

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):

- A.thaliana A.thaliana "genome":"A.thaliana","assembler":"wtDBG2":"cli_arguments":"-x":"sq"

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	10448	N/A	10448	N/A	N/A
median edge length	1	N/A	1	N/A	N/A
mean edge length	147.8	N/A	147.8	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 (≥ 0 bp)	394	360	376	315	315
# contigs (≥ 1000 bp)	394	360	376	315	315
# contigs (≥ 5000 bp)	352	318	337	280	280
# contigs (≥ 10000 bp)	211	183	206	155	157
# contigs (≥ 25000 bp)	145	115	126	73	74
# contigs (≥ 50000 bp)	116	85	98	48	48

Table 5: QUASt: total length of contigs

Parameter	Y-to-V sfa	wtdbg2 sfa	Y-to-V	frg Y-to-V	wtdbg2
Total length (≥ 0 bp)	223252288	119758630	224013245	120815035	120834200
Total length (≥ 1000 bp)	223252288	119758630	224013245	120815035	120834200
Total length (≥ 5000 bp)	223080290	119587342	223852937	120672362	120687216
Total length (≥ 10000 bp)	222117244	118662202	222965336	119824587	119854499
Total length (≥ 25000 bp)	221071737	117588044	221692684	118505727	118524470
Total length (≥ 50000 bp)	220047203	116595498	220721302	117676499	117672096

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

Parameter	Y-to-V sfa	wtdbg2 sfa	Y-to-V	frg Y-to-V	wtdbg2
# contigs	384	351	366	306	309
Largest contig	13259959	10282122	15350684	13976612	13976749
Total length	223227227	119734795	223987027	120791771	120818559
Reference length	122822733	122822733	122822733	122822733	122822733
GC (%)	35.90	36.23	35.93	36.28	36.28
Reference GC (%)	36.22	36.22	36.22	36.22	36.22
N50	5696482	4791028	6958495	10074979	10075074
NG50	7702241	4581882	10850727	10074979	10075074
N75	2422180	1837117	2851418	4850073	4850133
NG75	6224475	1475586	7702217	4850073	4850133
L50	14	9	11	5	5
LG50	6	10	5	5	5
L75	30	19	23	10	10
LG75	11	21	9	10	10

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

Parameter	Y-to-V sfa	wtdbg2 sfa	Y-to-V	frg Y-to-V	wtdbg2
# misassemblies	80	46	88	64	58
# unique misassemblies	66	44	76	63	57
# misassembled contigs	60	36	60	42	38
Misassembled contigs length	105623385	27500859	142568292	86809119	80435235
# local misassemblies	397	234	408	263	254
# unique local misassemblies	306	227	315	258	248
# scaffold gap ext. mis.	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0
# possible TEs	2	4	2	2	4
# unaligned mis. contigs	58	60	66	68	73
# unaligned contigs	61+291p	55+257p	56+293p	50+245p	49+249p
Unaligned length	4225259	3150686	4957175	4002184	4034568
Genome fraction (%)	95.090	94.778	95.105	94.956	94.950
Duplication ratio	1.875	1.002	1.875	1.001	1.001
# N's per 100 kbp	0.00	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	38.95	40.26	38.61	41.01	40.24
# indels per 100 kbp	139.13	140.87	139.03	140.47	141.37
Largest alignment	10388562	10273867	11129087	12957818	12952149
Total aligned length	218930603	116568152	218940816	116777728	116763198
EA50max	5066278	4192416	5690800	6062697	6062513
Strict EA50max	2397720	2159175	2530250	2804938	2398685
NGA50	6217971	4192416	6946215	6062697	6062513
EA75max	2159111	1474017	2460955	2159166	2159512
Strict EA75max	673960	472414	673960	673960	543419
NGA75	4852815	1474017	5066261	2159166	2159512
LGA50	8	11	7	8	8
LGA75	14	23	12	15	15

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

Parameter	Y-to-V sfa	wtdbg2 sfa	Y-to-V	frg Y-to-V	wtdbg2
# misassemblies	80	46	88	64	58
# contig misassemblies	80	46	88	64	58
# c. relocations	17	15	23	19	18
# c. translocations	58	30	61	44	39
# c. inversions	5	1	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	60	36	60	42	38
Misassembled contigs length	105623385	27500859	142568292	86809119	80435235
# local misassemblies	397	234	408	263	254
# 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	1	1	1
# possible TEs	2	4	2	2	4
# unaligned mis. contigs	58	60	66	68	73
# mismatches	85263	46931	84541	47894	46980
# indels	304606	164214	304390	164037	165069
# indels (≤ 5 bp)	304233	164003	304015	163841	164851
# indels (> 5 bp)	373	211	375	196	218
Indels length	340908	184766	340816	184439	185105

