

Figure 1. Geographic Distribution of Collected Lineages.

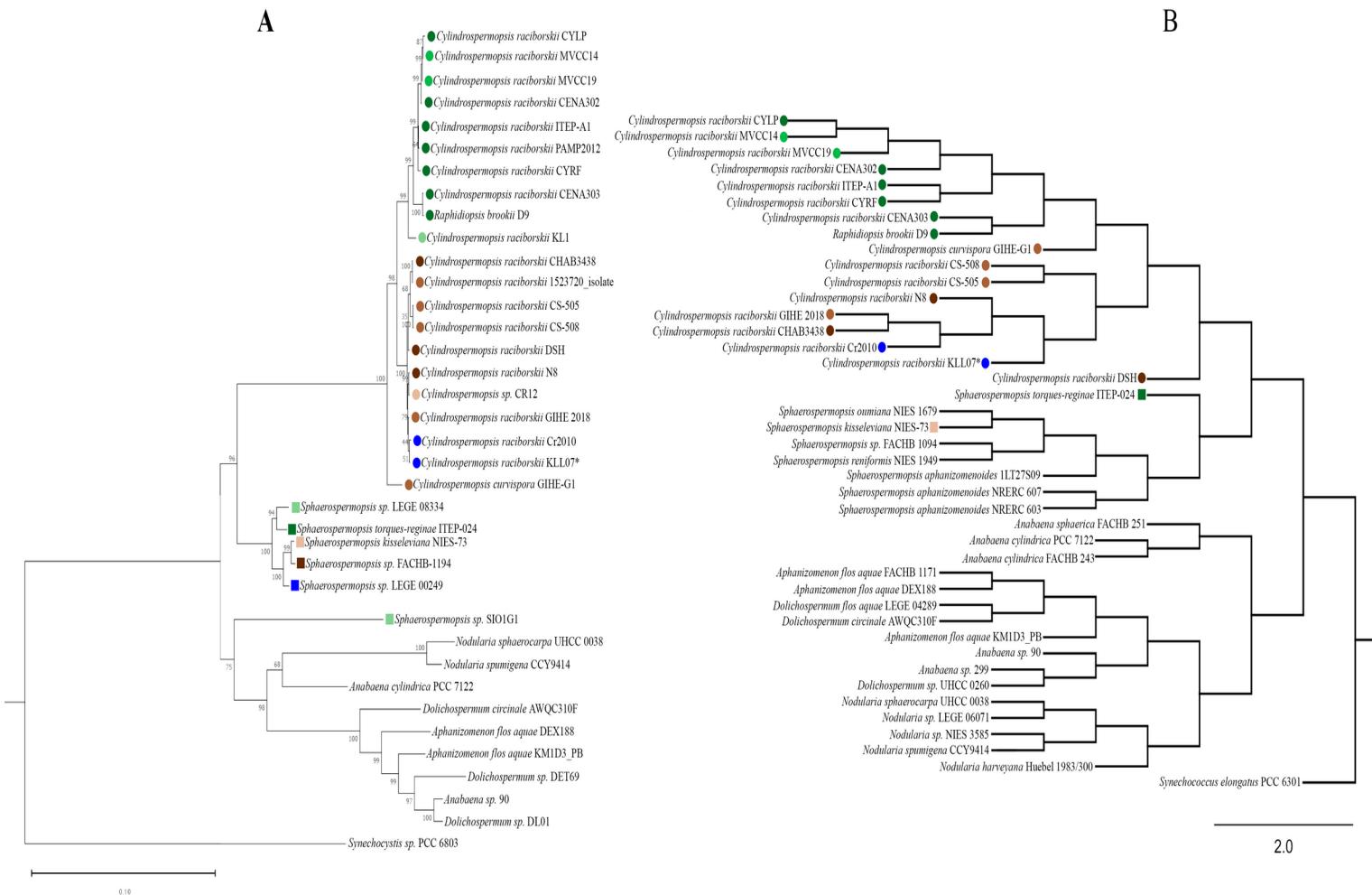


Figure 2. (A) Maximum Likelihood phylogenetic tree constructed from 31 conserved protein sequences of 37 cyanobacterial lineages. (B) Bayesian Inference phylogenetic tree derived from 16S rRNA gene nucleotide sequences of 42 cyanobacterial lineages.

