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_15kb_37x 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":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 (≥ 0 bp)	2,145	2,916	4,660	4,161	1,895	27,213	33,167	54,391	51,212	54,433
# contigs (≥ 1000 bp)	2,145	2,916	4,659	4,161	1,895	27,202	33,167	54,380	51,212	54,433
# contigs (≥ 5000 bp)	2,111	2,867	4,479	4,033	1,862	27,103	33,167	30,992	49,828	54,433
# contigs (≥ 10000 bp)	1,700	2,247	3,440	3,213	1,560	22,482	33,161	9,315	48,103	54,429
# contigs (≥ 25000 bp)	1,086	1,475	2,357	2,202	1,115	11,529	23,924	2,769	38,563	27,076
# contigs (≥ 50000 bp)	825	1,084	1,787	1,681	931	5,368	10,984	1,814	25,152	11,827

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)	2,710,148,694	2,801,669,904	5,371,774,140	5,385,785,649	5,188,215,705	3,586,681,568	5,982,135,458	3,229,928,771	5,714,819,445	6,164,499,418
Total length (≥ 1000 bp)	2,710,148,694	2,801,669,904	5,371,773,554	5,385,785,649	5,188,215,705	3,586,673,578	5,982,135,458	3,229,921,951	5,714,819,445	6,164,499,418
Total length (≥ 5000 bp)	2,710,004,398	2,801,461,642	5,371,060,560	5,385,260,532	5,188,074,215	3,586,333,893	5,982,135,458	3,141,848,600	5,710,415,920	6,164,499,418
Total length (≥ 10000 bp)	2,707,031,655	2,796,952,119	5,363,547,370	5,379,303,378	5,185,889,382	3,549,328,733	5,982,082,078	2,994,888,908	5,697,544,471	6,164,461,200
Total length (≥ 25000 bp)	2,697,493,053	2,784,932,660	5,346,742,083	5,363,408,623	5,179,018,299	3,371,274,581	5,810,363,497	2,902,098,390	5,525,939,457	5,710,291,578
Total length (≥ 50000 bp)	2,688,295,868	2,771,134,243	5,326,431,829	5,344,883,744	5,172,596,277	3,156,598,088	5,386,943,130	2,869,864,868	5,031,848,459	5,215,123,161

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	2,141	2,912	4,630	4,150	1,891	27,168	33,167	50,609	50,569	54,433
Largest contig	71,027,909	40,119,535	75,540,975	75,540,983	83,372,304	36,480,942	143,473,701	31,618,859	45,644,871	132,523,900
Total length	2,710,138,825	2,801,661,685	5,371,701,742	5,385,757,406	5,188,205,299	3,586,601,896	5,982,135,458	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
GC (%)	40.92	40.85	40.73	40.73	40.68	40.79	40.86	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
N50	14,522,088	9,907,950	15,728,017	16,881,131	25,703,187	2,019,624	2,510,882	3,947,737	260,865	986,873
NG50	11,774,680	8,703,232	24,873,801	26,508,307	42,018,699	2,623,367	68,318,907	4,158,865	504,342	38,046,558
N75	5,752,227	4,170,036	6,434,735	7,167,327	12,061,345	412,757	248,560	1,143,928	97,370	152,908
NG75	3,189,820	2,852,036	17,623,556	19,463,063	29,880,087	1,028,461	32,985,826	1,456,483	342,918	18,172,563
L50	51	83	101	92	58	405	93	211	5,410	309
LG50	65	99	41	38	27	297	16	195	1,727	25
L75	125	191	230	211	133	1,313	3,097	569	14,193	5,132
LG75	191	252	78	71	48	763	32	493	3,601	52
E-size	19,818,283	11,830,470	19,402,212	21,170,711	31,274,608	3,747,979	35,532,978	5,630,435	1,033,660	23,020,671

