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_13.5kb_29x 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","assembler":null,"assemb

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 (≥ 0 bp)	2,339	3,121	4,598	4,284	2,039	21,424	31,766	51,410	49,210	47,290
# contigs (≥ 1000 bp)	2,339	3,121	4,597	4,284	2,039	21,404	31,766	51,394	49,210	47,290
# contigs (≥ 5000 bp)	2,276	3,024	4,428	4,155	1,981	21,278	31,766	29,813	47,945	47,290
# contigs (≥ 10000 bp)	1,826	2,327	3,488	3,332	1,644	17,329	31,766	9,631	46,371	47,290
# contigs (≥ 25000 bp)	1,177	1,491	2,434	2,297	1,207	8,197	23,729	3,590	37,995	28,122
# contigs (≥ 50000 bp)	842	1,077	1,789	1,691	988	3,529	11,041	2,673	25,683	12,016

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 (≥ 0 bp)	2,742,483,193	2,805,083,979	5,041,927,742	5,044,851,396	5,784,296,206	3,434,598,829	5,952,916,243	3,134,624,158	5,598,628,726	6,065,329,698
Total length (≥ 1000 bp)	2,742,483,193	2,805,083,979	5,041,927,557	5,044,851,396	5,784,296,206	3,434,583,579	5,952,916,243	3,134,611,438	5,598,628,726	6,065,329,698
Total length (≥ 5000 bp)	2,742,228,028	2,804,702,537	5,041,298,342	5,044,356,895	5,784,067,747	3,434,168,093	5,952,916,243	3,052,876,266	5,594,572,705	6,065,329,698
Total length (≥ 10000 bp)	2,738,969,259	2,799,683,342	5,034,425,316	5,038,294,369	5,781,649,718	3,402,178,049	5,952,916,243	2,916,057,729	5,582,896,458	6,065,329,698
Total length (≥ 25000 bp)	2,728,746,178	2,786,618,732	5,017,714,078	5,021,763,405	5,774,821,549	3,253,898,671	5,803,070,098	2,830,473,814	5,431,647,642	5,735,362,561
Total length (≥ 50000 bp)	2,716,766,774	2,771,614,420	4,995,024,277	5,000,541,405	5,767,188,779	3,092,867,862	5,387,362,273	2,799,652,780	4,976,790,304	5,214,128,580

Table 6: QUAST: 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
# contigs	2,332	3,106	4,555	4,259	2,029	21,354	31,766	48,240	48,631	47,290
Largest contig	99,460,331	47,129,326	67,163,644	67,957,747	148,115,682	40,883,390	139,053,297	14,659,772	44,864,803	82,109,200
Total length	2,742,465,525	2,805,047,595	5,041,828,833	5,044,790,049	5,784,273,750	3,434,483,459	5,952,916,243	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
GC (%)	40.83	40.85	40.67	40.67	40.47	40.98	40.94	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
N50	13,822,859	9,909,747	14,488,950	15,557,518	28,993,361	4,618,521	2,601,436	1,745,031	249,037	1,029,121
NG50	11,107,829	8,519,361	24,442,605	26,449,135	53,136,945	5,442,036	68,645,173	1,782,625	456,617	25,904,525
N75	5,785,786	4,457,404	6,656,463	7,064,327	13,102,696	1,031,581	256,417	705,389	100,385	167,474
NG75	3,432,914	2,763,179	15,820,286	17,570,911	36,261,028	2,026,031	33,115,992	742,754	314,995	10,884,064
L50	49	77	94	85	54	178	91	507	5,720	334
LG50	63	92	41	37	20	144	16	496	1,934	39
L75	127	185	223	204	128	550	3,019	1,195	14,446	4,824
LG75	184	246	80	72	37	377	34	1,155	3,993	86
E-size	21,961,482	13,170,292	19,465,685	21,459,344	39,483,591	7,393,173	34,345,012	2,215,252	922,054	14,119,710

