Supplemental Table S1. Primers and Probes		
Gene Name	Primer names	Sequences/coordinates
Primers used in both qPCR and qRT-PCR		
psbA*	psbA_qPCR_F1	GTGGCTGCTCACGGTTATTT
	psbA_qPCR_R1	CCAAGCAGCCAAGAAGAAGT
psbC*	psbC_F1	CCGACGGGTTTAGGTAAATATC
	psbC_R1	GAAGGTCCCAAAAACGCATA
rpoB	rpoB_F1	CCGTTATAGCCCAACGCGAGGG
	rpoB_R1	CCCGCGGAACCCGAGGTTTT
atpI*	atpI_F1	CCAACCCCAATCCTTTTACC
	atpI_R1	CGACTAATTCATCCGCCAAT
atpH*	atpH_F1	CAGAAGCAGAAGGTAAAATAAGAGG
	atpH_R1	TGCCACAACCAGTCCATAAA
atpF*	atpF_F1	CTGGGAGTTTCGGGCTTAAT
	atpF_R1	AACTCGCACACACTCCCTTT
atpA	atpA_F1	GCGAGGCTTACTTGGGTCGTGT
	atpA_R1	CTCGCTGACCGCGCCCTATG
rps14**	rps14_F1 (Bendich)	ATCTTGTTGCACCCGGTAAC
	rps14_R2	CCTACACGCCTTCATCGACGTT
psaA*	psaA_F1	GGAAAATGCAGTCGGATGTT
	psaA_R1	AGAAATCTCGAAGCCAACCA
ndhC	ndhC_F1	CGTCGAAACTCATTGCCCAAGGGT
	ndhC_R1	AGCCCCGGTTAGTGAAGGACCA
atpB*	atpB_F1	GGGTTGATGAGAGGAATGGA

	atpB_R1	CGTTAAAAATTCGTCCGAGA
rbcL	rbcL_F1	ACTCCTCAGCTCGGGGTTCCG
	rbcL_R1	TCCCCAGGAACGGGCTCGAT
psaI*	psaI_F1	CTTACCCTCTATTTTCGTACCTTTAG
	psaI_R1	TGCACATAAAGAAATAAGGAAGTCA
petA**	petA_F1	TGGTTAAAGGAACAGATGATTCG
	petA_R1	AATGGCAATTGGCACATACA
psaJ*	psaJ_F1	CACCCGTGCTAAGTACTCTATGG
	psaJ_R1	GGGAATGACAAAGCATCTGG
clpP*	clpP_F1	TCGTTGCGAGATCACAAATC
	clpP_R1	TGTCACCGTTTGCATCGTAT
psbB	psbB_F1	TGCGCGGCGTGCTCAATTAG
	psbB_R1	CGGAACAAGGTTCGAGCGCCA
psbH*	psbH_F1	TCGGAATATGGGAAAGTTGC
	psbH_R1	TATCGCGAATAAAGCCATTG
petB*	petB_F1	TAATGACGGAGGCCAACTTT
	petB_R1	CGCCTGTGACCCAAGTTAAT
petD*	petD_F1	GGGAGTTAACAAAGAAACCTGACT
	petD_R1	AATTATGTCCCATCCCTTTAGC
rpl16*	rpl16_F1	CCATCGACTATAACCCCAAAA
	rpl16_R1	CATATTTTTCCACCACGACG
psaC	psaC_F1	CTGCGGGTTGTTTCAGGCCCT
	psaC_R1	TTGTGTACGAGCTTGCCCAACA

