

ERGA Assembly Report

v24.04.03_beta

Tags: ERGA-BGE

| | |
|---------|-------------------|
| TxID | 270879 |
| ToLID | ijBorWest1 |
| Species | Boreus westwoodi |
| Class | Insecta |
| Order | Mecoptera |

| Genome Traits | Expected | Observed |
|-------------------|-----------------------|-------------|
| Haploid size (bp) | 529,682,445 | 657,981,536 |
| Haploid Number | 13 (source: ancestor) | 24 |
| Ploidy | 2 (source: ancestor) | 2 |
| Sample Sex | F | F |

EBP metrics summary and curation notes

Obtained EBP quality metric for pri: 6.7.Q54

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

- . Observed Haploid size (bp) has >20% difference with Expected
- . Observed Haploid Number is different from Expected
- . Kmer completeness value is less than 90 for pri
- . More than 1000 gaps/Gbp for pri
- . Not 90% of assembly in chromosomes for pri

Curator notes

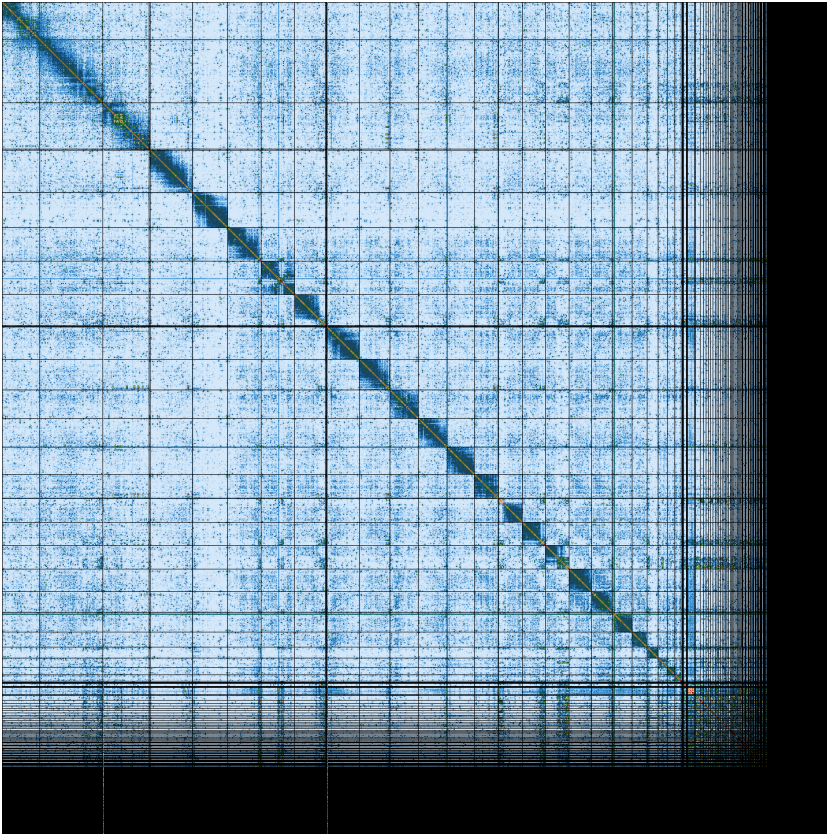
- . Interventions/Gb: 216
- . Contamination notes: "Contamination report for assembly labelled primary; Total length of scaffolds removed: 15 (0.0 %); Scaffolds removed: 0 (0.0 %); Largest scaffold removed: (15); FCS-GX contaminant species (number of scaffolds; total length of scaffolds):Barcodes (1; 15)"
- . Other observations: "hifiasm run in non-phasing mode; Hi-C is from 3 different individuals, ijBorWest2, ijBorWest4, ijBorWest5."

