

Supplementary Material

Genomic Insights into the Taxonomy and Metabolism of the Cyanobacterium *Pannus brasiliensis* CCIBt3594

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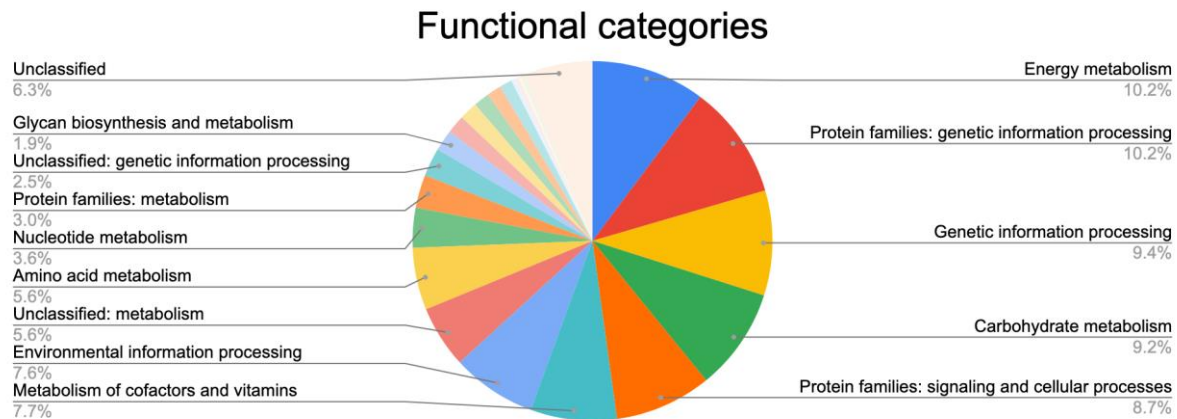


Figure S1. Functional classification of the genes annotated in the genome of *Pannus brasiliensis* CCIBt3594.

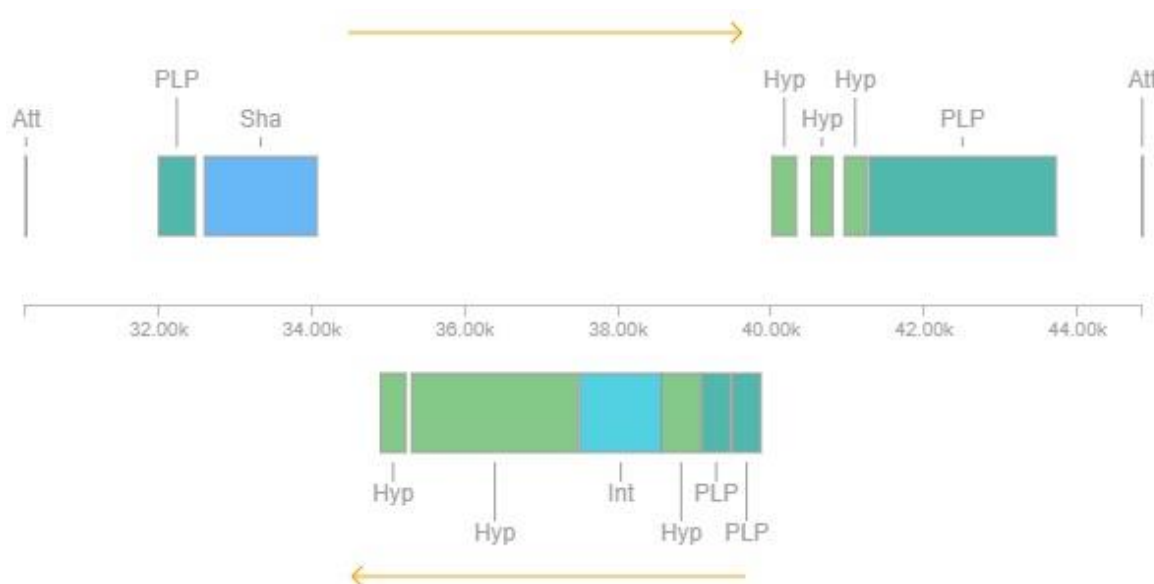


Figure S2. Prophage region identified in the contig number 17 in the genome of *Pannus brasiliensis* CCIBt3594. PLP: Phage-like Protein; Sha: Tail Shaft; Hyp: Hypothetical Protein; Int: Integrase.

