

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

Revision: b'bigraph@0.7.0-93-g522fddc'

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

- HG002_HiFi_20kb_16x_hodeco_simple HG002_HiFi_20kb_16x "retain_cm": "yes", "uniquify_ids": "yes", "genome": "HG002_HiFi_20kb_16x", "quast_mode": "hicanu", "read_downsampling_factor": "none", "homopolymer_compression": "none", "assembler": "n

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 (≥ 0 bp)	2,255	2,198	3,299	4,777	3,921	1,992	8,340	23,457	45,369	46,161	37,728
# contigs (≥ 1000 bp)	2,254	2,198	3,299	4,776	3,921	1,992	8,322	23,457	45,364	46,161	37,728
# contigs (≥ 5000 bp)	2,220	2,175	3,267	4,671	3,852	1,977	8,163	23,457	25,616	45,445	37,728
# contigs (≥ 10000 bp)	1,861	1,986	2,961	4,124	3,448	1,829	7,450	23,455	9,662	44,483	37,728
# contigs (≥ 25000 bp)	1,274	1,384	2,069	2,984	2,512	1,401	4,462	21,218	5,161	39,603	34,009
# contigs (≥ 50000 bp)	976	1,018	1,517	2,219	1,866	1,122	2,627	13,533	4,550	29,933	18,969

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 (≥ 0 bp)	2,785,753,546	2,775,726,426	2,804,483,658	4,128,045,972	4,127,030,155	4,439,815,248	3,173,378,180	5,882,154,531	2,437,921,680	5,200,080,087	5,952,937,636
Total length (≥ 1000 bp)	2,785,752,906	2,775,726,426	2,804,483,658	4,128,045,061	4,127,030,155	4,439,815,248	3,173,365,326	5,882,154,531	2,437,918,357	5,200,080,087	5,952,937,636
Total length (≥ 5000 bp)	2,785,621,513	2,775,633,177	2,804,355,456	4,127,649,657	4,126,752,856	4,439,750,955	3,172,847,858	5,882,154,531	2,364,063,143	5,197,754,800	5,952,937,636
Total length (≥ 10000 bp)	2,782,989,525	2,774,104,563	2,801,872,756	4,123,321,608	4,123,543,474	4,438,560,064	3,166,732,798	5,882,137,431	2,256,492,968	5,190,547,617	5,952,937,636
Total length (≥ 25000 bp)	2,773,391,401	2,764,082,851	2,787,185,407	4,104,998,990	4,108,294,745	4,431,405,633	3,117,973,368	5,836,652,666	2,192,925,217	5,099,681,772	5,877,879,448
Total length (≥ 50000 bp)	2,762,651,653	2,750,948,627	2,767,546,718	4,077,490,262	4,085,000,972	4,421,442,835	3,052,814,217	5,556,109,430	2,172,404,426	4,738,989,371	5,343,552,993

Table 6: QUAST: statistics for contigs ≥ 500 bp (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	2,245	2,196	3,296	4,752	3,913	1,992	8,261	23,457	42,100	45,844	37,728
Largest contig	109,683,034	88,028,093	52,877,139	70,612,739	70,612,739	98,827,424	41,615,215	47,637,577	3,527,865	5,734,769	10,610,862
Total length	2,785,732,030	2,775,722,016	2,804,476,329	4,127,988,539	4,127,009,601	4,439,815,248	3,173,245,686	5,882,154,531	2,429,676,854	5,199,363,167	5,952,937,636
Reference length	3,088,269,832	3,088,269,832	3,088,269,832	3,088,269,832	3,088,269,832	3,088,269,832	3,088,269,832	3,088,269,832	3,088,269,832	3,088,269,832	3,088,269,832
GC (%)	40.85	40.85	40.84	40.66	40.65	40.58	40.76	40.80	39.88	40.64	40.79
Reference GC (%)	40.87	40.87	40.87	40.87	40.87	40.87	40.87	40.87	40.87	40.87	40.87
N50	16,241,166	15,483,447	8,735,111	12,093,876	13,963,972	23,692,372	10,823,492	1,098,803	518,362	182,952	445,184
NG50	13,730,072	13,814,826	7,114,718	15,731,267	20,595,889	36,170,755	11,461,425	9,775,638	397,160	296,827	1,377,692
N75	5,300,858	4,764,183	2,989,099	3,791,178	5,036,339	10,152,801	2,945,225	259,509	299,153	93,449	145,744
NG75	2,991,964	2,847,148	1,735,532	9,515,377	12,176,680	21,653,242	3,273,387	4,004,428	6,559	206,441	747,156
L50	48	44	90	97	78	54	83	521	1,436	7,836	2,589
LG50	58	55	109	60	47	31	79	88	2,163	3,244	658
L75	120	122	234	249	193	125	222	3,738	2,970	17,746	8,612
LG75	177	185	325	121	98	58	202	211	17,211	6,374	1,428
E-size	24,546,083	23,789,249	11,009,484	15,498,763	19,245,472	29,290,734	12,788,058	6,853,565	636,662	305,165	1,031,070

