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_15kb_37x_hodeco_simple HG002_HiFi_15kb_37x "retain_cm":"yes","uniquify_ids":"yes","genome":"HG002_HiFi_15kb_37x","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 (≥ 0 bp)	2,145	2,297	2,913	3,413	3,156	2,059	27,213	33,167	58,585	56,285	56,285	54,391	51,212	54,433
# contigs (≥ 1000 bp)	2,145	2,297	2,913	3,413	3,156	2,059	27,202	33,167	58,585	56,285	56,285	54,380	51,212	54,433
# contigs (≥ 5000 bp)	2,111	2,279	2,889	3,334	3,096	2,030	27,103	33,167	58,585	56,285	56,285	30,992	49,828	54,433
# contigs (≥ 10000 bp)	1,700	1,964	2,482	2,868	2,719	1,762	22,482	33,161	58,582	56,285	56,285	9,315	48,103	54,429
# contigs (≥ 25000 bp)	1,086	1,187	1,537	1,940	1,864	1,103	11,529	23,924	56,644	54,604	54,604	2,769	38,563	27,076
# contigs (≥ 50000 bp)	825	869	1,116	1,519	1,453	850	5,368	10,984	39,486	38,033	38,033	1,814	25,152	11,827

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	H
Total length (≥ 0 bp)	2,710,148,694	2,743,626,278	2,796,824,550	5,360,317,965	5,361,907,129	4,934,073,437	3,586,681,568	5,982,135,458	7,458,371,445	7,432,192,686	7,432,192,686	3,229,928,771	5,714,819,445	6,164,49…
Total length (≥ 1000 bp)	2,710,148,694	2,743,626,278	2,796,824,550	5,360,317,965	5,361,907,129	4,934,073,437	3,586,673,578	5,982,135,458	7,458,371,445	7,432,192,686	7,432,192,686	3,229,921,951	5,714,819,445	6,164,49…
Total length (≥ 5000 bp)	2,710,004,398	2,743,552,597	2,796,731,921	5,360,023,190	5,361,663,515	4,933,953,564	3,586,333,893	5,982,135,458	7,458,371,445	7,432,192,686	7,432,192,686	3,141,848,600	5,710,415,920	6,164,49…
Total length (≥ 10000 bp)	2,707,031,655	2,741,035,875	2,793,458,105	5,356,285,471	5,358,651,204	4,931,807,804	3,549,328,733	5,982,082,078	7,458,349,849	7,432,192,686	7,432,192,686	2,994,888,908	5,697,544,471	6,164,40…
Total length (≥ 25000 bp)	2,697,493,053	2,728,625,472	2,778,382,317	5,341,395,358	5,344,725,500	4,921,318,434	3,371,274,581	5,810,363,497	7,419,406,313	7,398,259,693	7,398,259,693	2,902,098,390	5,525,939,457	5,710,29…
Total length (≥ 50000 bp)	2,688,295,868	2,717,448,603	2,763,432,540	5,326,413,204	5,330,099,179	4,912,508,287	3,156,598,088	5,386,943,130	6,753,536,046	6,753,611,609	6,753,611,609	2,869,864,868	5,031,848,459	5,215,11…

