

ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

TxID	40178
ToLID	bAleGra1
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

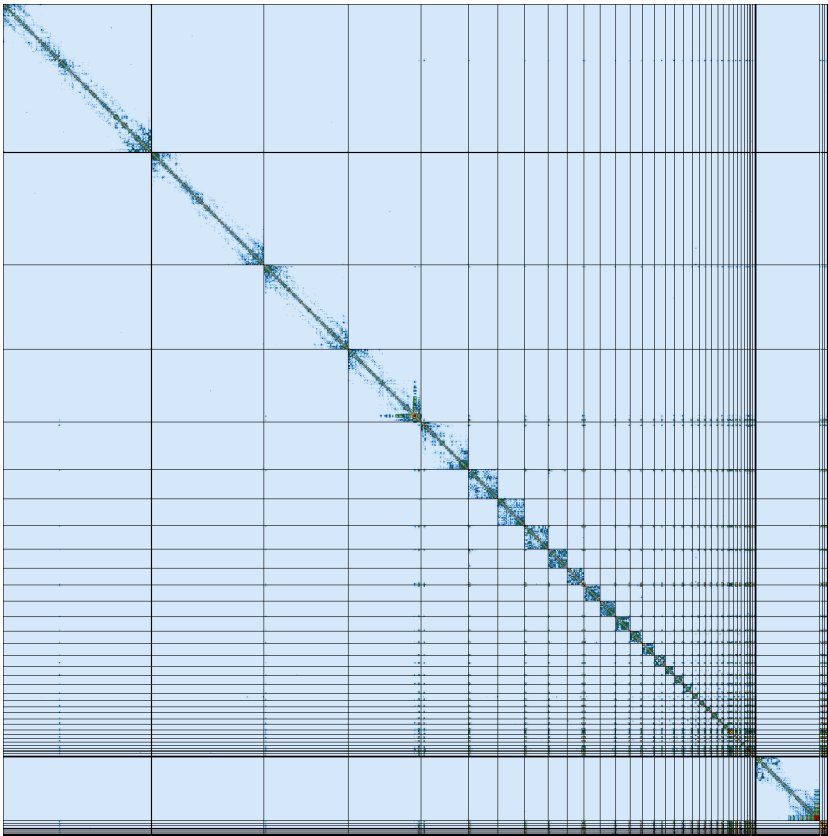
. Interventions/Gb: None
. Contamination notes: "No presence of contaminants."
. Other observations: "purging was manually done to avoid removing of large fractions of microchromosomes, guided by purge_dups dups.bed file. Microchromosomes were identified with MicroFinder and scaffolded with the guidance 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%

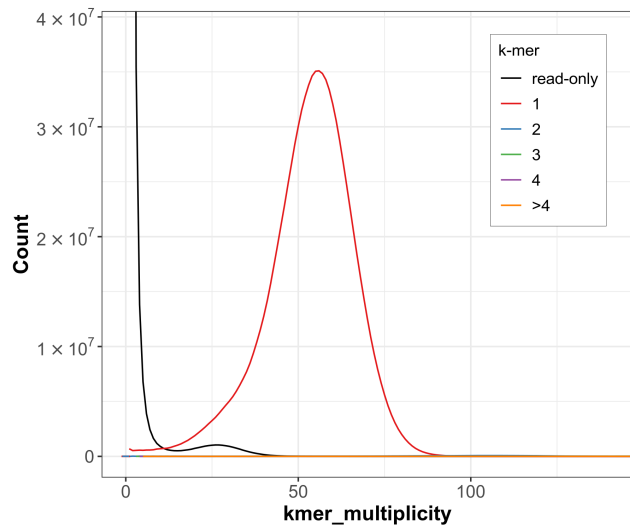
BUSCO: 5.8.3 (euk_genome_min, miniprot) / Lineage: aves_odb12 (genomes:80, BUSCOs:6251)

HiC contact map of curated assembly

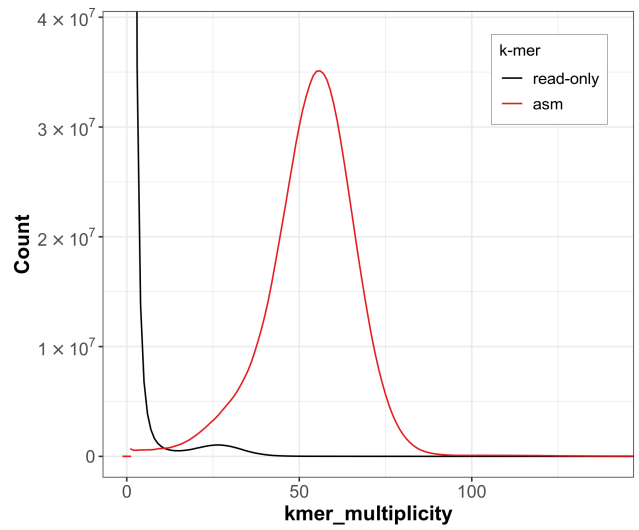


pri [\[LINK\]](#)

