

ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

| | |
|---------|---------------------|
| TxID | 1172132 |
| ToLID | cbLewAcum8.1 |
| Species | Lewinskya acuminata |
| Class | Bryopsida |
| Order | Orthotrichales |

| Genome Traits | Expected | Observed |
|-------------------|----------------------|-------------|
| Haploid size (bp) | 273,294,980 | 256,705,263 |
| Haploid Number | 6 (source: ancestor) | 6 |
| Ploidy | 1 (source: ancestor) | 2 |
| Sample Sex | Unknown | Unknown |

EBP metrics summary and curation notes

Obtained EBP quality metric for collapsed: 7.7.Q54

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

- . Observed Ploidy is different from Expected
- . BUSCO single copy value is less than 90% for collapsed
- . BUSCO duplicated value is more than 5% for collapsed

Curator notes

. Interventions/Gb: 85
. Contamination notes: ""
. Other observations: "The assembly of LEWINSKYA ACUMINATA (cbLewAcum8) is based on 69X PacBio data and 202X Arima Hi-C data generated as part of the European Reference Genome Atlas (ERGA, <https://www.erga-biodiversity.eu/>) via the Biodiversity Genomics Europe project (BGE, <https://biodiversitygenomics.eu/>). The assembly process included the following steps: initial PacBio assembly generation with Nextdenovo, removal of contaminant sequences using Context, removal of haplotypic duplications using purge_dups, and Hi-C-based scaffolding with YaHS. In total, 32 regions totaling 4 Mb were identified as haplotypic duplications and removed. Additionally, 114 contigs were identified as contaminants (bacterial, archaeal, or viral), totaling 23 Mb (with the largest being 4 Mb). The mitochondrial genome was assembled using OATK. Finally, the primary assembly was analyzed and manually improved using Pretext. During manual curation, 8 haplotypic regions and 5 contaminant sequences were removed, totaling 423,178 pb and 456,681 pb, respectively (with the largest being 180,566 pb and 162,112 pb). There is a large haplotypic inversion between ~3.79-4.36Mb (chr 1). Chromosome-scale scaffolds confirmed by Hi-C data were named in order of size and

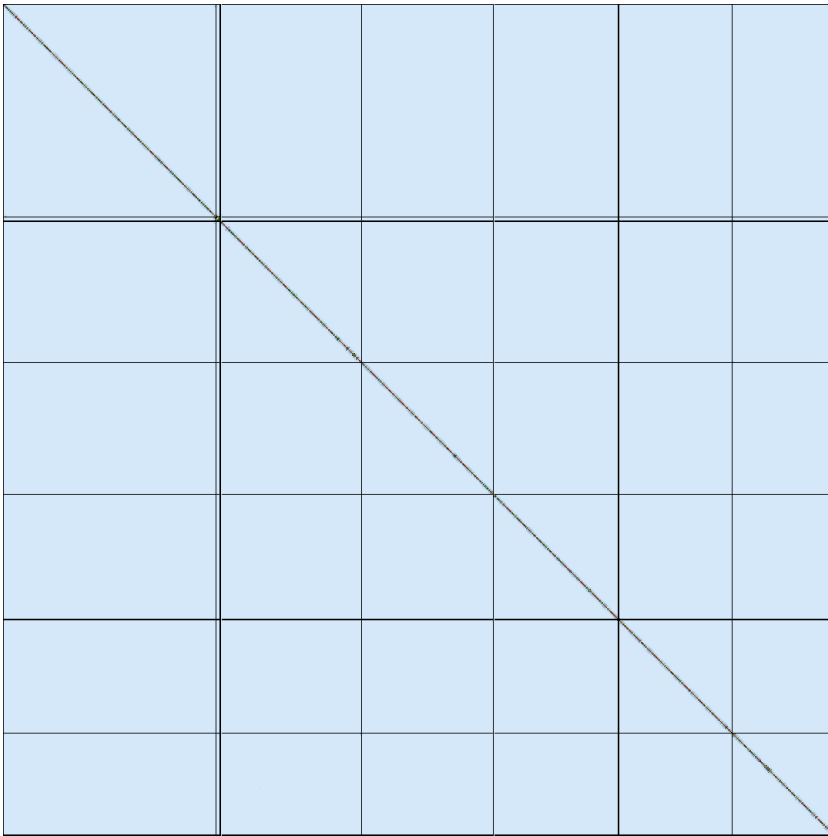
contigs were already mostly chromosome-scale. "

