

**Table S1 Primers used for plasmids construction**

Primers	Sequences (5'-3')
CrtE-F	GGGAACAAAAGCTGGGTACCTGCACCTATAGGAAAGAGGAGGAAAACCTAAATGGAC GTGACCAATCGGATCGAGCG
CrtE-R	TTTAAGCTTTCAGTGGTGGTGGTGGTGGTGGGCCGCAGTCGCGGCCAGTTT ACCACCACCACCACCCTGAAAGCTTACTGTTCGAAACGTTAGGAGGGATCTATGAGTC
CrtB-F:	TGCAATCCGATATGTTGG
CrtB-R	GAACTAGTGGATCCCCGGGCTGCAGCTACACCCGGCTGCGTT
CrtI-F:	GGGAACAAAAGCTGGGTACCCCTTACTGGAGGTATTTATATGCTCGATCCTGGCCCC
CrtI-R:	GCGGTGGCGGCCGCTCTAGAACTAGTTCATGATGTCACCAGACTGTCTG
CrtI-1-R:	TACCGTCGACCTCGAGTCAGTGGTGGTGGTGGTGGTGTGATGTCACCAGACTGTCTGGC GGGAACAAAAGCTGGGTACCAAGTTAAAGGGGGTTTTTCATGTGACCGAATTTAGTAAA
Dxs-3-F	ACACCGCTTCT
Dxs-3-R	TACCGTCGACCTCGAGTCAGTGGTGGTGGTGGTGGTGGGCCAGCTTCGAGGTCTCG GGGAACAAAAGCTGGGTACCTACGAAACCAGGAGGTTTCATATGACGGCGGACAACAA CT
IDisc-3-F	TACCGTCGACCTCGAGTCAGTGGTGGTGGTGGTGGTGGTGCAGCATGCGGTGGATCTGG ACCACTGACTCGAGCAATCAAAAAGGAGGATATCGTGACCGAATTTAGTAAAACACCG C
IDisc-3-R	GGAATTCGATATCAAGCTTTCAGTGGTGGTGGTGGTGGTGGTGGGCCAGCTTCGAGGTCTCG ACCACTGACTCGAGCACACAAAGGAAGGTATTTTATGACGGCGGACAACA ACT
Dxs-1-F	ATTCGATATCAAGCTTTCAGTGGTGGTGGTGGTGGTGGTGCAGCATGCGGTGGATCTGG CACCCTGAAAGCTTCAATCAAAAAGGAGGATATCGTGACCGAATTTAGTAAAACACC G
Dxs-1-R	CCCCGGGCTGCAGGAATTCTCAGTGGTGGTGGTGGTGGTGGTGGGCCAGCTTCGAGGTCTCG GTGGATCCCCCGGGCTGCAGTTAGTTTCGATAAGAGCGAACGG
IDisc-1-F	TACCGGGCCCCCTCGAGAAGGAGATATACCATGGAGGAGG
IDisc-1-R	CTAGTGGATCCCCGGGTTATAGCATTCTATGAATTTGCCTGTC GAACTAACTGCAGCCCGGAAGAGGTATATATTAATGTATCGATTAAATAAGGAGG
DXS-2-F	AATTCGATATCAAGCTTAAAGGAGCGCCACCATGGTGAGCAAG
Dxs-2-R	TGGAAAGCGGGCAGTGATTACTTGTACAGCTCGTCCATGCC
pBBR-upperMVA-F	TCACTGCCCCTTTCCAGT
pBBR-upperMVA-R	AAGCTTGATATCGAATTCCTGCAGC
pBBR-wholeMVA-F	CTCACTATAGGGCGAATTGGAGC
pBBR-wholeMVA-R	TCGTATTACGCGCTCA
EGFP-F	TGAGCGCGCGTAATACGAACCGTCTCCCCCTTTGAACGA
EGFP-R	ATTCGCCCTATAGTGAGGATGACTCCCCACAACGCAG
pBBR-vector-F	TGAGCGCGCGTAATACGAATATCTCGGCGCCACAC
pBBR-vector-R	CAATTCGCCCTATAGTGAGCCAATTTCTCCTCGCTGCAG
Vector-F	TGAGCGCGCGTAATACGATGTCGCCGGATGGAGGC
Vector-R	CAATTCGCCCTATAGTGAGGTCGTCCTCCTTGAAAGC
Primer-PcbbF-F	TGAGCGCGCGTAATACGACCGCGACGCAGGTCGGCA
Primer-PcbbF-R	CAATTCGCCCTATAGTGAGCCGTTTTCTCACTCCGGCTCAGCT
Primer-PcbbG-F	TGAGCGCGCGTAATACGAGGGTGTCTCCAGGCGTG
Primer-PcbbG-R	
Primer-PcbbL-F	
Primer-PcbbL-R	
Primer-PcrtD-F	
Primer-PcrtD-R	
Primer-PcrtE-F	

