

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	6	32	N/A
mean edge length	209.4	406.8	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)	240	275	194
# contigs (≥ 1000 bp)	240	275	194
# contigs (≥ 5000 bp)	234	263	187
# contigs (≥ 10000 bp)	203	227	150
# contigs (≥ 25000 bp)	152	177	105
# contigs (≥ 50000 bp)	127	154	93

Table 5: QUASt: total length of contigs

Parameter	uni	Y-to-V	wtdbg2
Total length (≥ 0 bp)	79783652	116714397	100493505
Total length (≥ 1000 bp)	79783652	116714397	100493505
Total length (≥ 5000 bp)	79763812	116669634	100468995
Total length (≥ 10000 bp)	79533260	116399943	100205456
Total length (≥ 25000 bp)	78696196	115596170	99520852
Total length (≥ 50000 bp)	77820175	114811215	99093065

Table 6: QUASt: statistics for contigs ≥ 500 bp

Parameter	uni	Y-to-V	wtdbg2
# contigs	240	275	194
Largest contig	4242749	4907136	5527820
Total length	79783652	116714397	100493505
Reference length	104169699	104169699	104169699
GC (%)	35.08	35.21	35.61
Reference GC (%)	35.67	35.67	35.67
N50	1048831	1163557	1849276
NG50	692949	1321297	1747713
N75	540100	653752	954436
NG75	40388	860829	944300
L50	23	30	18
LG50	37	24	19
L75	50	62	36
LG75	134	49	39

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

Parameter	uni	Y-to-V	wtdbg2
# misassemblies	17305	25819	142
# misassembled contigs	171	197	65
Misassembled contigs length	78859252	115729848	78800066
# local misassemblies	5054	7466	260
# scaffold gap ext. mis.	0	0	0
# scaffold gap loc. mis.	0	0	0
# unaligned mis. contigs	20	20	3
# unaligned contigs	20 + 201 part	21 + 238 part	8 + 60 part
Unaligned length	15516622	22355079	313152
Genome fraction (%)	55.201	59.742	96.129
Duplication ratio	1.118	1.516	1.000
# N's per 100 kbp	0.00	0.00	0.00
# mismatches per 100 kbp	297.87	401.29	30.60
# indels per 100 kbp	383.85	520.58	64.28
Largest alignment	91711	91711	3053773
Total aligned length	64211599	94247909	99995358
NA50	4092	4015	838474
NGA50	2082	6451	819705
NA75	1281	1316	501487
LA50	2851	2043	433021
LGA50	7417	4289	39
LA75	11695	3050	41