

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

Revision: b'bigraph-v0.2.0-63-gf9a4863'

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

- A.thaliana

Table 1: Genome Graph Statistics

Table 2: Algorithm Statistics

Parameter	inj uni sfa	inj Y-to-V sfa	wtdbg2 sfa	inj uni	inj Y-to-V	wtdbg2
min non-trivial omnitigs per macrotig	N/A	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	N/A
median non-trivial omnitigs per macrotig	N/A	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	N/A
min edge length	1	1	N/A	1	1	N/A
max edge length	8118	10448	N/A	8118	10448	N/A
median edge length	1	1	N/A	1	1	N/A
mean edge length	75.0	147.6	N/A	75.0	147.6	N/A

Table 3: ContigValidator

Parameter	inj uni sfa	inj Y-to-V sfa	wtdbg2 sfa	inj uni	inj Y-to-V	wtdbg2
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Table 4: QUASt: # of contigs

Parameter	inj uni sfa	inj Y-to-V sfa	wtdbg2 sfa	inj uni	inj Y-to-V	wtdbg2
# contigs (≥ 0 bp)	257	282	361	171	220	315
# contigs (≥ 1000 bp)	257	282	361	171	220	315
# contigs (≥ 5000 bp)	229	254	319	157	203	280
# contigs (≥ 10000 bp)	157	185	185	115	161	158
# contigs (≥ 25000 bp)	107	137	117	71	118	74
# contigs (≥ 50000 bp)	85	113	85	49	92	48

Table 5: QUASt: total length of contigs

Parameter	inj uni sfa	inj Y-to-V sfa	wtdbg2 sfa	inj uni	inj Y-to-V	wtdbg2
Total length (≥ 0 bp)	118550163	221637191	119764216	119102298	218201516	120835438
Total length (≥ 1000 bp)	118550163	221637191	119764216	119102298	218201516	120835438
Total length (≥ 5000 bp)	118453961	221533752	119592928	119049901	218134238	120688454
Total length (≥ 10000 bp)	117961584	221059387	118671377	118762197	217842037	119862528
Total length (≥ 25000 bp)	117162388	220296079	117608542	118032177	217129757	118518389
Total length (≥ 50000 bp)	116431079	219427422	116554555	117319638	216238384	117665999

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

Parameter	inj uni sfa	inj Y-to-V sfa	wtdbg2 sfa	inj uni	inj Y-to-V	wtdbg2
# contigs	245	274	352	166	217	309
Largest contig	10281502	13258666	10282109	14487410	15044586	13976658
Total length	118520933	221617474	119740381	119089113	218193882	120819797
Reference length	122822733	122822733	122822733	122822733	122822733	122822733
GC (%)	36.17	35.87	36.23	36.18	35.88	36.28
Reference GC (%)	36.22	36.22	36.22	36.22	36.22	36.22
N50	4791034	5695399	4791027	10075073	6220556	10075007
NG50	4581823	7697981	4581848	10075073	9895475	10075007
N75	1835623	2734216	1837140	4846733	2942957	4850122
NG75	1475607	6220566	1475589	4846733	6954983	4850122
L50	9	14	9	5	12	5
LG50	10	6	10	5	5	5
L75	19	29	19	10	23	10
LG75	21	11	21	10	9	10

