

# ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

TxID	1534607
ToLID	<b>drSemWulf4</b>
Species	Sempervivum wulfenii
Class	Magnoliopsida
Order	Saxifragales

Genome Traits	Expected	Observed
Haploid size (bp)	278,332,209	261,058,541
Haploid Number	9 (source: direct)	0
Ploidy	2 (source: ancestor)	2
Sample Sex	unknown	NA

## EBP metrics summary and curation notes

Obtained EBP quality metric for pri: 5.5.Q57

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

- . Observed Haploid Number is different from Expected
- . Observed sex is different from Sample sex
- . 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 library available for this species - contig level assembly submitted. Likely tetraploid"

## Quality metrics table

Metrics	Pre-curation pri	Curated pri
Total bp	261,058,541	261,058,541
GC %	38.03	38.03
Gaps/Gbp	0	0
Total gap bp	0	0
Scaffolds	551	551
Scaffold N50	811,835	811,835
Scaffold L50	101	101
Scaffold L90	315	315
Contigs	551	551
Contig N50	811,835	811,835
Contig L50	101	101
Contig L90	315	315
QV	57.8118	57.8118
Kmer compl.	91.3446	91.3446
BUSCO sing.	72.0%	72.0%
BUSCO dupl.	24.5%	24.5%
BUSCO frag.	0.9%	0.9%
BUSCO miss.	2.5%	2.5%

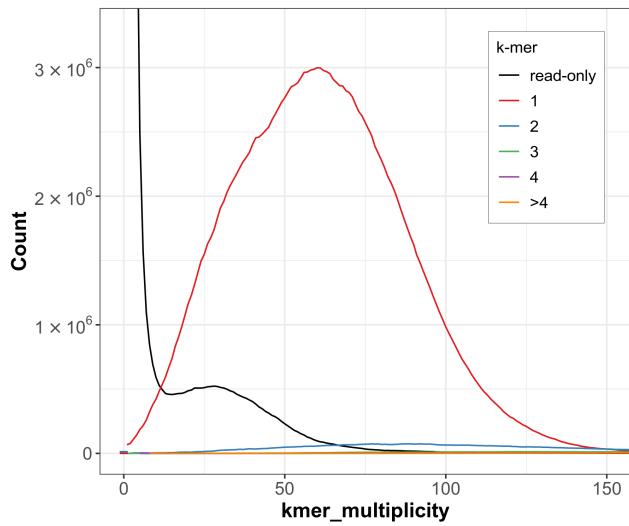
BUSCO: 6.0.0 (euk\_genome\_min, miniprot) / Lineage: eudicots\_odb12 (genomes:76, BUSCOs:2805)

## HiC contact map of curated assembly

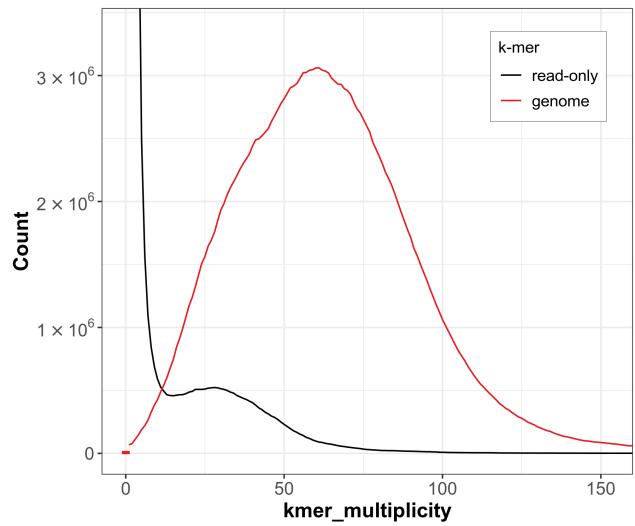
**pri** HiC PNG is missing!