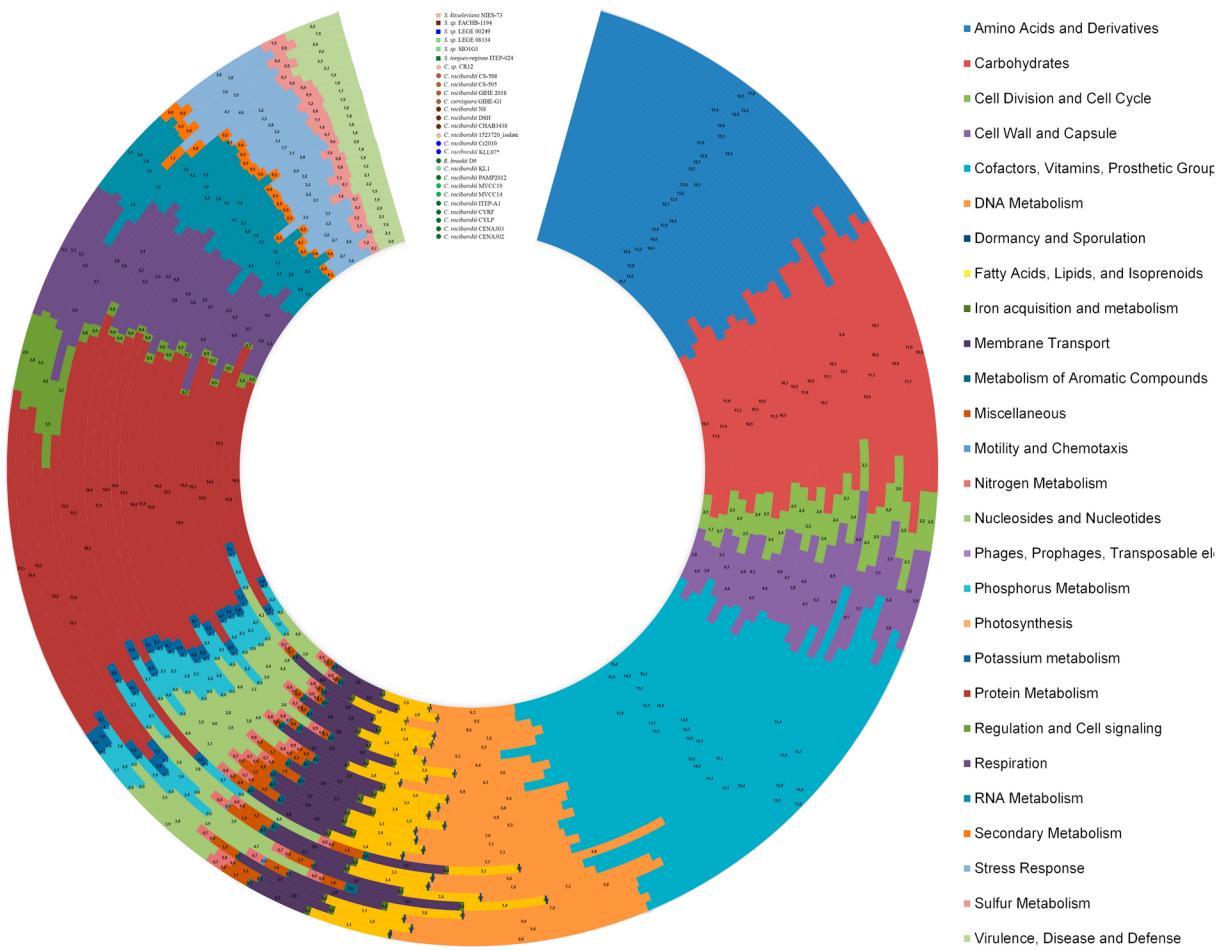


Figure S1. Comparison of automatic annotation of *Cylindrospermopsis raciborskii* strains and *Sphaerospermopsis* strains. Each layer of the circle represents a genome and each part of the layer represents a subsystem. The values represent the percentage of the subsystem of the genome strain.

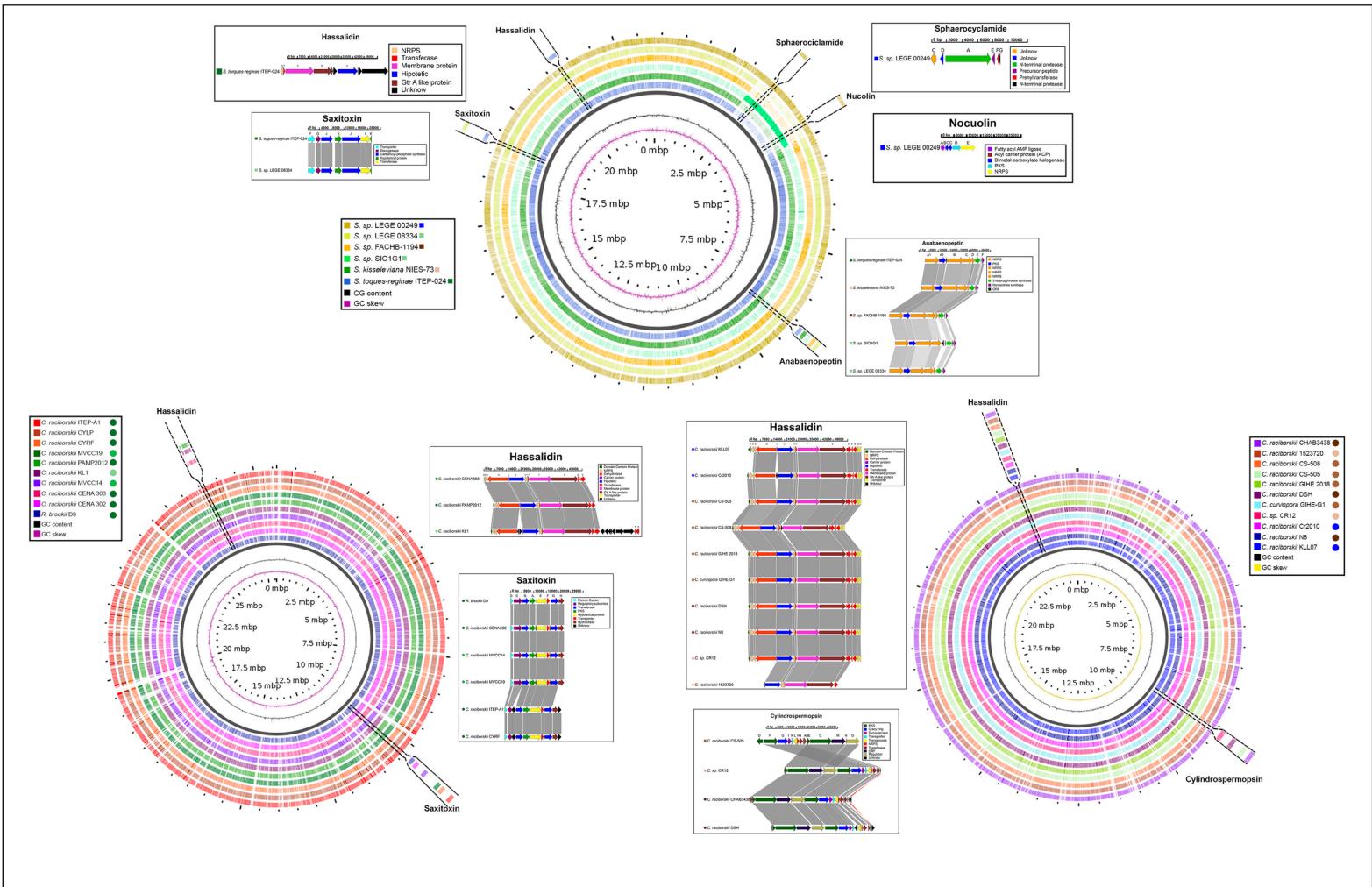


Figure 3. Blast Atlas analysis for 10 *Cylindrospermopsis raciborskii* strains from the Americas, 11 *Cylindrospermopsis raciborskii* strains Non Americas, and 6 *Sphaerospermopsis* strains. Identification of the saxitoxin (*sxt*), cylindrospermopsin (*cyr*), hassalidin (*has*), anabaenopeptin (*apt*), nocuolin (*noc*) and sphaerocyclamide (*sph*) gene clusters. These clusters are highlighted inside the boxes, and their locations in the genomes are indicated in the figure.

