

# ERGA Assembly Report

v24.10.15

Tags: ERGA-BGE

TxID	190562
ToLID	<b>tfGorWolt8</b>
Species	Gordionus wolterstorffii
Class	Gordioda
Order	Chordodea

Genome Traits	Expected	Observed
Haploid size (bp)	142,426,324	210,545,467
Haploid Number	4 (source: ancestor)	4
Ploidy	2 (source: ancestor)	2
Sample Sex	unknown	unknown

## EBP metrics summary and curation notes

Obtained EBP quality metric for pri: 7.7.Q70

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

- . Observed Haploid size (bp) has >20% difference with Expected
- . Kmer completeness value is less than 90 for pri
- . BUSCO single copy value is less than 90% for pri

### Curator notes

- . Interventions/Gb: None
- . Contamination notes: "FCS-GX identified 15 bacterial sequences that were removed from the base assembly (3,998,988 bp in total)"
- . Other observations: "It was not possible to get a good Hi-C library for this species but still we strongly believe that we have achieved a chromosome level assembly. Hifiiasm assembled 4 long sequences that seem to be full chromosomes. Due to the lack of Hi-C data, we have posted below an image of the distribution of telomeres along the 4 chromosomes."

# Quality metrics table

Metrics	Pre-curation pri	Curated pri
Total bp	214,544,449	210,545,467
GC %	29.86	29.51
Gaps/Gbp	0	0
Total gap bp	0	0
Scaffolds	23	8
Scaffold N50	53,486,554	53,486,554
Scaffold L50	2	2
Scaffold L90	4	4
Contigs	23	8
Contig N50	53,486,554	53,486,554
Contig L50	2	2
Contig L90	4	4
QV	60.8148	70.0004
Kmer compl.	73.9189	72.3129
BUSCO sing.	54.8%	55.0%
BUSCO dupl.	1.9%	0.9%
BUSCO frag.	11.8%	12.1%
BUSCO miss.	31.5%	32.0%

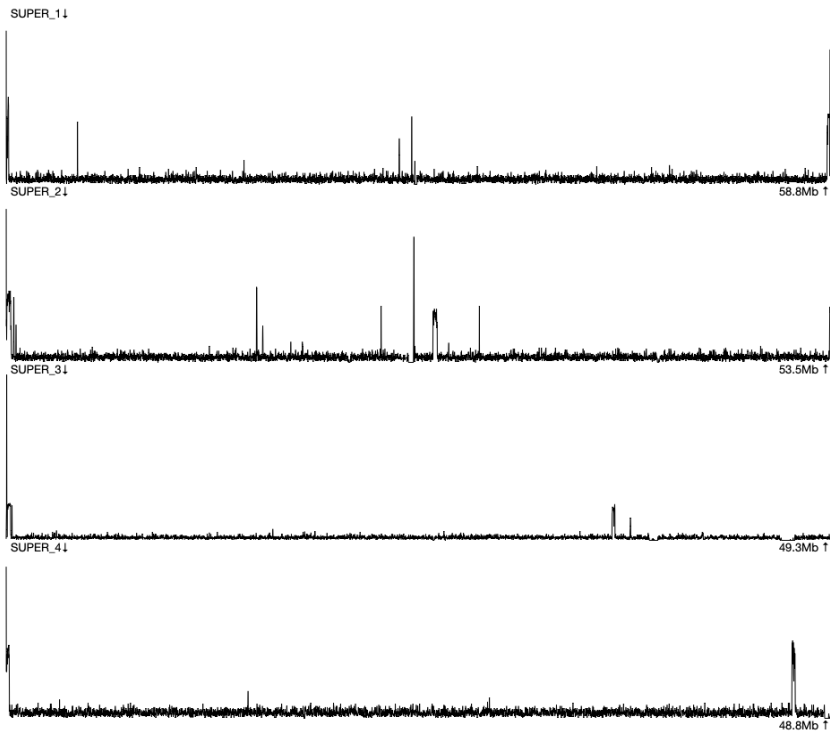
Warning! BUSCO versions or lineage datasets are not the same across results:

BUSCO: 5.4.0 (euk\_genome\_met, metaeuk) / Lineage: metazoa\_odb10 (genomes:65, BUSCOs:954)

