

ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

TxID	457762
ToLID	ddAlyUtri1
Species	Alyssoides utriculata
Class	Magnoliopsida
Order	Brassicales

Genome Traits	Expected	Observed
Haploid size (bp)	1,071,941,611	1,018,829,908
Haploid Number	4 (source: direct)	8
Ploidy	2 (source: ancestor)	2
Sample Sex	NA	NA

EBP metrics summary and curation notes

Obtained EBP quality metric for hap1: 8.8.Q64

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

- . Observed Haploid Number is different from Expected

Curator notes

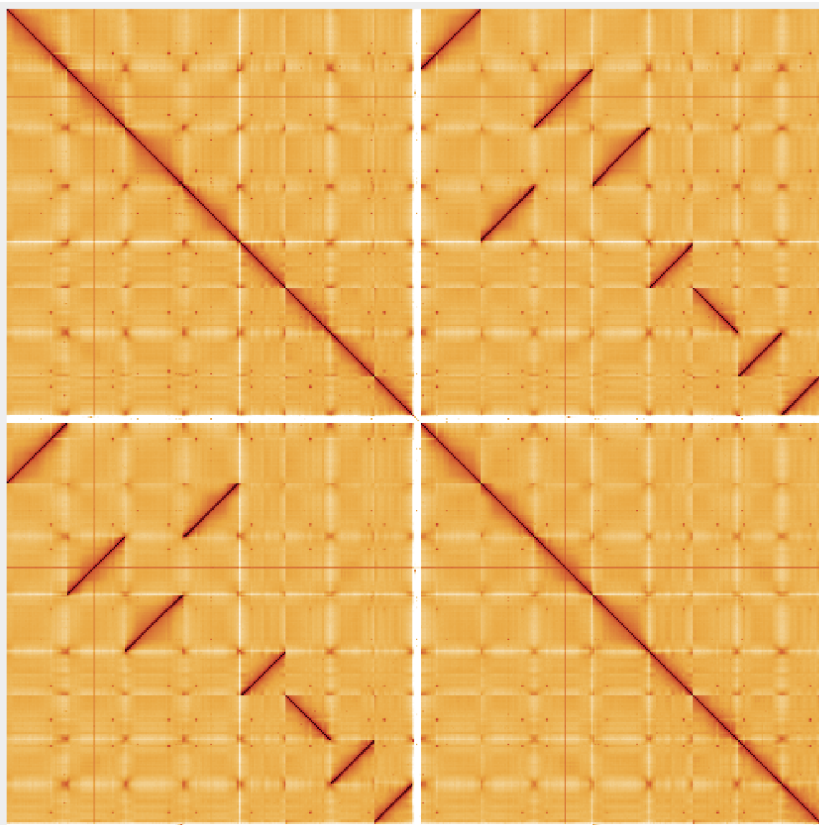
- . Interventions/Gb: 6
- . Contamination notes: "2 mycoplasma sequences removed"
- . Other observations: "Not many interventions to make after yahs. Need to reorder the chromosomes based on either size or sytneny, not sure yet"

Quality metrics table

Metrics	Pre-curation hap1	Curated hap1
Total bp	1,028,428,052	1,018,829,908
GC %	38.96	38.95
Gaps/Gbp	83.62	83.43
Total gap bp	17,200	17,000
Scaffolds	726	413
Scaffold N50	685,186,311	135,958,589
Scaffold L50	1	4
Scaffold L90	4	8
Contigs	812	498
Contig N50	108,093,000	108,093,000
Contig L50	5	5
Contig L90	10	10
QV	62.527	64.0782
Kmer compl.	98.0999	98.0773
BUSCO sing.	92.6%	92.5%
BUSCO dupl.	4.1%	4.0%
BUSCO frag.	1.5%	1.5%
BUSCO miss.	1.8%	1.9%

