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):

- C.elegans

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	5552	5552	N/A	5552	5552	N/A
median edge length	6	31	N/A	6	31	N/A
mean edge length	198.5	398.2	N/A	198.5	398.2	N/A

Table 3: ContigValidator

Parameter	inj uni sfa	inj Y-to-V sfa	wtdbg2 sfa	inj uni	inj Y-to-V	wtdbg2

Table 4: QUAST: # of contigs

Parameter	inj uni sfa	inj Y-to-V sfa	wtdbg2 sfa	inj uni	inj Y-to-V	wtdbg2
# contigs ($\geq$ 0 bp)	234	272	259	182	238	190
# contigs ($\geq$ 1000 bp)	234	272	259	182	238	190
# contigs ($\geq$ 5000 bp)	229	263	250	179	235	187
# contigs ($\geq$ 10000 bp)	196	230	207	149	202	150
# contigs ($\geq$ 25000 bp)	151	185	154	109	160	105
# contigs ($\geq$ 50000 bp)	132	159	134	95	142	89

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 ($\geq$ 0 bp)	100347783	151672313	100835892	99992086	151814759	100939469
Total length ($\geq$ 1000 bp)	100347783	151672313	100835892	99992086	151814759	100939469
Total length ($\geq$ 5000 bp)	100328882	151638130	100801255	99978213	151800798	100930287
Total length ($\geq$ 10000 bp)	100091232	151411395	100499127	99760254	151569877	100664859
Total length ($\geq$ 25000 bp)	99373587	150667695	99674841	99117002	150892552	99975709
Total length ($\geq$ 50000 bp)	98673877	149741663	98980274	98619180	150254230	99415340

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

Parameter	inj uni sfa	inj Y-to-V sfa	wtdbg2 sfa	inj uni	inj Y-to-V	wtdbg2
# contigs	233	270	257	182	238	188
Largest contig	6177007	6177007	6180070	6177007	6177007	6180090
Total length	100346378	151668689	100831458	99992086	151814759	100935035
Reference length	104169699	104169699	104169699	104169699	104169699	104169699
GC (%)	35.58	35.67	35.61	35.58	35.67	35.62
Reference GC (%)	35.67	35.67	35.67	35.67	35.67	35.67
N50	1204081	1426192	1205835	1901869	1618829	1906099
NG50	1203426	2037872	1204279	1849762	2268406	1854232
N75	720881	789977	720918	945991	946537	998289
NG75	639379	1417954	640359	926774	1601409	949752
L50	24	31	24	17	28	18
LG50	25	17	25	18	16	19
L75	51	67	51	36	59	36
LG75	55	32	55	39	29	38

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

Parameter	inj uni sfa	inj Y-to-V sfa	wtdbg2 sfa	inj uni	inj Y-to-V	wtdbg2
# misassemblies	66	125	66	77	135	81
# unique misassemblies	65	103	65	77	111	80
# misassembled contigs	45	81	45	42	76	47
Misassembled contigs length	51691406	94136614	50801528	63990831	101596193	68234193
# local misassemblies	164	286	161	156	283	170
# unique local misassemblies	164	199	161	156	197	167
# scaffold gap ext. mis.	0	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0	0
# possible TEs	2	16	6	2	14	6
# unaligned mis. contigs	0	0	1	0	1	0
# unaligned contigs	0 + 87 part	0 + 134 part	14 + 112 part	1 + 74 part	1 + 124 part	9 + 88 part
Unaligned length	512121	817858	688413	552198	857016	728640
Genome fraction (%)	95.879	96.359	96.179	95.497	96.435	96.231
Duplication ratio	1.000	1.503	1.000	1.000	1.503	1.000
# N's per 100 kbp	0.00	0.00	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	27.84	34.01	30.58	26.90	32.08	31.69
# indels per 100 kbp	48.14	49.34	49.36	48.51	49.56	49.83
Largest alignment	3147709	3147709	3150502	3147709	3147709	3150697
Total aligned length	99706946	150562511	100037038	99292602	150664438	100079261
EA50max	839952	976500	846349	923967	976500	949924
Strict EA50max	518393	604052	545657	604052	621381	650482
NGA50	839952	1359914	846349	923967	1524225	949924
EA75max	413044	535385	418864	510288	563673	536597
Strict EA75max	235044	309036	244082	275837	311372	308180
NGA75	413044	850442	416035	510288	851550	536597
LGA50	36	25	36	31	24	31
LGA75	79	50	79	68	49	66