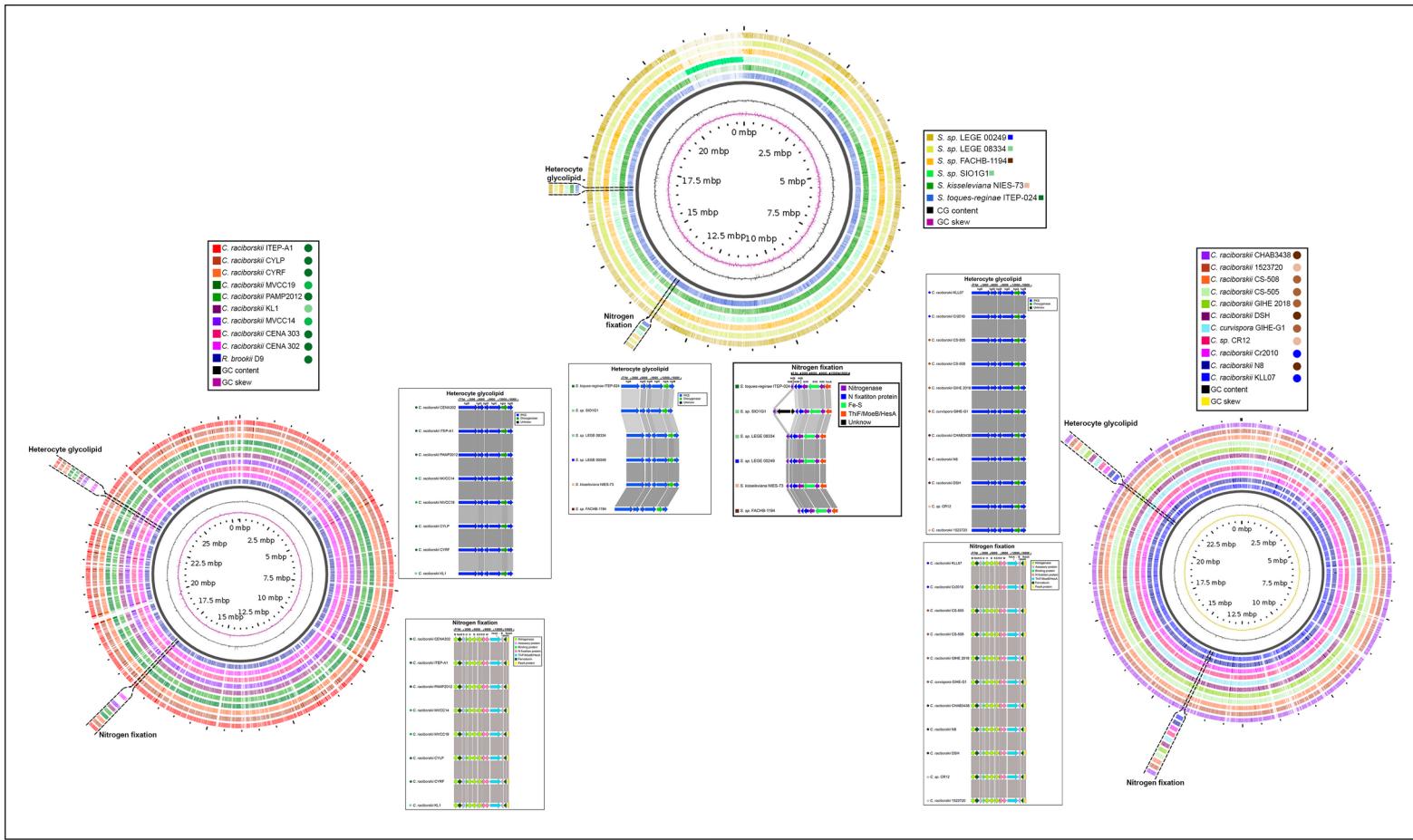


Figure S2. Blast Atlas analysis of *Cylindrospermopsis raciborskii* and *Sphaerospermopsis* strains. The figure compares 10 strains of *C. raciborskii* from the Americas, 11 strains of *C. raciborskii* from Non-Americas regions, and 6 strains of *Sphaerospermopsis*. Identified are the gene groups associated with heterocyst glycolipid (*hgl*) and nitrogen fixation (*nih*). The most conserved gene clusters among the groups, representing the core genome, are highlighted within the boxes, and their locations within the genomes are indicated in the figure.

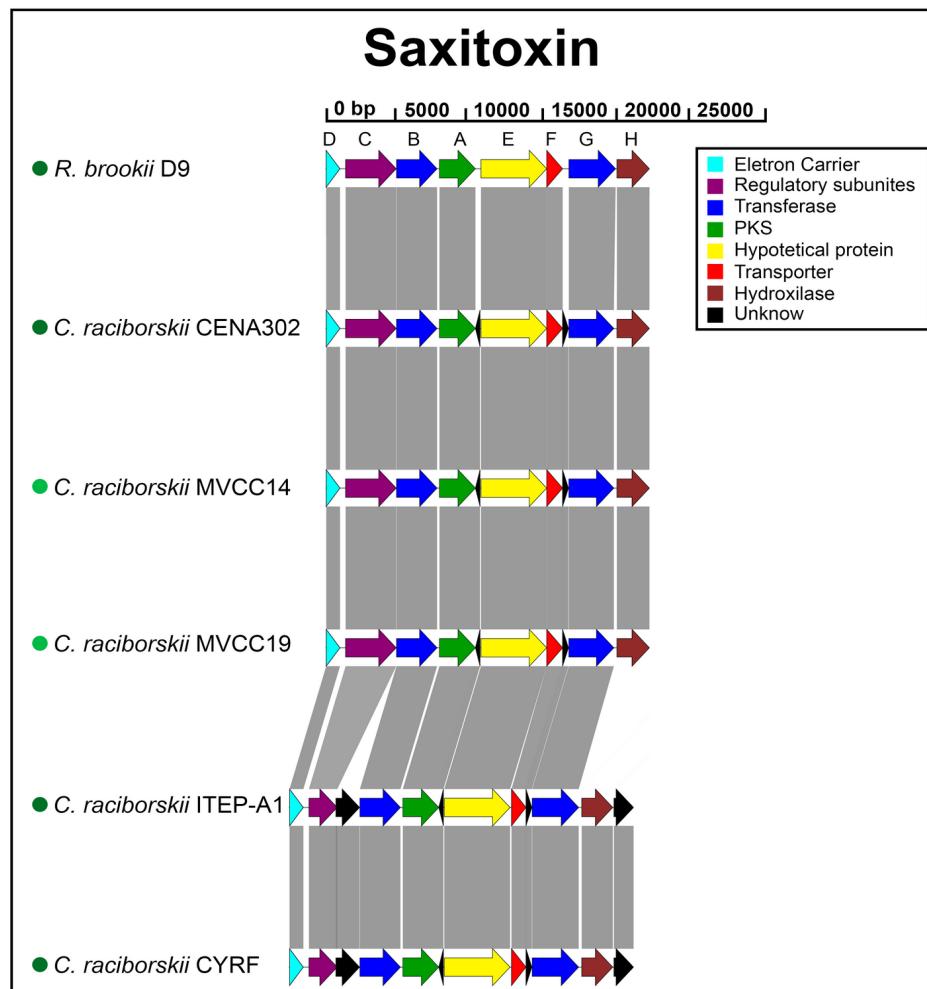


Figure S3. Clustering of saxitoxin genes (*sxt*) in *Cylindrospermopsis raciborskii* strains from the Americas. This figure shows the gene clusters associated with saxitoxin production in *Cylindrospermopsis raciborskii* strains located in the Americas. It includes the length of the gene clusters in base pairs (bp) and the function of each gene within the clusters.

