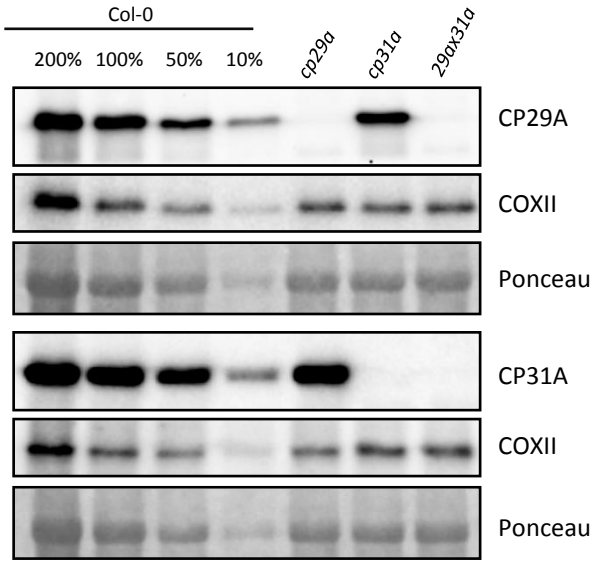
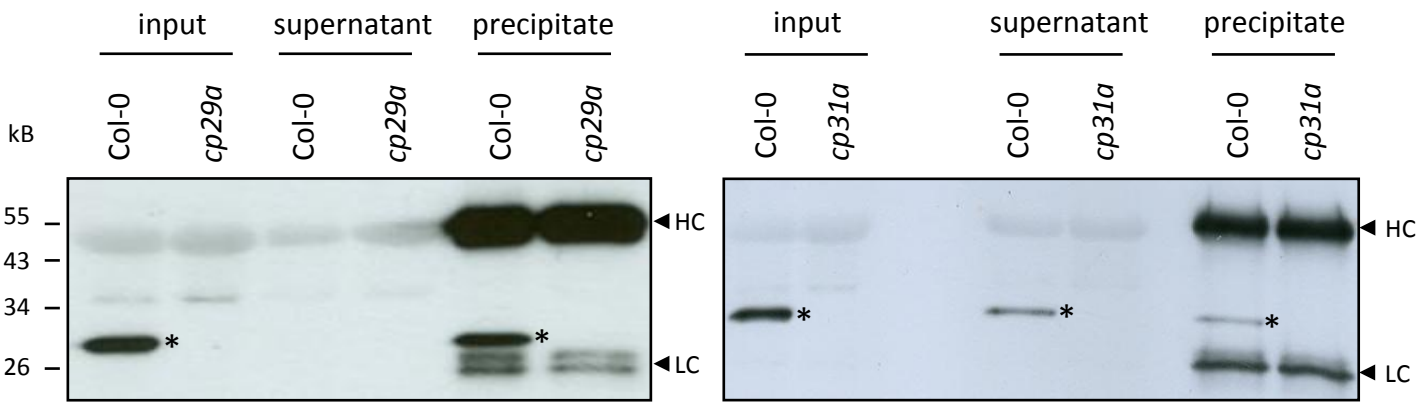


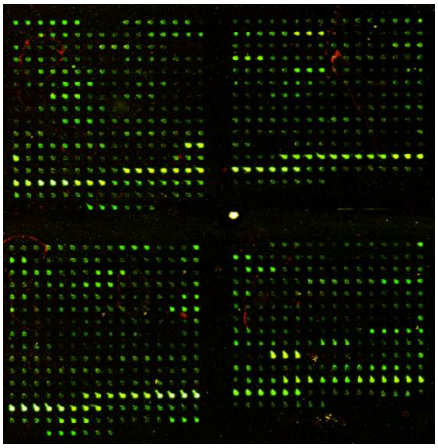
Supplemental Fig. 1: CP29A- and CP31A- protein levels are not altered by the presence or absence of CP31A and CP29A, respectively.
Immunoblots were performed with equal amounts of *cp29a*- and *cp31a*- single and double mutant total protein extracts and compared to a dilution series (200%, 100%, 50%, 10%) of a Col-0 total protein extract. The same blots were stripped and reprobed with antisera against the mitochondrial protein COXII. To demonstrate equal loading of samples, Ponceau-stained RbcL is shown to further support equal loading.



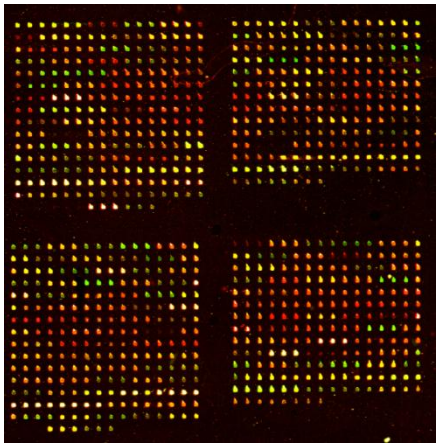
Supplemental Figure 2: Immunoprecipitation of CP29A and CP31A

Immunoblot analyses of immunoprecipitation experiments with anti-CP29A- and anti-CP31A-antibodies, respectively. Stromal extracts from Col-0 and the corresponding knockout mutants (input) were analyzed together with aliquots from precipitates and supernatants generated by immunoprecipitations. A twentieth of the total supernatant and a twentieth of the pellet fraction were loaded on the gel. CP29A and CP31A are indicated by asterisks. Arrowheads point to subunits of the antibody used (heavy chain HC, light chain LC).

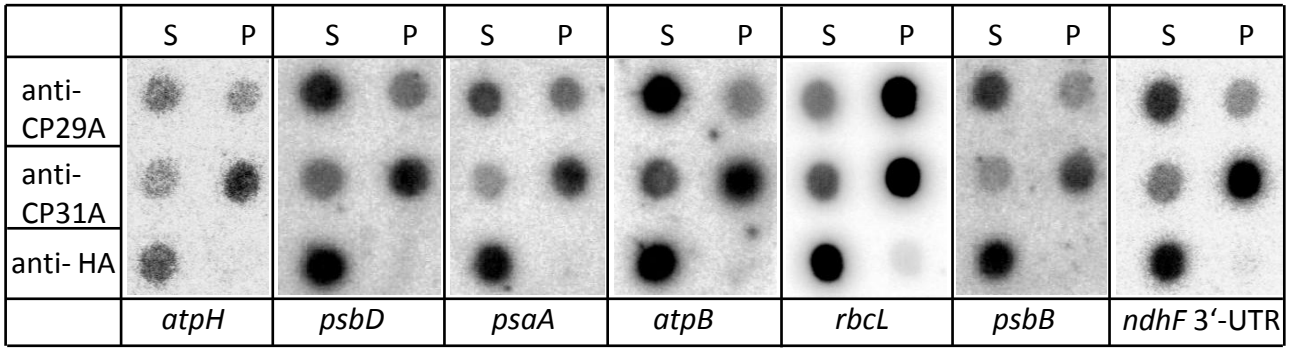
IP using pre-immune serum

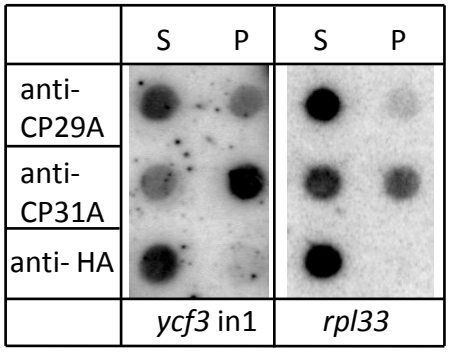


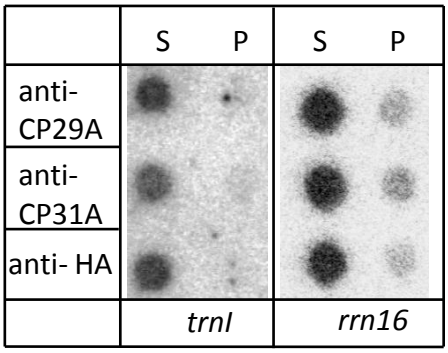
IP using anti-CP31A antibody



Supplemental Figure 3: Excerpt of a representative CP31A-RIP-Chip.
Overlays of fluorescence signals from pellet (Cy5; red) and supernatant (Cy3; green) of a representative CP31A- IP are shown. In the control-IP performed with pre-immune serum (left) RNA can be detected in the supernatant fraction (green fluorescence), but is almost absent from the pellet (no red or yellow signals). In the IP using the anti- CP31A- antibody (right) strong signals are obtained within the precipitate (red fluorescence). Both Chips were scanned using the same laser intensities.