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	1,112	941	3,009	3,167	2,471	10,665	25,446	11,101	20,980	21,964
# unique misassemblies	996	851	2,161	2,293	1,781	7,889	16,016	7,812	13,113	13,791
# misassembled contigs	471	448	1,427	1,415	846	1,789	1,358	6,591	1,472	1,551
Misassembled contigs length	1,430,801,787	829,195,375	3,412,506,370	3,740,890,760	5,242,008,629	1,282,674,486	3,149,115,614	851,556,215	502,795,746	2,536,839,997
# local misassemblies	3,002	2,893	5,805	6,273	5,032	15,071	21,298	39,134	19,916	21,993
# unique local misassemblies	2,589	2,600	3,622	3,669	3,135	6,765	9,941	27,866	8,987	9,880
# 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	186	192	402	406	346	1,190	3,722	1,478	2,882	3,492
# unaligned mis. contigs	121	125	227	234	121	427	373	1,797	386	487
# unaligned contigs	432+810p	543+929p	944+1859p	812+1890p	408+996p	631+3220p	777+2202p	8355+10866p	252+2951p	951+2772p
Unaligned length	21,148,599	19,967,571	44,116,641	45,269,593	28,267,086	116,889,875	171,881,025	116,762,033	148,710,968	174,356,855
Genome fraction (%)	92.43	94.62	95.63	95.64	95.20	97.78	98.42	92.18	98.11	98.42
Duplication ratio	1.00	1.00	1.78	1.78	2.06	1.16	2.00	1.11	1.89	2.04
# 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	120.33	119.76	136.13	137.09	124.46	204.90	180.65	250.41	181.03	180.81
# indels per 100 kbp	30.45	30.43	31.98	32.04	31.07	29.70	28.26	253.08	29.24	39.86
Largest alignment	51,408,586	39,696,882	61,440,986	61,440,990	61,449,461	39,638,271	90,729,089	13,232,485	30,573,091	50,519,606
Total aligned length	2,719,963,333	2,784,072,109	4,992,468,839	4,993,925,500	5,750,710,515	3,307,820,468	5,757,424,488	3,005,456,193	5,429,224,242	5,870,471,513
EAmeanmax	12,925,716	10,164,338	13,650,777	14,650,330	16,974,898	7,129,392	28,425,902	1,886,874	837,108	17,632,829
Strict EAmeanmax	3,366,865	3,213,278	3,617,263	3,628,670	3,773,223	3,245,068	5,296,926	331,400	423,204	4,850,369
EA50max	8,818,555	7,169,950	9,909,122	10,501,951	11,762,793	4,766,982	25,468,968	1,451,741	223,261	15,294,079
Strict EA50max	2,436,775	2,356,008	2,617,059	2,661,575	2,712,459	2,303,184	4,156,583	250,739	213,495	4,007,056
EA75max	2,621,380	2,456,290	3,096,892	3,429,913	3,568,481	1,659,403	8,615,153	535,471	77,413	5,271,608
Strict EA75max	832,740	847,873	934,560	970,050	987,790	867,578	1,601,397	90,210	74,837	1,489,464
P5k	0.88	0.90	0.91	0.91	0.91	0.93	0.93	0.87	0.93	0.93
P10k	0.88	0.90	0.91	0.91	0.91	0.93	0.93	0.87	0.93	0.93
P15k	0.88	0.90	0.91	0.91	0.90	0.93	0.93	0.87	0.92	0.93
P20k	0.88	0.90	0.91	0.91	0.90	0.92	0.93	0.86	0.91	0.93
Strict P5k	0.88	0.90	0.91	0.91	0.91	0.93	0.93	0.87	0.93	0.93
Strict P10k	0.88	0.90	0.91	0.91	0.90	0.93	0.93	0.86	0.93	0.93
Strict P15k	0.88	0.90	0.91	0.91	0.90	0.92	0.93	0.86	0.92	0.93
Strict P20k	0.88	0.90	0.91	0.91	0.90	0.92	0.93	0.85	0.91	0.93
NGA50	8,825,805	7,199,720	17,561,626	18,688,877	26,579,880	4,766,982	25,468,968	1,502,674	392,566	15,294,079
NGA75	2,663,185	2,456,290	11,558,659	12,181,138	22,385,773	1,665,682	8,615,153	610,047	270,135	5,271,608
LGA50	85	110	56	53	43	165	38	578	2,412	60
LGA75	240	286	110	105	74	447	90	1,354	4,790	142
EA-size	14,686,155	11,283,184	14,253,259	14,894,079	19,034,710	6,664,058	15,417,092	1,994,976	602,897	9,397,474

