

1 **Supplement**

2 **TABLE S1** Plasmids used in this work.

Plasmid	Characteristics	Reference
pDrive	Cloning vector	Qiagen, Germany
13K19	pBeloBAC11 with DNA of chromosome 17 including Cre17.g698750	CUGI, Clemson University, USA (1)
31O13	pBeloBAC11 with DNA of chromosome 10 including <i>RAA8</i> (Cre10.g440000)	CUGI, Clemson University, USA (1)
31O13-1	Ligation of 36 kb derived from 31O13: <i>Sgsl</i>	This work
31O13-2	Ligation of 48 kb derived from 31O13: <i>Sgsl</i>	This work
31O13-3	Ligation of 34 kb derived from 31O13: <i>BlnI</i>	This work
31O13-4	Ligation of 36 kb derived from 31O13: <i>BlnI</i>	This work
31O13-5	Ligation of 31O13: <i>SfuI</i> , <i>Clal</i>	This work
31O13-6	Subcloned DNA of <i>RAA8</i> , Cre10.g440050	This work
31O13-7	Subcloned DNA of <i>RAA8</i>	This work
pDrive_PCR250B	0.70 kb DNA of <i>RAA8</i> in pDrive	This work
pDrive_PCR252A	1.45 kb DNA of <i>RAA8</i> in pDrive	This work
pDrive_PCR253	0.80 kb DNA of <i>RAA8</i> in pDrive	This work
pDrive_PCR256B	1.28 kb DNA of <i>RAA8</i> in pDrive	This work
pIG637.1	0.9 kb <i>BglII</i> / <i>NsiI</i> fragment for <i>tscA</i> probes	(2, 3)

	in Northern analyses	
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5 **TABLE S2** Oligonucleotides used in PCR, RT-PCR or hybridization experiments.

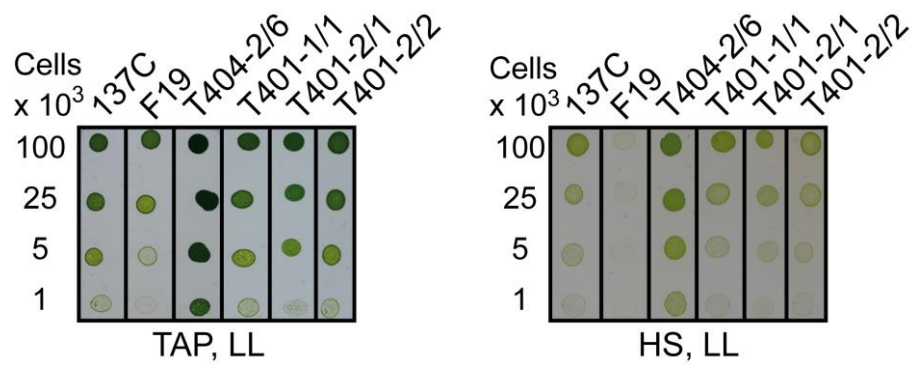
Oligonucleotide	Sequence (5' → 3')	Application, reference
Cloning and sequencing of <i>RAA8</i>		
for_IP2_Ex2-2	CAGTTGGTGCGGGTGTTGG	Specific for <i>RAA8</i> , this work
rev_IP2_Ex3	CTCAATGGCAGCGAGACCT	Specific for <i>RAA8</i> , this work
rev_raa8-F1-2	GCCCTTCCTGTACATAACC	Specific for <i>RAA8</i> , this work
for-2-IP2_Ex3	GCTGGCGGCGCTGTCACAC	Specific for <i>RAA8</i> , this work
rev_IP2_Ex4	TCGGGCTGGTAGCCCAGAC	Specific for <i>RAA8</i> , this work
for_raa8_F1	CTGGCATGCTCAGGGTCGC	Specific for <i>RAA8</i> , this work
rev_raa8_F1.1	AGCCGTCTGTGAAGGTTTG	Specific for <i>RAA8</i> , this work
for_raa8-F2-7	GACACACCGCAGGAGTTG	Specific for <i>RAA8</i> , this work
raa8_F3-for	TAGCATGGAGTGGCTACAG	Specific for <i>RAA8</i> , this work
rev_raa8-F2-4	TGCGGACCTCGCACTGAAG	Specific for <i>RAA8</i> , this work
for-raa8-F6-3	GGGCTACCAGCCCGAGGAC	Specific for <i>RAA8</i> , this work
for-raa8-Ex2-3	CGGCTGCTTACAAACCTTC	Specific for <i>RAA8</i> , this work
for_Raa8_Mutati on	TTGGCGGCGGCAGGTGTAG	Specific for <i>RAA8</i> , this work
rev_Raa8_Mutati on	TTTGCGCTTTCGCATGGG	Specific for <i>RAA8</i> , this work
rev-raa8-F6-4	ACTTCTTGCTTGCGCATCC	Specific for <i>RAA8</i> , this work
raa8-F2-for	GCAGGCGGTTATGTACAGG	Specific for <i>RAA8</i> , this work
rev-raa8-F2-4	TGCGGACCTCGCACTGAAG	Specific for <i>RAA8</i> , this work
for-raa8-F2-5	GGCGCTGCTTCAGTGCGAG	Specific for <i>RAA8</i> , this work