**pri** File link is missing!

# K-mer spectra of curated assembly

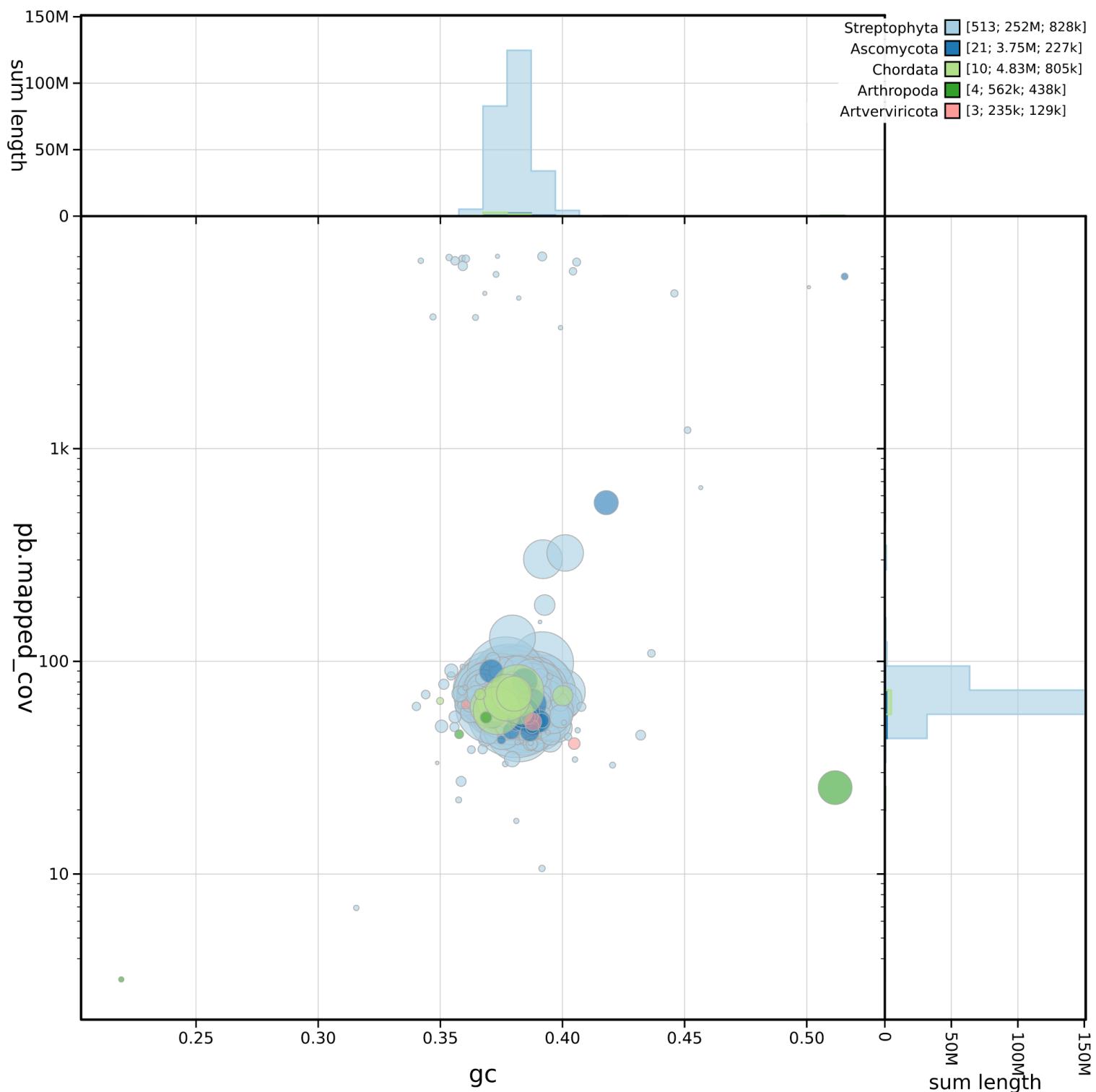


Distribution of k-mer counts per copy numbers found in asm



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

# 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	50

## Assembly pipeline

```
- hifiasm
  |_ ver: 0.25.0
  |_ key param: NA
- purge-dups
  |_ ver: 1.2.6
  |_ key param: NA
- fcs-gx
  |_ ver: 0.5.0
  |_ key param: NA
```

## Curation pipeline

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Date and time: 2026-02-17 11:49:10 CET