

Attention: this file was produced automatically, and some statistics might not make sense for certain pipelines.

Revision: b'bigraph@0.7.0-61-ga772b58'

This file contains statistics about the following genome(s):

- D.melanogaster_HiFi_hodeco_simple D.melanogaster_A4xISO1_HiFi24kb "quast_mode":"hicanu_misassemblies","filter_nw":"yes","genome":"D.melanogaster_A4xISO1_HiFi24kb","read_downsampling_factor":"none","homopolymer_compression":"none"

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	hifiasm YVr	hifiasm YVrbp	hifiasm YVp	mdbg	lja	HiCanu
# contigs (≥ 0 bp)	351	456	534	454	338	871	1871	1961	1790	1790	1620	1086	1110
# contigs (≥ 1000 bp)	351	456	534	454	338	866	1871	1961	1790	1790	1619	1086	1110
# contigs (≥ 5000 bp)	346	450	528	450	334	848	1870	1960	1789	1789	1611	891	1110
# contigs (≥ 10000 bp)	309	384	461	409	296	826	1870	1960	1789	1789	1563	732	1110
# contigs (≥ 25000 bp)	170	207	279	263	162	663	1766	1949	1780	1780	337	458	1054
# contigs (≥ 50000 bp)	84	112	169	158	84	467	811	1714	1568	1568	158	252	418

Table 5: QUAST: total length of contigs

Parameter	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)	142532285	142529390	397968422	398214666	234479452	281084814	370546663	604756937	617201172	617201172	207043564	303203818	334207136
Total length (≥ 1000 bp)	142532285	142529390	397968422	398214666	234479452	281081253	370546663	604756937	617201172	617201172	207043370	303203818	334207136
Total length (≥ 5000 bp)	142515992	142508429	397944194	398198717	234463503	281028825	370544201	604754475	617198710	617198710	207019512	302614531	334207136
Total length (≥ 10000 bp)	142207545	141958323	397403806	397870929	234159393	280861409	370544201	604754475	617198710	617198710	206626174	301450501	334207136
Total length (≥ 25000 bp)	139894833	139069829	394395514	395404908	231906950	278059008	368209985	604509013	616992426	616992426	188088663	297061042	332934376
Total length (≥ 50000 bp)	136928624	135848711	390506809	391691123	229243272	271008234	333526354	595194237	608586076	608586076	182172828	289616263	311235346

Table 6: QUAST: statistics for contigs ≥ 500 bp (or 3000bp for QUAST-LG)

Parameter	w2	w2 sfa	w2 YV sfa	w2 YV	w2 frg YV	flye	hifiasm	hifiasm YVr	hifiasm YVrbp	hifiasm YVp	mdbg	lja	HiCanu
# contigs	349	454	534	454	338	856	1870	1960	1789	1789	1615	980	1110
Largest contig	28533319	19897903	31629042	31628861	41677316	6795812	28128476	5098457	7394039	7394039	16458486	26917114	24409699
Total length	142527482	142524587	397968422	398214666	234479452	281060204	370544201	604754475	617198710	617198710	207035340	302963068	334207136
Reference length	137567484	137567484	137567484	137567484	137567484	137567484	137567484	137567484	137567484	137567484	137567484	137567484	137567484
GC (%)	42.09	42.07	42.17	42.17	41.93	41.73	41.48	41.61	41.34	41.34	41.30	41.53	41.37
Reference GC (%)	42.08	42.08	42.08	42.08	42.08	42.08	42.08	42.08	42.08	42.08	42.08	42.08	42.08
N50	18085012	8498462	14643909	14976343	23762707	1047285	3170105	728250	834270	834270	5398449	7248900	7217842
NG50	19897891	8498462	23685706	24010255	28542124	2268715	25819223	1911915	3297919	3297919	9652363	17808992	21898700
N75	5899208	4271473	10973854	14097987	21910664	514870	311336	295407	352147	352147	557885	2458514	1717026
NG75	14905921	4350705	19959847	23685706	23762707	1620739	24576786	1545331	2467479	2467479	5398449	11653815	20135459
L50	4	5	10	9	4	67	15	238	191	191	11	11	11
LG50	3	5	3	3	2	20	3	25	15	15	6	3	3
L75	6	11	17	16	7	164	118	552	466	466	50	28	36
LG75	5	10	5	4	4	38	4	46	27	27	11	6	5
E-size	16276394	10112438	15358034	16972976	23364318	1618454	10129664	959573	1366458	1366458	6012759	10468747	10155151