rev-raa8-F2-6	AACTCCTGCGGTGTGTCC	Specific for <i>RAA8</i> , this work
for-raa8-F6-4	GATGCGCAAGCAAGAAGTG	Specific for <i>RAA8</i> , this work
rev_ raa8-F5-2	GTTGTGCATCGCTATCTC	Specific for <i>RAA8</i> , this work
for-raa8-F2-3	GAGATAGCGATGCACAAC	Specific for <i>RAA8</i> , this work
rev-raa8-F6-2	GTCCACACGCCGGGCCTTG	Specific for <i>RAA8</i> , this work
for-raa8-F6	TGCCGTGCAGGCATGCAG	Specific for <i>RAA8</i> , this work
rev-raa8-F6-3	TGACACGCCAACATGCTC	Specific for <i>RAA8</i> , this work
for-raa8-F6-2	CAAGGCCCGGCGTGTGGAC	Specific for <i>RAA8</i> , this work
rev_IP2_Ex7	GGTCTGCCTGCTGCTCCTC	Specific for <i>RAA8</i> , this work
for-raa8-F7	AGCATGTTGGCGTGTGTCAG	Specific for <i>RAA8</i> , this work
rev_IP2-Ex8	CTGCAGCGCCAGCACCCAG	Specific for <i>RAA8</i> , this work
rev-raa8-F8	CGTGTGGTTGTGCATGTG	Specific for <i>RAA8</i> , this work
for-raa8-F9	ACGAACTCGCACACGTTG	Specific for <i>RAA8</i> , this work
rev_IP2_Ex9	ACGGAGGCACCAGCTTGTC	Specific for <i>RAA8</i> , this work
RT-PCR analyses		
for_psaAEx1	AGTACTCCAGAGCGCGAAG C	RT-PCR of <i>psaA</i> (4)
for_psaAEx2	TTGGAACCTTCACGCAGAT G	RT-PCR of <i>psaA</i> (4)
Oligo 19	TTGGTTAAGTGACCCTACTC A	RT-PCR of <i>psaA</i> (4)
Oligo 50	GTATTCAGTGCACACTTTGG TCAATTAGG	RT-PCR of <i>psaA</i> (4)

Oligo 53	AAAAGTAAAGATTGCGGTTG AT	RT-PCR of <i>psaA</i> , Northern analysis (4)
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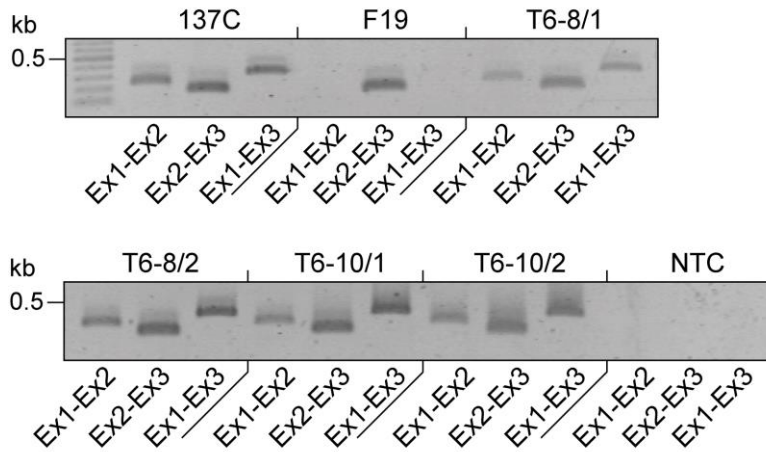
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9 **FIG S1 Functional complementation of *trans*-splicing mutant F19.** Test for

10 photoautotrophic growth of wild type 137C, *trans*-splicing mutant F19, and selected

11 transformants. Cells were spread onto acetate containing (TAP) or acetate lacking (HS)

12 agar plates at cell densities as indicated and incubated under low light (LL).



