

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

Revision: b'bigraph-v0.2.0-26-g6870ae8'

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	198.5	398.2	N/A	198.5	398.2	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)	234	272	259	183	237	189
# contigs (≥ 1000 bp)	234	272	259	183	237	189
# contigs (≥ 5000 bp)	229	263	250	180	234	186
# contigs (≥ 10000 bp)	196	230	207	150	201	149
# contigs (≥ 25000 bp)	151	185	154	110	159	104
# contigs (≥ 50000 bp)	132	159	134	97	141	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)	100341991	151666386	100831812	97817531	151810658	98765273
Total length (≥ 1000 bp)	100341991	151666386	100831812	97817531	151810658	98765273
Total length (≥ 5000 bp)	100323090	151632203	100797175	97803658	151796697	98756091
Total length (≥ 10000 bp)	100085438	151405466	100495047	97585697	151565774	98490663
Total length (≥ 25000 bp)	99367793	150661903	99670759	96951918	150888586	97809558
Total length (≥ 50000 bp)	98668083	149735871	98976192	96497212	150250264	97293076

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	272	259	183	237	189
Largest contig	6177006	6177007	6180070	6177006	6177005	6180070
Total length	100341991	151666386	100831812	97817531	151810658	98765273
Reference length	104169699	104169699	104169699	104169699	104169699	104169699
GC (%)	35.58	35.67	35.61	35.60	35.67	35.62
Reference GC (%)	35.67	35.67	35.67	35.67	35.67	35.67
N50	1203426	1426192	1205835	1840558	1692600	1908954
NG50	1201931	2037872	1204279	1783828	2268406	1906099
N75	720881	789977	720918	926774	946537	998289
NG75	639379	1417954	640359	835056	1618829	895623
L50	24	31	24	18	28	19
LG50	25	17	25	19	16	20
L75	51	67	51	38	59	36
LG75	55	32	55	43	29	41

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	117	212	118
# misassembled contigs	61	109	65	55	99	59
Misassembled contigs length	62911312	110248761	64806219	72912261	116823891	75730626
# local misassemblies	184	340	246	196	352	318
# 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 + 43 part	1 + 77 part	8 + 62 part
Unaligned length	195048	329360	310694	223473	362819	332278
Genome fraction (%)	96.119	96.609	96.433	93.668	96.709	94.435
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	25.20	43.25	28.93	25.25	42.84	29.84
# indels per 100 kbp	60.80	92.79	64.24	61.38	93.24	65.07
Largest alignment	3052603	3052603	3053766	3052603	3052603	3053766
Total aligned length	99927316	150908975	100324738	97372125	150973993	98241677
EA50max	603392	630842	615627	630730	656342	643763
NA50	735984	831508	736671	840560	831508	888388
NGA50	720881	977245	720918	793547	978073	851988
NA75	398779	479964	417128	495501	482415	519287
NGA75	379903	771244	385324	400885	778233	482415
LA50	42	62	41	38	62	35
LGA50	45	35	43	41	35	38
LA75	86	125	84	76	124	71
LGA75	93	65	90	86	65	79

























