

# ERGA Assembly Report

v24.10.15

Tags: ERGA-Pilot

TxID	136121
ToLID	<b>dmLauAzor1</b>
Species	Laurus azorica
Class	Magnoliopsida
Order	Lurales

Genome Traits	Expected	Observed
Haploid size (bp)	1,595,786,563	1,403,283,976
Haploid Number	24 (source: direct)	13
Ploidy	2 (source: ancestor)	2
Sample Sex	XXXY	NA

## EBP metrics summary and curation notes

Obtained EBP quality metric for : 7.8.Q61

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
- . Kmer completeness value is less than 90 for
- . BUSCO single copy value is less than 90% for
- . BUSCO duplicated value is more than 5% for
- . Assembly length loss > 3% for

### Curator notes

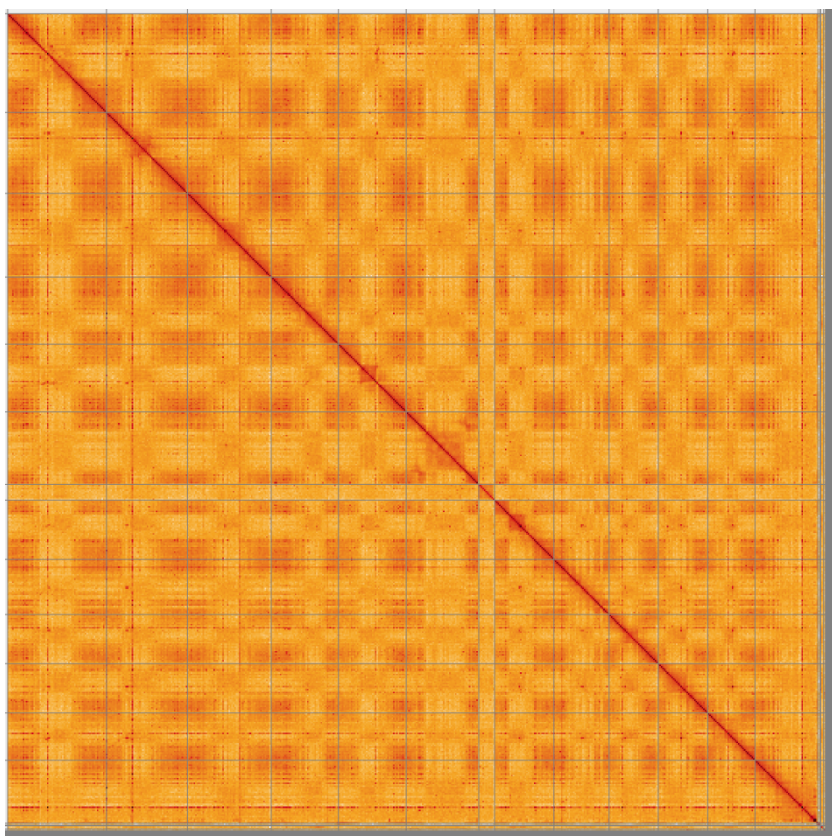
- . Interventions/Gb: 1000
- . Contamination notes: "Many contaminants removed"
- . Other observations: "The best we can do given the poor Hi-C signal"

# Quality metrics table

Metrics	Pre-curation <pri>	Curated <pri>
Total bp	1,649,185,159	1,403,283,976
GC %	41.47	41.16
Gaps/Gbp	110.96	123.99
Total gap bp	36,600	27,300
Scaffolds	298	193
Scaffold N50	72,886,773	113,755,423
Scaffold L50	8	6
Scaffold L90	22	11
Contigs	481	367
Contig N50	17,123,649	15,460,700
Contig L50	29	27
Contig L90	90	84
QV	61.7293	61.4311
Kmer compl.	66.6739	62.7795
BUSCO sing.	84.3%	88.8%
BUSCO dupl.	11.2%	6.5%
BUSCO frag.	1.5%	1.6%
BUSCO miss.	3.0%	3.1%

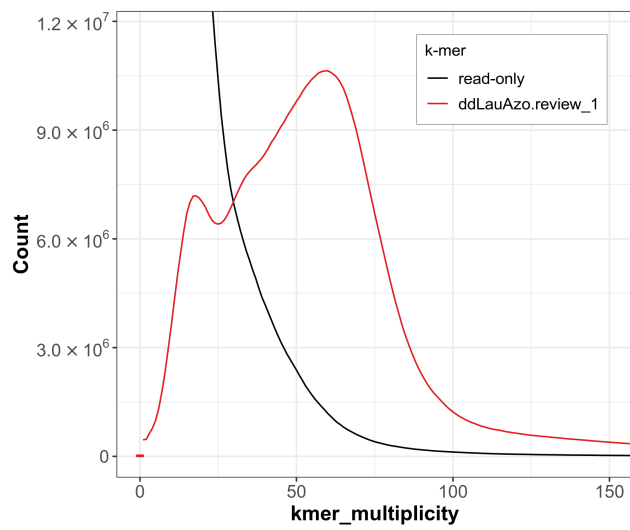
BUSCO: 5.8.2 (euk\_genome\_min, miniprot) / Lineage: eudicots\_odb10 (genomes:31, BUSCOs:2326)

