

ERGA Assembly Report

v24.10.15

Tags: non-curated[INVALID TAG]

TxID	350094
ToLID	icOmaFont1
Species	<i>Omalisus fontisbellaquei</i>
Class	Insecta
Order	Coleoptera

Genome Traits	Expected	Observed
Haploid size (bp)	321,564,405	355,235,907
Haploid Number	9 (source: ancestor)	20
Ploidy	2 (source: ancestor)	2
Sample Sex	unknown	unknown

EBP metrics summary and curation notes

Obtained EBP quality metric for pri: 4.5.Q61

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

- . Observed Haploid Number is different from Expected
- . More than 1000 gaps/Gbp for pri
- . Not 90% of assembly in chromosomes for pri

Curator notes

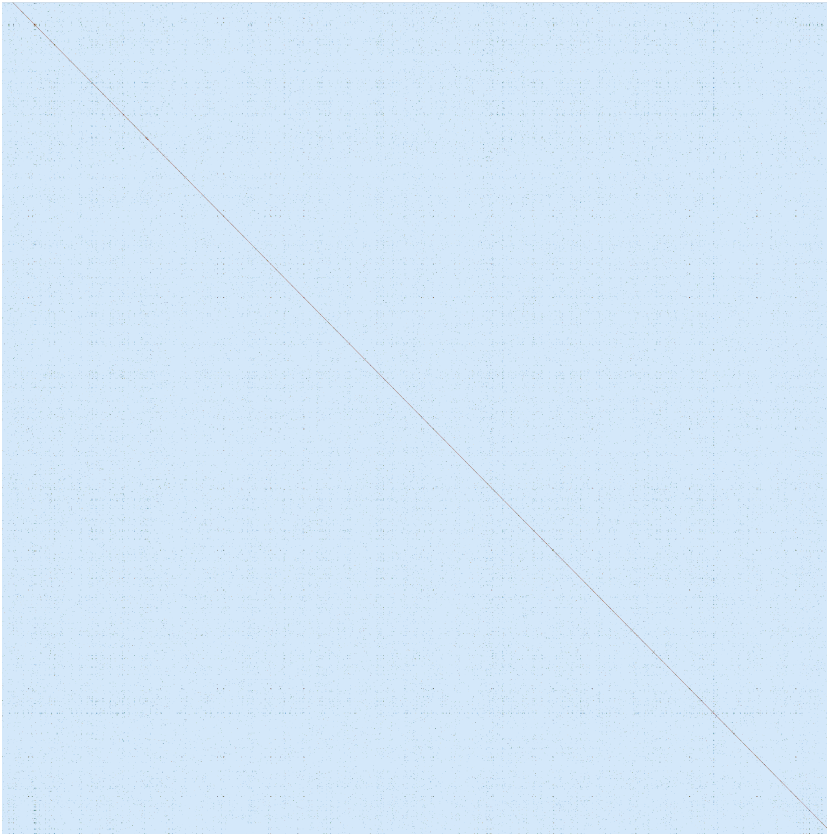
- . Interventions/Gb: 0
- . Contamination notes: "No contaminations were detected with FCS-GX."
- . Other observations: "This is a draft genome, not a manually curated assembly. No long range information from the Hi-C libraries, precluding the possibility to perform manual curation on this genome. I am providing the Hi-C map image and Pretext files anyway."

Quality metrics table

Metrics	Pre-curation pri	Curated pri
Total bp	355,235,907	355,235,907
GC %	34.11	34.11
Gaps/Gbp	11,685.19	11,685.19
Total gap bp	830,200	830,200
Scaffolds	4,605	4,605
Scaffold N50	178,600	178,600
Scaffold L50	558	558
Scaffold L90	2,306	2,306
Contigs	8,756	8,756
Contig N50	49,000	49,000
Contig L50	2,034	2,034
Contig L90	6,437	6,437
QV	59.0401	61.4911
Kmer compl.		
BUSCO sing.	93.9%	93.9%
BUSCO dupl.	3.4%	3.4%
BUSCO frag.	1.1%	1.1%
BUSCO miss.	1.7%	1.7%

