

ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

TxID	439822
ToLID	kaMicSqual
Species	Microcosmus squamiger
Class	Ascidacea
Order	Stolidobranchia

Genome Traits	Expected	Observed
Haploid size (bp)	192,802,479	188,886,422
Haploid Number	16 (source: ancestor)	10
Ploidy	2 (source: ancestor)	2
Sample Sex	unknown	unknown

EBP metrics summary and curation notes

Obtained EBP quality metric for pri: 6.7.Q61

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 pri

Curator notes

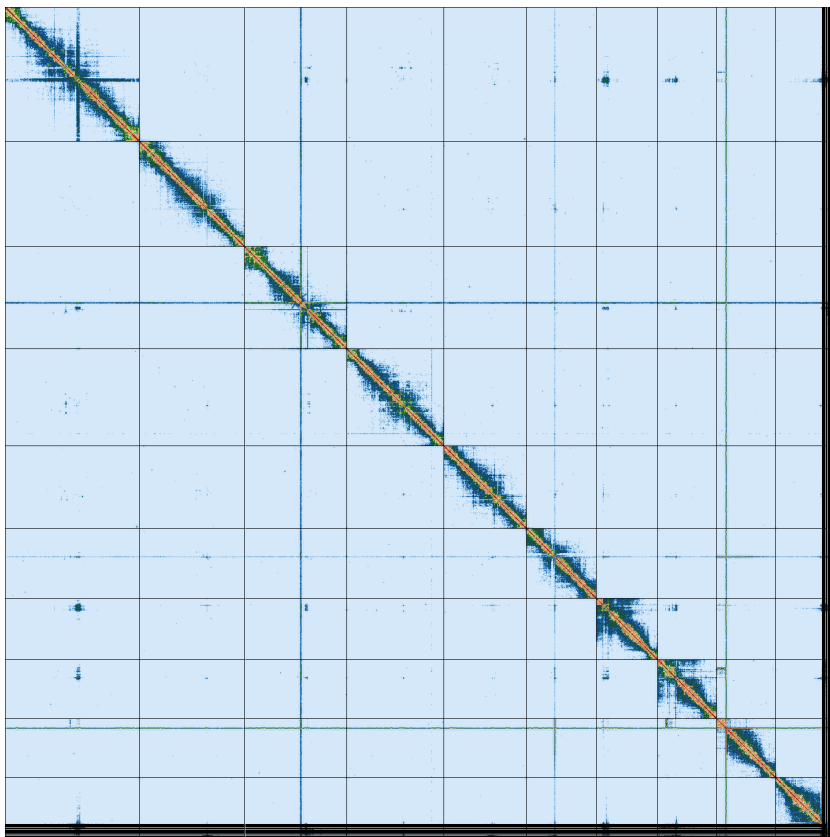
- . Interventions/Gb: 91
- . Contamination notes: "No contaminations were detected with FCS-GX."
- . Other observations: "Reads were assembled with hifiiasm (yield: 218M, N50: 5.3M, 666 contigs). FCS-GX detected no contaminations. Purge_dups removed 427 contigs (26Mb). HiC data is of a decent quality with 8.8M cis-reads pairs above 40Kb. The scaffolding was done in the manual curation steps."

Quality metrics table

Metrics	Pre-curation pri	Curated pri
Total bp	192,689,173	188,886,422
GC %	43.3	43.43
Gaps/Gbp	0	402.36
Total gap bp	0	15,200
Scaffolds	239	108
Scaffold N50	6,661,360	22,013,698
Scaffold L50	11	4
Scaffold L90	37	9
Contigs	239	184
Contig N50	6,661,360	5,359,238
Contig L50	11	12
Contig L90	37	39
QV	60.6774	61.1407
Kmer compl.	66.7366	66.5603
BUSCO sing.	96.1%	96.3%
BUSCO dupl.	0.3%	0.3%
BUSCO frag.	1.6%	1.6%
BUSCO miss.	1.9%	1.8%

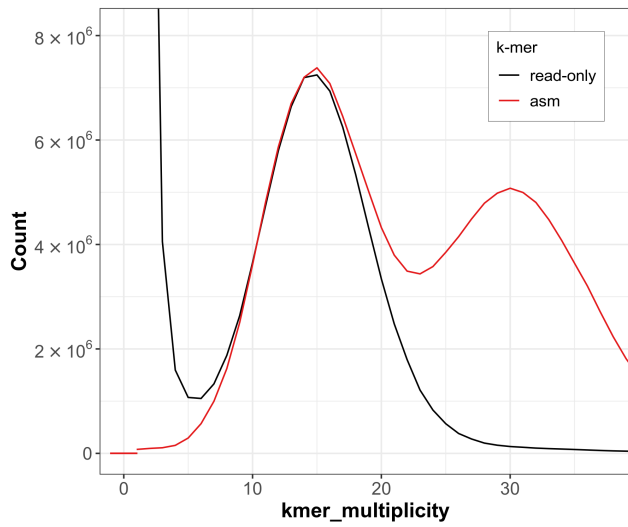
BUSCO: 5.8.3 (euk_genome_min, miniprot) / Lineage: metazoa_odb12 (genomes:206, BUSCOs:672)

