

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

Revision: b'omnitigs@0.6.1-27-gaf4f666'

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

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

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)	414	579	950	838	403	873	437	1961	1790	1790	1637	1086	1110
# contigs (≥ 1000 bp)	414	579	950	838	403	869	437	1961	1790	1790	1636	1086	1110
# contigs (≥ 5000 bp)	407	568	932	825	393	851	436	1960	1789	1789	1622	891	1110
# contigs (≥ 10000 bp)	337	446	720	672	331	829	436	1960	1789	1789	1576	732	1110
# contigs (≥ 25000 bp)	196	255	427	416	192	666	435	1949	1780	1780	345	458	1054
# contigs (≥ 50000 bp)	106	136	266	258	108	468	311	1714	1568	1568	161	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)	144174655	143256029	429969173	433005696	159733577	281064480	280147763	604756937	617201172	617201172	207071689	303203857	334207136
Total length (≥ 1000 bp)	144174655	143256029	429969173	433005696	159733577	281061582	280147763	604756937	617201172	617201172	207071507	303203857	334207136
Total length (≥ 5000 bp)	144150470	143213915	429901856	432955683	159695077	281009154	280145301	604754475	617198710	617198710	207023078	302614568	334207136
Total length (≥ 10000 bp)	143648701	142349156	428340403	431805727	159237870	280841738	280145301	604754475	617198710	617198710	206638389	301450539	334207136
Total length (≥ 25000 bp)	141198178	139203910	423611900	427561874	156820777	278073270	280121888	604509013	616992426	616992426	188043161	297061079	332934376
Total length (≥ 50000 bp)	138164287	135076627	417998645	422034780	153958810	270938452	275440003	595194237	608586076	608586076	181940053	289616297	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	413	578	948	837	402	859	436	1960	1789	1789	1632	980	1110
Largest contig	28519045	27858007	55743107	55753412	28514707	6795812	28128476	5098457	7394039	7394039	16460783	26917115	24409699
Total length	144172199	143253628	429965265	433002746	159731121	281040533	280145301	604754475	617198710	617198710	207063477	302963106	334207136
Reference length	137567484	137567484	137567484	137567484	137567484	137567484	137567484	137567484	137567484	137567484	137567484	137567484	137567484
GC (%)	42.04	42.04	42.05	42.03	41.96	41.73	41.71	41.61	41.34	41.34	41.31	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	19993503	5960472	12024517	13318571	15092921	1026517	12634472	728250	834270	834270	4485182	7248900	7217842
NG50	19993503	5960472	28509526	28514699	20000589	2268715	25819223	1911915	3297919	3297919	9652101	17808989	21898700
N75	5662636	2837120	5678826	7014908	5672284	518623	1456122	295407	352147	352147	558292	2458516	1717026
NG75	5666668	4331407	19924359	19929364	7159540	1567458	24576786	1545331	2467479	2467479	4485182	11653821	20135459
L50	3	5	10	10	4	68	7	238	191	191	11	11	11
LG50	3	5	2	2	3	20	3	25	15	15	6	3	3
L75	7	13	22	20	8	165	25	552	466	466	51	28	36
LG75	6	11	3	3	6	39	4	46	27	27	11	6	5
E-size	15893803	11217556	17220644	17542012	14826599	1608714	13230978	959573	1366458	1366458	5925851	10468749	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	3	1	18	18	7	5	3	6	9	9	1	2	1
# unique misassemblies	2	1	15	15	7	5	3	4	5	5	1	2	1
# misassembled contigs	3	1	18	18	7	5	2	6	7	7	1	2	1
Misassembled contigs length	20384017	173309	107318473	111185871	30725990	4736386	27480110	1969227	6529367	6529367	741369	11745123	23498506
# local misassemblies	293	264	871	916	371	289	360	547	528	528	1351	397	380
# unique local misassemblies	293	264	521	550	329	280	329	356	358	358	1348	356	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	0	0	2	2	0	2	2	0	0	0	0	0	2
# unaligned mis. contigs	2	1	3	4	2	20	6	23	22	22	8	6	8
# unaligned contigs	315+67p	436+86p	703+193p	594+195p	302+74p	232+193p	194+127p	720+482p	580+455p	580+455p	1480+94p	779+89p	685+134p
Unaligned length	14464418	14648592	34693908	34394351	16637549	47142661	52112905	127806628	144823128	144823128	66950176	63166278	83427372
