

ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

| | |
|---------|---------------------|
| TxID | 3049732 |
| ToLID | qdStyIlly1 |
| Species | Stygiulus illyricus |
| Class | Diplopoda |
| Order | Julida |

| Genome Traits | Expected | Observed |
|-------------------|-----------------------|-------------|
| Haploid size (bp) | 526,119,689 | 549,733,997 |
| Haploid Number | 12 (source: ancestor) | 13 |
| Ploidy | 2 (source: ancestor) | 2 |
| Sample Sex | NA | NA |

EBP metrics summary and curation notes

Obtained EBP quality metric for pri: 6.7.Q52

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
- . Not 90% of assembly in chromosomes for pri

Curator notes

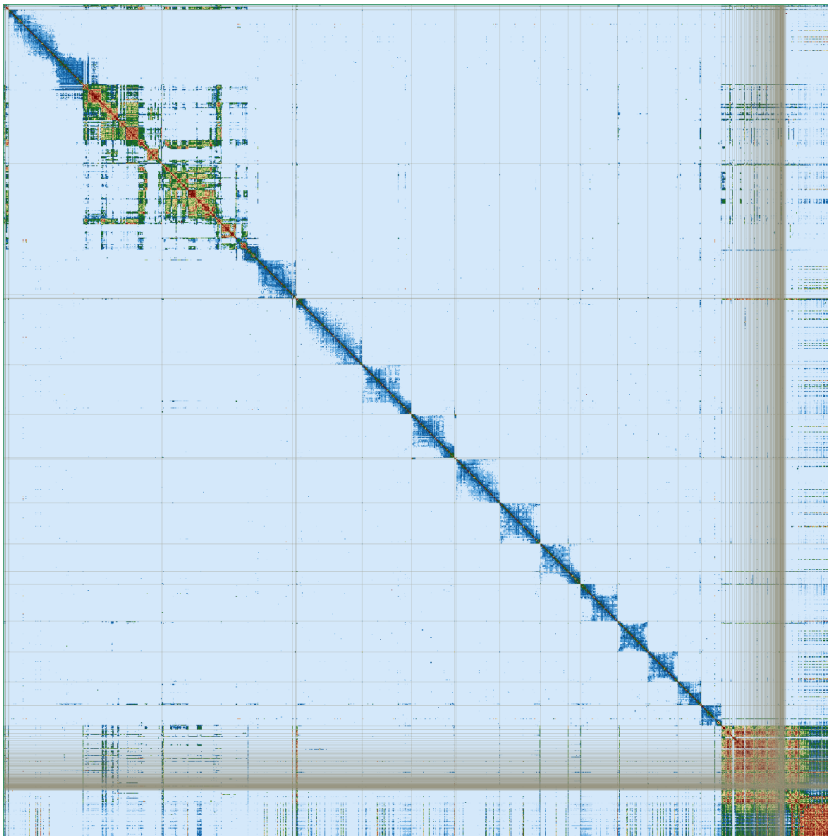
- . Interventions/Gb: None
- . Contamination notes: ""
- . Other observations: "Difficult to know if the first two scaffolds should be one or two chromosomes. Potentially the X and Y. Lots of repetitive sequences."

Quality metrics table

| Metrics | Pre-curation pri | Curated pri |
|--------------|---------------------|----------------|
| Total bp | 550,780,026 | 549,733,997 |
| GC % | 37.49 | 37.48 |
| Gaps/Gbp | 490.21 | 491.15 |
| Total gap bp | 54,000 | 54,000 |
| Scaffolds | 1,682 | 1,680 |
| Scaffold N50 | 29,700,184 | 29,024,683 |
| Scaffold L50 | 5 | 5 |
| Scaffold L90 | 36 | 34 |
| Contigs | 1,952 | 1,950 |
| Contig N50 | 2,585,720 | 2,585,720 |
| Contig L50 | 60 | 60 |
| Contig L90 | 235 | 234 |
| QV | 48.5773 | 52.7783 |
| Kmer compl. | 94.9653 | 87.5237 |
| BUSCO sing. | 97.1% | 97.1% |
| BUSCO dupl. | 0.6% | 0.5% |
| BUSCO frag. | 0.9% | 0.8% |
| BUSCO miss. | 1.4% | 1.5% |

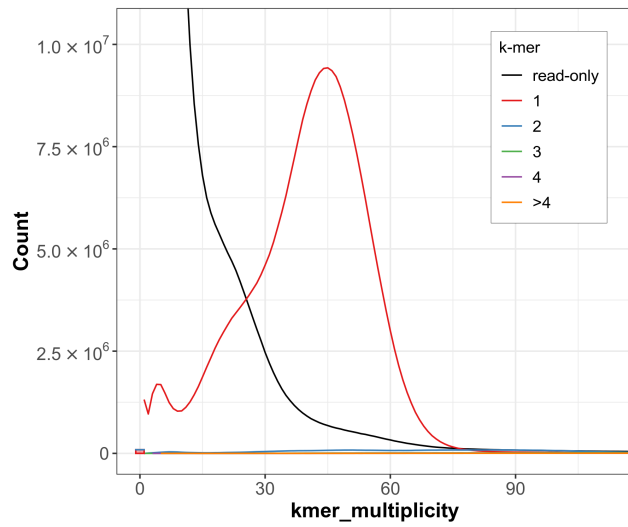
BUSCO: 6.0.0 (euk_genome_min, miniprot) / Lineage: arthropoda_odb12 (genomes:76, BUSCOs:1667)

