

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

**Revision:** b'bigraph-v0.2.0-313-g0a90677'

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

- D.melanogaster\_ISO1 D.melanogaster\_ISO1 'genome':"D.melanogaster\_ISO1","assembler":"wtDBG2":"cli\_arguments":"-x":"ont"

Table 1: Genome Graph Statistics

Table 2: Algorithm Statistics

Parameter	Y-to-V sfa	wtDBG2 sfa	Y-to-V frg	Y-to-V	wtDBG2
min non-trivial omnitigs per macrotig	N/A	N/A	N/A	N/A	N/A
max non-trivial omnitigs per macrotig	N/A	N/A	N/A	N/A	N/A
median non-trivial omnitigs per macrotig	N/A	N/A	N/A	N/A	N/A
mean non-trivial omnitigs per macrotig	N/A	N/A	N/A	N/A	N/A
min edge length	1	N/A	1	N/A	N/A
max edge length	25342	N/A	25342	N/A	N/A
median edge length	3	N/A	3	N/A	N/A
mean edge length	101.9	N/A	101.9	N/A	N/A

Table 3: ContigValidator

Parameter	Y-to-V sfa	wtDBG2 sfa	Y-to-V frg	Y-to-V	wtDBG2
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Table 4: QUAST: # of contigs

Parameter	Y-to-V sfa	wtdbg2 sfa	Y-to-V	frg Y-to-V	wtdbg2
# contigs ( $\geq 0$ bp)	1144	909	915	629	632
# contigs ( $\geq 1000$ bp)	1142	906	915	629	632
# contigs ( $\geq 5000$ bp)	974	746	824	545	543
# contigs ( $\geq 10000$ bp)	690	488	646	395	398
# contigs ( $\geq 25000$ bp)	389	247	393	207	212
# contigs ( $\geq 50000$ bp)	249	137	240	110	110

Table 5: QUAST: total length of contigs

Parameter	Y-to-V sfa	wtdbg2 sfa	Y-to-V	frg Y-to-V	wtdbg2
Total length ( $\geq 0$ bp)	246944249	134018566	245456117	141162677	136350953
Total length ( $\geq 1000$ bp)	246943011	134017222	245456117	141162677	136350953
Total length ( $\geq 5000$ bp)	246341054	133443828	245130337	140856056	136042809
Total length ( $\geq 10000$ bp)	244311817	131596421	243816156	139753162	134980727
Total length ( $\geq 25000$ bp)	239437563	127724980	239669982	136662080	131993068
Total length ( $\geq 50000$ bp)	234490421	123855044	234250230	133194877	128451920

Table 6: QUAST: statistics for contigs  $\geq 500$ bp (or 3000bp for QUAST-LG)

Parameter	Y-to-V sfa	wtdbg2 sfa	Y-to-V	frg Y-to-V	wtdbg2
# contigs	1092	861	886	605	602
Largest contig	31983088	13508885	31983106	23174436	23174440
Total length	246828682	133916153	245386900	141106420	136282945
Reference length	143726002	143726002	143726002	143726002	143726002
GC (%)	41.54	41.59	41.47	41.44	41.50
Reference GC (%)	42.01	42.01	42.01	42.01	42.01
N50	6540983	4906368	7065626	10621105	12019776
NG50	11948672	4171361	12769546	10621105	10619765
N75	1985379	1344728	2138745	2150356	1979102
NG75	10707151	816123	10707160	1979109	1344714
L50	9	8	8	5	4
LG50	4	9	4	5	5
L75	25	22	22	12	11
LG75	7	29	7	13	14

