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

Revision: b'bigraph-v0.2.0-66-ga19488e'

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

- Minghui63_sq

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	1487	2102	N/A	1487	2102	N/A
median edge length	3	5	N/A	3	5	N/A
mean edge length	19.3	42.5	N/A	19.3	42.5	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)	7602	7658	9951	5743	6545	7704
# contigs ($\geq$ 1000 bp)	7601	7657	9948	5743	6545	7704
# contigs ($\geq$ 5000 bp)	6953	7113	9763	5487	6310	7599
# contigs ($\geq$ 10000 bp)	5403	5743	7057	4365	5275	5823
# contigs ($\geq$ 25000 bp)	2886	3996	3207	2312	3773	2670
# contigs ($\geq$ 50000 bp)	1756	3034	1828	1455	2900	1552

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)	378647960	727712684	421432424	382462700	731705204	424221196
Total length ($\geq$ 1000 bp)	378647227	727711951	421430582	382462700	731705204	424221196
Total length ($\geq$ 5000 bp)	376458011	725843594	420617866	381452613	730774438	423735240
Total length ($\geq$ 10000 bp)	365268318	715951290	400913225	373266155	723230115	410596296
Total length ($\geq$ 25000 bp)	324785864	688084279	340433238	340148197	699041700	360420045
Total length ($\geq$ 50000 bp)	285336584	653043407	292553501	310318439	667238095	322149916

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	7346	7450	9933	5701	6503	7701
Largest contig	1600148	2258205	1598026	2585237	2278076	1843841
Total length	378081285	727246761	421399138	382346427	731588022	424213299
Reference length	387424359	387424359	387424359	387424359	387424359	387424359
GC (%)	43.20	43.00	43.50	43.22	43.01	43.53
Reference GC (%)	43.61	43.61	43.61	43.61	43.61	43.61
N50	147660	281721	126459	235294	307133	209261
NG50	143013	470611	144991	228628	523711	246081
N75	51144	122626	35557	80042	140288	53706
NG75	45738	354225	51383	76267	380605	84037
L50	650	747	803	398	690	478
LG50	683	270	677	409	249	398
L75	1721	1712	2387	1087	1551	1475
LG75	1866	513	1789	1136	471	1064

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	1002	2241	1533	1400	2640	2234
# unique misassemblies	903	1469	1237	1295	1870	1926
# misassembled contigs	556	1225	811	796	1454	1207
Misassembled contigs length	49987898	230305753	54637081	119547296	281590408	133832864
# local misassemblies	745	1944	937	766	1961	983
# unique local misassemblies	645	907	736	655	916	780
# scaffold gap ext. mis.	0	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0	0
# possible TEs	260	810	282	256	810	288
# unaligned mis. contigs	38	40	72	32	35	51
# unaligned contigs	19+669p	16+1146p	45+1096p	13+615p	10+1107p	16+1033p
Unaligned length	3155317	5695941	4777460	3133044	5723962	4614000
Genome fraction (%)	85.915	88.170	89.238	86.457	88.776	89.379
Duplication ratio	1.126	2.112	1.205	1.132	2.110	1.212
# N's per 100 kbp	0.00	0.00	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	83.71	83.30	118.04	85.45	83.27	118.10
# indels per 100 kbp	53.74	47.93	65.31	56.47	49.26	67.74
Largest alignment	1582708	2258133	1582707	2306387	2278004	1582707
Total aligned length	374697535	720588775	416309750	378858145	724766423	419178460
EA50max	132736	215844	135656	190477	241518	206414
Strict EA50max	116729	179514	120672	163389	198223	172807
NGA50	132867	393254	136181	190481	430425	206605
EA75max	39336	75618	44505	57858	85423	66083
Strict EA75max	35916	64801	40637	50955	73827	58713
NGA75	40799	300397	45720	59461	317459	68587
LGA50	724	308	716	488	289	471
LGA75	2029	589	1939	1370	554	1280

