# ERGA Assembly Report

v24.10.15

Tags: ATLASea[INVALID TAG]

| | |
|---|---|
| TxID | 1503747 |
| ToLID | **urMesExpa1** |
| Species | Mesophyllum expansum |
| Class | Florideophyceae |
| Order | Hapalidiales |

| Genome Traits | Expected | Observed |
|---|---|---|
| Haploid size (bp) | 139,914,054 | 134,486,399 |
| Haploid Number | 4 (source: ancestor) | 23 |
| Ploidy | 4 (source: ancestor) | 2 |
| Sample Sex | Unknown | Unknown |

## EBP metrics summary and curation notes

Obtained EBP quality metric for collapsed: 6.6.Q43

The following metrics were automatically flagged as below EBP recommended standards or different from expected:

. Observed Haploid Number is different from Expected
. Observed Ploidy is different from Expected

. Kmer completeness value is less than 90 for collapsed
. BUSCO single copy value is less than 90% for collapsed

### Curator notes

. Interventions/Gb: 119
. Contamination notes: ""
. Other observations: "The assembly of Mesophyllum expansum (urMesExpa1) is based on 103X PacBio data and 230X Arima Hi-C data generated as part of the ATLASea programme (https://www.atlasea.fr). The assembly process included the following steps: initial PacBio assembly generation with Hifiasm, removal of contaminant sequences using Context, removal of haplotypic duplications using purge_dups, and Hi-C-based scaffolding with YaHS. In total, 324 contigs were identified as contaminants (bacterial, archaeal, or viral), totaling 13.535 Mb (with the largest being 0.181 Mb). Additionally, 153 regions totaling 8.302 Mb (with the largest being 1.369 Mb) were identified as haplotypic duplications and removed. Mitochondrial and chloroplastic genomes were assembled using OATK. Finally, the primary assembly was analyzed and manually improved using Pretext. During manual curation, 9 contaminant sequences were removed, totaling 0.727Mb (with the largest being 0.257Mb). Additionally, several regions were identified as potential haplotypic duplications. However, in each case, the two copies were located within two different

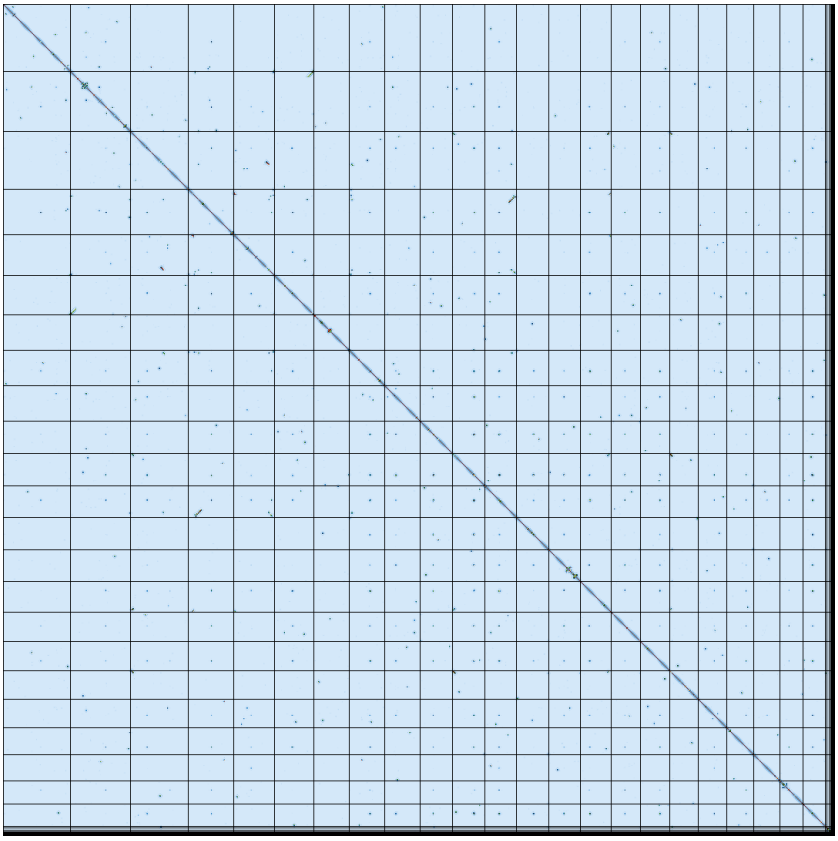
chromosome-scale scaffolds rather than corresponding to individual contigs. These regions were therefore retained in the final assembly. For example, potentially duplicated regions were identified on chromosome 3 (4.8-5.2 Mb) and chromosome 5 (5.2-5.6 Mb). Chromosome-scale scaffolds confirmed by Hi-C data were named in order of size. "