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

Parameter	Y-to-V sfa	wtdbg2 sfa	Y-to-V	frg Y-to-V	wtdbg2
# misassemblies	255	87	278	129	120
# unique misassemblies	178	87	202	124	120
# misassembled contigs	128	50	130	44	41
Misassembled contigs length	184881985	71581164	199395387	112856707	107884976
# local misassemblies	2294	1175	2291	1336	1231
# unique local misassemblies	1550	1174	1548	1281	1230
# scaffold gap ext. mis.	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0
# possible TEs	40	18	42	28	22
# unaligned mis. contigs	111	75	108	71	68
# unaligned contigs	517+537p	474+333p	410+447p	372+217p	370+215p
Unaligned length	21618977	13262558	23463095	16367633	15490849
Genome fraction (%)	86.547	85.580	84.419	85.641	85.679
Duplication ratio	1.825	0.989	1.844	1.022	0.989
# N's per 100 kbp	0.00	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	436.28	448.32	437.41	445.24	449.37
# indels per 100 kbp	1167.96	1176.35	1168.14	1177.34	1177.09
Largest alignment	11809134	8940712	11807717	12215745	12215178
Total aligned length	225083888	120618008	221796893	124648808	120757238
EA50max	2648366	2287235	2285494	2725102	2291323
Strict EA50max	231391	230722	221978	221140	223532
NGA50	5068803	2006239	5068380	2725102	2291323
EA75max	410656	394468	286145	613735	613735
Strict EA75max	56955	52212	47609	54115	54678
NGA75	4523949	289300	4523816	698247	538547
LGA50	10	17	10	14	14
LGA75	17	55	17	40	42

Table 8: QUASt: misassembly statistics for contigs  $\geq 500$ bp (or 3000bp for QUASt-LG)

Parameter	Y-to-V sfa	wtdbg2 sfa	Y-to-V	frg Y-to-V	wtdbg2
# misassemblies	255	87	278	129	120
# contig misassemblies	255	87	278	129	120
# c. relocations	179	56	196	95	90
# c. translocations	72	31	78	33	29
# c. inversions	4	0	4	1	1
# scaffold misassemblies	0	0	0	0	0
# s. relocations	0	0	0	0	0
# s. translocations	0	0	0	0	0
# s. inversions	0	0	0	0	0
# misassembled contigs	128	50	130	44	41
Misassembled contigs length	184881985	71581164	199395387	112856707	107884976
# local misassemblies	2294	1175	2291	1336	1231
# scaffold gap ext. mis.	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0
# mis. caused by frag. ref.	0	0	0	0	0
# possible TEs	40	18	42	28	22
# unaligned mis. contigs	111	75	108	71	68
# mismatches	981995	540751	970166	554982	542646
# indels	2628882	1418886	2590902	1467541	1421416
# indels ( $\leq 5$ bp)	2617300	1412494	2579488	1461014	1414981
# indels ( $> 5$ bp)	11582	6392	11414	6527	6435
Indels length	3282765	1776183	3234445	1823007	1781632