Table 7: QUAST: alignment statistics for contigs ≥ 500 bp (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	1,509	1,827	1,557	4,518	4,720	2,961	9,276	20,818	7,574	16,959	20,561
# unique misassemblies	1,393	1,741	1,476	3,457	3,613	2,425	6,749	12,421	5,002	11,114	12,785
# misassembled contigs	417	440	492	1,562	1,500	697	1,533	1,615	5,021	2,054	1,722
Misassembled contigs length	1,376,421,295	1,466,097,594	685,973,488	2,487,962,959	3,002,252,058	3,554,657,788	1,219,247,184	1,659,489,288	326,494,618	367,209,992	623,230,535
# local misassemblies	2,947	3,172	3,049	6,054	6,105	4,758	13,177	20,223	40,415	20,386	22,082
# unique local misassemblies	2,706	2,933	2,807	4,067	4,142	3,343	5,755	9,673	30,275	9,539	9,676
# 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	210	214	194	412	438	302	1,036	3,542	1,156	3,172	3,236
# unaligned mis. contigs	139	124	158	373	328	136	453	387	1,416	488	381
# unaligned contigs	351+756p	464+801p	589+1039p	999+2251p	853+1974p	440+949p	1026+2335p	464+2351p	8367+9093p	789+4942p	618+2741p
Unaligned length	23,270,287	30,015,565	28,364,486	58,912,307	59,048,689	37,447,923	129,051,438	183,039,216	94,966,921	168,140,893	186,242,523
Genome fraction (%)	93.83	93.26	94.30	95.41	95.44	94.89	97.55	98.28	70.42	97.95	98.20
Duplication ratio	1.00	1.00	1.00	1.45	1.45	1.58	1.06	1.97	1.13	1.75	2.00
# 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	120.44	121.12	120.38	145.08	145.34	126.34	194.86	179.05	252.20	183.06	181.46
# indels per 100 kbp	29.76	30.21	30.04	32.66	32.80	30.84	28.86	31.97	199.05	32.83	40.60
Largest alignment	62,959,951	74,369,105	34,558,828	61,448,688	61,448,688	74,371,287	41,604,502	37,338,644	3,503,179	5,732,588	10,602,224
Total aligned length	2,761,163,371	2,744,512,247	2,775,022,426	4,064,412,559	4,062,965,030	4,397,928,739	3,037,710,484	5,677,338,021	2,331,335,858	5,014,291,893	5,746,307,111
EAmeanmax	13,982,958	14,794,792	8,534,937	10,527,522	13,788,587	15,905,376	10,937,959	9,917,068	449,685	338,595	1,609,440
Strict EAmeanmax	3,211,040	3,067,318	2,793,154	3,021,872	3,198,474	3,214,949	4,179,186	4,250,500	137,726	306,255	1,315,026
EA50max	9,689,788	9,034,102	6,073,504	7,241,567	9,270,272	10,106,399	8,767,673	7,313,156	340,868	188,401	1,229,604
Strict EA50max	2,275,355	2,161,041	1,983,874	2,130,116	2,301,964	2,357,677	2,896,163	3,035,240	78,385	182,240	1,018,047
EA75max	2,229,624	2,147,408	1,546,961	1,847,398	2,483,101	2,669,775	2,879,602	2,638,125	0	86,177	540,888
Strict EA75max	854,242	757,673	681,422	737,089	853,383	852,773	1,123,864	1,189,185	0	82,957	449,137
P5k	0.89	0.89	0.90	0.91	0.91	0.90	0.93	0.93	0.67	0.93	0.93
P10k	0.89	0.89	0.90	0.91	0.91	0.90	0.92	0.93	0.66	0.93	0.93
P15k	0.89	0.89	0.90	0.91	0.91	0.90	0.92	0.93	0.66	0.92	0.93
P20k	0.89	0.88	0.89	0.91	0.91	0.90	0.92	0.93	0.66	0.92	0.93
Strict P5k	0.89	0.89	0.90	0.91	0.91	0.90	0.93	0.93	0.67	0.93	0.93
Strict P10k	0.89	0.89	0.90	0.91	0.91	0.90	0.92	0.93	0.66	0.93	0.93
Strict P15k	0.89	0.88	0.89	0.90	0.90	0.90	0.92	0.93	0.65	0.92	0.93
Strict P20k	0.89	0.88	0.89	0.90	0.90	0.90	0.92	0.93	0.64	0.92	0.93
NGA50	9,689,788	9,149,125	6,092,889	12,064,067	13,946,729	20,649,293	8,767,673	7,317,420	365,315	274,017	1,248,128
NGA75	2,234,408	2,147,408	1,549,787	7,022,283	8,094,842	12,464,132	2,897,718	2,668,966	2,648	187,628	633,706
LGA50	83	81	126	79	66	50	97	112	2,301	3,526	710
LGA75	248	257	374	161	136	98	245	283	32,632	6,963	1,591
EA-size	15,648,776	16,657,985	9,503,781	11,535,904	14,100,015	17,706,467	11,128,125	5,555,129	624,431	284,074	962,835

