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__A4 D.melanogaster__A4 "genome":"D.melanogaster__A4","assembler":"wtdbg2":"cli_arguments":"-x":"rs"

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	15350	N/A	15350	N/A	N/A
median edge length	4	N/A	4	N/A	N/A
mean edge length	320.2	N/A	320.2	N/A	N/A

Table 3:   ContigValidator

Parameter	Y-to-V sfa	wtdbg2 sfa	Y-to-V	frg Y-to-V	wtdbg2

Table 4: QUAST: # of contigs

Parameter	Y-to-V sfa	wtdbg2 sfa	Y-to-V	frg Y-to-V	wtdbg2
# contigs ($\geq$ 0 bp)	626	512	512	355	354
# contigs ($\geq$ 1000 bp)	626	512	512	355	354
# contigs ($\geq$ 5000 bp)	587	478	492	337	341
# contigs ($\geq$ 10000 bp)	432	333	404	267	269
# contigs ($\geq$ 25000 bp)	263	180	248	140	134
# contigs ($\geq$ 50000 bp)	212	129	190	86	83

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)	361140756	136879663	361805673	158071105	137740615
Total length ($\geq$ 1000 bp)	361140756	136879663	361805673	158071105	137740615
Total length ($\geq$ 5000 bp)	360990164	136750153	361728341	158007166	137692426
Total length ($\geq$ 10000 bp)	359854706	135707577	361086832	157498846	137182427
Total length ($\geq$ 25000 bp)	357129480	133238535	358553848	155415513	134977403
Total length ($\geq$ 50000 bp)	355413704	131373199	356592329	153580574	133181652

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

Parameter	Y-to-V sfa	wtdbg2 sfa	Y-to-V	frg Y-to-V	wtdbg2
# contigs	620	506	509	350	351
Largest contig	16844055	9814816	19613438	27923430	27922435
Total length	361128659	136866720	361798445	158059597	137734137
Reference length	144125362	144125362	144125362	144125362	144125362
GC (%)	41.97	42.00	41.95	41.86	41.97
Reference GC (%)	41.87	41.87	41.87	41.87	41.87
N50	5438673	5136262	7601377	18039744	17049466
NG50	8729882	4590037	12002297	18039744	17049466
N75	3385586	1517211	4232801	5345327	5136262
NG75	8038450	953699	9816912	13837779	5136262
L50	22	11	17	4	4
LG50	7	12	5	4	4
L75	42	23	34	7	7
LG75	11	27	9	6	7

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

Parameter	Y-to-V sfa	wtdbg2 sfa	Y-to-V	frg Y-to-V	wtdbg2
# misassemblies	273	144	294	173	167
# unique misassemblies	192	142	217	167	165
# misassembled contigs	102	53	106	53	50
Misassembled contigs length	104312130	29778310	141199846	121101521	100074526
# local misassemblies	680	320	681	361	331
# unique local misassemblies	475	314	476	344	325
# scaffold gap ext. mis.	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0
# possible TEs	14	8	16	10	8
# unaligned mis. contigs	65	58	65	63	65
# unaligned contigs	142+360p	136+275p	106+320p	101+217p	98+218p
Unaligned length	8047046	5809331	8910279	6966548	6733719
Genome fraction (%)	90.965	90.320	90.925	90.529	90.332
Duplication ratio	2.693	1.007	2.693	1.158	1.006
# N's per 100 kbp	0.00	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	30.07	43.07	29.83	39.08	42.14
# indels per 100 kbp	67.13	75.92	66.63	72.11	75.91
Largest alignment	16810763	9797262	19538157	27852333	27860630
Total aligned length	352787648	130967234	352576865	151000461	130912312
EA50max	5365059	3826158	5608461	8259524	8262226
Strict EA50max	2256858	1741841	2511300	2255138	2386475
NGA50	8580068	3826158	9999655	13386135	8262226
EA75max	1412288	953433	2355903	2109321	2255118
Strict EA75max	926525	523050	953029	953253	926525
NGA75	7668958	953433	8566040	4601065	2255118
LGA50	7	13	5	5	5
LGA75	11	31	9	9	12