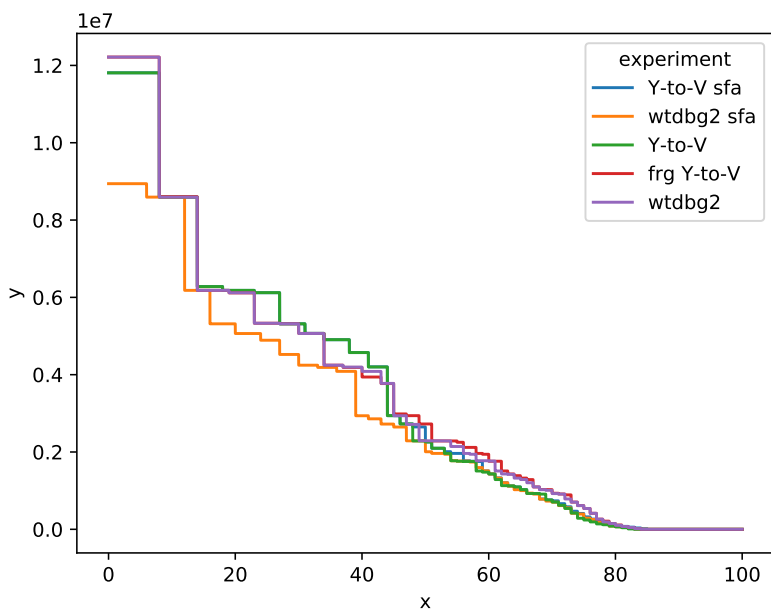


Figure 1: EAxmax

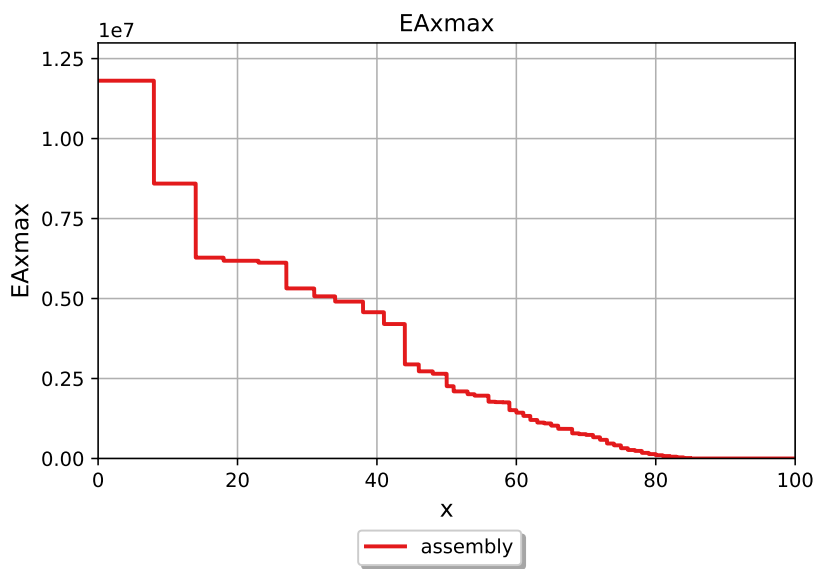


Figure 2: QUAST EAxmax graph for Y-to-V sfa

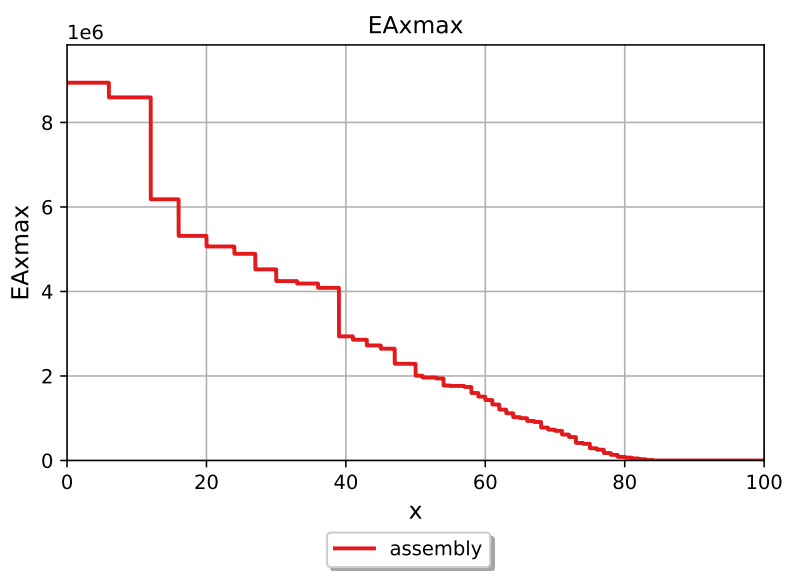


Figure 3: QUAST EAxmax graph for wtdbg2 sfa