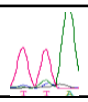
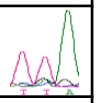
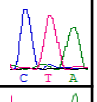
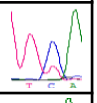
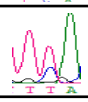
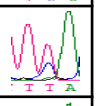
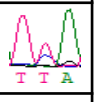






Supplemental Figure 4: Dot blot analyses for validation of RIP-Chip data.

RNAs were isolated from the precipitate and the supernatant of a representative CP29A- and a CP31A-immunoprecipitation, spotted onto uncharged nylon membranes and hybridized with ^{32}P- labeled riboprobes (see Suppl. Table1 online for primers). The upper panel displays dot blot hybridization of RNAs that were highly enriched in RIP-Chips, in the middle panel RNAs with moderate enrichment in RIP-Chips were selected and RNAs in the lower panel showed no enrichment in our RIP-Chips experiments. S = supernatant; P = precipitate.

gene	genome position	Col-0	*cp29a*
matK	2931		
atpF	12707		
rpoC1	21806		
rpoB	23898		
rpoB	25779		
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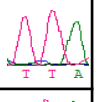
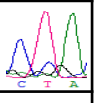
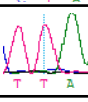
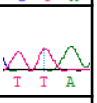
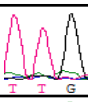
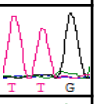
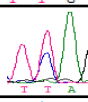
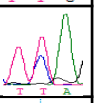
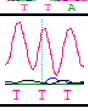
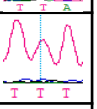
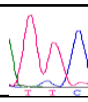
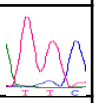
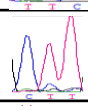
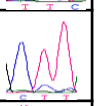
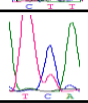
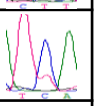
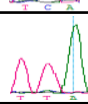
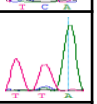
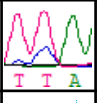
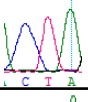
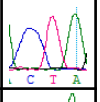
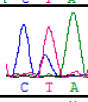
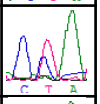
psbZ	35800		
rps14	37092		
rps14	37161		
accD	57868		
accD	58642		
psbF	63985		
psbE	64109		
petL	65716		
rps12	69553		
clpP	69942		
rpoA	78691		

gene	genome position	Col-0	*cp29a*
rpl23	86055		
ndhB	94999		
ndhB	95225		
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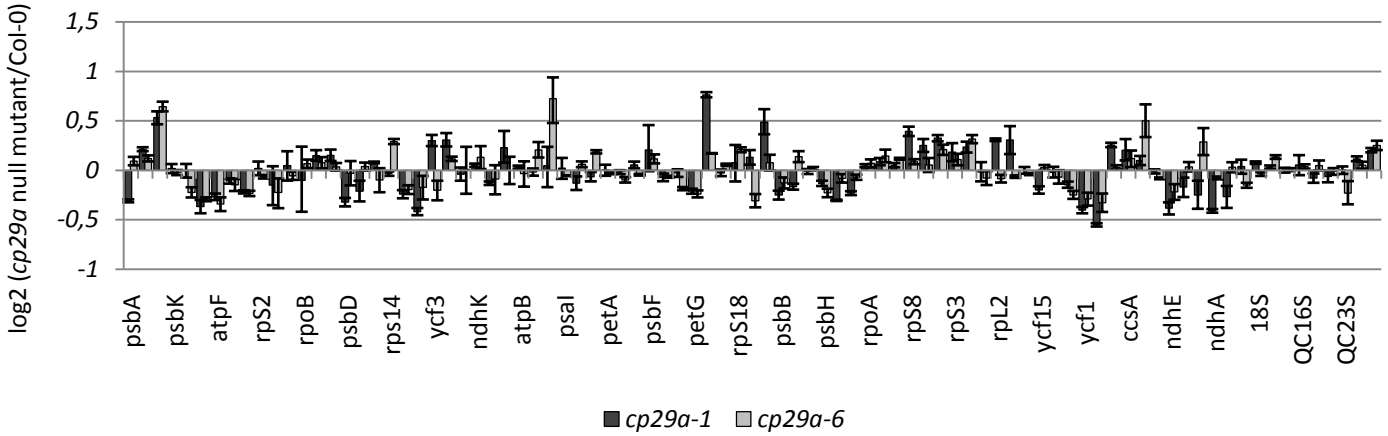
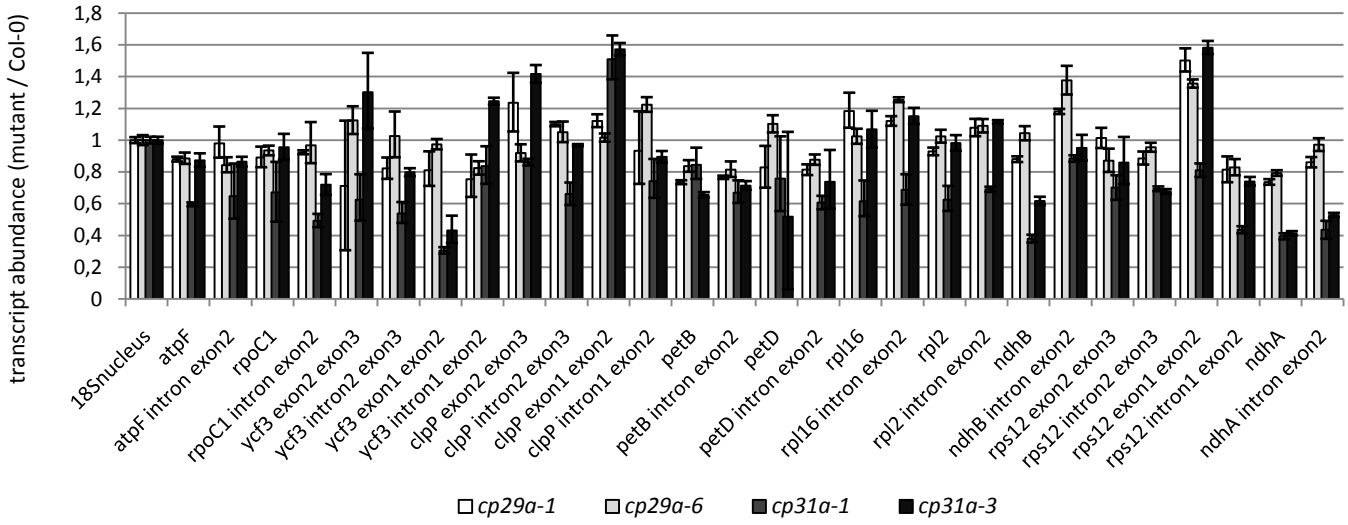
ndhF	112349		
ndhD	116281		
ndhD	116290		
ndhD	116494		
ndhD	116785		
ndhD	117166		
ndhG	118858		

Supplemental Figure 5: Editing in cp29A

Leaves from 3 weeks old Col-0 and *cp29a* plants were used for total RNA isolation and subsequent cDNA amplification. PCR products from RT-PCRs harboring all 34 Arabidopsis plastid editing sites were sequenced (Primers are listed in Suppl. Table1 online). Excerpts of sequencing chromatographs each showing a triplet, which harbors the editing site in the middle, are displayed. Genome positions are given according to the Arabidopsis plastid genome annotation (Genebank accession: AP000423; Sato et al., 1999).



