

# ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

TxID	40178
ToLID	<b>bAleGra1</b>
Species	<i>Alectoris graeca</i>
Class	Aves
Order	Galliformes

Genome Traits	Expected	Observed
Haploid size (bp)	1,015,215,291	1,114,500,572
Haploid Number	39 (source: direct)	39
Ploidy	2 (source: ancestor)	2
Sample Sex	ZZ	ZZ

## EBP metrics summary and curation notes

Obtained EBP quality metric for pri: 7.7.Q65

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

### Curator notes

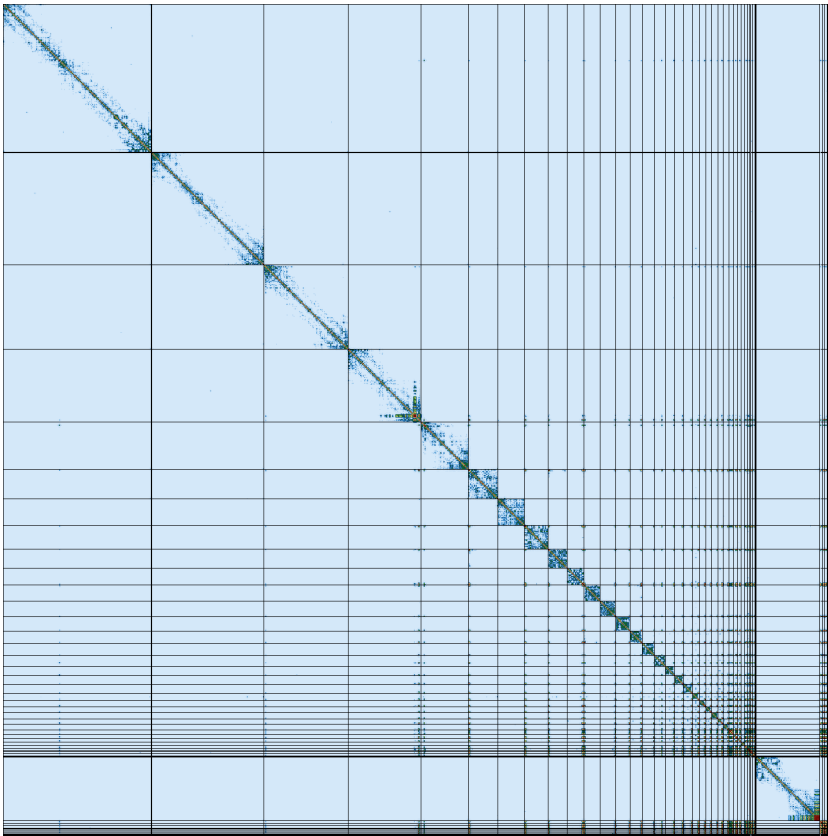
. Interventions/Gb: None  
. Contamination notes: "No presence of contaminants."  
. Other observations: "purging was manually done to avoid removing of large fractions of microchromosomes, guided by purge\_dups dups.bed file. Microchromosomes were identified with MicroFinder and scaffolded with the guidance of the alignments against the T2T chicken assembly. Microchromosomes 34-38 are probably not complete due to very low sequencing coverage 3-7X. Includes the mitochondrion (MT) - assembled with MitoHifi."

# Quality metrics table

Metrics	Pre-curation pri	Curated pri
Total bp	1,131,325,264	1,114,500,572
GC %	42.08	41.99
Gaps/Gbp	0	134.59
Total gap bp	0	30,000
Scaffolds	379	116
Scaffold N50	43,679,502	97,991,491
Scaffold L50	8	4
Scaffold L90	45	20
Contigs	379	266
Contig N50	43,679,502	43,679,502
Contig L50	8	8
Contig L90	45	42
QV	65.2645	65.8096
Kmer compl.	98.0477	98.0031
BUSCO sing.	98.4%	98.5%
BUSCO dupl.	0.3%	0.2%
BUSCO frag.	0.7%	0.7%
BUSCO miss.	0.7%	0.7%

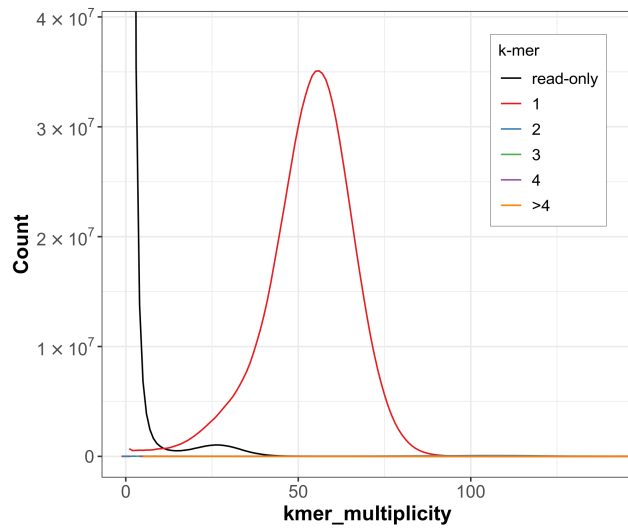
BUSCO: 5.8.3 (euk\_genome\_min, miniprot) / Lineage: aves\_odb12 (genomes:80, BUSCOs:6251)