BUSCO: 5.5.0 (euk\_genome\_met, metaeuk) / Lineage: metazoa\_odb10 (genomes:65, BUSCOs:954)

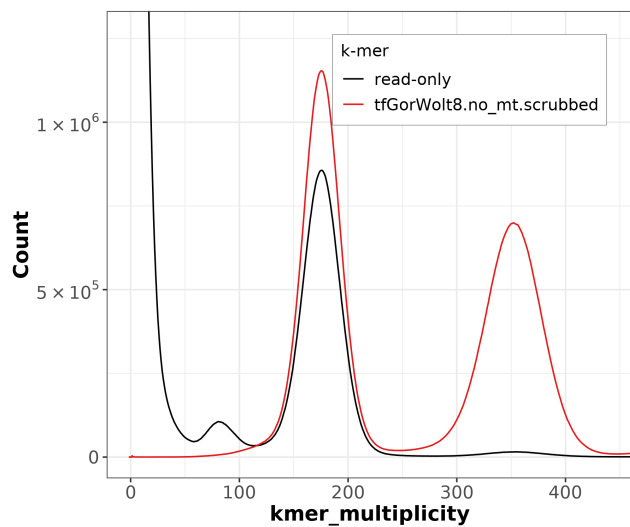
# HiC contact map of curated assembly

Telomeric regions

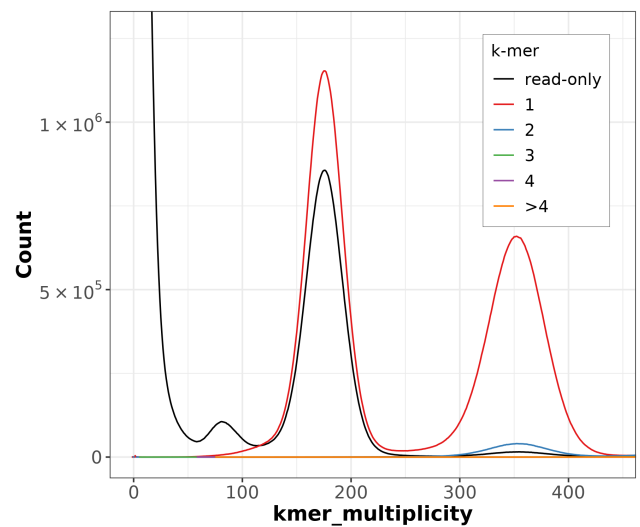


**pri** File link is missing!

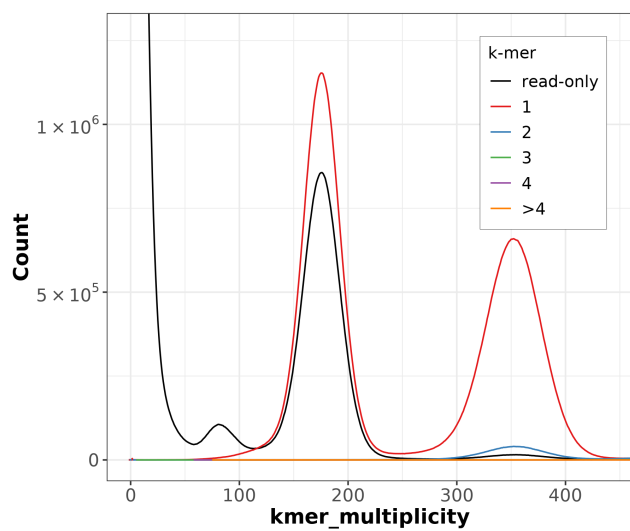
# K-mer spectra of curated assembly



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



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



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

# Post-curation contamination screening

## Data profile

Data	ONT	Illumina
Coverage	143	220

## Assembly pipeline

- **CLAWS**
  - |\_ *ver*: v2.3.0
  - |\_ *key param*: NA
- **Filtlong**
  - |\_ *ver*: v0.2.1
  - |\_ *key param*: -t target\_bases 30000000000
- **Hifiasm**
  - |\_ *ver*: 0.24.0
  - |\_ *key param*: --ont

## Curation pipeline

- **FCS-GX**
  - |\_ *ver*: None
  - |\_ *key param*: NA

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Date and time: 2025-09-23 15:41:18 CEST