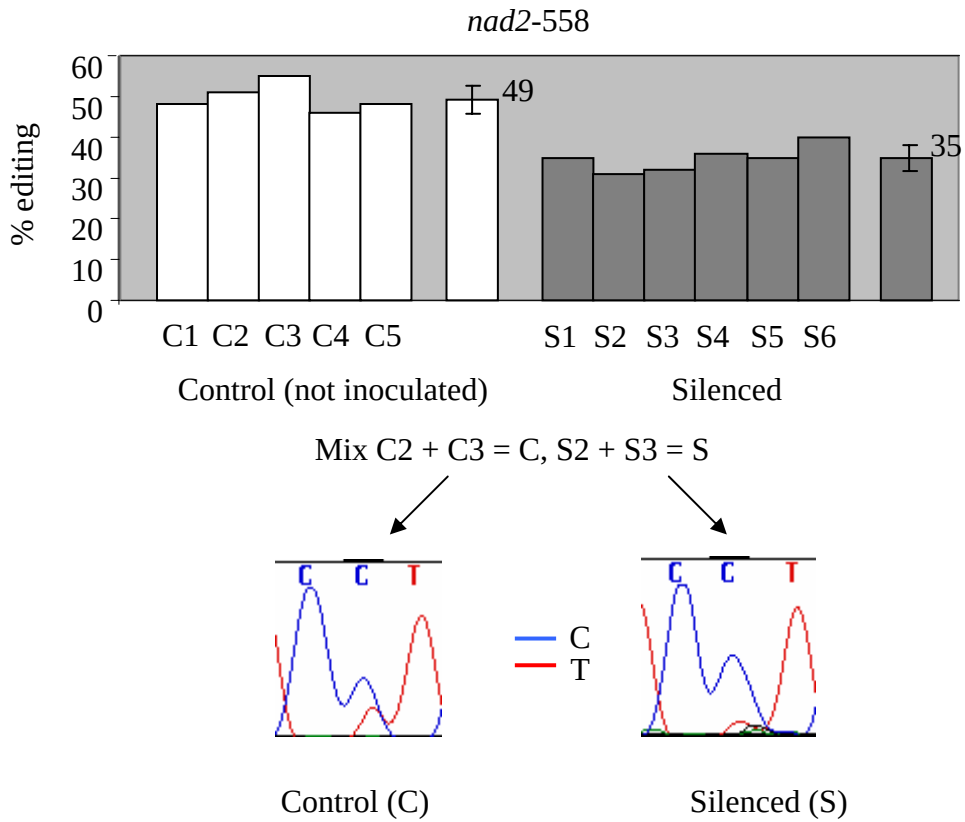
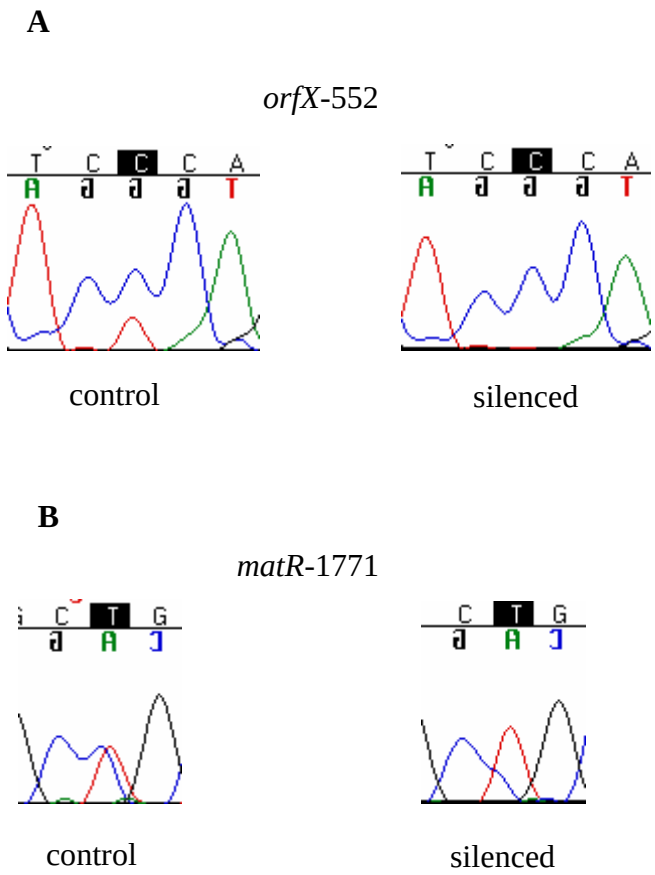