HiC contact map of curated assembly

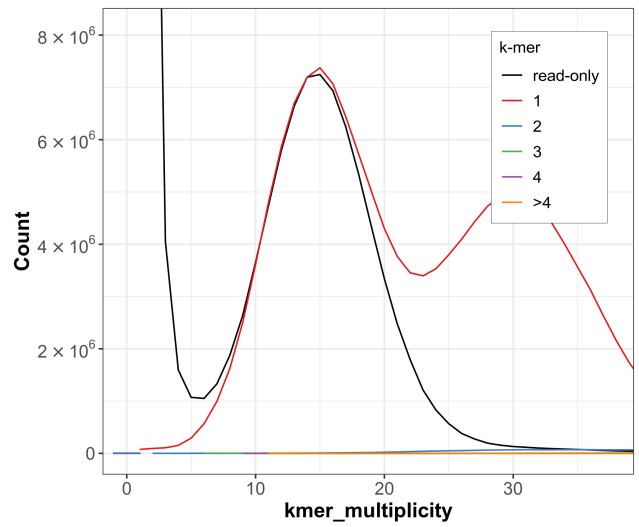


pri [\[LINK\]](#)

K-mer spectra of curated assembly

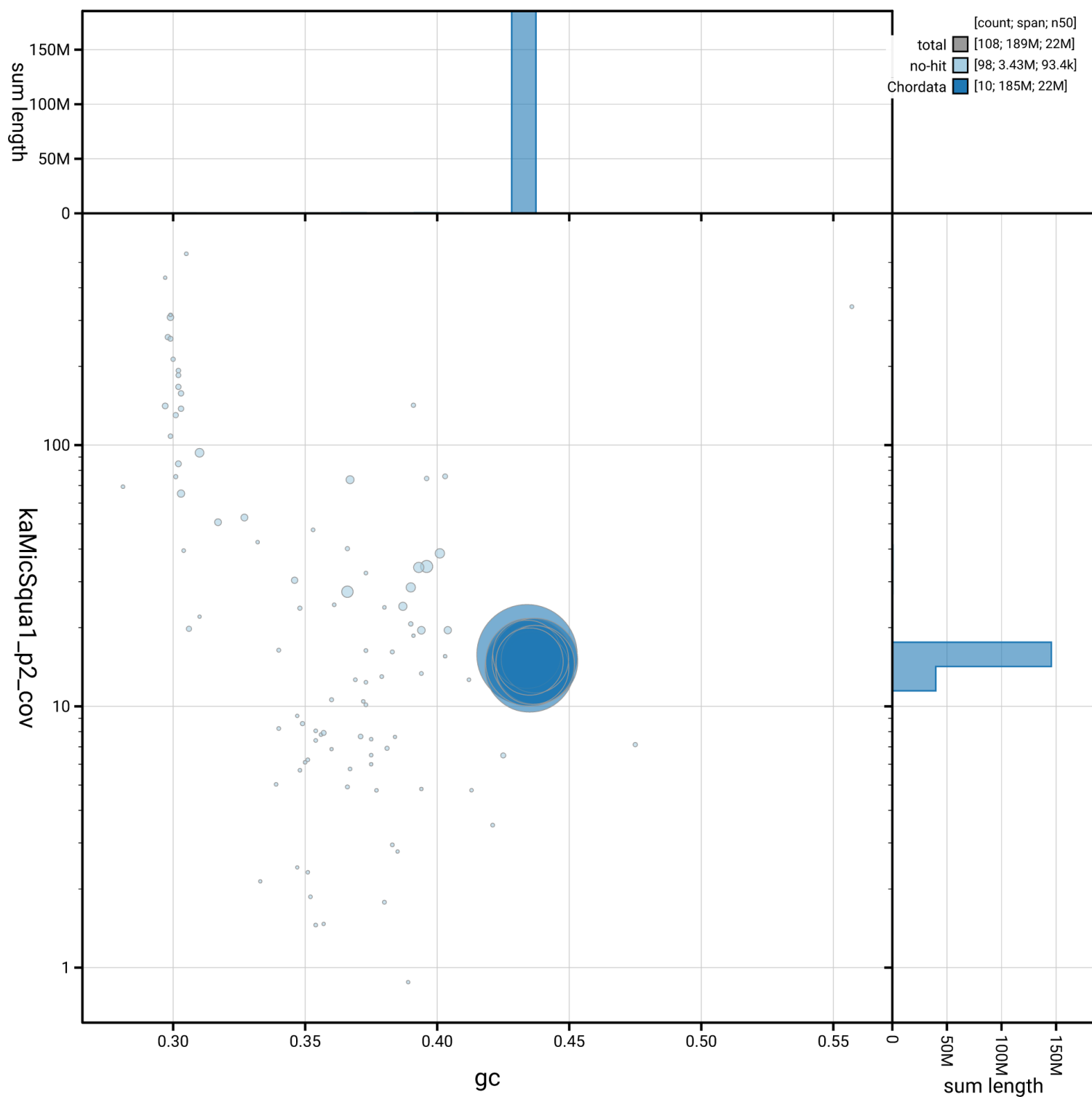


Distribution of k-mer counts coloured by their presence in reads/assemblies



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

Post-curation contamination screening



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	33x	176x

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

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