

ERGA Assembly Report

v24.04.03_beta

Tags: ERGA-BGE

TxID	478306
ToLID	drAlcFaer1
Species	<i>Alchemilla faeroensis</i>
Class	Magnoliopsida
Order	Rosales

Genome Traits	Expected	Observed
Haploid size (bp)	2,546,153,876	4,888,224,412
Haploid Number	85 (source: direct)	211
Ploidy	6 (source: ancestor)	2
Sample Sex	H	H

EBP metrics summary and curation notes

Obtained EBP quality metric for hap1: 7.7.Q66

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
- . BUSCO single copy value is less than 90% for hap1
- . BUSCO duplicated value is more than 5% for hap1

Curator notes

. Interventions/Gb: 127
. Contamination notes: "Contamination report for assembly labelled hap1; Total length of scaffolds removed: 109,943,101 (3.6 %); Scaffolds removed: 2155 (82.9 %); Largest scaffold removed: (292,073); FCS-GX contaminant species (number of scaffolds; total length of scaffolds): *Hymenobacter baengnokdamensis*, CFB group bacteria (19; 1,055,728); *Hymenobacter ginkgonis*, CFB group bacteria (14; 1,062,421); *Hymenobacter polaris*, CFB group bacteria (11; 763,362); *Hymenobacter setariae*, CFB group bacteria (5; 240,257); *Hymenobacter coccineus*, CFB group bacteria (4; 334,246); *Hymenobacter caeli*, CFB group bacteria (2; 132,038); *Hymenobacter monticola*, CFB group bacteria (1; 79,444); *Hymenobacter lapidarius*, CFB group bacteria (1; 54,659); *Hymenobacter artigasi*, CFB group bacteria (1; 40,243); *Hymenobacter terrenus*, CFB group bacteria (1; 37,644); *Curvularia* sp. IFB-Z10, ascomycetes (1; 34,725); *Hymenobacter norwichensis*, CFB group bacteria (1; 33,411); *Hymenobacter nivis*, CFB group bacteria (1; 22,579); Mitochondrion (115; 5,317,778); Plastid (1978; 100,734,566);
Contamination report for assembly labelled hap2; Total length of scaffolds removed:

14,665,935 (0.8 %); Scaffolds removed: 193 (40.8 %) ;Largest scaffold removed: (229,862); FCS-GX contaminant species (number of scaffolds; total length of scaffolds): *Hymenobacter baengnokdamensis*, CFB group bacteria (7; 502,816); *Hymenobacter polaris*, CFB group bacteria (2; 99,620); *Hymenobacter caeli*, CFB group bacteria (1; 170,274); *Hymenobacter coccineus*, CFB group bacteria (1; 69,749); *Hymenobacter ginkgonis*, CFB group bacteria (1; 66,773); Mitochondrion (2; 103,209); Plastid (179; 13,653,494)"

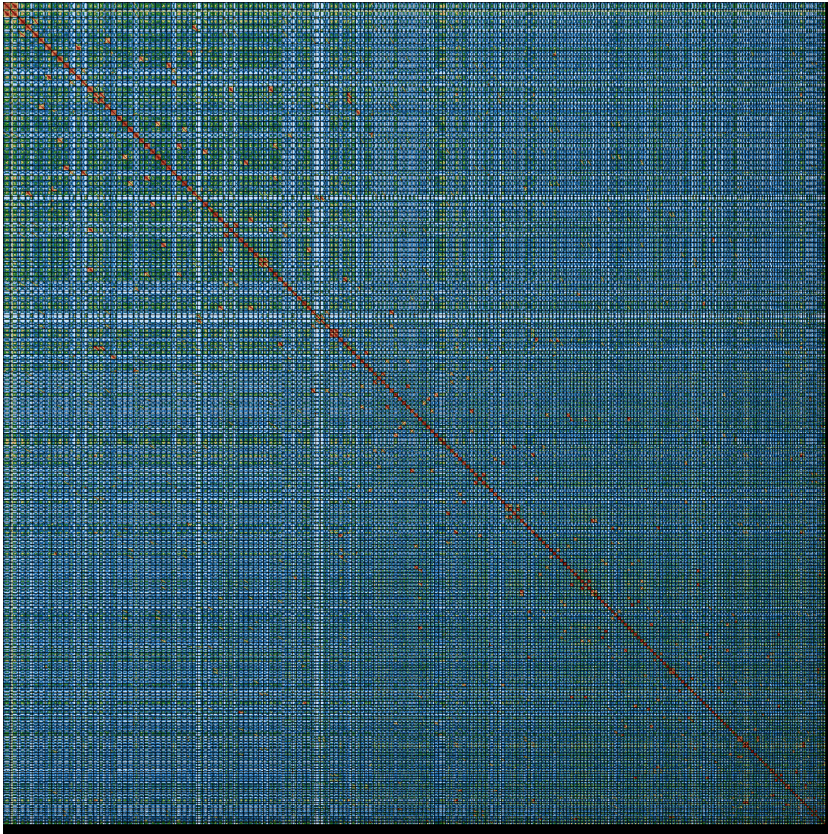
. Other observations: "Assembly was Hi-C phased; The species shows a high chromosome number and different chromosome distribution patterns. In addition, it shows a history of many rearrangements and hybridisation events. The number of chromosomes may vary within the species. It was not possible to infer ploidy. The haplotypes could not be separated during curation, so a complete set of chromosomes were submitted."