Table 6: QUAST: 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	hifiasm YVr	hifiasm YVrbp	hifiasm YVp	mdbg	lja	HiCanu
# contigs	2,141	2,296	2,910	3,392	3,150	2,055	27,168	33,167	58,585	56,285	56,285	50,609	50,569	54,433
Largest contig	71,027,909	74,405,341	44,024,760	62,286,514	62,286,512	149,584,362	36,480,942	143,473,701	19,535,553	33,815,206	33,815,206	31,618,859	45,644,871	132,523,900
Total length	2,710,138,825	2,743,623,429	2,796,817,553	5,360,269,916	5,361,893,767	4,934,065,233	3,586,601,896	5,982,135,458	7,458,371,445	7,432,192,686	7,432,192,686	3,220,392,699	5,713,400,799	6,164,499,418
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 (%)	40.92	40.86	40.84	40.51	40.51	40.40	40.79	40.86	40.82	40.80	40.80	40.64	40.83	40.85
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	14,522,088	13,049,512	9,129,109	16,063,095	16,550,044	32,947,791	2,019,624	2,510,882	226,928	244,535	244,535	3,947,737	260,865	986,873
NG50	11,774,680	11,087,647	7,770,579	25,164,941	26,493,939	48,303,382	2,623,367	68,318,907	561,465	632,495	632,495	4,158,865	504,342	38,046,558
N75	5,752,227	5,201,732	3,999,840	7,275,466	8,241,862	13,248,984	412,757	248,560	87,028	89,194	89,194	1,143,928	97,370	152,908
NG75	3,189,820	3,089,156	2,563,463	18,253,839	18,968,970	34,217,238	1,028,461	32,985,826	412,540	447,490	447,490	1,456,483	342,918	18,172,563
L50	51	59	89	101	94	47	405	93	8,009	7,162	7,162	211	5,410	309
LG50	65	73	106	43	40	23	297	16	1,723	1,441	1,441	195	1,727	25
L75	125	141	205	216	204	112	1,313	3,097	21,741	20,172	20,172	569	14,193	5,132
LG75	191	204	273	80	74	43	763	32	3,341	2,904	2,904	493	3,601	52
E-size	19,818,283	17,837,603	11,387,312	19,259,191	20,490,856	37,117,100	3,747,979	35,532,978	519,287	875,960	875,960	5,630,435	1,033,660	23,020,671

