

ERGA Assembly Report

v24.09.10

Tags: ERGA-BGE

TxID	754874
ToLID	drEbeCret
Species	<i>Ebenus cretica</i>
Class	Magnoliopsida
Order	Fabales

Genome Traits	Expected	Observed
Haploid size (bp)	988,901,153	944,538,891
Haploid Number	7 (source: direct)	6
Ploidy	2 (source: ancestor)	2
Sample Sex	Unknown	Unknown

EBP metrics summary and curation notes

Obtained EBP quality metric for collapsed: 7.8.Q59

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

- . Observed Haploid Number is different from Expected
- . Kmer completeness value is less than 90 for collapsed
- . BUSCO single copy value is less than 90% for collapsed
- . BUSCO duplicated value is more than 5% for collapsed

Curator notes

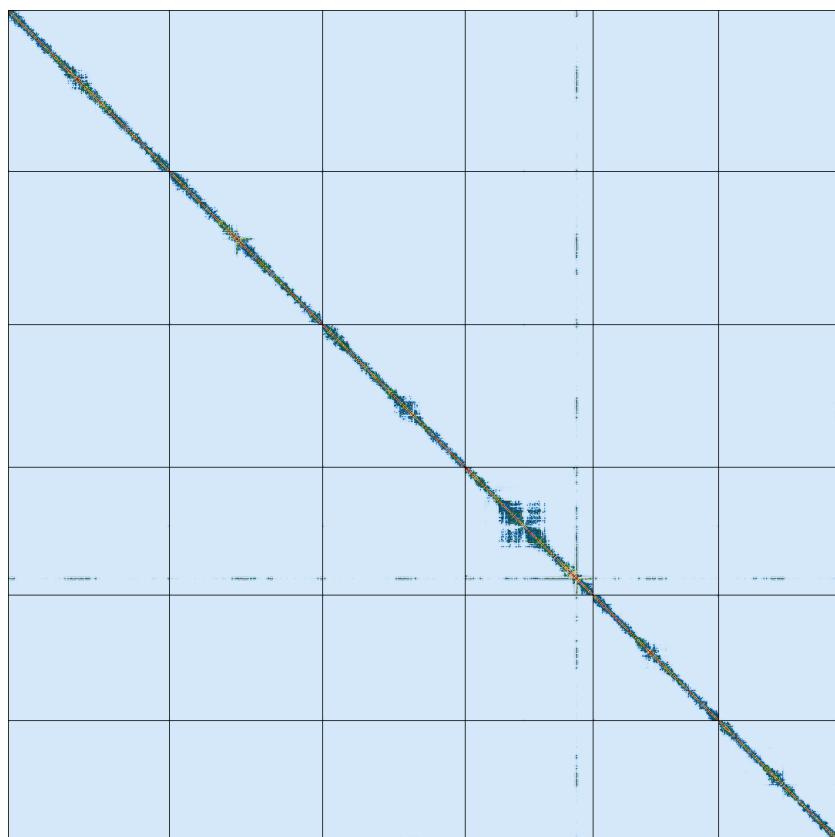
- . Interventions/Gb: 3
- . Contamination notes: "One bacterial sequence of 77kb was detected and removed. "
- . Other observations: ""

Quality metrics table

Metrics	Pre-curation collapsed	Curated collapsed
Total bp	946,087,149	944,538,891
GC %	34.54	34.54
Gaps/Gbp	27.48	18
Total gap bp	2,600	1,800
Scaffolds	69	55
Scaffold N50	174,068,480	161,678,577
Scaffold L50	2	3
Scaffold L90	5	6
Contigs	95	72
Contig N50	92,227,207	92,227,207
Contig L50	4	4
Contig L90	10	10
QV	58.9172	59.1885
Kmer compl.	89.3262	89.3335
BUSCO sing.	64.3%	64.4%
BUSCO dupl.	34.6%	34.5%
BUSCO frag.	0.1%	0.1%
BUSCO miss.	1.0%	1.0%

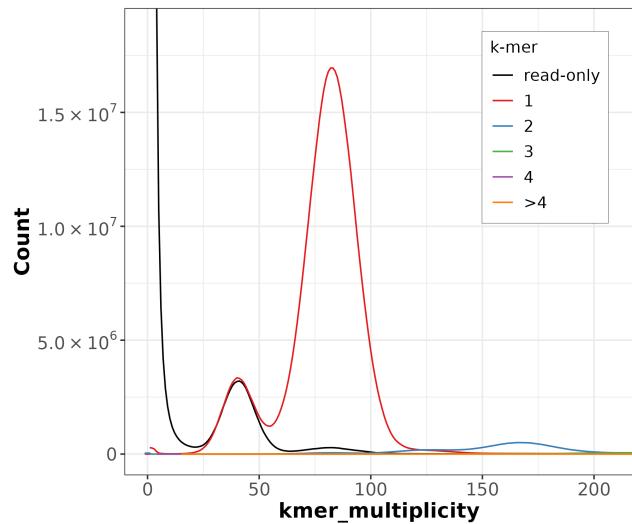
BUSCO 5.4.3 Lineage: embryophyta_odb10 (genomes:50, BUSCOs:1614)