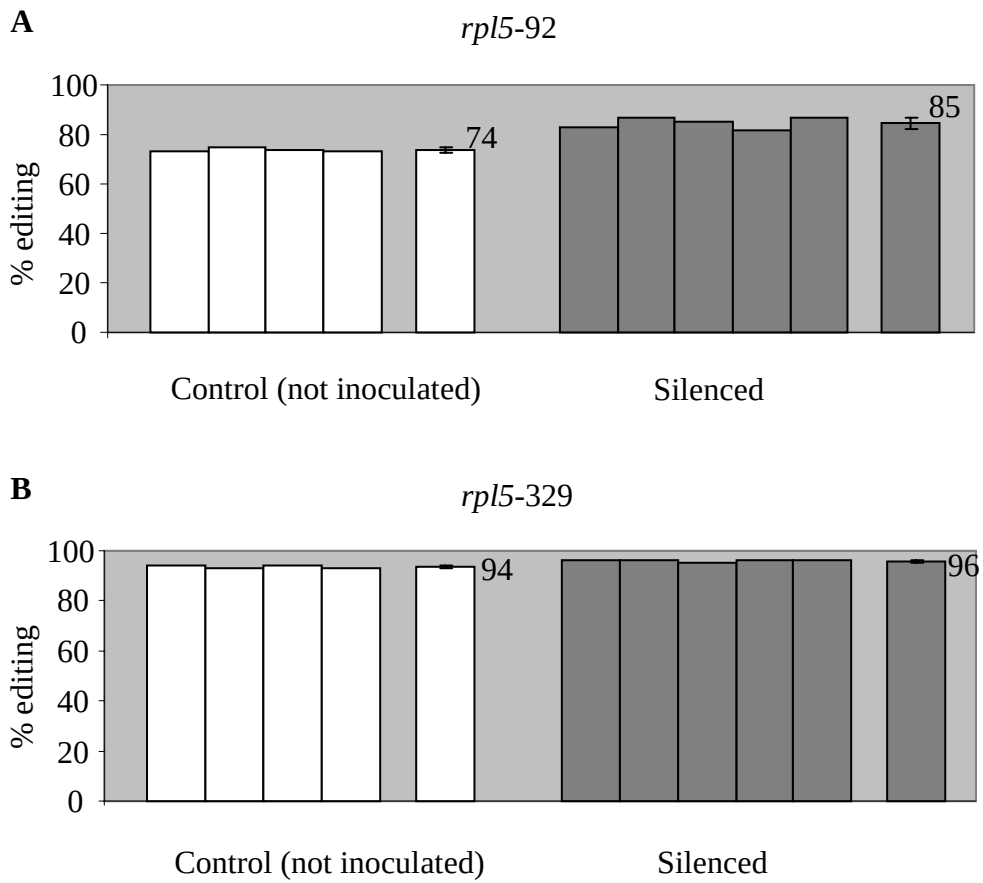


