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_ccs

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	3178	3737	N/A	3178	3737	N/A
median edge length	2	115	N/A	2	115	N/A
mean edge length	49.2	232.0	N/A	49.2	232.0	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)	2838	3863	2806	1704	3481	1610
# contigs ($\geq$ 1000 bp)	2838	3863	2806	1704	3481	1610
# contigs ($\geq$ 5000 bp)	2772	3817	2797	1678	3449	1602
# contigs ($\geq$ 10000 bp)	2531	3641	2544	1554	3322	1478
# contigs ($\geq$ 25000 bp)	2068	3346	2071	1317	3081	1242
# contigs ($\geq$ 50000 bp)	1606	2963	1610	1084	2768	1021

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)	366986376	1093739058	367877842	354159624	1089076861	351240619
Total length ($\geq$ 1000 bp)	366986376	1093739058	367877842	354159624	1089076861	351240619
Total length ($\geq$ 5000 bp)	366751283	1093568057	367844594	354058522	1088948642	351212248
Total length ($\geq$ 10000 bp)	365020651	1092282694	366027152	353169109	1088006109	350328658
Total length ($\geq$ 25000 bp)	357356653	1087437038	358168394	349245599	1084026685	346409836
Total length ($\geq$ 50000 bp)	340490208	1073576708	341335458	340848140	1072746305	338236071

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	2818	3853	2802	1702	3478	1606
Largest contig	3258383	3868404	3258382	4279158	3868404	4273861
Total length	366940338	1093717141	367867822	354154899	1089069236	351230599
Reference length	387424359	387424359	387424359	387424359	387424359	387424359
GC (%)	43.43	43.46	43.43	43.50	43.46	43.50
Reference GC (%)	43.61	43.61	43.61	43.61	43.61	43.61
N50	280845	562856	279334	498982	601358	513597
NG50	262375	1090100	262375	445494	1137525	459469
N75	134228	288783	133922	235394	314664	255646
NG75	112168	914062	113316	170577	949636	174561
L50	369	592	370	199	559	187
LG50	407	132	406	235	127	224
L75	840	1265	843	454	1177	426
LG75	965	229	961	578	220	555

Table 7: QUAST: alignment 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
# misassemblies	659	3231	663	742	3299	780
# unique misassemblies	634	2237	638	717	2285	752
# misassembled contigs	216	1595	221	235	1585	241
Misassembled contigs length	27722352	559535450	27447884	63332601	600850980	74820787
# local misassemblies	428	1306	414	421	1329	403
# unique local misassemblies	359	621	351	362	625	338
# scaffold gap ext. mis.	0	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0	0
# possible TEs	44	180	56	48	184	62
# unaligned mis. contigs	23	30	24	17	21	15
# unaligned contigs	2+237p	7+617p	2+255p	1+218p	7+579p	1+217p
Unaligned length	2239281	5714515	2356153	2268707	5797064	2296932
Genome fraction (%)	93.542	97.513	93.702	90.182	97.457	89.388
Duplication ratio	1.006	2.880	1.007	1.007	2.869	1.008
# N's per 100 kbp	0.00	0.00	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	36.33	48.28	35.96	39.64	48.76	40.47
# indels per 100 kbp	28.78	29.73	28.99	29.52	29.82	30.11
Largest alignment	3258383	3868396	3258382	4279158	3868396	4273861
Total aligned length	364554928	1086680471	365363871	351668693	1081867838	348730655
EA50max	254805	562451	255434	406744	600683	412263
Strict EA50max	242152	539491	242084	373364	563003	382859
NGA50	254805	896152	255434	406744	926961	412263
EA75max	105654	290779	106918	149648	319480	149184
Strict EA75max	100651	271049	102135	139942	299485	140875
NGA75	105708	704473	106918	149648	735273	149184
LGA50	422	162	421	261	156	253
LGA75	1011	285	1006	644	274	634