---

Primer-PcrtE-R	CAATTCGCCCTATAGTGAGGGCCACACTCCCGCGCTTC
Primer-Ptrc-F	GAGCGCGCGTAATACGAGCGCCGACATCATAACGGTT
Primer-Ptrc-R	CAATTCGCCCTATAGTGAGATTCCGGTCGAGTGCCCA
Primer-PnifH-F	GCGCGCGTAATACGATTCTCCCAACCTCAATGATCATCATG
Primer-PnifH-R	CAATTCGCCCTATAGTGAGCTCTCCGTTGACCTAATGCCG
Primer-PpckA-F	TGAGCGCGCGTAATACGAGATCTGACCGGCGCAGAG
Primer-PpckA-R	CAATTCGCCCTATAGTGAGGAATAGATCCTCCTCGAATCCGCG
WholeMVA-PCR-F	CCTGTCGTGCCAGCTGCATTAATG
WholeMVA-PCR-R	TTTCACACAGGAAACAGCTATGACCATGATTAC
PpckA-F	GCTGTTTCCTGTGTGAAAGAATAGATCCTCCTCGAATCCGCG
PpckA-R	GCAGCTGGCACGACAGGGATCTGACCGGCGCAGAGG
PcbbG-F	GCTGTTTCCTGTGTGAAACCAATTTCTCCTCGCTGCAGATG
PcbbG-R	GCAGCTGGCACGACAGGATATCTCGGCGCCCACACTC
PMG103-MVAzp-F	CTCTAGAGTCGACGGTACCATGATGCAGAACGAAGAAGCGGAAGC
PMG103-MVAzp-R	TTGCATGCCTGCAGGTCGACTCAACGCCCTCGAACGGCG
PMG103-SacII-F	GTCGACCTGCAGGCATGC
PMG103-SacII-R	ATGGTACCGTCGACTCTAGAGGATC

---

Underlined letters, the restriction sites

Bold letters, the RBS sequence

**Table S2 Codon-optimized gene sequence**

Gene name	Sequence (5'-3')
<i>IDI<sub>sc</sub></i>	ATGACGGCGGACAACAACCTCGATGCCGCACGGCGCGGTGTCGTTCGTAC GCGAAGCTGGTCCAGAACCAGACCCCGGAGGACATCCTGGAGGAGTTC CCGGAGATCATCCCGCTCCAGCAGCGCCCGAACACGCGGTTCGTTCGGAG ACCAGCAACGACGAGTCGGGGCAGACGTGCTTCTCCGGCCACGACGAG GAGCAGATCAAGCTGATGAACGAGAACTGCATCGTGCTGGACTGGGAC GACAACGCCATCGGCGCCGGCACCAAGAAGGTCTGCCACCTGATGGAG AACATCGAGAAGGGCCTCCTGCACCGCGCCTTCTCCGTCTTCATCTTCA ACGAGCAGGGCGAATTACTCCTGCAGCAGCGGGCCACCGAGAAGATCA CCTTCCCGGACCTGTGGACCAACACGTGCTGCTCGCACCCGCTGTGCAT CGACGACGAACTAGGCCTGAAGGGCAAGCTCGACGACAAGATCAAGG GCGCGATCACGGCCGCGGTGCGCAAGCTGGACCACGAGCTAGGCATCC CGGAGGACGAGACCAAGACGCGGGGCAAGTTCCACTTCTCAACCGCA TCCACTACATGGCCCCGTCCAACGAGCCGTGGGGCGAGCACGAGATCG ACTACATCCTGTTCTACAAGATCAACGCGAAGGAGAACCTCACGGTGA ACCCGAACGTGAACGAGGTCCGGGACTTCAAGTGGGTGAGCCCGAACG ACCTGAAGACCATGTTCCGCCACCCGTCCTACAAGTTCACGCCGTGGTT CAAGATCATCTGCGAGAACTACCTCTTCAACTGGTGGGAGCAGCTGGA CGACCTCTCGGAGGTGGAGAACGACCGCCAGATCCACCGCATGCTGCA CCACCACCACCACCACTGA