Quality metrics table

| Metrics | Pre-curation pri | Curated pri |
|--------------|---------------------|----------------|
| Total bp | 667,801,017 | 657,981,536 |
| GC % | 33.59 | 33.6 |
| Gaps/Gbp | 1,758.01 | 1,759.93 |
| Total gap bp | 117,400 | 130,900 |
| Scaffolds | 764 | 739 |
| Scaffold N50 | 17,691,776 | 21,986,458 |
| Scaffold L50 | 12 | 11 |
| Scaffold L90 | 94 | 69 |
| Contigs | 1,938 | 1,897 |
| Contig N50 | 1,007,420 | 1,012,485 |
| Contig L50 | 197 | 184 |
| Contig L90 | 828 | 800 |
| QV | 54.0 | 54.0 |
| Kmer compl. | 99.24 | 65.72 |
| BUSCO sing. | 93.4% | 95.2% |
| BUSCO dupl. | 4.7% | 3.3% |
| BUSCO frag. | 0.4% | 0.0% |
| BUSCO miss. | 1.5% | 1.5% |

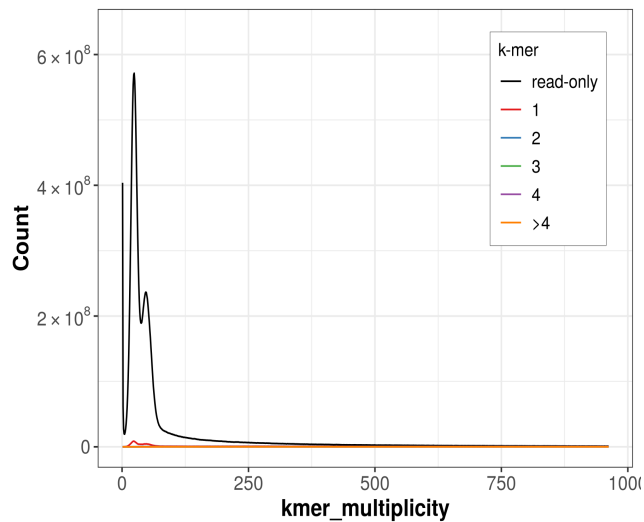
Warning: BUSCO versions or lineage datasets are not the same across results

HiC contact map of curated assembly

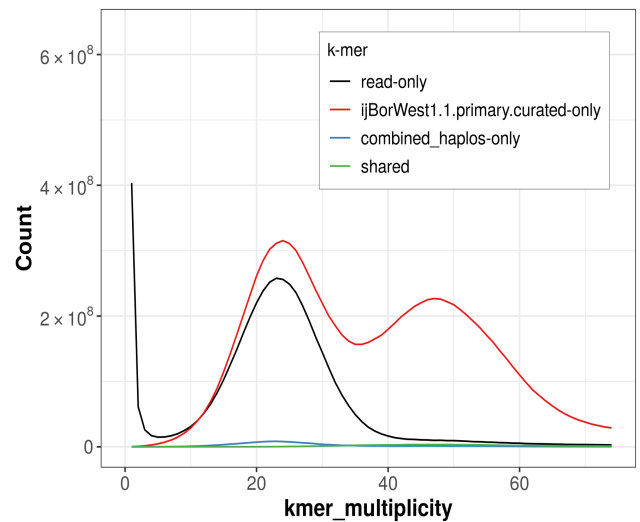


pri [\[LINK\]](#)