Supplemental Figure 6: Plastid transcript levels in two *cp29a*-mutants.
Transcript quantities assayed by qRT-PCR are shown as $\log_2$ of the ratios of transcript amounts in mutant versus wild-type extracts. The resulting values were normalized to the median of expression ratios (mutant/WT) of all chloroplast genes analyzed. The cytosolic 18S rRNA was used as a non-plastid control. Genes are sorted by their physical location on the plastome. The full data set is given in Suppl. Table2 online.



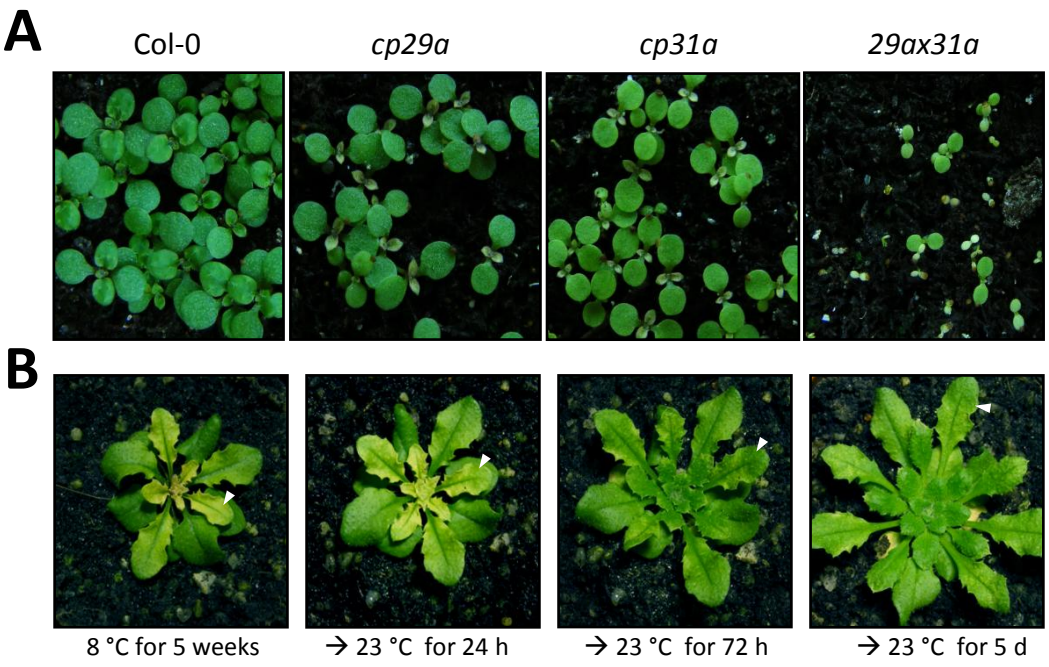
Supplemental Figure 7: Splicing analyses in cpRNP mutants.

Quantitative RT-PCR was used to analyze spliced and unspliced introns in *cp29a* and *cp31a* mutants compared with wild-type plants. Data are normalized to control amplifications of cDNA for nuclear 18S rRNA. There is a reduction in the accumulation of several spliced, but not unspliced RNAs in *cp31a* mutants (*ycf3* first intron; *rpoC1*, *ndhB*). The other splicing events are not or only mildly affected in both mutants. The full data set is given in Suppl. Table.4 online.

	Col-0	*cp29a*	*cp31a*	*cp29axcp31a*
high light conditions (500-600 µmol*m^{-2}*s^{-1})				
low light conditions (20-30 µmol*m^{-2}*s^{-1})				
normal light conditions (180 µmol*m^{-2}*s^{-1})				

Supplemental Figure 8: Light stress phenotypes

Col-0 plants and *cp29a*, *cp31a* and *cp29axcp31a* mutants were grown under standard growth conditions (long day [16 h light/ 8 h dark]; normal light [180 µmol*m^{-2}*s^{-1}]) for 12 days and then shifted to either high light (500-600 µmol*m^{-2}*s^{-1}; upper panel) or low light (20-30 µmol*m^{-2}*s^{-1}; middle panel) or kept at the primary standard conditions (lower panel) for three weeks.



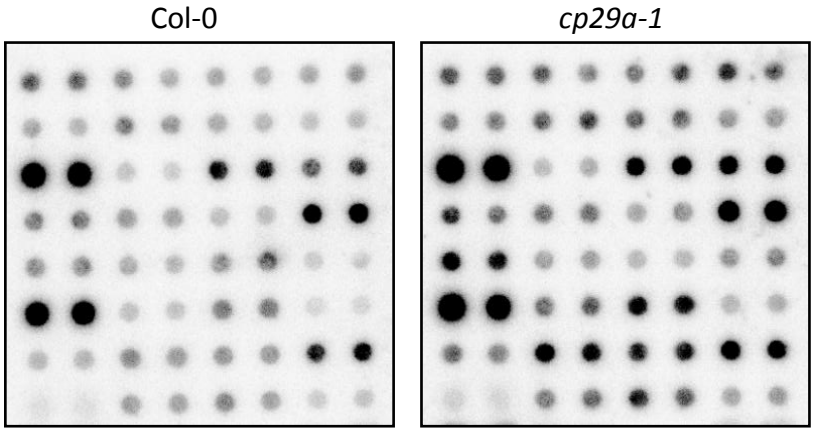
Supplemental Figure 9: Phenotypes of *cp29a*- and *cp31a*- single and double mutants germinated under cold stress conditions.

Seeds from Col-0 plants and from *cp29a*, *cp31a,* and *cp29a*x*cp31a* mutants were germinated and grown at 8 °C for three weeks.

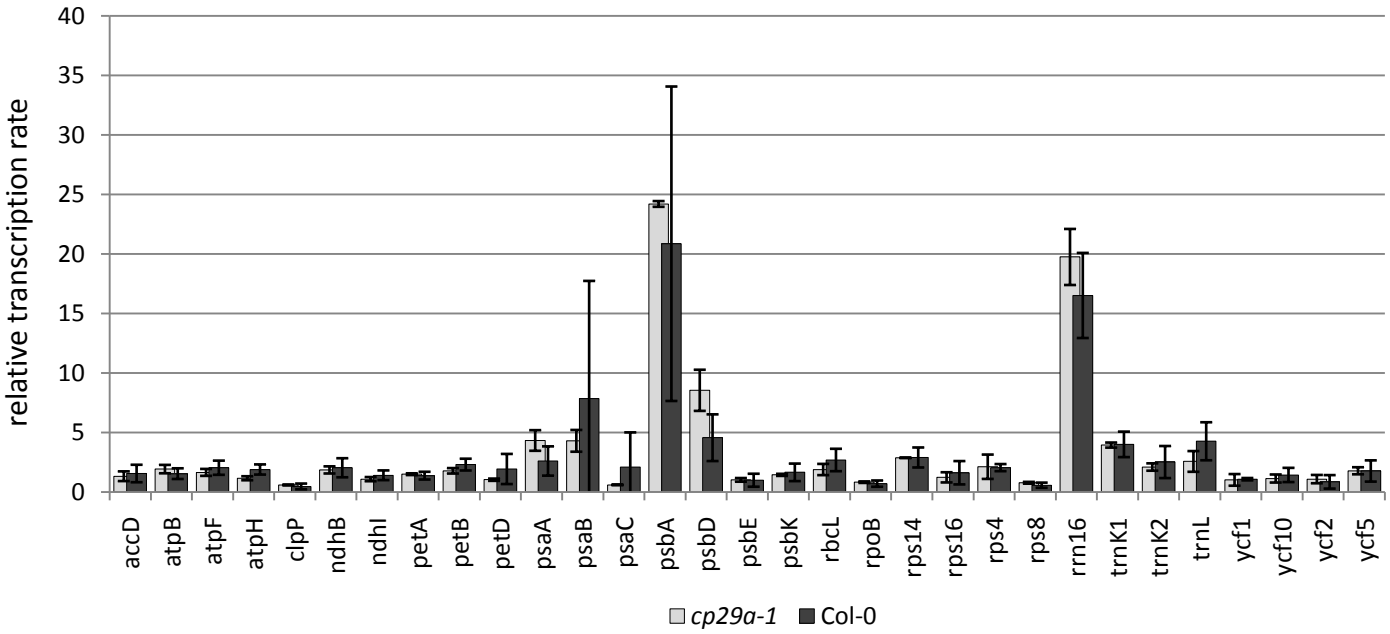
A *cp29a* x *cp31a* double mutant was germinated and grown for 5 weeks at 8°C and then shifted to 23 °C . The phenotype was documented 0 h, 24 h, 72 h and 5 days after the low temperature stress. Arrowhead indicates same leaf in all four pictures.