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

| Parameter	inj uni sfa	inj Y-to-V sfa	wtdbg2 sfa	inj uni	inj Y-to-V	wtdbg2
# misassemblies	66	125	66	77	135	81
# contig misassemblies	66	125	66	77	135	81
# c. relocations	16	29	16	19	32	19
# c. translocations	50	95	49	58	102	61
# c. inversions	0	1	1	0	1	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	45	81	45	42	76	47
Misassembled contigs length	51691406	94136614	50801528	63990831	101596193	68234193
# local misassemblies	164	286	161	156	283	170
# 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	0	0	0
# possible TEs	2	16	6	2	14	6
# unaligned mis. contigs	0	0	1	0	1	0
# mismatches	27758	51212	30595	26712	48337	31719
# indels	48000	74289	49377	48171	74665	49871
# indels (≤ 5 bp)	46955	72525	48317	47113	72893	48781
# indels (> 5 bp)	1045	1764	1060	1058	1772	1090
Indels length	145423	226126	159161	151582	234268	157493
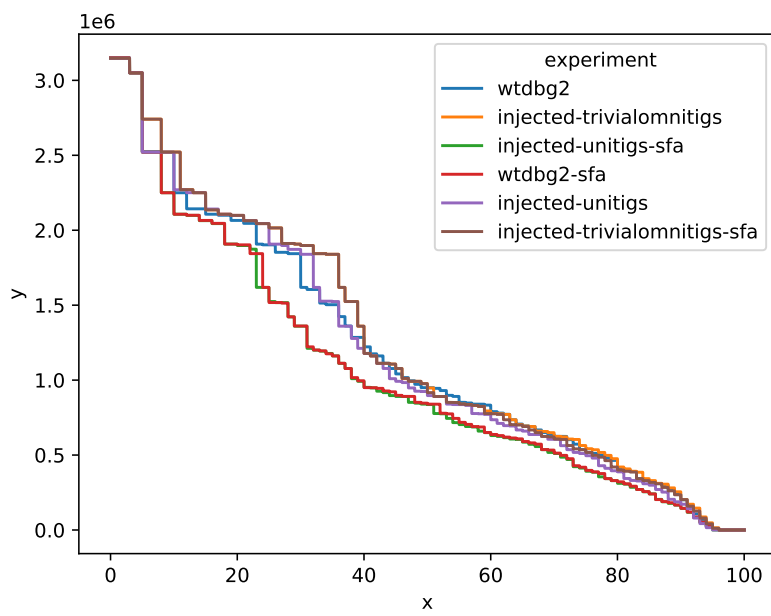
Figure 1: EAxmax
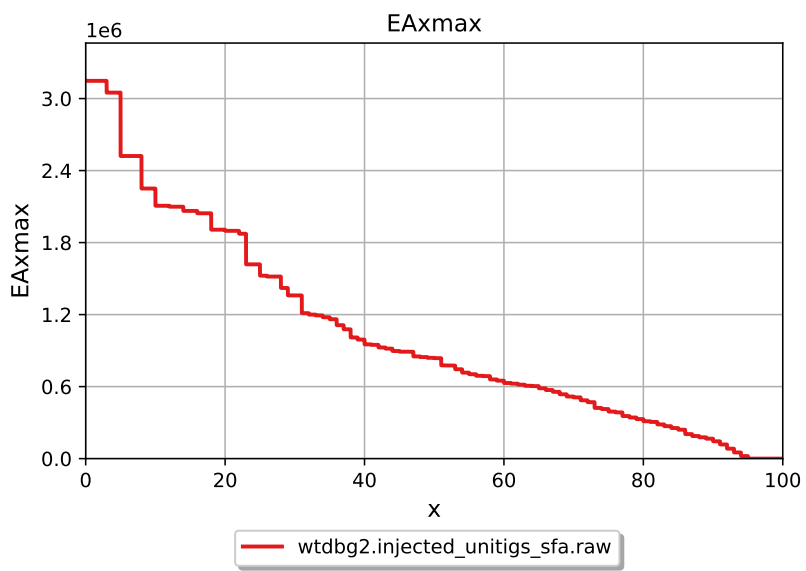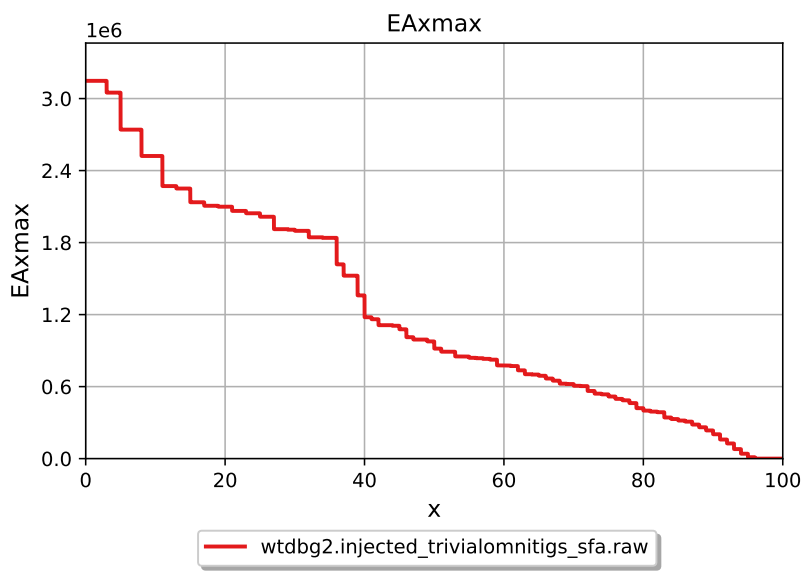
Figure 2: QUAST EAxmax graph for inj uni sfa