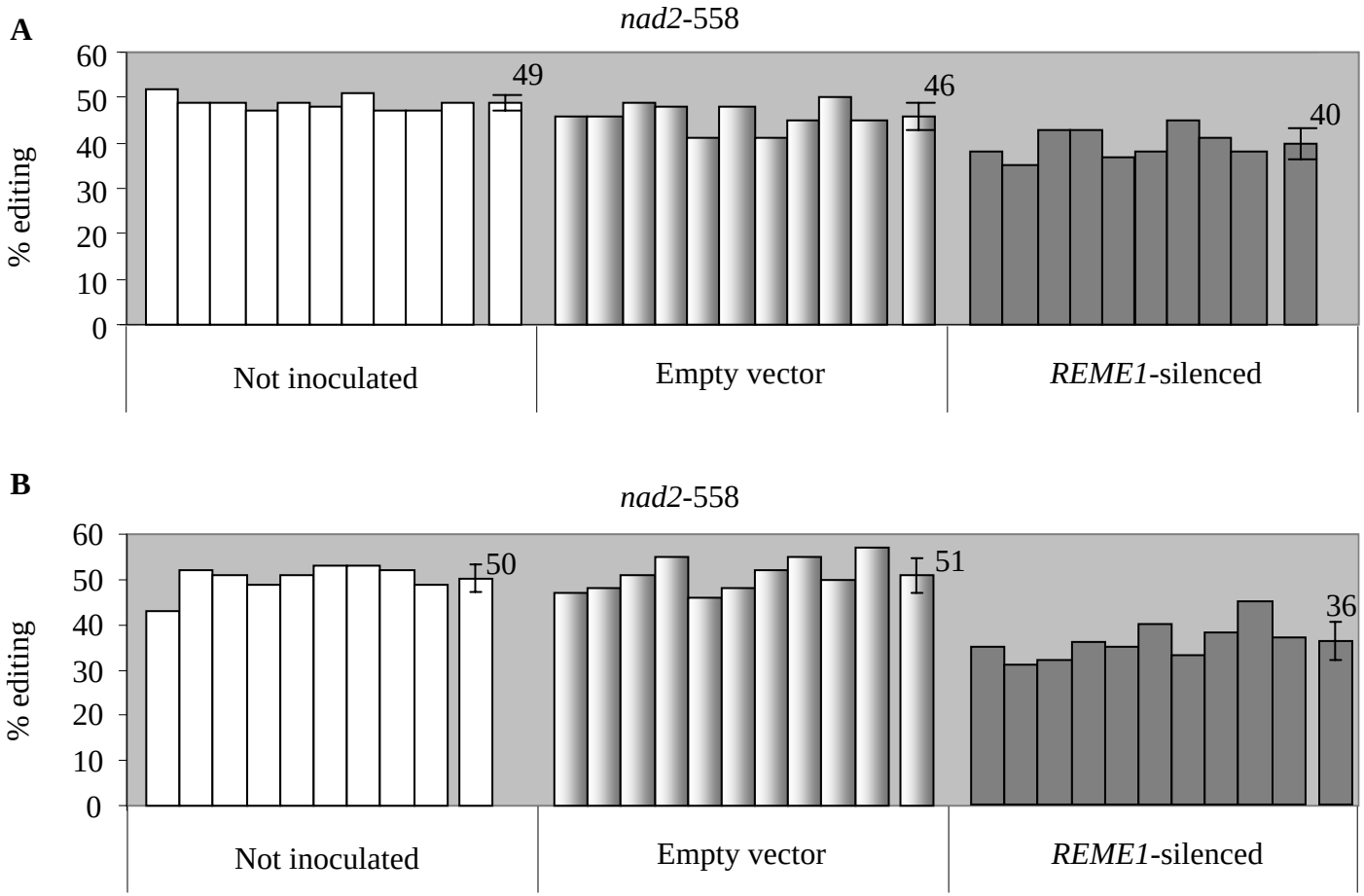
Supplemental Figure 1. RNA from pooled samples can be used to detected editing differences between control and silenced plants. Comparison of the sequencing electrophoretograms of *nad2* RT-PCR products obtained from control and silenced pools shows a noticeable difference in the height of the T peak at position 558. The difference in the T peaks reflects the differential editing extent of *nad2*-558 between control and silenced pools.



