

Supporting Information

Figure S1. Variation of particulate nitrogen and carbon of CS-505 and D9 under alternative N regimes.

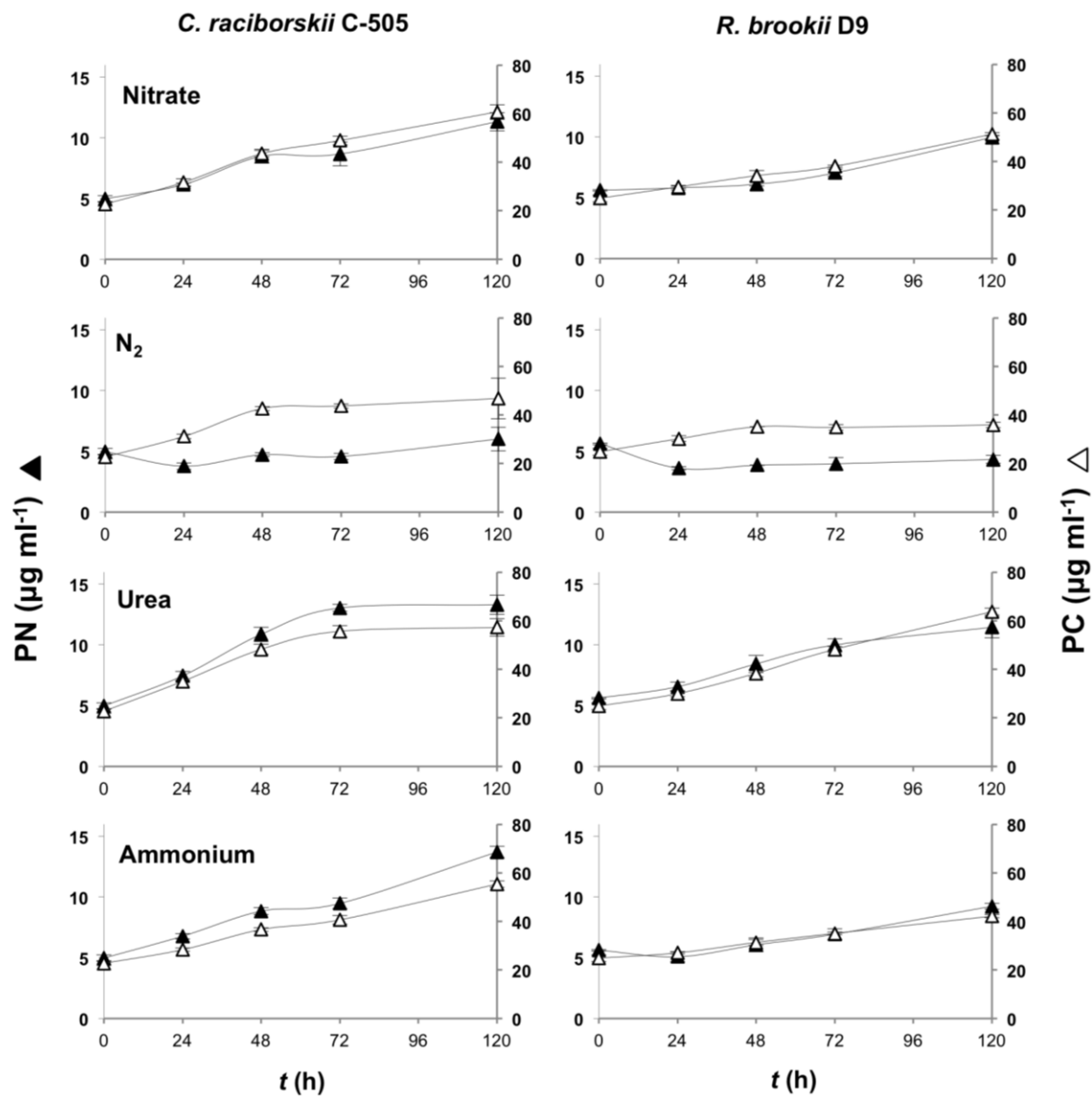


Figure S2. *In silico* analysis of transcriptional units (TU), NtcA binding boxes and promoters outside and within the *cyr* gene cluster. (A) Graphical representation of the *cyr* gene cluster and predicted TUs. Genes forming part of TUs are marked by black lines across them. (B–E) Nucleotide sequence of regions containing predicted NtcA binding boxes. NtcA binding boxes are shown as a thick red line within the cluster and enclosed in rectangles in the sequences. The −10 and −35 regulatory boxes are shown only for the −10 box with the conserved motif TAN₃T.