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	1,112	941	3,009	3,167	2,471	10,665	25,446	11,101	20,980	21,964
# contig misassemblies	1,112	941	3,009	3,167	2,471	10,665	25,446	11,101	20,980	21,964
# c. relocations	857	723	2,025	2,170	1,691	8,504	19,477	9,923	16,797	17,799
# c. translocations	221	197	936	949	703	2,113	5,857	1,124	4,094	4,061
# c. inversions	34	21	48	48	77	48	112	54	89	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	471	448	1,427	1,415	846	1,789	1,358	6,591	1,472	1,551
Misassembled contigs length	1,430,801,787	829,195,375	3,412,506,370	3,740,890,760	5,242,008,629	1,282,674,486	3,149,115,614	851,556,215	502,795,746	2,536,839,997
# local misassemblies	3,002	2,893	5,805	6,273	5,032	15,071	21,298	39,134	19,916	21,993
# 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	186	192	402	406	346	1,190	3,722	1,478	2,882	3,492
# unaligned mis. contigs	121	125	227	234	121	427	373	1,797	386	487
# mismatches	3,272,812	3,334,271	6,796,370	6,846,037	7,157,424	6,777,743	10,400,883	7,526,080	9,828,372	10,614,563
# indels	828,196	847,158	1,596,635	1,600,176	1,786,896	982,489	1,627,153	7,606,136	1,587,445	2,340,084
# indels (≤ 5 bp)	699,210	714,937	1,353,464	1,356,480	1,514,684	802,571	1,319,689	6,918,920	1,301,212	2,030,063
# indels (> 5 bp)	128,986	132,221	243,171	243,696	272,212	179,918	307,464	687,216	286,233	310,021
Indels length	8,643,487	8,775,386	15,848,626	15,967,103	17,532,465	11,222,916	18,804,889	20,607,333	16,839,256	19,460,051

Table 9: Resource usage

Parameter	w2	w2 sfa	w2 YV sfa	w2 YV	w2 frg YV	flye	hifiasm	mdbg	lja	HiCanu
time [s]	28,750.42	27,708.76	33,686.51	34,851.55	35,601.38	79,392.00	62,380.00	830.18	31,693.00	91,623.00
mem [GiB]	111.33	111.25	111.25	111.33	111.33	151.03	115.35	17.07	167.93	48.79
trivial_omnitigs time			351.89	414.19	0.07	N/A	N/A	N/A	N/A	N/A
trivial_omnitigs mem			29.43	29.43	0.00	N/A	N/A	N/A	N/A	N/A
assembly time	23,483.00	22,350.00	22,350.00	23,483.00	23,483.00	79,392.00	62,380.00	830.18	31,693.00	91,623.00
assembly mem	111.33	111.25	111.25	111.33	111.33	151.03	115.35	17.07	167.93	48.79
wtdbg2_extract time	722.42	674.76	674.76	722.42	722.42	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			1,713.86	1,714.94	1,669.89	N/A	N/A	N/A	N/A	N/A
contig_assembly mem			107.12	107.12	107.12	N/A	N/A	N/A	N/A	N/A
wtdbg2_consensus time	4,545.00	4,684.00	8,596.00	8,517.00	9,726.00	N/A	N/A	N/A	N/A	N/A
wtdbg2_consensus mem	6.89	7.33	8.67	8.48	7.23	N/A	N/A	N/A	N/A	N/A

EAxmax

EAxmax

EAxmax

EAxmax

EAxmax

NGAx