**Table S3 Sequence of promoters tested**

Promoter name	Sequence (5'-3')
<i>P<sub>cbbF</sub></i>	ACCGTCTCCCCCTTTGAACGACGGCGGCCGTCGCGAGCATC GCTCCGGTCGCTCAACCATCTGTTTTGGTTCAGTTTTCTATGT CCAAAAATGCGACGGAAGCTCAAGGGACGTCGCGCTGCAGC ATCTTGGCTCGCCTCGGCAGCGGCAAAGACCCGCAGGGTGTGG ATACGCGGCGCTGCTAAAGTATAAGAGTGTCGACTCTCCGACC GATCGGGGCCAAATCACCCCGATCTGGGGCCGTGTCTTCTGAT CTAAATCACGGCGGTCTTCGACTAATTGTGCAGAATGCGCGCC GCGCCGCGTTTTCCGGTAAAAAATACAGGGCAGCGGCGCTT CATATAAAAATTCCTTTGGTGGTACCAAGGAAAATGCAATTC TCTTATGTGACCGATCGGCTCACAAGCTCCGCGCAACGGAGCT CGCGGAACCATTTGGTTCGCGCTGCGTTGTGGGGGAGTCATC ATATCTCGGCGCCCACTCGGGCGATTAAGGATCGCGCAGTT TTTCAGGCGCGGCGGTTACCGCATCAGGTGGGCCGCGCCTGC GGTAAGTCTTTGATCTGAATCATGAACGAGCGGATTGCAACTG <i>P<sub>cbbG</sub></i>
<i>P<sub>cbbL</sub></i>	CTCGGCATTTTGGGCATGAAACCGCGCAAGAGTACGGGGCGGG CTCCGCCATAGAACTGAAAATCATCTGCAGCGAGGAGAAATTG G TGTCGCCGGATGGAGGCCGCTGCGCGCCTCACAGGGATATCC ACGACGCGTTTGCGGCGCTGCATGCCGCGCTCGACAATGCCGA ACCGGTGCTCGACGCCCCGCACGAGCTGACCTGATCGCGCCTG CCGCGATATAAGAAATACTTTTGCATATCGAAGATAATAAAA TTTCTCTATTTTCGGCGTTGTGGTCAAAGTCTCCCGCACGCA TCCCGCGACGCTGATCGGCATAGCGGAACTTCGCGACCGAGT TCCCGAACGGCGTCGACCATCCAGCCGCTCGGCCGGCCAGGG CTTTCAAGGAGGACGAC CCGCGACGCAGGTCGGCACCATCGAAGCACGGAAGATCGTCA TGGATCAGCGAGGCACAGTGCATCAGCTCAAGTGCGGCACCGG CAGCTTCGGTAATTCGGGATTGTCTTCGCCGCAAGCAAGCGC CACGCTGTGGCAGAGCCGCGGACGAACGCGCGCCCCGCGCGG GAACACCGCACTGCGCATTGCTGCCGCCAGCCGCGGCGGACAT CCGGCCATGTCGGCCTGATTGAGCGCTTCTGTCAGAGCACGCT CGATCCGATTGGTCACGTCCATGGCCACACTCCCGCGCTTACG GCACAAGTGTCAGTTTAACTTGTCATGCCAAACTGTAAGTTATT GTGGACACCTGTCAATGATATGGCTCAAAGACAGCTGAGCCGG AGTGAGAAAACGG GCGCCGACATCATAACGGTTCTGGCAAATATTCTGAAATGAGC TGTTGACAATTAATCATCCGGCTCGTATAATGTGTGGAATTGTG <i>P<sub>irc</sub></i>
<i>P<sub>nifH</sub></i>	AGCGGATAACAATTCACACAGGAAACAGCGCCGCTGAGAAA AAGCGAAGCGGCACTGCTCTTTAACAATTTATCAGACAATCTG TGTGGGCACTCGACCGGAAT TTCTCCAACCTCAATGATCATCATGGCCGGGCTCGTCCCGGCC ATTCACGTTCTTGCTCCGGGCTCTGCCGTAGTCGTGGATGCCCG

---

GCACAAGGCCGGGCATGACGATGCGTGCACTCGCTATCCTCGT  
GATTGCGGGGAGCCTAATCCAGGATCCCCATGCACCGGGCCTT  
GGATTGCGTCGCTTCGCACGCAATGACGCAGCGCAGTCGATCT  
CAAGTTGCGACAGAGTCTCGCTTAGCTCCCCGGCCGGTATCAG  
TTTGTTTCGTTTCTAACAGCCGTTCCCTGGGATGTCGTCCGCTC  
GGCAGCGATGTCCGATTCTAAACATCTACGTACATTCTGCCCG  
GACATTCTACATCTCCGCGAAAACACACACTTTTTTCGTCTCCGG  
CGACGCTTGGCACGCTCGTTGCAAACAGGGATCAGCAAGGCC  
AGGGATGGTTGGCCGAGCAGGTACTGCAAAGGGCAACGTCCG  
CATCTGAGCCGTGCGACGGTTTTGAACGGAAGAAGGCTGCGCC  
TCGGCGCAAATCGATCAAGCGGCATTAGGTCAACGGAGAG