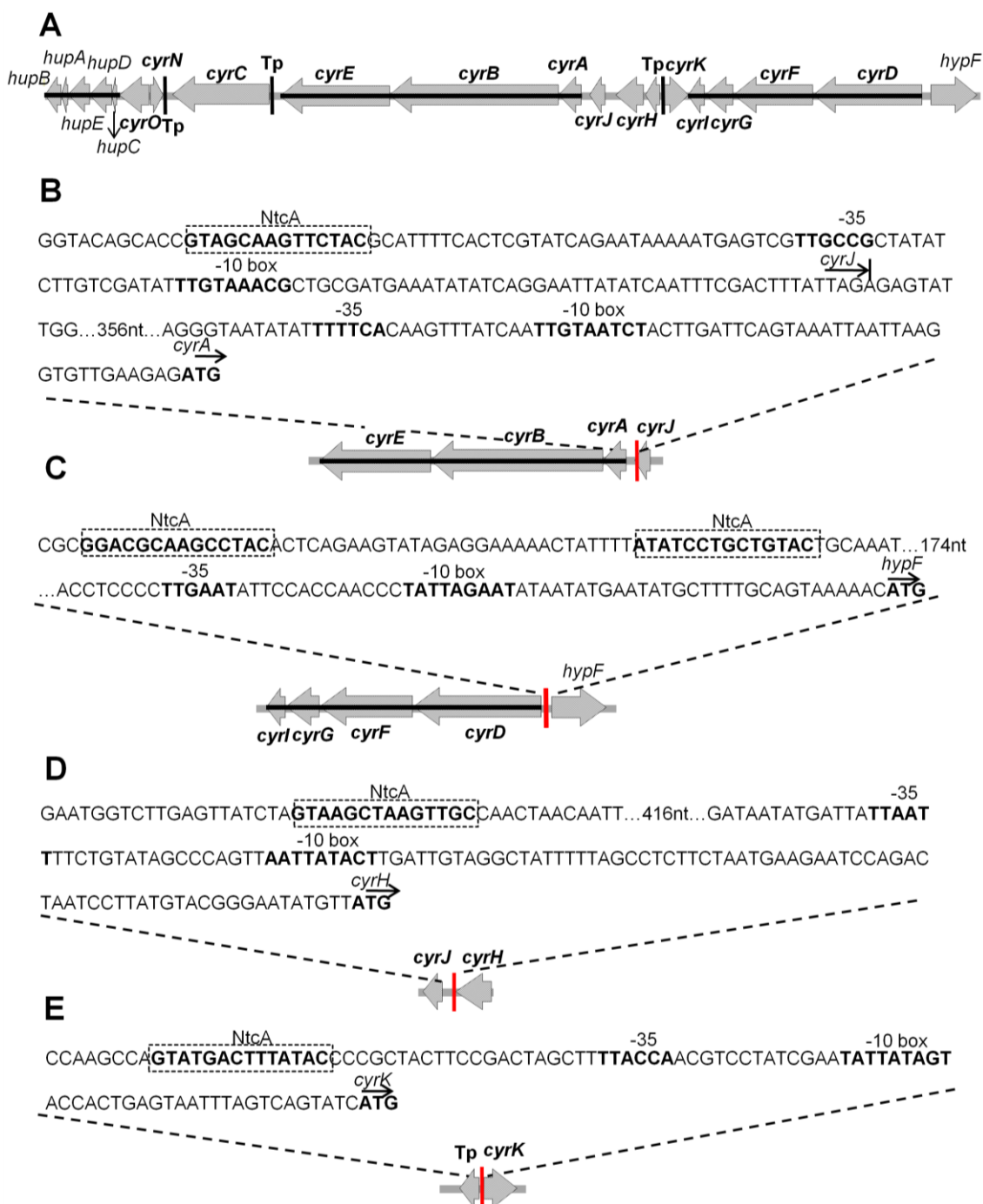


Figure S3. *In silico* analysis of transcriptional units (TU), NtcA binding boxes and promoters outside and within the *sxt* gene cluster. (A) Graphical representation of the *sxt* gene cluster and predicted TUs. Genes forming part of TUs are marked by black lines across them. (B–E) Nucleotide sequence of regions containing predicted NtcA binding boxes. NtcA binding boxes are shown as a thick red line within the cluster and enclosed in rectangles in the sequences. The –10 and –35 regulatory boxes are shown only for the –10 box with the conserved motif TAN₃T. In the presence of two possible –10 and –35 boxes within the same intergenic region, the second sequence appears underlined.