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

Parameter	Y-to-V sfa	wtdbg2 sfa	Y-to-V	frg Y-to-V	wtdbg2
# misassemblies	273	144	294	173	167
# contig misassemblies	273	144	294	173	167
# c. relocations	128	66	138	91	81
# c. translocations	143	78	154	82	86
# c. inversions	2	0	2	0	0
# 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	102	53	106	53	50
Misassembled contigs length	104312130	29778310	141199846	121101521	100074526
# local misassemblies	680	320	681	361	331
# 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	14	8	16	10	8
# unaligned mis. contigs	65	58	65	63	65
# mismatches	106075	56411	105179	59013	55171
# indels	236838	99432	234929	108885	99378
# indels ($\leq$ 5 bp)	235777	98849	233867	108278	98798
# indels ($>$ 5 bp)	1061	583	1062	607	580
Indels length	324256	144420	320230	161614	150417
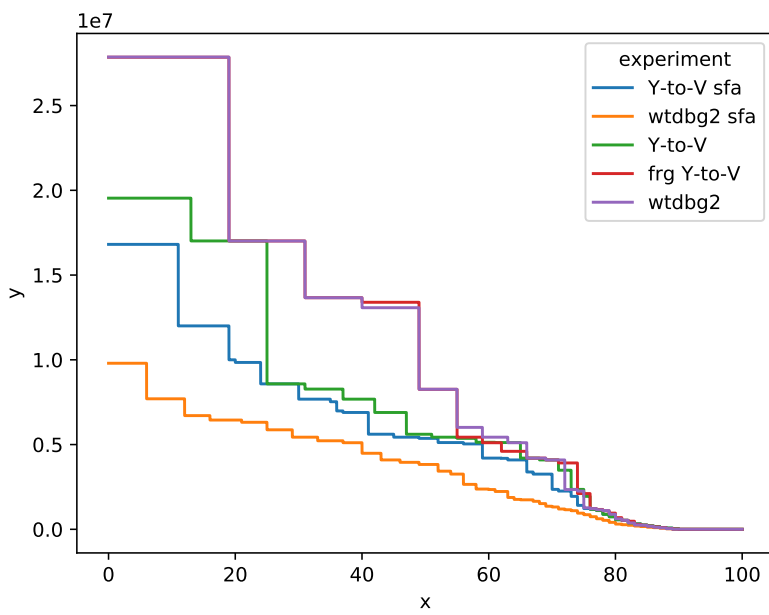
Figure 1: EAxmax
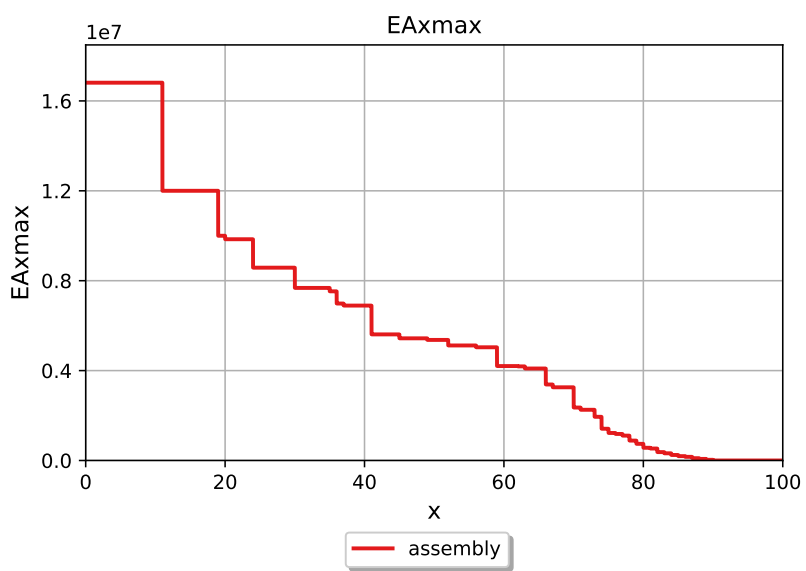
Figure 2: QUAST EAxmax graph for Y-to-V sfa
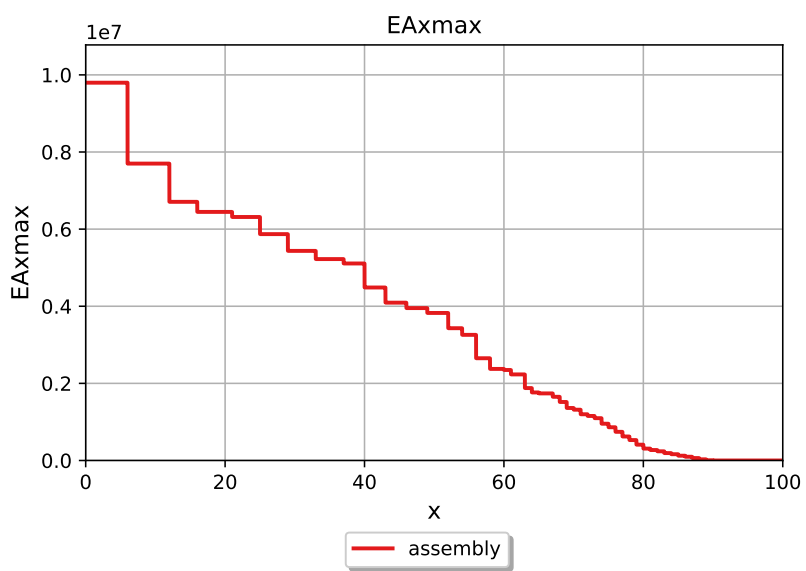
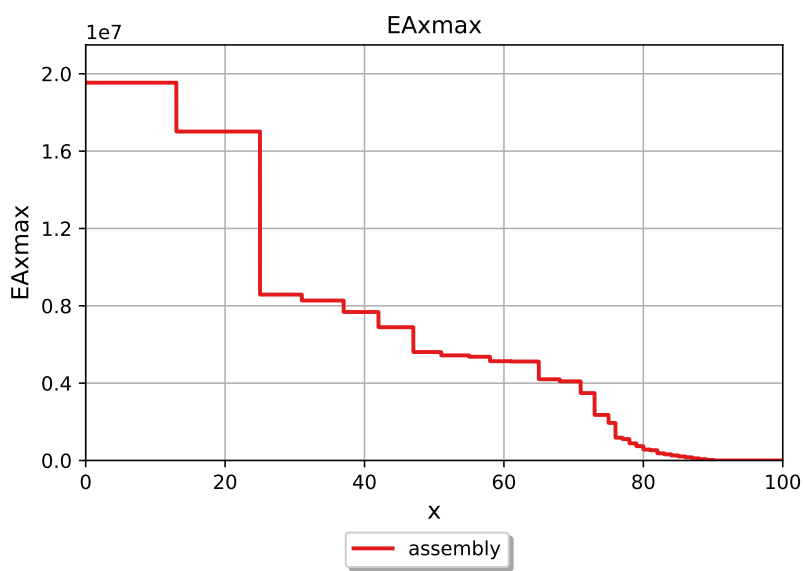Figure 3: QUAST EAxmax graph for wtdbg2 sfa
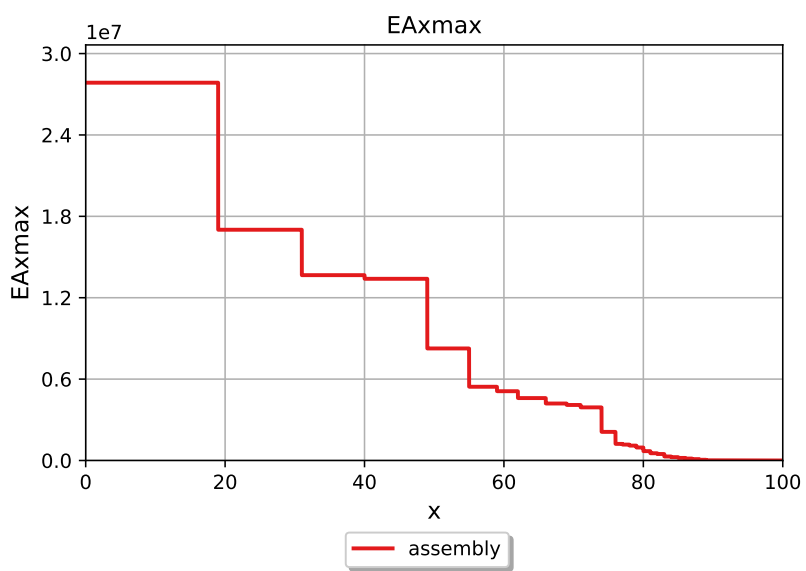
Figure 4: QUAST EAxmax graph for Y-to-V