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

Parameter	inj uni sfa	inj Y-to-V sfa	wtdbg2 sfa	inj uni	inj Y-to-V	wtdbg2
# misassemblies	33	57	46	38	62	55
# unique misassemblies	32	45	45	37	50	55
# misassembled contigs	24	44	36	23	44	37
Misassembled contigs length	29675567	93198467	27501564	76162087	116661435	80418792
# local misassemblies	197	340	232	206	344	252
# unique local misassemblies	197	254	229	206	261	252
# scaffold gap ext. mis.	0	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0	0
# possible TEs	2	2	4	4	2	4
# unaligned mis. contigs	33	31	60	32	29	72
# unaligned contigs	50 + 163 part	55 + 193 part	55 + 259 part	33 + 126 part	38 + 164 part	49 + 250 part
Unaligned length	2570157	3501419	3150873	2984749	3894035	4009157
Genome fraction (%)	94.408	94.673	94.804	94.540	94.648	94.794
Duplication ratio	1.000	1.876	1.001	1.000	1.843	1.000
# N's per 100 kbp	0.00	0.00	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	38.73	36.99	40.27	40.19	36.95	40.27
# indels per 100 kbp	136.70	136.76	140.50	137.10	137.07	140.50
Largest alignment	10274093	10388530	10273882	12953438	10388902	12951438
Total aligned length	115904295	218032028	116573963	116073252	214240759	116783963
EA50max	4097311	5065728	4192402	6061486	5690067	6062486
Strict EA50max	2077345	2397718	2159186	2397733	2397711	2397711
NGA50	4097311	6216813	4192402	6061486	6301794	6062486
EA75max	1353183	2158494	1474020	2158316	2160630	2159143
Strict EA75max	504560	673960	514786	643884	681826	543884
NGA75	1353183	4852903	1474020	2158316	5065724	2159143
LGA50	11	8	11	8	7	11
LGA75	24	14	23	15	13	23

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

Parameter	inj uni sfa	inj Y-to-V sfa	wtdbg2 sfa	inj uni	inj Y-to-V	wtdbg2
# misassemblies	33	57	46	38	62	55
# contig misassemblies	33	57	46	38	62	55
# c. relocations	10	10	16	11	11	17
# c. translocations	22	42	29	26	46	37
# c. inversions	1	5	1	1	5	1
# scaffold misassemblies	0	0	0	0	0	0
# s. relocations	0	0	0	0	0	0
# s. translocations	0	0	0	0	0	0
# s. inversions	0	0	0	0	0	0
# misassembled contigs	24	44	36	23	44	37
Misassembled contigs length	29675567	93198467	27501564	76162087	116661435	80418792
# local misassemblies	197	340	232	206	344	252
# scaffold gap ext. mis.	0	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0	0
# mis. caused by frag. ref.	0	0	0	1	1	1
# possible TEs	2	2	4	4	2	4
# unaligned mis. contigs	33	31	60	32	29	72
# mismatches	44892	80641	46943	46649	79164	47028
# indels	158443	298188	163792	159134	293668	164821
# indels (≤ 5 bp)	158254	297833	163579	158935	293314	164596
# indels (> 5 bp)	189	355	213	199	354	225
Indels length	177821	333844	184373	179122	328950	184954

