SUPPLEMENTAL MATERIAL.

Supplemental Figure Legends.

Supplemental Figure 1. Map of the *RAA1* locus.

A: Cloning of the *RAA1* locus. Phage λ P23 contains a DNA fragment from the *raa1-314B* mutant, with part of the *ARG* marker used for insertional mutagenesis. Cosmid #2 was isolated from a wild-type genomic library, using a fragment of λ P23 as probe.

B: Restriction map of the *RAA1* locus. Open bars represent the 18 exons of *Raa1*. The ATG start codon and the STOP codon are indicated.

C: The *Raa1* cDNA. The cDNA is depicted with an open bar, as deduced from the overlapping cDNA clones (thin lines). The five black triangles represent the 38 amino-acid repeats (see figure 4).

D: The midigene construct (mWT) contains a genomic fragment fused, at the Sal I site in exon 6, to the cDNA for the 3' part of the gene. The construct is tagged with three copies of the HA epitope (HA3).

Supplemental Figure 2. The *raa1-314B* and *L137H* mutants are allelic.

A. To test whether *raa1-314B* and *L137H* are allelic, vegetative diploids were constructed and analyzed for genetic complementation. A deletion mutant for another factor also involved in *psaA* trans-splicing (*raa2-A18*) was used as a positive control. The two pairs of parental strains were used to generate diploids by PEG-mediated fusion as depicted by the brackets and arrows. The relevant genetic markers are indicated in parenthesis: $Paro^R$ (insertion of the *aphVIII* cassette conferring resistance to paromomycin); Spc^R (chloroplast mutation conferring resistance to spectinomycin); pARG7.8 (insertion of the *Arg7* gene used for insertional mutagenesis); *raa2Δ* (partial deletion in *raa2-A18*); *RAA1*, *RAA2* (wild-type alleles).

B. PCR genotyping of the parental strains and of two selected diploids from each fusion. The primers for *Raa2* amplification are within the region that is deleted in *raa2-A18*.

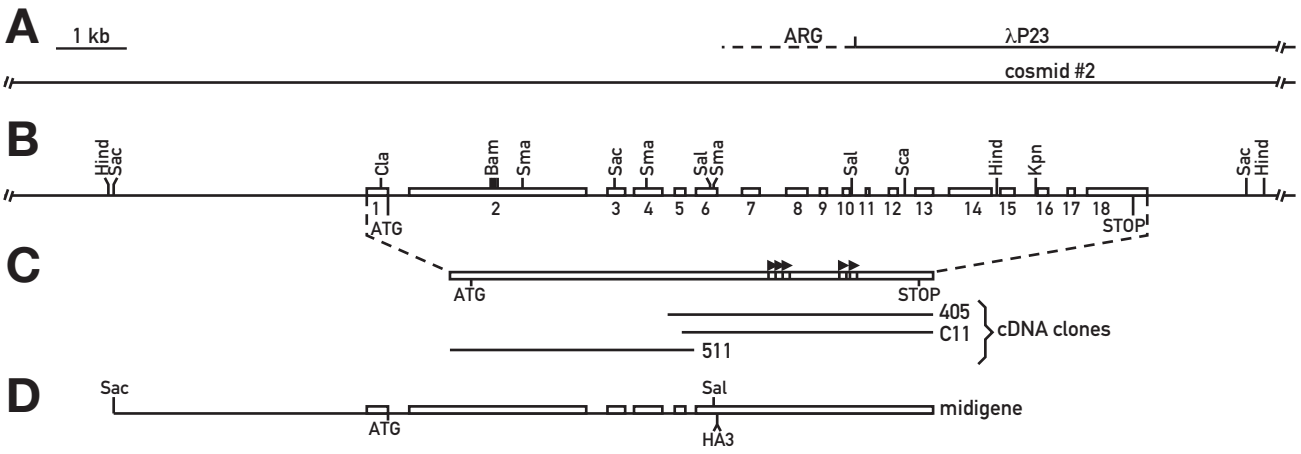
C. Immunoblot analysis with anti-PsaA serum of total protein extracts from the diploids and the parental strains (upper panels). Anti-Rubisco serum was used as a control (ss Rubisco, lower panels). The control diploids, *raa2-A18* / *raa1-314B* (strains 3 and 8), were phototrophic (not shown) and had wild-type amounts of PsaA, showing complementation of *Raa1* and *Raa2*. In contrast, the *raa1-314B* / *L137H* diploids (strains 1 and 2) were not phototrophic and did not accumulate detectable levels of PsaA, showing lack of complementation.

Supplemental Table I.

Oligonucleotides used in this work (5'→3').

cDNA library:	
i2	AAACCCGCCGCCTGCTTGAA
m3	CCTTGCGGCGCGACCAA
Deletion constructs:	
Paro Bgl 5'	CGAAGATCTAATGTGAGTTAGCTCACTC
Paro 3'	TATGACCATGATTACGCCAAG
Paro Kpn 5'	GCGGTACCGATAATGTGAGTTAGCTCACTC
Paro Mlu 5'	ACGCGTAATGTGAGTTAGCTCACTC
Paro Mlu 3'	ACGCGTATGACCATGATTACGCCAAG
Complementation :	
Paro2-5'	GTCCGTTCGATCGCAGTCTCG
Paro2-3'	CGCTCCAGCTCGGCGAGAAG
pBRBam2	GTTCTCGGAGCACTGTCCGAC
ArgSau2	GGACGGGTGTGACAGAGTTAC
A18/rbcS	GGACGCGGGCAGGGG
A18/Nci1	TCACCGTTGGCACTACCAGCG
RT-PCR:	
AUG 2	GTGCACTCTCCGCATCACCATC
middle 4	TCCGTCGTTGCCTGCCGCATG
AUG 5'-1	CGATTCGGGGCTCAGATGAGG
AUG 3'-1	CACTGCGTCCCTCCAAACCG
m5'-3	CCTCATGCCGCTGATGACGGG
m3'-3	CTCGTTGCGAGCGCCATGAGC
STOP5'-6	GTGCTGCTGTATTGCGCAGTAG
STOP3'-6	CGCCCAGCACCAGGCCAATG
UP	GACGTCATCCACTGCCTGTG
DOWN	CGACGCATCCTCAACACACC
Arg7ex11	CCGACATGCTCGCCACGGACTT

Supplementary Figure 1



Supplementary Figure 2