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	1,037	905	3,167	3,322	2,239	10,615	24,550	10,939	21,969	21,346
# unique misassemblies	957	839	2,206	2,338	1,647	7,724	15,559	7,517	12,650	13,400
# misassembled contigs	449	449	1,475	1,445	741	1,814	1,307	6,400	1,500	1,560
Misassembled contigs length	1,401,181,134	942,776,745	3,636,085,712	3,917,664,938	4,575,290,793	842,057,669	3,102,880,165	1,082,365,816	535,378,803	2,792,253,308
# local misassemblies	2,705	2,721	5,980	6,015	4,588	14,862	22,082	31,026	21,108	22,421
# unique local misassemblies	2,407	2,471	3,638	3,669	2,959	6,716	9,630	18,968	9,073	10,042
# 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	166	162	392	390	314	1,116	3,768	1,528	2,832	3,226
# unaligned mis. contigs	113	116	228	217	130	420	481	1,540	432	525
# unaligned contigs	361+719p	426+866p	835+1986p	733+1838p	346+902p	912+3314p	558+2297p	11149+10522p	442+2993p	1040+2803p
Unaligned length	19,734,000	18,852,746	42,948,792	43,291,998	30,740,825	139,622,427	191,202,834	134,740,112	176,983,395	200,297,559
Genome fraction (%)	91.39	94.55	95.43	95.44	95.04	97.78	98.40	95.78	98.18	98.42
Duplication ratio	1.00	1.00	1.90	1.91	1.85	1.20	2.00	1.10	1.92	2.06
# 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	118.00	117.51	133.26	133.26	121.34	202.45	180.88	242.47	178.70	180.52
# indels per 100 kbp	29.67	29.61	31.13	31.14	29.92	29.68	27.49	187.78	27.59	36.23
Largest alignment	47,921,947	38,189,409	61,464,827	61,464,856	74,394,234	32,046,407	90,496,567	31,574,696	32,050,878	90,221,157
Total aligned length	2,689,347,269	2,781,976,338	5,324,333,078	5,337,800,926	5,154,078,511	3,438,541,411	5,771,642,014	3,081,217,872	5,517,535,823	5,945,192,324
EAmeanmax	12,181,695	9,326,854	13,340,113	14,106,038	16,632,027	3,894,055	29,821,065	4,807,323	1,051,676	24,970,912
Strict EAmeanmax	3,405,595	3,260,999	3,720,871	3,745,386	3,852,047	2,256,757	5,564,594	649,471	473,214	5,296,691
EA50max	8,261,576	7,079,372	9,696,205	10,600,239	11,352,986	2,389,466	25,620,191	3,317,710	228,815	21,929,637
Strict EA50max	2,529,467	2,459,351	2,818,542	2,831,189	2,879,849	1,582,183	4,301,869	493,607	219,118	4,167,533
EA75max	2,368,326	2,387,363	3,216,674	3,278,862	3,792,253	895,996	10,224,387	1,077,309	73,548	7,094,515
Strict EA75max	810,871	889,034	1,004,423	1,027,374	1,055,466	602,162	1,650,652	208,213	71,194	1,526,825
P5k	0.87	0.90	0.91	0.91	0.90	0.93	0.93	0.91	0.93	0.93
P10k	0.87	0.90	0.91	0.91	0.90	0.93	0.93	0.90	0.93	0.93
P15k	0.87	0.90	0.91	0.91	0.90	0.93	0.93	0.90	0.92	0.93
P20k	0.87	0.90	0.91	0.91	0.90	0.92	0.93	0.90	0.91	0.93
Strict P5k	0.87	0.90	0.91	0.91	0.90	0.93	0.93	0.91	0.93	0.93
Strict P10k	0.87	0.90	0.91	0.91	0.90	0.93	0.93	0.90	0.93	0.93
Strict P15k	0.87	0.90	0.91	0.91	0.90	0.92	0.93	0.90	0.92	0.93
Strict P20k	0.86	0.89	0.90	0.90	0.90	0.92	0.93	0.89	0.91	0.93
NGA50	8,261,576	7,079,372	17,209,134	17,693,961	24,294,180	2,389,466	25,620,191	3,376,207	428,635	21,929,637
NGA75	2,368,326	2,387,363	12,938,557	13,513,713	15,869,273	897,039	10,224,387	1,165,405	290,138	7,094,515
LGA50	89	116	61	58	44	331	36	239	2,165	44
LGA75	252	295	113	108	84	855	85	614	4,366	103
EA-size	13,998,976	10,361,645	13,762,202	14,266,271	19,052,790	3,506,248	16,122,283	4,888,781	729,740	13,091,772

