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

Revision: b'bigraph@0.7.0-91-gc178fcd'

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

- D.melanogaster_HiFi_hodeco_simple D.melanogaster_A4xISO1_HiFi24kb "quast_mode":"hicanu_misassemblies","filter_nw":"yes","genome":"D.melanogaster_A4xISO1_HiFi24kb","read_downsampling_factor":"none","homopolymer_compression":"none

Table 1: Genome Graph Statistics

Table 2: Algorithm Statistics

Parameter

Table 3: ContigValidator

Parameter

Table 4: QUAST: # of contigs

Parameter	w2 noho	w2	w2 sfa	w2 YV sfa	w2 YV	w2 frg YV	flye	hifiasm	mdbg	lja	HiCanu
# contigs ($\geq$ 0 bp)	414	369	495	596	478	359	862	1,871	1,626	1,086	1,110
# contigs ($\geq$ 1000 bp)	414	369	494	596	478	359	857	1,871	1,626	1,086	1,110
# contigs ($\geq$ 5000 bp)	407	366	489	591	475	356	838	1,870	1,617	891	1,110
# contigs ($\geq$ 10000 bp)	335	327	418	519	436	319	815	1,870	1,571	732	1,110
# contigs ($\geq$ 25000 bp)	194	184	225	312	290	179	655	1,766	346	458	1,054
# contigs ($\geq$ 50000 bp)	106	96	112	199	196	98	461	811	162	252	418

Table 5: QUAST: total length of contigs

Parameter	w2 noho	w2	w2 sfa	w2 YV sfa	w2 YV	w2 frg YV	flye	hifiasm	mdbg	lja	HiCanu
Total length ($\geq$ 0 bp)	144,151,804	136,454,697	142,388,881	319,376,149	330,991,551	186,947,242	280,485,510	370,546,663	206,961,557	303,203,843	334,207,136
Total length ($\geq$ 1000 bp)	144,151,804	136,454,697	142,388,652	319,376,149	330,991,551	186,947,242	280,481,949	370,546,663	206,961,557	303,203,843	334,207,136
Total length ($\geq$ 5000 bp)	144,127,619	136,443,207	142,369,900	319,356,756	330,978,998	186,934,689	280,426,534	370,544,201	206,933,669	302,614,393	334,207,136
Total length ($\geq$ 10000 bp)	143,609,546	136,130,035	141,790,312	318,781,589	330,672,629	186,646,510	280,250,030	370,544,201	206,547,093	301,450,361	334,207,136
Total length ($\geq$ 25000 bp)	141,160,688	133,732,703	138,626,342	315,437,317	328,222,095	184,273,657	277,533,416	368,209,985	188,008,490	297,060,903	332,934,376
Total length ($\geq$ 50000 bp)	138,201,375	130,691,720	134,681,537	311,585,298	325,048,905	181,487,912	270,505,298	333,526,354	181,903,470	289,616,158	311,235,346

Table 6: QUAST: statistics for contigs $\geq$ 500bp (or 3000bp for QUAST-LG)

Parameter	w2 noho	w2	w2 sfa	w2 YV sfa	w2 YV	w2 frg YV	flye	hifiasm	mdbg	lja	HiCanu
# contigs	413	369	494	595	478	359	846	1,870	1,622	980	1,110
Largest contig	28,513,870	28,480,067	17,998,823	31,584,896	31,584,899	41,582,611	6,795,813	28,128,476	16,459,800	26,917,111	24,409,699
Total length	144,149,348	136,454,697	142,388,652	319,373,543	330,991,551	186,947,242	280,457,913	370,544,201	206,953,527	302,962,930	334,207,136
Reference length	137,567,484	137,567,484	137,567,484	137,567,484	137,567,484	137,567,484	137,567,484	137,567,484	137,567,484	137,567,484	137,567,484
GC (%)	42.04	42.03	42.07	42.33	42.34	42.18	41.75	41.48	41.30	41.53	41.37
Reference GC (%)	42.08	42.08	42.08	42.08	42.08	42.08	42.08	42.08	42.08	42.08	42.08
N50	19,988,504	14,421,878	10,766,281	14,411,730	14,891,726	24,031,187	1,026,517	3,170,105	4,485,434	7,248,900	7,217,842
NG50	19,988,504	14,421,878	10,766,281	23,546,907	23,546,907	28,492,352	2,267,476	25,819,223	9,676,322	17,808,991	21,898,700
N75	5,643,332	7,236,486	4,258,420	6,379,575	10,638,128	14,860,864	523,609	311,336	552,231	2,458,513	1,717,026
NG75	5,666,668	7,236,486	4,258,420	14,891,726	19,368,005	20,859,823	1,568,695	24,576,786	4,485,434	11,653,812	20,135,459
L50	3	4	5	9	8	3	67	15	11	11	11
LG50	3	4	5	3	3	2	20	3	6	3	3
L75	7	7	10	16	15	6	165	118	52	28	36
LG75	6	7	10	5	5	4	38	4	11	6	5
E-size	15,888,745	15,197,531	9,604,046	13,649,137	14,889,241	22,596,649	1,626,968	10,129,664	5,918,256	10,468,752	10,155,151