Supplemental Figure 2. An example of differential editing between pools of control and silenced plants assessed by electophoretogram traces of bulk RT-PCR products. Editing T is shown in red. A, *OrfX*-552 is more edited in control than in silenced pools. B, *MatR*-1771 is less edited in control than in silenced pools. Note that the height of the peaks does not reflect the actual editing extent as evaluated by PPE (43% vs. 26% and 60% vs. 76% for *orfX*-552 and *matR*-1771 respectively).

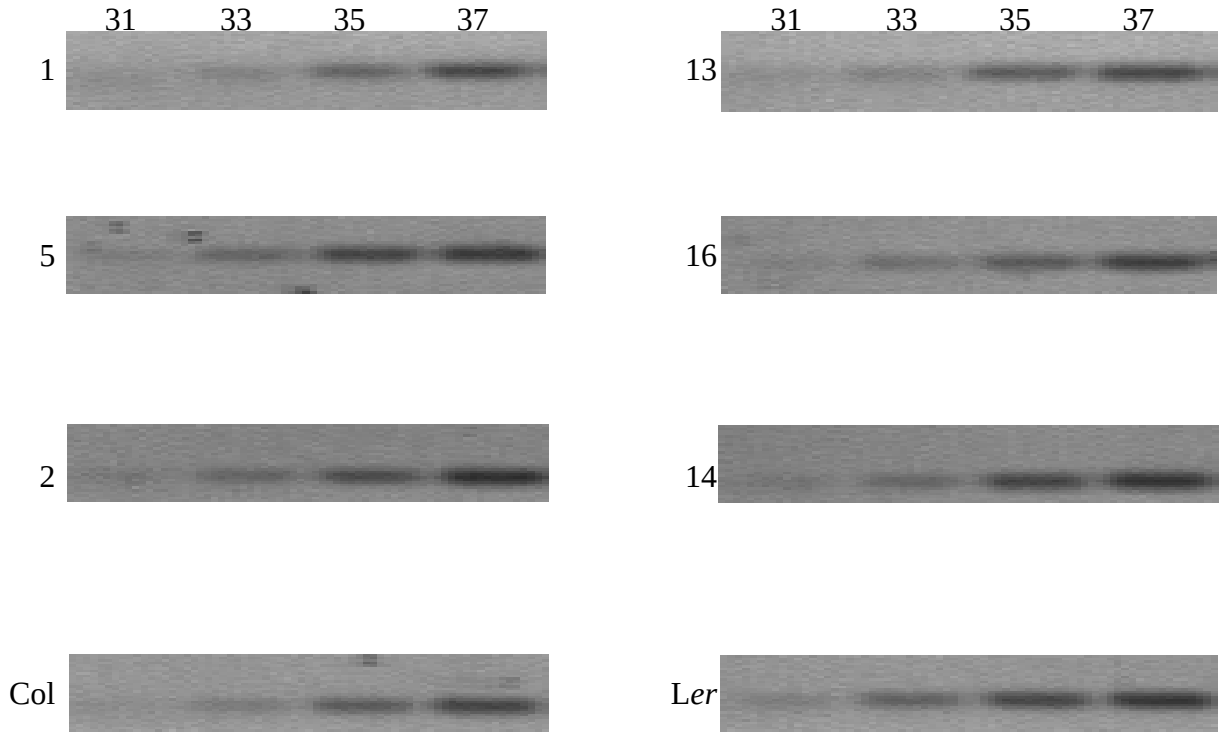


Supplemental Figure 3. Virus induced gene silencing (VIGS) of *REME1* results in increased editing of sites found in *rpl5*. A, Editing extent of C at position 92 is increased by an average of 15% in silenced plants ((85-74)/74 = 0.15, $P < 5\ 10^{-5}$). B, The increase in editing is much less pronounced for the edited C at position 329 ($P < 3\ 10^{-4}$). On the right of each group is the average editing extent with s.d.