Table S1. Identity of the amino acid sequences of the of *nif*, *isc*, *fdx* and *hsc* genes in *Pannus brasiliensis* CCIBt3594 genome.

Gene	Protein	% Identity	Specie	NCBI Accession
<i>nifK</i>	nitrogenase molybdenum-iron protein subunit beta	85.55	<i>Hydrococcus</i> sp. C42_A2020_068	MBF2018560.1
		86.12	<i>Hydrococcus rivularis</i>	WP_073598932.1
<i>nifD</i>	nitrogenase molybdenum-iron protein alpha chain	91.84	<i>Pleurocapsa</i> sp. PCC 7327	WP_015145032.1
		90.38	<i>Hydrococcus rivularis</i>	WP_073599038.1
<i>nifH</i>	nitrogenase iron protein	90	<i>Cyanothece</i> sp. BG0011	WP_198648223.1
		89.66	<i>Crocospaera subtropica</i>	WP_009546639.1
<i>iscU</i>	Fe-S cluster assembly protein NifU	78.41	<i>Crocospaera</i> sp.	MDJ0658368.1
		77.7	<i>Rippkaea orientalis</i>	WP_012595103.1
<i>nifS</i>	cysteine desulfurase NifS	85.5	<i>Gloeocapsa</i> sp. DLM2.Bin57	TVQ43199.1
		82.75	<i>Oscillatoria salina</i>	WP_224411706.1
<i>fdx</i>	4Fe-4S binding protein	57.27	<i>Gloeocapsa</i> sp. DLM2.Bin57	TVQ43198.1
		54.27	<i>Cyanobacterium</i> sp. uoEpiScrs1	WP_267383980.1

<i>nifB</i>	nitrogenase cofactor biosynthesis protein NifB	78.05	<i>Pleurocapsa</i> sp. PCC 7327	WP_015145027. 1
		77.85	<i>Hydrococcus rivularis</i>	WP_073598927. 1
<i>nifJ</i>	pyruvate: ferredoxin (flavodoxin) oxidoreductase	86.42	<i>Microcystis aeruginosa</i> W13-16	NCQ69820.1
		86.33	<i>Microcystis aeruginosa</i> L111-01	NCR22450.1
<i>nifW</i>	nitrogenase- stabilizing/prote ctive protein NifW	69.16	<i>Eubalotheca natronophila</i>	WP_146294458. 1
		69.72	<i>Crocospaera</i> sp.	WP_007305809. 1
<i>hesA</i>	HesA/MoeB/Thi F family protein	81.96	<i>Hydrococcus rivularis</i>	WP_073598939. 1
		81.57	<i>Pleurocapsa</i> sp. PCC 7327	WP_015145041. 1
<i>hesB</i>	iron-sulfur cluster assembly accessory protein	77.69	<i>Hydrococcus rivularis</i>	WP_073598940. 1
		76.03	<i>Pleurocapsa</i> sp. PCC 7327	WP_015145042. 1
<i>iscS</i>	cysteine desulfurase	74.87	<i>Microcystis aeruginosa</i> TA09	REJ46172.1
		74.62	<i>Microcystis</i> sp. M04BS1	MCA2552547.1

