

ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

TxID	595348
ToLID	daLeoNival
Species	Leontopodium nivale
Class	Magnoliopsida
Order	Asterales

Genome Traits	Expected	Observed
Haploid size (bp)	805,889,386	2,421,255,336
Haploid Number	12 (source: ancestor)	0
Ploidy	2 (source: ancestor)	4
Sample Sex	unknown	unknown

EBP metrics summary and curation notes

Obtained EBP quality metric for pri: 7.7.Q65

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

- . Observed Haploid size (bp) has >20% difference with Expected
- . Observed Haploid Number is different from Expected
- . Observed Ploidy is different from Expected
- . Kmer completeness value is less than 90 for pri
- . BUSCO single copy value is less than 90% for pri
- . BUSCO duplicated value is more than 5% for pri
- . Not 90% of assembly in chromosomes for pri

Curator notes

- . Interventions/Gb: None
- . Contamination notes: "No contaminants detected by fcs-gx"
- . Other observations: "No Hi-C data available, so a contig-level assembly was submitted. Likely tetraploid"

Quality metrics table

Metrics	Pre-curation pri	Curated pri
Total bp	2,421,255,336	2,421,255,336
GC %	36.52	36.52
Gaps/Gbp	0	0
Total gap bp	0	0
Scaffolds	548	548
Scaffold N50	38,282,995	38,282,995
Scaffold L50	22	22
Scaffold L90	70	70
Contigs	548	548
Contig N50	38,282,995	38,282,995
Contig L50	22	22
Contig L90	70	70
QV	65.8845	65.8845
Kmer compl.	86.6709	86.6709
BUSCO sing.	1.3%	1.3%
BUSCO dupl.	98.3%	98.3%
BUSCO frag.	0.1%	0.1%
BUSCO miss.	0.4%	0.4%

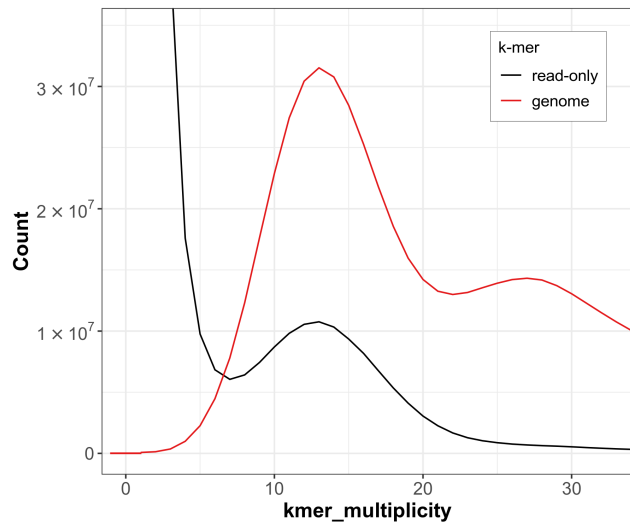
BUSCO: 6.0.0 (euk_genome_min, miniprot) / Lineage: eudicotyledons_odb12 (genomes:76, BUSCOs:2805)

HiC contact map of curated assembly

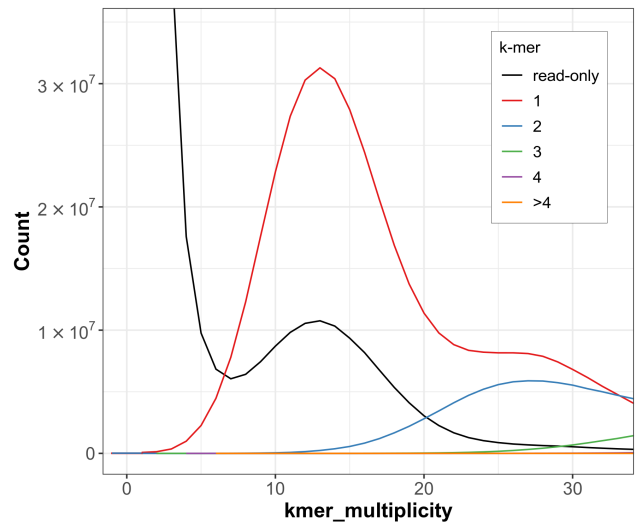
pri HiC PNG is missing!

pri File link is missing!