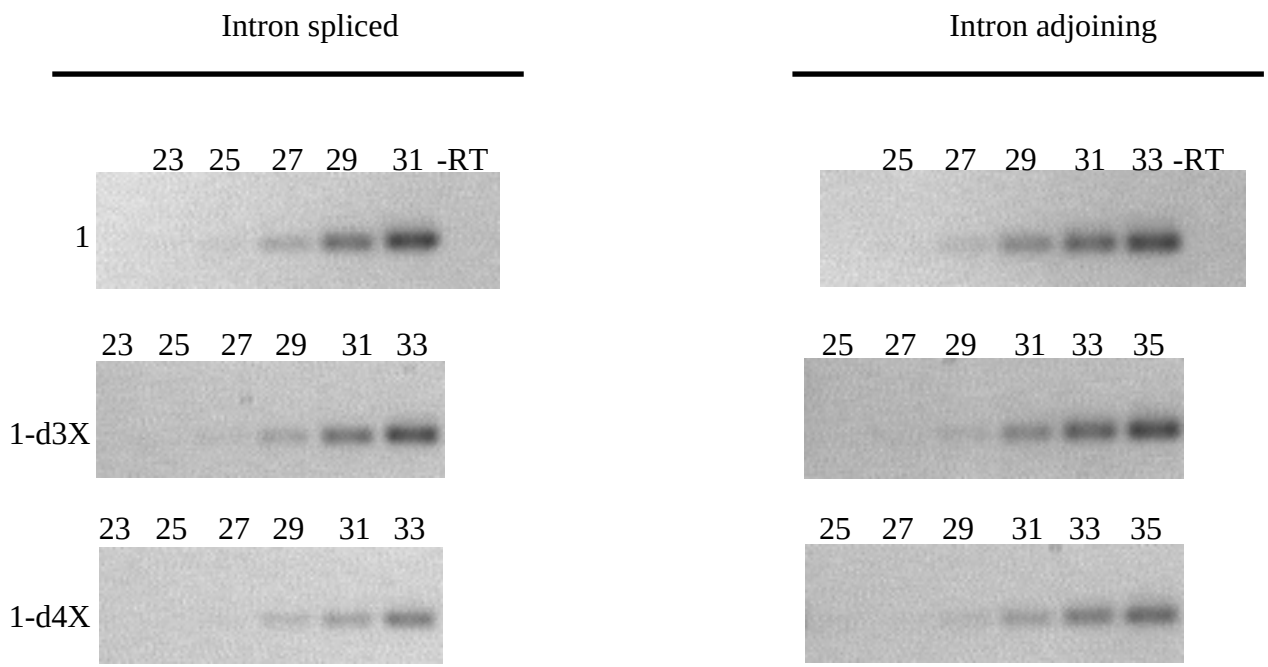


Supplemental Figure 4. Editing extent of *nad2*-558 is decreased in *REME1* silenced plants. Editing extents were assayed by PPE. A and B show data from two independent experiments. A, Virus inoculation induces a significant decrease of *nad2*-558 editing extent (not inoculated vs. empty vector, $P<2\ 10^{-2}$), but half the range of *REME1* specific silencing (empty vector vs. REME1-silenced, $P< 7\ 10^{-4}$). B, No effect of virus inoculation on *nad2*-558 editing extent was detectable (not inoculated vs. empty vector, P = 0.7).The decrease in *nad2*-558 editing extent in *REME1* silenced plants is more pronounced in B than in A (29% = (50-36)/36 x 100 vs. 18% (49-40)/49 x 100). On the right of each group is the average editing extent with s.d.

Supplemental Figure 5. REME1 is targeted to mitochondria. In the panels are shown the subcellular localization in onion epidermal cells of REME1 fused to GFP (left panel) and of the Cherry fluorescent marker addressed to mitochondria (right panel). In the middle panel is shown an overlay of the two pictures showing a clear co-localization of both fluorescent markers.



Supplemental Figure 6. Semi-quantitative RT-PCR of a reference gene (At4g26410) shows no difference in expression level between transgenic lines and parental accessions. RT-PCR products were amplified and electrophoresed on 1% agarose gels after a completed number of cycles indicated above each lane. On the left of each gel are indicated the origin of the RNA used for the RT-PCR: 1, 13, 5, 16, 2, and 14 are T_0 L*er* plants expressing *REME1* Col allele and showing a high, low, and medium level of *nad2*-558 editing extent respectively. The same amount of template RNA (50 ng) was used for each reverse transcription reaction. The abundance of RT-PCR products is very similar for each template. This control experiment validates the difference observed in *REME1* expression level reported in Figure 10.