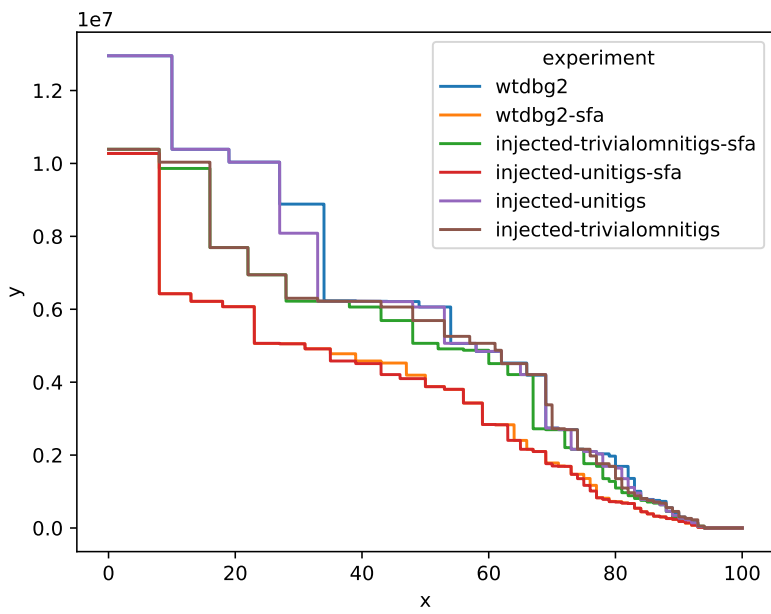


Figure 1: EAxmax

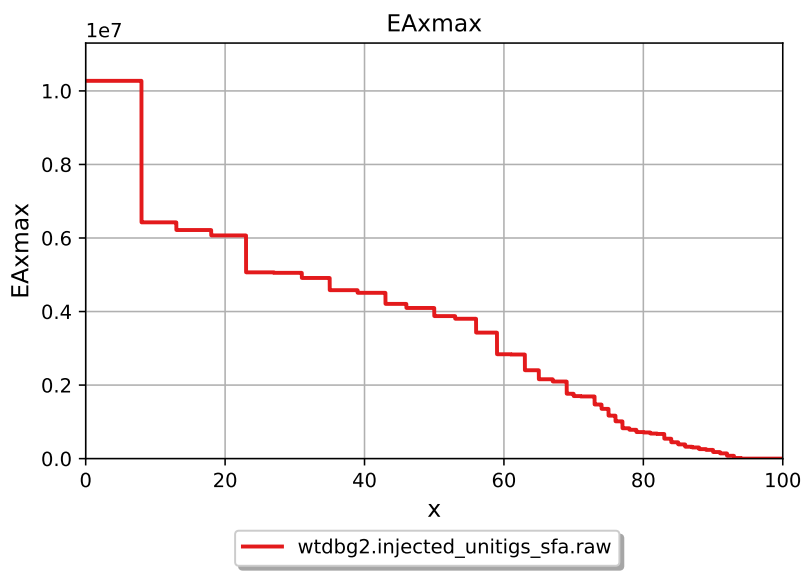


Figure 2: QUAST EAxmax graph for inj uni sfa

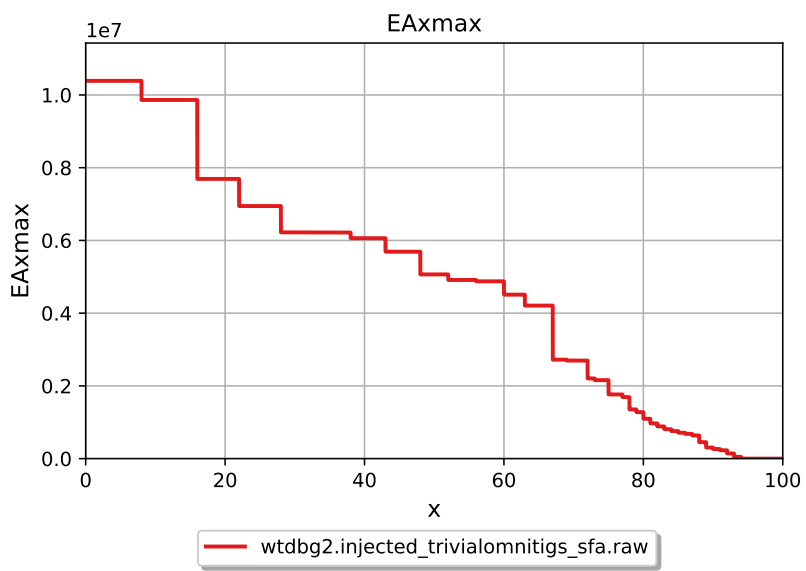


Figure 3: QUAST EAxmax graph for inj Y-to-V sfa

