

ERGA Assembly Report

v24.04.03_beta

Tags: ERGA-BGE

TxID	345151
ToLID	drZizLotu1
Species	<i>Ziziphus lotus</i>
Class	Magnoliopsida
Order	Rosales

Genome Traits	Expected	Observed
Haploid size (bp)	307,042,740	293,261,554
Haploid Number	12 (source: direct)	12
Ploidy	2 (source: ancestor)	2
Sample Sex	H	H

EBP metrics summary and curation notes

Obtained EBP quality metric for pri: 7.7.Q62

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

- . Assembly length loss > 3% for pri

Curator notes

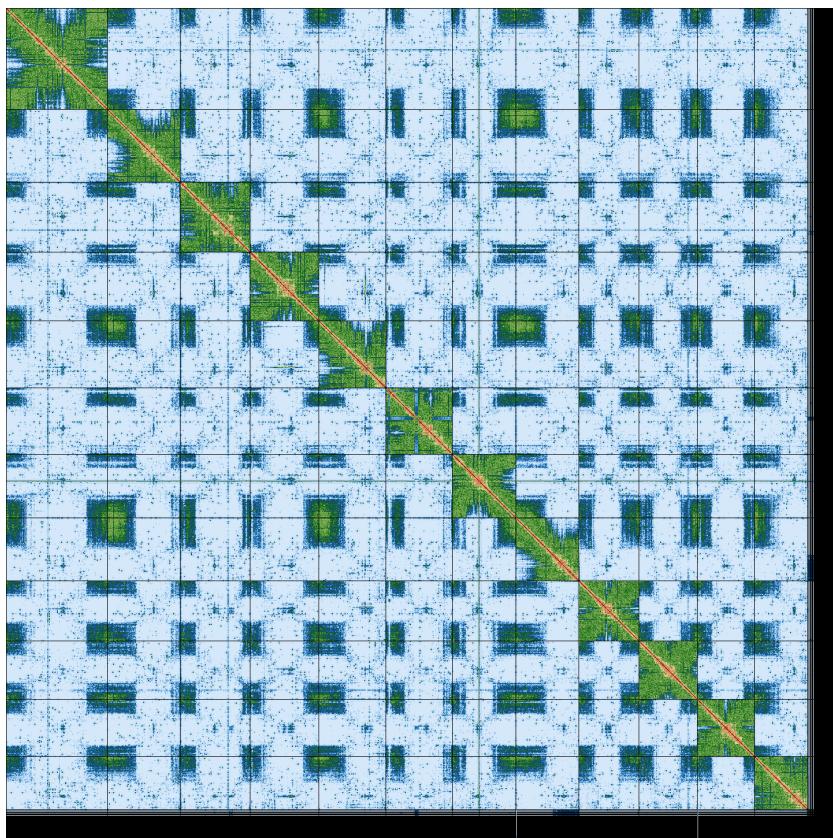
- . Interventions/Gb: 22
- . Contamination notes: "Contamination report for assembly labelled hap1; Total length of scaffolds removed: 200,777,297 (40.4 %); Scaffolds removed: 3555 (95.2 %); Largest scaffold removed: (341,751); FCS-GX contaminant species (number of scaffolds; total length of scaffolds):: Brevundimonas sp. UBA6550, a-proteobacteria (4; 167,575); Delftia acidovorans, b-proteobacteria (1; 8,026); Homo sapiens, primates (1; 7,632); Mitochondrion (1621; 85,342,075); Plastid (1928; 115,251,989)"
- . Other observations: "Assembly was Hi-C phased;"

Quality metrics table

Metrics	Pre-curation pri	Curated pri
Total bp	496,389,500	293,261,554
GC %	36.18	33.33
Gaps/Gbp	16.12	57.97
Total gap bp	800	2,900
Scaffolds	3,735	142
Scaffold N50	20,141,524	23,263,395
Scaffold L50	10	6
Scaffold L90	2,349	12
Contigs	3,743	159
Contig N50	12,725,994	20,141,524
Contig L50	12	6
Contig L90	2,357	15
QV	51.4	62.6
Kmer compl.	99.47	99.24
BUSCO sing.	97.8%	98.3%
BUSCO dupl.	1.4%	0.8%
BUSCO frag.	0.2%	0.2%
BUSCO miss.	0.6%	0.7%