Saxitoxin

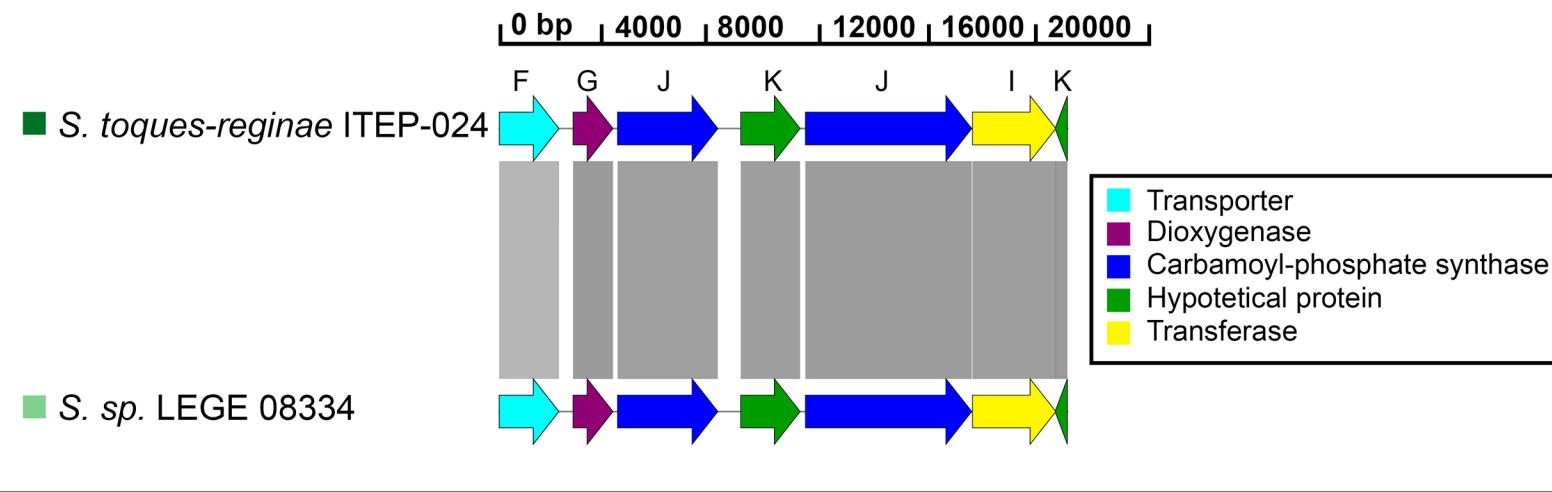


Figure S4. Saxitoxin gene clustering (*sxt*) in *Sphaerospermopsis*. This figure shows the gene clusters associated with saxitoxin production in *Sphaerospermopsis*. It includes the length of the gene clusters in base pairs (bp) and the function of each gene within the clusters. A difference of 5000 base pairs is observed when compared to the saxitoxin gene cluster in *Cylindrospermopsis raciborskii* from the Americas.

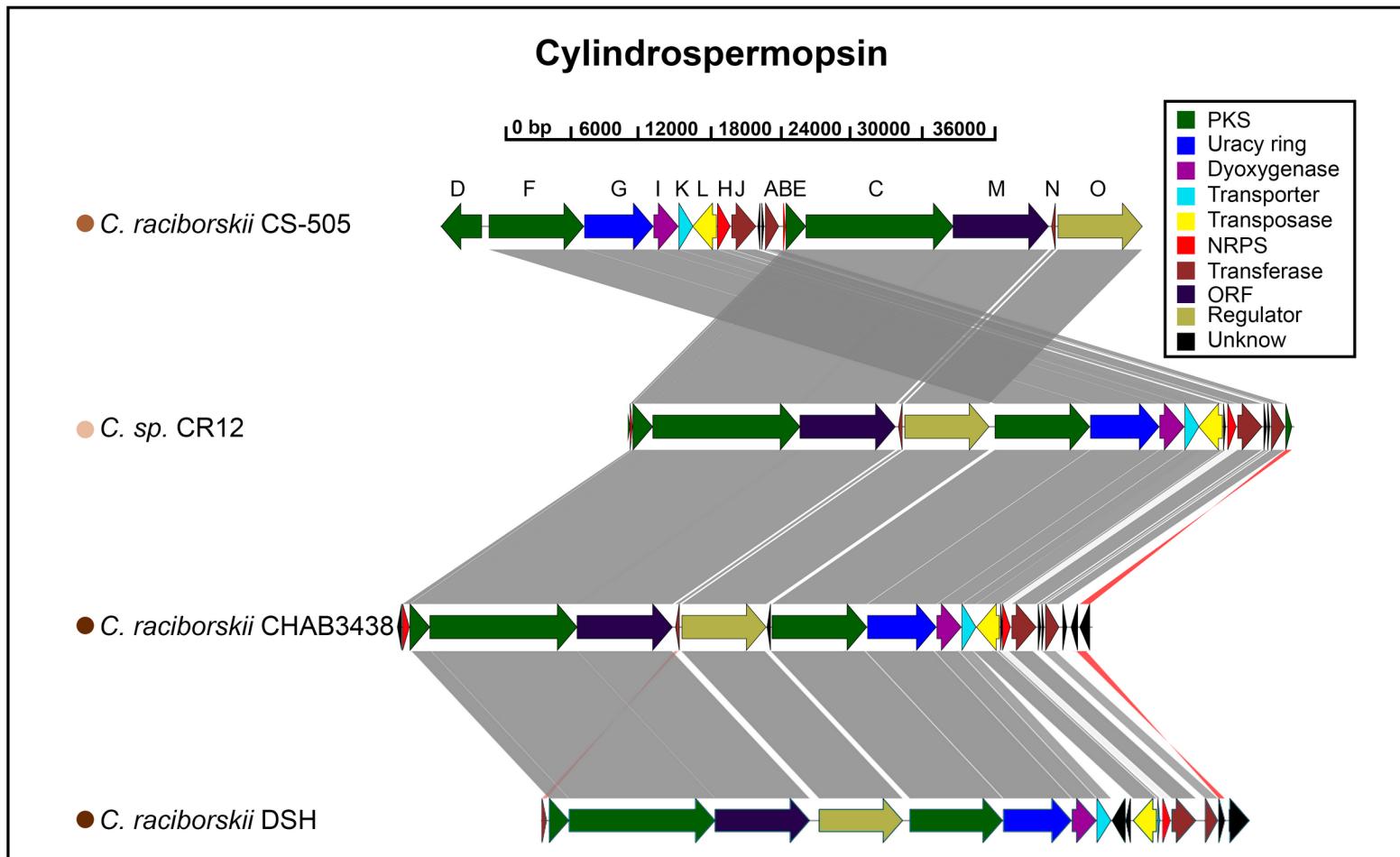


Figure S5. Cylindrospermopsin gene clustering (*cyr*) in *Cylindrospermopsis raciborskii* strains from Non-Americas regions. This figure shows the gene clusters associated with cylindrospermopsin production in *Cylindrospermopsis raciborskii* strains from the Non-Americas group. It includes the length of the gene clusters in base pairs (bp) and the function of each gene within the clusters.