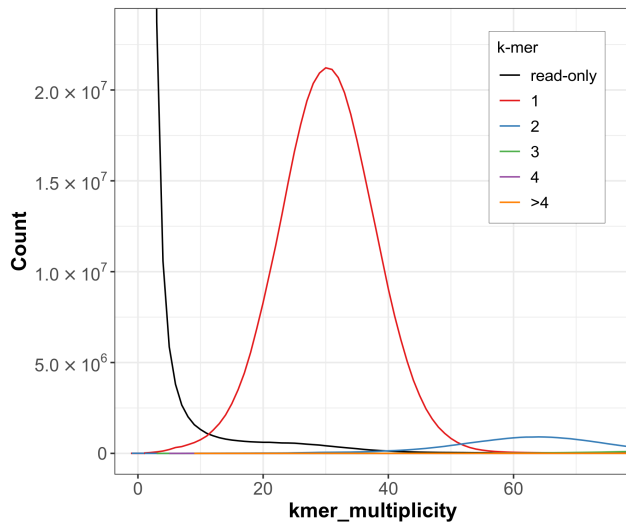
BUSCO: 5.8.2 (euk_genome_min, miniprot) / Lineage: eudicotyledons_odb12 (genomes:76, BUSCOs:2805)

HiC contact map of curated assembly

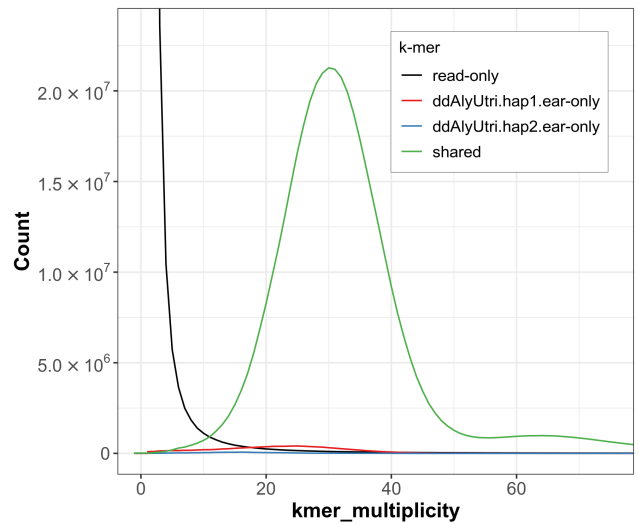


hap1 [\[LINK\]](#)

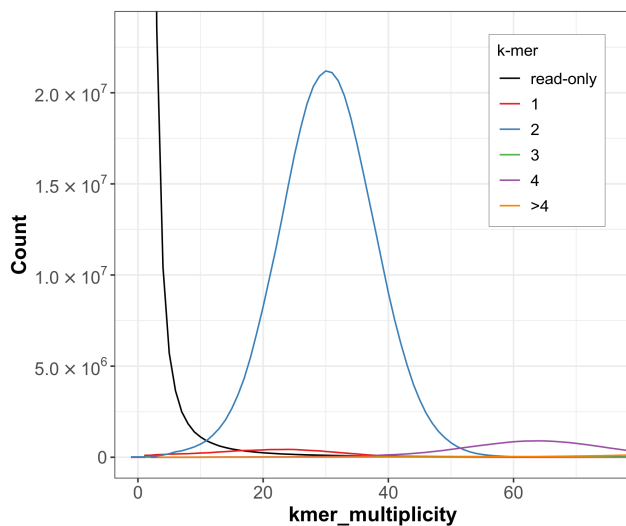
K-mer spectra of curated assembly



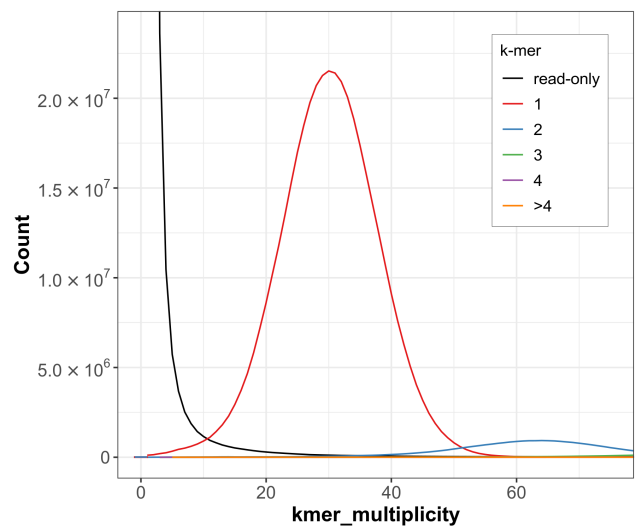
Distribution of k-mer counts per copy numbers found in **hap2** (hap1.)