Quality metrics table

Metrics	Pre-curation hap1	Curated hap1
Total bp	3,064,326,706	4,888,224,412
GC %	38.46	38.49
Gaps/Gbp	67.88	89.81
Total gap bp	20,800	54,100
Scaffolds	2,598	648
Scaffold N50	22,932,066	23,747,037
Scaffold L50	53	82
Scaffold L90	125	180
Contigs	2,806	1,087
Contig N50	11,440,633	10,806,000
Contig L50	98	165
Contig L90	266	421
QV	61.3	66.9
Kmer compl.	99.20	100.00
BUSCO sing.	0.4%	0.3%
BUSCO dupl.	97.9%	98.0%
BUSCO frag.	0.1%	0.1%
BUSCO miss.	1.5%	1.5%

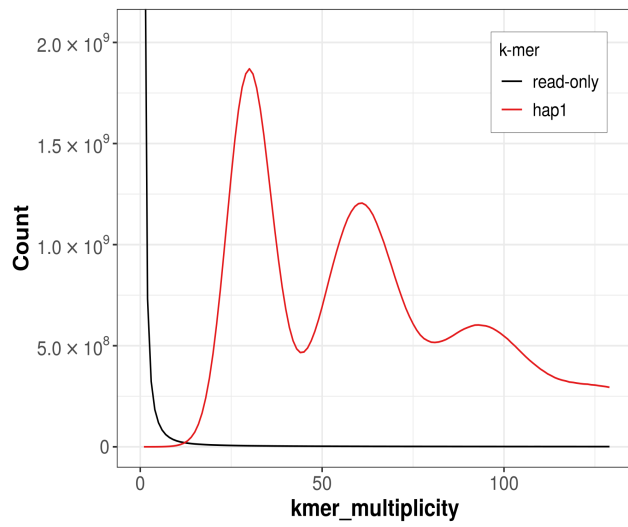
BUSCO 6.0.0 Lineage: eudicots_odb10 (genomes:31, BUSCOs:2326)

HiC contact map of curated assembly

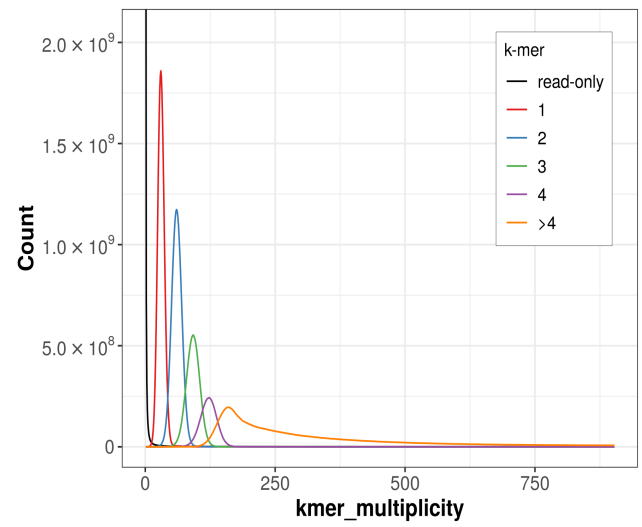


hap1 [\[LINK\]](#)

