

**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\_hoco D.melanogaster\_A4xISO1\_HiFi24kb "quast\_mode":"hicanu\_misassemblies","filter\_nw":"yes","genome":"D.melanogaster\_A4xISO1\_HiFi24kb","homopolymer\_compression":"yes","read\_downsampling\_factor":"none","uniquify

Table 1: Genome Graph Statistics

Table 2: Algorithm Statistics

Parameter
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Table 3: ContigValidator

Parameter
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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 ( $\geq 0$ bp)	331	445	568	474	323	763	172	1189	774	774	1582	1049	1110
# contigs ( $\geq 1000$ bp)	331	444	568	474	323	763	172	1189	774	774	1581	1049	1110
# contigs ( $\geq 5000$ bp)	321	426	551	464	312	758	172	1189	774	774	1558	817	1110
# contigs ( $\geq 10000$ bp)	252	304	407	378	241	739	172	1189	774	774	943	634	1110
# contigs ( $\geq 25000$ bp)	117	141	233	229	116	582	169	1170	762	762	188	363	640
# contigs ( $\geq 50000$ bp)	63	76	150	148	62	435	86	937	582	582	109	171	207

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 ( $\geq 0$ bp)	95398488	99852594	206238421	229322134	173202282	199296544	118211012	349699795	313725498	313725498	138906824	212881219	234952683
Total length ( $\geq 1000$ bp)	95398488	99851692	206238421	229322134	173202282	199296544	118211012	349699795	313725498	313725498	138906630	212881219	234952683
Total length ( $\geq 5000$ bp)	95366913	99790779	206181354	229292948	173168232	199281274	118211012	349699795	313725498	313725498	138831907	212187204	234952683
Total length ( $\geq 10000$ bp)	94844575	98902825	205113202	228635095	172628325	199129495	118211012	349699795	313725498	313725498	133455489	210835405	234952683
Total length ( $\geq 25000$ bp)	92580392	96325968	202286647	226120559	170505354	196219806	118147990	349304347	313475156	313475156	122915947	206475793	225429248
Total length ( $\geq 50000$ bp)	90721561	94055948	199458516	223323690	168656351	190819459	115007145	340327503	306533583	306533583	120344566	199766529	210123559

Table 6: QUAST: statistics for contigs  $\geq 500$ 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	327	438	562	469	318	761	172	1189	774	774	1573	925	1110
Largest contig	20107902	14531035	16709540	20099224	29127551	3818276	19947077	4640061	10104373	10104373	12908506	18985180	17132268
Total length	95391526	99839518	206227531	229313636	173193784	199294152	118211012	349699795	313725498	313725498	138890588	212615207	234952683
Reference length	96857709	96857709	96857709	96857709	96857709	96857709	96857709	96857709	96857709	96857709	96857709	96857709	96857709
GC (%)	46.53	46.57	46.52	46.56	46.55	46.34	45.89	46.08	46.01	46.01	45.84	46.07	45.87
Reference GC (%)	46.58	46.58	46.58	46.58	46.58	46.58	46.58	46.58	46.58	46.58	46.58	46.58	46.58
N50	10036599	9400473	10033784	14522764	15873771	731784	15389360	874562	2438774	2438774	4508115	5885951	4816137
NG50	10036599	9903743	11622349	16697856	20108724	1352699	17243526	2164932	7352123	7352123	8704692	12467834	15355488
N75	4144127	3845696	4508765	7723140	10469069	332485	6637176	317041	546005	546005	450707	1679919	1212055
NG75	3872461	3845696	10302075	16495899	16610537	1055110	15151919	1734155	5629860	5629860	4313730	8215565	14259904
L50	4	5	9	7	5	74	4	118	34	34	8	10	12
LG50	4	4	4	3	2	23	3	17	6	6	5	3	3
L75	6	8	15	13	8	176	6	282	96	96	37	29	36
LG75	7	8	6	5	4	43	5	30	10	10	9	6	5
E-size	10742821	8168361	8841706	11279142	16062073	1011268	13721508	1086478	3206216	3206216	5353075	7351127	7134569