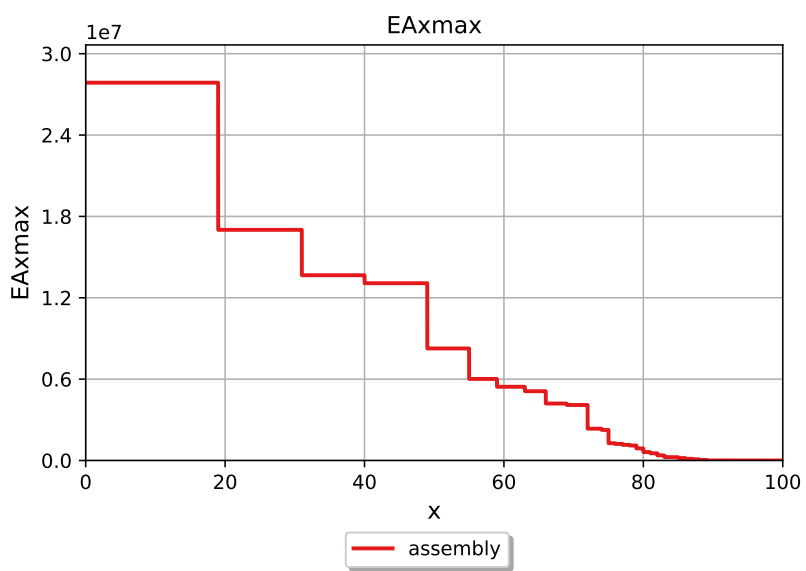Figure 5: QUAST EAxmax graph for frg Y-to-V
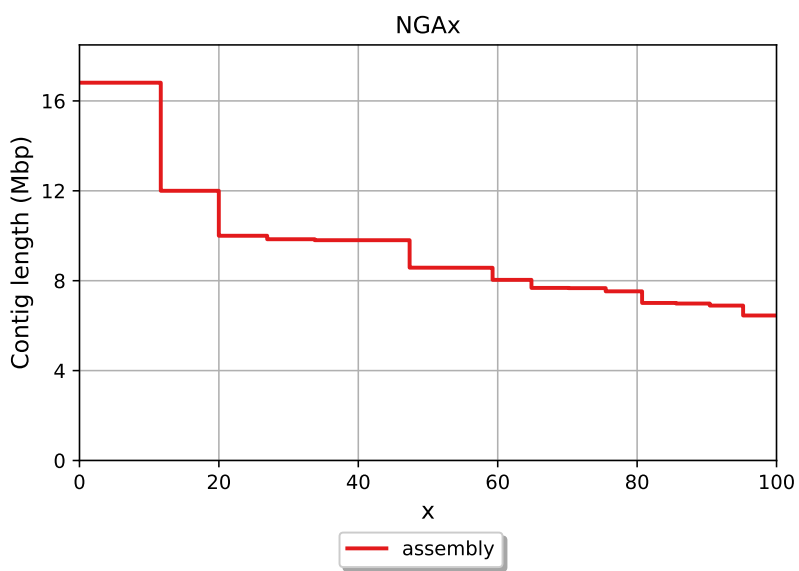
Figure 6: QUAST EAxmax graph for wtdbg2

