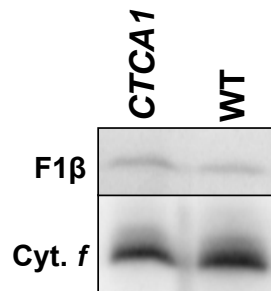


**Supplemental Figure 1.** Characterization of the *mca1-6* and *mH* strains.

A: MCA1-HA and cytochrome *f* accumulation assessed by immunoblots in the *mH* strain, compared to the wild-type control strain. The OEE2 from PSII was used as a loading control.

B: *petA* mRNA accumulation in the wild type, in the mutant strain *mca1-6* and in its complemented derivative *mH*. The *psbB* transcript serves as a loading control.



**Supplemental Figure 2.** Accumulation of cytochrome *f*, detected by immunoblot in the wild type and in the *CTCA1* strain (the *tca1-8* mutant complemented with the C-terminal domain of TCA1). F1 $\beta$  provides a loading control.

Supplemental Table 1: Oligonucleotides used in this study

Name	Oligonucleotide sequence 5' to 3' <sup>1</sup>
<i>petACod1</i>	TTTATAAAGATCTTCCATGCATGAACTATG
<i>petA<sub>Stop</sub>Rev</i>	<u>CAATTGGTTAG</u> <b>CTA</b> AATTTTATTAATCTTAAAACGAAACT AGAATAAA
<i>petA<sub>Stop</sub>Cod</i>	ATTAATAAAATT <b>TAG</b> TCTAAC <u>CAATTG</u> TTTACTACTTTACG CGCAGCAACA
<i>petARev2</i>	ACCTGGAAGCTGGACCAACAAC
Test_ <i>petA</i> _For	CCTGCTCGTATTCAAGGTTTATTAG
Test_ <i>petA</i> _Rev	AAATTAATTGGCAGCTAAATTGCCAAC
<i>TCA1_EcoRI_814_dir</i>	CGC <u>GAAATTC</u> ATGGCGCCCGCCTCCAACCTGCAC
<i>TCA1_1212_rev</i>	TGCAGCCTGCTGCTGCTGCTGGGTTCGG
<i>TCA1_EcoRV_dir</i>	GGAAGCT <u>GATATCA</u> AAAAATGCTGCTGTCGCTGCAAAATGG
<i>MCA1_EcoRI_dir</i>	CGC <u>GAAATTC</u> CCTATCACTGCAAGGCCGCCTATTC
<i>MCA1_AscI_SalI_rev</i>	GCGG <u>TGCACAGCGC</u> ATTCGGAGATGAGGAC <u>GGCGCGCC</u>
<i>MBB1_dir_EcoRI-1</i>	CC <u>GAAATTC</u> ATGAGCTTGGTGCCCTTCTC
<i>MBB1_rev_410</i>	CTTACGCTCATTC AAGTCAA
MCA1cod3	GTCTCTGGCTTCAGCGCTGGTGCT
MCA1rev3	GAACTGAATTCCCAACACGGGGAAG

<sup>1</sup> restriction sites, underlined in the sequences of the oligonucleotides, were used for the construction of plasmids and/or RFLP analysis of transformed strains. Nucleotides indicated in bold differ from the wild type gene sequence. The Stop codon, replacing the initiation codon, is boxed.