Table 7: QUASt: alignment statistics for contigs  $\geq 500$ 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	8	8	5	16	1	10	5	5	0	1	0
# unique misassemblies	0	0	8	8	4	15	1	4	3	3	0	1	0
# misassembled contigs	0	0	8	8	5	16	1	10	5	5	0	1	0
Misassembled contigs length	0	0	3785552	37853350	63460230	11889527	19947077	6230091	6567651	6567651	0	64601	0
# local misassemblies	279	265	617	691	508	266	202	452	484	484	1088	366	346
# unique local misassemblies	279	265	376	402	353	254	199	343	372	372	1086	330	326
# 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	0	0	0	0	0	0	0	0
# unaligned mis. contigs	1	3	3	2	2	15	3	22	10	10	6	7	8
# unaligned contigs	260+44p	351+60p	410+113p	324+109p	257+45p	180+213p	141+28p	555+342p	386+205p	386+205p	1482+63p	749+76p	796+90p
Unaligned length	11376766	11487945	22334648	23472149	14486518	36444285	31949901	84189081	65332484	65332484	47509730	47676235	64726746
Genome fraction (%)	85.735	90.217	90.923	90.965	91.226	96.310	88.567	95.025	96.475	96.475	86.038	96.458	96.853
Duplication ratio	1.012	1.011	2.088	2.336	1.796	1.746	1.006	2.885	2.658	2.658	1.097	1.765	1.815
# 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	187.09	173.79	177.52	180.64	190.19	169.93	133.50	157.10	151.08	151.08	100.71	157.84	166.15
# indels per 100 kbp	581.13	585.68	578.35	579.55	609.09	569.37	541.39	577.92	555.32	555.32	544.10	567.38	563.30
Largest alignment	19617570	13769845	15583026	19607552	19639939	3146890	17903256	4616505	10098821	10098821	10502352	18872984	17106868
Total aligned length	83916054	88278093	183745289	205643795	158536401	162795726	86117224	265416751	248179534	248179534	91346009	164662315	170073297
EAmearmax	9525967	7597276	8727446	11583033	12196333	924414	12384941	1656882	4418514	4418514	4929454	7742856	11663020
Strict EAmearmax	550927	578244	623653	609301	598827	707601	1256015	1196620	2034314	2034314	132078	3118628	2738398
EA50max	9505060	9030758	9990824	13853031	15464124	711505	15316056	1321659	3823669	3823669	5676826	6974717	13628452
Strict EA50max	467235	485775	520324	511392	520324	509416	757222	875891	1430062	1430062	90777	1711430	1938456
EA75max	891194	2710589	2704940	3677160	9850372	332155	13392937	570039	1035226	1035226	814215	1711430	13123991
Strict EA75max	130445	186417	205810	199440	196754	230562	247698	386859	509928	509928	43081	944297	823969
P5k	0.857	0.902	0.909	0.910	0.912	0.963	0.886	0.950	0.965	0.965	0.860	0.965	0.969
P10k	0.857	0.902	0.909	0.910	0.912	0.963	0.886	0.950	0.965	0.965	0.860	0.965	0.969
P15k	0.857	0.902	0.909	0.910	0.912	0.963	0.886	0.950	0.965	0.965	0.860	0.965	0.969
P20k	0.857	0.902	0.909	0.910	0.912	0.963	0.886	0.950	0.965	0.965	0.860	0.965	0.969
Strict P5k	0.857	0.902	0.909	0.910	0.912	0.963	0.886	0.950	0.965	0.965	0.860	0.965	0.968
Strict P10k	0.857	0.902	0.909	0.910	0.912	0.963	0.886	0.950	0.965	0.965	0.860	0.965	0.968
Strict P15k	0.857	0.902	0.909	0.910	0.912	0.963	0.886	0.950	0.965	0.965	0.860	0.965	0.968
Strict P20k	0.856	0.902	0.909	0.910	0.912	0.963	0.886	0.950	0.965	0.965	0.860	0.965	0.968
NGA50	9505060	9030758	11297503	15586196	15464124	1044847	15316056	1914329	6384228	6384228	5712463	10317890	13628452
NGA75	1214195	2710589	9642022	15382888	15344501	737294	13392937	1458743	4813312	4813312	1228864	7022003	13123991
LGA50	4	5	4	3	3	31	3	18	7	7	6	4	4
LGA75	8	9	6	5	5	59	5	32	11	11	14	6	5
EA-size	11104530	8417170	8663386	11057007	13576939	859360	13919259	1194504	3331458	3331458	5567966	7767021	7831887

Table 8: QUASt: misassembly statistics for contigs  $\geq 500$ 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	8	8	5	16	1	10	5	5	0	1	0
# contig misassemblies	0	0	8	8	5	16	1	10	5	5	0	1	0
# c. relocations	0	0	0	0	0	2	0	0	0	0	0	0	0
# c. translocations	0	0	1	1	2	12	0	4	2	2	0	0	0
# c. inversions	0	0	7	7	3	2	1	6	3	3	0	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	8	8	5	16	1	10	5	5	0	1	0
Misassembled contigs length	0	0	3785552	37853350	63460230	11889527	19947077	6230091	6567651	6567651	0	64601	0
# local misassemblies	279	265	617	691	508	266	202	452	484	484	1088	366	346
# 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	0	0	0	0	0	0	0	0
# unaligned mis. contigs	1	3	3	2	2	15	3	22	10	10	6	7	8
# mismatches	156998	153420	326186	371472	301527	276645	114969	416965	374938	374938	91998	259897	282580
# indels	487665	517028	1062692	1191806	965626	926910	466226	1533908	1378199	1378199	497012	934264	958015
# indels ( $\leq 5$ bp)	472651	501010	1030501	1155466	934871	898757	452796	1486086	1337970	1337970	484302	905900	929130
# indels ( $> 5$ bp)	15014	16018	32191	36340	30755	28153	13430	47822	40229	40229	12710	28364	28885
Indels length	2445661	2616469	5453517	6129826	4958520	4208452	2243372	7341431	6799216	6799216	1761295	4592891	4652866



























