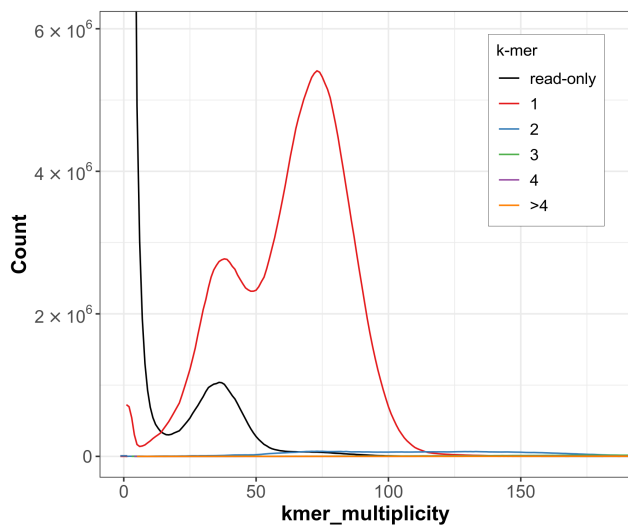
BUSCO: 6.0.0 (euk_genome_min, miniprot) / Lineage: arthropoda_odb10 (genomes:90, BUSCOs:1013)

HiC contact map of curated assembly

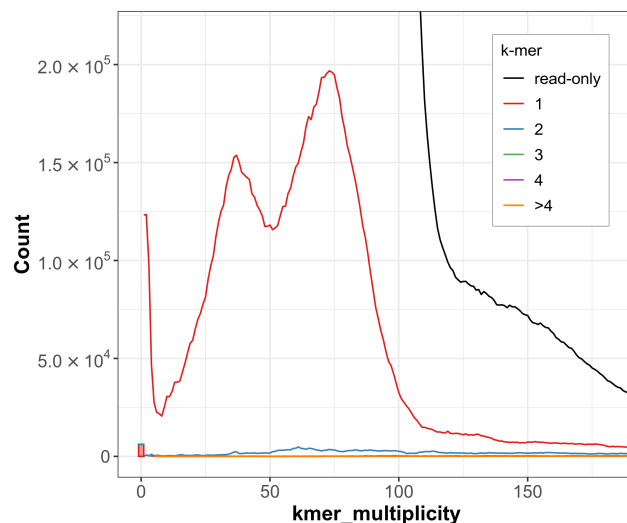


pri [\[LINK\]](#)

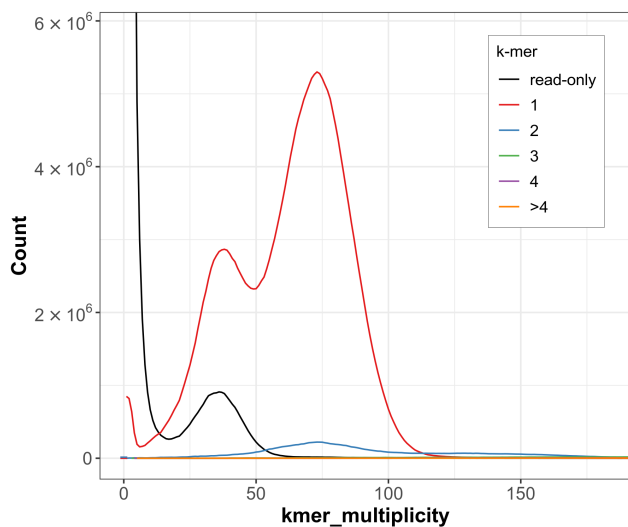
K-mer spectra of curated assembly



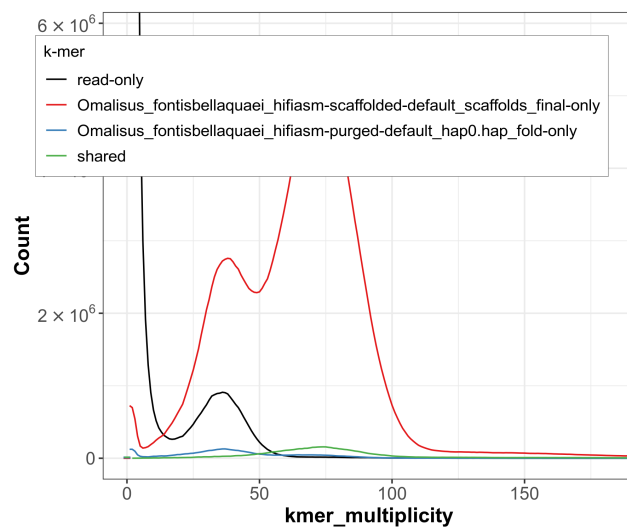
Distribution of k-mer counts per copy numbers found in **Omalisus_fontisbellaquaei_hifi.asm-sc affolded-default_scaffolds_final** (hap1.)



Distribution of k-mer counts per copy numbers found in **Omalisus_fontisbellaquaei_hifi.asm-purged-default_hap0 hap_fold** (hap1.)