ndhE*	ndhE_F1	GATCACAAGCCGAAACATGG
	ndHE_R1	AAAAATTGCGAAAATGTCTCC
ndhG*	ndhG_F1	ATTTGGGGGATTTGGTCTTC
	ndhG_R1	CGAAAAGGCAGAATAAATTGG
ndhI*	ndhI_F1	CAATTACATCGGAGCGTTTC
	ndhI_R1	GCATACGCGAACACATACTTC
ndhA*	ndhA_F1	TGGTCTTCTCATGGCAGGAT
	ndhA_R1	TTGCTAGTACACAAAAAGTTAATGGT
HMG 1/2	zmHMG_F4	GAGGTGTAGAGGATAAGGAGCGATA
	zmHMG_R4	TGACAGCAGCATATCATCTTGGCT
Primers used specifically for qPCR (includes sequence in both exons and introns)		
psbC**	psbC_F1	CTACCACGTGGAAACGCTCT
	psbC_R1	ATACGATTAATCCGGCATGG
atpF	atpF_F2	AGCGGGAGAGCCAAATGAATCGA
	atpF_R2	AGGGTCCCTTTACGCAATTCTTCCG
ycf3-int2	ycf3-int2_F2	TCCTGGAGTAAGCGCTATAGCTTGT
	ycf3-int2-R2	AGCAATTTCTGAGCCGTATGAGGT
petD	petD_F2	TGTCCGGTTCCTTTGGGGGATGG
	petD_R2	AAAGATCGTTGGGCCACGCGG
rps12-int1	rps12-int1_F2	TGGATTTGCACCAAAGGAAACCA
	rps12-int1_R2	GCCGCGCTTAAGGGATGTCC
rpl2	rpl2_F2	TCAATGGGAAATGCCCTACCTTTG

	rpl2_R2	TGAACTCAATCACTTGCTGCCGT
ndhA	ndhA_F2	AGGCTGACGCCAAAGATTCCATCC
	ndhA_R2	AGAGGAGCCGTATGAAGCTAAGGTT
psbC***	psbC-F	TAATGTAGGGTCTGCCCAAGG
	psbC-R	TTCTAACCACGGAGCACGAAG
ndhA***	ndhA-F	GATAACATCACAGTTCCCACCG
	ndhA-R	GATACCGAAACGAAACAATCCT
cox2** (mitochondria)	cox2_F2	ACAGCAGTGGCATACAACTTTGG
	cox2_R2	AAGGAGGAGCAGGAACAACAGG
ccmfc** (mitochondria)	ccmfc_F2	TCAGCGAAGCGTGAGCGG
	ccmfc_R2	AACAAGCACCACTCGACGAGG
nad4** (mitochondria)	nad4_F2	GCAAAAGTCCTTCCACGGCA
	nad4_R1	AGCAAGCGTAGGCAACCAAAC
atp6 (mitochondria)***	atp6-F	TGCTACTCACTCTCGGTTTGG
	atp6-R	CGGCACGAAATCATAAATAAGC
rps12 (mitochondria)***	rps12-F	ATTATGACCTTCGCCTGGAATG
	rps12-R	GGAGTATGCCTGCGTGTTTC
18S***	18S-F	CAACCATAAACGATGCCGAC
	18S-R	TTTCAGCCTTGCGACCATAC
Primers used only in qRT-PCR		
psaB	psaB_F1	GGACCCCACTACTCGTCGTA
	psaB_R1	ATCCGGACGTCCATAGAAAGA