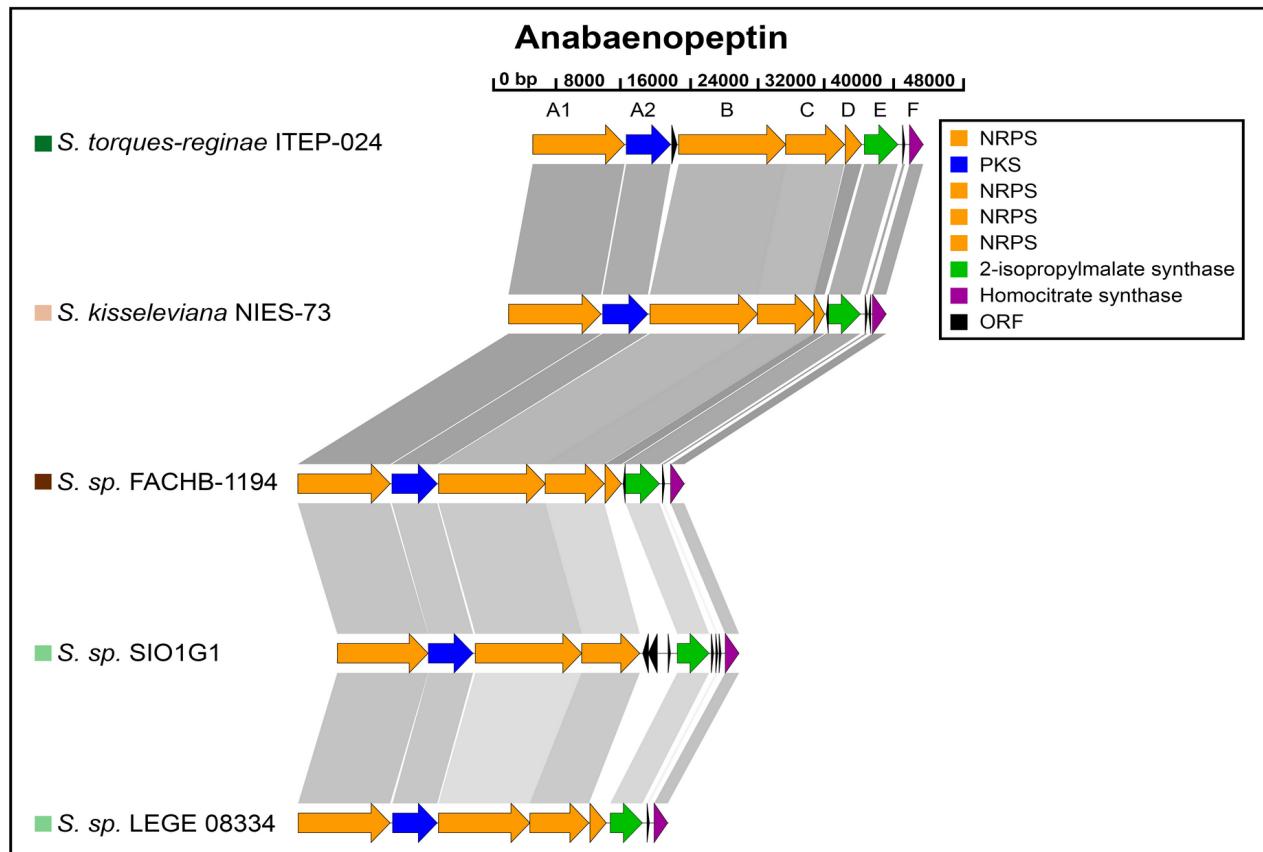


Figure S6. Anabaenopeptin gene clustering (*apt*) exclusive to the *Sphaerospermopsis* group. This figure shows the gene clusters associated with anabaenopeptin production that are exclusive to the *Sphaerospermopsis* group. It includes the length of the gene clusters in base pairs (bp) and the function of each gene within these clusters.

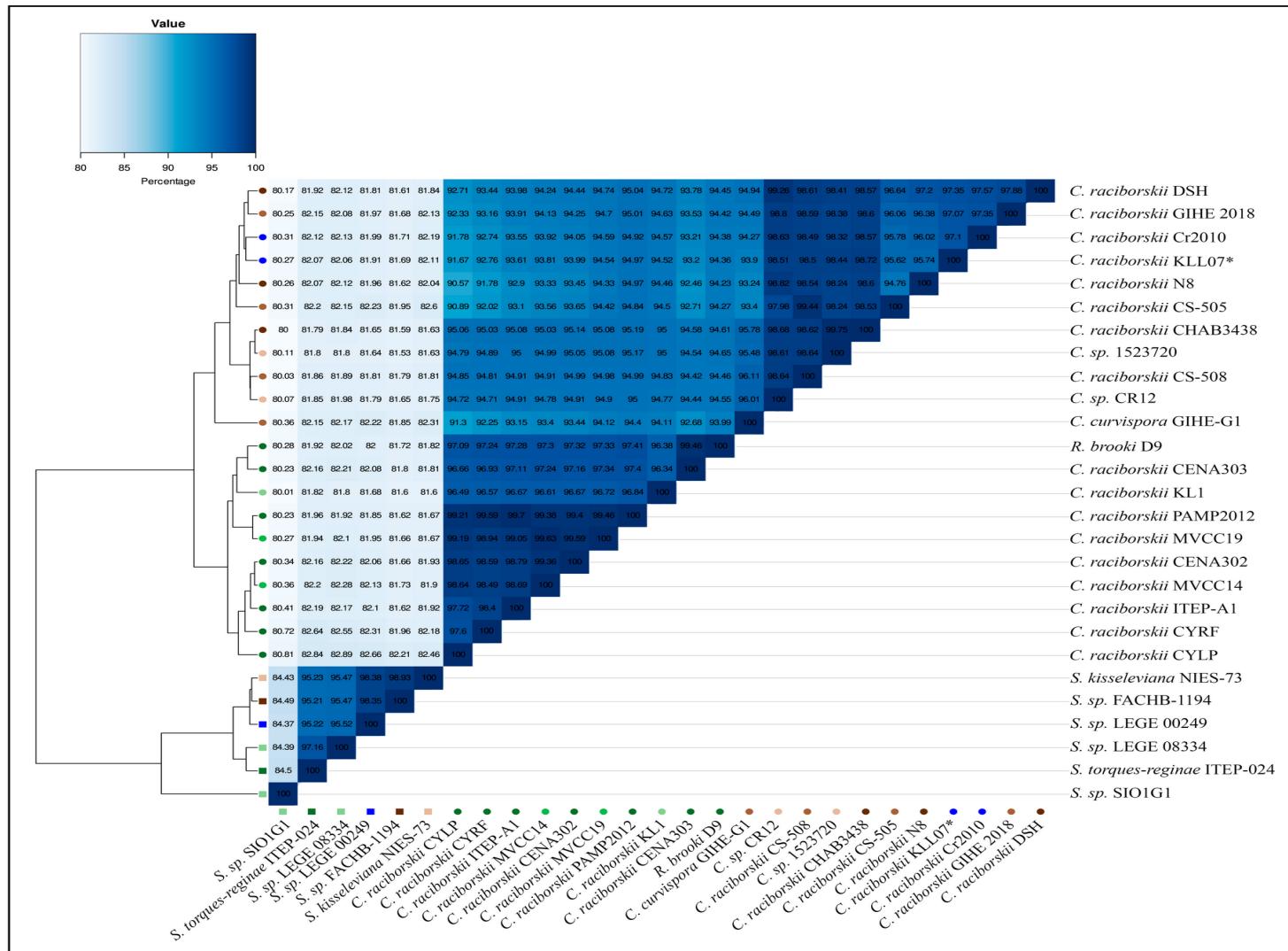


Figure S7. Pangenomic tree: Calculation of average nucleotide identity between the genera *Cylindrospermopsis* and *Sphaerospermopsis*, obtained using the Get_Homologues tool.