Table 8: QUAST: misassembly 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
# misassemblies	659	3231	663	742	3299	780
# contig misassemblies	659	3231	663	742	3299	780
# c. relocations	176	826	179	224	860	235
# c. translocations	479	2382	477	514	2416	538
# c. inversions	4	23	7	4	23	7
# 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	216	1595	221	235	1585	241
Misassembled contigs length	27722352	559535450	27447884	63332601	600850980	74820787
# local misassemblies	428	1306	414	421	1329	403
# 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	44	180	56	48	184	62
# unaligned mis. contigs	23	30	24	17	21	15
# mismatches	132449	524616	131393	139400	527466	141119
# indels	104920	323094	105930	103814	322598	105008
# indels ($\leq$ 5 bp)	103701	317372	104659	102620	316884	103716
# indels ($>$ 5 bp)	1219	5722	1271	1194	5714	1292
Indels length	343621	1382898	381505	368205	1385626	428361
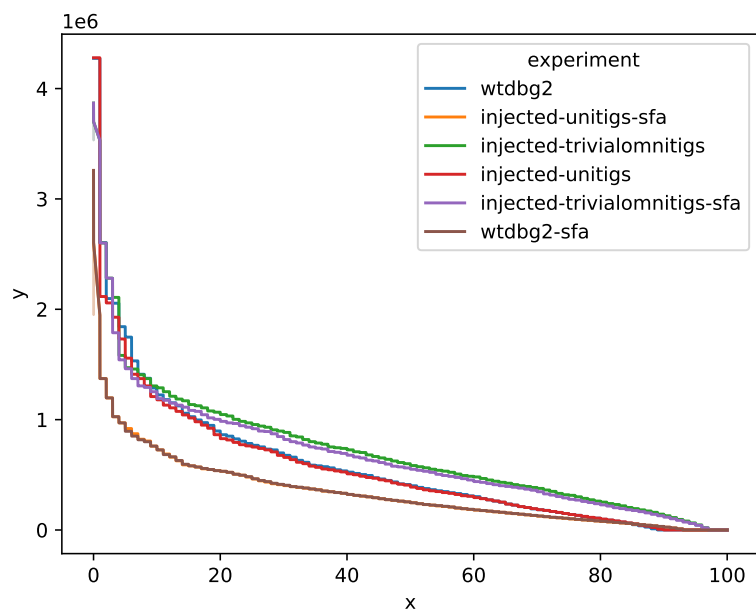
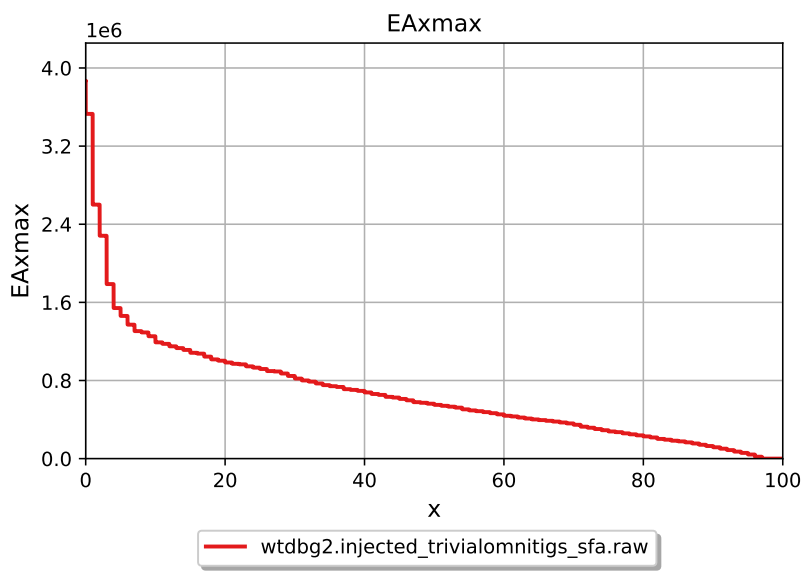Figure 1: EAxmax
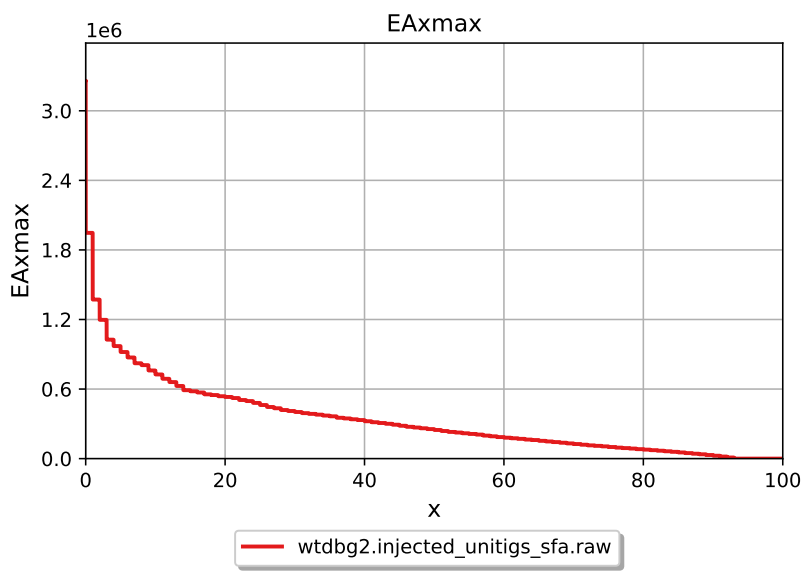
Figure 2: QUAST EAxmax graph for inj uni sfa

