcccc
At1g62670-Kompl.R	tgactccgaggcttaattaattccagcacctgatgagttttctcatcc
At1g62670-Kompl.H3	ttcacaagtacccgggcctatgaggatatcgtttgcgattgc
At1g62670-Kompl.R5	tgactccgaggcttcccgggggaagggaagggacgagacttg

At1g62670-Kompl.R3	tgactccgaggcttcccgggcgaagaaagcatatcgaggaagct
At1g62670UEx.H2	atgcagtcgagcggatccggtaatgctgcaactgtttctcc
At1g62670UEx.R	gacttagagtttctgcagttaagaaagcatatcgaggaagcttttgtc
Atccb2-8	aaaggtgcaggaggaaaagg
Atccb2-Mega5'	gccgcgtaacatcatcttcaaccaacc
Atccb2-Mega3'	gttcgtatctctttttccaatttcggtctcga
Atrpl5-1	cacacaatccaggaacttcc
Atrpl5-5	tttgagcaacagatcttgacg
Atcob-3	attctgggacgagttggaag
Atatp6-1-NS.R	ttatatccgccgcctgtcccac
Atatp6-3	accggacgcttgaccactag
Atatp6-2	ggtctggaattaggtgtagc
Atatp8-pu2	tacaccattgggatacttcg
Atatp8-1	gtactccatctccatcattgc
Atatp8-4	agtggctcacgaggaatgg
Atnad7-2	tatgtggttccgcacgttcc
Atnad7-7	tgcacctaaaggagaatttggtgtctttctgg
Atnad7-8	ttttaatttgccttttcctagtcgtcatggg
Atrpl2-2	gtctaagtgctcttgctctc
Atrpl2-3	gaggaagtgcttcgtttcag
AtorfX-3	cacagctgctcttttcacac
Atnad4-3	gactgcatgcatacatccg
Atnad4-5	ttgtatccgaggaacaggag
Atnad4-15	aacccttcccgtgtatacg
Atatp9-14	agagcaaagcccaaaatgg
Atatp9-Mega.5'	agagcaaagcccaaaatggcataacc
Atatp9-Mega.3'	gccccaatgatggccttttgatcttattcg

Supplemental Table S2, continued

Atrps7-2	gctttatattctctacggcg
Atrps7-7	atcaatagtttttgctcaccatccaagccc
Atrps7-8	gaagtttcgcgcatttcagatggtgg
Atcox1-1	cccaccaagaatttgatcg
Atcox1-2	tacgaatcagtactgagaagc
Atcox1-4	gaatggatggtacaaagtcc
Atnad2ab-1	acccacattactggctaacg
Atnad2ab-2	aaagatctctggggaaaccg
Atnad2cde-3	gtcgttactactagcaatgac
Atnad1a-2	gtaacaatccgaacgatccc
Atnad1a-Mega.5‘.B	ttccaagtatttcagctggaacagctatgtaca
Atnad1de-Mega.3‘.B	tggtcttttagtcacctttcaatggcttcc
Atatp1-3	caatcccatctccaactgag
Atatp1-8	ttcgcgtaaaagttcctaattcgactttcg
Atatp1-9	gcagctgtcaatggattctgtgatcg
Atatp6-2.Mega5'	taatatatccggcctgaatcactccctcg
Atatp6.Mega3'	tcttgcattaaccggtctggaattaggtg
Atnad3-1	aaacgacttctggcatcacc
Atnad3-5	aaggatcgaaaccacattcgtaggcc
Atrps12-6	aggagtaaaggatttgatgggaattccgg
Atccb6n2-1	ttcgaattggttcctggtcc
Atccb6n2-5	tcctgatcagagaccactgtgttcgc
Atccb6n2-6	agcaggcatcggtccgtagaacg
Atccb3-5	caataatactcatccgagcc
Atccb3-Mega3'nah	tgggagcattagccgatttggtacatc
Atccb3-Mega5' nah	cttgtgcgtggcactccttgct
Atccb6n1-1	caaaatgcaagtgctgcacc
Atccb6n1-Mega.5'	tgtaagtgaatgcaacgaaaagacccaga

Supplemental Table S2, continued

Atcccb6n1-Mega.3'	agcgagaagccactcgactaaaaggtactg
Atnad5ab-1	ttccgatgagatccatggag
Atnad5ab-2	atgaaacgcacgtagtggtc
Atnad5de-4	tgcctttgcaatgttacttgg
Atnad4L-1	agctgccaccgttagaacc
Atnad4L-2	aggaggattccccaaatacc
Atorf25-3	tcattcgagagagcttggtg
Atrps4-2	ctctgttccgaacatttcctg
Atrps4-4	taggtcatatccctcacgac
Atnad6-1	agtaaacctgaagtgtcgcg
Atnad6-2	gcacgtacaaccatcaaacc
Atnad6-4	ttagtagccatgattggggc
Atccb6-1	catttcaatagtacgggtg
Atccb6-2	gaatagggcgacttgctctg
Atccb6-3	gagaaagttccgtggagttc
Atcox2-5	aaggttccttcattttctgc
Atcox2-6	ttgtatggcaggaataccac
Atrps3-1	tacacctaccgagacgaaag
Atrps3-2	aaggtgagtctcataggtgg
Atrpl16-3	ccaagtttgttcagtggtcg
CER479928.H	cagttcccaatgagcaatgtacacatgg
CER479928.R	ccttgttggatgtaaaatagtttcgggttcc
CER449403.H	tgattccagcgggtaggcatgacc
CER449403.R	cgaaacattcaaaaagtggttatgggagag
CER449629.H	ccaaaaggcaacatgaatgacatgg
CER449629.R	ttttggggtttttgcagaaacatgg
CER458621.H	cagcctcattgcctgatgtcaagaatgc

Supplemental Table S2, continued

CER458621.R	cgggtgaatgggcagcatgg
CER464947.H	tttggttgctttgaagaacaaatgttatatcg
CER464947.R	cgtgctgtgtgcgcatgc
CER470109.H	ttttgtgattctatgttggcatcagtgg
CER470109.R	caaaccgtagtgcaaattagagcatagtttcc
CER460528.H	caatgatttggtgggtcaagagtcaagac
CER460528.R	gcaaaagtcattacggacaataccaaacg
CER456657.H	ccttcagaatcaccaactgtggagtcc
CER456657.R	gaaagaaaccatatgcatcaaatctaccttcg
CER464694.H	tgagaaacatcatcggatgttgatagtacatcg
CER464694.R	gctcttagttgttgtaatgaatatgaaatcttagtcg
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MASC00581.H	ttttttggttatgtagctagcggttcttgatttcaatgc
MASC00581.R	gcctaaccgtttttctcactctctgctc
MASC04181.H	ggggtcagttacattactagc
MASC04181.R	gtacggttcttcttccctta
MASC03744.H	caattctctgataatctaatttaaaagacaaaaaaattacaaataaaattttcga
MASC03744.R	tcgaattctaacatggtttctccagaccac

Supplemental Table S2, continued