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	1,037	905	3,167	3,322	2,239	10,615	24,550	10,939	21,969	21,346
# contig misassemblies	1,037	905	3,167	3,322	2,239	10,615	24,550	10,939	21,969	21,346
# c. relocations	799	670	2,105	2,234	1,582	8,352	18,548	9,854	18,021	17,414
# c. translocations	207	217	1,007	1,026	601	2,205	5,906	1,030	3,868	3,842
# c. inversions	31	18	55	62	56	58	96	55	80	90
# 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	449	449	1,475	1,445	741	1,814	1,307	6,400	1,500	1,560
Misassembled contigs length	1,401,181,134	942,776,745	3,636,085,712	3,917,664,938	4,575,290,793	842,057,669	3,102,880,165	1,082,365,816	535,378,803	2,792,253,308
# local misassemblies	2,705	2,721	5,980	6,015	4,588	14,862	22,082	31,026	21,108	22,421
# 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	166	162	392	390	314	1,116	3,768	1,528	2,832	3,226
# unaligned mis. contigs	113	116	228	217	130	420	481	1,540	432	525
# mismatches	3,173,515	3,269,236	7,095,344	7,113,281	6,254,060	6,961,350	10,439,981	7,470,963	9,859,716	10,732,429
# indels	798,002	823,638	1,657,721	1,662,168	1,542,115	1,020,607	1,586,770	5,785,884	1,522,171	2,153,717
# indels (≤ 5 bp)	670,007	691,596	1,398,491	1,402,268	1,298,838	831,766	1,276,870	5,066,202	1,230,237	1,838,425
# indels (> 5 bp)	127,995	132,042	259,230	259,900	243,277	188,841	309,900	719,682	291,934	315,292
Indels length	8,546,640	8,747,652	16,867,666	16,979,797	16,223,784	11,491,876	18,778,818	19,743,048	16,927,204	19,251,051

Table 9: Resource usage

Parameter	w2	w2 sfa	w2 YV sfa	w2 YV	w2 frg YV	flye	hifiasm	mdbg	lja	HiCanu
time [s]	35,127.96	34,104.22	41,583.72	42,756.64	41,586.22	98,493.00	97,377.00	1,072.00	34,878.00	160,198.00
mem [GiB]	144.05	143.87	143.87	144.05	144.05	199.61	155.84	18.40	168.11	77.63
trivial_omnitigs time			636.64	618.02	0.08	N/A	N/A	N/A	N/A	N/A
trivial_omnitigs mem			40.77	40.77	0.00	N/A	N/A	N/A	N/A	N/A
assembly time	29,305.00	28,160.00	28,160.00	29,305.00	29,305.00	98,493.00	97,377.00	1,072.00	34,878.00	160,198.00
assembly mem	144.05	143.87	143.87	144.05	144.05	199.61	155.84	18.40	168.11	77.63
wtdbg2_extract time	851.96	884.22	884.22	851.96	851.96	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			2,038.86	2,150.66	1,986.18	N/A	N/A	N/A	N/A	N/A
contig_assembly mem			135.71	135.71	135.71	N/A	N/A	N/A	N/A	N/A
wtdbg2_consensus time	4,971.00	5,060.00	9,864.00	9,831.00	9,443.00	N/A	N/A	N/A	N/A	N/A
wtdbg2_consensus mem	6.39	6.76	8.65	8.21	6.69	N/A	N/A	N/A	N/A	N/A

NGAx

NGAx