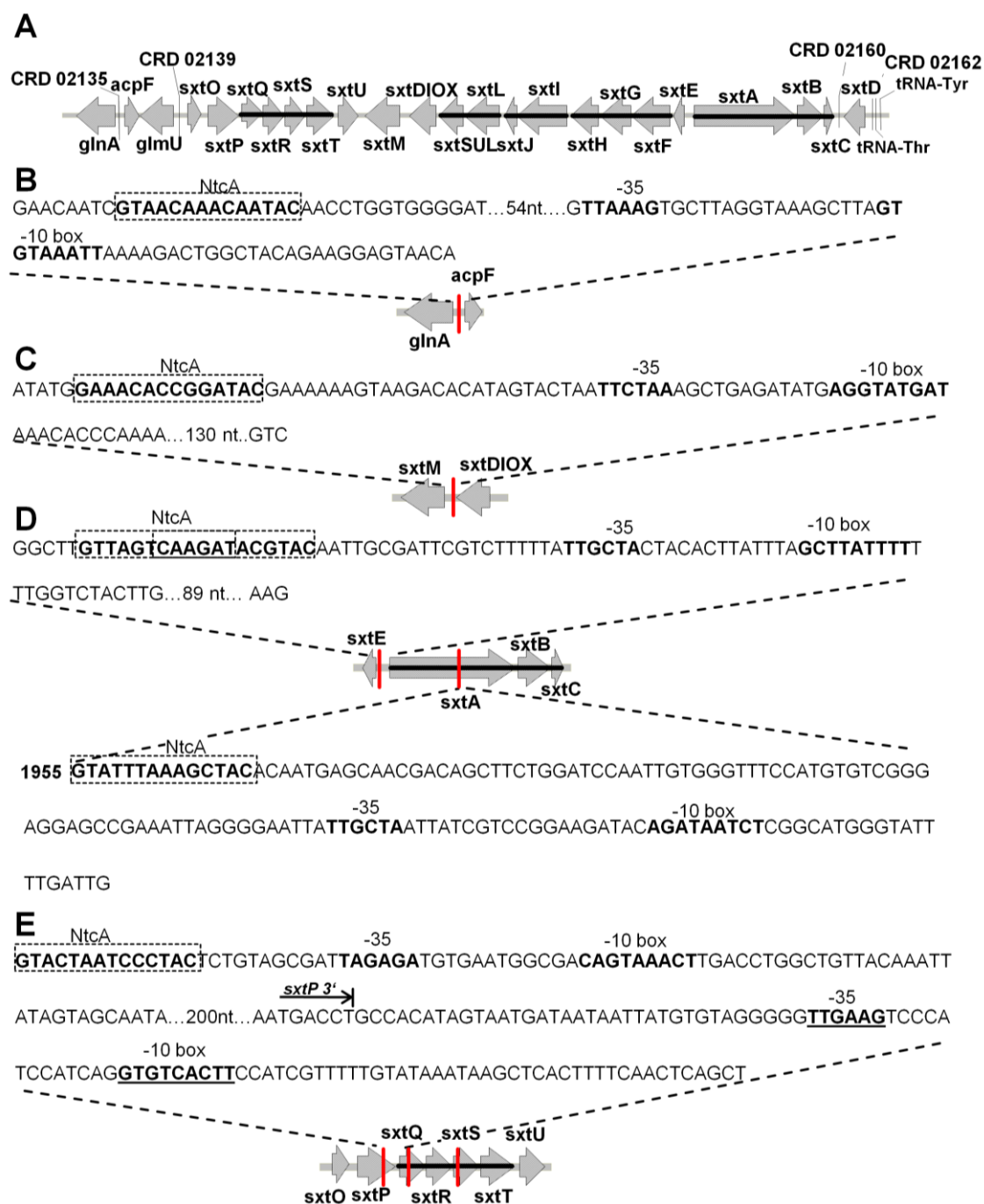


Table S1. Pearson correlation coefficients ($p < 0.001$) between biomass estimations based on chlorophyll *a* (chl_a), optical density (OD) and dry weight (DW).

Biomass estimation	Pearson Corr (r) <i>C. raciborskii</i> CS-505				Pearson Corr (r) <i>R. brookii</i> D9			
	Nitrate	N2	Urea	Ammonium	Nitrate	N2	Urea	Ammonium
chl _a vs. DW	0.90	0.14	0.95	0.79	0.97	−0.35	0.90	0.82
chl _a vs. OD	0.97	0.25	0.95	0.91	0.95	−0.25	0.88	0.48
OD vs. DW	0.93	0.81	0.97	0.90	0.97	0.95	0.99	0.80

Values in green boxes have $p > 0.001$.

Table S2. qPCR primer sequences, efficiencies and amplicon sizes.

Gene	Amplicon Size (nt)	qRT-PCR Primer Sequence 5'-3'	Slope	Efficiency (%)
<i>ntcA</i>	60	qD9ntcAF TCGCTGAAGCAATAGGATCCA	−3.33	100.3
		qD9ntcAR TCCCGCAAGTCTCCTAGCAA		
	60	q505ntcAF TTTTACTGCGGTGGAATTGCT	−3.41	102.7
		q505ntcAR TTCCTTGAGGGCCTGCTCTAC		
<i>sxtSUL</i>	79	qsxt14F CTGAAGTAGCGGCTCAACAGATAA	−3.67	110.5
		qsxt14R CAGGAGGATTGCGAAGCATAA		