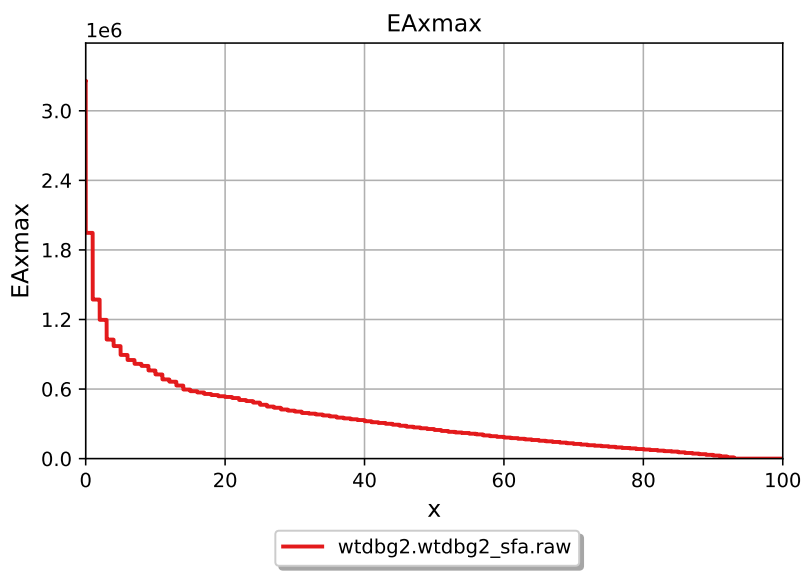Figure 3: QUAST EAxmax graph for inj Y-to-V sfa

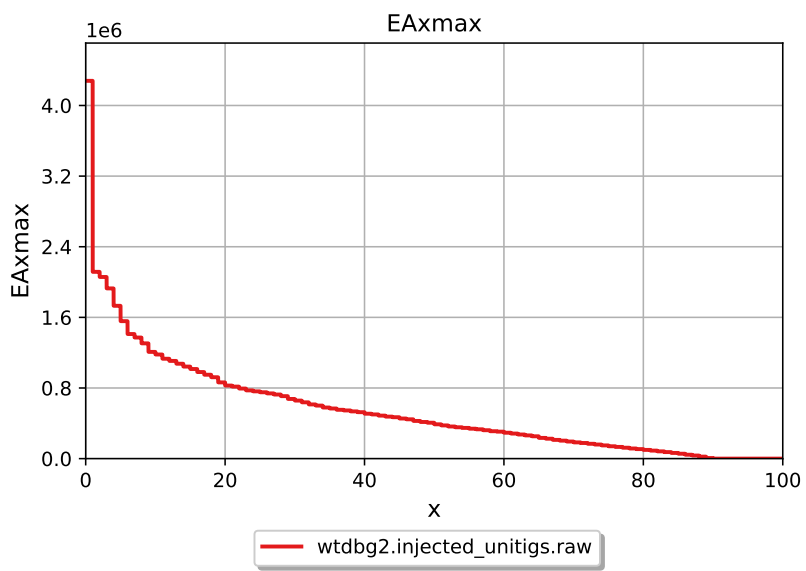Figure 4: QUAST EAxmax graph for wtdbg2 sfa