Quality metrics table

| Metrics | Pre-curation collapsed | Curated collapsed |
|--------------|---------------------------|----------------------|
| Total bp | 257,229,379 | 256,705,263 |
| GC % | 37.5 | 37.51 |
| Gaps/Gbp | 0 | 148.03 |
| Total gap bp | 0 | 4,700 |
| Scaffolds | 63 | 16 |
| Scaffold N50 | 10,772,754 | 40,771,022 |
| Scaffold L50 | 7 | 3 |
| Scaffold L90 | 22 | 6 |
| Contigs | 63 | 54 |
| Contig N50 | 10,772,754 | 11,461,491 |
| Contig L50 | 7 | 7 |
| Contig L90 | 22 | 20 |
| QV | 54.3675 | 54.4078 |
| Kmer compl. | 97.548 | 97.4963 |
| BUSCO sing. | 77.1% | 77.0% |
| BUSCO dupl. | 5.7% | 5.7% |
| BUSCO frag. | 2.0% | 2.0% |
| BUSCO miss. | 15.2% | 15.3% |

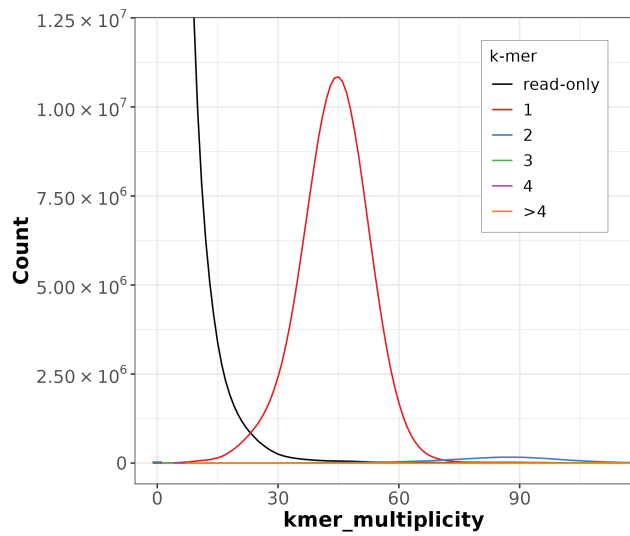
BUSCO: 5.4.3 (euk_genome_met, metaeuk) / Lineage: embryophyta_odb10 (genomes:50, BUSCOs:1614)

HiC contact map of curated assembly

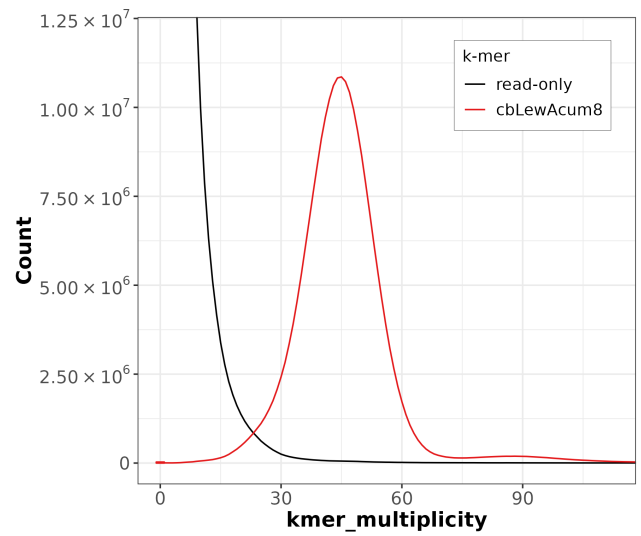


collapsed [\[LINK\]](#)