A

ndhB	*atpH*	*atpF*	*atpB*
petD	*petB*	*petA*	*ndhI*
psbA	*psaC*	*psaB*	*psaA*
rbcL	*psbK*	*psbE*	*psbD*
rps4	*rpoB*	*clpP*	*accD*
rrn16	*rps16*	*rps14*	*rps8*
ycf1	*trnL*	*trnK2*	*trnK1*
	ycf10	*ycf5*	*ycf2*



B

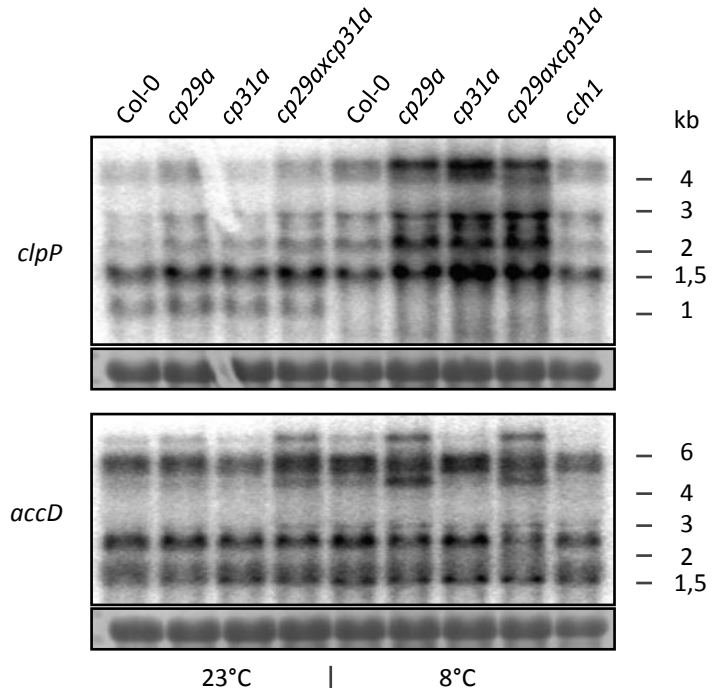


Supplemental Figure 10: Run-on transcription assay of selected chloroplast genes in a *cp29a*-knockout mutant.

Relative transcription rates in the *cp29a-1* mutant and the wildtype (Col-0) were determined as described (Zubo et al., 2008).

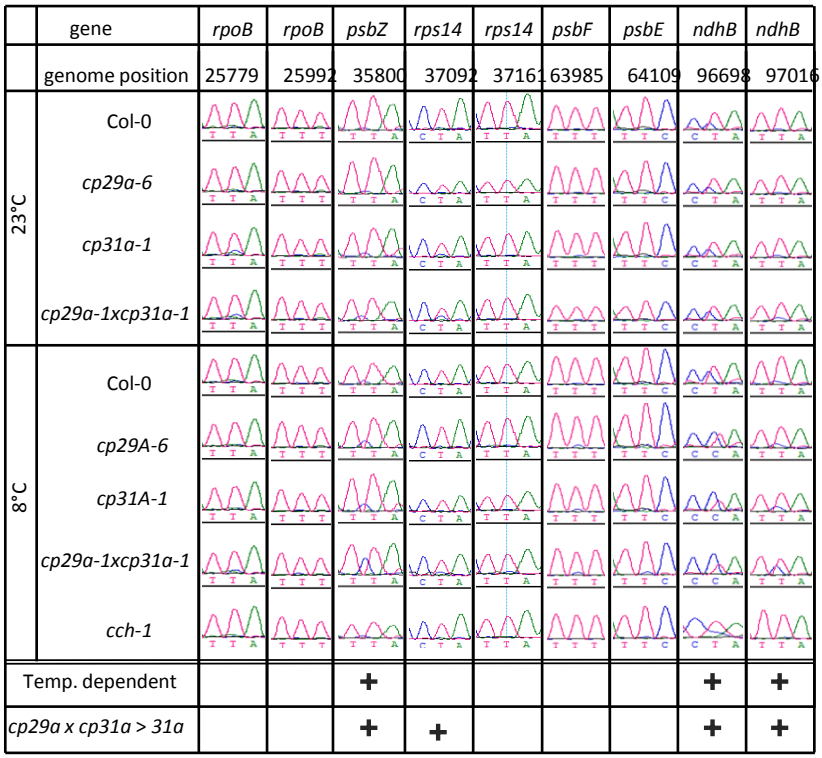
(A) Hybridisation of ^{32}P- labeled chloroplast RNA from Col-0 and *cp29a-1* seedlings with a macroarray containing DNA-probes for 31 selected chloroplast genes. Signals were detected using the Personal Molecular Imager (PMI) System (Bio-Rad).

(B) represents the quantification of (A) Autoradiographs from wild-type and the *cp29a-1*- mutant shown in (A) were quantified using the Quantity One Software (Biorad).The relative transcription rates were obtained by calculating wild-type to mutant ratios (see also Suppl. Table.3 online).



Supplemental Figure 11: Transcript accumulation of selected NEP-dependent mRNAs under standard- (23 °C) and cold stress (8 °C) conditions.

4 µg of total RNA from 2 weeks old whole plants grown at 23 °C (left) and from bleached tissue after 18 days of cold stress (right) were fractionated on denaturing agarose gels and analyzed by hybridization to ^{32}P- labeled riboprobes for the plastid RNAs *clpP* and *accD*. Equal loading was controlled by methylene blue staining (cytosolic 25S rRNA is shown).



Supplemental Figure 12: Analysis of chloroplast RNA editing in cpRNP mutants.
cDNAs were prepared from total leaf RNA from wild-type, *cp31a* and *cp29a* mutants, either grown at standard growth temperatures for 18 days or additionally cold-stressed for three weeks. Selected cDNAs were amplified by PCR and sequenced to identify changes in RNA-editing site processing. Excerpts of sequencing chromatograms are displayed with the editing site always being in the centre of the base triplet shown. Overall, effects on RNA editing either by genotype or by low temperatures were only mild. Most prominently, editing of the site in *psbZ* is reduced after cold treatment, in particular in double mutants. Similarly, RNA editing of the two sites in the *ndhB* transcript decreases in cpRNP mutants in a temperature-dependent manner (indicated by plus signs below the chart). Parallel analysis of *cch* mutants demonstrates that the defects observed are specific for cpRNP mutants.