# HiC contact map of curated assembly

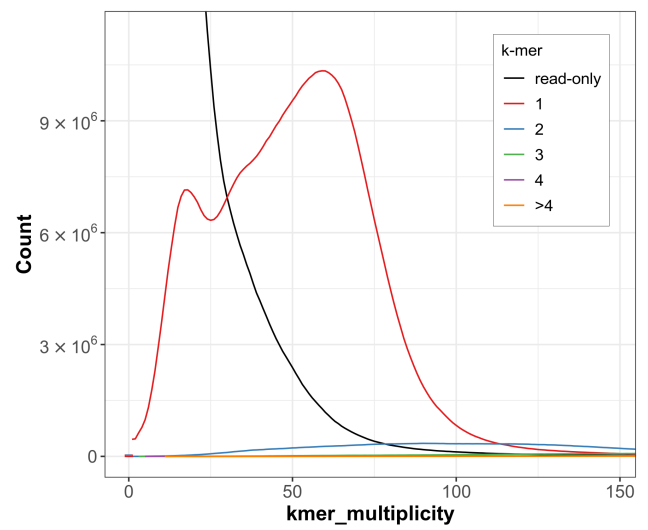


[\[LINK\]](#)

# K-mer spectra of curated assembly

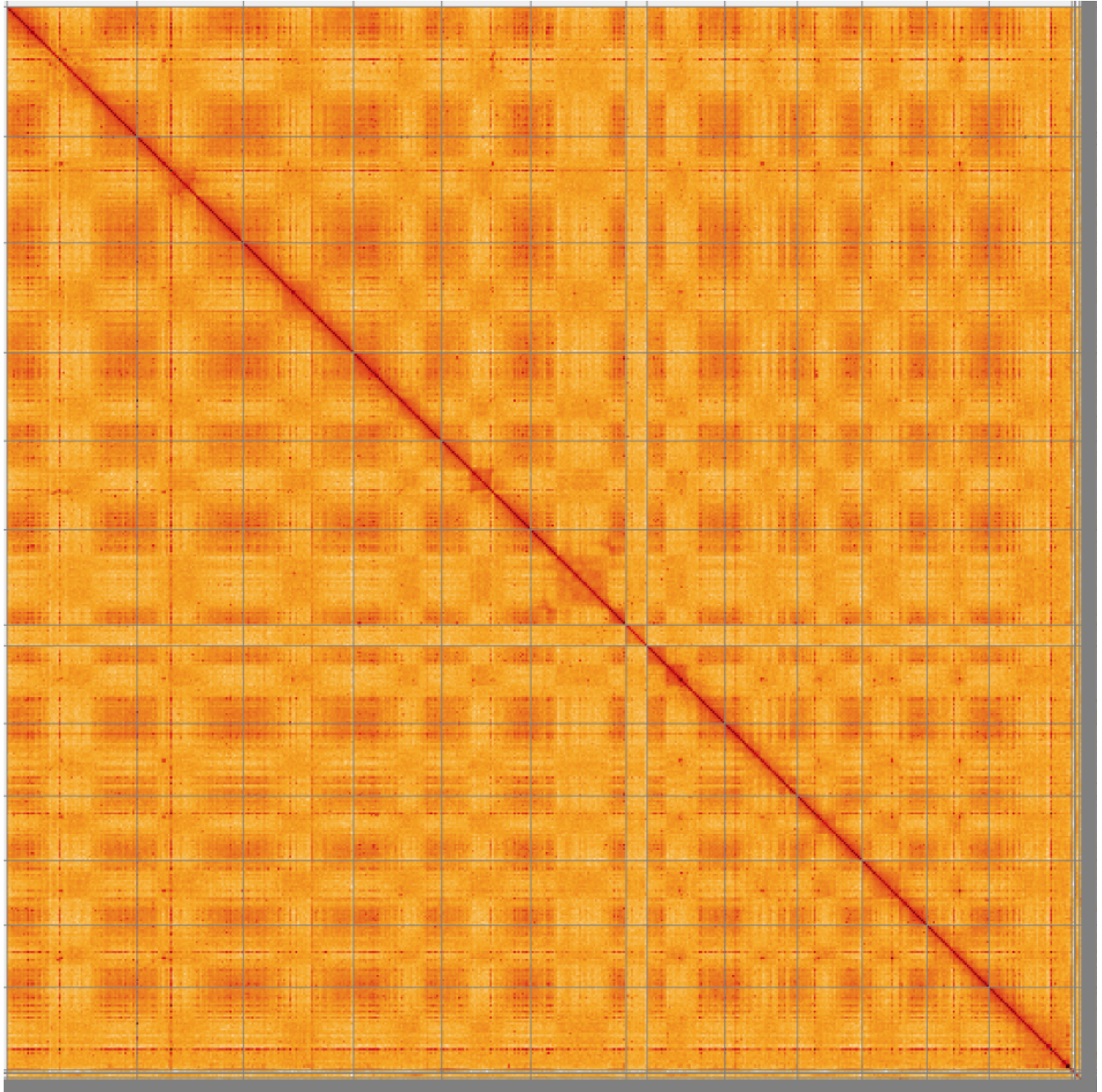


Distribution of k-mer counts coloured by their presence in reads/assemblies



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

## Post-curation contamination screening



. 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	40x	10x

# Assembly pipeline

- **HiFiasm**
  - |\_ *ver*: 0.19.4
  - |\_ *key param*: HiC
  - |\_ *key param*: 10
- **purge\_dups**
  - |\_ *ver*: 1.2.6
  - |\_ *key param*: NA
- **YaHS**
  - |\_ *ver*: 1.1
  - |\_ *key param*: NA

# Curation pipeline

- **GRIT\_Rapid**
  - |\_ *ver*: 2.0
  - |\_ *key param*: NA
- **HiGlass**
  - |\_ *ver*: 1.0
  - |\_ *key param*: NA

Submitter: Tom Brown

Affiliation: IZW

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