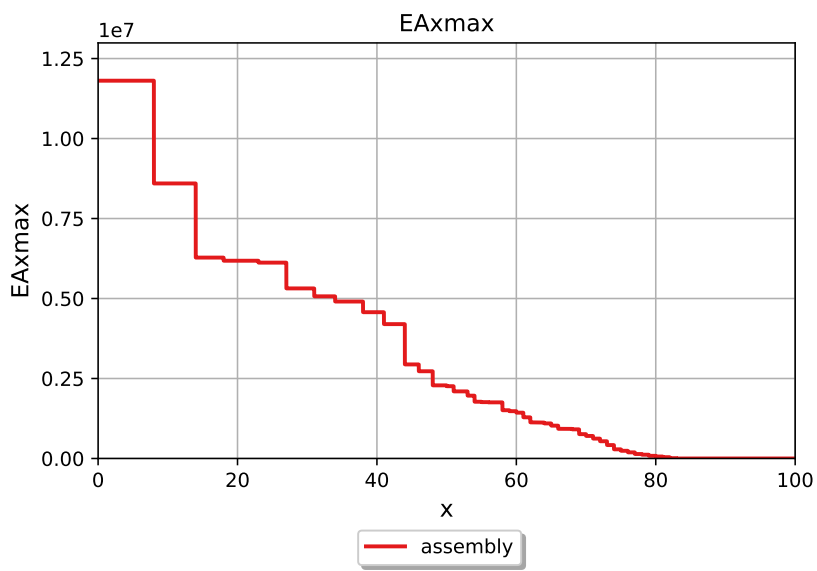


Figure 4: QUAST EAxmax graph for Y-to-V

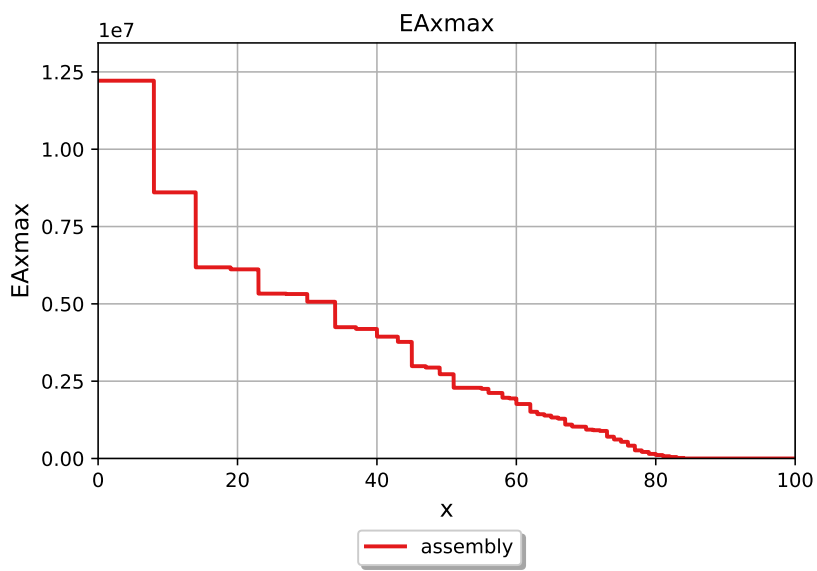


Figure 5: QUAST EAxmax graph for frg Y-to-V



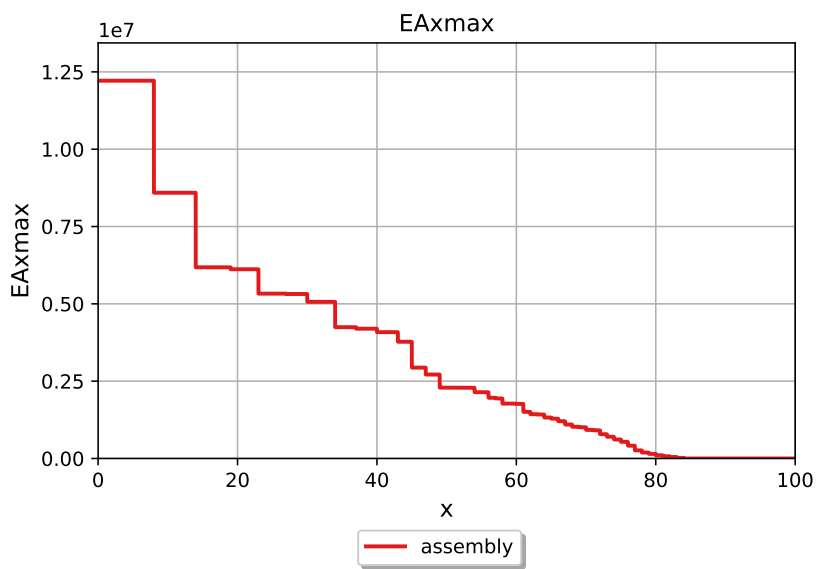


