

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_13.5kb_29x_hodeco_simple HG002_HiFi_13.5kb_29x "retain_cm": "yes", "uniquify_ids": "yes", "genome": "HG002_HiFi_13.5kb_29x", "quast_mode": "hicanu", "read_downsampling_factor": "none", "homopolymer_compression": "none", "assemb

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 (≥ 0 bp)	2,339	2,228	2,959	3,590	3,250	2,027	21,424	31,766	55,873	54,231	54,231	51,410	49,210	47,290
# contigs (≥ 1000 bp)	2,339	2,228	2,959	3,588	3,250	2,027	21,404	31,766	55,873	54,231	54,231	51,394	49,210	47,290
# contigs (≥ 5000 bp)	2,276	2,192	2,908	3,498	3,189	1,998	21,278	31,766	55,873	54,231	54,231	29,813	47,945	47,290
# contigs (≥ 10000 bp)	1,826	1,899	2,526	3,008	2,807	1,743	17,329	31,766	55,873	54,231	54,231	9,631	46,371	47,290
# contigs (≥ 25000 bp)	1,177	1,198	1,597	2,096	1,992	1,137	8,197	23,729	54,508	52,999	52,999	3,590	37,995	28,122
# contigs (≥ 50000 bp)	842	852	1,146	1,596	1,520	840	3,529	11,041	39,155	38,125	38,125	2,673	25,683	12,016

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 (≥ 0 bp)	2,742,483,193	2,749,128,292	2,800,033,701	5,379,243,042	5,381,342,123	4,384,178,479	3,434,598,829	5,952,916,243	7,414,560,848	7,387,073,666	7,387,073,666	3,134,624,158	5,598,628,726	6,065,329,698
Total length (≥ 1000 bp)	2,742,483,193	2,749,128,292	2,800,033,701	5,379,242,029	5,381,342,123	4,384,178,479	3,434,583,579	5,952,916,243	7,414,560,848	7,387,073,666	7,387,073,666	3,134,611,438	5,598,628,726	6,065,329,698
Total length (≥ 5000 bp)	2,742,228,028	2,748,987,939	2,799,839,591	5,378,914,594	5,381,107,815	4,384,070,765	3,434,168,093	5,952,916,243	7,414,560,848	7,387,073,666	7,387,073,666	3,052,876,266	5,594,572,705	6,065,329,698
Total length (≥ 10000 bp)	2,738,969,259	2,746,600,126	2,796,734,046	5,375,063,051	5,378,083,371	4,382,045,970	3,402,178,049	5,952,916,243	7,414,560,848	7,387,073,666	7,387,073,666	2,916,057,729	5,582,896,458	6,065,329,698
Total length (≥ 25000 bp)	2,728,746,178	2,735,286,924	2,781,899,055	5,360,652,543	5,365,125,300	4,372,414,291	3,253,898,671	5,803,070,098	7,386,523,648	7,361,699,224	7,361,699,224	2,830,473,814	5,431,647,642	5,735,329,698
Total length (≥ 50000 bp)	2,716,766,774	2,723,253,805	2,766,036,048	5,343,081,069	5,348,591,595	4,362,118,912	3,092,867,862	5,387,362,273	6,787,804,378	6,780,981,625	6,780,981,625	2,799,652,780	4,976,790,304	5,214,118,912

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	hifiasm YVr	hifiasm YVrbp	hifiasm YVp	mdbg	lja	HiCanu
# contigs	2,332	2,221	2,948	3,565	3,240	2,021	21,354	31,766	55,873	54,231	54,231	48,240	48,631	47,290
Largest contig	99,460,331	77,289,823	53,667,001	66,653,164	66,653,158	123,154,765	40,883,390	139,053,297	16,076,876	21,778,805	21,778,805	14,659,772	44,864,803	82,109,200
Total length	2,742,465,525	2,749,110,979	2,800,007,134	5,379,190,939	5,381,318,187	4,384,166,003	3,434,483,459	5,952,916,243	7,414,560,848	7,387,073,666	7,387,073,666	3,126,620,709	5,597,326,445	6,065,329,698
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 (%)	40.83	40.88	40.85	40.53	40.53	40.65	40.98	40.94	40.94	40.92	40.92	40.80	40.95	40.96
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	13,822,859	14,311,131	9,747,533	16,916,971	18,338,325	23,032,173	4,618,521	2,601,436	235,246	247,852	247,852	1,745,031	249,037	1,029,121
NG50	11,107,829	12,201,491	7,684,580	33,207,938	34,899,991	38,405,726	5,442,036	68,645,173	586,784	627,822	627,822	1,782,625	456,617	25,904,525
N75	5,785,786	6,010,857	3,597,017	7,141,815	8,048,008	11,065,962	1,031,581	256,417	90,853	92,654	92,654	705,389	100,385	167,474
NG75	3,432,914	3,357,179	2,454,517	20,357,479	21,800,663	20,428,079	2,026,031	33,115,992	420,859	447,727	447,727	742,754	314,995	10,884,064
L50	49	48	80	83	78	51	178	91	7,690	7,122	7,122	507	5,720	334
LG50	63	61	97	33	31	26	144	16	1,663	1,490	1,490	496	1,934	39
L75	127	121	201	199	183	120	550	3,019	20,747	19,665	19,665	1,195	14,446	4,824
LG75	184	176	272	63	59	57	377	34	3,230	2,956	2,956	1,155	3,993	86
E-size	21,961,482	22,972,128	12,835,754	23,269,999	24,729,764	32,253,619	7,393,173	34,345,012	484,213	594,016	594,016	2,215,252	922,054	14,119,710