K-mer spectra of curated assembly

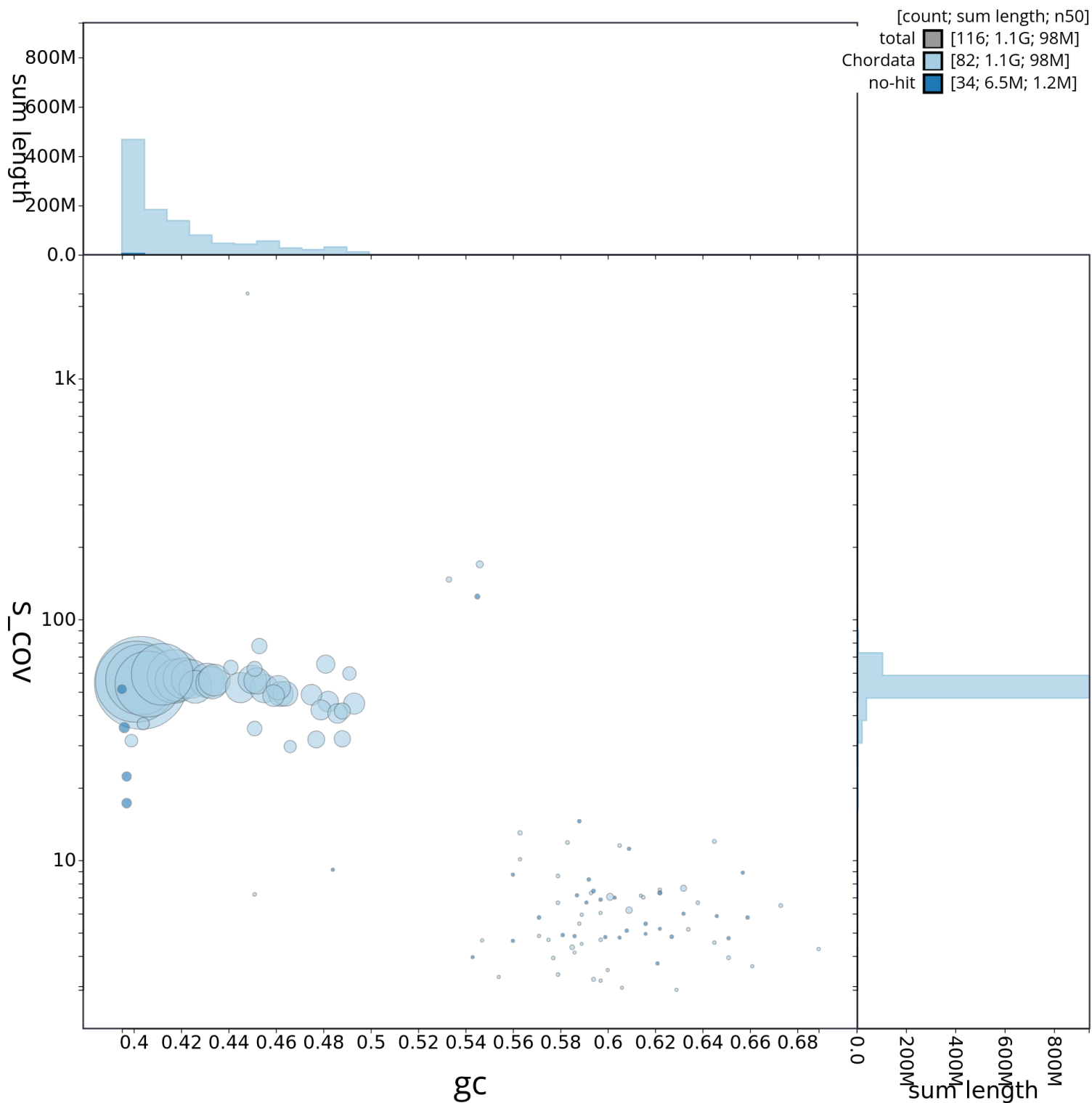


Distribution of k-mer counts per copy numbers found in asm



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

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