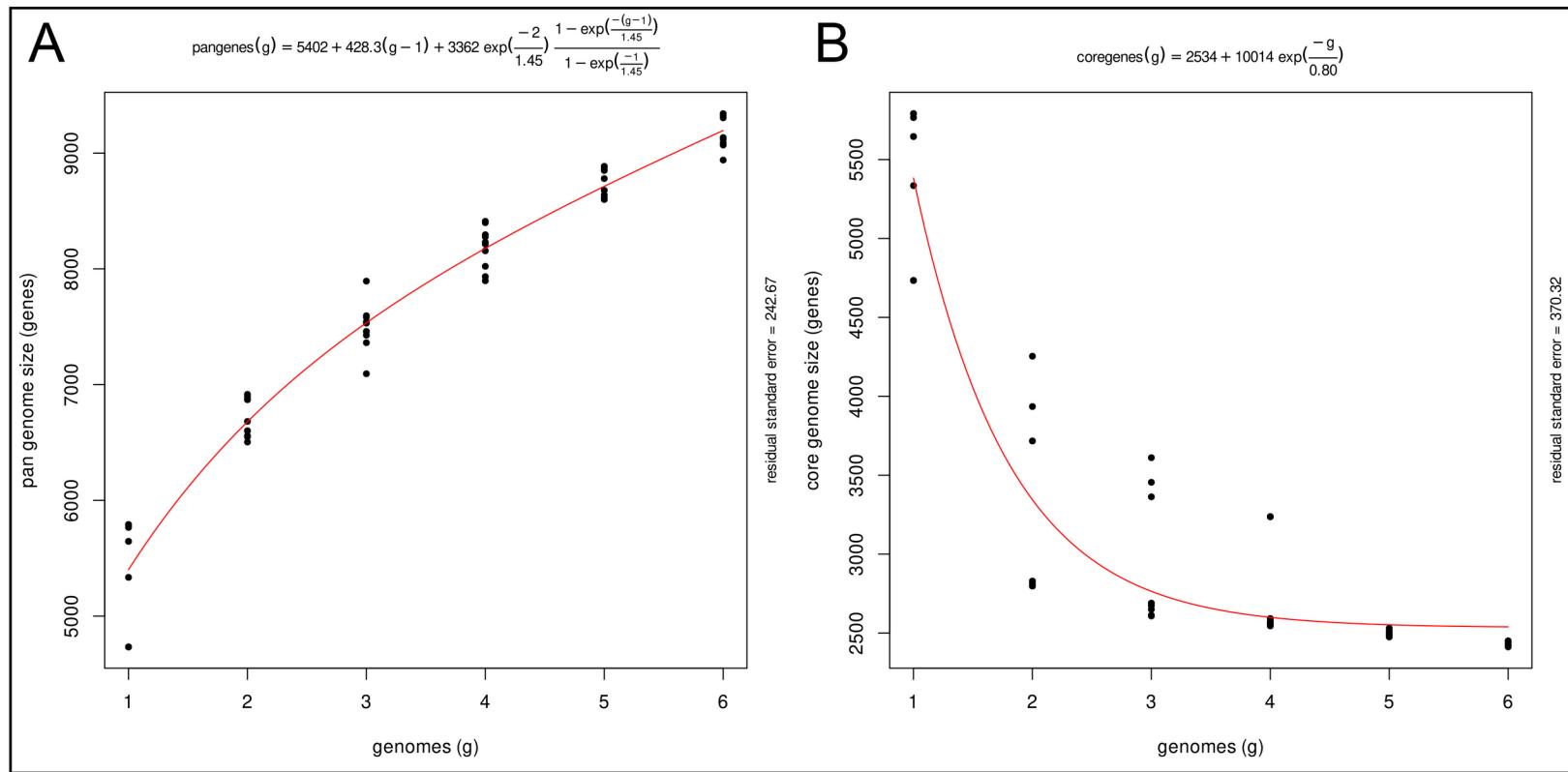


Figure S8. (A) Quantitative estimation of the pangenome in *Sphaerospermopsis* strains based on 6 available genomes. The x-axis represents the number of resampled genomes used for the estimation, and the y-axis shows the estimated number of genes. (B) Estimation of the core genome in *Sphaerospermopsis* strains based on 6 genomes. The x-axis shows the number of resampled genomes used for the estimation, while the y-axis indicates the estimated number of genes. The estimated asymptote is 2.375 genes. The evident plateau from the fifteenth genome onward demonstrates statistical robustness in the estimation.