Figure 6: QUAST EAxmax graph for wtdbg2

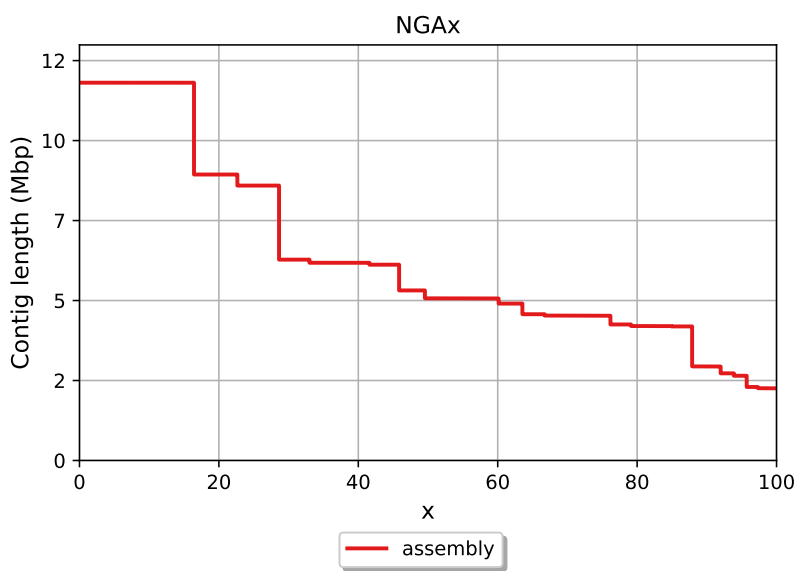


Figure 7: QUAST NGAx graph for Y-to-V sfa

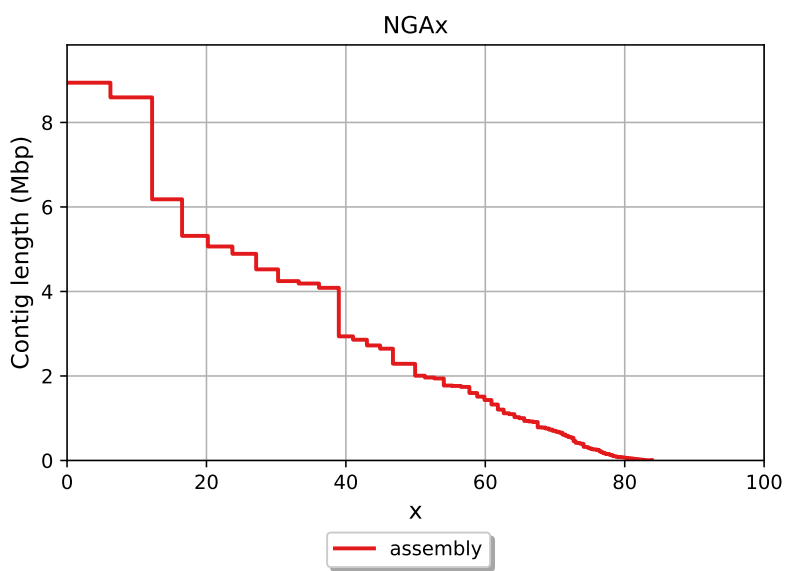


Figure 8: QUAST NGAx graph for wtdbg2 sfa