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	hifiasm YVr	hifiasm YVrbp	hifiasm YVp	mdbg	lja	
# misassemblies	1,112	1,566	1,307	3,711	3,884	2,481	10,665	25,446	17,408	23,717	23,717	11,101	20,980	
# unique misassemblies	996	1,441	1,205	2,768	2,928	1,957	7,889	16,016	11,357	13,925	13,925	7,812	13,113	
# misassembled contigs	471	517	512	1,411	1,380	711	1,789	1,358	2,638	2,108	2,108	6,591	1,472	
Misassembled contigs length	1,430,801,787	1,606,561,303	900,546,447	4,110,435,032	4,348,874,884	3,739,687,904	1,282,674,486	3,149,115,614	524,834,489	597,557,122	597,557,122	851,556,215	502,795,746	2,536,839,997
# local misassemblies	3,002	3,179	3,138	6,510	6,546	4,625	15,071	21,298	21,898	23,532	23,532	39,134	19,916	
# unique local misassemblies	2,589	2,804	2,793	3,816	3,852	3,212	6,765	9,941	10,717	10,798	10,798	27,866	8,987	
# 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	186	246	240	446	446	286	1,190	3,722	1,550	3,406	3,406	1,478	2,882	
# unaligned mis. contigs	121	145	178	287	266	149	427	373	664	543	543	1,797	386	
# unaligned contigs	432+810p	524+895p	621+1070p	783+1948p	703+1824p	520+994p	631+3220p	777+2202p	862+4002p	728+3538p	728+3538p	8355+10866p	252+2951p	95,121,102
Unaligned length	21,148,599	27,098,016	25,944,657	45,470,181	46,655,683	30,931,108	116,889,875	171,881,025	171,559,307	196,194,265	196,194,265	116,762,033	148,710,968	174,000,000
Genome fraction (%)	92.43	92.44	94.22	95.12	95.14	94.65	97.78	98.42	97.92	98.20	98.20	92.18	98.11	
Duplication ratio	1.00	1.00	1.00	1.91	1.91	1.57	1.16	2.00	2.52	2.49	2.49	1.11	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	0.00	0.00	
# mismatches per 100 kbp	120.33	122.06	121.27	132.25	132.53	124.87	204.90	180.65	163.93	171.77	171.77	250.41	181.03	
# indels per 100 kbp	30.45	30.67	30.61	31.54	31.55	31.02	29.70	28.26	27.54	27.64	27.64	253.08	29.24	
Largest alignment	51,408,586	62,963,967	39,694,190	62,963,952	62,963,952	75,752,841	39,638,271	90,729,089	16,070,308	21,774,175	21,774,175	13,232,485	30,573,091	56,000,000
Total aligned length	2,719,963,333	2,720,857,729	2,773,106,040	5,327,923,911	5,328,810,275	4,348,255,608	3,307,820,468	5,757,424,488	7,221,602,213	7,167,380,777	7,167,380,777	3,005,456,193	5,429,224,242	5,870,000,000
EAmeanmax	12,925,716	13,848,423	9,626,538	13,530,742	13,884,243	17,018,045	7,129,392	28,425,902	647,257	792,633	792,633	1,886,874	837,108	1,700,000
Strict EAmeanmax	3,366,865	3,268,771	3,122,729	3,508,017	3,542,343	3,479,716	3,245,068	5,296,926	477,042	508,190	508,190	331,400	423,204	4,000,000
EA50max	8,818,555	8,954,444	6,630,935	9,997,644	10,109,133	10,862,360	4,766,982	25,468,968	273,154	276,353	276,353	1,451,741	223,261	13,000,000
Strict EA50max	2,436,775	2,254,875	2,166,336	2,488,095	2,534,495	2,509,972	2,303,184	4,156,583	258,005	260,474	260,474	250,739	213,495	4,000,000
EA75max	2,621,380	2,529,268	2,220,578	2,980,264	3,144,923	3,255,934	1,659,403	8,615,153	107,146	108,643	108,643	535,471	77,413	5,000,000
Strict EA75max	832,740	837,724	834,885	927,471	952,910	948,530	867,578	1,601,397	103,371	104,897	104,897	90,210	74,837	1,000,000
P5k	0.88	0.88	0.90	0.90	0.90	0.90	0.93	0.93	0.93	0.93	0.93	0.87	0.93	
P10k	0.88	0.88	0.90	0.90	0.90	0.90	0.93	0.93	0.93	0.93	0.93	0.87	0.93	
P15k	0.88	0.88	0.89	0.90	0.90	0.90	0.93	0.93	0.93	0.93	0.93	0.87	0.92	
P20k	0.88	0.88	0.89	0.90	0.90	0.90	0.92	0.93	0.93	0.93	0.93	0.86	0.91	
Strict P5k	0.88	0.88	0.90	0.90	0.90	0.90	0.93	0.93	0.93	0.93	0.93	0.87	0.93	
Strict P10k	0.88	0.88	0.89	0.90	0.90	0.90	0.93	0.93	0.93	0.93	0.93	0.86	0.93	
Strict P15k	0.88	0.88	0.89	0.90	0.90	0.90	0.92	0.93	0.93	0.93	0.93	0.86	0.92	
Strict P20k	0.88	0.88	0.89	0.90	0.90	0.90	0.92	0.93	0.92	0.93	0.93	0.85	0.91	
NGA50	8,825,805	9,020,390	6,630,935	19,989,866	19,996,930	18,704,684	4,766,982	25,468,968	552,489	553,300	553,300	1,502,674	392,566	13,000,000
NGA75	2,663,185	2,529,268	2,265,997	14,144,422	14,217,084	11,572,602	1,665,682	8,615,153	394,769	394,929	394,929	610,047	270,135	5,000,000
LGA50	85	86	116	52	52	52	165	38	1,778	1,759	1,759	578	2,412	1,000,000
LGA75	240	244	311	99	98	104	447	90	3,446	3,426	3,426	1,354	4,790	1,000,000
EA-size	14,686,155	15,729,080	10,728,071	15,112,720	15,370,586	18,091,171	6,664,058	15,417,092	454,460	517,768	517,768	1,994,976	602,897	9,000,000

