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 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":null,"assembler_a

Table 1: Genome Graph Statistics

Table 2: Algorithm Statistics

Parameter

Table 3: ContigValidator

Parameter

Table 4: QUAST: # of contigs

Parameter	w2	w2 sfa	w2 YV sfa	w2 YV	w2 frg YV	flye	hifiasm	mdbg	lja	HiCanu
# contigs ($\geq$ 0 bp)	2,255	3,370	5,976	4,989	2,054	8,340	23,457	45,369	46,161	37,728
# contigs ($\geq$ 1000 bp)	2,254	3,369	5,972	4,989	2,054	8,322	23,457	45,364	46,161	37,728
# contigs ($\geq$ 5000 bp)	2,220	3,314	5,697	4,798	2,023	8,163	23,457	25,616	45,445	37,728
# contigs ($\geq$ 10000 bp)	1,861	2,722	4,491	3,851	1,802	7,450	23,455	9,662	44,483	37,728
# contigs ($\geq$ 25000 bp)	1,274	1,896	3,107	2,617	1,417	4,462	21,218	5,161	39,603	34,009
# contigs ($\geq$ 50000 bp)	976	1,453	2,338	1,944	1,185	2,627	13,533	4,550	29,933	18,969

Table 5: QUAST: total length of contigs

Parameter	w2	w2 sfa	w2 YV sfa	w2 YV	w2 frg YV	flye	hifiasm	mdbg	lja	HiCanu
Total length ($\geq$ 0 bp)	2,785,753,546	2,809,006,701	4,356,852,208	4,355,155,499	4,002,295,305	3,173,378,180	5,882,154,531	2,437,921,680	5,200,080,087	5,952,937,636
Total length ($\geq$ 1000 bp)	2,785,752,906	2,809,006,061	4,356,849,370	4,355,155,499	4,002,295,305	3,173,365,326	5,882,154,531	2,437,918,357	5,200,080,087	5,952,937,636
Total length ($\geq$ 5000 bp)	2,785,621,513	2,808,791,622	4,355,859,372	4,354,428,070	4,002,172,189	3,172,847,858	5,882,154,531	2,364,063,143	5,197,754,800	5,952,937,636
Total length ($\geq$ 10000 bp)	2,782,989,525	2,804,493,855	4,347,097,482	4,347,531,883	4,000,570,838	3,166,732,798	5,882,137,431	2,256,492,968	5,190,547,617	5,952,937,636
Total length ($\geq$ 25000 bp)	2,773,391,401	2,791,124,128	4,325,200,678	4,327,772,494	3,994,239,990	3,117,973,368	5,836,652,666	2,192,925,217	5,099,681,772	5,877,879,448
Total length ($\geq$ 50000 bp)	2,762,651,653	2,774,994,236	4,297,837,812	4,303,964,202	3,985,607,352	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 $\geq$ 500bp (or 3000bp for QUAST-LG)

Parameter	w2	w2 sfa	w2 YV sfa	w2 YV	w2 frg YV	flye	hifiasm	mdbg	lja	HiCanu
# contigs	2,245	3,356	5,899	4,957	2,050	8,261	23,457	42,100	45,844	37,728
Largest contig	109,683,034	40,811,204	73,898,056	73,898,058	109,687,827	41,615,215	47,637,577	3,527,865	5,734,769	10,610,862
Total length	2,785,732,030	2,808,976,491	4,356,688,273	4,355,077,039	4,002,286,195	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
GC (%)	40.85	40.86	40.85	40.85	40.86	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
N50	16,241,166	9,526,322	12,141,252	14,689,045	18,238,295	10,823,492	1,098,803	518,362	182,952	445,184
NG50	13,730,072	8,234,496	16,682,454	19,469,691	21,594,138	11,461,425	9,775,638	397,160	296,827	1,377,692
N75	5,300,858	3,482,975	3,968,777	5,206,142	7,570,785	2,945,225	259,509	299,153	93,449	145,744
NG75	2,991,964	1,894,353	10,595,131	13,417,853	15,601,876	3,273,387	4,004,428	6,559	206,441	747,156
L50	48	85	106	86	64	83	521	1,436	7,836	2,589
LG50	58	100	62	49	40	79	88	2,163	3,244	658
L75	120	208	261	204	144	222	3,738	2,970	17,746	8,612
LG75	177	290	118	96	83	202	211	17,211	6,374	1,428
E-size	24,546,083	11,717,563	14,951,528	18,836,098	25,322,604	12,788,058	6,853,565	636,662	305,165	1,031,070