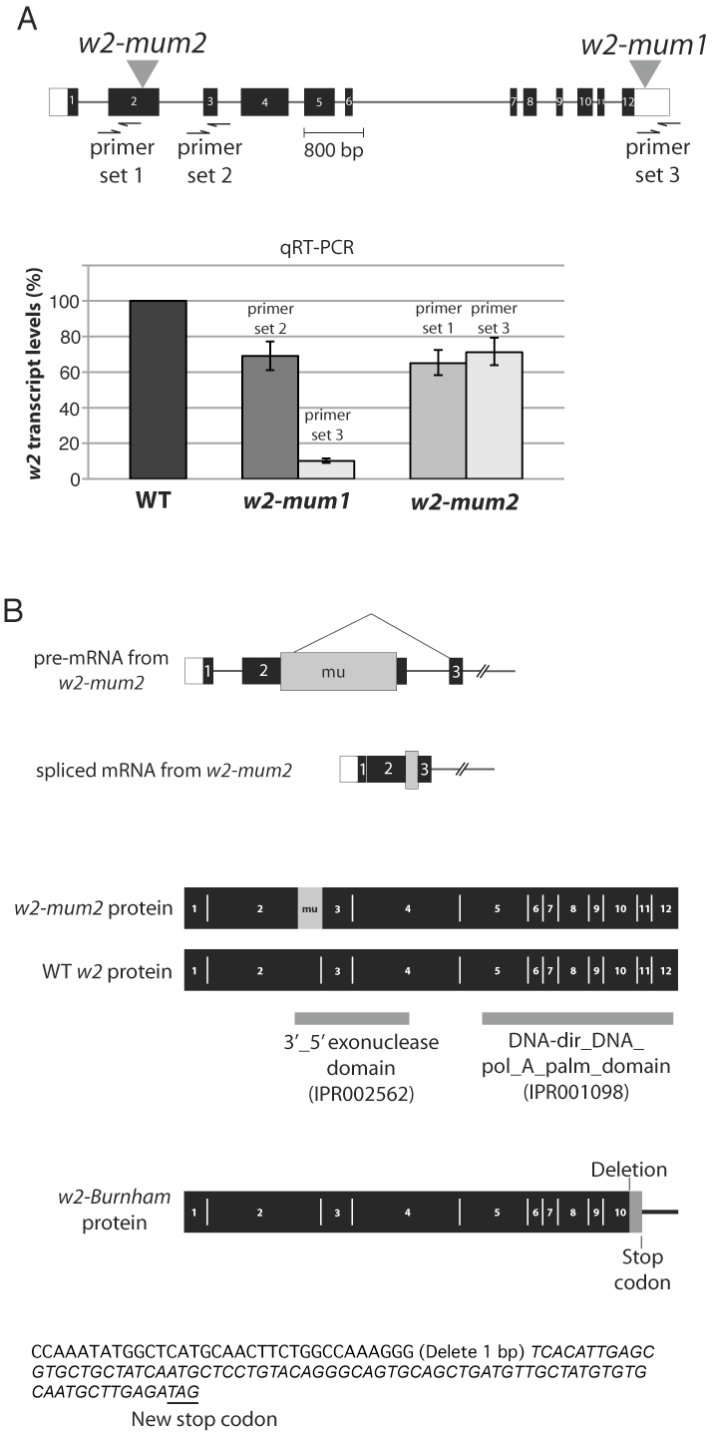
psbE	psbE_F1 psbE_R1	CTATTCATTGCGGGTTGGTT GAATTCCTTGTCGGCTTTCC
rpoA	rpoA_F1 rpoA_R1	CCACCCCTTTTAACCTTTCA TTGGCCCTTTTGAGACAATTA
Primers used for *w2* transcript qRT-PCR		
Primer set 1	DU_Pol_F2 DU_Pol_R2	GTCCTTGGAATTCAAGACAACCG ACCATTACTATTGCCGGCTTTGCT
Primer set 2	DU_Pol_F3 DU_Pol_R3	TCATGCATGTGACACAGAGGTAGC TCCACCCAAATGCATGTCTTGCCA
Primer set 3	DU_Pol_F5 DU_Pol_R5	GCTGATGTGTTGAGTTGCTGACCA AAGACGCACAGTTCAACAGCAGA
Primers used for analysis of *w2-mum2* mis-splicing		
	DU_Pol_F2 DNA_Pol_exon_R1	GTCCTTGGAATTCAAGACAACCG GCCTCAGCACCTTTAGTGCCAGA
Primers for genotyping *w2-mum1*		
Amplifies WT allele	tk8051_5' tk8579_3'	GGCCTTCAGAGTCTGCGGAG AACATTGTTGCAGTGCGTGC
Amplifies mutant allele	tk8051_5' Eomumix	GGCCTTCAGAGTCTGCGGAG CCCTAAGCTGCTTTACCTCCG GCCTAAGCTGCTTTATCTCCG (mix of two *Mu* specific primers)
Primers for genotyping w2-mum2		
Amplifies WT allele	tk1507pol15'	GCTGACGAGAGCAGGAGGTT