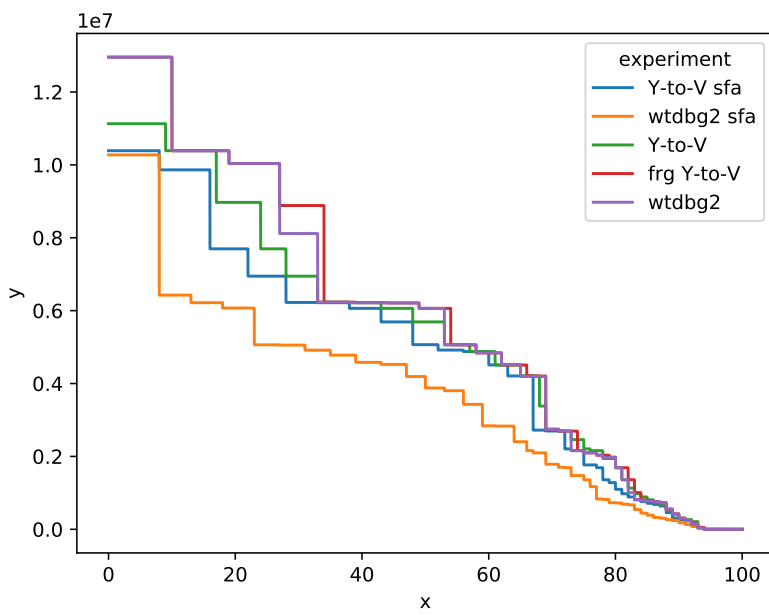


Figure 1: EAxmax

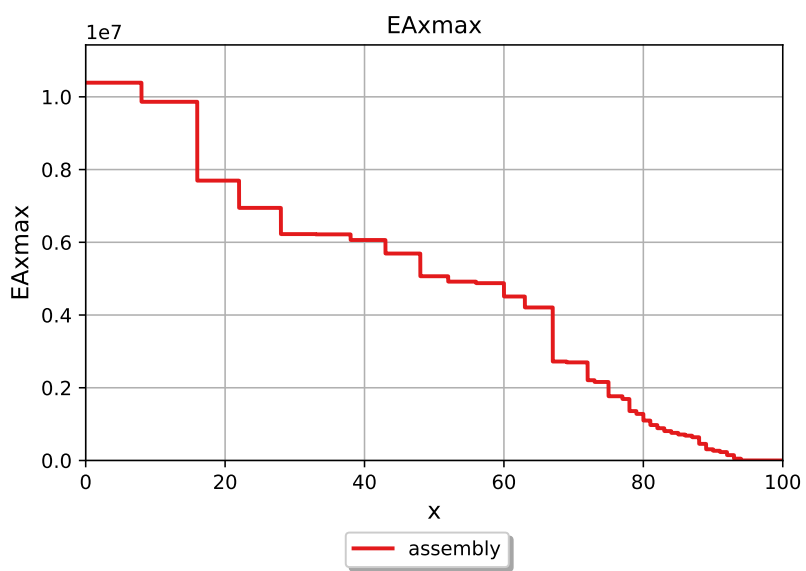


Figure 2: QUAST EAxmax graph for Y-to-V sfa

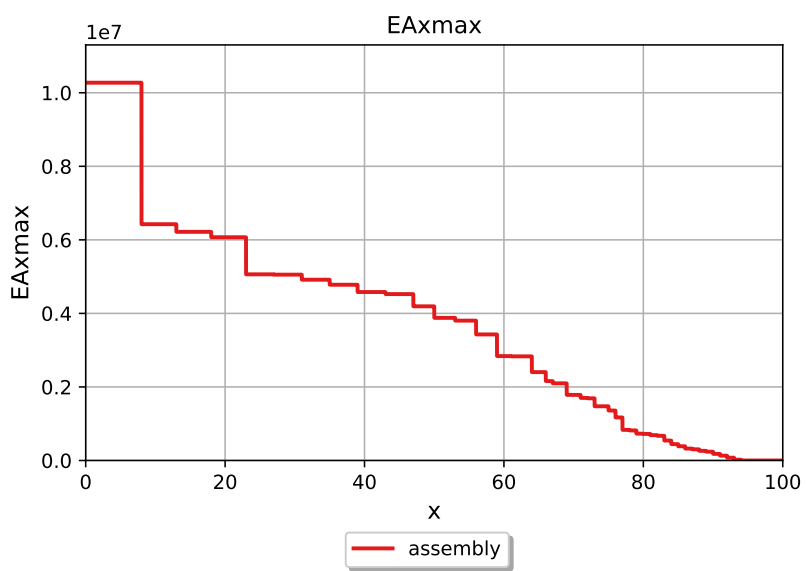


Figure 3: QUAST EAxmax graph for wtdbg2 sfa