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

Parameter	w2	w2 sfa	w2 YV sfa	w2 YV	w2 frg YV	flye	hifiasm	hifiasm YVr	hifiasm YVrbp	hifiasm YVp	mdbg	lja	HiCanu
# misassemblies	0	0	14	19	4	5	3	6	9	9	1	2	1
# unique misassemblies	0	0	13	16	4	5	3	4	5	5	1	2	1
# misassembled contigs	0	0	14	18	4	5	2	6	7	7	1	2	1
Misassembled contigs length	0	0	98095111	99913719	90005545	4732020	27480110	1969227	6529367	6529367	741261	11745117	23498506
# local misassemblies	318	295	828	846	537	292	401	547	528	528	1347	395	380
# unique local misassemblies	318	295	469	484	381	282	359	356	358	358	1344	355	360
# 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	2	2	2	2	2	2	2	0	0	0	2	0	2
# unaligned mis. contigs	3	1	2	2	4	20	10	23	22	22	8	6	8
# unaligned contigs	268+52p	333+76p	370+127p	310+115p	265+54p	231+191p	757+299p	720+482p	580+455p	580+455p	1471+87p	779+89p	685+134p
Unaligned length	14132283	13928985	26475123	26582493	17622086	47068880	89995770	127806628	144823128	144823128	66974864	63587555	83427372
Genome fraction (%)	91.960	92.171	92.902	92.872	92.445	96.540	97.324	95.420	95.361	95.361	88.703	96.711	97.080
Duplication ratio	1.019	1.018	2.917	2.919	1.711	1.768	2.103	3.646	3.614	3.614	1.152	1.806	1.885
# 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	329.86	328.86	343.47	343.09	369.18	291.62	305.85	300.14	298.00	298.00	252.06	288.59	281.13
# indels per 100 kbp	78.32	77.80	80.15	80.26	83.85	51.74	53.85	52.67	52.03	52.03	271.51	51.98	54.31
Largest alignment	27883671	19392861	23182174	27868243	27863849	6225533	26077520	5097052	5097052	5097052	14412967	26749443	24372115
Total aligned length	128340289	128551258	371348879	371463204	216674202	233867072	280113718	476487275	472145540	472145540	139988033	238902397	250556642
EAmearmax	15640457	9733945	12227574	16096527	17828559	1765987	15813336	1540121	1540327	1540327	5942796	10990526	16842834
Strict EAmearmax	803959	821601	894111	885122	859863	1197779	4562008	1201876	1202210	1202210	179562	4386589	4408802
EA50max	17459538	8292864	14315984	20112482	21941267	1011661	20140010	1309067	1309067	1309067	5409123	9893263	20378876
Strict EA50max	673799	709965	715962	715962	715358	756879	2594722	1110696	1110696	1110696	123358	2458514	2910474
EA75max	5450936	3908607	5607067	11192877	14317358	462633	6795652	772888	772888	772888	1142098	2458514	18554192
Strict EA75max	267953	259811	301776	295492	285964	318481	1228573	578144	578144	578144	57640	1228571	1163025
P5k	0.916	0.918	0.926	0.925	0.921	0.962	0.970	0.951	0.950	0.950	0.884	0.964	0.967
P10k	0.916	0.918	0.926	0.925	0.921	0.962	0.970	0.951	0.950	0.950	0.884	0.964	0.967
P15k	0.916	0.918	0.926	0.925	0.921	0.962	0.970	0.951	0.950	0.950	0.884	0.964	0.967
P20k	0.916	0.918	0.926	0.925	0.921	0.962	0.970	0.951	0.950	0.950	0.884	0.964	0.967
Strict P5k	0.916	0.918	0.926	0.925	0.921	0.962	0.970	0.951	0.950	0.950	0.884	0.964	0.967
Strict P10k	0.916	0.918	0.926	0.925	0.921	0.962	0.970	0.951	0.950	0.950	0.884	0.964	0.967
Strict P15k	0.916	0.918	0.925	0.925	0.921	0.962	0.970	0.951	0.950	0.950	0.884	0.964	0.967
Strict P20k	0.916	0.918	0.925	0.925	0.921	0.962	0.970	0.951	0.950	0.950	0.884	0.963	0.967
NGA50	17459538	8292864	19468969	22938830	22873621	1957438	23921119	1798846	1798846	1798846	6319289	17799519	20378876
NGA75	5450936	3908607	19448930	20104994	21931624	1143509	14781569	1449957	1449957	1449957	1609587	10179335	18554192
LGA50	4	5	4	3	3	23	26	26	26	26	8	3	4
LGA75	6	11	5	5	5	47	5	48	48	48	16	6	5
EA-size	17024173	10564856	13947360	15575217	19848410	1540884	10857647	1040463	1046744	1046744	6413038	11078452	11085585

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

Parameter	w2	w2 sfa	w2 YV sfa	w2 YV	w2 frg YV	flye	hifiasm	hifiasm YVr	hifiasm YVrbp	hifiasm YVp	mdbg	lja	HiCanu
# misassemblies	0	0	14	19	4	5	3	6	9	9	1	2	1
# contig misassemblies	0	0	14	19	4	5	3	6	9	9	1	2	1
# c. relocations	0	0	2	5	0	1	1	0	2	2	0	1	1
# c. translocations	0	0	2	4	1	1	0	1	1	1	0	0	0
# c. inversions	0	0	10	10	3	3	2	5	6	6	1	1	0
# scaffold misassemblies	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
# s. translocations	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
# misassembled contigs	0	0	14	18	4	5	2	6	7	7	1	2	1
Misassembled contigs length	0	0	98095111	99913719	90005545	4732020	27480110	1969227	6529367	6529367	741261	11745117	23498506
# local misassemblies	318	295	828	846	537	292	401	547	528	528	1347	395	380
# 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	2	2	2	2	2	2	2	0	0	0	2	0	2
# unaligned mis. contigs	3	1	2	2	4	20	10	23	22	22	8	6	8
# mismatches	423344	422759	1275463	1274470	799908	682014	856715	1430146	1406975	1406975	352860	689442	704380
# indels	100515	100008	297644	298121	181687	121008	150832	250976	245640	245640	380081	124185	136074
# indels (≤ 5 bp)	78908	78395	233846	234328	142492	81455	101982	168685	165397	165397	348797	83517	94132
# indels (> 5 bp)	21607	21613	63798	63793	39195	39553	48850	82291	80243	80243	31284	40668	41942
Indels length	3256273	3287953	9641039	9587208	5711001	5023127	6136551	10372501	10219780	10219780	2388610	5548890	5765567





















