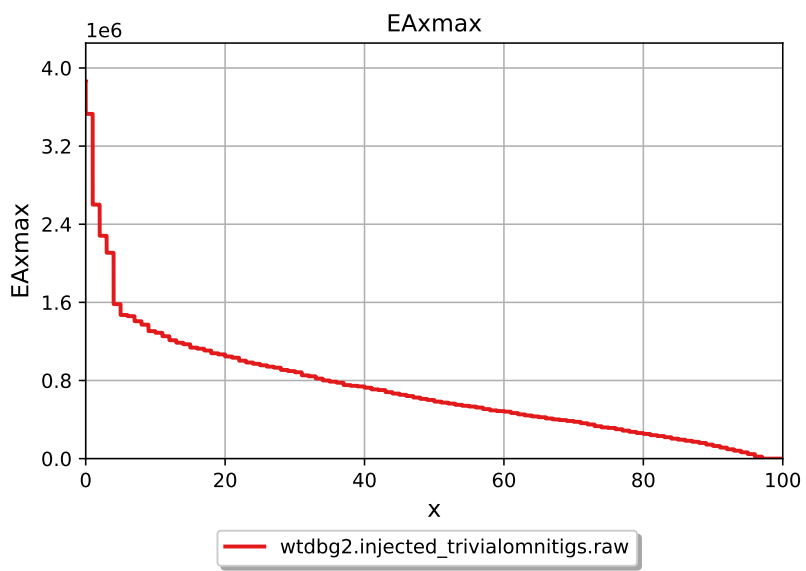Figure 5: QUAST EAxmax graph for inj uni
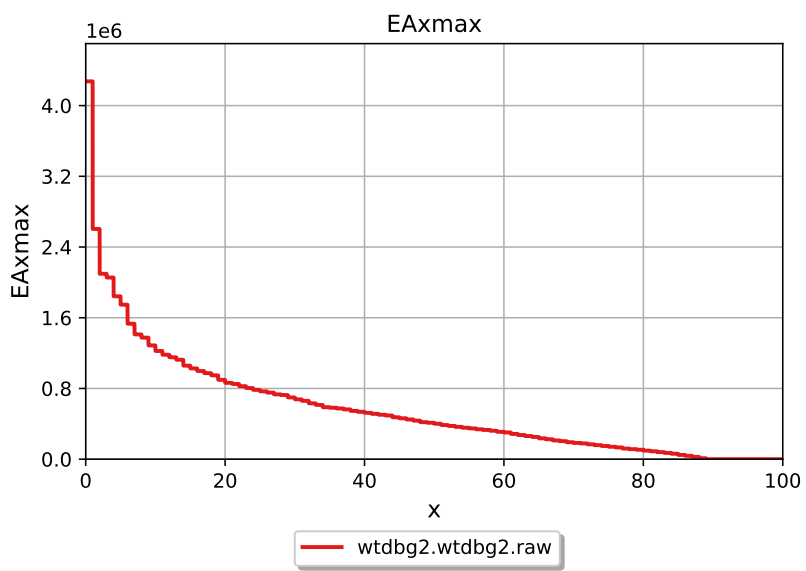
Figure 6: QUAST EAxmax graph for inj Y-to-V