*P<sub>pckA</sub>*

GATCTGACCGGCGCAGAGGCGCTGCTCGAGGTCGAGGCTTCGG  
CGGTCGAGCACATCAATGCCGATCATCCAGATAACAATGAAGTT  
GTACGCCACTCAGCTACTCGGCTCTGGCGAAGCCGACTGGCGC  
TGACCGGCATCGATCCGGAAGGGCTGGATCTGCAATGCGAGC  
GTGCGACGCTGCGGCTCGATTTTCCAAGTCGCGTGGAAAAC  
TGCTGCATTGCGGGACATGCTGAAACGCATGGCTGACATTGCC  
CGCAAACGGAATGACTTGAGCCAGCGCAATGTCGCTCGGCGG  
TAAACGAAATAATGCCGGCCGGGTTGGCAAACCCCTCGTTCGC  
CACTATTCAGTCGCCCCACTGGATCAGGGCGGTATATATTGAC  
GTTACCGCGGCCAGTGATGCGCGTTGGCGGCAATCGCGCGATC  
GAGACAACGCGGATTCGAGGAGGATCTATTC

---

**Table S4 Primers used for gene knockout**

Primers	Sequence (5'-3')
$\Delta crtC$ -up-F:	AAATCTAGAAGATCGCCGCTCCCTTCGAT
$\Delta crtC$ -up-R:	GGCTACGCCTGGTGGTACATTCTGAAGACACTCCGTTCTAC
$\Delta crtC$ -down-F:	GTAGAACGGAGTGTCTTCGAATGTACCACCAGGCGTAGCC
$\Delta crtC$ -down-R:	5-TTG <u>TCTAGA</u> ATGACCTGGAGCATGGTGGC-3
$\Delta crtC$ -yz-F	GCAACGGCGTTAGTTGTGGC
$\Delta crtC$ -yz-R	CTGCTTCCAAGACGACGTGA
$\Delta crtD$ -UP-F	GTGGATCCCCCGGGCTGCAGGCTCGTTGCCATTGGTGCAT
$\Delta crtD$ -UP-R	AAGCCGAGATCGGCCGAACAGACTACGACGCGATTCCCTCGC
$\Delta crtD$ -down-F	GCGAGGAATCGCGTTCGTAGTCTGTTCGCCGATCTCGGCTT
$\Delta crtD$ -down-R	TTGATATCGAATTCCTGCAGACCATCGAGCGGGCGTAGAA
$\Delta crtD$ -yz-F	CACGGAAGATCGTCATGGAT
$\Delta crtD$ -yz-R	ATACAACGCGACGTTGATGG
$\Delta crtF$ -UP-F	GTGGATCCCCCGGGCTGCAGTCAATCAGGCCGACATGGCC
$\Delta crtF$ -UP-R	CATTCTCCAACATCGCCTGCACGAGGTCGAACATCGCCAC
$\Delta crtF$ -down-F	GTGGCGATGTTTCGACCTCGTGCAGGCGATGTTGGAGAATG
$\Delta crtF$ -down-R	TTGATATCGAATTCCTGCAG AGATGCTGCGATAGTCGCGA
$\Delta crtF$ -yz-F	TGCGGTTCGTGATCATGTC
$\Delta crtF$ -yz-R	ATGATAAGCAGTCGCAGCCA CCGGGGGATCCACTAGTTCTAGAACCGGATCCGGCAAGGAT
$\Delta RPA1208$ -up-F	G
$\Delta RPA1208$ -up-R	CCCCGCGTCGTATCGTAACGCTGCGAGAATCGCAGCGAC
$\Delta RPA1208$ -down-F	GTCGCTGCGATTCTCGCAGCGTTACGATACGACGCGCGGC
$\Delta RPA1208$ -down-R	CCGCGGTGGCGGCCGCTCTAGAGCAGTCACAGCAAGGCTCC CCGGGGGATCCACTAGTTCTAGACCAACAATCCGCAGCACA
$\Delta PhbC$ -UP-F	C GCCAGGCCTTAGCGACGATGACCATCGGCAACGAAGCCTAC
$\Delta PhbC$ -UP-R	C
$\Delta PhbC$ -down-F	GTAGGCTTCGTTGCCGATGGTCATCGTCGCTAAGGCCTGGC
$\Delta PhbC$ -down-R	CCGCGGTGGCGGCCGCTCTAGACCTCGACTCCGGGTAACG
$\Delta phbC$ -yz-F	TGCAGGTGATCGGCGGATT
$\Delta phbC$ -yz-R	CAATCGTCGCACTCGAGGAT
$\Delta RPA1208$ -yz-F	GGAACAGACCCGGTCACTACT
$\Delta RPA1208$ -yz-R	GCCCGAAGCACGACCAAGA