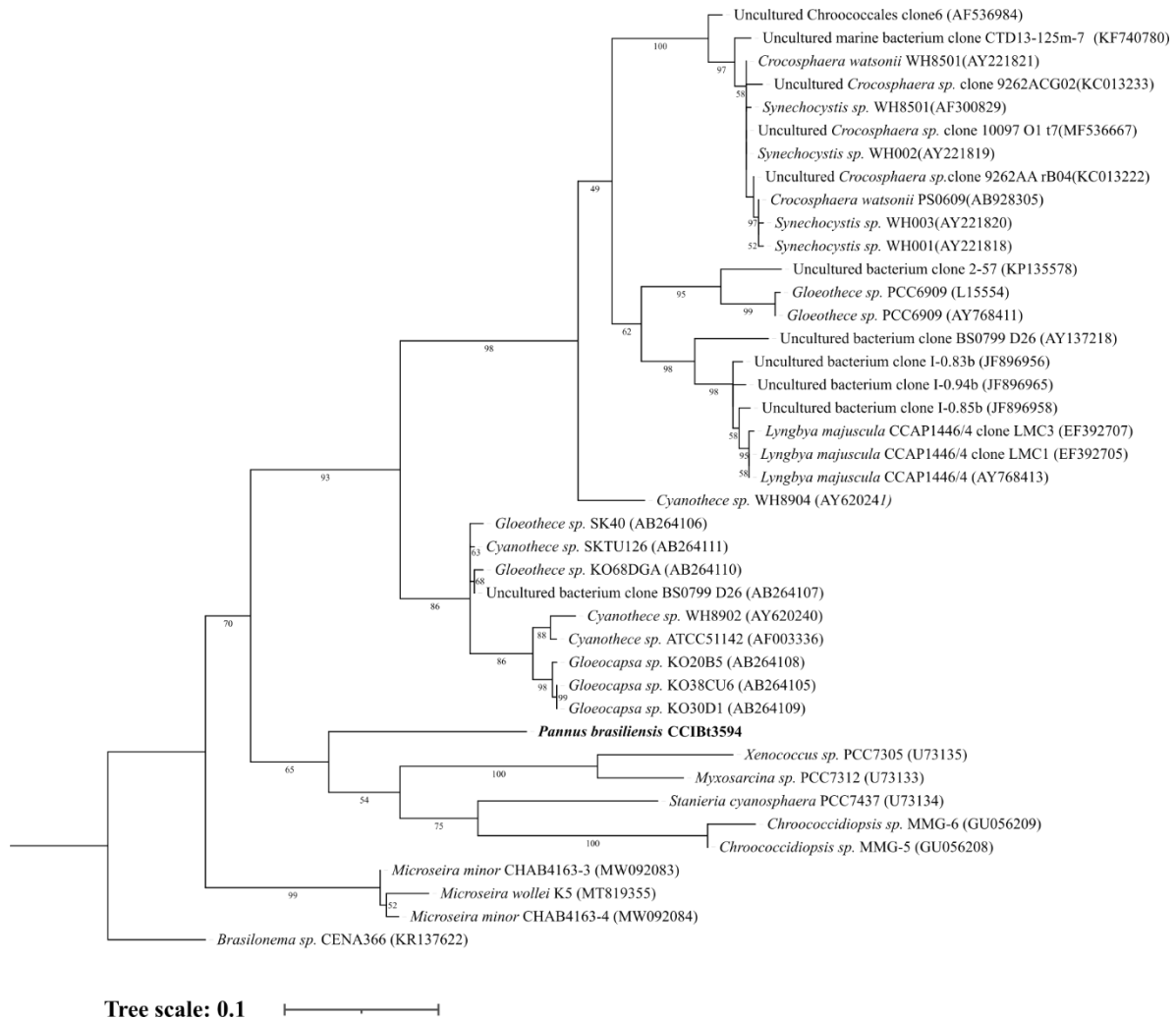


Figure S3. Maximum-likelihood Phylogenetic tree using *nifH* gene displaying the relationship of *Pannus brasiliensis* CCIBt3594 (in bold). 1000 resampling bootstrap test was performed. Bootstrap values 50% are displayed at nodes.