Amplifies WT allele	tk1507pol15' tk2203pol13'	GCTGACGAGAGCAGGAGGTT CATTAGATTTAGGTAACAAGCCATGACCGA (use this set to check for WT product)
Amplifies mutant allele	tk1507pol15' Eomumix	GCTGACGAGAGCAGGAGGTT CCCTAAGCTGCTTTACCTCCG GCCTAAGCTGCTTTATCTCCG (mix of two *Mu* specific primers)
Coordinates for probes used in RNA and DNA gel blot hybridizations		
rps12 intron 1		68,793 – 69,302
ycf3 intron 2		44,383 – 45,116
psbA		295 – 1,074
atpA		36,690 – 37,679
psaB		40,716 – 41,052
psaJ		66,399 – 66,673
petB		73,971 – 74,538
rpoB		23,258 – 24,475
trnT-UGU		48,065 - 48,215
trnG-UCC		13,248 – 14,013
trnV-UAC		53,796 – 53,836
rrn23		99,065 – 99,688
mt-rps4		19,631 - 21,050 (mitochondrial genome)
Primers used to		CCAATAGCGTATATTTAAGTTGTTGC

*Sharpe RM, Dunn SN, Cahoon AB: **A plastome primer set for comprehensive quantitative real time RT-PCR analysis of *Zea mays*: a starter primer set for other *Poaceae* species.** *Plant Methods* 2008, **4**:14.

** Kumar RA, Bendich AJ: **Distinguishing authentic mitochondrial and plastid DNAs from similar DNA sequences in the nucleus using the polymerase chain reaction**. *Current Genetics* 2011, **57**: 287-95.

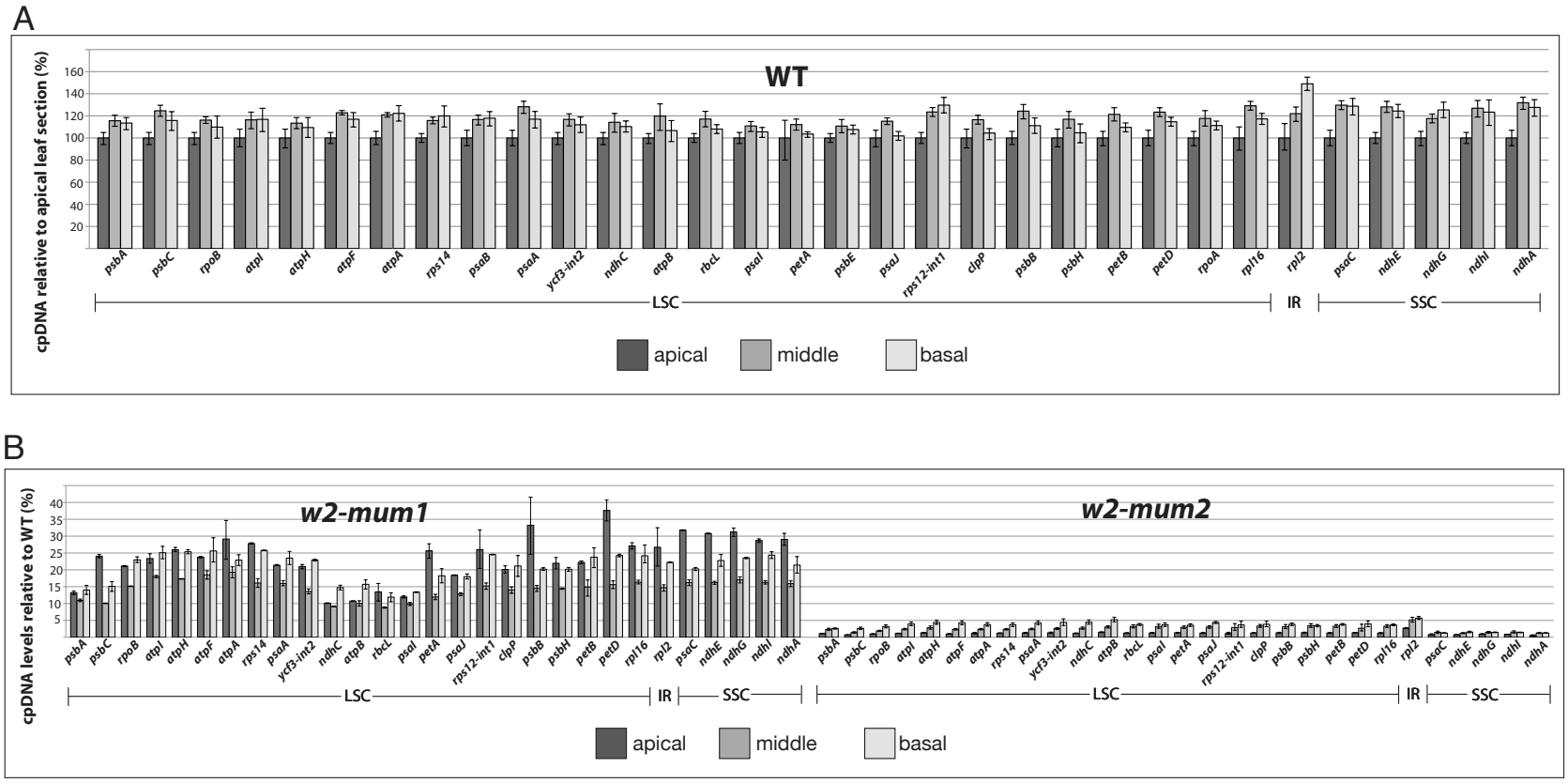
*** Primers used in supplemental Figure S3