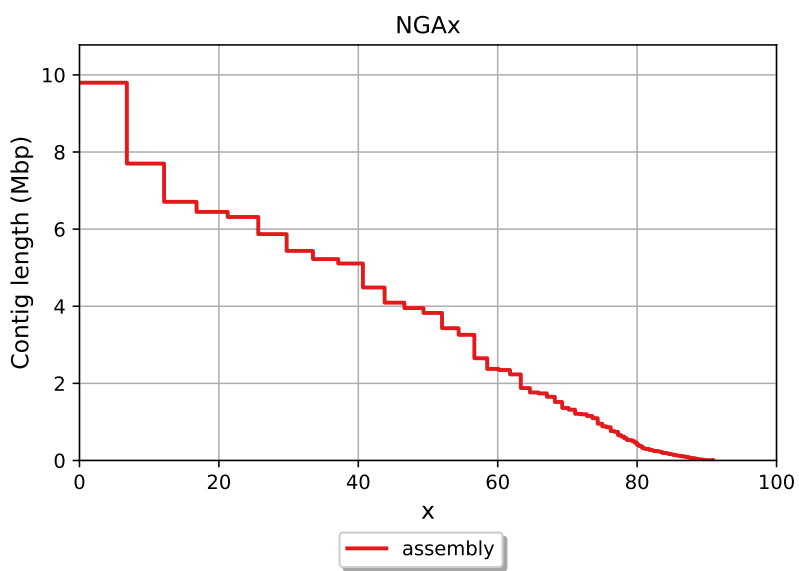Figure 7: QUAST NGAx graph for Y-to-V sfa