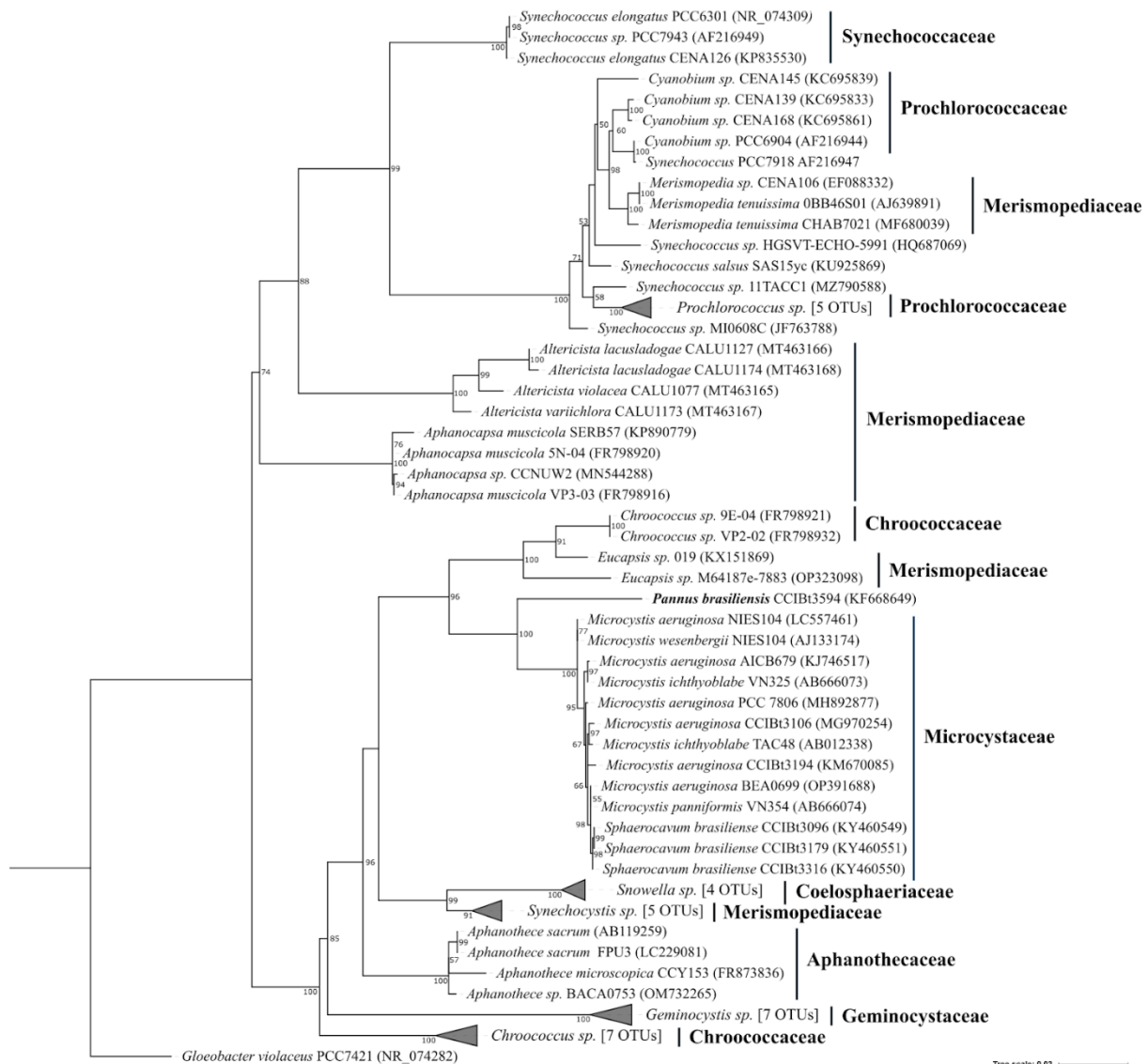


Figure S4. Phylogenetic tree using 16S rDNA gene displaying the relationship of *Pannus brasiliensis* CCIBt3594 (in bold) with other species of order Synechococcales and Chroococcales available in NCBI. Maximum-likelihood and 1000 resampling bootstrap test was performed. Bootstrap values 50% are displayed at nodes.