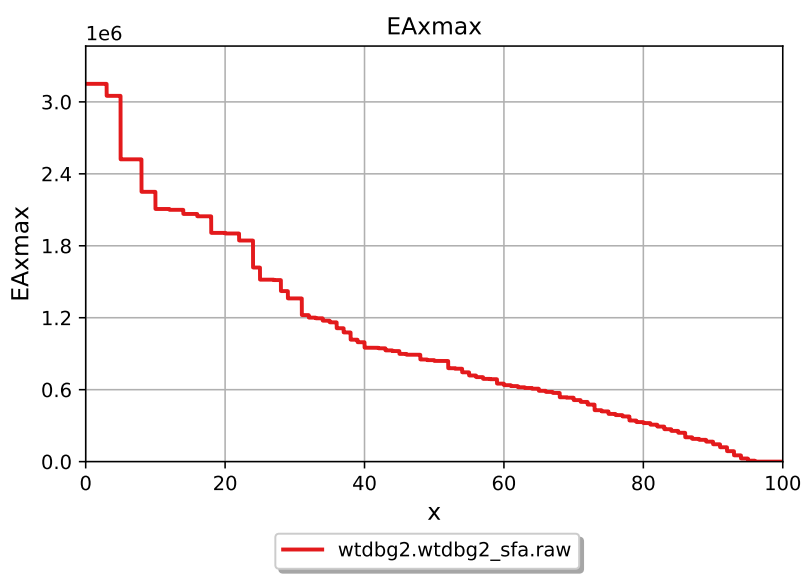Figure 3: QUAST EAxmax graph for inj Y-to-V sfa
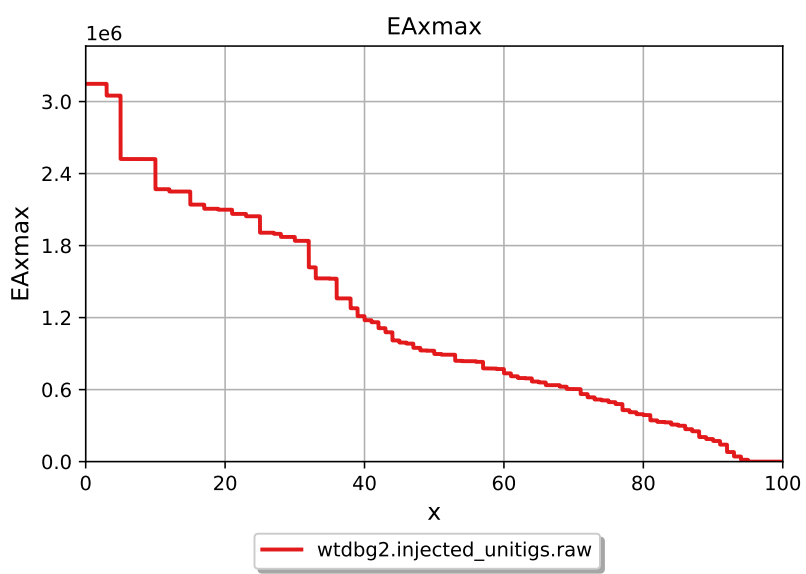
Figure 4: QUAST EAxmax graph for wtdbg2 sfa

