

Attention: this file was produced automatically, and some statistics might not make sense for certain pipelines.

This file contains statistics about the following genome(s):

- C.elegans

Table 1: Genome Graph Statistics

Table 2: Algorithm Statistics

Parameter	uni	Y-to-V	wtdbg2
min non-trivial omnitigs per macrotig	N/A	N/A	N/A
max non-trivial omnitigs per macrotig	N/A	N/A	N/A
median non-trivial omnitigs per macrotig	N/A	N/A	N/A
mean non-trivial omnitigs per macrotig	N/A	N/A	N/A
min edge length	1	1	N/A
max edge length	4876	5648	N/A
median edge length	7	37	N/A
mean edge length	214.9	408.3	N/A

Table 3: ContigValidator

Parameter	uni	Y-to-V	wtdbg2
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Table 4: QUASt: # of contigs

Parameter	uni	Y-to-V	wtdbg2
# contigs (≥ 0 bp)	242	271	194
# contigs (≥ 1000 bp)	242	271	194
# contigs (≥ 5000 bp)	237	262	189
# contigs (≥ 10000 bp)	205	227	151
# contigs (≥ 25000 bp)	154	181	106
# contigs (≥ 50000 bp)	128	157	94

Table 5: QUASt: total length of contigs

Parameter	uni	Y-to-V	wtdbg2
Total length (≥ 0 bp)	79798818	115953601	100492986
Total length (≥ 1000 bp)	79798818	115953601	100492986
Total length (≥ 5000 bp)	79783906	115921048	100475058
Total length (≥ 10000 bp)	79543715	115658958	100206081
Total length (≥ 25000 bp)	78706651	114913930	99521477
Total length (≥ 50000 bp)	77780368	114078713	99091743

Table 6: QUASt: statistics for contigs ≥ 500 bp

Parameter	uni	Y-to-V	wtdbg2
# contigs	242	271	194
Largest contig	4243953	4908340	5526902
Total length	79798818	115953601	100492986
Reference length	104169699	104169699	104169699
GC (%)	35.08	35.21	35.61
Reference GC (%)	35.67	35.67	35.67
N50	1002386	1093467	1849275
NG50	674926	1236932	1753949
N75	540100	652385	947170
NG75	40388	760056	929356
L50	24	31	18
LG50	38	26	19
L75	51	65	37
LG75	136	52	40

Table 7: QUAST: alignment statistics for contigs ≥ 500 bp

Parameter	uni	Y-to-V	wtdbg2
# misassemblies	17294	25675	142
# misassembled contigs	173	199	66
Misassembled contigs length	78869707	115003890	79479330
# local misassemblies	5055	7445	279
# scaffold gap ext. mis.	0	0	0
# scaffold gap loc. mis.	0	0	0
# unaligned mis. contigs	20	20	3
# unaligned contigs	20 + 203 part	20 + 237 part	8 + 58 part
Unaligned length	15513418	22180822	316190
Genome fraction (%)	55.216	59.749	96.144
Duplication ratio	1.118	1.507	1.000
# N's per 100 kbp	0.00	0.00	0.00
# mismatches per 100 kbp	297.91	401.91	30.49
# indels per 100 kbp	384.04	518.45	64.40
Largest alignment	91711	91711	3053773
Total aligned length	64229985	93660166	99998285
NA50	4093	4017	838474
NGA50	2082	6273	819705
NA75	1285	1317	501487
LA50	2849	2026	433021
LGA50	7407	4267	39
LA75	11688	3087	41