Supplemental Figure 7. Semi-quantitative RT-PCR is able to detect a three to four-fold reduction in *nad2* second intron spliced or intron adjoining product. Intron-spliced and intron-adjoining RT-PCR products for the second intron were amplified and electrophoresed on 2% agarose gels after a completed number of cycles indicated above each lane. –RT indicates a negative control in which the reverse transcriptase was omitted and was performed for each combination of primers at the maximum number of cycles (e.g. 31 for intron2-spliced). On the left of each gel are indicated the origin of the RNA used for the RT-PCR: 1 is a T_0 L*er* plant expressing *REME1* Col allele, 1-d3X and 1-d4X indicate a three and four times dilution of the cDNA from 1. The difference between 1 and 1-d3X is readily observable as there is a shift of about 2 cycles to obtain the same amount of PCR product (e.g., intron-spliced amplification, 27 cycles for 1 vs. 29 cycles for 1-d3X). The difference in PCR products abundance is even more pronounced between 1 and 1-d4X.

Supplemental Table 1. Markers used in *REME1* fine mapping

Marker[a]	Category	Primers[b]	Amplicon length	Enzyme	Allele cut	Polymorphism coordinates (AGI map) [c]
1027K	CAPs	1027K-F1 = CCTTGATATAAACTTGACGATTGT 1027K-R1 = ACGAACCGACAATATTATGTATGT	556 bp	RsaI	L*er*	1027083
1113K	CAPs	1113K-F1 = AAAGATCGGTAGACAAATCATTGA 1113K-F1 = ATTCGCCGAGTTATTTGTAAAAA	381 bp	MfeI	L*er*	1112836
1135K	CAPs	1135K-F1 = ACTCTAGTGAGCCCAAAAGATGAC 1135K-R1 = AGACCGGATGTGTTACCATCTG	406 bp	TscI	Col	1134935
1150K	sequencing	1150K-F1 = GCGGCTTGCATACCAGTA 1150K-R1 = CGTCACTAATCCTAAATCAGGTAC	442 bp			11 SNPs 1149913-1150153
1170K	sequencing	1170K-F1 = CTATTAAGCTATTTCAAGGGAAAAA 1170K-R1 = TCGATCGGTTATACTATGTTTAATC	416 bp			1170362
1181K	CAPs	1181K-F1 = AGACGCCTTGGTTTGATTGT 1181K-R1 = ATTCGATTTTTCCGGTTTACTTC	471 bp	PstI	Col	1181241
At2g03880	sequencing	At2g03880-F1 = ACCGGAAAAATCGAATGTCTGAGT At2g03880-5' = TGGATTCATTGCAAAGTCATGG At2g03880-F2 = TGGTGGGTTTGCTCAGAATAGTA At2g03880-F3 = CGGAGTATGCAGCTAAAAAGGTC At2g03880-R1 = GTGCAGCAAGTGTCTTCCCATTAA	2316 bp			51 SNPs, 3 indels 1181511-1183701
1184K,1186K	sequencing	1184K-F1 = TCATGTCATCGCTACATCCTATTA 1184K-F2 = TTCCACTGCAAAGGTATTAAATA 1186K-R1 = CATCCCCAAAACACAACCAGT	1917 bp			4 SNPs, 3 indels 1184613-1185817
1193K	CAPs	1193K-F1 = AAATCGATCTCTAGCTTCAACTAA 11931K-R1 = CTATCTTAGTGGCGAGCATGATC	398 bp	EarI	L*er*	1192628
1220K	CAPs	1220K-F1 = AATGTTTCCCAATTAATAGTATAGATG 1220K-R1 = AAGCGACAATATAATAAAATTAGTTTT	402 bp	EcoRV	L*er*	1220166
1276K	CAPs	1276K-F1 = GCATAAGTTAGGAGCAAGAAAGTT 1276K-R1 = GACGCGGATCAAAGAAAATA	381 bp	ClaI	Col	1275626

[a]Markers 1027K and 1276K were used to screen the 692 F2 plants. Recombinants were then genotyped with the other markers.

[b]For sequencing markers the internal markers used for sequencing are also given, the amplification were obtained with the pair marker-F1, marker-R1.

[c]Physical coordinates of the polymorphism are given in bp; when several SNPs correspond to a marker, the number is given and the coordinates of the first and the last SNP are also provided.