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	1002	2241	1533	1400	2640	2234
# contig misassemblies	1002	2241	1533	1400	2640	2234
# c. relocations	235	595	311	323	680	411
# c. translocations	761	1637	1213	1070	1950	1812
# c. inversions	6	9	9	7	10	11
# 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	556	1225	811	796	1454	1207
Misassembled contigs length	49987898	230305753	54637081	119547296	281590408	133832864
# local misassemblies	745	1944	937	766	1961	983
# 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	260	810	282	256	810	288
# unaligned mis. contigs	38	40	72	32	35	51
# mismatches	313654	600243	491407	323722	603509	495040
# indels	201368	345357	271894	213925	356984	283952
# indels (≤ 5 bp)	199782	340360	269791	212234	351925	281756
# indels (> 5 bp)	1586	4997	2103	1691	5059	2196
Indels length	379618	902320	496964	467727	956435	587457
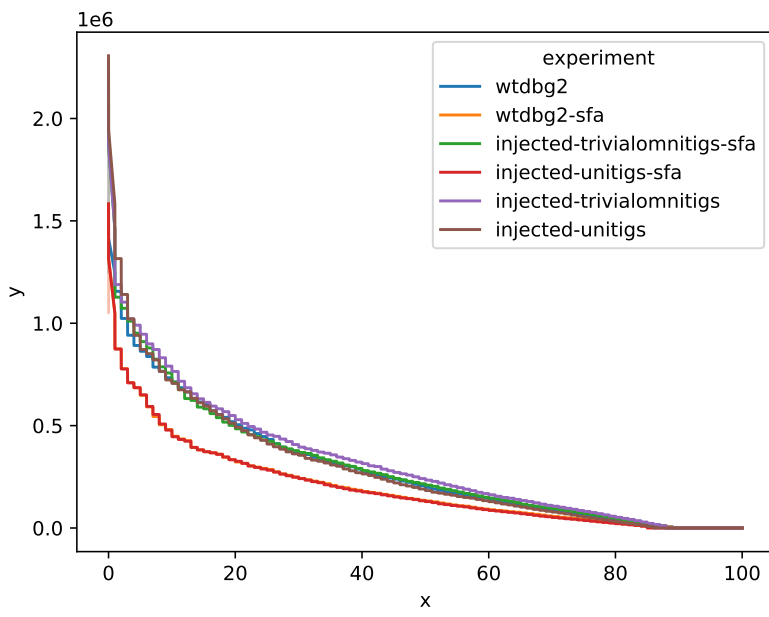
Figure 1: EAxmax
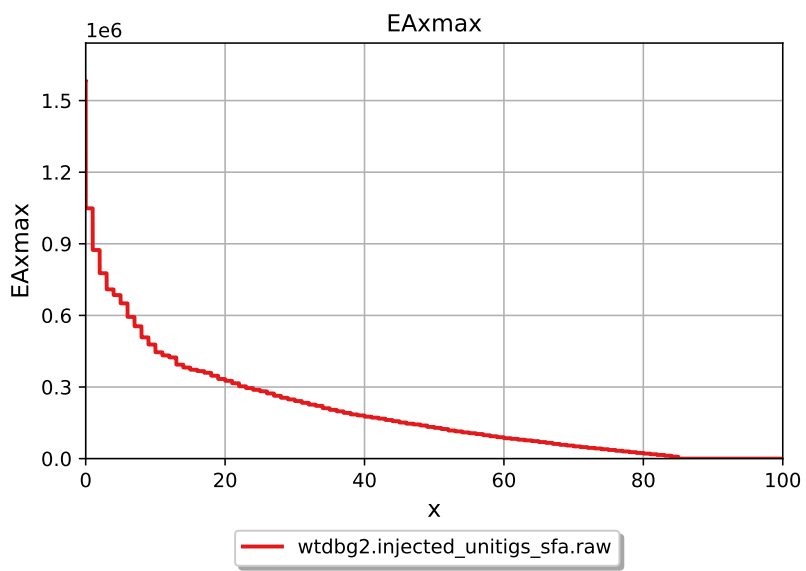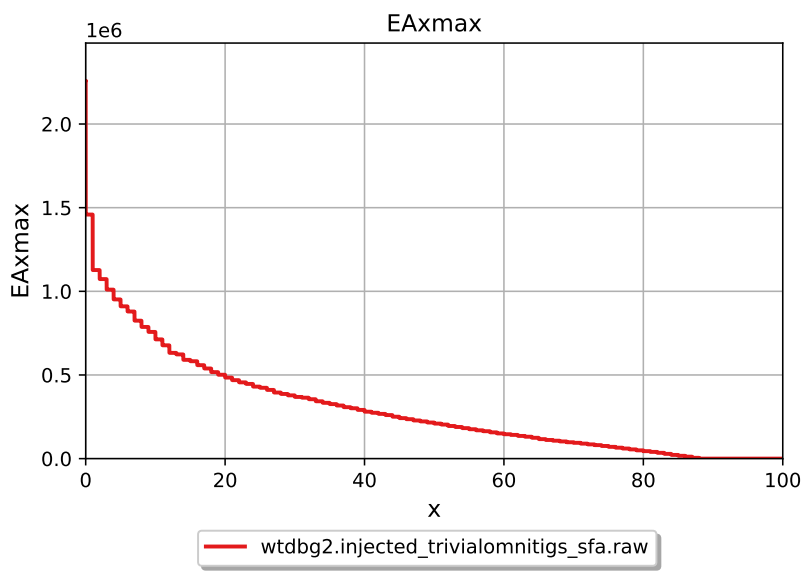
Figure 2: QUAST EAxmax graph for inj uni sfa