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	hifiasm YVr	hifiasm YVrbp	hifiasm YVp	mdbg	lja	
# misassemblies	1,037	1,571	1,353	3,491	3,723	2,437	10,615	24,550	19,087	25,290	25,290	10,939	21,969	
# unique misassemblies	957	1,450	1,265	2,596	2,782	1,920	7,724	15,559	12,166	15,022	15,022	7,517	12,650	
# misassembled contigs	449	561	551	1,362	1,362	724	1,814	1,307	2,696	1,997	1,997	6,400	1,500	
Misassembled contigs length	1,401,181,134	1,485,206,940	875,538,566	3,809,283,394	4,124,446,179	4,222,179,816	842,057,669	3,102,880,165	537,119,658	671,186,992	671,186,992	1,082,365,816	535,378,803	2,79...
# local misassemblies	2,705	3,077	2,980	6,020	6,173	4,463	14,862	22,082	23,299	25,585	25,585	31,026	21,108	
# unique local misassemblies	2,407	2,788	2,740	3,613	3,691	3,087	6,716	9,630	10,903	10,497	10,497	18,968	9,073	
# 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	166	204	208	436	430	348	1,116	3,768	2,088	4,056	4,056	1,528	2,832	
# unaligned mis. contigs	113	144	151	218	196	154	420	481	780	622	622	1,540	432	
# unaligned contigs	361+719p	570+917p	636+1037p	780+1778p	729+1691p	566+979p	912+3314p	558+2297p	819+4257p	558+3570p	558+3570p	11149+10522p	442+2993p	10...
Unaligned length	19,734,000	25,668,873	24,481,216	43,026,389	43,798,578	30,634,458	139,622,427	191,202,834	192,770,231	222,372,127	222,372,127	134,740,112	176,983,395	2...
Genome fraction (%)	91.39	92.31	94.17	94.97	94.99	94.58	97.78	98.40	97.53	98.08	98.08	95.78	98.18	
Duplication ratio	1.00	1.00	1.00	1.91	1.91	1.76	1.20	2.00	2.54	2.50	2.50	1.10	1.92	
# 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	118.00	120.91	120.13	131.66	132.10	120.48	202.45	180.88	166.67	177.37	177.37	242.47	178.70	
# indels per 100 kbp	29.67	30.01	29.99	31.29	31.32	30.06	29.68	27.49	26.82	26.98	26.98	187.78	27.59	
Largest alignment	47,921,947	74,389,239	44,016,462	56,946,514	56,946,513	74,384,115	32,046,407	90,496,567	19,525,717	31,356,030	31,356,030	31,574,696	32,050,878	9...
Total aligned length	2,689,347,269	2,716,638,451	2,771,232,004	5,310,842,047	5,311,649,189	4,898,948,974	3,438,541,411	5,771,642,014	7,245,656,022	7,189,840,158	7,189,840,158	3,081,217,872	5,517,535,823	5,94...
EAmeanmax	12,181,695	11,571,860	8,947,360	12,882,900	13,152,452	16,081,291	3,894,055	29,821,065	688,537	1,068,707	1,068,707	4,807,323	1,051,676	
Strict EAmeanmax	3,405,595	3,122,146	3,031,055	3,401,611	3,425,141	3,433,567	2,256,757	5,564,594	471,870	499,658	499,658	649,471	473,214	
EA50max	8,261,576	8,164,963	6,744,390	10,010,056	10,030,572	10,091,829	2,389,466	25,620,191	260,318	264,488	264,488	3,317,710	228,815	
Strict EA50max	2,529,467	2,358,674	2,263,458	2,578,478	2,670,188	2,560,581	1,582,183	4,301,869	248,216	251,689	251,689	493,607	219,118	
EA75max	2,368,326	2,272,024	2,159,649	2,985,083	3,084,569	3,003,362	895,996	10,224,387	100,998	103,445	103,445	1,077,309	73,548	
Strict EA75max	810,871	827,969	841,911	972,310	977,370	963,900	602,162	1,650,652	98,042	100,039	100,039	208,213	71,194	
P5k	0.87	0.88	0.90	0.90	0.90	0.90	0.93	0.93	0.93	0.93	0.93	0.91	0.93	
P10k	0.87	0.88	0.89	0.90	0.90	0.90	0.93	0.93	0.92	0.93	0.93	0.90	0.93	
P15k	0.87	0.88	0.89	0.90	0.90	0.90	0.93	0.93	0.92	0.93	0.93	0.90	0.92	
P20k	0.87	0.88	0.89	0.90	0.90	0.90	0.92	0.93	0.92	0.93	0.93	0.90	0.91	
Strict P5k	0.87	0.88	0.90	0.90	0.90	0.90	0.93	0.93	0.93	0.93	0.93	0.91	0.93	
Strict P10k	0.87	0.88	0.89	0.90	0.90	0.90	0.93	0.93	0.92	0.93	0.93	0.90	0.93	
Strict P15k	0.87	0.88	0.89	0.90	0.90	0.90	0.92	0.93	0.92	0.93	0.93	0.90	0.92	
Strict P20k	0.86	0.87	0.89	0.90	0.90	0.90	0.92	0.93	0.92	0.92	0.92	0.89	0.91	
NGA50	8,261,576	8,164,963	6,744,390	17,256,574	17,266,299	29,837,383	2,389,466	25,620,191	530,353	535,135	535,135	3,376,207	428,635	
NGA75	2,368,326	2,280,694	2,174,040	13,205,281	13,567,632	16,197,583	897,039	10,224,387	385,072	386,008	386,008	1,165,405	290,138	
LGA50	89	101	124	60	58	37	331	36	1,843	1,788	1,788	239	2,165	
LGA75	252	271	314	111	108	73	855	85	3,565	3,497	3,497	614	4,366	
EA-size	13,998,976	13,164,487	9,978,229	14,243,069	14,509,266	21,454,715	3,506,248	16,122,283	476,347	737,052	737,052	4,888,781	729,740	1...