Supplemental Table 2. New primers used in mitochondrial genes screening

Gene	Primers[a]	Amplicon length
Coding sequences		
atp1	atp1-F1 = CGCGGAATTAGACCTGCTATTAAC	469 bp
	atp1-R1 = TGATTGAGGATTCCTAATGTGATG	
ccb206	ccb206-F1 = CAGCCTTGAAGTGAATGAATT	661 bp
	ccb206-R1* = TTAATCTTGTAAACTAATCGAGACC	
ccb382	**ccb382-R2 = GATTAGACCATGTTCCTGAGATTT**	
ccb452	**ccb452-F2 = GAATCACTTCATGCCGACCTC**	
	ccb452-R2 = AAGTGTTTGGCCTTTCCTTCT	
cox2	cox2-F1 = ATGATTGTTCTAAAATGGTTATT	770 bp
	cox2-R1* = GTTTGGGGGATTAATTGATTGG	
	cox2-R2 = TCAGAATACTCATAAGTCCGATACC	
matR	matR-F1 = AGAGGCGATCAGAATGGTACTCGA	1927 bp
	matR-R1 = GTCTTGACCGGGTCCGAGCTTCC	
nad1	nad1-F1 = AGGCCAGATCATGAGTAAATAAAA	995 bp
	nad1-R1* = AAAGGTGACTAAAAGACCAGAAAC	
nad2	nad2-F1 = GACCGTAACGTAAGTGACTCAGTG	1578 bp
	nad2-R1 = ACGGCCTACCCTTTCTTTGAA	
	nad2-F2 = TTGATGCTTTTGAATTCATTGTAT	
	nad2-F3 = GGCAAACCCGTGTCAAAT	
nad3	nad3-F1 = AGCAAGGAGCGAGAAAACAAAGT	414 bp
	nad3-R1 = CCCCCATTTTGTGCCCTATC	
nad4	nad4-F1 = ATGTTAGAACATTTCTGTGAATGCTATT	1479 bp
	nad4-R1* = TTTGCCATGTTGCACTAAGTTACT	
	nad4-R2 = CACGCTTTCGGGAAAAACA	
nad5	nad5-F1 = TTTTTCGGACGTTTTCTAGGA	1937 bp
	nad5-R1 = TAAAAACTACTCACTATCAAAATGAAAG	
	nad5-F2 = GGTGATTTTGGATTAGCTCTTG	
	nad5-F3 = GAAGTCTCATTCGAAGCTTTAGAC	
nad6	nad6-F1 = ATGATACTTTCTGTTTTGTCGAG	536 bp
	nad6-R1 = CTTTTCACCTTAGTAGTCCTATGC	
nad7	nad7-F1 = ATGACGACTAGGAAAAGGCAAAT	1179 bp
	nad7-R1* = ATCCACCTCTCCAAACACAATA	
	nad7-R2 = TTCTCCCGCTCCTCAAAA	
	nad7-F2 = AAAGGATTGGGGATTCAGTG	
orf114	orf114-F1* = CAACCGGCGATTGGATG	381 bp
	orf114-R1 = AATGGAAAAGGAACACCGAGTAG	
rps3	**rps3-F2 = CGCCCCTCCTTGAATTTT**	
	rps3-F3 = GGGTGGAGGGAATCCGTATA	

	rps3-R2 = AGAATAATACACCTACCGAGACGA	
rps4	**rps4-F2 = AAGTTTGGATCCGAAAAAGTATG**	
	rps4-R2 = CACAAACCCTTCGATGACTTAT	
UTR and introns		
cox3-trailer	cox3-tr-F1 = TTCGGCAATATCTTGGTCATCTG	341 bp
	cox3-tr-R1 = TTCGGGTCATTTCTTGGTGAAC	
nad5 -intron	nad5-intr-F1 = GTGGGGCAGAGGGCTCGTAGTACC	406 bp
	nad5-intr-R1 = CGGTCGGGCTATCGAACACAGAGT	
nad6- leader	nad6-ld-F1 = AAGGGCTTGGAAGAAGAAAATG	375 bp
	nad6-ld-R1 = ATAGCGCAATACTTCTTCGTGAAT	
nad7- leader	nad7-ld-F1: GGAGATGCATTTCTGGTACAAGTG	203 bp
	nad7-ld-R1: GTTCCGCACGTTCCACCAC	
nad7 -2nd-intron	nad7-2ndintr-F1 = CTCCGCCCGGTGACTAAGAAAG	343 bp
	nad7-2ndintr-R1 = AGCGTGTTCTTGGGCCATCATAG	
rpl5 -trailer	rpl5-tr-F1 = TATTCGGGGGTTCAATGTGACTATTA	338 bp
	rpl5-tr-R1 = TTCGAAAGAACTCAGATACAGAACGA	
rpl16 -trailer	rpl16-tr-F1= ATTAGCGGCTCATAAACCATGTTC	469 bp
	rpl16-tr-R1= CCATACATATCGAGGGCTTTATCA	
rps7 -leader	rps7-ld-F1 = ACAAACTCGACTAAAAGAAGAGGT	410 bp
	rps7-ld-R1 = CGTCAACCATAAGTTTGATTACAT	