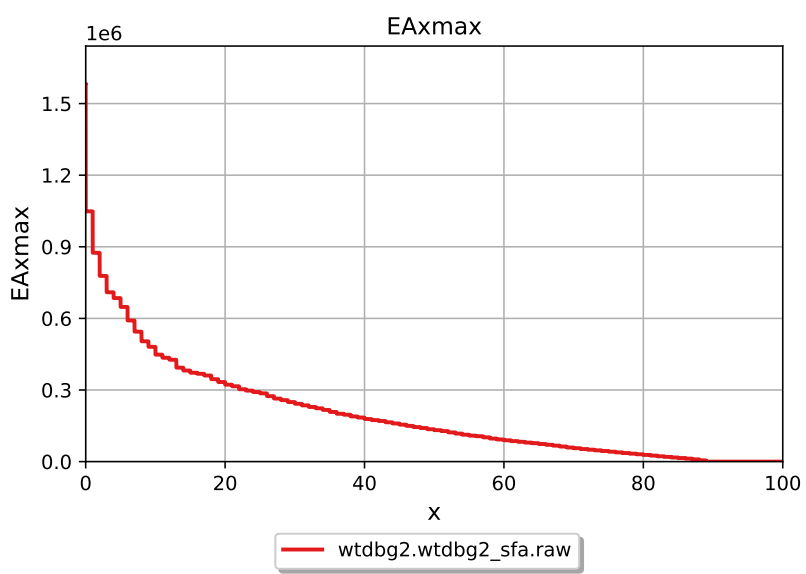Figure 3: QUAST EAxmax graph for inj Y-to-V sfa
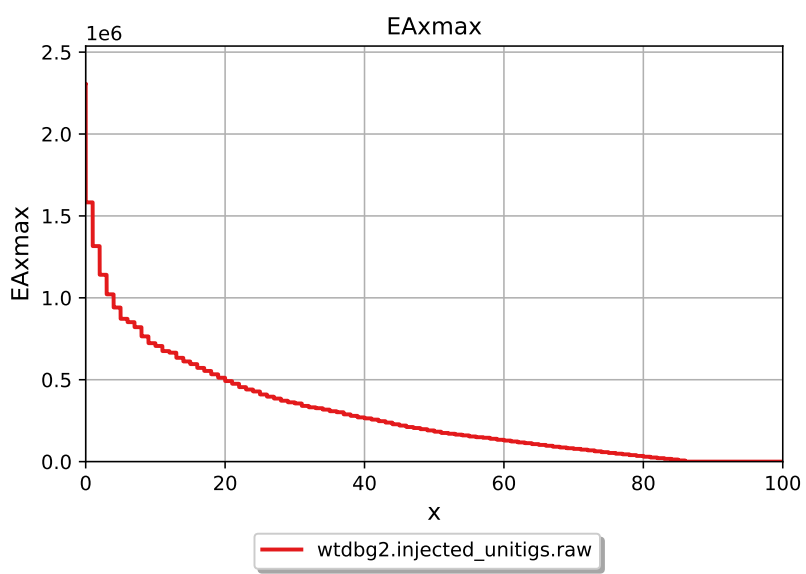
Figure 4: QUAST EAxmax graph for wtdbg2 sfa