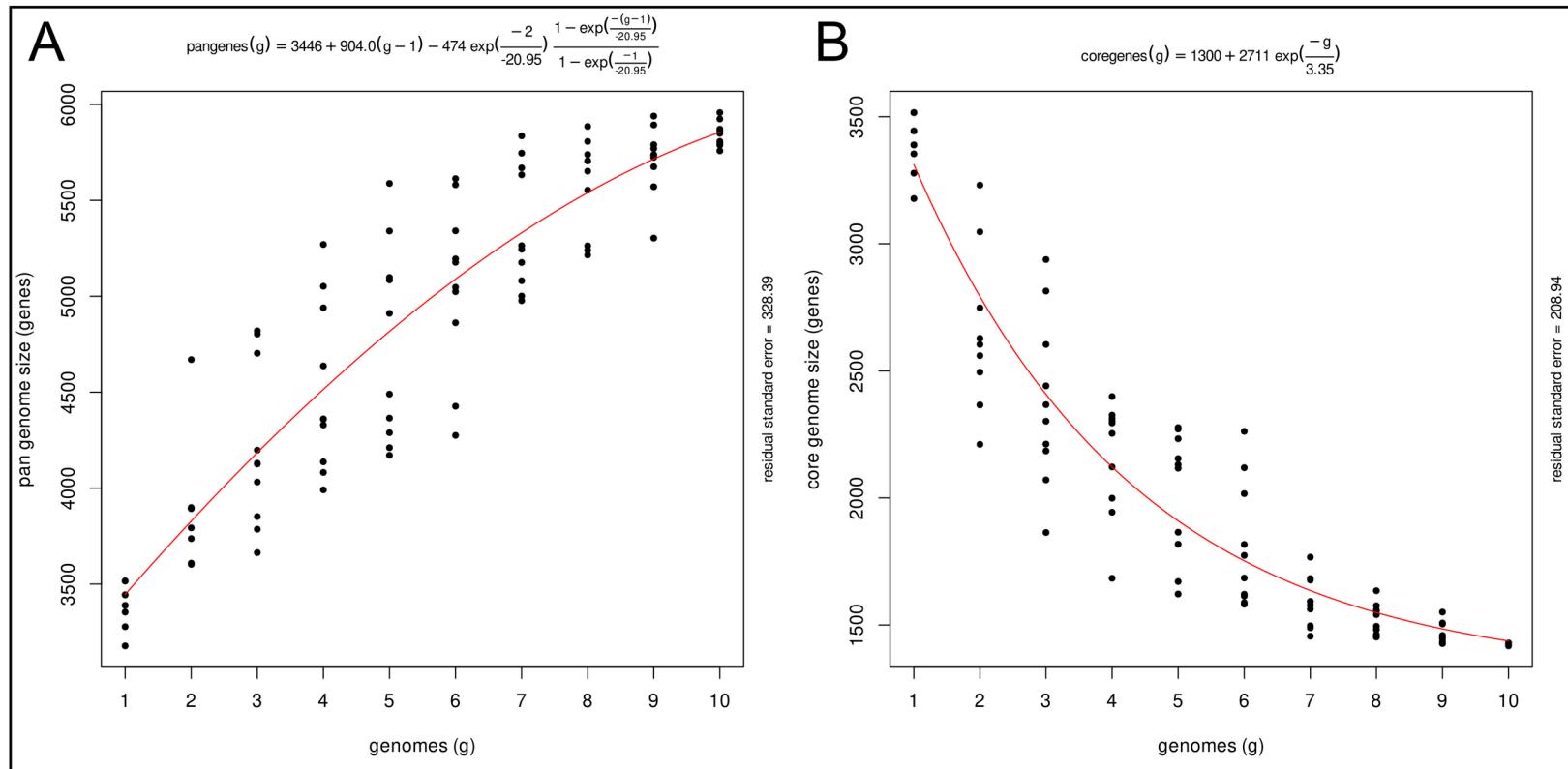


Figure S9. Pangome and core genome plot of ten *Cylindrospermopsis raciborskii* strains from the Americas. (A) Shows the progression of the pangome: the y-axis indicates the number of non-redundant genes and the x-axis indicates the number of genomes. (B) Shows the progression of the core genome: the y-axis indicates the number of genes present in all strains and the x-axis indicates the number of genomes. The estimated asymptote is 1.410 genes. estimation.

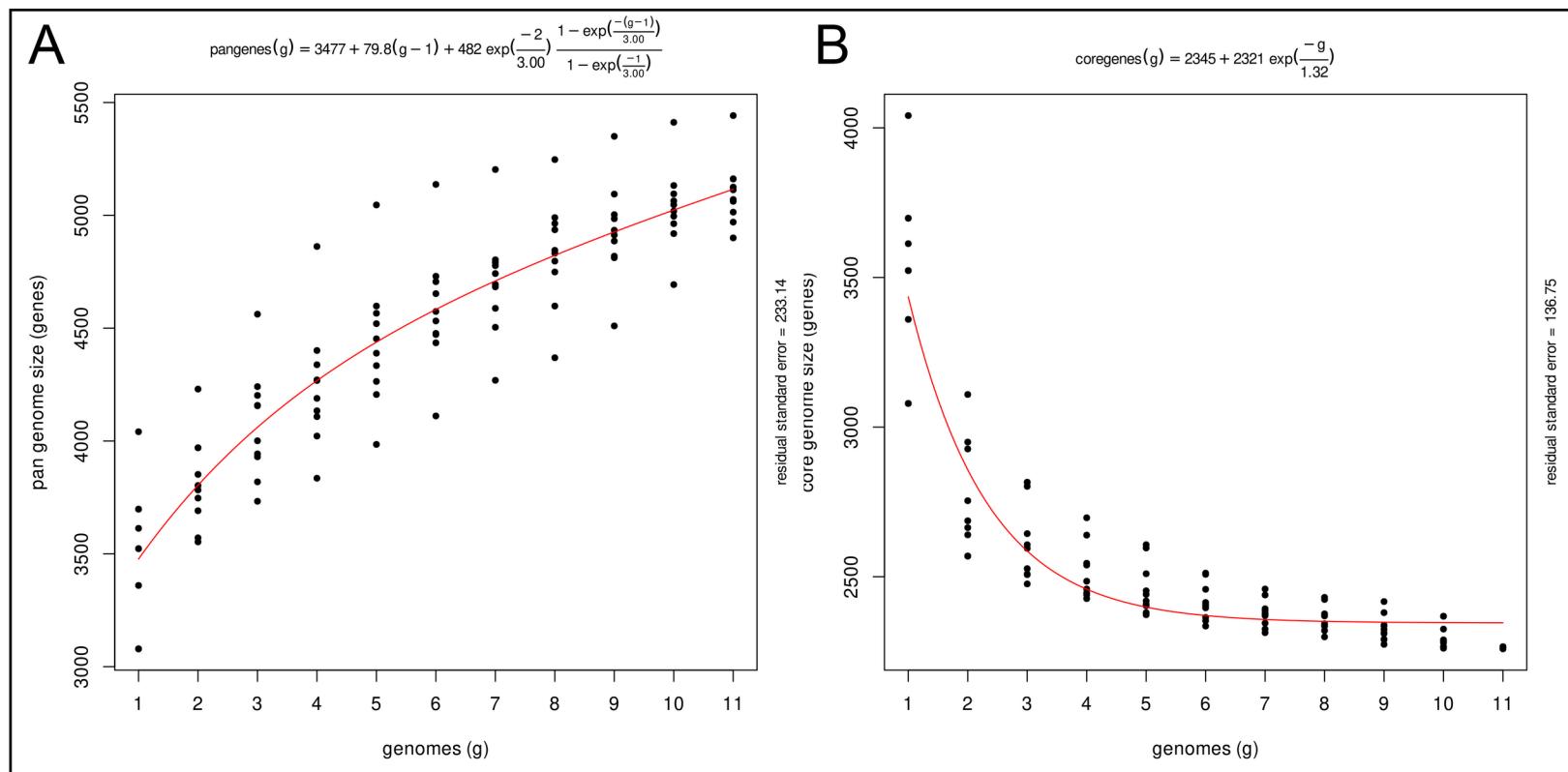


Figure S10. Pangenome and core genome plot of eleven *Cylindrospermopsis raciborskii* strains from the Non Americas. (A) Shows the progression of the pangenome: the y-axis indicates the number of non-redundant genes and the x-axis indicates the number of genomes. (B) Shows the progression of the core genome: the y-axis indicates the number of genes present in all strains and the x-axis indicates the number of genomes. The estimated asymptote is 2.249 genes. The evident plateau from the eighth genome onward demonstrates statistical robustness in the estimation.

Sphaerocyclamide

0 bp | 2000 | 4000 | 6000 | 8000 | 10000

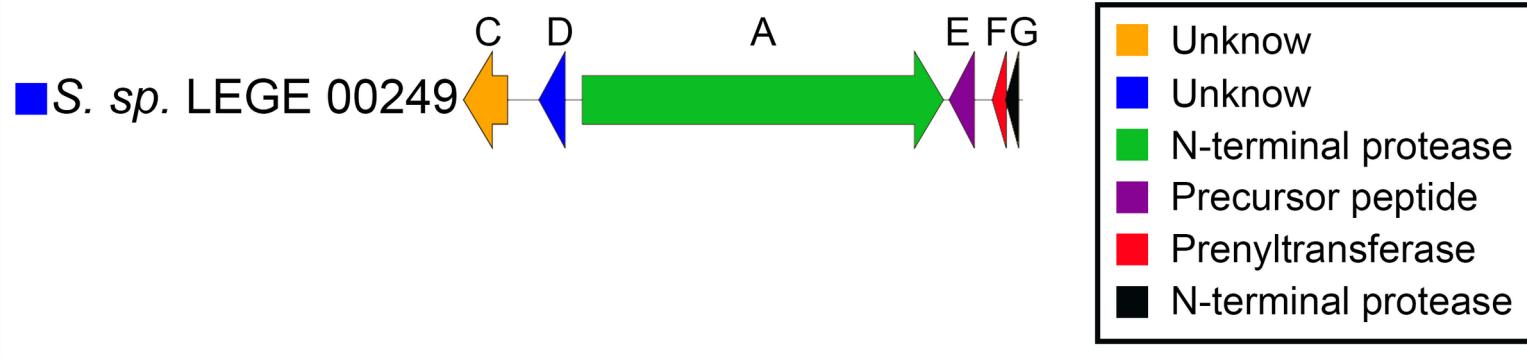


Figure S11. Cluster of Sphaerocyclamide (*sph*) genes in the *S. sp. LEGE 00249* strain. This figure shows the gene clusters associated with Sphaerocyclamide production in the *S. sp. LEGE 00249* strain, including the length of the gene clusters in base pairs (bp) and the function of each gene within these clusters.