**Table S5 Primers used for real time quantitative PCR**

Primers	Sequences (5'-3')
cbbP-F	TAACCGCCACTTCAGCCATT
cbbP-R	TCGTCTGTAACGTAGTGACG
cbbF-F	GGCTGCTCTACGAAACCCAT
cbbF-R	GATCGTCTTGGCGGTGAGAT
cbbK-F	GTCTCTGTGCGAGAAGGACC
cbbK-R	CTCGAAGTGATAGGCCACGG
cbbI-F	CATGCTTTCGTCACCGATGG
cbbI-R	ACAACCCATGCTCGACTACG
cbbJ-F	TTGAGTCTCGCAATCGGCTC
cbbJ-R	CAGGCCGTTTCATCTTCCAGT
glpX-F	ACATGGTGAAGGGTGACTGC
glpX-R	TCCGCCTTGATGTAGCGAAC
RPA3384-F	CCTCGGTGATGACGACCAA
RPA3384-R	ATCGACCTTGATTGGCGTGT
RPA0232-F	GGAAGTGATGGTGATCGGCT
RPA0233-R	ACGATGTGCTTCACCCTGAG
RPA0794-F	CGTCAGCGCCAATCTGTTTC
RPA0794-R	CTGGGGCGATGGAAATGGAA
RPA0799-F	TCGCTAGTCTCGAATACGGC
RPA0799-R	CCGCAGATCCTCCTCCTTC
cbbX-F	GATCGTGAGTTGATCGGGCT
cbbX-R	CATGTGCAAGGTGGGATTGC
cbbRR1-F	GAGATCCGTGACCGCTTCAG
cbbRR1-R	AAACCATAGATCCCGGCGAC
cbbRR2-F	GAAGAAGCTCGGGATCGAGG
cbbRR2-R	CGGCATGTGATAGTCGGTGA
cbbSR-F	GGGCTGTTCAAGCGTTTCAG
cbbSR-R	GCTGGCTGTCGATCTTGAGT
cbbX-F	GATCGTGAGTTGATCGGGCT
cbbX-R	CATGTGCAAGGTGGGATTGC
cbbR-F	AGCCTGATGGAGCAGTTCTT
cbbR-R	ACGGTGTGGGCCGAAATAAA
cbbL-F	AGTATCGCGCCAAGTGCTAC
cbbL-R	ATGATCGACGCGGTGAGATT
cbbS-F	GACTGACCCAAGGCTGTTTCT
cbbS-R	AATAAGTGTTGCGGGGATGC
cbbA-F	AAATCGTGCGTGGCATCAAG
cbbA-R	TCGAACTCCGCCTTGTTCTG
cbbT1-F	TCCTACCTGCACTACGGCAT
cbbT1-R	AGTCGTGGGTCATCACATGG
cbbG-F	GAAGGCCACCACCAAGGAAG
cbbG-R	CATGTGGAAGGTGGACGAGT
cbbM-F	TGGGTTTCGGCAAGATGGAA
cbbM-R	AGCCACTCCTGGTGGAAAGTA
ugpC-F	GAAATCCGCAAGCTACAGCG
ugpC-R	ATGAACGAAGCCACGAAGGT
ugpA-F	CGCCGACGATTTTCTTCTG

ugpA-R	AGCAGGCCATCCTGATACAC
gpsA-F	CTGGCGGAAGGCTACTACAC
gpsA-R	TATTCCTCCGCCTTGAGAGG
glpK-F	CGGGCGATTCTGTTTCGTTC
glpK-R	CGACAGGTAGCAATGGTCGT
glpD-F	CGGATGTGGTGTGGACCTTC
glpD-R	CAGCTTCTCCAACGCCTCTT
glpR-F	AGTGTCGGCACAGACCATTC
glpR-R	GAGCAGCCGTTGGGAATCT
cbbE-F	AGCGCCGTTCAGAAGATCAA
cbbE-R	TGGCCTTATACGCTTCCAGC

---



**Table S6 OD<sub>660</sub> and generation time of *R. palustris* LMJ01 using different seed culture**

Strain	Seed culture source	Carbon source and electron donor		OD <sub>660</sub>	Generation time (h)
		CO <sub>2</sub> (mM)	Na <sub>2</sub> S <sub>2</sub> O <sub>3</sub> (mM)		
LMJ01	Bacteria culture medium with 20 mM CO <sub>2</sub> and 4 mM Na <sub>2</sub> S <sub>2</sub> O <sub>3</sub>	20	4	0.43±0.05	36.25±0.47
LMJ01	Frozen stock solution with 25% glycerol	20	4	2.35±0.14	20.99±0.41

**Table S7 Generation time of *R. palustris* with thiosulfate of different concentration as electron donor**

Strain	Carbon source/electron donor			Generation time (h)
	CO <sub>2</sub> (mM)	Na <sub>2</sub> S <sub>2</sub> O <sub>3</sub> (mM)	Glycerol (mM)	
LMJ01	20	0	0	-
LMJ01	20	2	0	31.01±0.25
LMJ01	20	4	0	36.25±0.47
LMJ01	20	6	0	36.50±0.24
LMJ01	20	8	0	35.60±0.16
LMJ01	20	0	20	28.00±0.33
LMJ01	20	2	20	22.83±0.32
LMJ01	20	4	20	21.57±0.31
LMJ01	20	6	20	25.67±0.22
LMJ01	20	8	20	25.02±0.28