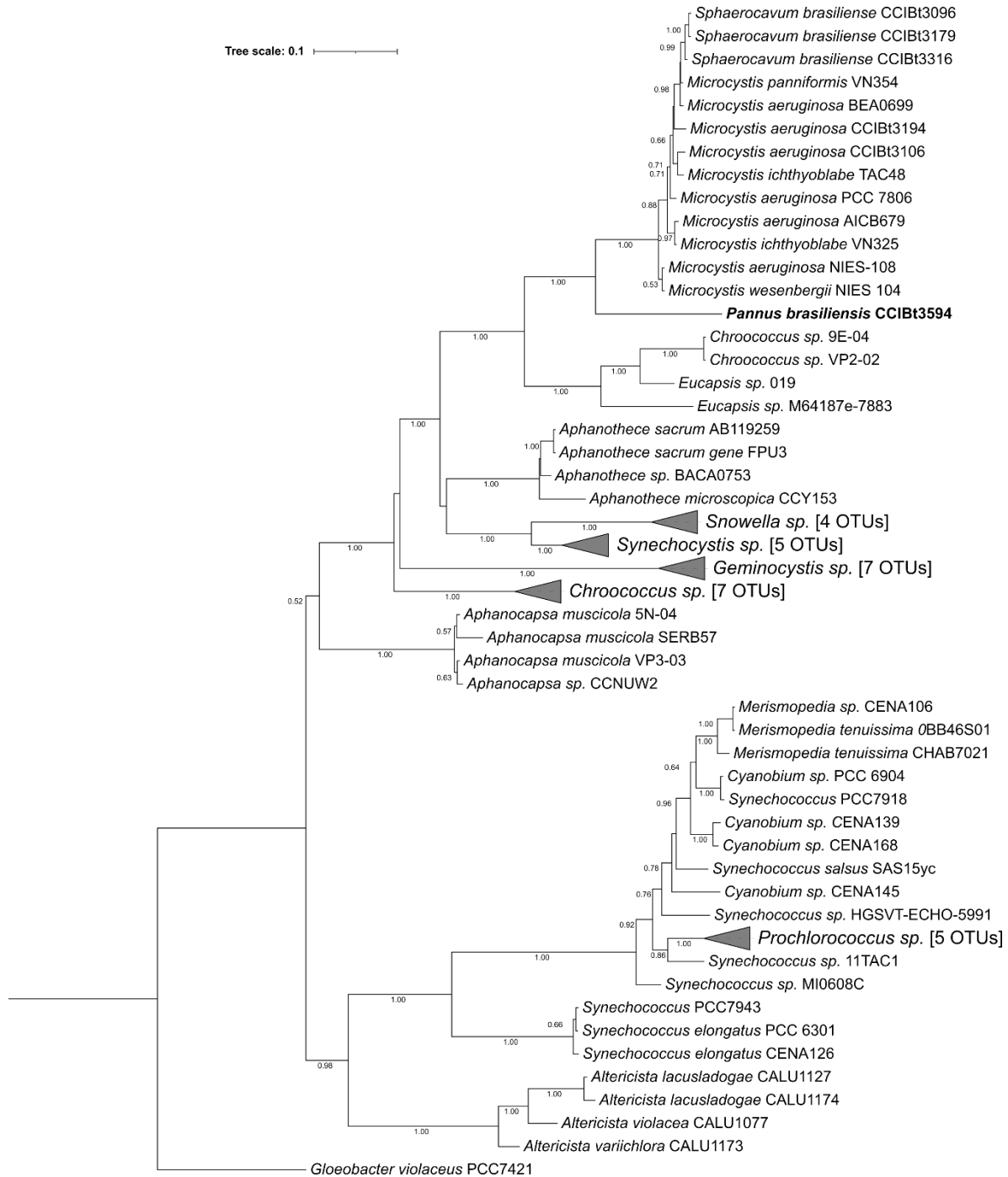


Figure S5 Phylogenetic tree reconstructed by the Bayesian Inference method displaying the relationship of *Pannus brasiliensis* CCIBt3594 (in bold) with other species of order Synechococcales and Chroococcales available in NCBI. Bayesian posterior probabilities are represented on each node.