Table 7: QUAST: alignment statistics for contigs ≥ 500bp (or 3000bp for QUAST-LG)

Parameter	w2 noho	w2	w2 sfa	w2 YV sfa	w2 YV	w2 frg YV	flye	hifiasm	mdbg	lja	HiCanu
# misassemblies	3	1	0	14	14	5	5	3	1	2	1
# unique misassemblies	2	1	0	12	12	5	5	3	1	2	1
# misassembled contigs	3	1	0	14	14	5	5	2	1	2	1
Misassembled contigs length	20,379,018	24,026,054	0	112,814,669	135,763,338	85,701,942	4,727,083	27,480,110	741,405	11,745,114	23,498,506
# local misassemblies	298	305	291	624	649	438	291	401	1,345	396	380
# unique local misassemblies	298	305	291	411	433	366	281	359	1,342	358	360
# scaffold gap ext. mis.	0	0	0	0	0	0	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0	0	0	0	0	0	0
# possible TEs	0	2	2	2	2	2	2	2	0	0	2
# unaligned mis. contigs	2	1	1	4	7	1	20	10	8	6	8
# unaligned contigs	315+66p	278+56p	369+79p	415+133p	316+125p	269+58p	222+193p	757+299p	1471+93p	779+89p	685+134p
Unaligned length	14,390,580	15,049,793	14,847,661	26,253,290	26,075,430	17,082,472	46,396,610	89,995,770	67,054,402	62,989,641	83,427,372
Genome fraction (%)	92.62	86.98	91.42	92.20	92.30	91.96	96.52	97.32	88.47	96.71	97.08
Duplication ratio	1.02	1.02	1.02	2.32	2.41	1.35	1.77	2.10	1.15	1.81	1.89
# N's per 100 kbp	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	298.09	324.28	328.87	333.97	329.12	343.11	291.71	305.85	257.68	288.80	281.13
# indels per 100 kbp	77.34	76.86	77.74	78.46	77.91	81.33	51.79	53.85	272.71	52.07	54.31
Largest alignment	27,882,095	27,938,614	17,439,269	23,115,982	23,232,072	27,960,446	6,225,533	26,077,520	14,428,909	26,749,447	24,372,115
Total aligned length	129,684,837	121,332,458	127,493,794	292,985,144	304,778,648	169,739,671	233,901,594	280,113,718	139,834,626	239,502,644	250,556,642
EAmeanmax	15,595,734	13,823,579	9,200,408	11,373,390	14,101,590	16,982,342	1,742,897	15,813,336	5,861,626	10,996,172	16,842,834
Strict EAmeanmax	886,995	801,017	868,782	954,994	971,923	839,771	1,189,950	4,562,008	178,283	4,400,916	4,408,802
EA50max	19,601,726	13,426,596	10,274,006	11,954,517	16,925,996	19,868,314	1,010,149	20,140,010	5,420,556	9,893,262	20,378,876
Strict EA50max	761,416	650,915	711,058	756,015	792,972	722,256	757,944	2,594,722	122,376	2,458,513	2,910,474
EA75max	5,359,690	1,775,090	1,775,090	6,375,560	11,311,484	14,188,994	469,152	6,795,652	1,037,091	2,458,513	18,554,192
Strict EA75max	271,882	178,344	246,854	256,289	286,100	247,624	322,141	1,228,573	57,111	1,228,571	1,163,025
P5k	0.92	0.87	0.91	0.92	0.92	0.92	0.96	0.97	0.88	0.96	0.97
P10k	0.92	0.87	0.91	0.92	0.92	0.92	0.96	0.97	0.88	0.96	0.97
P15k	0.92	0.87	0.91	0.92	0.92	0.92	0.96	0.97	0.88	0.96	0.97
P20k	0.92	0.87	0.91	0.92	0.92	0.92	0.96	0.97	0.88	0.96	0.97
Strict P5k	0.92	0.87	0.91	0.92	0.92	0.92	0.96	0.97	0.88	0.96	0.97
Strict P10k	0.92	0.87	0.91	0.92	0.92	0.92	0.96	0.97	0.88	0.96	0.97
Strict P15k	0.92	0.87	0.91	0.92	0.92	0.92	0.96	0.97	0.88	0.96	0.97
Strict P20k	0.92	0.87	0.91	0.92	0.92	0.92	0.96	0.97	0.88	0.96	0.97
NGA50	19,601,726	13,426,596	10,274,006	15,441,323	18,575,154	19,868,314	1,899,476	23,921,119	6,360,793	17,799,518	20,378,876
NGA75	5,539,348	6,565,547	3,926,232	14,117,465	15,442,729	19,769,332	1,115,050	14,781,569	1,464,502	10,179,332	18,554,192
LGA50	3	4	5	4	4	3	23	3	8	3	4
LGA75	6	7	10	6	6	5	48	5	17	6	5
EA-size	16,805,471	15,888,047	10,062,307	12,055,666	13,341,183	18,291,210	1,520,002	10,857,647	6,333,376	11,145,676	11,085,585