Supplemental Table 1: Oligonucleotides

Oligonucleotide	Sequence (5'>3')	Target(s)	Purpose
accD_for	TTCATTTGTAGTGAAAGCGG	*accD*	riboprobe for Northern
accD_T7_rev	GTAATACGACTCACTATAGGGTTCGCCTACTACGGATCCC	*accD*	riboprobe for Northern
atpB_for2	GGAATGGACGTGGTTGATATGG	*atpB*	riboprobe for dot blot
atpB_T7_rev2	TAATACGACTCACTATAGGGCAGTCAGACCAACTCTCATACG	*atpB*	riboprobefordotblot
atpH5'_for	GATTTAGATAGGGATTCGATTAG	*atpH*	riboprobe for dot blot
atpH5'_T7_rev	GTAATACGACTCACTATAGGGTCCAGGTCCAATAGAAGCAAG	*atpH*	riboprobefordotblot
clpP_ex2_for	GAGGTTGATACCGAAATCTCG	*clpP*	riboprobe for Northern
clpP_ex2_T7_rev	GTAATACGACTCACTATAGGGCGTTTGGTAATTGCTCCTCC	*clpP*	riboprobefor Northern
ndhB_ex1_for	CTGAGCAATCGCAATAATCG	*ndhB*	riboprobe for Northern
ndhB_ex1_T7_rev	GTAATACGACTCACTATAGGGTACCGGAACTGATAACATTCG	*ndhB*	riboprobefor Northern
petB_for	CGTCCAACCGTTACTGAAGC	*petB*	riboprobe for Northern
petB_T7_rev	GTAATACGACTCACTATAGGGAATAGCGTCAGGTACACC	*petB*	riboprobefor Northern
psaA_for	TGGCATGTATTTCCATGGTG	*psaA*	riboprobe for Northern and dot blot
psaA_T7_rev	GTAATCGACTCACTATAGGGAACCAAGCCAATTTTGGAG	*psaA*	riboprobe for Northern and dot blot
psbB_for	TTTGCAGCTTTTGTTGTTGC	*psbB*	riboprobe for Northern and dot blot
psbB_T7_rev	GTAATACGACTCACTATAGGGCTTCTAAACGGGACGTCAGC	*psbB*	riboprobe for Northern and dot blot
psbD_for	CTATTTCGCTTTAGGGGGTTGG	*psbD*	riboprobe for Northern and dot blot
psbD_T7_rev	TAATACGACTCACTATAGGGCAGCAATGGGACCAGAGAATGC	*psbD*	riboprobe for Northern and dot blot
psbF_for	GTCTGGAAGCACAGGAGAACG	*psbF*	riboprobe for Northern
psbF_T7_rev	GTAATACGACTCACTATAGGGCAAAACGGCCTGTTATTAATGG	*psbF*	riboprobefor Northern
rbcL_for	GCAGCATTCCGAGTAACTCC	*rbcL*	riboprobe for Northern and dot blot
rbcL_T7_rev	GTAATACGACTCACTATAGGGCCACGTAGACATTCATAAACTGC	*rbcL*	riboprobe for Northern and dot blot
rpl33_for	ATGGCCAAGGGTAAAGATGTTCG	*rpl33*	riboprobe for Northern and dot blot
rpl33_T7_rev	GTAATACGACTCACTATAGGGCTCAATTCCAATCGACTAGG	*rpl33*	riboprobe for Northern and dot blot
rps4_rp	CGTCTGGGGGCTTTACCGGG	*rps4*	riboprobe for Northern
rps4_T7	GTAATACGACTCACTATAGGGTGGTTTGGCAATTCCTCAGGGGC	*rps4*	riboprobefor Northern
rrn16_for	ATGGATACTAGGCGCTGTGC	*16 S* rRNA	riboprobe for Northern and dot blot
rrn16_T7_rev	GTAATCGACTCACTATAGGGACCTTCCTCCGGCTTATCAC	*16 S*rRNA	riboprobe for Northern and dot blot
rrn23_3'_for	GCAAGACCCACCCGTCGAGC	*23S* rRNA	riboprobe for Northern
rrn23_3'_T7_rev	GTAATCGACTCACTATAGGGCGCTCCGCACTTGGCTACCC	*23S* rRNA	riboprobefor Northern
ycf3_exon2_for	CGGATGTCGGCTCAATCTGAAGG	*ycf3*	riboprobe for Northern
ycf3_exon2_T7_rev	TAATACGACTCACTATAGGGAGAGGGGTTTCGTTCTAATGCCCGA	*ycf3*	riboprobefor Northern
ycf3_intron1_for	AGGGGAAGAAGCACTACGCCG	*ycf3*	riboprobe for Northern and dot blot

ycf3_intron1_T7_rev	TAATACGACTCACTATAGGGAGACGGCTCCTCCTTTAGGTGCAT	*ycf3*	riboprobe for Northern and dot blot
ndhF_3'UTR_for	TCGAACGTGGAATTCATCATC	*ndhF,ycf1as*	riboprobe for Northern and dot blot
ndhF_3'UTR_T7_rev	GTAATCGACTCACTATAGGGTGAGAAATTCTATGGCTCGAATC	*ndhF,ycf1as*	riboprobe for Northern and dot blot
ycf1as_for	GATTCTTCCCCGAGAGATTCC	*ycf1as*	riboprobe for Northern
ycf1as_T7_rev	GTAATCGACTCACTATAGGGAAGATGGAATCGACCAAACC	*ycf1as*	riboprobefor Northern
ndhF_for	TTTTTCACGCCGTCAATAAACC	*ndhF*	riboprobe for Northern
ndhF_T7_rev	TAATACGACTCACTATAGGGAGAAGAGATGCGACTTCCAC	*ndhF*	riboprobefor Northern
trnIex1	TTATCAGGGGCGCGCTCTACCACTGAGCTAATAGCCC	*trnI*	oligoprobe for dot blot
accD.AT.for2	ATTGCATTTGCGGGTAAAAGAG	*accD-2*	Editing
accD.AT.rev2	GGGAAATGCAAAAAGATGGAAG		Editing
accD.AT.for	TTCATTTGTAGTGAAAGCGG	*accD-1*	Editing
accD.AT.rev	TTTCGCCTACTACGGATCCC		Editing
ATPHfor2	ATAAGAGGAGATTGTATGAAA	*atpF-1*	Editing
AT7atpF	GTAATACGACTCACTATAGGGCTAATGGTACGTAAATGTAACTC		Editing
clpP.AT.for	GTAATGATCCATCAACCCGC	*clpP-1*	Editing
clpP.AT.2rev	TGAACCGCTACAAGATCAAC		Editing
matK.AT.for	CGTTACCGGGTAAAAGATGC	*matK-2*	Editing
matK.AT.rev	AGCGGCGTATCCTTTGTTGC		Editing
matK.seq	TTTGTTGCCAGAATGCATCTTC		Editing
ndhBfor2	TCATGATCTGGCATGTACAG	*ndhB-1,2*	Editing
ndhBedIII	ATTTCTTGAAGCTCAATCTCTCCCCCGGAT		Editing
ndhB1seq	TGAACCATATAGCCAAGAGAAACC		Editing
nb11	TTCATGCTTGTTTGAGTAATAGC	*ndhB-3,4,5,6,7,8,9,11*	Editing
P12	GGTCTAATGAGGCTACTATG		Editing
ndhBrev2	CTAAAAAAGGCTATCCTGAGC	*ndhB-10,12*	Editing
AndhB	GTCGTTGCTTTTCTTTCTG		Editing
ndhB3seq	CAGGCAGGCCTATATTTCTTGG		Editing
ndhDstart5´	GGTCCAAGTGTATCTTGTC	*ndhD-1*	Editing
ndhD.AT.3rev	ACAGTTGAATTAATGGATCG		Editing
ndhDstart5´	GGTCCAAGTGTATCTTGTC	*ndhD-2*	Editing
iz	AGGAATTAATTCTAACTCCC		Editing
ndhD.AT.for4	ACGGGATTTATTACTACTTTAGC	*ndhD-2,3,4,5*	Editing
ndhD.AT.for	CAAGCCTAATTCTATCATAACTCG		Editing
ndhF.AT.for	AAAACCTTCGCCGCATGTGG	*ndhF-2*	Editing
ndhF.AT.rev	GCATTCGCTGCAATAGGTCG		Editing
ndhGforM	TAGAATGGATTTGCCTGGAC	*ndhG-1*	Editing
ndhG.AT.rev	AGAATTATTGAAATGAGTTC		Editing
petL.AT.for	AAATTTGGTAATTAACACGG	*petL-1*	Editing
petL.AT.rev	ATTTCAATTGAAACTTAGGG		Editing
petLseq	GGTAATTAACACGGTAAGGAACTATCG		Editing
psbF.AT.rev	CGTTGGATGAACTGCATTGC	*psbE-1, psbF-1*	Editing
psbE.AT.for	ACAGGAGAACGTTCTTTTGC		Editing