**Table S8 Predicated genes encoding HCO<sub>3</sub><sup>-</sup> transporter**

Gene name	Locus Tag	Protein function	Homologous gene in cyanobacteria	%ID
<i>sulP</i> <sup>a</sup>	RPA432 6	sulfate transporter family protein	<i>bicA</i>	45
-	RPA338 3	taurine transport system permease	<i>cmpB</i>	24.8
-	RPA338 4	nitrate/sulfonate/bicarbonate ABC related periplasmic binding protein	<i>cmpA</i>	35.7
<i>nrtC2</i> <sup>a</sup>	RPA338 5	nitrate transport system ATP-binding protein	<i>cmpD</i>	39.8
<i>nrtA</i> <sup>a</sup>	RPA211 2	nitrate transporter component nrtA	<i>cmpA</i>	50
<i>nrtB</i> <sup>a</sup>	RPA211 3	nitrate transport system permease	<i>cmpB</i>	47.1
<i>nrtC1</i> <sup>a</sup>	RPA211 4	nitrate transport system ATP-binding protein	<i>cmpD</i>	49.4
-	RPA370 7	nitrate transporter component nrtA	<i>cmpA</i>	50

<sup>a</sup> Gene name was computationally analyzed.

**Table S9 Predicated genes encoding carbonic dehydratase**

Gene name	Locus Tag	Protein function	Homologous gene in cyanobacteria	%ID
-	RPA0232	carbonate dehydratase	<i>ecaA</i>	50
<i>acaP</i> <sup>a</sup>	RPA0794	carbonate dehydratase	<i>ecaA</i>	42.3
-	RPA0799	carbonic anhydrase	<i>ecaA</i>	63.2

<sup>a</sup> Gene name was computationally analyzed.

Figure S1 Linear fitting relationship between OD<sub>660</sub> and biomass

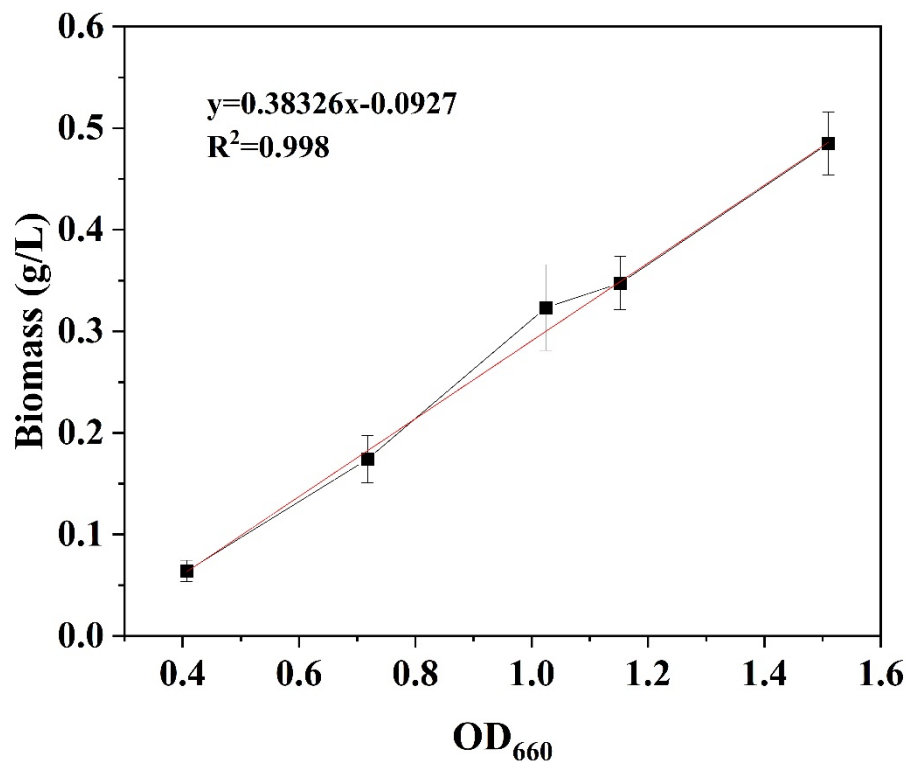
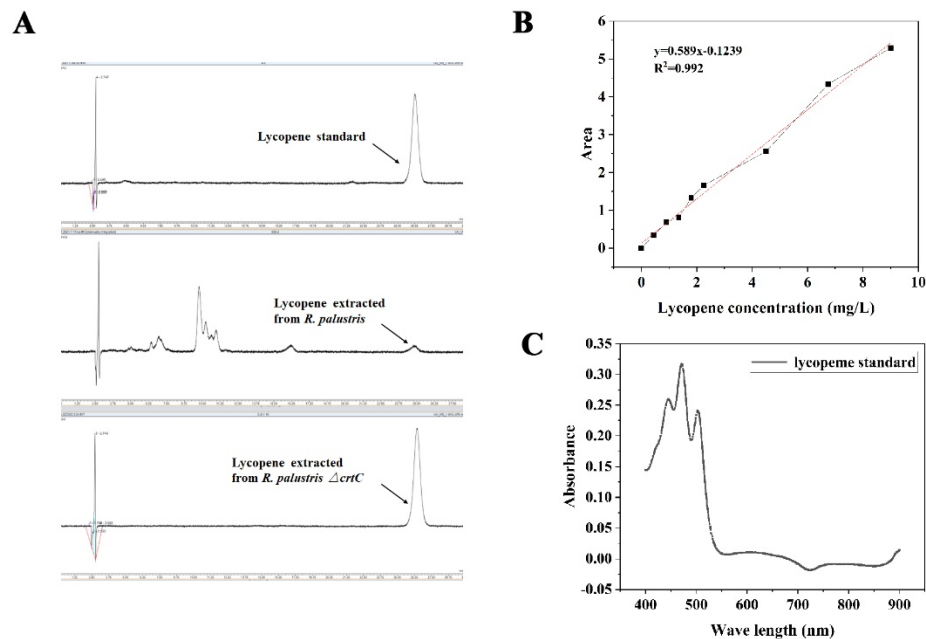


