

**Table S1.** Summary of long-read algal genomics and associated assembly metrics.

| Reference           | Reported algae                     | Algal group   | DNA extraction kit                          | Sequencing platforms                                              | Assembly metrics (size, contigs, N50, BUSCOs (C))                                                              |
|---------------------|------------------------------------|---------------|---------------------------------------------|-------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------|
| Guo et al., 2019    | <i>Nannochloropsis oceanica</i>    | Ochrophyta    | CTAB protocol                               | Sequel (PacBio),<br>HiSeq X (Illumina),<br>HiSeq 4000 (Illumina)  | Size: 29.3 Mb<br>Contigs: 129<br>N50: 664.749 kb<br>BUSCO: 87.1 % (C)                                          |
| Liu et al., 2020    | <i>Mychonastes homosphaera</i>     | Chlorophyta   | Genomic DNA Extraction Kit (Qiagen)         | Sequel (PacBio)                                                   | Size: 24.23 Mb<br>Contigs: 31<br>N50: 2 Mb<br>BUSCO: 89.4% (C)                                                 |
| Wang et al., 2020   | <i>Pyropia yezoensis</i>           | Rhodophyta    | HMW DNA extraction from plant               | RSII (PacBio),<br>HiSeq 2000 (Illumina),<br>Irys (Bionano)        | Size: 108 Mb<br>Contigs: 660<br>N50: 340.8 kb<br>BUSCO: 84%                                                    |
| Zhang et al., 2020  | <i>Chlamydomonas</i> sp. ICE-L     | Chlorophyta   | DNeasy Plant Mini Kit (Qiagen)              | HiSeq X (Illumina),<br>GemCode (10X Genomics),<br>Sequel (PacBio) | Size: 541.86 Mb<br>Superscaffold (>100 bp): 946<br>N50: 19.23 Mb<br>BUSCO: 83.7% (C)                           |
| Dreher et al., 2021 | Nostocales (ADA clade; 16 genomes) | Cyanobacteria | DNeasy PowerBiofilm extraction kit (Qiagen) | Sequel (PacBio),<br>HiSeq 3000 (Illumina)                         | 16 genomes (9 C)<br>Size: 4.36-6.07 Mbp<br>Contigs:1 (C); Others: 4-286<br>N50: N/A<br>BUSCO: 94.19-99.89% (C) |

|                         |                                                             |             |                                                                                      |                                                                                             |                                                                                                                                   |
|-------------------------|-------------------------------------------------------------|-------------|--------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------|
| Hulatt et al.,<br>2021  | <i>Diacronema lutheri</i> (former <i>Pavlova lutheri</i> )  | Haptophyta  | N/A                                                                                  | MiSeq (Illumina),<br>Sequel (PacBio)                                                        | Size: 43.5 Mb<br>Contigs: 103<br>N50: 852.26 kbp<br>BUSCO: 80.80 % (C)                                                            |
| Chen et al.,<br>2022    | <i>Neoporphyra haitanensis</i>                              | Rhodophyta  | CTAB protocol                                                                        | Sequel (PacBio),<br>HiSeq (Illumina)                                                        | Size: 49.67 Mb<br>Contig N50: 650 kb<br>Scaffold N50: 7.796Mb<br>BUSCO: 85.8%                                                     |
| Cho et al., 2023        | 6 genomes <i>Cyanidiophyceae</i>                            | Rhodophyta  | CTAB protocol                                                                        | Sequel II (PacBio),<br>PromethION (ONT),<br>HiSeq2500 (Illumina),<br>NovaSeq6000 (Illumina) | 6 genomes <i>Cyanidiophyceae</i><br>Size: 8.79-16.5 Mb<br>Scaffolds: 20; 76-433<br>N50: 172.3-202.1 kbp<br>BUSCO: 94.1-96.7 % (C) |
| Gueidan et al.,<br>2023 | <i>Diplosphaera chodatii</i> strain CS-1475                 | Chlorophyta | Illumina: Phenol-<br>chloroform and SDS/BME<br>lysis buffer<br>PacBio: CTAB protocol | NextSeq 500 (Illumina),<br>Sequel (PacBio)                                                  | Size: 85.6 Mb<br>Contigs: 62<br>N50: 2.626 Mb<br>BUSCO: 88.4% (C)                                                                 |
| Chen et al.,<br>2024    | <i>Phaeocystis globosa</i>                                  | Haptophyta  | Plant DNA Mini Kit<br>(Omega)                                                        | Sequel (PacBio),<br>Illumina platform                                                       | Size: 129.7 Mb<br>Contigs: 396<br>N50: 569.7 kbp<br>Scaffolds: 85; N50 scaff.: 6601.8<br>kbp<br>BUSCO: 80.9 % (C)                 |
| Jian et al., 2024       | <i>Prymnesium parvum</i> strains CCMP 3037<br>and UTEX 2797 | Haptophyta  | DNeasy Plant Kit (Qiagen)                                                            | MGISEQ-2000 (MGI),<br>Sequel II (PacBio)                                                    | Size: UTEX 2797 - 97.56 Mb<br>CCMP 3037 - 107.32 Mb<br>Contigs: 463 & 362<br>N50: 596.99 kbp & 968.39 kbp                         |