HiC contact map of curated assembly

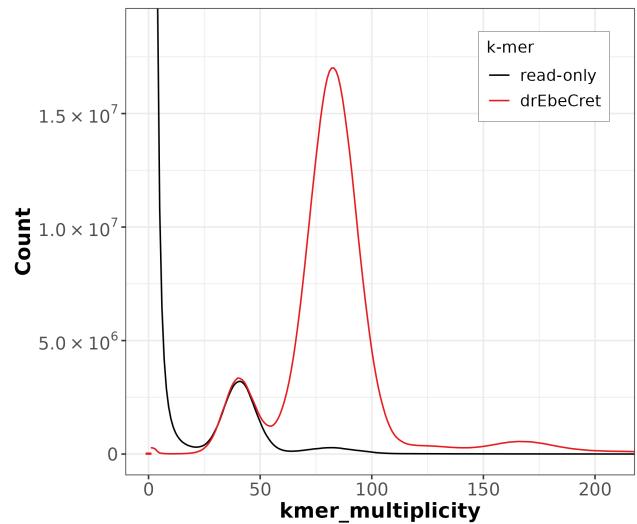


collapsed [\[LINK\]](#)

K-mer spectra of curated assembly

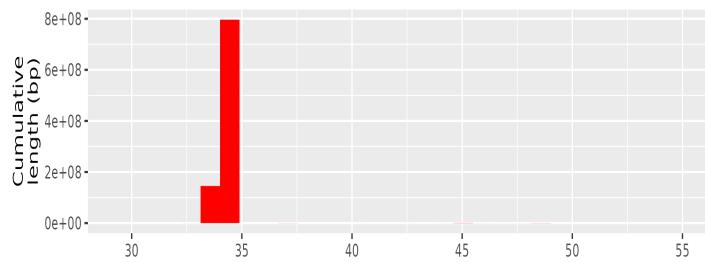


Distribution of k-mer counts per copy numbers found in asm

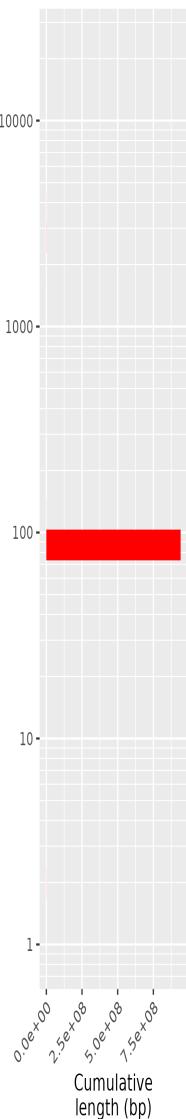
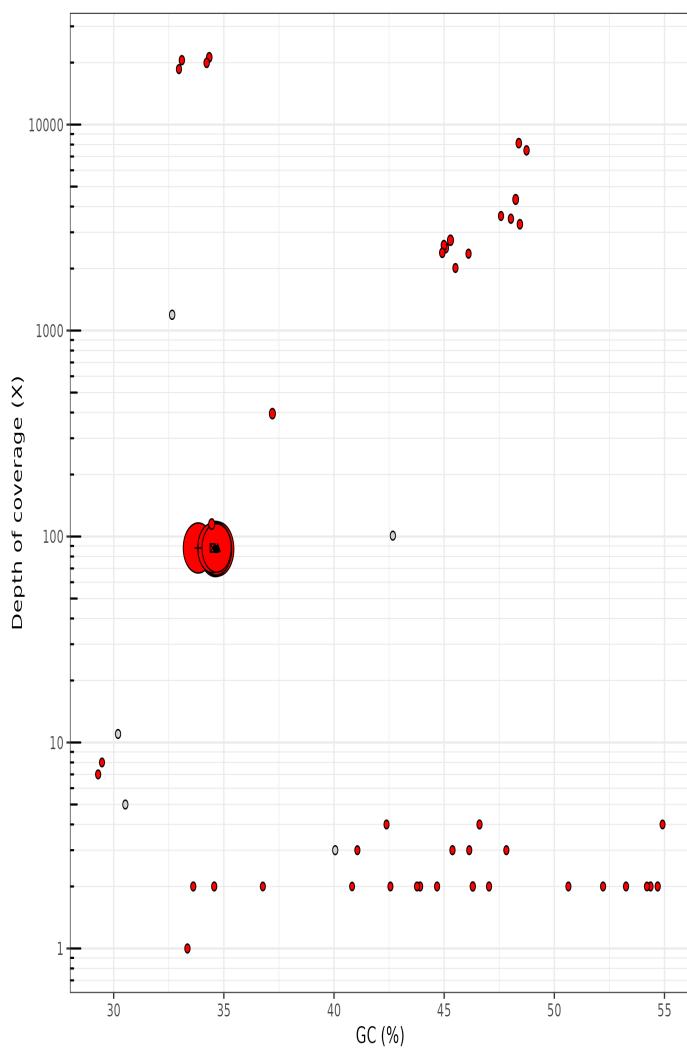


Distribution of k-mer counts coloured by their presence in reads/assemblies

Post-curation contamination screening



TAPAs summary Graph



Data profile

Data	PACBIO Hifi	Omnic
Coverage	75	43

Assembly pipeline

- **Hifiasm**
 - |_ ver: 0.19.5-r593
 - |_ key param: NA
- **purge_dups**
 - |_ ver: 1.2.5
 - |_ key param: NA
- **YaHS**
 - |_ ver: 1.2
 - |_ key param: NA

Curation pipeline

- **PretextMap**
 - |_ ver: 0.1.9
 - |_ key param: NA
- **PretextView**
 - |_ ver: 0.2.5
 - |_ key param: NA

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Affiliation: Genoscope

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