Supplemental Figure S1. Effects of *w2* mutations on *w2* gene expression. (A) qRT-PCR was performed with the primer sets diagramed above. (B) Aberrant proteins produced by the *w2-mum2* and *w2*-Burnham alleles. RT-PCR followed by DNA sequencing revealed the diagrammed mis-splicing event for *w2-mum2*: the RNA lacks 52 codons from exon 2, and these are replaced by 47 codons from the *Mu* terminal inverted repeat. This insertion/deletion map to the conserved 3'-->5' exonuclease domain of DNA polymerase I. End-point PCR and RT-PCR of *w2*-Burnham material detected a 1-bp deletion in exon 10. The gray box represents amino acids that are translated out of frame. The sequence context of the deletion is shown below; the italicized nucleotides are translated out of frame until termination at an in-frame stop codon.

Supplemental Figure S2. Additional qPCR assays of plastid DNA content in wild-type and *w2* basal, middle, and apical leaf sections. Genes are listed according to their order in the plastid genome. LSC- large single copy region; IR- inverted repeat; SSC- small single copy region.
(A) Ratio of plastid-to-nuclear DNA copy number in wild-type (WT) leaf sections. Values are plotted relative to the ratio in the apical leaf section.
(B) Ratio of plastid-to-nuclear DNA copy number in *w2* mutants. Values are expressed as a percent of the ratio in the corresponding wild-type tissue.

Supplementary Figure S2



Supplemental Figure S3. qPCR survey of chloroplast and mitochondrial DNA levels in independently-arising albino mutants in the PML mutant collection. The chloroplast *psbC* and *ndhA* genes and the mitochondrial *rps12* and *atp6* genes were assayed by qPCR, and normalized to the nuclear 18S rRNA gene. The cpDNA and mtDNA values indicated are the mean of the results obtained with the respective amplicons. Results for the *w2*-Burnham allele are marked. The causal nuclear mutations in most of these mutants are not known. The mutants were ordered according to their content of plastid DNA.