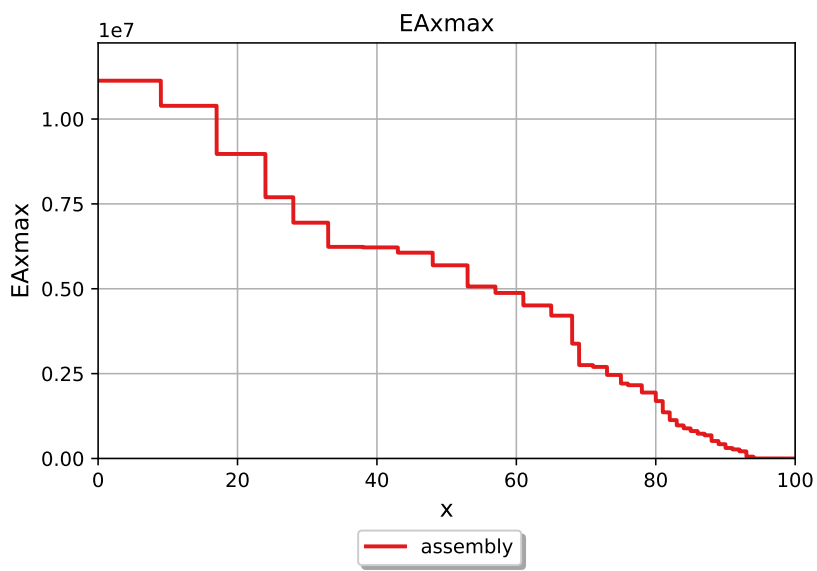


Figure 4: QUAST EAxmax graph for Y-to-V

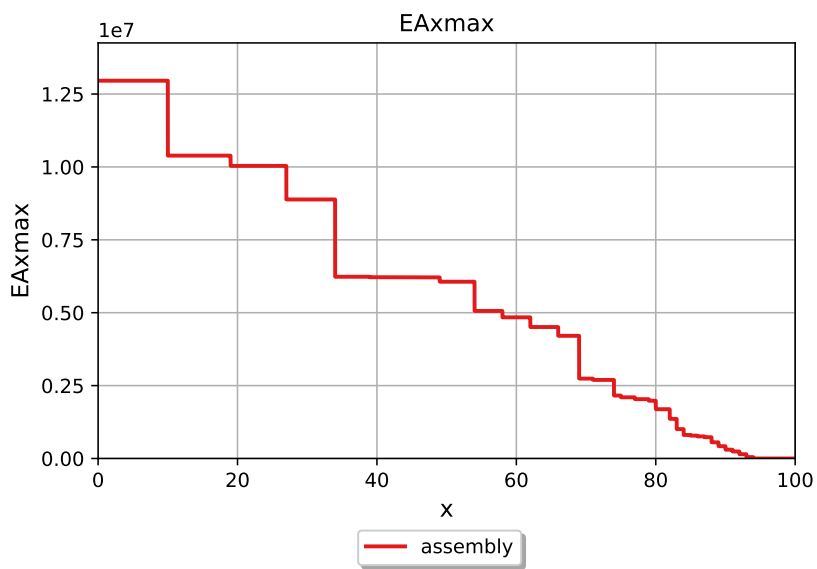


Figure 5: QUAST EAxmax graph for frg Y-to-V

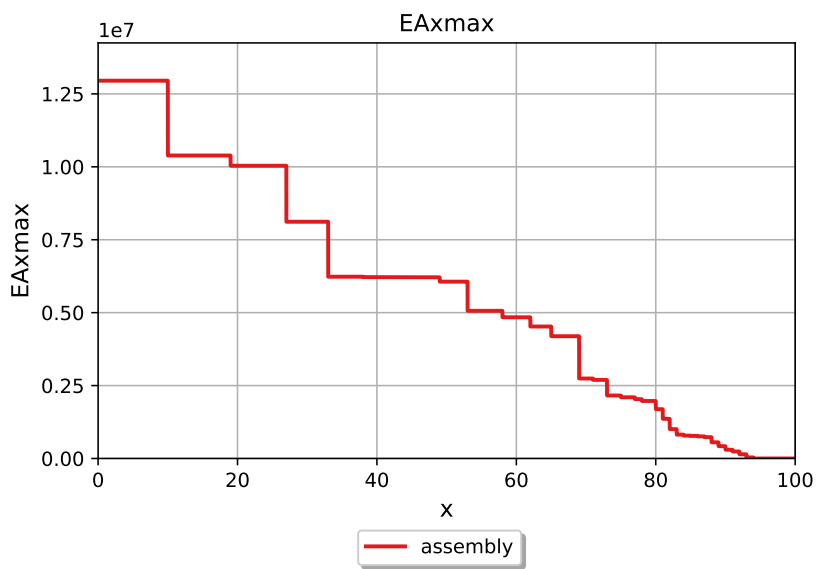