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	hifiasm YVr	hifiasm YVrbp	hifiasm YVp	mdbg	lja	HiCanu
# misassemblies	1,112	1,566	1,307	3,711	3,884	2,481	10,665	25,446	17,408	23,717	23,717	11,101	20,980	21,964
# contig misassemblies	1,112	1,566	1,307	3,711	3,884	2,481	10,665	25,446	17,408	23,717	23,717	11,101	20,980	21,964
# c. relocations	857	1,305	1,087	2,821	2,965	1,832	8,504	19,477	13,757	19,228	19,228	9,923	16,797	17,799
# c. translocations	221	226	196	826	856	606	2,113	5,857	3,547	4,361	4,361	1,124	4,094	4,061
# c. inversions	34	35	24	64	63	43	48	112	104	128	128	54	89	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	471	517	512	1,411	1,380	711	1,789	1,358	2,638	2,108	2,108	6,591	1,472	1,551
Misassembled contigs length	1,430,801,787	1,606,561,303	900,546,447	4,110,435,032	4,348,874,884	3,739,687,904	1,282,674,486	3,149,115,614	524,834,489	597,557,122	597,557,122	851,556,215	502,795,746	2,536,839,997
# local misassemblies	3,002	3,179	3,138	6,510	6,546	4,625	15,071	21,298	21,898	23,532	23,532	39,134	19,916	21,993
# 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	186	246	240	446	446	286	1,190	3,722	1,550	3,406	3,406	1,478	2,882	3,492
# unaligned mis. contigs	121	145	178	287	266	149	427	373	664	543	543	1,797	386	487
# mismatches	3,272,812	3,321,189	3,362,908	7,046,091	7,062,262	5,429,657	6,777,743	10,400,883	11,838,503	12,311,295	12,311,295	7,526,080	9,828,372	10,614,563
# indels	828,196	834,458	848,739	1,680,162	1,681,253	1,349,010	982,489	1,627,153	1,988,639	1,981,410	1,981,410	7,606,136	1,587,445	2,340,084
# indels (≤ 5 bp)	699,210	704,986	717,084	1,425,595	1,426,545	1,142,759	802,571	1,319,689	1,615,447	1,610,191	1,610,191	6,918,920	1,301,212	2,030,063
# indels (> 5 bp)	128,986	129,472	131,655	254,567	254,708	206,251	179,918	307,464	373,192	371,219	371,219	687,216	286,233	310,021
Indels length	8,643,487	8,664,231	8,757,979	16,104,102	16,143,546	13,276,700	11,222,916	18,804,889	22,116,125	21,871,033	21,871,033	20,607,333	16,839,256	19,460,051

Resource usage

[illegible]

























































