

**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):

- 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	hifiasm YVr	hifiasm YVrbp	hifiasm YVp	mdbg	lja	HiCanu
# contigs ( $\geq 0$ bp)	2,255	2,198	3,299	4,777	3,921	1,992	8,340	23,457	39,447	38,207	38,207	45,369	46,161	37,728
# contigs ( $\geq 1000$ bp)	2,254	2,198	3,299	4,776	3,921	1,992	8,322	23,457	39,447	38,207	38,207	45,364	46,161	37,728
# contigs ( $\geq 5000$ bp)	2,220	2,175	3,267	4,671	3,852	1,977	8,163	23,457	39,447	38,207	38,207	25,616	45,445	37,728
# contigs ( $\geq 10000$ bp)	1,861	1,986	2,961	4,124	3,448	1,829	7,450	23,455	39,444	38,206	38,206	9,662	44,483	37,728
# contigs ( $\geq 25000$ bp)	1,274	1,384	2,069	2,984	2,512	1,401	4,462	21,218	39,314	38,083	38,083	5,161	39,603	34,009
# contigs ( $\geq 50000$ bp)	976	1,018	1,517	2,219	1,866	1,122	2,627	13,533	35,437	34,441	34,441	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	hifiasm YVr	hifiasm YVrbp	hifiasm YVp	mdbg	lja	HiCanu
Total length ( $\geq 0$ 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	7,346,691,482	7,326,863,530	7,326,863,530	2,437,921,680	5,200,080,087	5,952,937,636
Total length ( $\geq 1000$ 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	7,346,691,482	7,326,863,530	7,326,863,530	2,437,918,357	5,200,080,087	5,952,937,636
Total length ( $\geq 5000$ 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	7,346,691,482	7,326,863,530	7,326,863,530	2,364,063,143	5,197,754,800	5,952,937,636
Total length ( $\geq 10000$ 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	7,346,671,777	7,326,856,127	7,326,856,127	2,256,492,968	5,190,547,617	5,952,937,636
Total length ( $\geq 25000$ 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	7,343,798,742	7,324,149,752	7,324,149,752	2,192,925,217	5,099,681,772	5,877,811,428
Total length ( $\geq 50000$ 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	7,182,722,981	7,173,058,586	7,173,058,586	2,172,404,426	4,738,989,371	5,343,511,428

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

Parameter	w2 noho	w2	w2 sfa	w2 YV sfa	w2 YV	w2 frg YV	flye	hifiasm	hifiasm YVr	hifiasm YVrbp	hifiasm YVp	mdbg	lja	HiCanu
# contigs	2,245	2,196	3,296	4,752	3,913	1,992	8,261	23,457	39,447	38,207	38,207	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	6,556,963	6,556,963	6,556,963	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	7,346,691,482	7,326,863,530	7,326,863,530	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	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	40.81	40.81	40.81	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	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	303,709	317,287	317,287	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	638,634	664,406	664,406	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	135,987	141,091	141,091	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	485,938	505,491	505,491	6,559	206,441	747,156
L50	48	44	90	97	78	54	83	521	6,612	6,347	6,347	1,436	7,836	2,589
LG50	58	55	109	60	47	31	79	88	1,672	1,620	1,620	2,163	3,244	658
L75	120	122	234	249	193	125	222	3,738	15,738	15,081	15,081	2,970	17,746	8,612
LG75	177	185	325	121	98	58	202	211	3,062	2,963	2,963	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	428,071	444,683	444,683	636,662	305,165	1,031,070