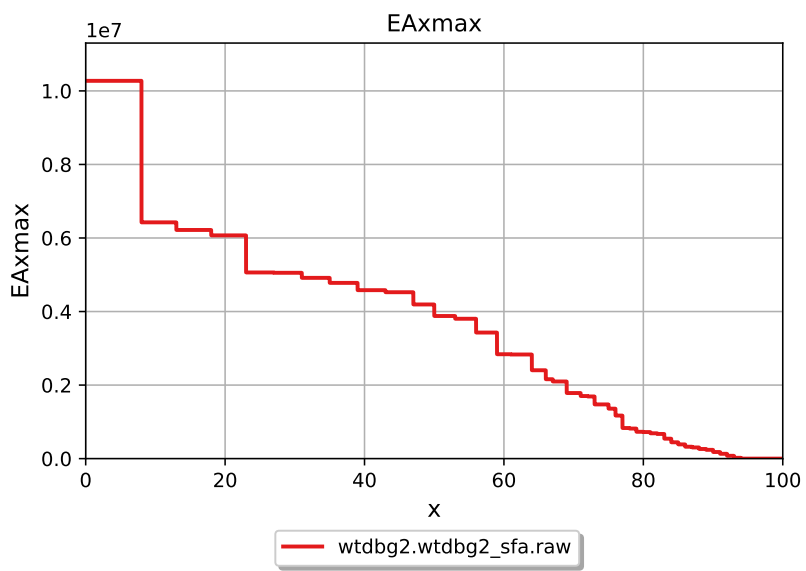


Figure 4: QUAST EAxmax graph for wtdbg2 sfa

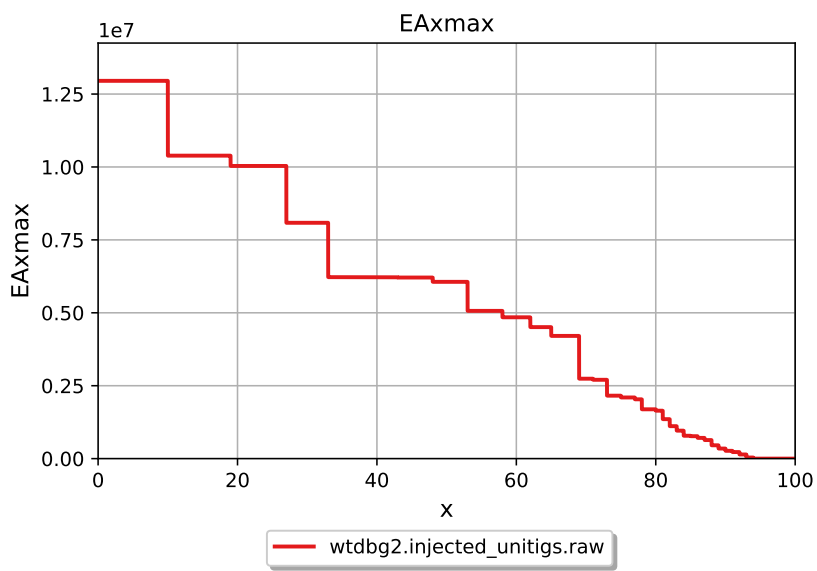


Figure 5: QUAST EAxmax graph for inj uni

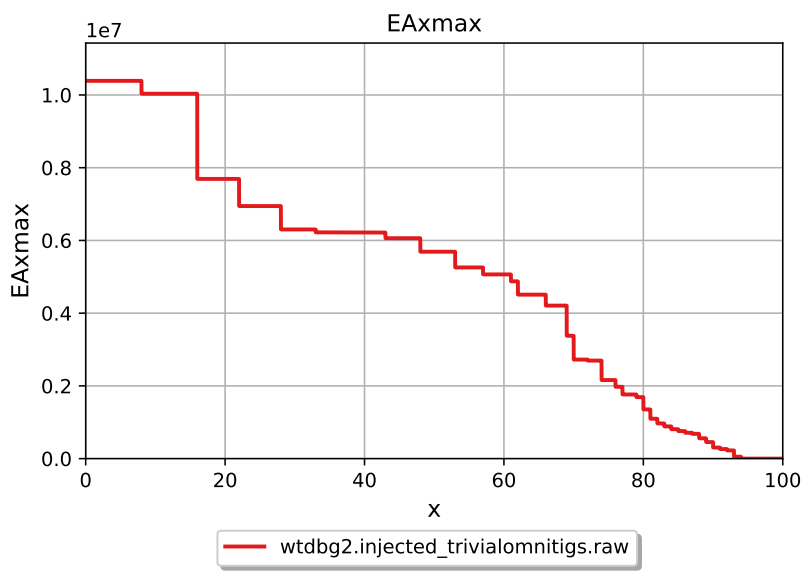