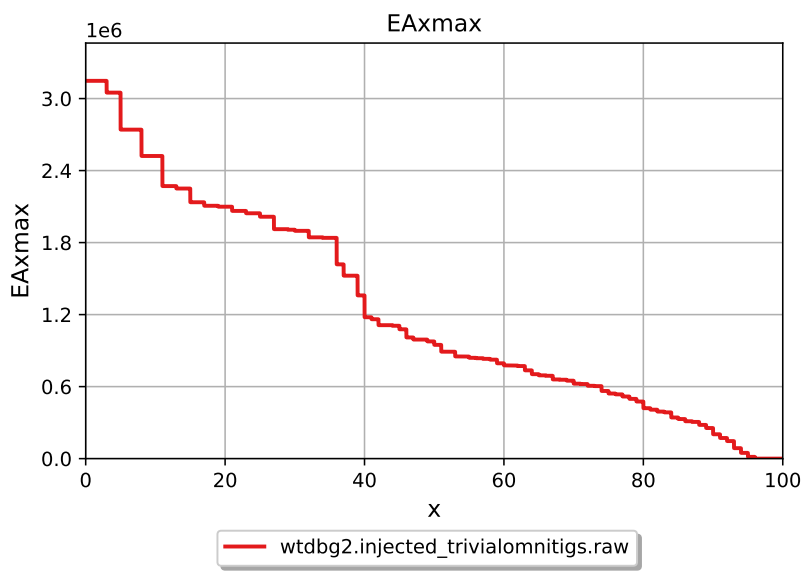Figure 5: QUAST EAxmax graph for inj uni
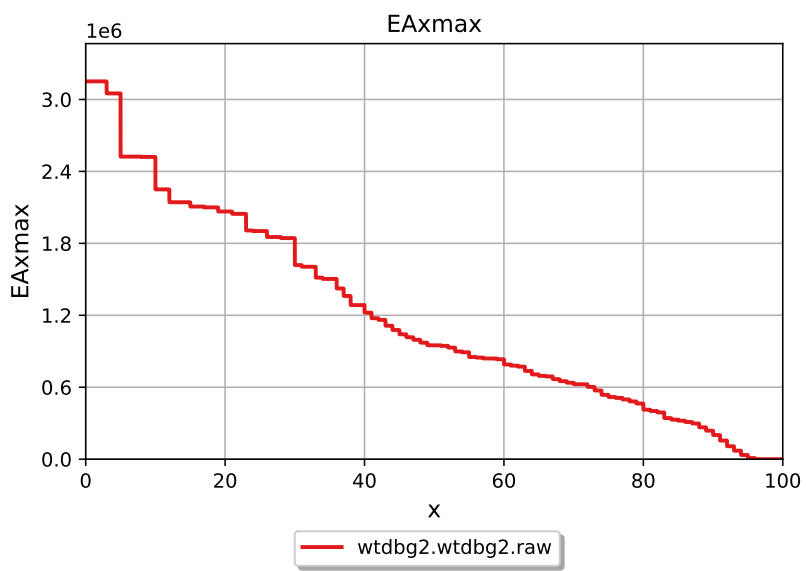
Figure 6: QUAST EAxmax graph for inj Y-to-V