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	hifiasm YVr	hifiasm YVrbp	hifiasm YVp	mdbg	lja	HiCanu
# misassemblies	1,037	1,571	1,353	3,491	3,723	2,437	10,615	24,550	19,087	25,290	25,290	10,939	21,969	21,346
# contig misassemblies	1,037	1,571	1,353	3,491	3,723	2,437	10,615	24,550	19,087	25,290	25,290	10,939	21,969	21,346
# c. relocations	799	1,305	1,122	2,562	2,765	1,789	8,352	18,548	15,597	20,409	20,409	9,854	18,021	17,414
# c. translocations	207	230	211	883	910	598	2,205	5,906	3,386	4,751	4,751	1,030	3,868	3,842
# c. inversions	31	36	20	46	48	50	58	96	104	130	130	55	80	90
# 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	449	561	551	1,362	1,362	724	1,814	1,307	2,696	1,997	1,997	6,400	1,500	1,560
Misassembled contigs length	1,401,181,134	1,485,206,940	875,538,566	3,809,283,394	4,124,446,179	4,222,179,816	842,057,669	3,102,880,165	537,119,658	671,186,992	671,186,992	1,082,365,816	535,378,803	2,792,253,308
# local misassemblies	2,705	3,077	2,980	6,020	6,173	4,463	14,862	22,082	23,299	25,585	25,585	31,026	21,108	22,421
# 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	166	204	208	436	430	348	1,116	3,768	2,088	4,056	4,056	1,528	2,832	3,226
# unaligned mis. contigs	113	144	151	218	196	154	420	481	780	622	622	1,540	432	525
# mismatches	3,173,515	3,284,752	3,329,042	6,992,265	7,016,906	5,902,152	6,961,350	10,439,981	12,076,653	12,752,887	12,752,887	7,470,963	9,859,716	10,732,429
# indels	798,002	815,128	831,189	1,661,904	1,663,691	1,472,592	1,020,607	1,586,770	1,943,609	1,940,057	1,940,057	5,785,884	1,522,171	2,153,717
# indels (≤ 5 bp)	670,007	686,089	699,630	1,404,711	1,406,294	1,243,826	831,766	1,276,870	1,570,021	1,566,501	1,566,501	5,066,202	1,230,237	1,838,425
# indels (> 5 bp)	127,995	129,039	131,559	257,193	257,397	228,766	188,841	309,900	373,588	373,556	373,556	719,682	291,934	315,292
Indels length	8,546,640	8,546,771	8,690,018	16,527,152	16,555,050	14,732,079	11,491,876	18,778,818	21,778,779	21,596,053	21,596,053	19,743,048	16,927,204	19,251,051

Table 9: Resource usage

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
time [s]	35,127.96	69,508.90	66,659.66	77,942.09	81,198.64	85,877.10	98,493.00	97,377.00	98,625.20	98,610.68	98,610.54	1,072.00	34,878.00	160,198.00
mem [GiB]	144.05	136.04	135.93	135.93	136.04	136.04	199.61	155.84	155.84	155.84	155.84	18.40	168.11	77.63
hoco time		448.05	448.05	448.05	448.05	448.05	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
hoco mem		0.38	0.38	0.38	0.38	0.38	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
hodeco time		36,631.00	34,278.00	39,482.00	41,693.00	47,956.00	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
hodeco mem		1.79	1.79	1.95	1.94	1.94	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
assembly time									97,377.00	97,377.00	97,377.00	1,072.00	34,878.00	160,198.00
assembly mem									155.84	155.84	155.84	18.40	168.11	77.63
trivial_omnitigs time				423.67	397.92	0.47	N/A	N/A	1,248.20	1,233.68	1,233.54	N/A	N/A	N/A
trivial_omnitigs mem				26.77	26.77	0.00	N/A	N/A	1.70	1.72	1.72	N/A	N/A	N/A
assembly time	29,305.00	27,270.00	26,625.00	26,625.00	27,270.00	27,270.00	98,493.00	97,377.00	N/A	N/A	N/A	N/A	N/A	N/A
assembly mem	144.05	136.04	135.93	135.93	136.04	136.04	199.61	155.84	N/A	N/A	N/A	N/A	N/A	N/A
wtdbg2_extract time	851.96	571.85	584.61	584.61	571.85	571.85	N/A	N/A	N/A	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	N/A	N/A	N/A
contig_assembly time				1,326.76	1,371.82	1,308.73	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
contig_assembly mem				125.01	125.02	125.02	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
wtdbg2_consensus time	4,971.00	4,588.00	4,724.00	9,052.00	9,446.00	8,322.00	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
wtdbg2_consensus mem	6.39	7.41	7.56	9.15	8.86	7.38	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A

NGAx

NGAx

NGAx

NGAx

- contigs

NGAx

NGAx

NGAx