Figure 6: QUASt EAXmax graph for inj Y-to-V

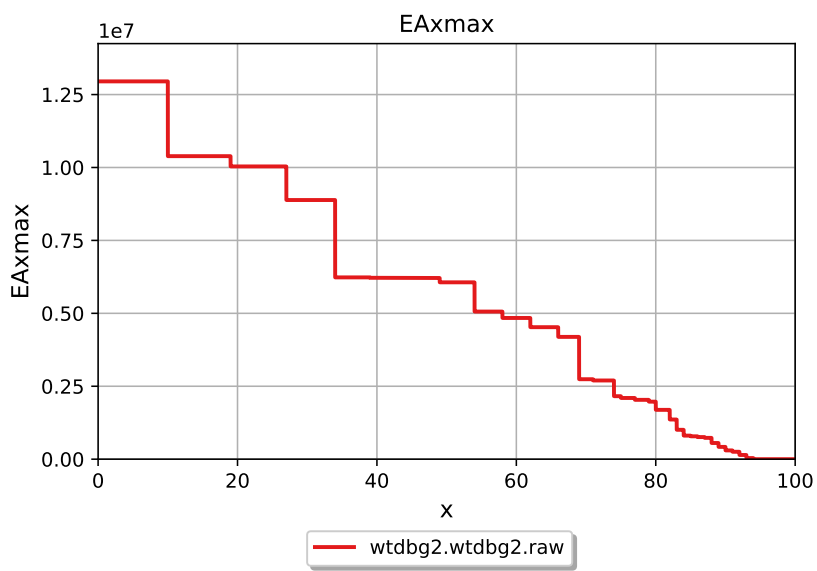


Figure 7: QUAST EAxmax graph for wtdbg2

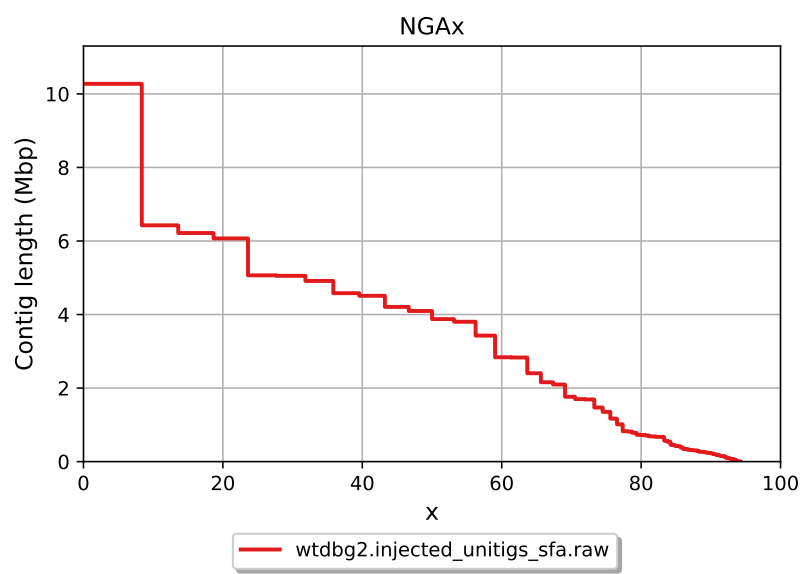


Figure 8: QUAST NGAx graph for inj uni sfa