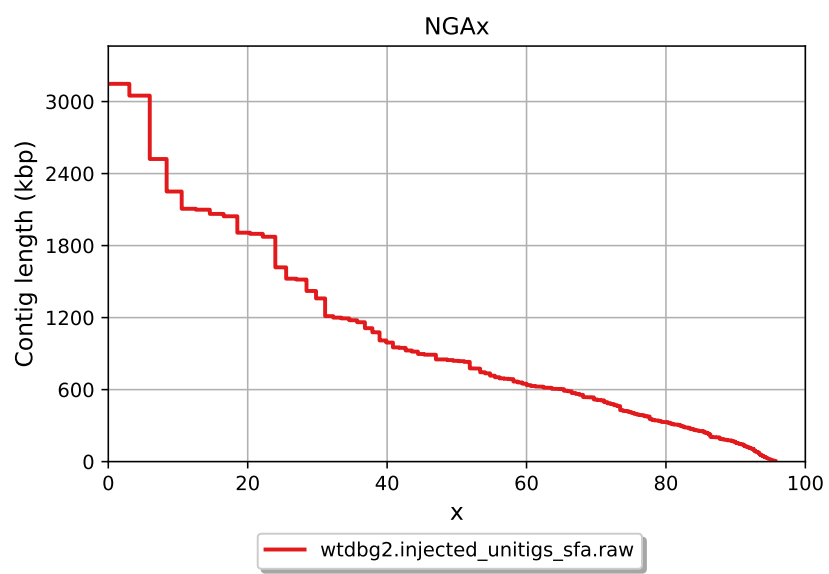Figure 7: QUAST EAxmax graph for wtdbg2

Figure 8: QUAST NGAx graph for inj uni sfa

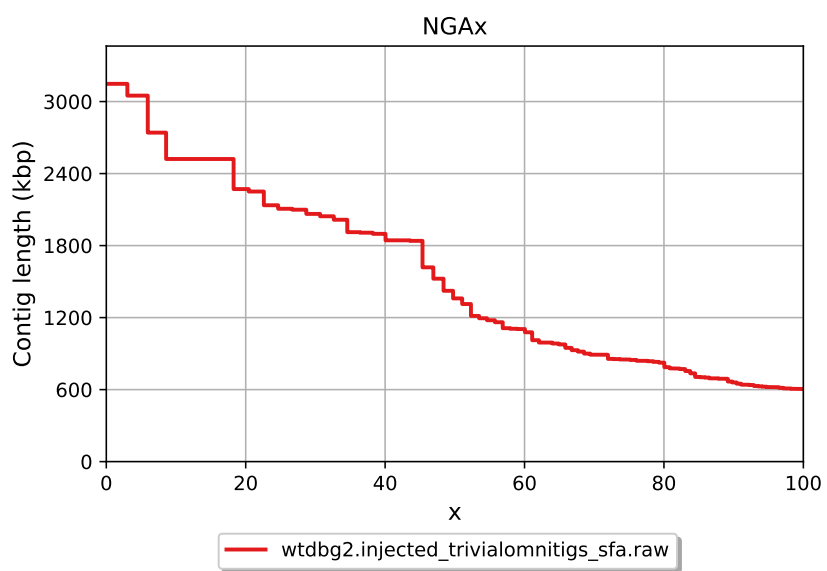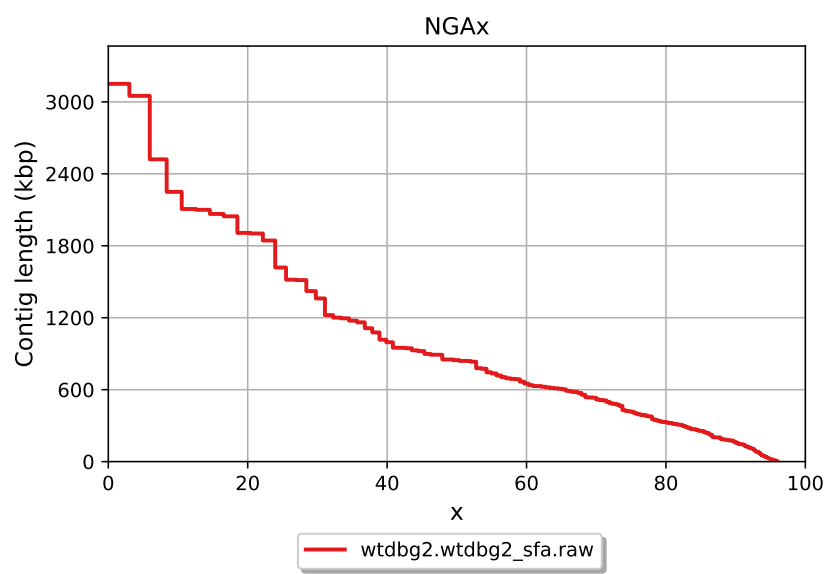Figure 9: QUAST NGAx graph for inj Y-to-V sfa
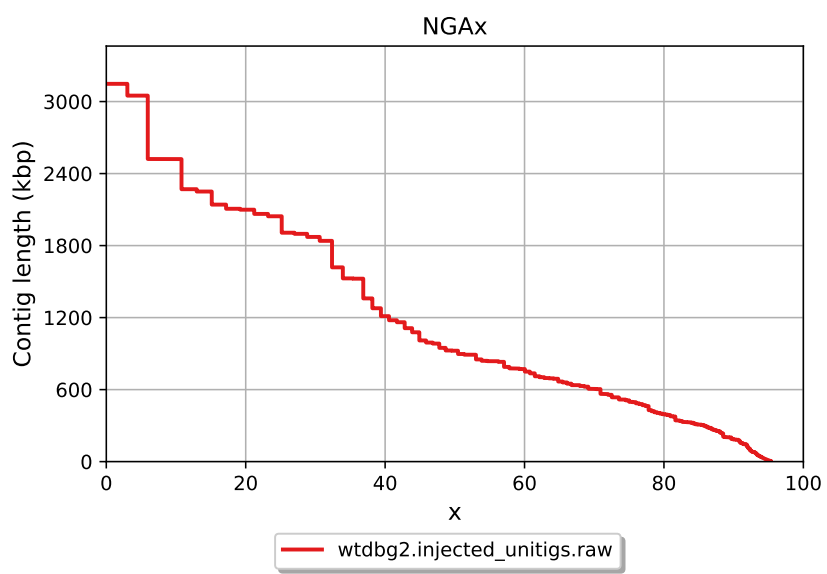