Table 8: QUAST: misassembly statistics for contigs ≥ 500 bp (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	1,509	1,827	1,557	4,518	4,720	2,961	9,276	20,818	7,574	16,959	20,561
# contig misassemblies	1,509	1,827	1,557	4,518	4,720	2,961	9,276	20,818	7,574	16,959	20,561
# c. relocations	1,255	1,558	1,358	3,470	3,620	2,180	7,403	17,422	6,915	13,676	17,003
# c. translocations	221	238	175	983	1,030	735	1,821	3,285	630	3,207	3,454
# c. inversions	33	31	24	65	70	46	52	111	29	76	104
# 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	417	440	492	1,562	1,500	697	1,533	1,615	5,021	2,054	1,722
Misassembled contigs length	1,376,421,295	1,466,097,594	685,973,488	2,487,962,959	3,002,252,058	3,554,657,788	1,219,247,184	1,659,489,288	326,494,618	367,209,992	623,230,535
# local misassemblies	2,947	3,172	3,049	6,054	6,105	4,758	13,177	20,223	40,415	20,386	22,082
# 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	210	214	194	412	438	302	1,036	3,542	1,156	3,172	3,236
# unaligned mis. contigs	139	124	158	373	328	136	453	387	1,416	488	381
# mismatches	3,325,655	3,324,265	3,340,499	5,896,694	5,905,239	5,556,256	5,919,192	10,165,248	5,879,539	9,178,928	10,427,234
# indels	821,830	828,991	833,531	1,327,511	1,332,504	1,356,177	876,675	1,814,895	4,640,553	1,646,245	2,332,852
# indels (≤ 5 bp)	691,523	699,551	702,829	1,126,009	1,130,710	1,147,826	717,091	1,512,726	4,242,146	1,383,347	2,032,243
# indels (> 5 bp)	130,307	129,440	130,702	201,502	201,794	208,351	159,584	302,169	398,407	262,898	300,609
Indels length	8,608,802	8,566,069	8,610,318	12,889,511	12,937,266	13,597,153	10,045,353	18,566,292	12,546,236	14,907,754	18,431,713

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]	15,455.97	17,553.34	21,525.28	25,644.03	24,534.68	23,221.41	47,286.00	27,423.00	364.77	35,359.00	42,503.00
mem [GiB]	64.86	61.67	61.69	61.69	61.67	61.67	137.76	67.91	6.23	135.06	47.33
hoco time		164.67	164.67	164.67	164.67	164.67	N/A	N/A	N/A	N/A	N/A
hoco mem		0.42	0.42	0.42	0.42	0.42	N/A	N/A	N/A	N/A	N/A
hodeco time		3,449.82	5,779.00	7,605.00	7,954.00	6,349.00	N/A	N/A	N/A	N/A	N/A
hodeco mem		1.68	1.62	1.73	1.73	1.72	N/A	N/A	N/A	N/A	N/A
trivial_omnitigs time				107.56	180.48	0.02	N/A	N/A	N/A	N/A	N/A
trivial_omnitigs mem				11.33	11.33	0.00	N/A	N/A	N/A	N/A	N/A
assembly time	10,785.00	10,447.00	12,127.00	12,127.00	10,447.00	10,447.00	47,286.00	27,423.00	364.77	35,359.00	42,503.00
assembly mem	64.86	61.67	61.69	61.69	61.67	61.67	137.76	67.91	6.23	135.06	47.33
wtdbg2_extract time	346.97	385.56	241.65	241.65	385.56	385.56	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				598.15	637.97	661.16	N/A	N/A	N/A	N/A	N/A
contig_assembly mem				59.96	59.96	59.96	N/A	N/A	N/A	N/A	N/A
wtdbg2_consensus time	4,324.00	3,106.29	3,212.96	4,800.00	4,765.00	5,214.00	N/A	N/A	N/A	N/A	N/A
wtdbg2_consensus mem	6.77	9.27	8.90	11.56	10.92	9.56	N/A	N/A	N/A	N/A	N/A













