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

Parameter	w2	w2 sfa	w2 YV sfa	w2 YV	w2 frg YV	flye	hifiasm	mdbg	lja	HiCanu
# misassemblies	1,509	1,281	4,063	4,217	3,198	9,276	20,818	7,574	16,959	20,561
# unique misassemblies	1,393	1,182	2,931	3,094	2,206	6,749	12,421	5,002	11,114	12,785
# misassembled contigs	417	425	1,687	1,611	769	1,533	1,615	5,021	2,054	1,722
Misassembled contigs length	1,376,421,295	874,429,843	2,613,998,480	2,999,188,806	2,974,975,040	1,219,247,184	1,659,489,288	326,494,618	367,209,992	623,230,535
# local misassemblies	2,947	2,868	6,468	6,413	4,411	13,177	20,223	40,415	20,386	22,082
# unique local misassemblies	2,706	2,628	3,857	3,849	3,124	5,755	9,673	30,275	9,539	9,676
# scaffold gap ext. mis.	0	0	0	0	0	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0	0	0	0	0	0
# possible TEs	210	168	422	426	306	1,036	3,542	1,156	3,172	3,236
# unaligned mis. contigs	139	162	509	461	169	453	387	1,416	488	381
# unaligned contigs	351+756p	422+950p	955+2605p	820+2332p	310+989p	1026+2335p	464+2351p	8367+9093p	789+4942p	618+2741p
Unaligned length	23,270,287	21,636,307	54,898,849	54,893,151	35,727,558	129,051,438	183,039,216	94,966,921	168,140,893	186,242,523
Genome fraction (%)	93.83	94.69	95.83	95.87	95.37	97.55	98.28	70.42	97.95	98.20
Duplication ratio	1.00	1.00	1.53	1.53	1.42	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
# mismatches per 100 kbp	120.44	119.53	146.52	146.42	134.29	194.86	179.05	252.20	183.06	181.46
# indels per 100 kbp	29.76	29.59	32.37	32.45	31.50	28.86	31.97	199.05	32.83	40.60
Largest alignment	62,959,951	36,758,990	62,966,425	62,966,427	62,966,425	41,604,502	37,338,644	3,503,179	5,732,588	10,602,224
Total aligned length	2,761,163,371	2,786,541,074	4,297,201,774	4,295,600,204	3,961,686,864	3,037,710,484	5,677,338,021	2,331,335,858	5,014,291,893	5,746,307,111
EAmeanmax	13,982,958	8,851,581	10,663,204	13,753,715	15,041,096	10,937,959	9,917,068	449,685	338,595	1,609,440
Strict EAmeanmax	3,211,040	2,967,794	3,197,849	3,399,433	3,384,752	4,179,186	4,250,500	137,726	306,255	1,315,026
EA50max	9,689,788	6,892,624	7,563,761	10,039,068	10,547,631	8,767,673	7,313,156	340,868	188,401	1,229,604
Strict EA50max	2,275,355	2,078,946	2,237,275	2,373,958	2,388,454	2,896,163	3,035,240	78,385	182,240	1,018,047
EA75max	2,229,624	1,737,918	2,020,238	2,730,780	2,891,654	2,879,602	2,638,125	0	86,177	540,888
Strict EA75max	854,242	746,708	810,312	924,990	926,239	1,123,864	1,189,185	0	82,957	449,137
P5k	0.89	0.90	0.91	0.91	0.91	0.93	0.93	0.67	0.93	0.93
P10k	0.89	0.90	0.91	0.91	0.91	0.92	0.93	0.66	0.93	0.93
P15k	0.89	0.90	0.91	0.91	0.91	0.92	0.93	0.66	0.92	0.93
P20k	0.89	0.90	0.91	0.91	0.91	0.92	0.93	0.66	0.92	0.93
Strict P5k	0.89	0.90	0.91	0.91	0.91	0.93	0.93	0.67	0.93	0.93
Strict P10k	0.89	0.90	0.91	0.91	0.91	0.92	0.93	0.66	0.93	0.93
Strict P15k	0.89	0.90	0.91	0.91	0.91	0.92	0.93	0.65	0.92	0.93
Strict P20k	0.89	0.90	0.91	0.91	0.90	0.92	0.93	0.64	0.92	0.93
NGA50	9,689,788	6,892,624	12,436,231	14,002,559	15,553,998	8,767,673	7,317,420	365,315	274,017	1,248,128
NGA75	2,234,408	1,740,622	7,889,423	9,134,845	10,048,218	2,897,718	2,668,966	2,648	187,628	633,706
LGA50	83	120	85	71	58	97	112	2,301	3,526	710
LGA75	248	340	162	138	119	245	283	32,632	6,963	1,591
EA-size	15,648,776	9,816,487	10,978,778	13,212,739	16,372,759	11,128,125	5,555,129	624,431	284,074	962,835