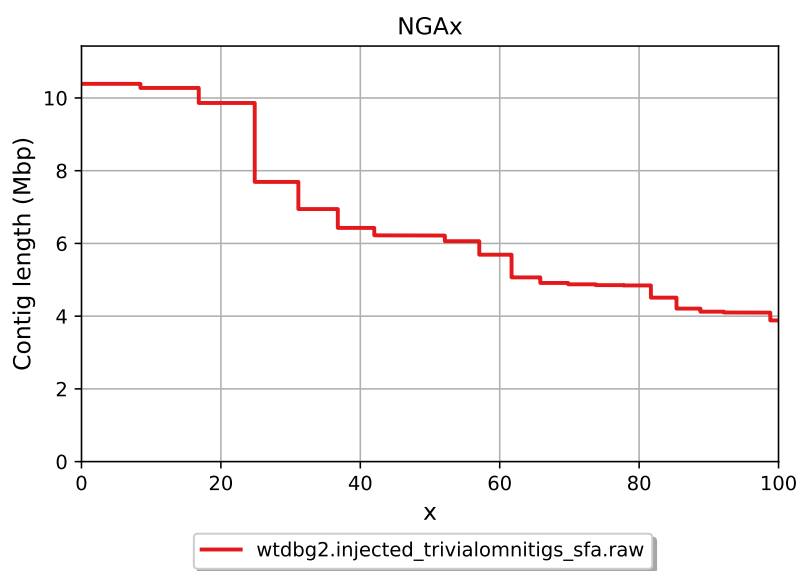


Figure 9: QUAST NGAx graph for inj Y-to-V sfa

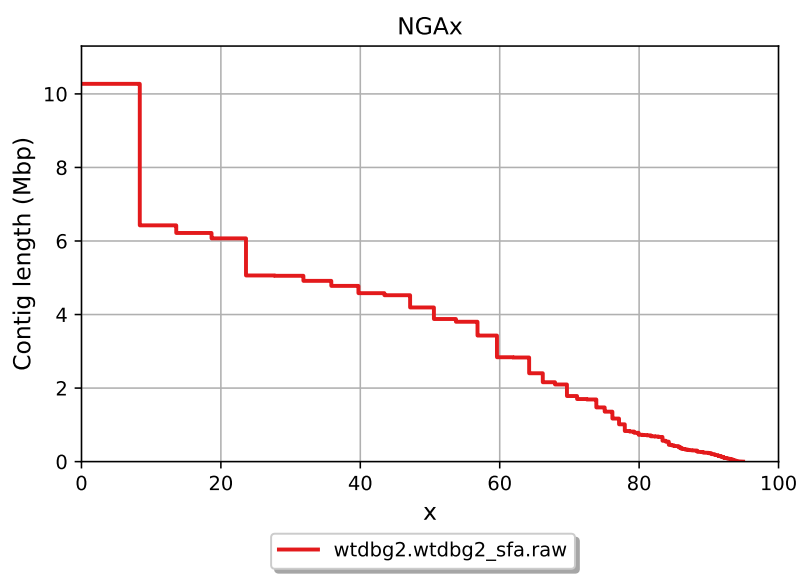


Figure 10: QUAST NGAx graph for wtdbg2 sfa

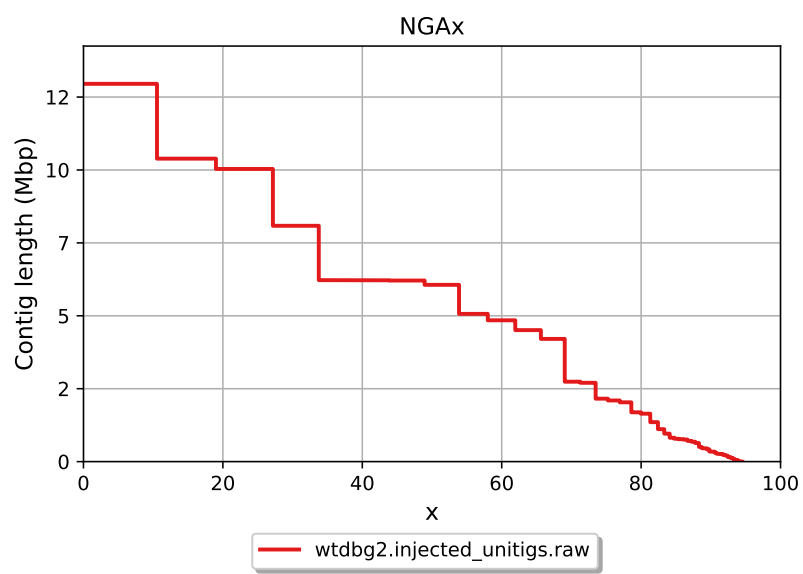