# HiC contact map of curated assembly

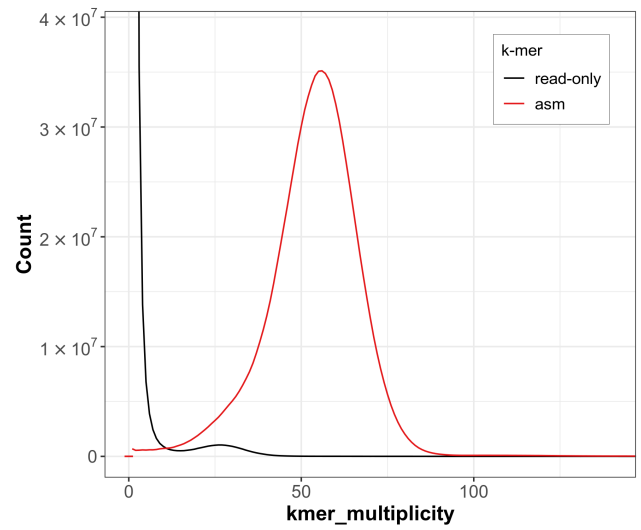


pri [\[LINK\]](#)

# K-mer spectra of curated assembly

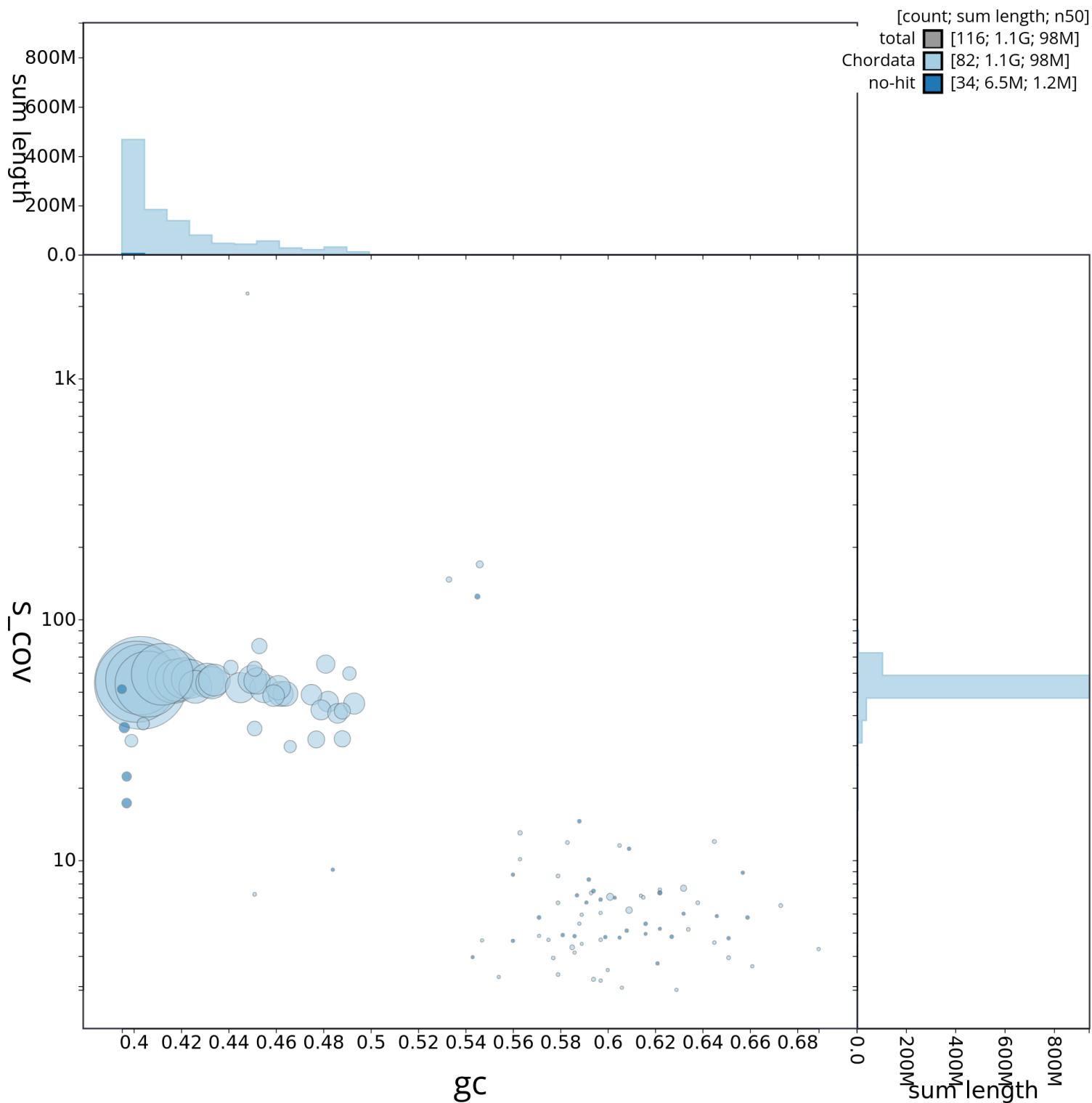


Distribution of k-mer counts per copy numbers found in asm



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	HiFi	Bionano	OmniC
Coverage	53x	NA	143x

## Assembly pipeline

- **Hifiasm**
  - |\_ *ver*: 0.25.0-r726
  - |\_ *key param*: HiC
  - |\_ *key param*: 13
- **purge\_dups**
  - |\_ *ver*: 1.2.5
  - |\_ *key param*: NA
- **YaHS**
  - |\_ *ver*: 1.2.2
  - |\_ *key param*: NA
- **MicroFinder**
  - |\_ *ver*: 0.1
  - |\_ *key param*: NA

## Curation pipeline

- **GRIT\_Rapid**
  - |\_ *ver*: 1a3d79a8
  - |\_ *key param*: NA
- **HiGlass**
  - |\_ *ver*: 0.10.4
  - |\_ *key param*: NA

Submitter: Martin Pippel

Affiliation: SciLifeLab

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