|                         |                                                                                                                                                                                                                          |               |                                            |                                                                 |  |                                                                                                                                                                            |
|-------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------|--------------------------------------------|-----------------------------------------------------------------|--|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|                         |                                                                                                                                                                                                                          |               |                                            |                                                                 |  | Scaffolds: 34; N50 scaff.: 5.35 Mb<br>& 3.61 Mb<br>BUSCO: 81.2% (C) & 77.2% (C)                                                                                            |
| Moretto et al.,<br>2024 | <i>Umezakia ovalisporum</i> BLCC-F208,<br><i>Microcystis</i> sp. BLCC-F209, <i>Microcystis</i> sp.<br>BLCC-F210, <i>Pelatocladus</i> sp. BLCC-F211,<br><i>U. ovalisporum</i> BLCC-F215, <i>Raphidiopsis</i><br>BLCC-F218 | Cyanobacteria | DNeasy PowerSoil Kit<br>(Qiagen)           | HiSeq (Illumina),<br>N/A (ONT)                                  |  | Size: 4.9 Mb<br>Contigs: 1(ONT); 55-349<br>(Illumina)<br>N50: 4.9 Mb (ONT); 22.4-135.4<br>kbp (Illumina)<br>BUSCO (ONT): 99.1% (C),<br>BUSCO (Illumina): 85-99.96 %<br>(C) |
| Raymond et<br>al., 2024 | <i>Sanguina aurantia</i><br><i>C.reinhardtii</i> (reference)                                                                                                                                                             | Chlorophyta   | Plant DNA Isolation Kit<br>(Norgen Biotek) | PromethION (ONT),<br>HiSeq (Illumina)                           |  | A & B genomes<br>Size: 96 Mb & 102 Mb<br>Scaffolds: 38 & 50<br>N50: 5.42 Mb & 6.41 Mb<br>BUSCO: 87.4% (C) & 81.9%<br>(C):98.9% (ref.)                                      |
| Petroll et al.,<br>2025 | <i>Bostrychia moritziana</i>                                                                                                                                                                                             | Rhodophyta    | CTAB protocol                              | MinION (ONT),<br>Sequel II (PacBio),<br>NextSeq 2000 (Illumina) |  | Size: 1.04 Gb<br>Contigs: 32<br>N50: N/A<br>BUSCO: 74.5% (C)                                                                                                               |

**Abbreviations:** CTAB - cetyltrimethylammonium bromide; HMW - high molecular weight; (C) - genome completeness %; N/A - not available.

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