Nocuolin

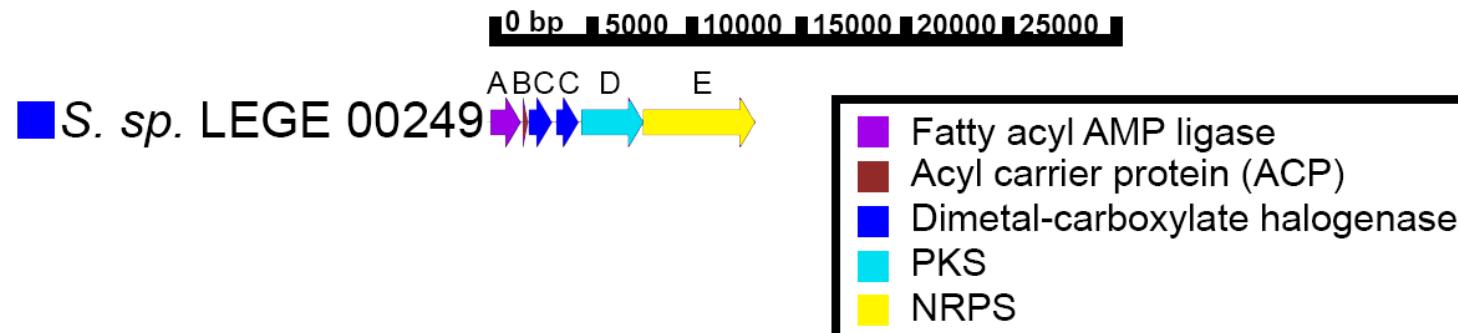


Figure S12. Cluster of Nocuolin (*noc*) genes in the *S. sp.* LEGE 00249 strain. This figure shows the gene clusters associated with Nocuolin production in the *S. sp.* LEGE 00249 strain, including the length of the gene clusters in base pairs (bp) and the function of each gene within these clusters.

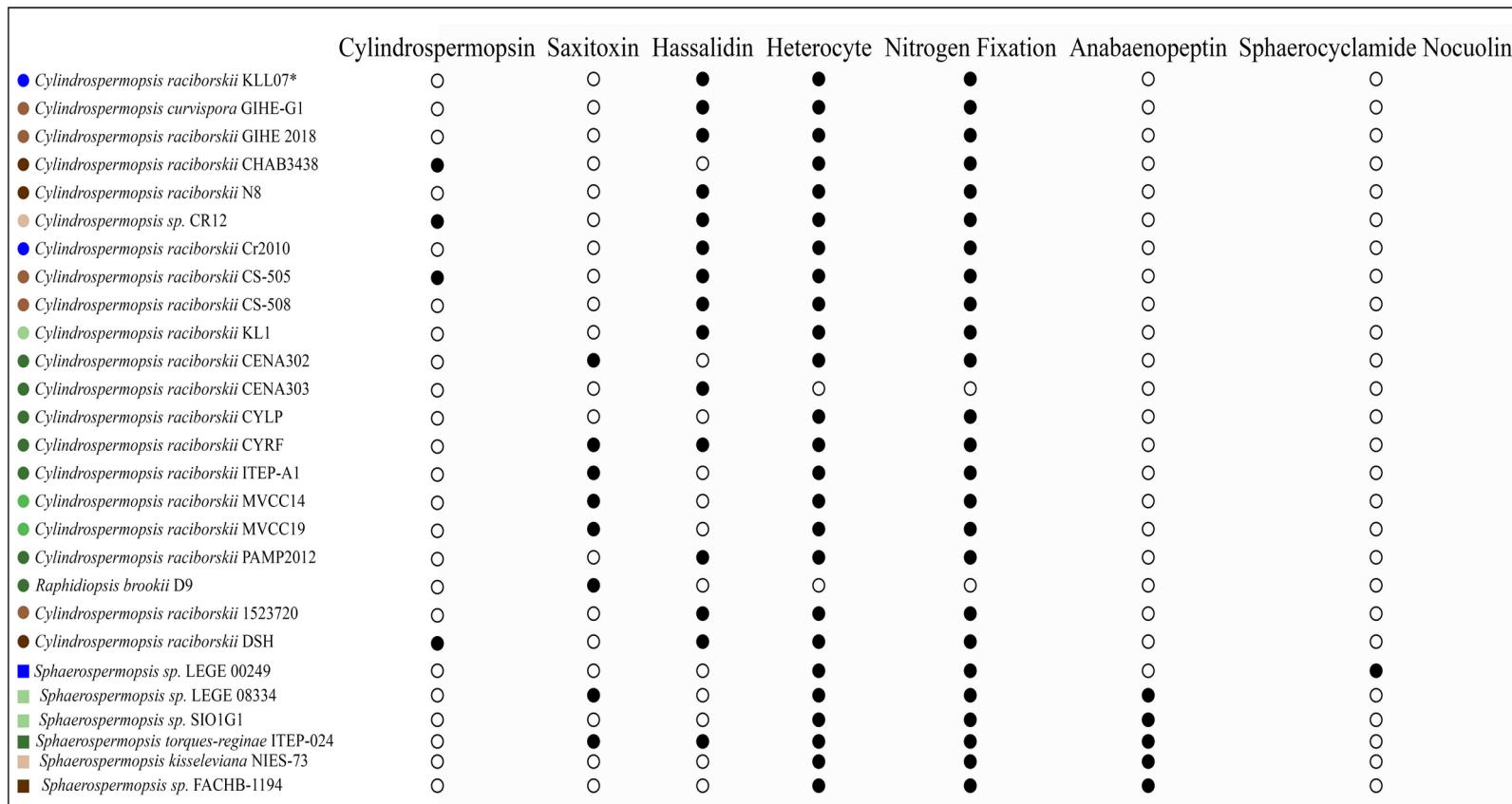


Figure S13. Comparison of the presence (filled circles) or absence (empty circles) of the genotypes assessed in this study (hassallidin, cylindrospermopsin, saxitoxin, heterocyte glycolipides, nitrogen fixation, anabaenopeptin, sphaerocyclamide, and nocuolin).