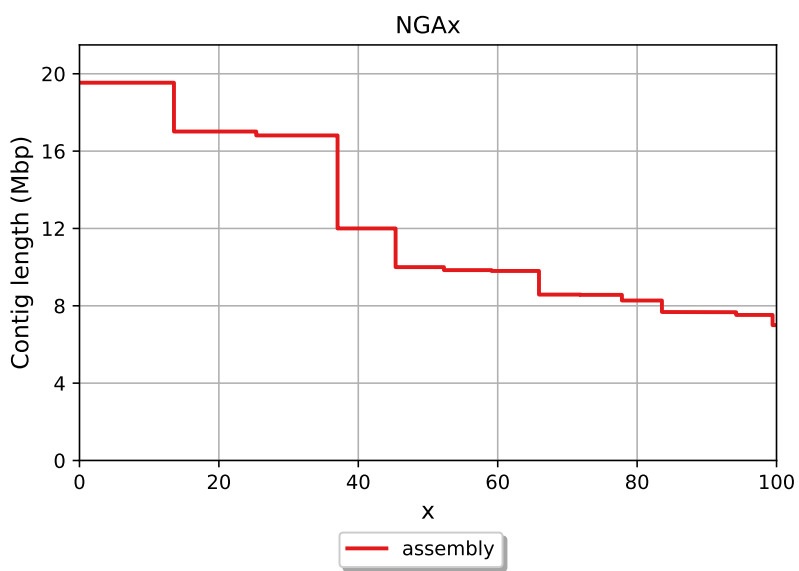Figure 8: QUAST NGAx graph for wtdbg2 sfa
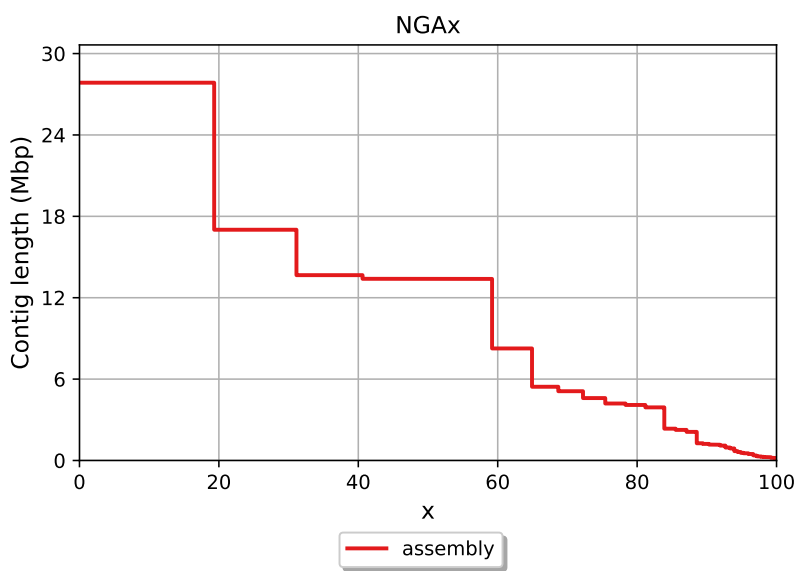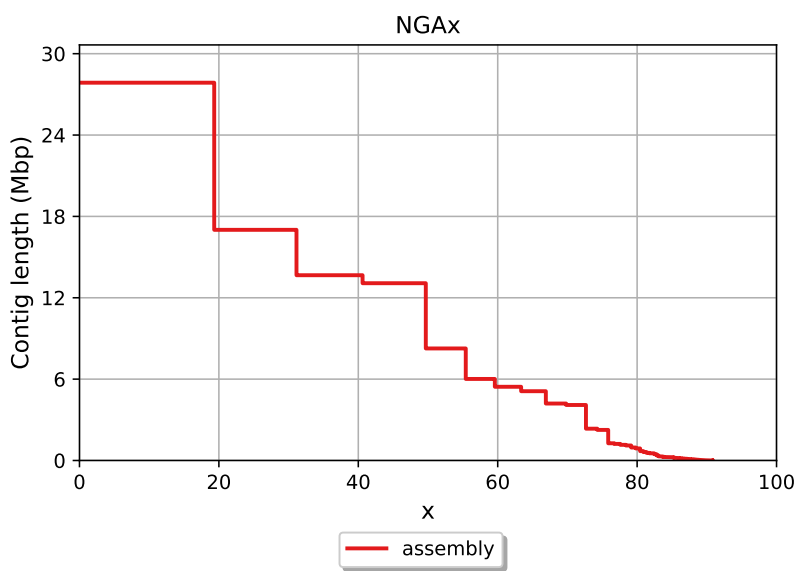
Figure 9: QUAST NGAx graph for Y-to-V

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

Figure 11: QUAST NGAx graph for wtdbg2