[a]Primers in bold are internal primers used for bulk-sequencing the RT-PCR products.
Primers with * have already been reported (Bentolila et al., 2008)

Supplemental Table 3. New PPE primers used in this report

Gene	Position of differentially edited site[a]	PPE primers[b]
Coding sequences		
ccb206	80	ccb206-80 = CACCAATCACGAGTTTTTCTTTATTCCTC
ccb256	184	ccb256-184R = GCCGTGGCGATATAAACAATAATACTCATC
	421	ccb256-421 = CATCTTGTTTTTTATTTACCTGGGTGCAC
ccb382	709	ccb382-709 = GCTCTTGGCATTGCTTTGTTTTTCTC
ccb452	1246	ccb452-1246 = ATAATGAAACTGCCTTTTATTTTTTTTAT
	1280	ccb452-1280 = ATTTATGTTGGCTTCGTTGGGAGGC
matR	374	matR-374R = GATCGAGCTTGTGTAGGTAGATGTTGCC
	461	matR-461 = CGAAATTCCGATTGTTCAGAGAGTCAG
	1771	matR-1771R = CGTTCGGACTTGATAAAGGTTGTCG
	1807	matR-1807R = GAATATTGCAGACCAGCGAATCTGG
orf114	327	orf114-327 = GGATCAAAGAAACTAGCAGACTAATCACTAAATAG
orfX	552	orfX-552 = CGTATTTTGTTCATTTCATCGGTATGCTC
rpl5	92	rpl5-92R = GGGTGCCTTTGGTACTACTCTTATTTCAC
	329	rpl5-329R = CGACCGGAAAATCTAATAGAGACATTACTG
rps14	194	rps14-194 = CCTTTGCACGAGTCAGAAACCGATG
rps4	967	rps4-967 = GGATCGAACTACCTACTCATTATTTGGAGG
UTR and introns		
nad5-intron	803	nad5-int-803R = CTCGTAATTCACTTTTGACTCTGTGTTCG
nad7-leader	-39	nad7-ld-39 = TTTCTGGTACAAGTGGTATTGGACAAGATC
rpl5-trailer	195	rpl5-tr-195 = CCTTTGCACGAGTCAGAAACCGATG

[a]Site differentially edited in silenced vs. control plants was detected by bulk sequencing. Position of the edited C in the coding sequence is given relative to the start codon. In leader and trailer, the position of the edited C is relative to the start codon and stop codon respectively.

[b]ddCTP is used with gene-site, ddGTP is used with gene-siteR.

Supplemental Table 4. Primers used for semi quantitative RT-PCR

Product	Primers	Amplicon length
nad2-intron2 spliced	nad2-ex2-F1 = AATATTTGATCTTAGGTGCATTTTC nad2-ex3-R1 = AAAGGAACTGCAGTGATCTTGA	205 bp
nad2-intron2 adjoining	nad2-ex2-F1 = AATATTTGATCTTAGGTGCATTTTC nad2-int2-R1 = CCCGATCCGATAGTTTACAA	145 bp
nad2-intron3 spliced	nad2-ex3-F1 = CTATGGGTCTACTGGAGCTACCC nad2-ex4-R1 = GCGCAATAGAAAGGAATGCT	215 bp
nad2-intron3 adjoining	nad2-int3-F1 = GGCGAATTTCAAACTTGTGG nad2-ex4-R1 = GCGCAATAGAAAGGAATGCT	156 bp