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

Parameter	w2 noho	w2	w2 sfa	w2 YV sfa	w2 YV	w2 frg YV	flye	hifiasm	hifiasm YVr	hifiasm YVrbp	hifiasm YVp	mdbg	lja
# misassemblies	1,509	1,827	1,557	4,518	4,720	2,961	9,276	20,818	19,803	21,538	21,538	7,574	16,959
# unique misassemblies	1,393	1,741	1,476	3,457	3,613	2,425	6,749	12,421	13,007	13,093	13,093	5,002	11,114
# misassembled contigs	417	440	492	1,562	1,500	697	1,533	1,615	2,299	2,050	2,050	5,021	2,054
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	516,401,952	538,435,180	538,435,180	326,494,618	367,209,992
# local misassemblies	2,947	3,172	3,049	6,054	6,105	4,758	13,177	20,223	21,811	22,498	22,498	40,415	20,386
# unique local misassemblies	2,706	2,933	2,807	4,067	4,142	3,343	5,755	9,673	10,655	10,176	10,176	30,275	9,539
# scaffold gap ext. mis.	0	0	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	0	0
# possible TEs	210	214	194	412	438	302	1,036	3,542	2,404	3,984	3,984	1,156	3,172
# unaligned mis. contigs	139	124	158	373	328	136	453	387	561	491	491	1,416	488
# unaligned contigs	351+756p	464+801p	589+1039p	999+2251p	853+1974p	440+949p	1026+2335p	464+2351p	577+3562p	447+3312p	447+3312p	8367+9093p	789+4942p
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	212,949,825	218,279,317	218,279,317	94,966,921	168,140,893
Genome fraction (%)	93.83	93.26	94.30	95.41	95.44	94.89	97.55	98.28	98.14	98.15	98.15	70.42	97.95
Duplication ratio	1.00	1.00	1.00	1.45	1.45	1.58	1.06	1.97	2.48	2.46	2.46	1.13	1.75
# 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	0.00	0.00
# mismatches per 100 kbp	120.44	121.12	120.38	145.08	145.34	126.34	194.86	179.05	169.04	172.83	172.83	252.20	183.06
# indels per 100 kbp	29.76	30.21	30.04	32.66	32.80	30.84	28.86	31.97	30.86	30.87	30.87	199.05	32.83
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	5,902,261	5,902,261	5,902,261	3,503,179	5,732,588
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	7,111,198,985	7,085,615,090	7,085,615,090	2,331,335,858	5,014,291,893
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	498,803	507,098	507,098	449,685	338,595
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	462,644	469,070	469,070	137,726	306,255
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	363,675	368,536	368,536	340,868	188,401
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	339,258	343,303	343,303	78,385	182,240
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	158,504	161,449	161,449	0	86,177
Strict EA75max	854,242	757,673	681,422	737,089	853,383	852,773	1,123,864	1,189,185	150,829	153,044	153,044	0	82,957
P5k	0.89	0.89	0.90	0.91	0.91	0.90	0.93	0.93	0.93	0.93	0.93	0.67	0.93
P10k	0.89	0.89	0.90	0.91	0.91	0.90	0.92	0.93	0.93	0.93	0.93	0.66	0.93
P15k	0.89	0.89	0.90	0.91	0.91	0.90	0.92	0.93	0.93	0.93	0.93	0.66	0.92
P20k	0.89	0.88	0.89	0.91	0.91	0.90	0.92	0.93	0.93	0.93	0.93	0.66	0.92
Strict P5k	0.89	0.89	0.90	0.91	0.91	0.90	0.93	0.93	0.93	0.93	0.93	0.67	0.93
Strict P10k	0.89	0.89	0.90	0.91	0.91	0.90	0.92	0.93	0.93	0.93	0.93	0.66	0.93
Strict P15k	0.89	0.88	0.89	0.90	0.90	0.90	0.92	0.93	0.93	0.93	0.93	0.65	0.92
Strict P20k	0.89	0.88	0.89	0.90	0.90	0.90	0.92	0.93	0.93	0.93	0.93	0.64	0.92
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	608,903	614,433	614,433	365,315	274,017
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	455,176	460,480	460,480	2,648	187,628
LGA50	83	81	126	79	66	50	97	112	1,742	1,725	1,725	2,301	3,526
LGA75	248	257	374	161	136	98	245	283	3,212	3,180	3,180	32,632	6,963
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	411,554	417,197	417,197	624,431	284,074

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

Parameter	w2 noho	w2	w2 sfa	w2 YV sfa	w2 YV	w2 frg YV	flye	hifiasm	hifiasm YVr	hifiasm YVrbp	hifiasm YVp	mdbg	lja	HiCanu
# misassemblies	1,509	1,827	1,557	4,518	4,720	2,961	9,276	20,818	19,803	21,538	21,538	7,574	16,959	20,561
# contig misassemblies	1,509	1,827	1,557	4,518	4,720	2,961	9,276	20,818	19,803	21,538	21,538	7,574	16,959	20,561
# c. relocations	1,255	1,558	1,358	3,470	3,620	2,180	7,403	17,422	15,971	17,871	17,871	6,915	13,676	17,003
# c. translocations	221	238	175	983	1,030	735	1,821	3,285	3,736	3,561	3,561	630	3,207	3,454
# c. inversions	33	31	24	65	70	46	52	111	96	106	106	29	76	104
# scaffold misassemblies	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# s. relocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# s. translocations	0	0	0	0	0	0	0	0	0	0	0	0	0	0
# s. inversions	0	0	0	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	2,299	2,050	2,050	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	516,401,952	538,435,180	538,435,180	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	21,811	22,498	22,498	40,415	20,386	22,082
# scaffold gap ext. mis.	0	0	0	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	0	0	0
# possible TEs	210	214	194	412	438	302	1,036	3,542	2,404	3,984	3,984	1,156	3,172	3,236
# unaligned mis. contigs	139	124	158	373	328	136	453	387	561	491	491	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	12,020,877	12,245,999	12,245,999	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	2,194,418	2,187,628	2,187,628	4,640,553	1,646,245	2,332,852
# indels ( $\leq 5$ bp)	691,523	699,551	702,829	1,126,009	1,130,710	1,147,826	717,091	1,512,726	1,826,734	1,819,187	1,819,187	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	367,684	368,441	368,441	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	22,097,575	22,140,838	22,140,838	12,546,236	14,907,754	18,431,713

Resource usage

[illegible]

































