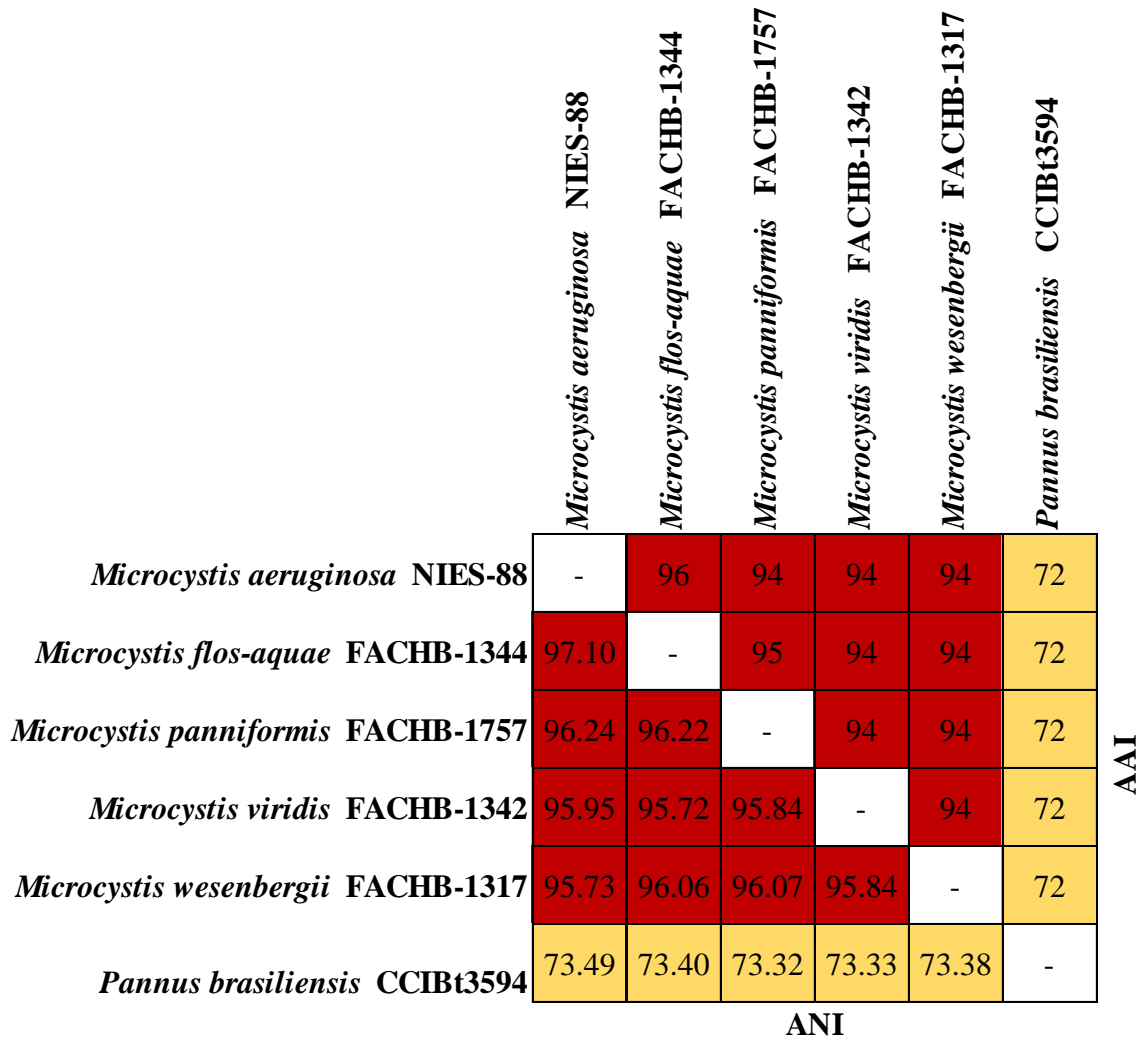


Figure S6. Heatmap showing the Average Nucleotide Identity (ANI) and the Average Amino acids Identity (AAI) among the genomes of *Pannus brasiliensis* CCIBT3594 and related species of the genus *Microcystis* spp.

Table S2. The *in silico* DDH values for *Pannus brasiliensis* CCIBt3594 and selected reference genomes of *Microcystis* genera.

Reference genome	DDH	Distance	Prob. DDH >= 70%	G+C difference
<i>Microcystis aeruginosa</i> NIES-88	21.20	0.2068	0	9.31
<i>Microcystis flos-aquae</i> FACHB-1344	20.80	0.2110	0	9.41
<i>Microcystis panniformis</i> FACHB-1757	20.80	0.2108	0	9.69
<i>Microcystis viridis</i> FACHB-1342	20.90	0.2098	0	9.46
<i>Microcystis wesenbergii</i> FACHB-1317	21.10	0.2085	0	9.53