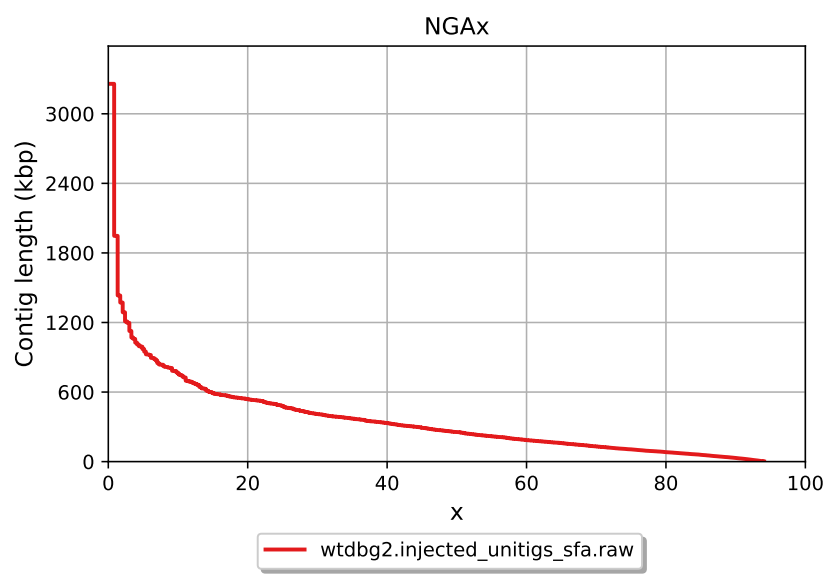Figure 7: QUAST EAxmax graph for wtdbg2

Figure 8: QUAST NGAx graph for inj uni sfa

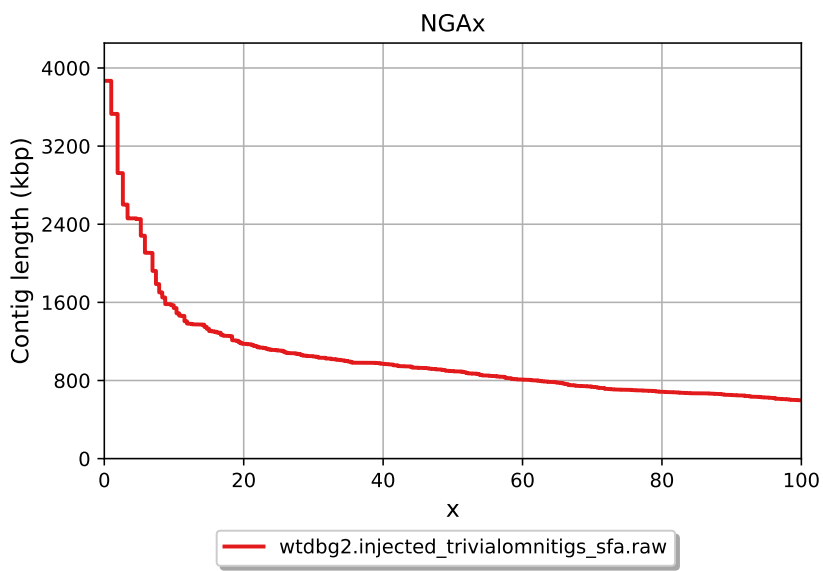Figure 9: QUAST NGAx graph for inj Y-to-V sfa

