

ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

TxID	2750798
ToLID	qcLitStygl
Species	Lithobius stygius
Class	Chilopoda
Order	Lithobiomorpha

Genome Traits	Expected	Observed
Haploid size (bp)	2,782,836,479	2,899,779,427
Haploid Number	20 (source: ancestor)	21
Ploidy	2 (source: ancestor)	2
Sample Sex	unknown	unknown

EBP metrics summary and curation notes

Obtained EBP quality metric for pri: 7.8.Q66

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

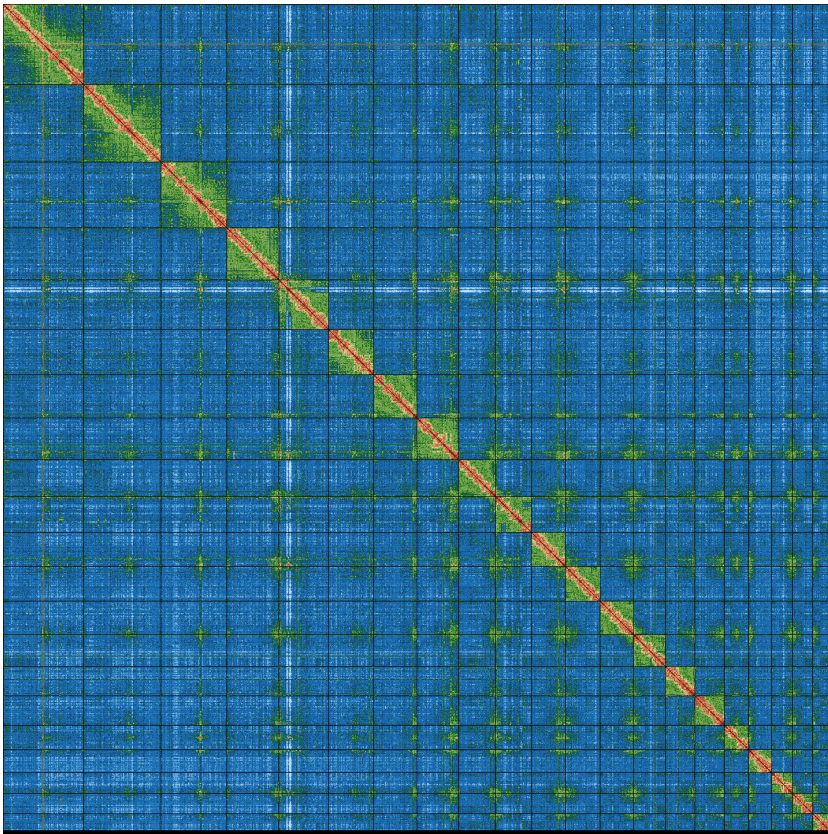
- . Interventions/Gb: None
- . Contamination notes: "No presence of contaminants."
- . Other observations: "many interventions on the contig level were necessary. Three manual curation rounds were done with the following interventions round 1: (Curation made 31 cuts in contigs, 15 breaks at gaps and 47 joins), round 2: (Curation made 50 cuts in contigs, 41 breaks at gaps and 49 joins) and round 3: (Curation made 16 cuts in contigs, 18 breaks at gaps and 17 joins). The final blobtools plot is misleading in my point of view. FCS reported nothing on contig assembly and the blobtools classification is only based on the diamond hits. Blast reported not a single alignment. A manual web-blast for some of the putative contaminations did not report anything either. Super_5 has an odd HiC signal and a 20Mb region where the coverage drops to half. But there is not any haplotig off-diagonal signal visible. In a previous curation round I had SUPER_5 split into two chromosomes separated at the 32Mb gap, but that did not look good either."

Quality metrics table

Metrics	Pre-curation pri	Curated pri
Total bp	2,938,307,048	2,899,779,427
GC %	40.82	40.86
Gaps/Gbp	77.6	92.42
Total gap bp	22,800	36,300
Scaffolds	166	139
Scaffold N50	138,650,401	145,659,984
Scaffold L50	6	8
Scaffold L90	17	18
Contigs	394	407
Contig N50	17,735,187	16,382,918
Contig L50	48	54
Contig L90	157	170
QV	66.7765	66.9532
Kmer compl.	86.5003	86.188
BUSCO sing.	94.2%	94.2%
BUSCO dupl.	0.9%	0.9%
BUSCO frag.	2.8%	2.8%
BUSCO miss.	2.0%	2.1%

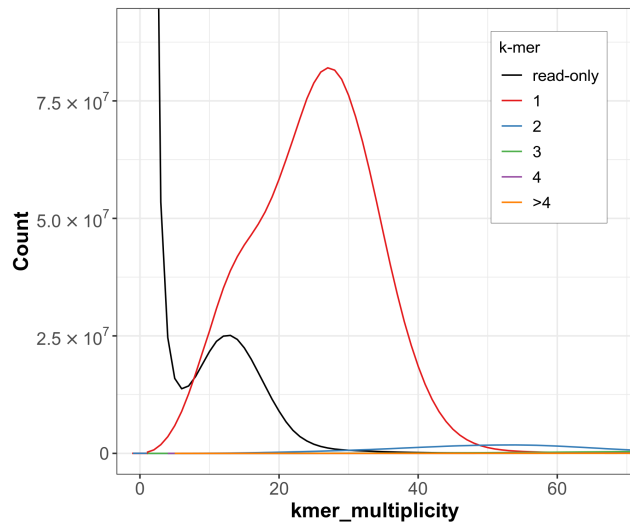
BUSCO: 5.8.3 (euk_genome_min, miniprot) / Lineage: arthropoda_odb12 (genomes:76, BUSCOs:1667)