K-mer spectra of curated assembly

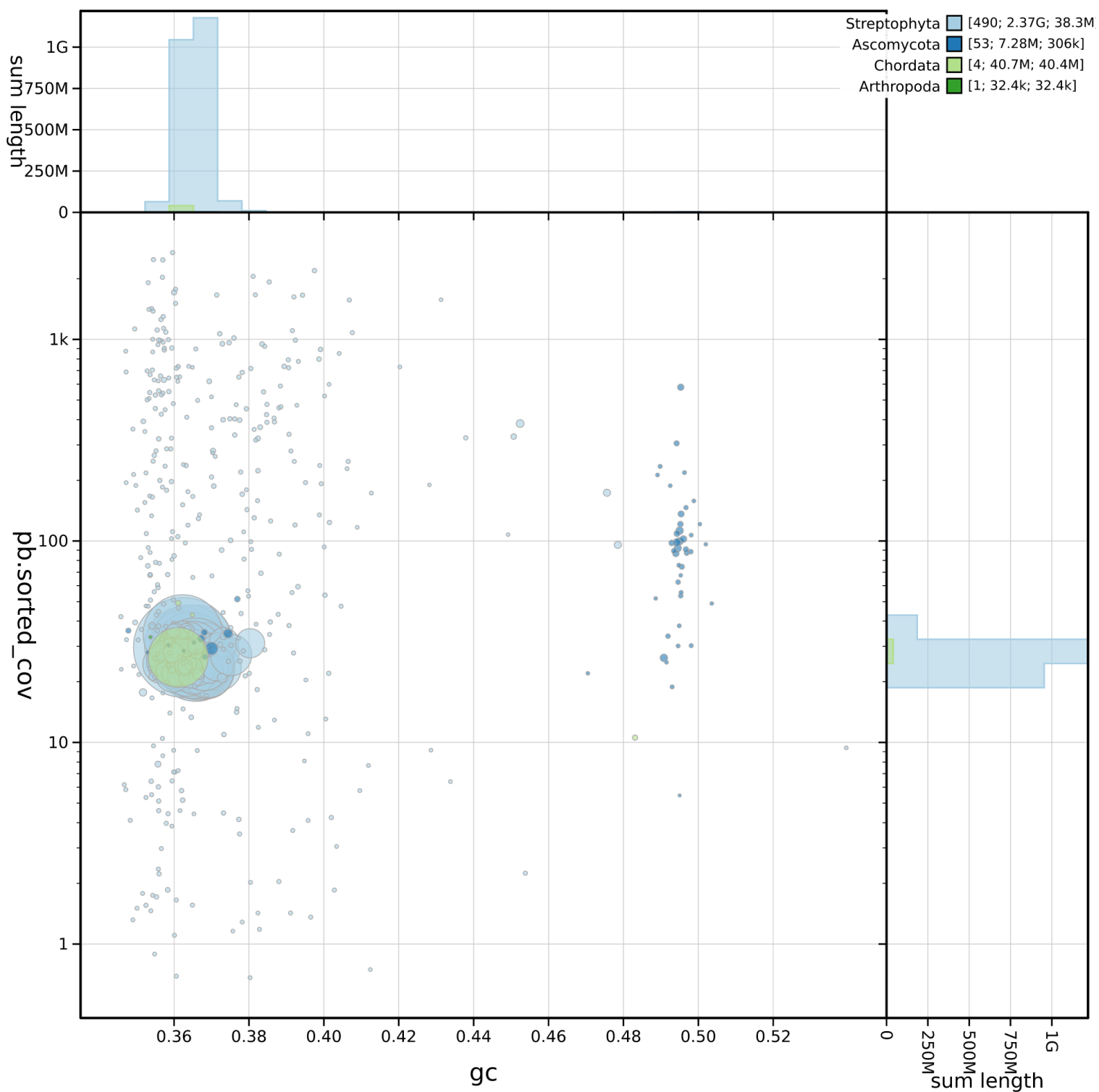


Distribution of k-mer counts coloured by their presence in reads/assemblies



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

Post-curation contamination screening



pri. 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
Coverage	28

Assembly pipeline

- **HiFiasm**
 - |_ *ver*: 0.25.0
 - |_ *key param*: NA
- **fcs-gx**
 - |_ *ver*: 0.5.0
 - |_ *key param*: NA

Curation pipeline

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Date and time: 2026-02-20 11:53:55 CET