K-mer spectra of curated assembly

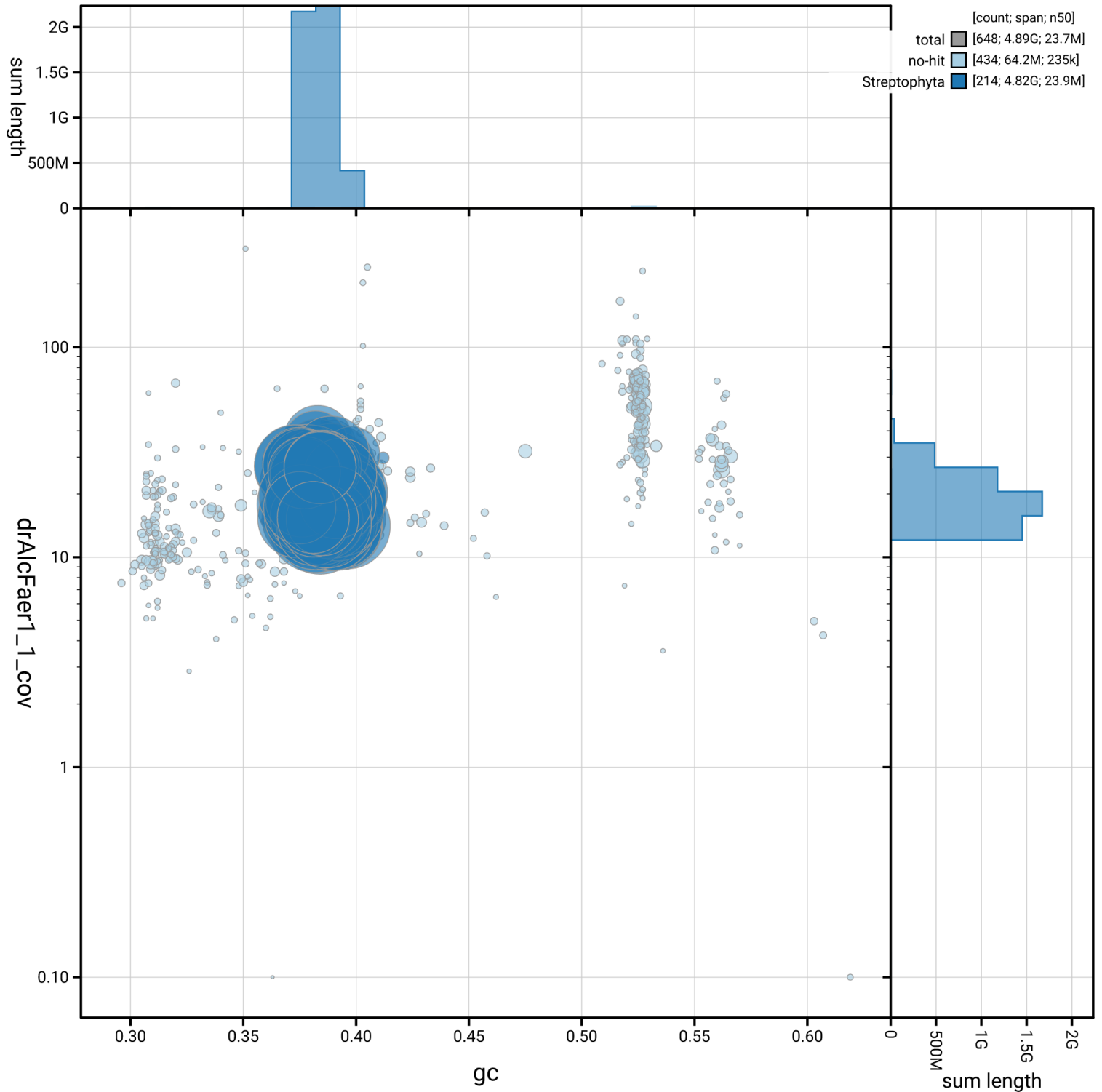


Distribution of k-mer counts coloured by their presence in reads/assemblies



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

Post-curation contamination screening



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	PacBio HiFi	Arima v2
Coverage	47x	175x

Assembly pipeline

- **hifiasm-hic**
 - |_ *ver*: 0.19.8-r603
 - |_ *key param*: --h1/--h2
- **yahs**
 - |_ *ver*: 1.2.2
 - |_ *key param*: NA

Curation pipeline

- **hifiasm-hic**
 - |_ *ver*: 0.19.8-r603
 - |_ *key param*: --h1/--h2
- **yahs**
 - |_ *ver*: 1.2.2
 - |_ *key param*: NA
- **TreeVal**
 - |_ *ver*: 1.2.1
 - |_ *key param*: NA

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