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

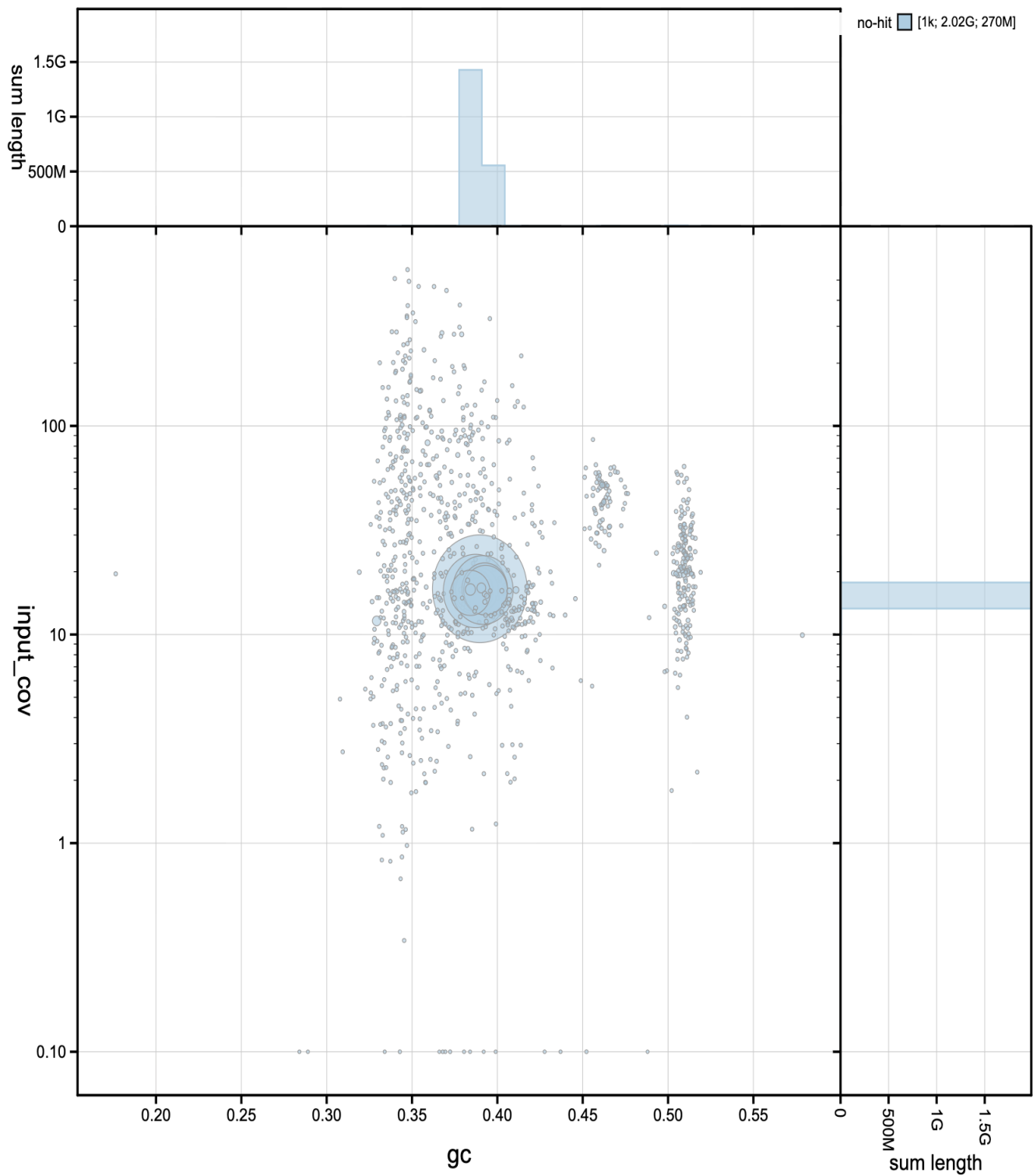


Distribution of k-mer counts per copy numbers found in asm (dipl.)



Distribution of k-mer counts per copy numbers found in **hap1** (hap1.)

Post-curation contamination screening



hap1. 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	HiFi	HiC
Coverage	32	130

Assembly pipeline

- **HiFiasm**
 - |_ *ver*: 0.25.0
 - |_ *key param*: --hom-cov 32
- **purge-dups**
 - |_ *ver*: 1.2.6
 - |_ *key param*: NA
- **yahs**
 - |_ *ver*: 1.1a
 - |_ *key param*: NA

Curation pipeline

- **PretextViewAI**
 - |_ *ver*: 1.0.0
 - |_ *key param*: NA

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