HiC contact map of curated assembly

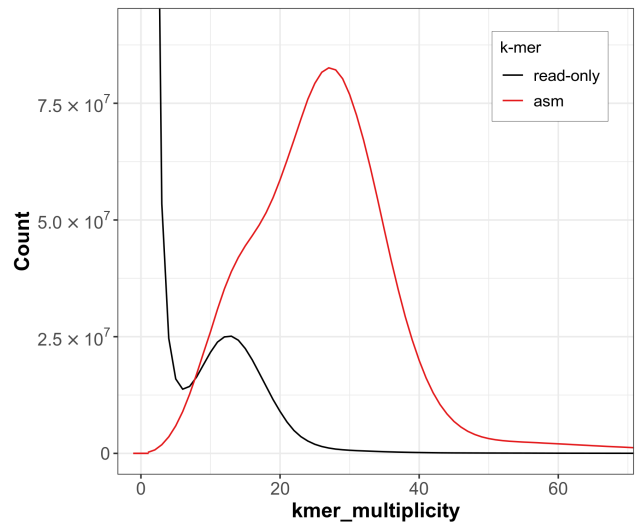


pri [\[LINK\]](#)

K-mer spectra of curated assembly

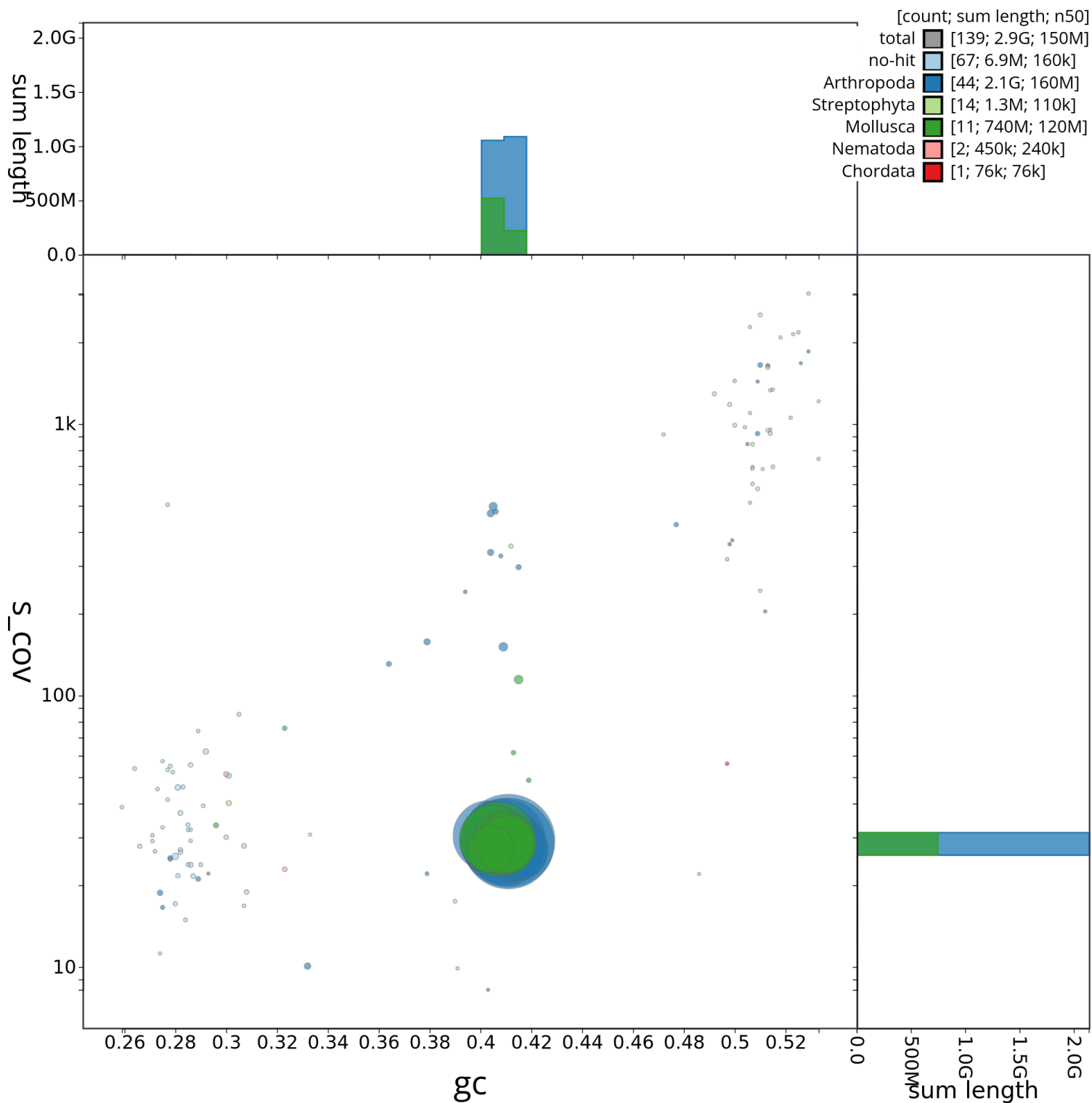


Distribution of k-mer counts per copy numbers found in asm



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	HiC
Coverage	28x	76x

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

Curation pipeline

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

Submitter: Martin Pippel

Affiliation: SciLifeLab

Date and time: 2025-07-08 09:08:20 CEST