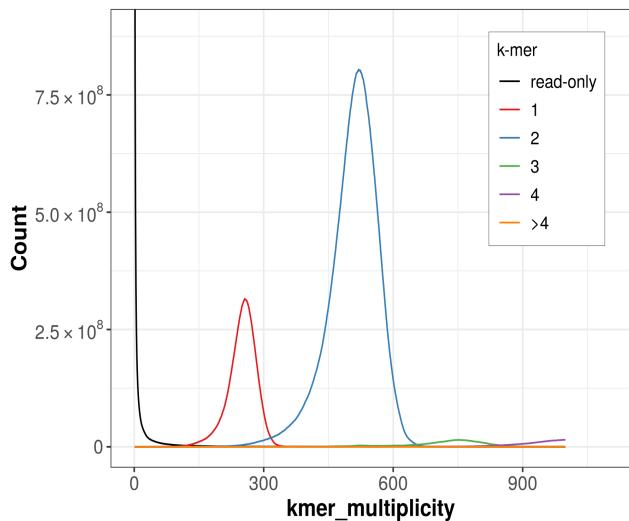
BUSCO 6.0.0 Lineage: eudicots_odb10 (genomes:31, BUSCOs:2326)

HiC contact map of curated assembly

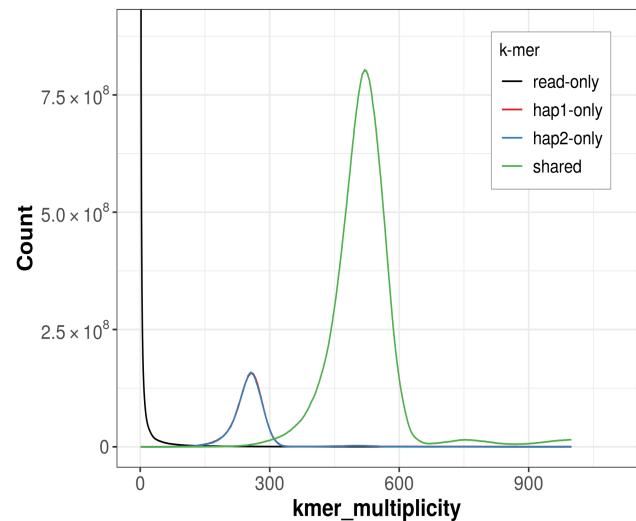


pri [LINK]

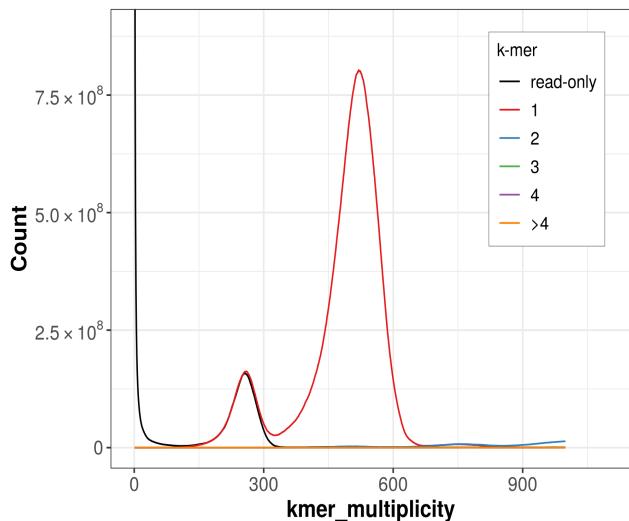
K-mer spectra of curated assembly



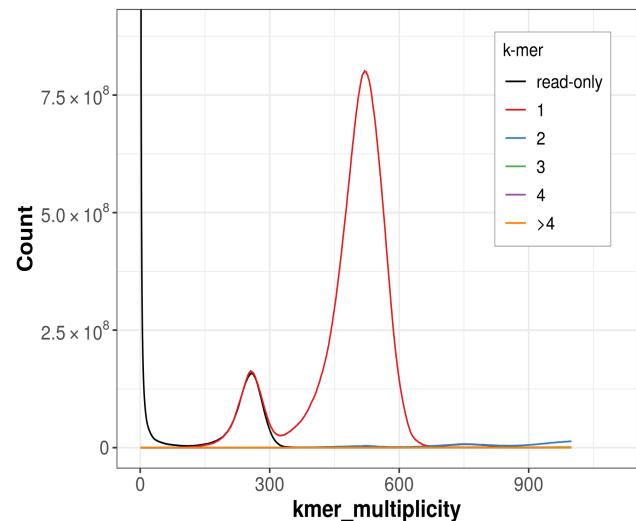
Distribution of k-mer counts per copy numbers found in asm (dipl.)