pebEseq	CACCGGTTTAGCTTACGATGTG		Editing
psbZ.AT.for	GCTTTCCAATTGGCAGTTTTTG	*psbZ-1*	Editing
psbZ.AT.rev	CCACCAAGAAGACTAATCCAATCC		Editing
rpl23.AT.for	TTACAGACAAAAGTATTCGGTTATTGG	*rpl23-1*	Editing
rpl23.AT.rev	ATAACCCGGTTGAAGCGTAATG		Editing
rpoA.AT.for	GGACACTACAGTGGAAGTGTGTTG	*rpoA-1*	Editing
rpoA.AT.rev	CCAGGACCTTGGACACAAATAAG		Editing
rpoB.AT.for	GAAAACCAGTAGGAATATGC	*rpoB-1,3*	Editing
rpoB.AT.rev	GTCTCCAATTAATATTTCGGCG		Editing
rpoB1seq1	TCCTTTAATGAATTCCCTTGGAAC		Editing
rpoB1seq2	TCCCCACCTACACAAGAAAATTG		Editing
rpoB.AT.3for	GAGGTGGGTTCAGAAAAAGG	*rpoB-7*	Editing
rpoB.AT.3rev	TATCTGTCCTACATTCATGCG		Editing
rpoC1.AT.rev	CGGCTAATTGTTCTCGGATAGC	*rpoC1*	Editing
rpoC1.AT.for	CCCAAAGTTTTGTGAACAATGTG		Editing
rps12.AT.for	TACAAGACAGCCAATCCGAAAC	*rps12-1*	Editing
rps12.AT.rev	GTTGATTGGATTTGCACCAATG		Editing
rps14.AT.for	TTATAGGGAGAAGAAGAGGC	*rps14-1,2*	Editing
rps14.AT.rev	TACCAGCTTGATCTTGTTGC		Editing
T7 withoverlap	TAATACGACTCACTATAGGGAGACAGG	T7 promoter	RNase protection
ndhF footprint	TAAAATGTGACCAATTAACCAACCAACAAAACTACTTGCCTGTCTC	*ndhF*	RNase protection
ndhF3RACE	GTCGCATCTCTTCTTATCTGTTC	*ndhF*	3'RACE
ycf1as3RACE	CGAAAACGAGAGTTACAAATGG	*ycf1as*	3'RACE

Supplemental Table 2: Full data set of quantitative RT-PCRs to determine the transcript accumulation levels in *cp29a*- mutant lines

	cp29a-1			***cp29a-6***		
gene	log2(mutant/WT)	SD-	SD+	log2(mutant/WT)	SD-	SD+
psbA	-0,308405573	0,01478404	0,01487582	0,093562711	0,04255459	0,04212409
matK	0,213410958	0,01938086	0,01954235	0,12021388	0,03083574	0,0306896
rpS12A	0,531690239	0,0663808	0,06387123	0,644154161	0,04833883	0,04936726
psbK	0,017222846	0,04606198	0,04609677	-0,022767693	0,02563558	0,02571511
psbI	-0,005469711	0,06821807	0,06977166	-0,222581654	0,0515945	0,05115693
atpA	-0,367084946	0,06682182	0,0673772	-0,292692633	0,01948995	0,01943572
atpF	-0,267715948	0,03300013	0,0332586	-0,341388625	0,07061334	0,06803832
atpH	-0,107714657	0,02676288	0,02706794	-0,147510091	0,06161574	0,06030011
atpI	-0,217426905	0,01605861	0,01598818	-0,233648421	0,02642356	0,02687418
rpS2	0,018046473	0,06757473	0,07062984	-0,0654047	0,01727369	0,01745945
rpoC2	-0,150293411	0,20153942	0,19159103	-0,224824483	0,15744568	0,14287651
rpoC1	0,047295833	0,1512611	0,14522745	-0,054993896	0,04126455	0,04085919
rpoB	-0,100316417	0,31848033	0,3396508	0,065831149	0,04363173	0,04255747
petN	0,149103371	0,05392125	0,05444864	0,07743167	0,05738696	0,05568124
psbM	0,15158363	0,05693476	0,05809682	0,035228799	0,03904684	0,03877639
psbD	-0,321883531	0,04254471	0,0425286	-0,030790238	0,12136672	0,12436366
psbC	-0,210630757	0,10351006	0,10540503	0,037523469	0,04073921	0,04073742
psbZ	0,079453336	0,00835804	0,00833688	-0,09684972	0,12449021	0,11831917
rps14	-0,033125219	0,02245161	0,02241754	0,290774926	0,02563488	0,02571099
psaB	-0,241193537	0,04150941	0,04110315	-0,195215167	0,04407312	0,04429442
psaA	-0,416966427	0,03649244	0,03635349	-0,171740847	0,12313123	0,11608167
ycf3	0,300859295	0,05607927	0,05668101	-0,201269046	0,10149144	0,096555
rps4	0,307280784	0,06610499	0,06916151	0,115917602	0,02201703	0,02214886
ndhJ	-0,03887838	0,06587592	0,067027	0,007613683	0,24467753	0,22979342
ndhK	0,050943594	0,01656246	0,01674604	0,132131288	0,1191684	0,11239532
ndhC	-0,130360945	0,01778333	0,0178125	-0,089006104	0,15387285	0,14079193
atpE	0,230048813	0,15197693	0,16779084	0	0,13903597	0,13696237
atpB	0,032077171	0,01539415	0,01537261	-0,032960949	0,13181929	0,12379318
rbcL	-0,017594895	0,0366103	0,03619888	0,206023104	0,07638347	0,07948386
accD	0,046162	0,21616346	0,19112171	0,72262421	0,24479733	0,21632904
psaI	0,023364043	0,10929604	0,10182696	-0,054362759	0,00355328	0,00354573
ycf4	-0,129247068	0,06968094	0,06716335	0,06074097	0,02881204	0,02935022
cemA	-0,064759941	0,047116	0,04749303	0,186728866	0,01650058	0,01659818
petA	0,001581193	0,05650531	0,05459648	-0,029828969	0,00886032	0,00883598
psbJ	-0,018906986	0,02012177	0,02033593	-0,09632326	0,0272173	0,02742314
psbL	0,054032108	0,03476806	0,03405198	-0,044824096	0,00837072	0,00841431
psbF	0,206952357	0,2158894	0,24993588	0,115192426	0,04524851	0,04565104
psbE	-0,071311688	0,03859082	0,03860894	-0,065139323	0,00986995	0,00991599
petI	-0,028010491	0,03883234	0,03828736	-0,185182292	0,0160937	0,01604089
petG	-0,211498102	0,02541062	0,02522903	-0,238503994	0,03510587	0,03580378
psaJ	0,763779691	0,02574896	0,02595166	0,17137016	0,00236332	0,00235979
rpL33	-0,025535863	0,0333036	0,03370574	0,056011589	0,0112724	0,01129044
rpS18	0,07638034	0,18907958	0,17948231	0,207970294	0,02501149	0,02463304