Figure S2 Analysis of lycopene standard and extracted lycopene.

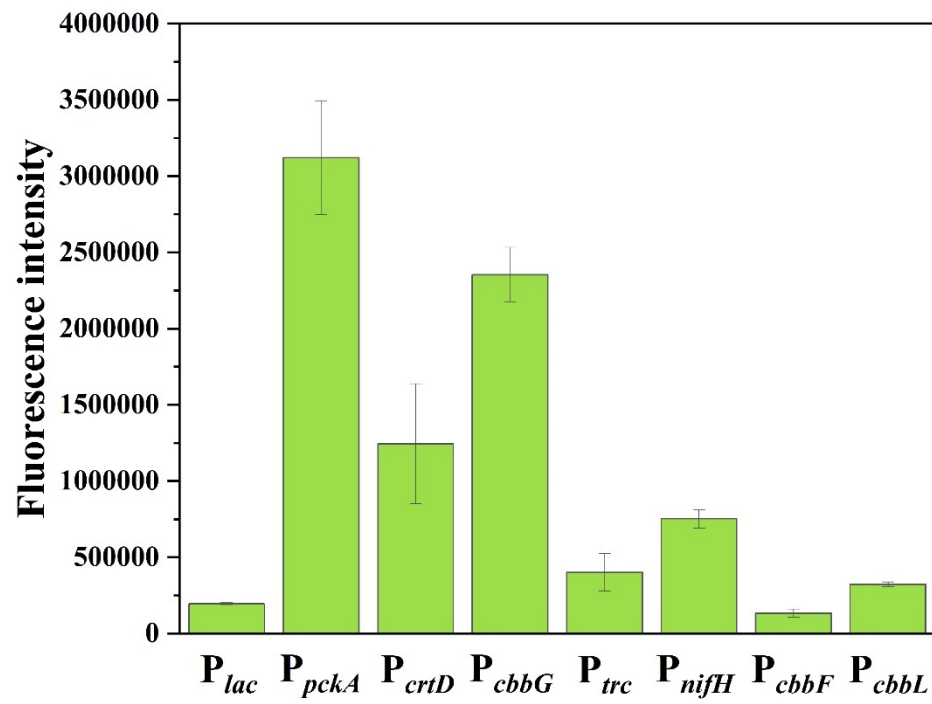


**A.** HPLC spectrum; **B.** Standard curve of lycopene standard, which was corrected by the percentage of actual lycopene (45%) in the standard, using HPLC; **C.** UV-visible absorption spectrum (400-900 nm) of lycopene standard.

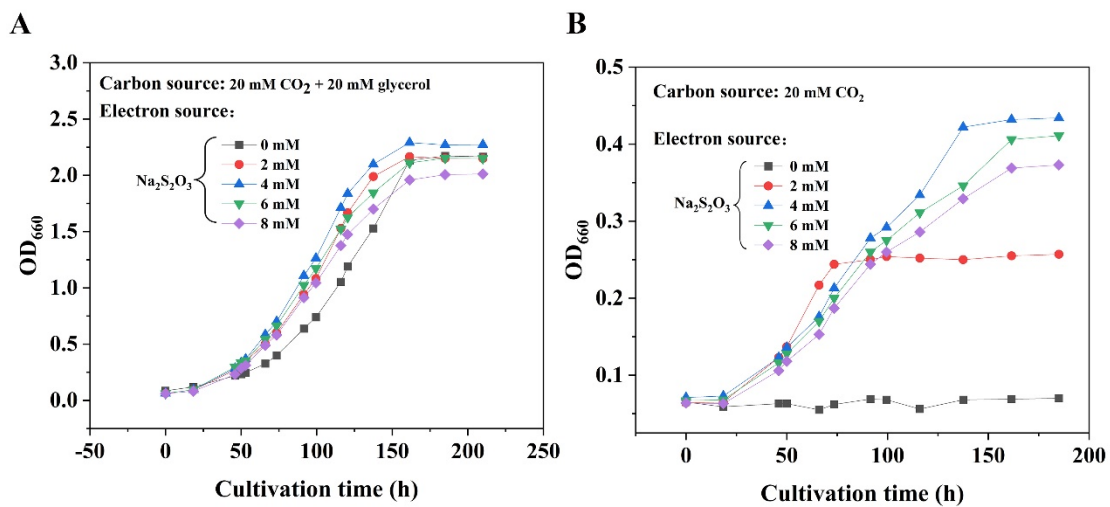
**Figure S3 Color change of *R. palustris* with *crtC*, *crtD* or *crtF* deletion**



