

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

Revision: b'bigraph-v0.2.0-44-gc65be72'

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

- C.elegans

Table 1: Genome Graph Statistics

Table 2: Algorithm Statistics

Parameter	inj uni sfa	inj Y-to-V sfa	wtdbg2 sfa	inj uni	inj Y-to-V	wtdbg2
min non-trivial omnitigs per macrotig	N/A	N/A	N/A	N/A	N/A	N/A
max non-trivial omnitigs per macrotig	N/A	N/A	N/A	N/A	N/A	N/A
median non-trivial omnitigs per macrotig	N/A	N/A	N/A	N/A	N/A	N/A
mean non-trivial omnitigs per macrotig	N/A	N/A	N/A	N/A	N/A	N/A
min edge length	1	1	N/A	1	1	N/A
max edge length	5552	5552	N/A	5552	5552	N/A
median edge length	6	31	N/A	6	31	N/A
mean edge length	198.1	397.0	N/A	198.1	397.0	N/A

Table 3: ContigValidator

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

Parameter	inj uni sfa	inj Y-to-V sfa	wtdbg2 sfa	inj uni	inj Y-to-V	wtdbg2
# contigs (≥ 0 bp)	235	273	259	180	238	191
# contigs (≥ 1000 bp)	235	273	259	180	238	191
# contigs (≥ 5000 bp)	230	264	250	177	235	188
# contigs (≥ 10000 bp)	196	230	207	147	202	151
# contigs (≥ 25000 bp)	151	185	154	108	160	104
# contigs (≥ 50000 bp)	132	159	134	96	142	89

Table 5: QUASt: total length of contigs

Parameter	inj uni sfa	inj Y-to-V sfa	wtdbg2 sfa	inj uni	inj Y-to-V	wtdbg2
Total length (≥ 0 bp)	100327583	151651912	100835745	99589989	151794835	99188638
Total length (≥ 1000 bp)	100327583	151651912	100835745	99589989	151794835	99188638
Total length (≥ 5000 bp)	100308682	151617729	100801108	99576116	151780874	99179456
Total length (≥ 10000 bp)	100062994	151382956	100498980	99358157	151549953	98914028
Total length (≥ 25000 bp)	99345349	150639393	99674694	98742458	150872765	98202073
Total length (≥ 50000 bp)	98645639	149713361	98980127	98314918	150234443	97685591

Table 6: QUASt: statistics for contigs ≥ 500 bp

Parameter	inj uni sfa	inj Y-to-V sfa	wtdbg2 sfa	inj uni	inj Y-to-V	wtdbg2
# contigs	234	271	257	180	238	189
Largest contig	6177007	6177006	6180070	6177007	6177007	6180070
Total length	100326178	151648288	100831311	99589989	151794835	99184204
Reference length	104169699	104169699	104169699	104169699	104169699	104169699
GC (%)	35.58	35.67	35.61	35.58	35.67	35.63
Reference GC (%)	35.67	35.67	35.67	35.67	35.67	35.67
N50	1203426	1426192	1205835	1840559	1692600	2010311
NG50	1201931	2037872	1204279	1776636	2143059	1906099
N75	720881	789977	720918	932235	933067	998289
NG75	639379	1417954	640359	890688	1601409	936038
L50	24	31	24	17	28	18
LG50	25	17	25	18	16	20
L75	51	67	51	37	60	36
LG75	55	32	55	41	30	40

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

Parameter	inj uni sfa	inj Y-to-V sfa	wtdbg2 sfa	inj uni	inj Y-to-V	wtdbg2
# misassemblies	66	125	65	75	136	78
# misassembled contigs	46	82	45	45	78	49
Misassembled contigs length	52869792	95954692	50801533	67672365	103939846	68787778
# local misassemblies	163	288	162	154	280	165
# scaffold gap ext. mis.	0	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0	0
# possible TEs	2	16	6	4	14	6
# unaligned mis. contigs	0	0	1	0	1	0
# unaligned contigs	0 + 87 part	0 + 134 part	14 + 112 part	1 + 74 part	1 + 125 part	9 + 87 part
Unaligned length	505674	812753	688670	547762	849892	723003
Genome fraction (%)	95.862	96.341	96.180	95.110	96.424	94.559
Duplication ratio	1.000	1.503	1.000	1.000	1.503	1.000
# N's per 100 kbp	0.00	0.00	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	27.35	50.82	30.59	26.53	48.82	31.48
# indels per 100 kbp	48.02	73.95	49.28	48.27	74.24	49.98
Largest alignment	3147709	3148195	3150502	3147709	3147709	3150502
Total aligned length	99710183	150564231	100036634	98893361	150654909	98338119
EA50max	839879	947855	846349	891038	947855	949214
Strict EA50max	518389	604052	545657	604052	621381	629563
NA50	851530	854174	851910	916466	861527	995676
NGA50	839879	1313040	846349	891038	1359914	949214
EA75max	405683	535385	418864	511062	563673	513053
Strict EA75max	235044	309036	244082	275837	311372	292317
NA75	479606	506912	481743	562625	517517	602709
NGA75	405683	850442	416035	497788	851550	513053
LA50	34	49	34	29	47	28
LGA50	36	25	36	31	24	30
LA75	73	106	73	63	104	59
LGA75	80	51	79	70	50	66

Table 8: QUASt: misassembly statistics for contigs ≥ 500 bp

Parameter	inj uni sfa	inj Y-to-V sfa	wtdbg2 sfa	inj uni	inj Y-to-V	wtdbg2
# misassemblies	66	125	65	75	136	78
# contig misassemblies	66	125	65	75	136	78
# c. relocations	17	30	15	19	33	19
# c. translocations	49	94	49	56	102	58
# c. inversions	0	1	1	0	1	1
# scaffold misassemblies	0	0	0	0	0	0
# s. relocations	0	0	0	0	0	0
# s. translocations	0	0	0	0	0	0
# s. inversions	0	0	0	0	0	0
# misassembled contigs	46	82	45	45	78	49
Misassembled contigs length	52869792	95954692	50801533	67672365	103939846	68787778
# local misassemblies	163	288	162	154	280	165
# scaffold gap ext. mis.	0	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0	0
# mis. caused by frag. ref.	0	0	0	0	0	0
# possible TEs	2	16	6	4	14	6
# unaligned mis. contigs	0	0	1	0	1	0
# mismatches	27311	50999	30648	26288	49041	31005
# indels	47957	74215	49371	47825	74570	49227
# indels (≤ 5 bp)	46909	72456	48309	46796	72793	48163
# indels (> 5 bp)	1048	1759	1062	1029	1777	1064
Indels length	148518	229312	159173	150296	242429	156680

