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

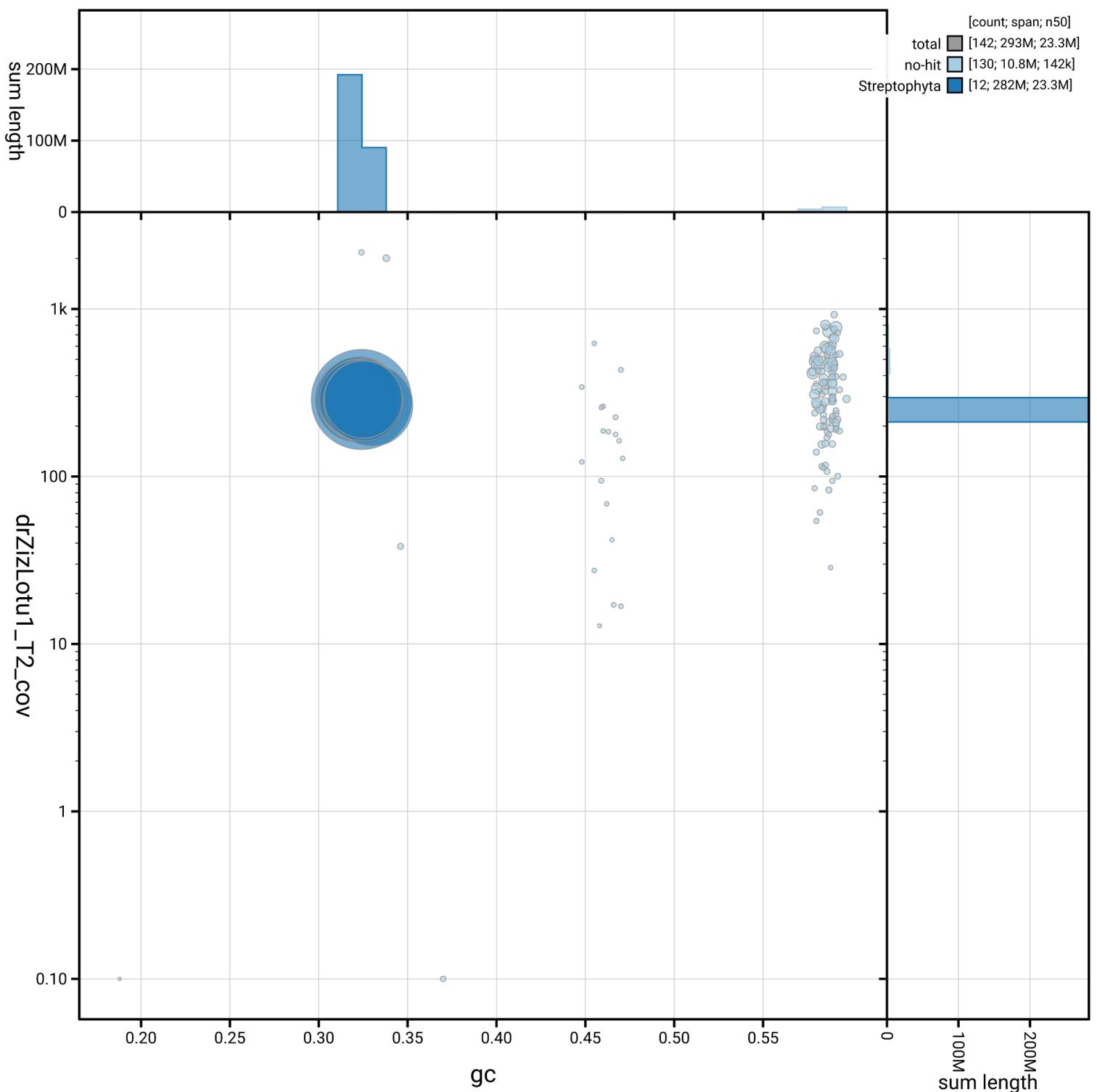


Distribution of k-mer counts per copy numbers found in **hap1** (hapl.)



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

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	Arima v2
Coverage	514x	524x

Assembly pipeline

```
- hifiasm
  |_ ver: 0.25.0-r726
  |_ key param: --h1/--h2
- yahs
  |_ ver: 1.2.2
  |_ key param: NA
```

Curation pipeline

```
- hifiasm
  |_ ver: 0.25.0-r726
  |_ key param: --h1/--h2
- yahs
  |_ ver: 1.2.2
  |_ key param: NA
- TreeVal
  |_ ver: 1.2.2
  |_ key param: NA
```

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