Figure 6: QUAST EAxmax graph for wtdbg2

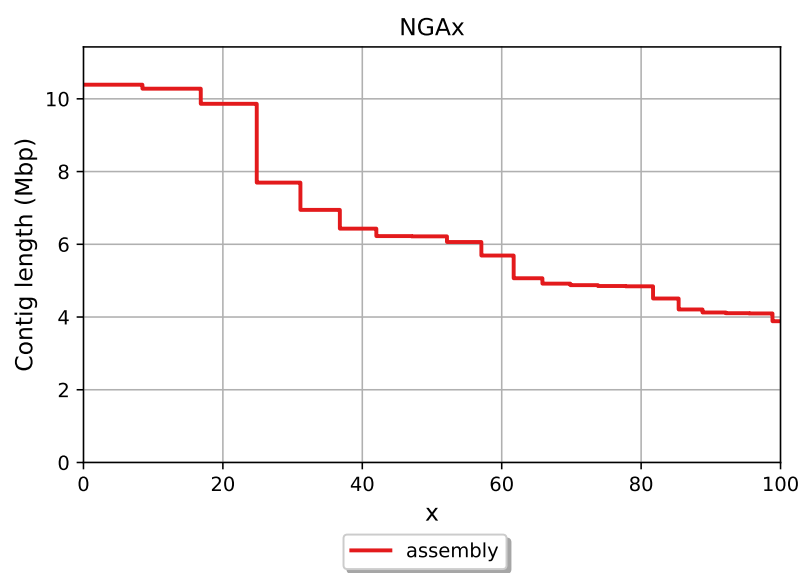


Figure 7: QUAST NGAx graph for Y-to-V sfa

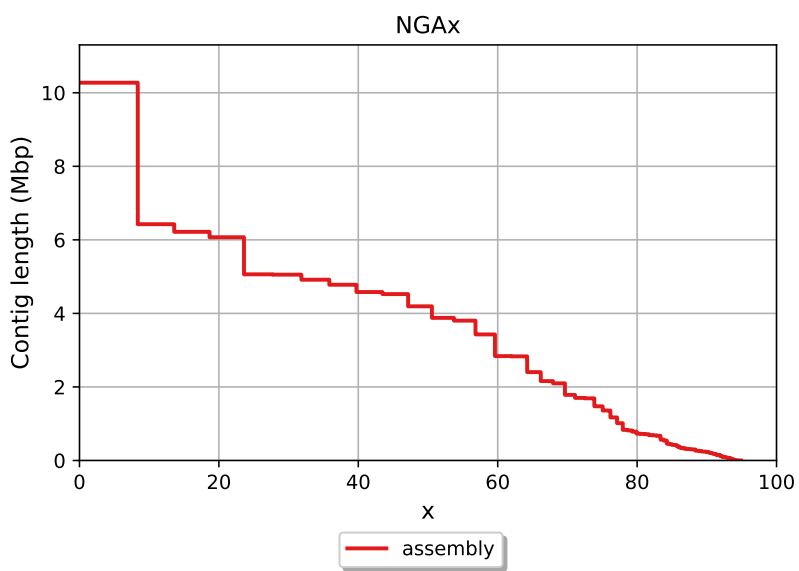


Figure 8: QUAST NGAx graph for wtdbg2 sfa