# Quality metrics table

| Metrics | Pre-curation collapsed | Curated collapsed |
|---|---|---|
| Total bp | 134,997,649 | 134,486,399 |
| GC % | 45.36 | 45.4 |
| Gaps/Gbp | 125.93 | 111.54 |
| Total gap bp | 1,700 | 1,900 |
| Scaffolds | 238 | 43 |
| Scaffold N50 | 4,498,349 | 5,678,113 |
| Scaffold L50 | 13 | 9 |
| Scaffold L90 | 30 | 20 |
| Contigs | 255 | 58 |
| Contig N50 | 4,390,000 | 5,207,890 |
| Contig L50 | 13 | 10 |
| Contig L90 | 39 | 23 |
| QV | 41.9396 | 43.2828 |
| Kmer compl. | 74.3183 | 74.3703 |
| BUSCO sing. | 74.1% | 74.5% |
| BUSCO dupl. | 3.1% | 2.7% |
| BUSCO frag. | 7.5% | 7.5% |
| BUSCO miss. | 15.3% | 15.3% |

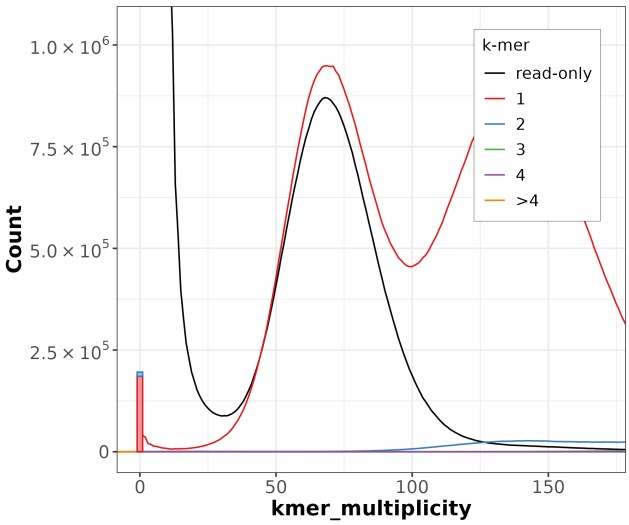
BUSCO: 5.4.3 (euk_genome_met, metaeuk) / Lineage: eukaryota_odb10 (genomes:70, BUSCOs:255)