Table 8: QUAST: misassembly statistics for contigs ≥ 500bp (or 3000bp for QUAST-LG)

Parameter	w2 noho	w2	w2 sfa	w2 YV sfa	w2 YV	w2 frg YV	flye	hifiasm	mdbg	lja	HiCanu
# misassemblies	3	1	0	14	14	5	5	3	1	2	1
# contig misassemblies	3	1	0	14	14	5	5	3	1	2	1
# c. relocations	0	0	0	1	1	1	1	1	0	1	1
# c. translocations	0	0	0	2	2	0	1	0	0	0	0
# c. inversions	3	1	0	11	11	4	3	2	1	1	0
# scaffold misassemblies	0	0	0	0	0	0	0	0	0	0	0
# s. relocations	0	0	0	0	0	0	0	0	0	0	0
# s. translocations	0	0	0	0	0	0	0	0	0	0	0
# s. inversions	0	0	0	0	0	0	0	0	0	0	0
# misassembled contigs	3	1	0	14	14	5	5	2	1	2	1
Misassembled contigs length	20,379,018	24,026,054	0	112,814,669	135,763,338	85,701,942	4,727,083	27,480,110	741,405	11,745,114	23,498,506
# local misassemblies	298	305	291	624	649	438	291	401	1,345	396	380
# scaffold gap ext. mis.	0	0	0	0	0	0	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0	0	0	0	0	0	0
# possible TEs	0	2	2	2	2	2	2	2	0	0	2
# unaligned mis. contigs	2	1	1	4	7	1	20	10	8	6	8
# mismatches	386,584	393,456	419,295	978,470	1,003,084	582,401	682,315	856,715	360,319	691,673	704,380
# indels	100,292	93,256	99,113	229,863	237,448	138,042	121,145	150,832	381,349	124,719	136,074
# indels (≤ 5 bp)	78,577	73,012	77,554	180,525	186,596	107,990	81,539	101,982	349,667	83,849	94,132
# indels (> 5 bp)	21,715	20,244	21,559	49,338	50,852	30,052	39,606	48,850	31,682	40,870	41,942
Indels length	3,460,107	3,110,923	3,329,360	7,625,591	7,942,209	4,448,701	5,050,564	6,136,551	2,412,596	5,624,748	5,765,567

Table 9: Resource usage

Parameter	w2 noho	w2	w2 sfa	w2 YV sfa	w2 YV	w2 frg YV	flye	hifiasm	mdbg	lja	HiCanu
time [s]	960.53	1,309.37	1,361.43	1,902.06	1,968.79	1,524.49	21,938.00	72,413.00	164.24	63,002.00	37,853.00
mem [GiB]	16.96	15.31	15.25	15.25	15.31	15.31	121.30	116.44	0.51	68.60	19.22
hoco time		70.61	70.61	70.61	70.61	70.61	N/A	N/A	N/A	N/A	N/A
hoco mem		0.77	0.77	0.77	0.77	0.77	N/A	N/A	N/A	N/A	N/A
hodeco time		393.74	433.88	529.90	542.33	452.11	N/A	N/A	N/A	N/A	N/A
hodeco mem		1.59	1.63	1.71	1.71	1.69	N/A	N/A	N/A	N/A	N/A
trivial_omnitigs time				22.84	37.75	0.06	N/A	N/A	N/A	N/A	N/A
trivial_omnitigs mem				1.65	1.65	0.00	N/A	N/A	N/A	N/A	N/A
assembly time	637.32	547.98	546.17	546.17	547.98	547.98	21,938.00	72,413.00	164.24	63,002.00	37,853.00
assembly mem	16.96	15.31	15.25	15.25	15.31	15.31	121.30	116.44	0.51	68.60	19.22
wtdbg2_extract time	58.98	37.90	39.19	39.19	37.90	37.90	N/A	N/A	N/A	N/A	N/A
wtdbg2_extract mem	0.00	0.00	0.00	0.00	0.00	0.00	N/A	N/A	N/A	N/A	N/A
contig_assembly time				89.77	91.47	63.84	N/A	N/A	N/A	N/A	N/A
contig_assembly mem				11.50	11.50	11.50	N/A	N/A	N/A	N/A	N/A
wtdbg2_consensus time	264.23	259.14	271.58	603.58	640.75	351.99	N/A	N/A	N/A	N/A	N/A
wtdbg2_consensus mem	7.61	8.53	8.02	9.42	9.26	9.27	N/A	N/A	N/A	N/A	N/A

EAxmax

EAxmax

NGAx

NGAx

NGAx