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14 **FIG S2 Molecular characterization of F19 and complemented strains.** PCR analysis

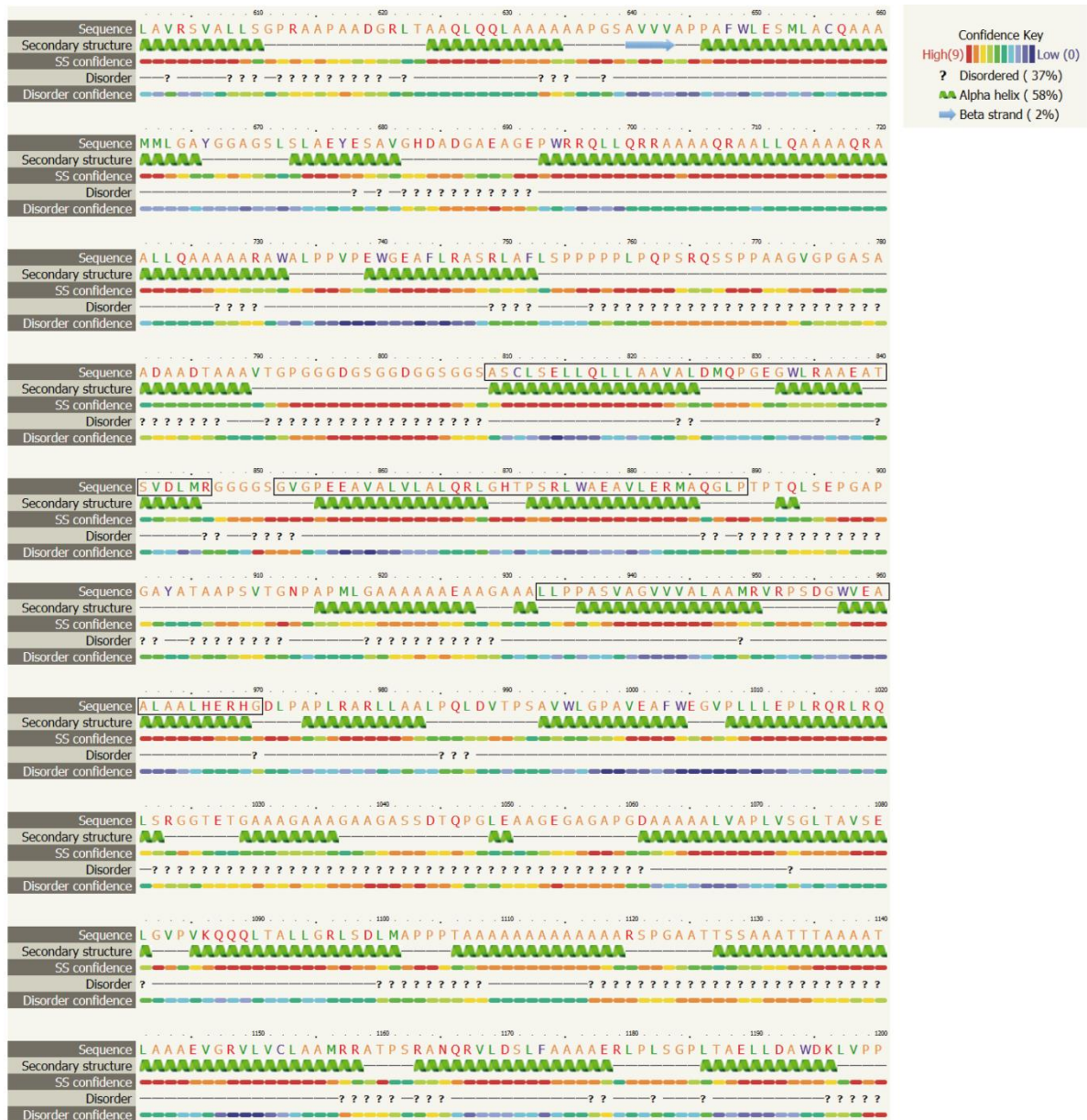
15 using cDNA of 137C, F19, two transformants derived from transformation with 31O13-6

16 (T6-8/1, -8/2), and two transformants of 31O13-7 (T6-10/1, -10/2). Different primer

17 combinations were used to amplify *psaA* exon 1 - exon 2, exon 2 - exon 3, and exon 1 -

18 exon 3.

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 23 **FIG S3 Secondary structure prediction of a partial Raa8 sequence (from A1,546 to**
 24 **P2,745).** Prediction of α -helices (green), β -strands (blue arrows), and coil regions (faint
 25 lines) by the program Phyre² (5). Scale of confidence key is given in highest (9, red) to
 26 lowest (0, blue). Predicted OPR repeats are marked as black boxes. Residues were
 27 coloured according to a property based scheme (A,S,T,G,P small/polar; M,I,L,V
 28 hydrophobic; K,R,E,N,D,H,Q charged; W,Y,F,C aromatic/cysteine). Question marks
 29 indicate the prediction of disordered regions.

30 Supplemental references

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- 34 2. **Herdenberger F, Holländer V, Kück U.** 1994. Correct *in vivo* RNA splicing of a
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