# HiC contact map of curated assembly

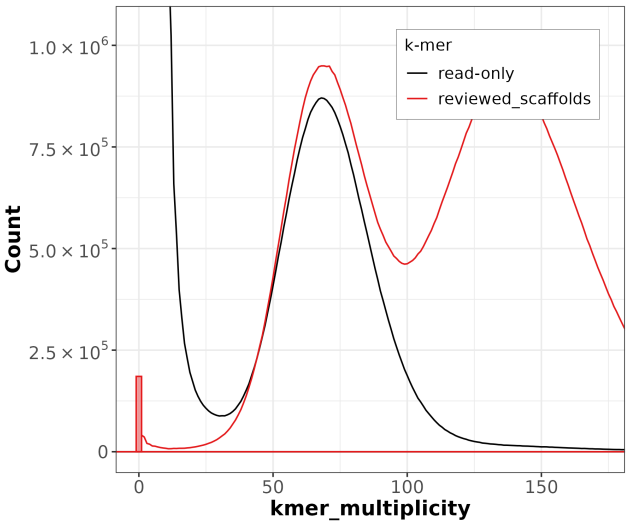


**collapsed** [LINK]

# K-mer spectra of curated assembly

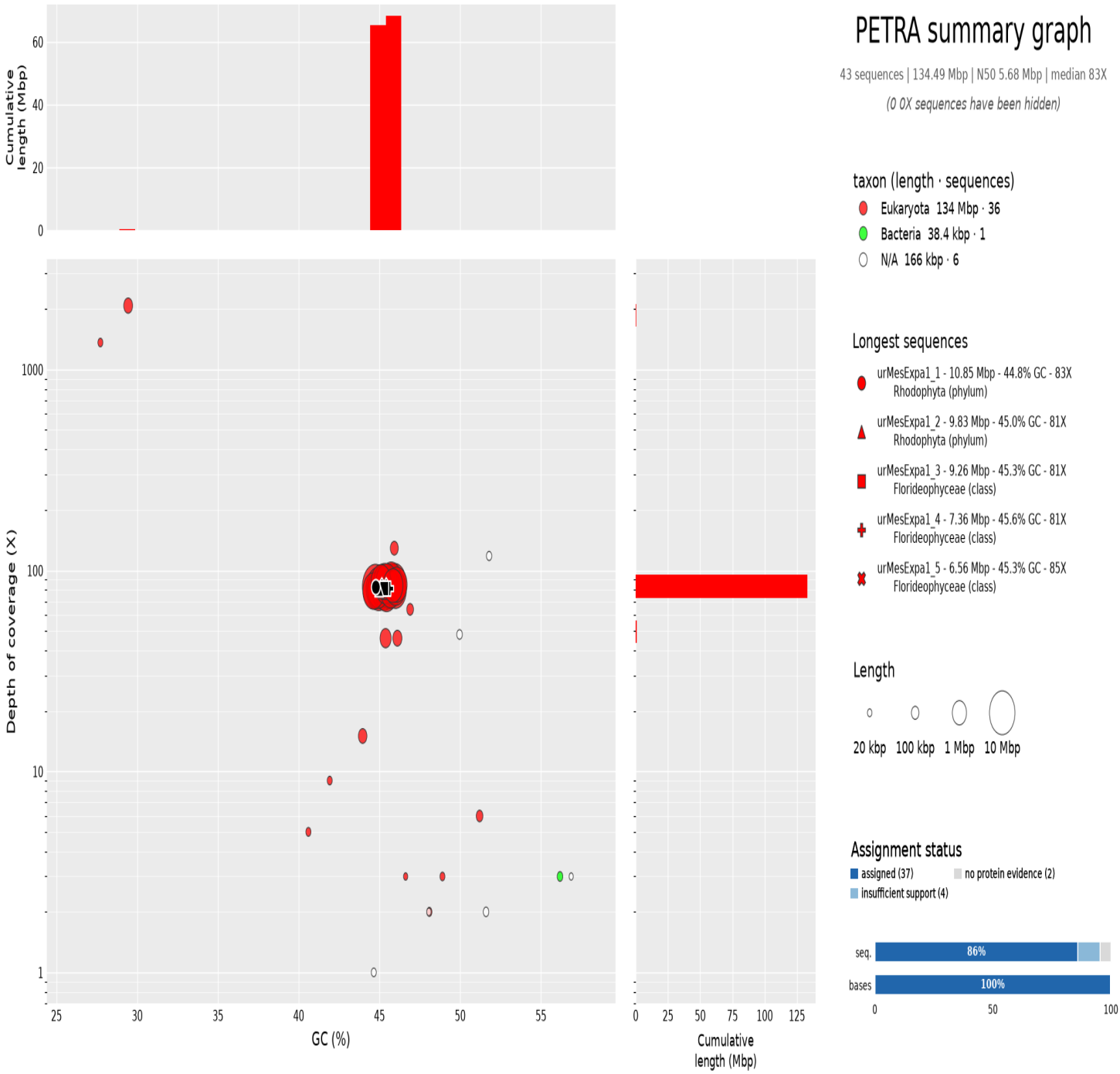



Distribution of k-mer counts per copy numbers found in asm




Distribution of k-mer counts coloured by their presence in reads/assemblies

# Post-curation contamination screening




**collapsed.** Bubble plot circles are scaled by sequence length, positioned by coverage and GC proportion, and coloured by taxonomy. Histograms show total assembly length distribution on each axis.

# Data profile

| Data | Long reads | Arima |
|---|---|---|
| Coverage | 103 | 230 |

# Assembly pipeline

- **Hifiasm**
    |_ *ver:* 0.19.5-r593
    |_ *key param:* NA
- **purge_dups**
    |_ *ver:* 1.2.5
    |_ *key param:* NA
- **YaHS**
    |_ *ver:* 1.2
    |_ *key param:* NA

# Curation pipeline

- **PretextMap**
    |_ *ver:* 0.2.4
    |_ *key param:* NA
- **PretextView**
    |_ *ver:* 1.0.7
    |_ *key param:* NA

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