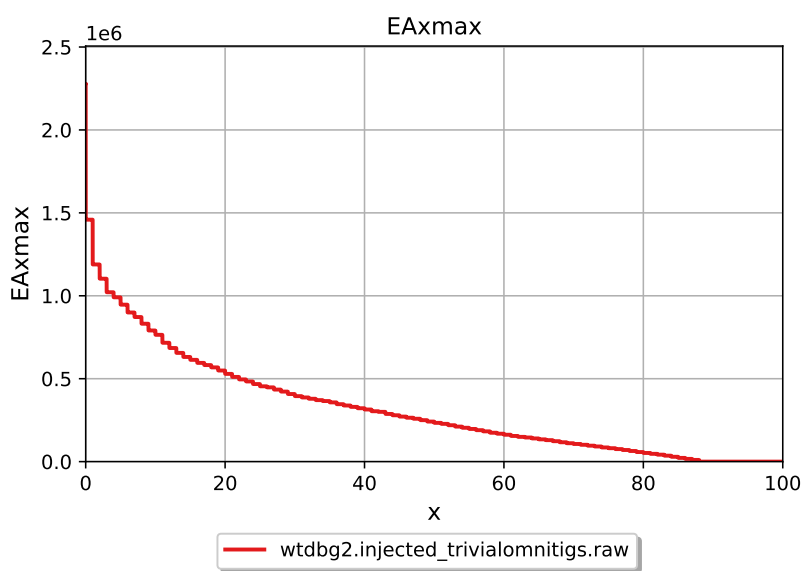Figure 5: QUAST EAxmax graph for inj uni
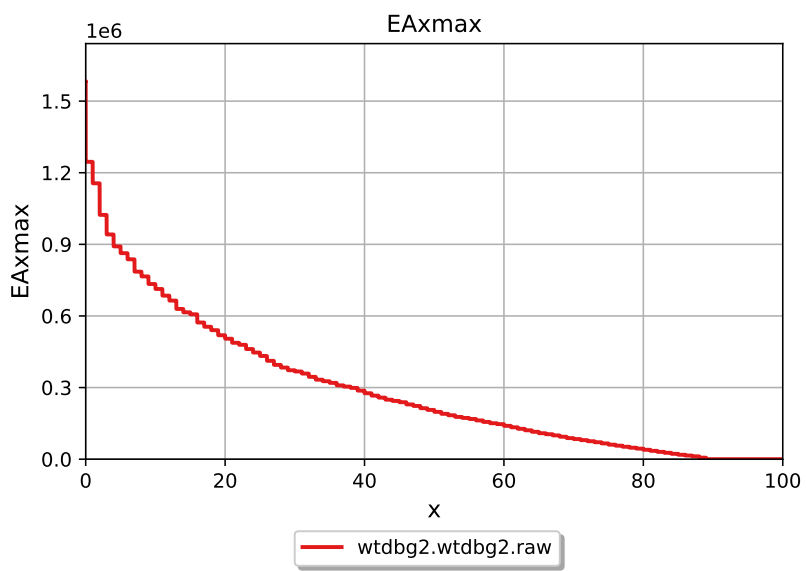
Figure 6: QUAST EAxmax graph for inj Y-to-V