rpL20	0,131925944	0,07457473	0,07264815	-0,308143452	0,06589417	0,068445
clpP1	0,486495225	0,12236073	0,13139575	0,076352739	0,07841435	0,08105609
psbB	-0,251227696	0,04442311	0,04481071	-0,128347889	0,05507769	0,05606247
psbT	-0,165467543	0,02982736	0,030238	0,138611296	0,05593157	0,05496006
psbN	-0,012050104	0,02513407	0,02510576	0,016616281	0,01685183	0,01695135
psbH	-0,131929841	0,02644396	0,02692147	-0,22849194	0,04317011	0,0431875
petB	-0,303287636	0,00675474	0,00674493	-0,081101099	0,04289848	0,04302192
petD	-0,230789068	0,01943513	0,01947918	-0,070224263	0,02625929	0,02666277
rpoA	0,046038435	0,01595019	0,01597726	0,069561265	0,04070504	0,04083132
rpS11	0,08761172	0,03641386	0,03672384	0,144784122	0,06378685	0,06431317
rpL36	0,052028393	0,02203107	0,02184349	0,117113787	0,00932581	0,00934367
rpS8	0,394251839	0,04795939	0,04693499	0,087033672	0,02559715	0,02565035
rpL14	0,250166105	0,06450276	0,06612289	0,054081206	0,07115067	0,0703307
rpL16	0,324651661	0,0317053	0,03143824	0,208342387	0,05250051	0,05122393
rpS3	0,182348368	0,08945457	0,09233599	0,109338423	0,05878661	0,05765654
rpL22	0,235194513	0,05578907	0,05418887	0,315000977	0,04126901	0,04124601
rpS19	-0,015357612	0,09606281	0,09772183	-0,077928612	0,07066856	0,06820275
rpL2	0,308818476	0,01318726	0,01326008	-0,084075631	0,03915935	0,03826957
rpL23	0,305669229	0,14165393	0,14080905	-0,063983936	0,01262681	0,01259567
ycf2.1	0	0,03397167	0,0334639	-0,038455791	0,00996405	0,00991006
ycf15	-0,198651724	0,03696535	0,0371376	0,029073812	0,02515729	0,02493643
ndhB	-0,018755938	0,05377252	0,05442461	-0,067606257	0,06681117	0,06866137
rpS7	-0,145221257	0,03107372	0,03152018	-0,248746672	0,03989009	0,04049651
ycf1	-0,402592043	0,0318257	0,03219067	-0,289965968	0,06624097	0,06417544
ndhF	-0,551391306	0,01664637	0,01658441	-0,327438091	0,09316085	0,09289452
rpL32	0,255940045	0,02217327	0,02224298	0,02908994	0,02216244	0,02229649
ccsA	0,20440134	0,10404229	0,11136342	0,117909613	0,08503234	0,08188703
ndhD	0,098248166	0,04540946	0,04677473	0,500812594	0,1651471	0,16539321
psaC	-0,011338638	0,02063322	0,02086726	-0,0813676	0,00882306	0,00887404
ndhE	-0,383651637	0,06250327	0,06031794	-0,2176313	0,08082534	0,07774404
ndhG	-0,169945487	0,10033964	0,09585357	0,035260195	0,04717738	0,04806869
ndhI	-0,248699429	0,13977635	0,14349788	0,285342712	0,1318692	0,14141658
ndhA	-0,409827066	0,01862744	0,01854095	-0,077049555	0,0142767	0,01434018
ndhH	-0,267277721	0,1124837	0,10888585	0,031236453	0,05105751	0,05038942
rpS15	0,036619797	0,0712452	0,07087126	-0,15108761	0,02534018	0,02537962
18S	0,077374429	0,01242462	0,01241586	-0,037773557	0,01875914	0,01864399
18S	0,032492365	0,01639459	0,01650402	0,134186498	0,01838876	0,01846863
18S	0,001295177	0,024078	0,02399951	0,006918298	0,0147918	0,01491309
QC16S	0,053195244	0,10235864	0,09999512	0,038775818	0,02169949	0,02184592
QC16S	-0,079472866	0,04647324	0,04725979	0,048830631	0,04918109	0,05047213
QC16S	-0,063326767	0,05761224	0,05726447	-0,012080439	0,0337441	0,03423117
QC23S	0,001783324	0,03809949	0,03735972	-0,230727281	0,11245258	0,12161601
QC23S	0,116756883	0,02441273	0,02419174	0,051973391	0,0350072	0,03463573
QC23S	0,203585052	0,02168644	0,02192682	0,250963885	0,04628146	0,04777931

Supplemental Table 3: Run on transcription experiments in *cp29a* mutants. Quantification of five independent experiments with wild-type (Col-0) and two with the *cp29a-1* mutant

	Col-0							***cp29a***			
	Col-0 exp 1	Col-0 exp 25	Col-0 exp 26	Col-0 exp 27	Col-0 exp 29	mean (Col-0)	+-SD (Col-0)	*cp29a* exp1	*cp29a* exp2	meanc *p29a*	+-SD (*cp29*)
accD	1,44	0,66	1,22	1,79	2,64	1,55	0,73	1,03	1,61	1,32	0,41
atpB	1,20	1,04	1,45	1,89	2,10	1,54	0,45	1,67	2,17	1,92	0,35
atpF	1,48	1,32	2,30	2,63	2,45	2,04	0,60	1,44	1,85	1,64	0,29
atpH	2,55	1,51	2,01	1,86	1,51	1,89	0,43	1,27	1,03	1,15	0,17
clpP	0,88	0,29	0,29	0,40	0,46	0,46	0,24	0,62	0,56	0,59	0,04
ndhB	1,17	1,78	3,34	2,04	1,84	2,03	0,80	1,64	2,06	1,85	0,30
ndhI	1,77	0,75	1,39	1,37	1,73	1,40	0,41	0,95	1,20	1,08	0,17
petA	1,12	0,94	1,47	1,66	1,66	1,37	0,33	1,44	1,55	1,49	0,07
petB	2,75	1,90	2,83	2,30	1,71	2,30	0,49	1,61	1,94	1,78	0,23
petD	4,13	1,44	1,84	1,16	1,08	1,93	1,27	1,10	0,96	1,03	0,09
psaA	0,70	2,06	3,69	3,09	3,46	2,60	1,23	3,71	4,94	4,33	0,87
psaB	25,54	3,49	3,07	3,61	3,47	7,84	9,90	3,65	4,94	4,30	0,91
psaC	7,31	0,55	0,81	0,76	0,99	2,08	2,92	0,62	0,57	0,60	0,03
psbA	0,90	37,13	26,03	22,09	18,15	20,86	13,21	24,04	24,38	24,21	0,24
psbD	1,52	4,50	6,24	6,35	4,17	4,56	1,96	7,32	9,77	8,54	1,73
psbE	1,96	0,77	0,70	0,76	0,75	0,99	0,54	0,91	1,13	1,02	0,15
psbK	0,58	1,31	2,30	1,70	2,35	1,65	0,74	1,37	1,50	1,44	0,09
rbcL	2,18	3,53	3,84	2,19	1,69	2,69	0,94	1,55	2,22	1,89	0,47
rpoB	1,11	0,47	0,52	0,61	0,81	0,70	0,26	0,87	0,78	0,82	0,06
rps14	1,75	2,92	2,44	3,56	3,82	2,90	0,84	2,88	2,85	2,86	0,02
rps16	0,47	1,05	1,49	2,03	3,03	1,62	0,98	1,53	0,93	1,23	0,43
rps4	2,23	1,84	1,74	1,96	2,47	2,05	0,30	2,84	1,39	2,12	1,02
rps8	0,85	0,32	0,39	0,57	0,70	0,57	0,22	0,72	0,83	0,77	0,08
rrn16	21,96	17,61	13,59	13,09	16,33	16,51	3,58	21,42	18,08	19,75	2,36
trnK1	4,12	2,73	3,73	5,68	3,73	4,00	1,07	3,79	4,09	3,94	0,21
trnK2	1,60	1,15	1,96	3,54	4,31	2,51	1,35	2,31	1,88	2,10	0,31
trnL	1,82	3,87	4,28	5,95	5,38	4,26	1,60	3,18	1,95	2,56	0,87
ycf1	1,06	1,06	0,99	1,01	1,24	1,07	0,10	1,36	0,67	1,01	0,49
ycf10	0,70	0,93	2,14	1,66	1,72	1,43	0,60	1,37	0,89	1,13	0,34
ycf2	1,70	0,40	0,35	0,66	1,14	0,85	0,57	0,83	1,33	1,08	0,35
ycf5	1,46	0,68	1,56	2,02	3,11	1,76	0,89	1,99	1,57	1,78	0,30

