

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	235	273	259	180	238	191
Largest contig	6177007	6177006	6180070	6177007	6177007	6180070
Total length	100327583	151651912	100835745	99589989	151794835	99188638
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	111	205	102	120	211	119
# misassembled contigs	62	110	65	56	100	59
Misassembled contigs length	62896853	110234318	64806280	76694567	116808070	75834094
# local misassemblies	185	339	245	185	331	321
# scaffold gap ext. mis.	0	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0	0
# unaligned mis. contigs	1	1	6	1	2	3
# unaligned contigs	0 + 54 part	0 + 85 part	9 + 74 part	1 + 45 part	1 + 78 part	8 + 62 part
Unaligned length	194781	328755	312893	231076	360605	335388
Genome fraction (%)	96.104	96.595	96.431	95.350	96.700	94.825
Duplication ratio	1.000	1.504	1.001	1.000	1.503	1.001
# N's per 100 kbp	0.00	0.00	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	25.18	43.19	28.93	25.30	42.73	30.02
# indels per 100 kbp	60.76	92.73	64.22	61.19	93.15	65.14
Largest alignment	3052603	3052603	3053766	3052603	3052603	3053766
Total aligned length	99933050	150914975	100323145	99127525	150960460	98642019
EA50max	720881	858024	720918	831508	858024	851988
Strict EA50max	616247	656106	615317	649575	656106	642610
NA50	735984	831508	736671	848409	831508	888388
NGA50	720881	977245	720918	831508	978073	851988
EA75max	379903	490743	385324	413478	498341	482415
Strict EA75max	296702	347279	293620	328446	347279	331457
NA75	398779	479964	417128	495501	482415	519287
NGA75	379903	771233	385324	413478	771233	482415
LA50	42	62	41	38	62	35
LGA50	45	35	43	41	35	38
LA75	86	125	84	77	124	71
LGA75	93	65	90	85	65	79

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	111	205	102	120	211	119
# contig misassemblies	111	205	102	120	211	119
# c. relocations	65	100	57	65	102	63
# c. translocations	43	100	43	53	106	54
# c. inversions	3	5	2	2	3	2
# 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	62	110	65	56	100	59
Misassembled contigs length	62896853	110234318	64806280	76694567	116808070	75834094
# local misassemblies	185	339	245	185	331	321
# 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
# unaligned mis. contigs	1	1	6	1	2	3
# mismatches	25213	43462	29059	25126	43038	29656
# indels	60823	93311	64513	60778	93828	64343
# indels (≤ 5 bp)	58749	90024	62178	58691	90500	61991
# indels (> 5 bp)	2074	3287	2335	2087	3328	2352
Indels length	135917	205554	139407	135333	206749	138921

