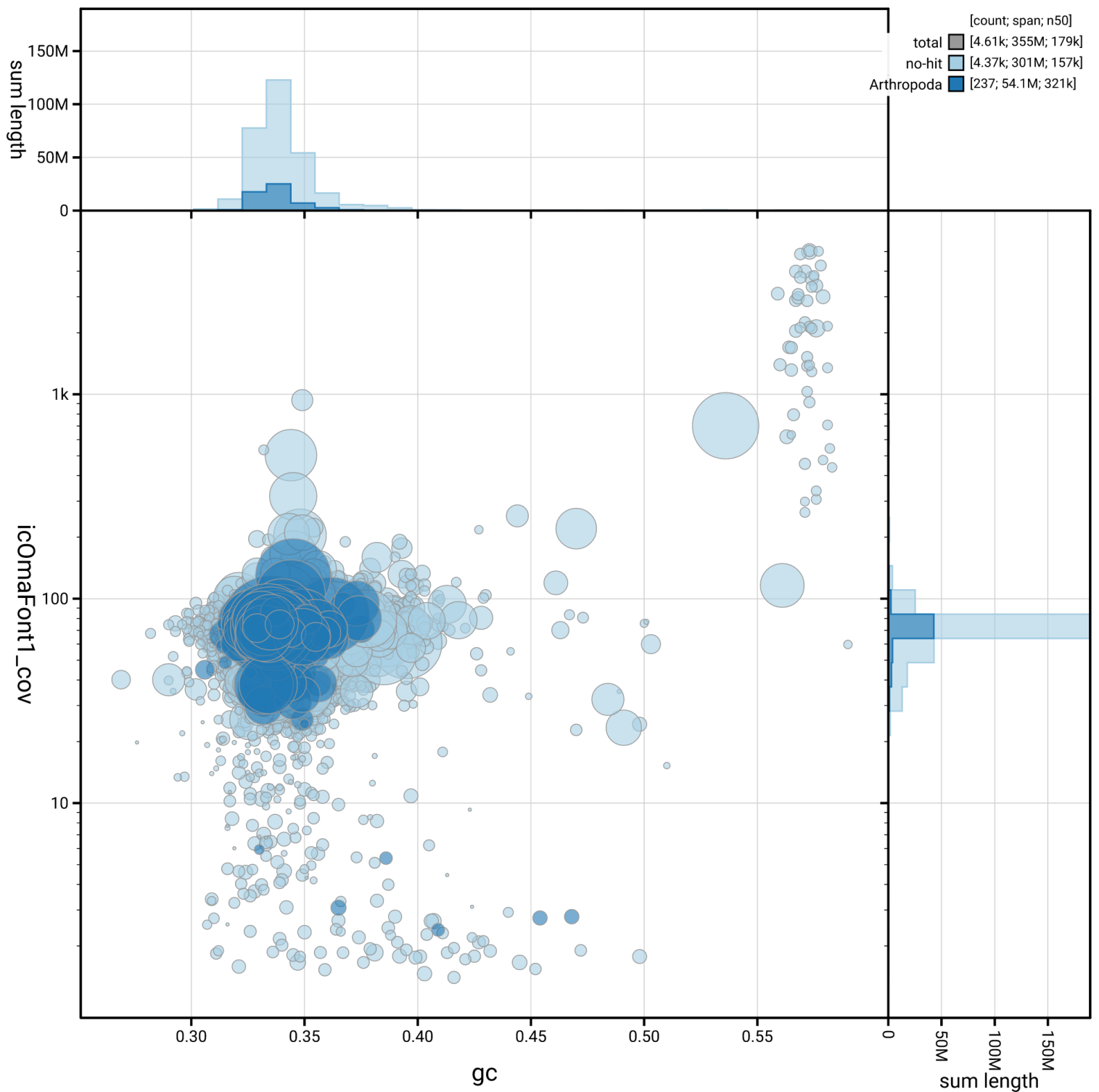


Distribution of k-mer counts per copy numbers found in **asm** (dipl.)



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	HiC
Coverage	68x	195x

Assembly pipeline

- **Hifiasm**
 - |_ *ver*: 0.25.0-r726
 - |_ *key param*: 13
- **purge_dups**
 - |_ *ver*: 1.2.6
 - |_ *key param*: NA

Curation pipeline

- **GRIT_Rapid**
 - |_ *ver*: 0
 - |_ *key param*: NA
- **HiGlass**
 - |_ *ver*: 0
 - |_ *key param*: NA

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