Fig. 1 Suppl. The schematic diagram of genomic structure of the *COR15B* gene. The *black filled boxes and line* indicate exons and an intron, respectively. The *grey filled boxes* indicate the untranslated regions (UTR) of the *COR15B* gene. The *dashed lines* indicate the flanking regions of the *COR15B* gene. The position of T-DNA insertion is indicated by the triangle.

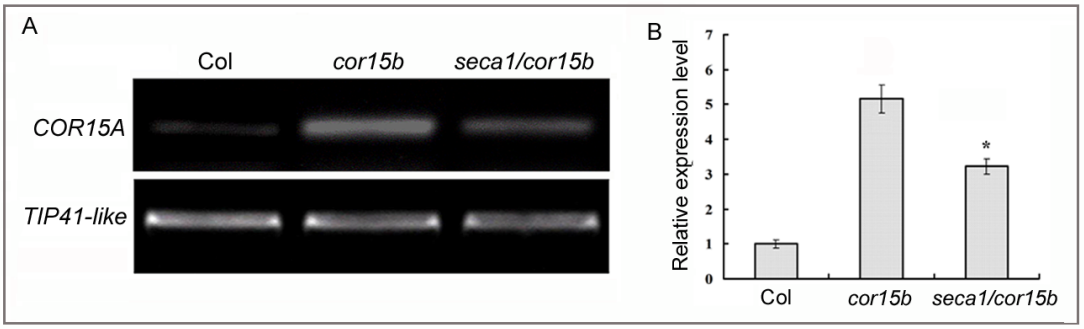

Fig. 2 Suppl. Expressional reprogramming between *COR15* homologous genes requires functional chloroplasts. *A* – The semi-quantitative RT-PCR analysis of *COR15A* transcripts in the Col, *cor15b* single and *seca1/cor15b* double mutants. The *TIP41-like* gene was used as internal control. The typical results from three independent experiments. *B* – The real-time quantitative PCR analysis of *COR15A* transcripts in the Col, *cor15b* single and *seca1/cor15b* double mutants. There were three biological replicates with at least three technical repeats. The *asterisks* above the bars indicate significant differences ($P \leq 0.05$) between *cor15b* and *seca1/cor15b*, as determined by the Student's *t*-test.

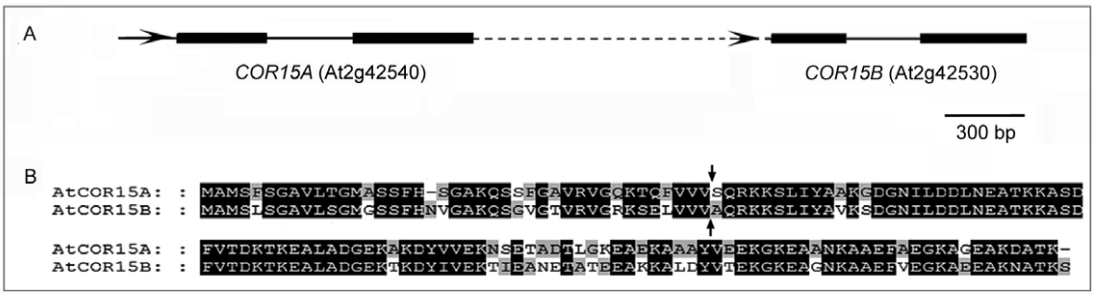

Fig. 3 Suppl. The sequence analysis of *COR15A/B* genes. *A* – The genes *COR15A* and *COR15B* are aligned in tandem on the second chromosome. Exons and introns are indicated by the *black filled boxes* and *lines*, respectively. Transcription orientations are indicated by the *arrows*. *B* - An alignment of amino acid sequences of COR15A and COR15B. The *downward and upward arrows* indicate the putative cleavage site of the chloroplast transit peptide of COR15A and COR15B, respectively. Sequences were aligned by the *ClustalW2* software and displayed by the *GenDoc* program.

Table 1. The list of primers used in this study.

Gene	Primer Sequence (5′-3′)	Purpose
LBb1.3	ATTTTGCCGATTTCGGAAC	Identifying *cor15b* mutant
COR15B-DF	CGTGACTTTAGAAGGGAAGGG	
COR15B-DR	CGTAGGAGCAAAGCAGAGTGG	
COR15A-F	GCCAGAAAACTCAGTTCGTCG	Semi-quantitative and real-time quantitative PCR of the *COR15A* gene
COR15A-R	ATACGCCGCAGCTTTCTCAGC	
COR15B-F	CGTAGGAGCAAAGCAGAGTGG	Semi-quantitative and real-time quantitative PCR of the *COR15B* gene
COR15B-R	CTCAGTCGCAGTTTCATTGGC	
TIP41-like-F	GAAATTCAGGAGCAAGCCGTCTCAG	Semi-quantitative PCR of the *TIP41-like* gene
TIP41-like-R	ATCAACTCTCAGCCAAAATCGCAAG	
LHCB1-F	GGTTTGTGTTTGTGGTGGATGGTA	Semi-quantitative PCR of the *LHCB1* gene
LHCB1-R	GTGAACCCAAGAACTGAAAATCCA	
RBCS-F	GGTCGCTCCTTTCAACGGACTT	Semi-quantitative PCR of the *RBCS* gene
RBCS-R	ATTCGGAATCGGTAAGGTCAGG	
rTIP41-like-F	GTATGAAGATGAACTGGCTGACAAT	Real-time quantitative PCR of the *TIP41-like* gene
rTIP41-like-R	ATCAACTCTCAGCCAAAATCGCAAG	
OEcor15b-F	CATGCCATGGCGATGTCTTTATCAGGAGCT	The amplification of the *COR15B* coding region for cloning into pCAMBIA1301
OEcor15b-R	GGGTAACCTCAGGACTTTGTGGCATTAGCC	