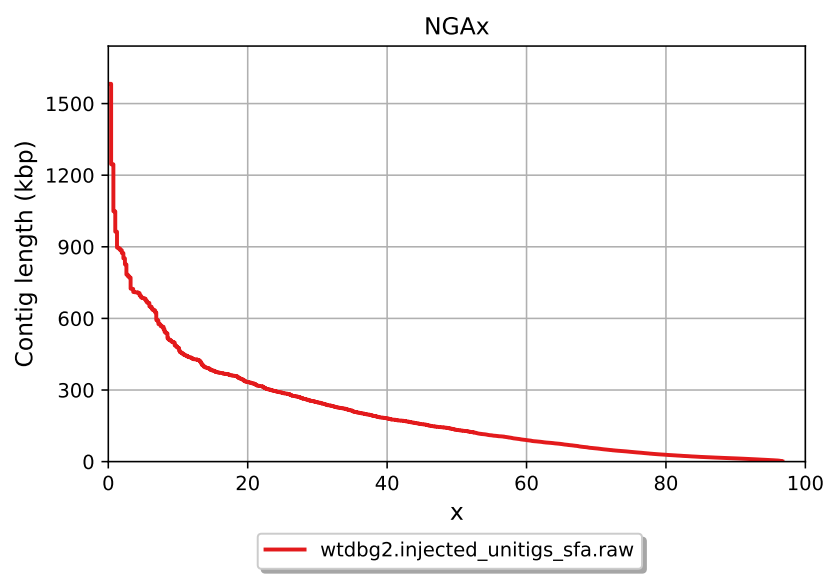Figure 7: QUAST EAxmax graph for wtdbg2

Figure 8: QUAST NGAx graph for inj uni sfa

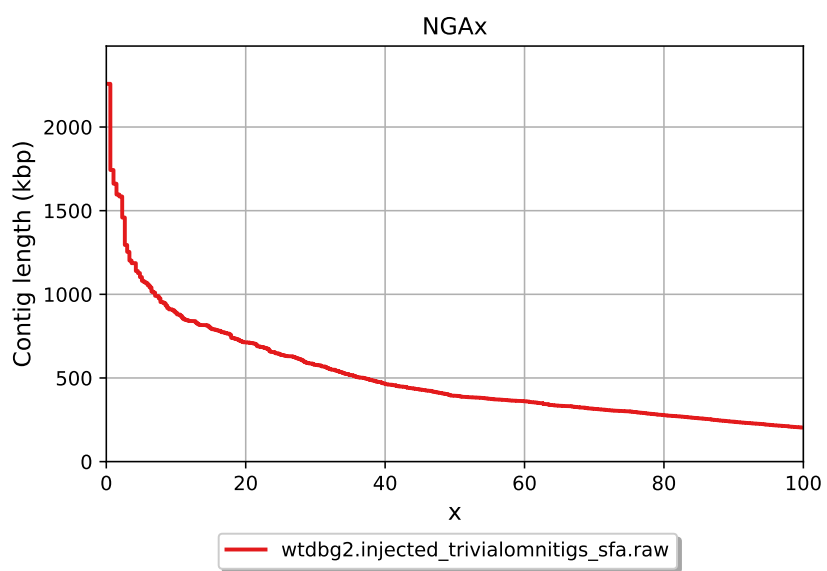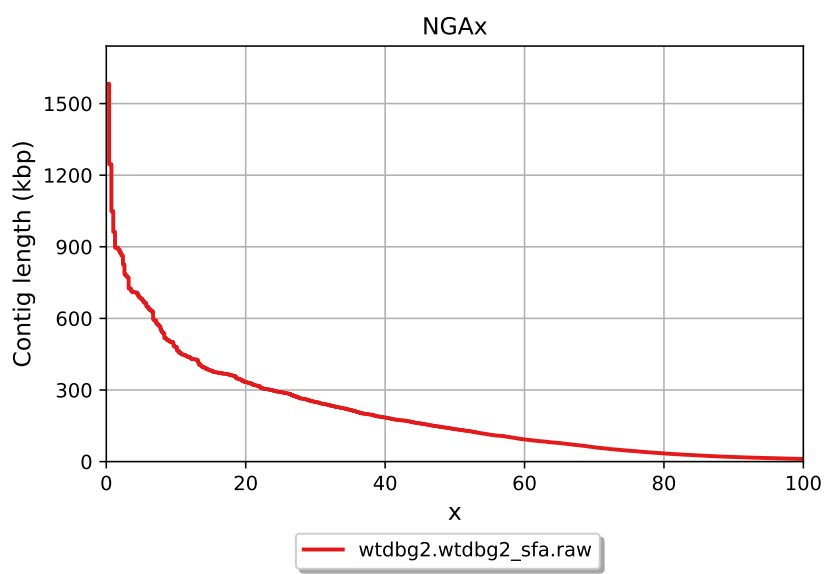Figure 9: QUAST NGAx graph for inj Y-to-V sfa
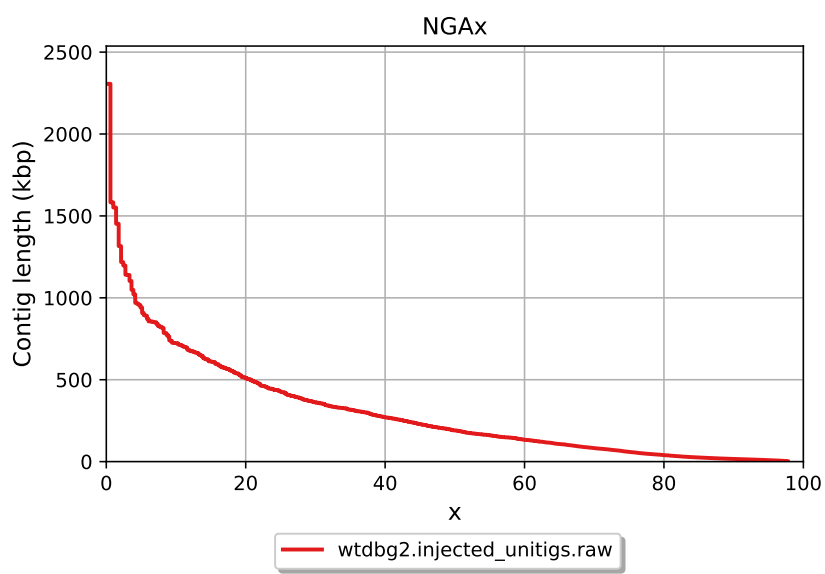