HiC contact map of curated assembly

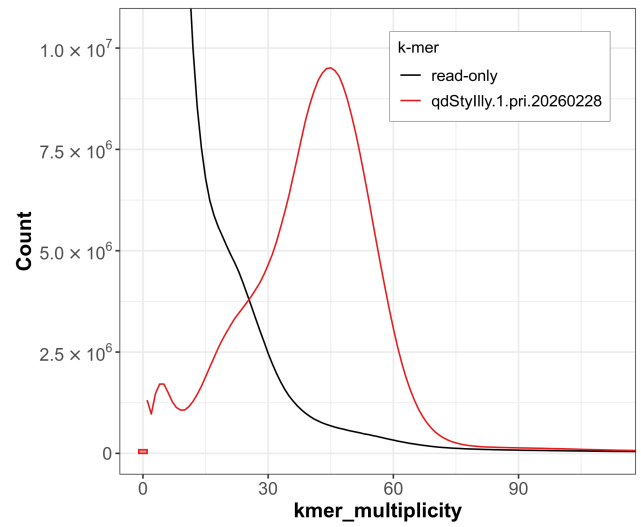


pri [\[LINK\]](#)

K-mer spectra of curated assembly

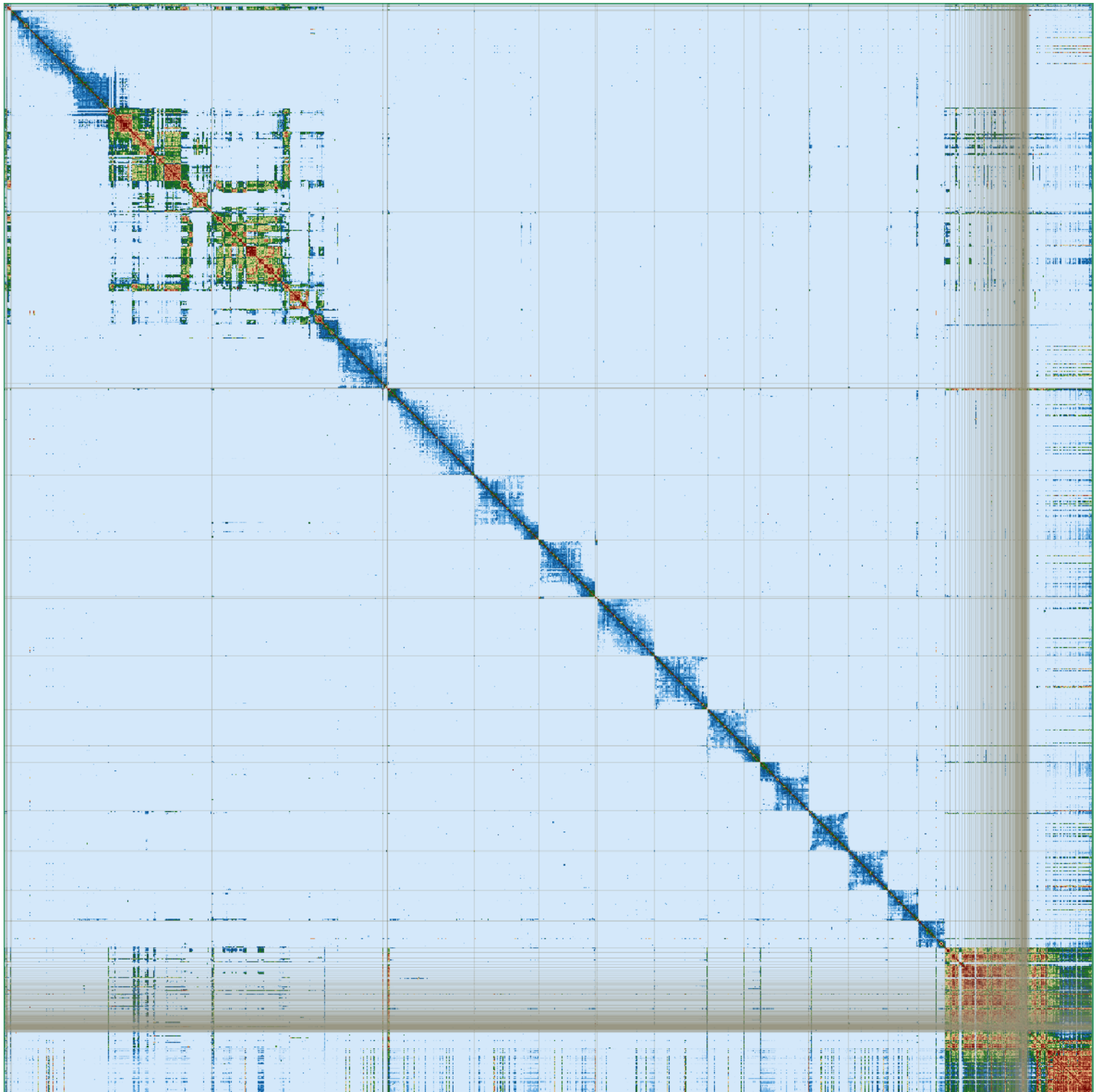


Distribution of k-mer counts per copy numbers found in asm



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 | ONT | HiC |
|----------|-----|-----|
| Coverage | NA | NA |

Assembly pipeline

- **HiFiasm**
 - |_ *ver*: 0.25.0
 - |_ *key param*: NA
- **purge-dups**
 - |_ *ver*: 1.2.6
 - |_ *key param*: NA
- **yahs**
 - |_ *ver*: 1.1a
 - |_ *key param*: NA
- **fcs-gx**
 - |_ *ver*: 0.5.0
 - |_ *key param*: NA

Curation pipeline

- **PretextView**
 - |_ *ver*: 1.0.0
 - |_ *key param*: NA

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