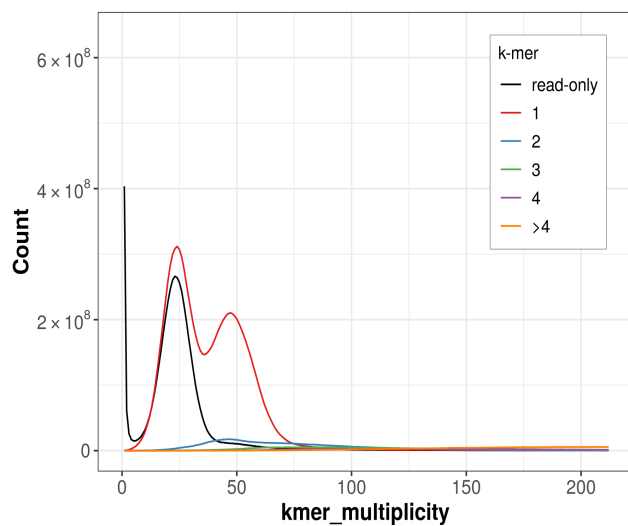
K-mer spectra of curated assembly



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

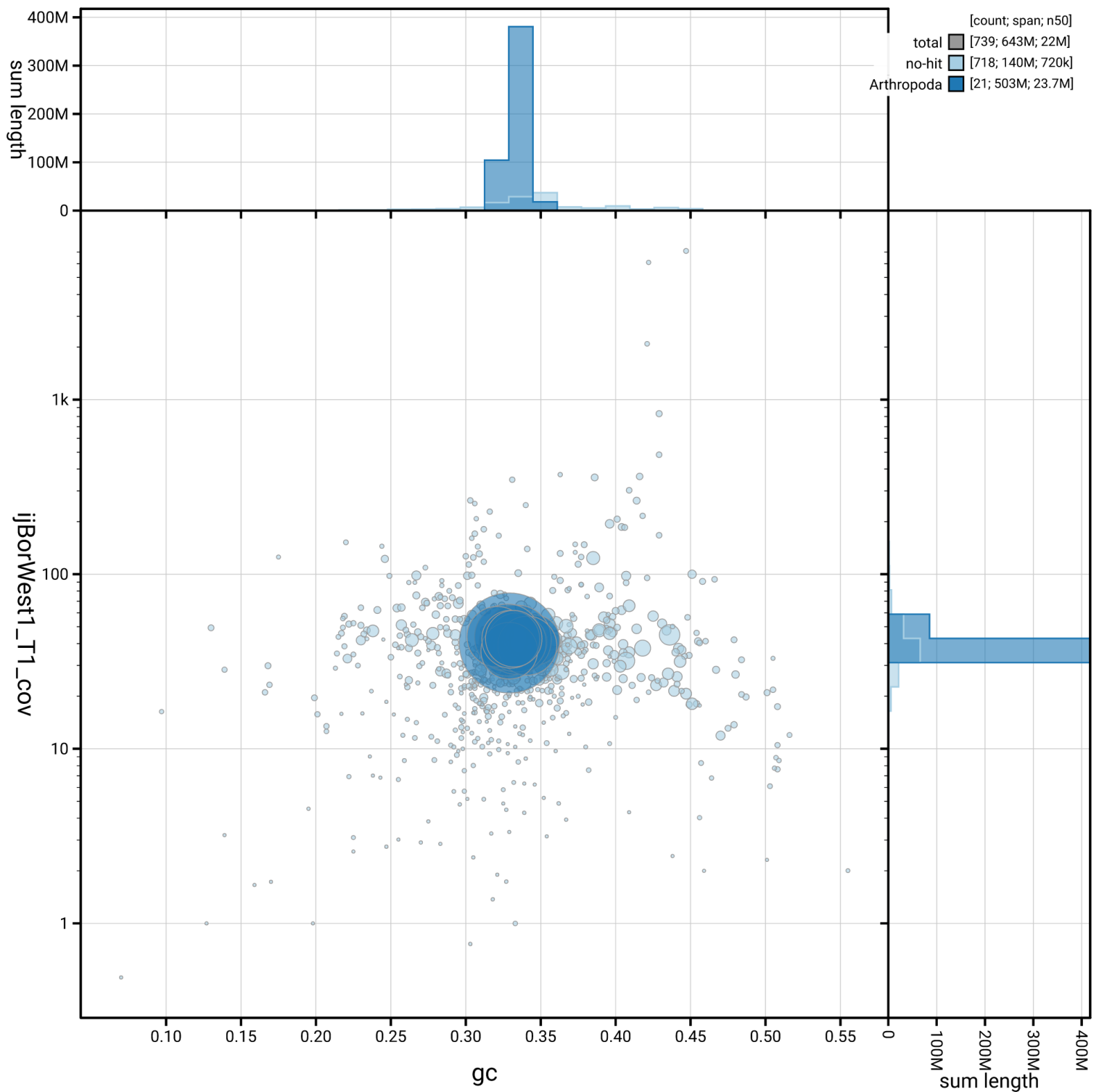


Distribution of k-mer counts coloured by their presence in reads/assemblies



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 | PacBio HiFi | Arima v3 |
|----------|-------------|----------|
| Coverage | 46x | 819x |

Assembly pipeline

- **hifiasm**
 - |_ *ver*: 0.19.8-r603
 - |_ *key param*: --primary
- **yahs**
 - |_ *ver*: 1.2.2
 - |_ *key param*: NA

Curation pipeline

- **hifiasm**
 - |_ *ver*: 0.19.8-r603
 - |_ *key param*: --primary
- **yahs**
 - |_ *ver*: 1.2.2
 - |_ *key param*: NA
- **TreeVal**
 - |_ *ver*: 1.2.1
 - |_ *key param*: NA

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