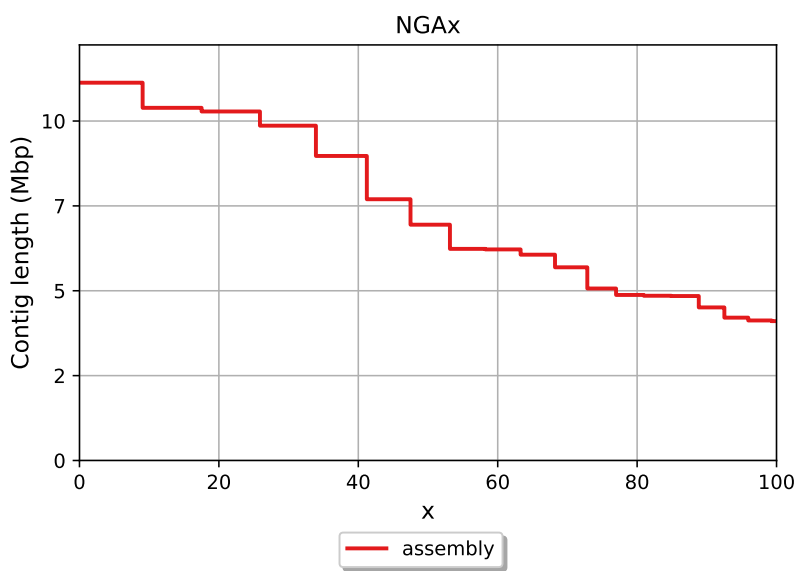


Figure 9: QUASt NGAx graph for Y-to-V

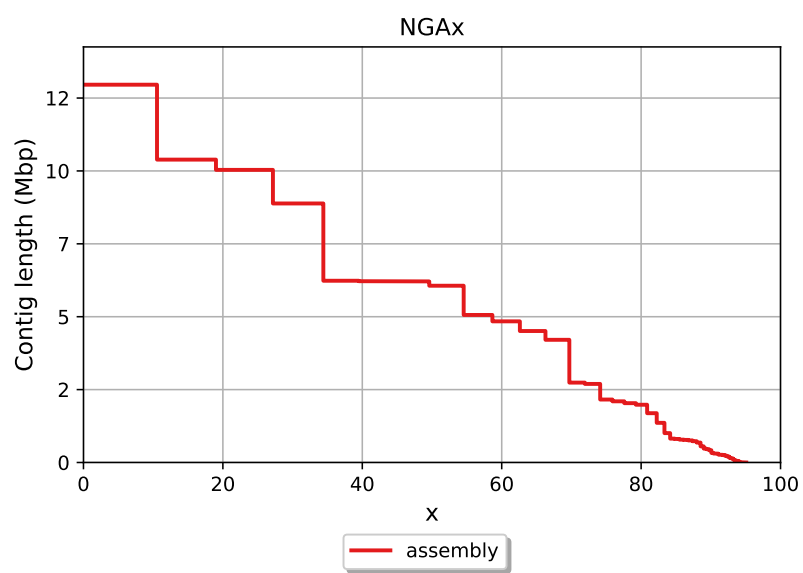


Figure 10: QUAST NGAx graph for frg Y-to-V

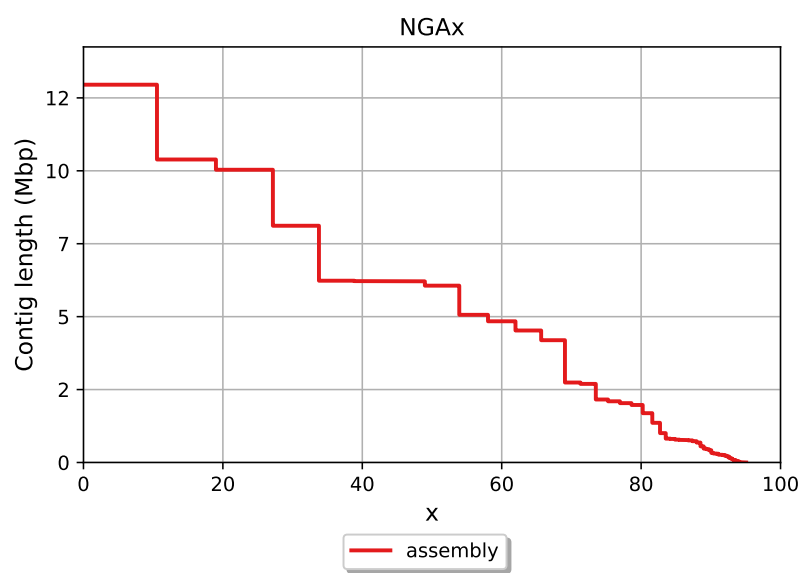


Figure 11: QUASt NGAx graph for wtdbg2