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

Parameter	w2	w2 sfa	w2 YV sfa	w2 YV	w2 frg YV	flye	hifiasm	mdbg	lja	HiCanu
# misassemblies	1,509	1,281	4,063	4,217	3,198	9,276	20,818	7,574	16,959	20,561
# contig misassemblies	1,509	1,281	4,063	4,217	3,198	9,276	20,818	7,574	16,959	20,561
# c. relocations	1,255	1,051	2,980	3,140	2,442	7,403	17,422	6,915	13,676	17,003
# c. translocations	221	202	1,032	1,022	706	1,821	3,285	630	3,207	3,454
# c. inversions	33	28	51	55	50	52	111	29	76	104
# scaffold misassemblies	0	0	0	0	0	0	0	0	0	0
# s. relocations	0	0	0	0	0	0	0	0	0	0
# s. translocations	0	0	0	0	0	0	0	0	0	0
# s. inversions	0	0	0	0	0	0	0	0	0	0
# misassembled contigs	417	425	1,687	1,611	769	1,533	1,615	5,021	2,054	1,722
Misassembled contigs length	1,376,421,295	874,429,843	2,613,998,480	2,999,188,806	2,974,975,040	1,219,247,184	1,659,489,288	326,494,618	367,209,992	623,230,535
# local misassemblies	2,947	2,868	6,468	6,413	4,411	13,177	20,223	40,415	20,386	22,082
# scaffold gap ext. mis.	0	0	0	0	0	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0	0	0	0	0	0
# possible TEs	210	168	422	426	306	1,036	3,542	1,156	3,172	3,236
# unaligned mis. contigs	139	162	509	461	169	453	387	1,416	488	381
# mismatches	3,325,655	3,330,867	6,296,068	6,289,464	5,320,196	5,919,192	10,165,248	5,879,539	9,178,928	10,427,234
# indels	821,830	824,650	1,390,841	1,394,045	1,247,889	876,675	1,814,895	4,640,553	1,646,245	2,332,852
# indels (≤ 5 bp)	691,523	693,197	1,176,124	1,179,382	1,055,482	717,091	1,512,726	4,242,146	1,383,347	2,032,243
# indels (> 5 bp)	130,307	131,453	214,717	214,663	192,407	159,584	302,169	398,407	262,898	300,609
Indels length	8,608,802	8,583,359	13,939,039	14,015,016	12,758,202	10,045,353	18,566,292	12,546,236	14,907,754	18,431,713

Table 9: Resource usage

Parameter	w2	w2 sfa	w2 YV sfa	w2 YV	w2 frg YV	flye	hifiasm	mdbg	lja	HiCanu
time [s]	15,455.97	20,048.20	20,628.10	18,234.59	17,204.30	47,286.00	27,423.00	364.77	35,359.00	42,503.00
mem [GiB]	64.86	64.84	66.07	66.07	66.07	137.76	67.91	6.23	135.06	47.33
trivial_omnitigs time			436.70	328.18	0.15	N/A	N/A	N/A	N/A	N/A
trivial_omnitigs mem			16.74	16.74	0.00	N/A	N/A	N/A	N/A	N/A
assembly time	10,785.00	13,098.00	13,098.00	10,785.00	10,785.00	47,286.00	27,423.00	364.77	35,359.00	42,503.00
assembly mem	64.86	64.84	64.84	64.86	64.86	137.76	67.91	6.23	135.06	47.33
wtdbg2_extract time	346.97	348.20	348.20	346.97	346.97	N/A	N/A	N/A	N/A	N/A
wtdbg2_extract mem	0.00	0.00	0.00	0.00	0.00	N/A	N/A	N/A	N/A	N/A
contig_assembly time			968.20	987.44	885.18	N/A	N/A	N/A	N/A	N/A
contig_assembly mem			66.07	66.07	66.07	N/A	N/A	N/A	N/A	N/A
wtdbg2_consensus time	4,324.00	6,602.00	5,777.00	5,787.00	5,187.00	N/A	N/A	N/A	N/A	N/A
wtdbg2_consensus mem	6.77	6.67	9.59	9.33	7.56	N/A	N/A	N/A	N/A	N/A

EAxmax

EAxmax

EAxmax

EAxmax

EAxmax

EAxmax

NGAx