<i>sxtDIOX</i>	99	qsxt15F CGATGGGAGAAATTGCGAAT	−3.76	113.1
		qsxt15R ATGTCAGGGTGAGCTGGGATA		
<i>sxtO</i>	69	qsxtOF TTGGGTGAGGTTGCCAAACT	−3.53	106.3
		qsxtOR CGGTCATTCTGTAGGGTGAGA		
<i>sxtU</i>	69	qsxtUF GCGATCGCCGCAAGAC	−3.31	99.7
		qsxtUR CTTGACCACCACTGGCTTCA		
<i>sxtA</i>	59	qACPR GGGAGAGCGAGCCTTGAAT	−3.30	99.0
		qACPR ATGCGGGACAACATAGGAGTGT		
<i>sxtI</i>	69	qsxtIF TTGTTGCTGCAGCTCAGGAA	−3.29	99.1
		qsxtIR ATCGCTCCAGTCGGAAACC		
<i>sxtM</i>	100	qsxtMF GGCTAGCAACGGCCTTGTC	−3.16	95.2
		qsxtMR TGCCAGTAACACATTGCTTTGTT		
<i>sxtF</i>	60	qsxtFF GCCCATGATATTGGCTTCCA	−3.47	104.5
		qsxtFR TGCCGACTCCGAGTGGTATAAC		
<i>cyrB</i>	99	qcyrBF ACTGCACAGACTGCGATTTC	−3.48	104.8
		qcyrBR TGCGCCCCATGTTAATGTATT		
<i>cyrI</i>	94	qcyrIF TCCCGGTCATCCATCAGTAAG	−3.65	109.9
		qcyrIR ATGTGGGTGCGTCTTCTTGATA		
<i>cyrJ</i>	60	qcyrJF TGAACGATCCGCGGAGAA	−3.32	100.0
		qcyrJR TCGGTAACTCAACCCCTACAAC		
<i>cyrK</i>	99	qcyrKF AGATGACCGAGAGGGCGTACT	−3.97	119.5
		qcyrKR CACCCCTAACGGGTACTGTAACA		