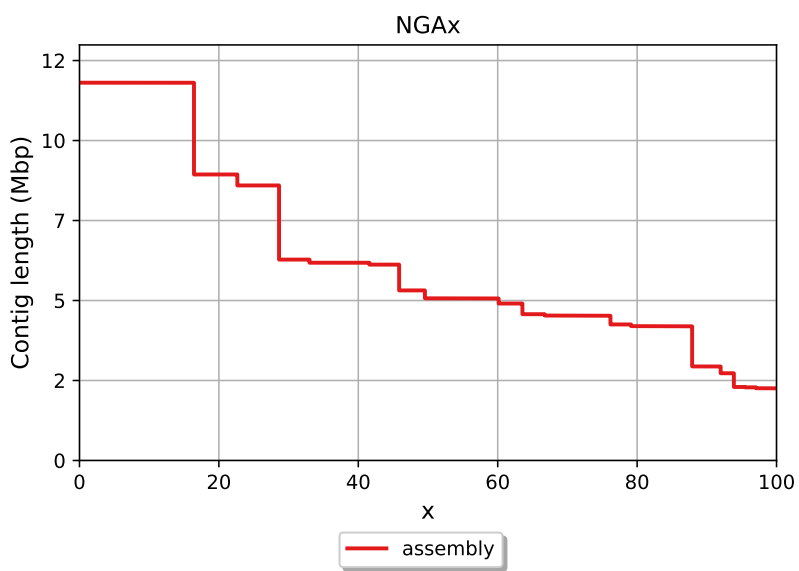


Figure 9: QUASt NGAx graph for Y-to-V

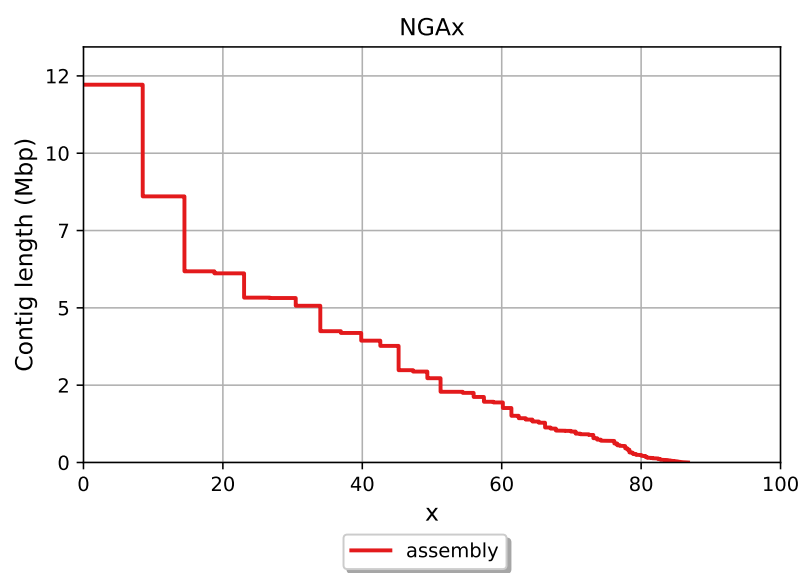


Figure 10: QUAST NGAx graph for frg Y-to-V

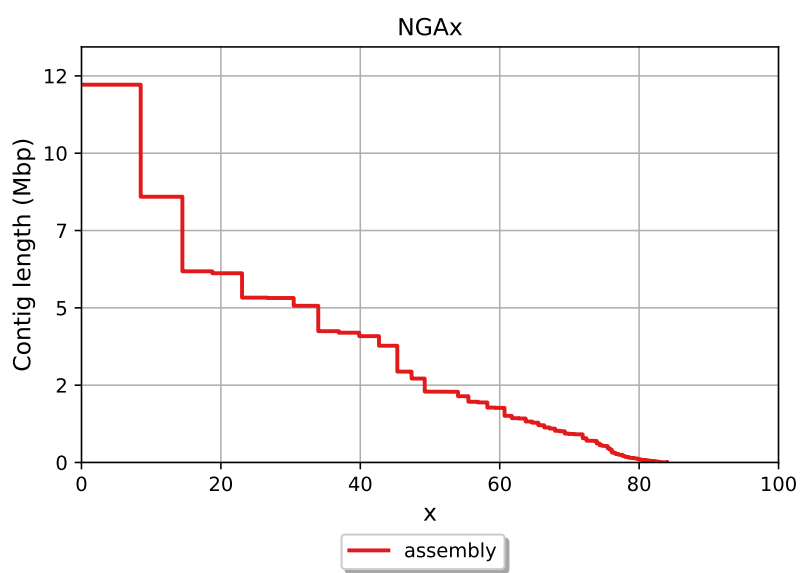


Figure 11: QUAST NGAx graph for wtdbg2