K-mer spectra of curated assembly

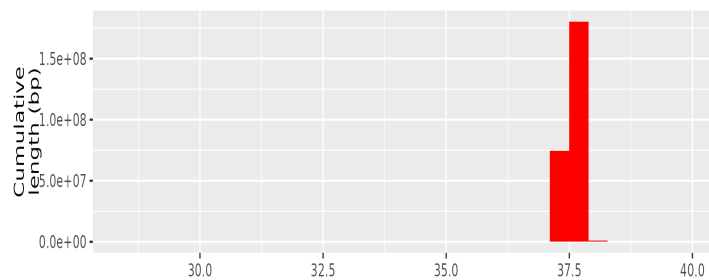


Distribution of k-mer counts per copy numbers found in asm

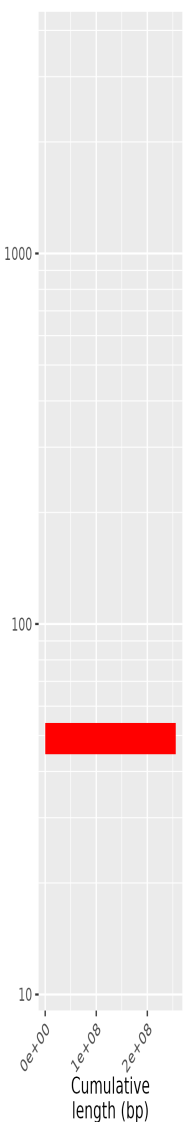
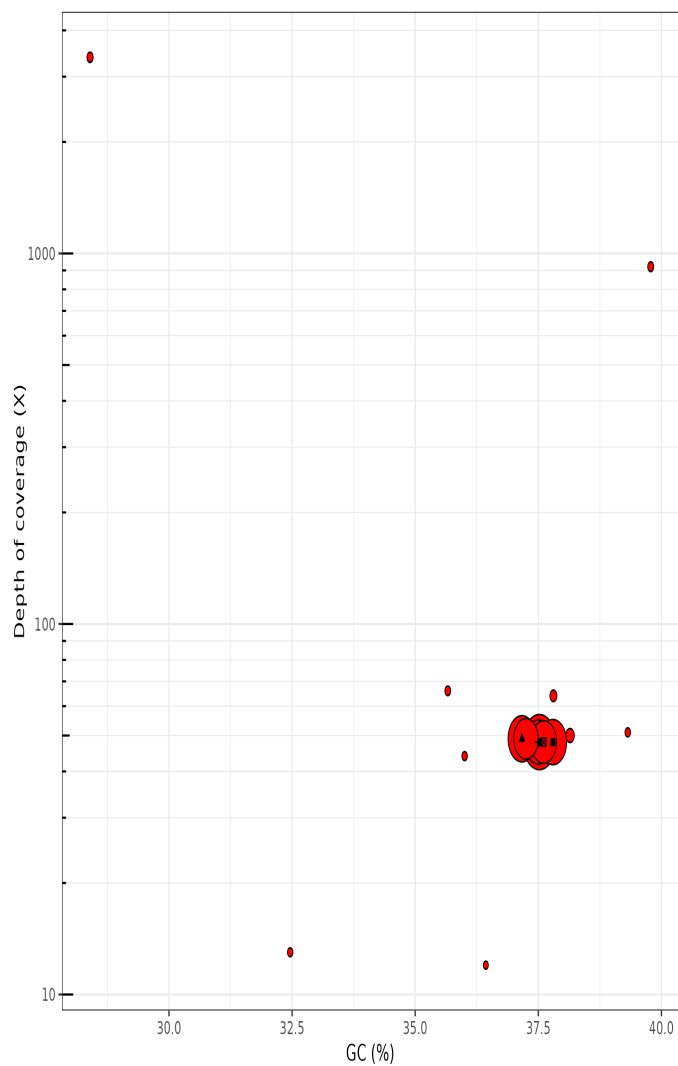


Distribution of k-mer counts coloured by their presence in reads/assemblies

Post-curation contamination screening



TAPAs summary Graph



- Longest sequences (bp)
- cbLewAcum8_1 - 65748008 (Eukaryota)
 - ▲ cbLewAcum8_2 - 43280964 (Eukaryota)
 - cbLewAcum8_3 - 40771022 (Eukaryota)
 - + cbLewAcum8_4 - 38499793 (Eukaryota)
 - ▣ cbLewAcum8_5 - 35003652 (Eukaryota)

- Length (bp)
- 2e+07
 - 4e+07
 - 6e+07

- superkingdom
- Eukaryota

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 | PACBIO Hifi | Arima |
|----------|-------------|-------|
| Coverage | 69 | 202 |

Assembly pipeline

- **Nextdenovo**
 - |_ *ver*: 2.5.1
 - |_ *key param*: NA
- **purge_dups**
 - |_ *ver*: 1.2.5
 - |_ *key param*: NA
- **YaHS**
 - |_ *ver*: 1.2
 - |_ *key param*: NA

Curation pipeline

- **PretextMap**
 - |_ *ver*: 0.1.9
 - |_ *key param*: NA
- **PretextView**
 - |_ *ver*: 0.2.5
 - |_ *key param*: NA

Submitter: Lola Demirdjian

Affiliation: Genoscope

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