Figure 10: QUAST NGAx graph for wtdbg2 sfa
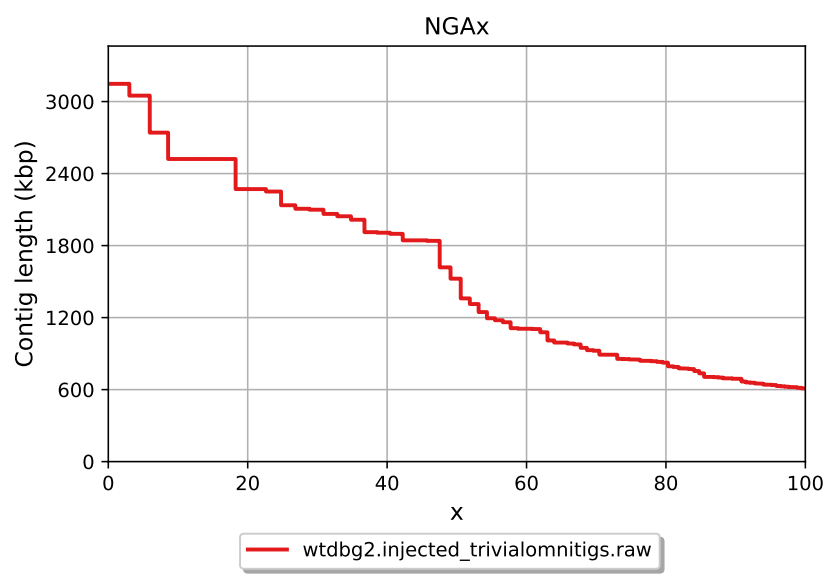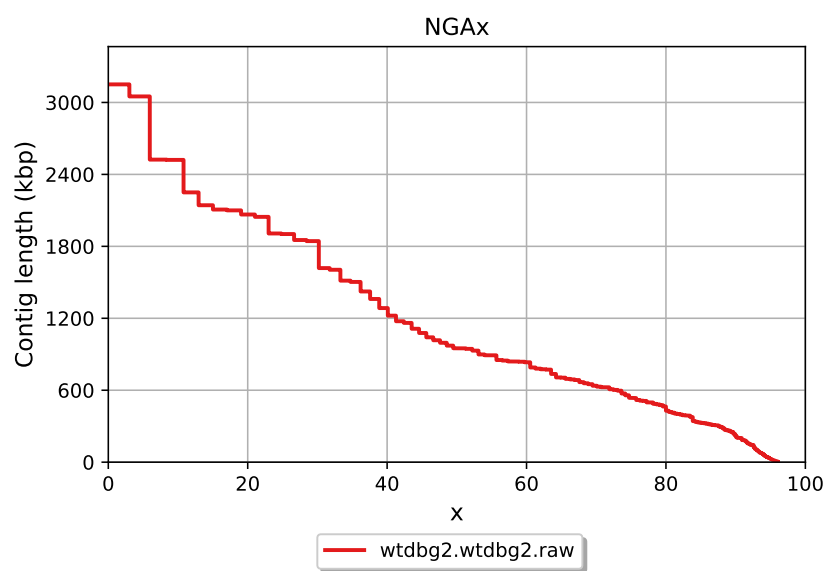
Figure 11: QUAST NGAx graph for inj uni

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

Figure 13: QUAST NGAx graph for wtdbg2