Figure 11: QUASt NGAx graph for inj uni

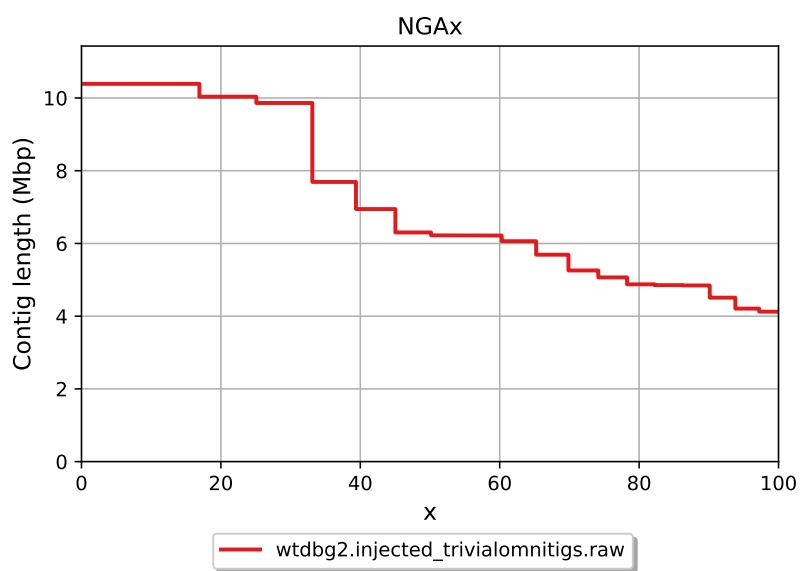


Figure 12: QUAST NGAx graph for inj Y-to-V

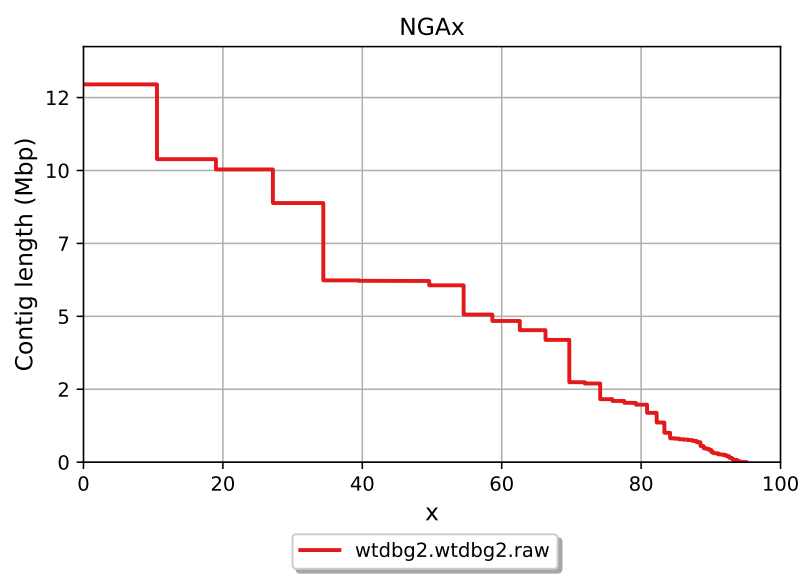


Figure 13: QUAST NGAx graph for wtdbg2