Genome fraction (%)	92.606	91.921	93.066	93.496	92.717	96.522	96.103	95.420	95.361	95.361	88.582	96.713	97.080
Duplication ratio	1.022	1.021	3.098	3.110	1.126	1.768	1.731	3.646	3.614	3.614	1.154	1.809	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	297.97	311.72	329.50	328.16	292.18	291.36	303.00	300.14	298.00	298.00	256.56	288.62	281.13
# indels per 100 kbp	77.27	76.94	78.27	78.31	75.37	51.69	50.73	52.67	52.03	52.03	271.94	52.03	54.31
Largest alignment	27898395	27331482	28110048	28099838	28109305	6225533	26077520	5097052	5097052	5097052	14423060	26742518	24372115
Total aligned length	129593949	128531150	394956113	398203654	142897075	233738882	227614773	476487275	472145540	472145540	140019672	239362224	250556642
EAmearmax	15597834	10989862	12537850	13716218	15691750	1765817	15801460	1540121	1540327	1540327	5854918	10990619	16842834
Strict EAmearmax	909479	852042	936157	926639	841227	1199028	4545272	1201876	1202210	1202210	178131	3442110	4408802
EA50max	19613700	5849663	11733152	13197902	19435977	1011676	20140010	1309067	1309067	1309067	5421838	9893317	20378876
Strict EA50max	791991	788384	883076	851279	761423	756879	2594722	1110696	1110696	1110696	122062	2458516	2910474
EA75max	5315822	2815288	5069366	6559203	6526004	462633	6795652	772888	772888	772888	1037082	2458516	18554192
Strict EA75max	269550	261791	317633	317633	274437	320846	1163093	578144	578144	578144	57067	1228571	1163025
P5k	0.923	0.916	0.927	0.932	0.924	0.962	0.958	0.951	0.950	0.950	0.883	0.964	0.967
P10k	0.923	0.916	0.927	0.932	0.924	0.962	0.958	0.951	0.950	0.950	0.883	0.964	0.967
P15k	0.923	0.916	0.927	0.932	0.924	0.962	0.958	0.951	0.950	0.950	0.883	0.964	0.967
P20k	0.923	0.916	0.927	0.932	0.924	0.962	0.958	0.951	0.950	0.950	0.883	0.964	0.967
Strict P5k	0.923	0.916	0.927	0.932	0.924	0.962	0.958	0.951	0.950	0.950	0.883	0.964	0.967
Strict P10k	0.923	0.916	0.927	0.932	0.924	0.962	0.958	0.951	0.950	0.950	0.883	0.964	0.967
Strict P15k	0.923	0.916	0.927	0.932	0.924	0.962	0.958	0.951	0.950	0.950	0.883	0.964	0.967
Strict P20k	0.922	0.916	0.927	0.932	0.923	0.962	0.958	0.951	0.950	0.950	0.882	0.964	0.967
NGA50	19613700	5849663	27300933	27316359	19435977	1932516	23921119	1798846	1798846	1798846	6319404	17799516	20378876
NGA75	5539348	2885169	19430536	19605786	6526004	1133801	14781569	1449957	1449957	1449957	1464421	10179341	18554192
LGA50	3	5	3	3	3	23	3	26	26	26	8	3	4
LGA75	6	12	5	5	6	47	5	48	48	48	17	6	5
EA-size	16821523	11949865	13898496	14267170	15602516	1538115	13278879	1040463	1046744	1046744	6319089	11144029	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	3	1	18	18	7	5	3	6	9	9	1	2	1
# contig misassemblies	3	1	18	18	7	5	3	6	9	9	1	2	1
# c. relocations	0	0	5	5	1	1	1	0	2	2	0	1	1
# c. translocations	0	0	5	5	1	1	0	1	1	1	0	0	0
# c. inversions	3	1	8	8	5	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	3	1	18	18	7	5	2	6	7	7	1	2	1
Misassembled contigs length	20384017	173309	107318473	111185871	30725990	4736386	27480110	1969227	6529367	6529367	741369	11745123	23498506
# local misassemblies	293	264	871	916	371	289	360	547	528	528	1351	397	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	0	0	2	2	0	2	2	0	0	0	0	0	2
# unaligned mis. contigs	2	1	3	4	2	20	6	23	22	22	8	6	8
# mismatches	386152	400660	1301398	1306732	417515	681014	689665	1430146	1406975	1406975	359230	690841	704380
# indels	100137	98886	309140	311823	107707	120824	115476	250976	245640	245640	380766	124551	136074
# indels (≤ 5 bp)	78456	77304	240516	242958	84088	81347	77661	168685	165397	165397	349314	83782	94132
# indels (> 5 bp)	21681	21582	68624	68865	23619	39477	37815	82291	80243	80243	31452	40769	41942
Indels length	3475828	3428353	10654051	10802277	3772341	5023576	5044155	10372501	10219780	10219780	2380153	5604087	5765567





















































