

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	4875	4875	N/A
median edge length	23	23	N/A
mean edge length	306.9	306.9	N/A

Table 3: ContigValidator

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

Parameter	uni	Y-to-V	wtdbg2
# contigs (≥ 0 bp)	230	230	191
# contigs (≥ 1000 bp)	230	230	191
# contigs (≥ 5000 bp)	224	224	186
# contigs (≥ 10000 bp)	201	201	150
# contigs (≥ 25000 bp)	150	150	104
# contigs (≥ 50000 bp)	127	127	93

Table 5: QAST: total length of contigs

Parameter	uni	Y-to-V	wtdbg2
Total length (≥ 0 bp)	79388023	79388023	100600033
Total length (≥ 1000 bp)	79388023	79388023	100600033
Total length (≥ 5000 bp)	79369274	79369274	100582105
Total length (≥ 10000 bp)	79199000	79199000	100329617
Total length (≥ 25000 bp)	78389170	78389170	99633877
Total length (≥ 50000 bp)	77572756	77572756	99238426

Table 6: QAST: statistics for contigs ≥ 500 bp

Parameter	uni	Y-to-V	wtdbg2
# contigs	230	230	191
Largest contig	4243665	4243665	5526899
Total length	79388023	79388023	100600033
Reference length	104169699	104169699	104169699
GC (%)	35.07	35.07	35.61
Reference GC (%)	35.67	35.67	35.67
N50	1044376	1044376	1751993
NG50	670801	670801	1716774
N75	542967	542967	949768
NG75	30581	30581	936468
L50	23	23	18
LG50	38	38	19
L75	50	50	37
LG75	141	141	40

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

Parameter	uni	Y-to-V	wtdbg2
# misassemblies	17172	17172	141
# misassembled contigs	166	166	64
Misassembled contigs length	78496414	78496414	77880928
# local misassemblies	5012	5012	268
# scaffold gap ext. mis.	0	0	0
# scaffold gap loc. mis.	0	0	0
# unaligned mis. contigs	18	18	2
# unaligned contigs	20 + 197 part	20 + 197 part	8 + 58 part
Unaligned length	15406544	15406544	303326
Genome fraction (%)	55.012	55.012	96.240
Duplication ratio	1.116	1.116	1.000
# N's per 100 kbp	0.00	0.00	0.00
# mismatches per 100 kbp	295.48	295.48	30.46
# indels per 100 kbp	385.23	385.23	64.39
Largest alignment	91711	91711	3053773
Total aligned length	63927419	63927419	100113565
NA50	4119	4119	838474
NGA50	2076	2076	819705
NA75	1290	1290	501487
LA50	2807	2807	433021
LGA50	7445	7445	39
LA75	11566	11566	41