Figure S4 Promoter screening by detection of GFP fluorescence intensity.



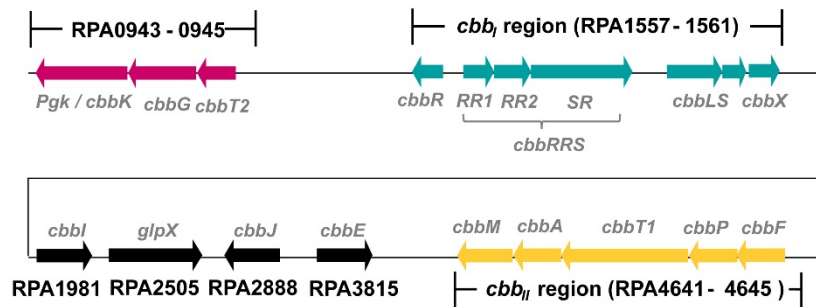
**Figure S5 Growth curve of *R. palustris* LMJ01 using  $\text{Na}_2\text{S}_2\text{O}_3$  of different concentration as electron donor**



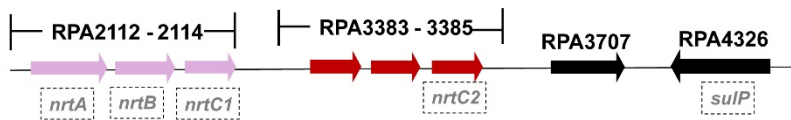
$\text{Na}_2\text{S}_2\text{O}_3$  of different concentration (0, 2, 4, 6, 8 mM) was utilized as the electron donor, using 20 mM  $\text{CO}_2$  with glycerol of 0 mM (**B**) and 20 mM (**A**) as the carbon source. Three biological replicates were performed.

**Figure S6 Arrangement of genes related to CBB cycle in the genome of *R. palustris***

Arrangement of genes related to CBB cycle directly in the genome of *R. palustris*



Arrangement of predicated genes encoding  $\text{HCO}_3^-$  transporter in the genome of *R. palustris*.



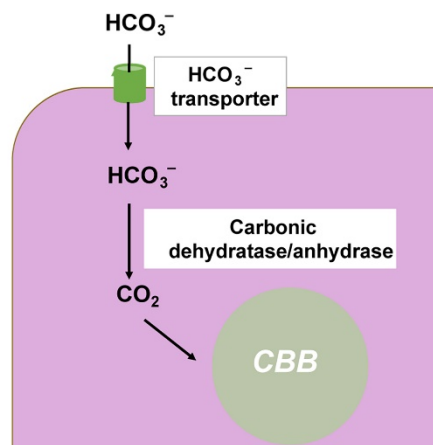
Arrangement of predicated genes encoding carbonic dehydratase/ anhydrase in the genome of *R. palustris*



In *R. palustris*, most genes required for a functional CBB cycle are organized into two operons, *cbb<sub>I</sub>* and *cbb<sub>II</sub>*. The *cbb<sub>I</sub>* operon contains the *cbbLS* genes encoding the large and small subunits of form I RubisCO which is regulated by a LysR transcriptional activator. In *cbb<sub>II</sub>* operon, *cbbM* encodes the form II RubisCO, and *cbbA*, *cbbT1*, *cbbP* and *cbbF* are known to be present in this region. The other three genes related to the CBB cycle, *cbbK*, *cbbG* and *cbbT2*, were clustered together, and other four genes related to CBB cycle, *cbbI*, *glpX*, *cbbJ* and *cbbE*, were scattered in the genome. The putative genes encoding  $\text{HCO}_3^-$  transporter and carbonic anhydrase/dehydratase were also listed.

**Figure S7 Illustration of the process of bicarbonate entered into the CBB cycle in**

*R. palustris*



The bicarbonate ( $\text{HCO}_3^-$ ) in the medium is transported into the cytoplasm by bicarbonate transporter; and, subsequently, the  $\text{HCO}_3^-$  is converted to  $\text{CO}_2$  by carbonic anhydrase/dehydratase.