Shown are differential values for each transcript, calculated by dividing the sum of the spot intensities of all transcripts analyzed by the spot intensity of each single transcript**.** exp = independent experiments

Supplemental Table 4: Quantitative RT-PCRs amplifying spliced and unspliced forms of the 12 chloroplast intron containing mRNAs in *cp29a* and *cp31a* mutant lines. Values were obtained by dividing quantities measured for the mutants with the ones measured for the wild-type (WT). Data were normalized to cytosolic 18S rRNA.

PCR product	***cp29a-1***			***cp29a-6***			***cp31a-1***			***cp31a-3***		
	ratiomutant/WT	STD+	STD-	ratiomutant/WT	STD+	STD-	ratiomutant/WT	STD+	STD-	ratiomutant/WT	STD+	STD-
16S	0,8727	0,0282	0,0273	1,0572	0,0210	0,0208	0,7308	0,0146	0,0142	0,8533	0,0764	0,0675
23S	0,9611	0,0722	0,0632	0,9275	0,0722	0,0625	1,2152	0,2257	0,1807	1,7317	0,0791	0,0753
18Snucleus	1,0000	0,0190	0,0187	1,0000	0,0317	0,0311	1,0000	0,0213	0,0207	1,0000	0,0213	0,0209
atpF	0,8806	0,0155	0,0151	0,8855	0,0364	0,0350	0,5959	0,0120	0,0119	0,8738	0,0435	0,0419
*atpF*intron exon2	0,9799	0,1059	0,0901	0,8429	0,0496	0,0450	0,6467	0,2060	0,1409	0,8644	0,0309	0,0300
rpoC1	0,8907	0,0686	0,0612	0,9349	0,0306	0,0302	0,6717	0,1917	0,1845	0,9555	0,0842	0,0780
*rpoC1*intron exon2	0,9236	0,0127	0,0124	0,9684	0,1455	0,1133	0,4909	0,0452	0,0387	0,7199	0,0665	0,0641
ycf3 exon2 exon3	0,7119	0,4110	0,4049	1,1257	0,0875	0,0871	0,6252	0,1601	0,1317	1,3018	0,2477	0,2281
ycf3 intron2 exon3	0,8227	0,0682	0,0663	1,0254	0,1549	0,1331	0,5388	0,0716	0,0600	0,7980	0,0255	0,0246
ycf3 exon1 exon2	0,8105	0,1191	0,0984	0,9740	0,0332	0,0319	0,3051	0,0214	0,0197	0,4320	0,0928	0,0792
ycf3 intron1 exon2	0,7546	0,1551	0,1121	0,8243	0,0430	0,0414	0,8365	0,1251	0,1115	1,2454	0,0219	0,0217
*clpP*exon2 exon3	1,2360	0,1877	0,1814	0,9199	0,0541	0,0538	0,8614	0,0213	0,0213	1,4173	0,0557	0,0555
clpP intron2 exon3	1,1008	0,0138	0,0134	1,0507	0,0665	0,0630	0,6604	0,0729	0,0687	0,9680	0,0071	0,0070
clpP exon1 exon2	1,1211	0,0418	0,0390	1,0157	0,0264	0,0251	1,5097	0,1494	0,1265	1,5724	0,0392	0,0382
clpP intron1 exon2	0,9329	0,2486	0,2082	1,2235	0,0471	0,0451	0,7408	0,1410	0,1040	0,8943	0,0374	0,0356
petB	0,7354	0,0124	0,0124	0,8373	0,0370	0,0360	0,8454	0,1073	0,0896	0,6555	0,0175	0,0168
*petB*intron exon2	0,7660	0,0105	0,0102	0,8150	0,0512	0,0466	0,6697	0,0772	0,0645	0,7140	0,0282	0,0265
petD	0,8294	0,1345	0,1283	1,1026	0,0545	0,0540	0,7577	0,2665	0,2040	0,5173	0,5348	0,4551
*petD*intron exon2	0,8139	0,0338	0,0336	0,8762	0,0337	0,0314	0,6058	0,0441	0,0409	0,7382	0,2002	0,1686
rpl16	1,1823	0,1165	0,1040	1,0234	0,0485	0,0461	0,6157	0,1307	0,0939	1,0680	0,1169	0,1142
*rpl16*intron exon2	1,1201	0,0310	0,0298	1,2543	0,0156	0,0153	0,6880	0,0975	0,0941	1,1508	0,0525	0,0493
rpl2	0,9288	0,0247	0,0239	1,0241	0,0413	0,0397	0,6247	0,0876	0,0703	0,9810	0,0506	0,0479
*rpl2*intron exon2	1,0776	0,0566	0,0528	1,0899	0,0432	0,0416	0,6906	0,0165	0,0161	1,1150	0,0110	0,0109
ndhB	0,8799	0,0182	0,0178	1,0432	0,0451	0,0442	0,3799	0,0247	0,0243	0,6170	0,0268	0,0253
*ndhB*intron exon2	1,1804	0,0164	0,0160	1,3764	0,0916	0,0890	0,8843	0,0206	0,0203	0,9513	0,0822	0,0791
rps12 exon2 exon3	1,0139	0,0638	0,0634	0,8713	0,0753	0,0714	0,7006	0,0787	0,0762	0,8590	0,1613	0,1354
rps12 intron2 exon3	0,8859	0,0427	0,0393	0,9551	0,0286	0,0279	0,6936	0,0151	0,0147	0,6768	0,0150	0,0146
rps12 exon1 exon2	1,5027	0,0754	0,0705	1,3563	0,0259	0,0257	0,8103	0,0433	0,0420	1,5826	0,0420	0,0404
rps12 intron1 exon2	0,8149	0,0828	0,0800	0,8280	0,0530	0,0493	0,4355	0,0229	0,0214	0,7407	0,0278	0,0260
ndhA	0,7367	0,0179	0,0174	0,7929	0,0179	0,0172	0,3948	0,0193	0,0191	0,4142	0,0132	0,0129
*ndhA*intron exon2	0,8606	0,0332	0,0321	0,9710	0,0411	0,0392	0,4344	0,0581	0,0556	0,5289	0,0135	0,0134