Figure 10: QUAST NGAx graph for wtdbg2 sfa
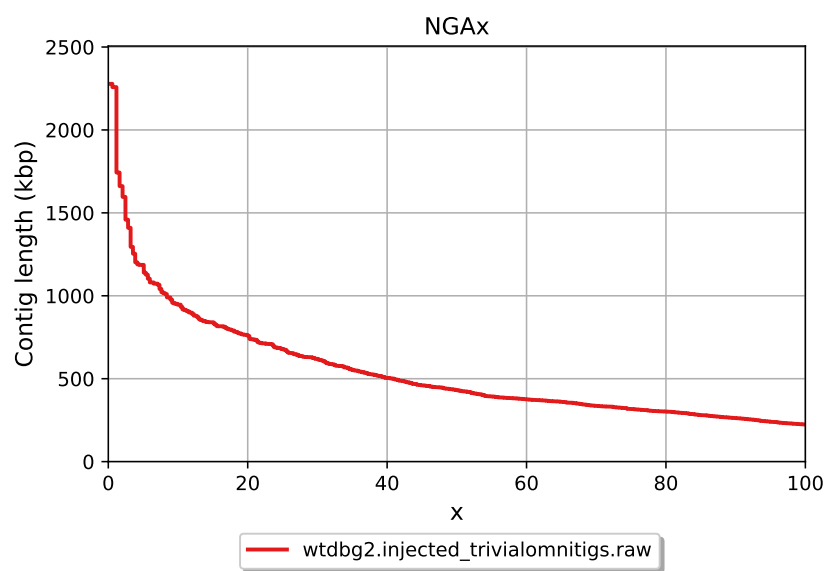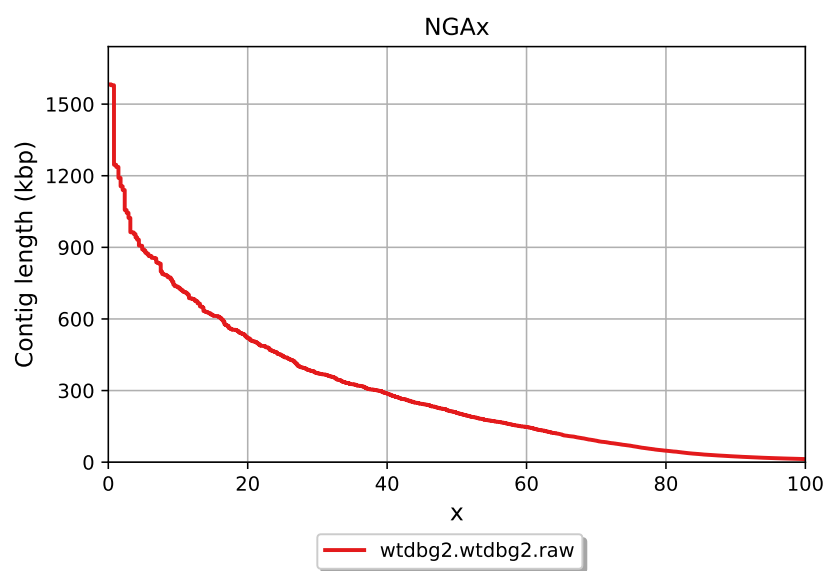
Figure 11: QUAST NGAx graph for inj uni

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

Figure 13: QUAST NGAx graph for wtdbg2