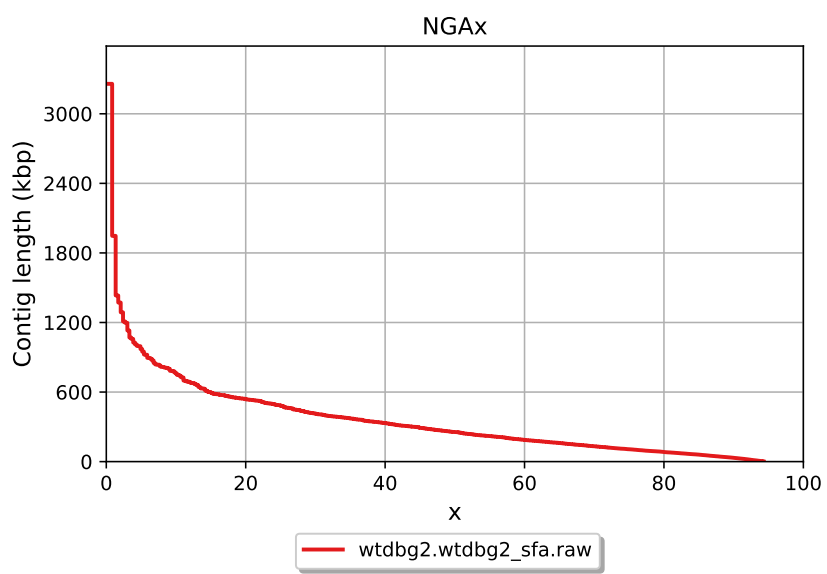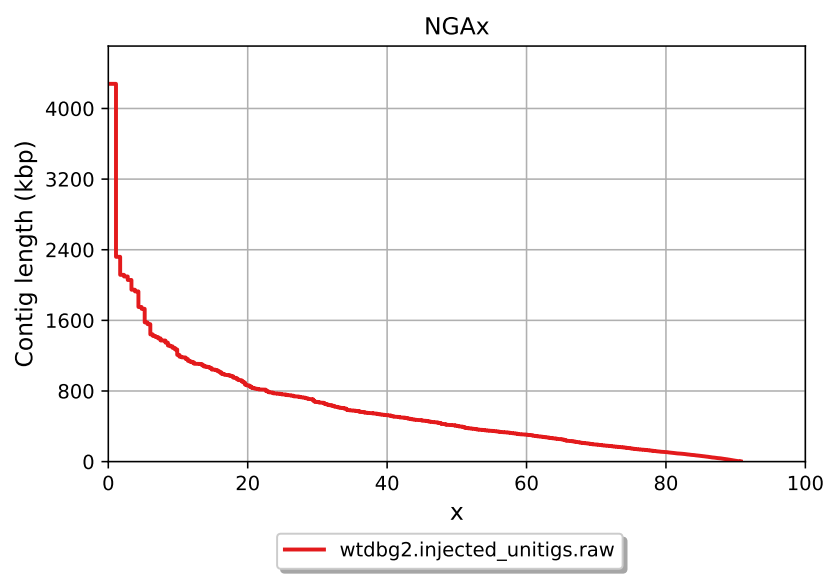Figure 10: QUAST NGAx graph for wtdbg2 sfa
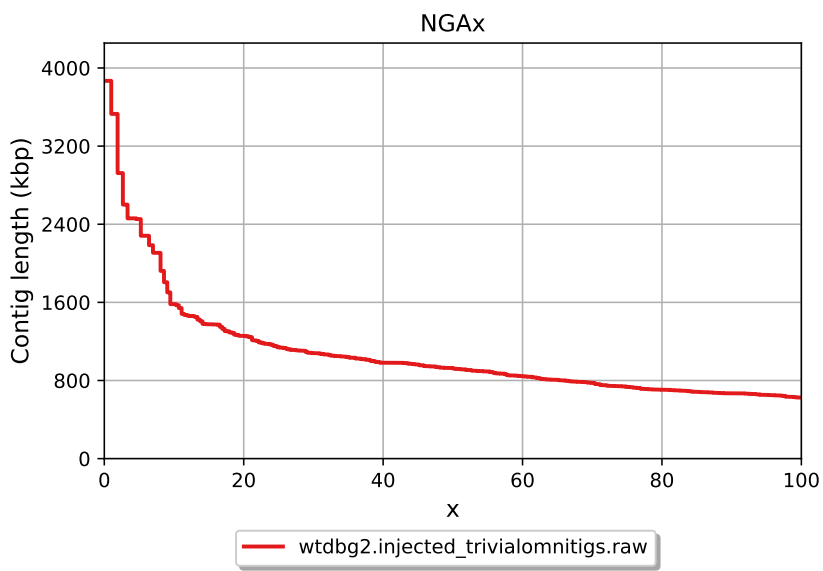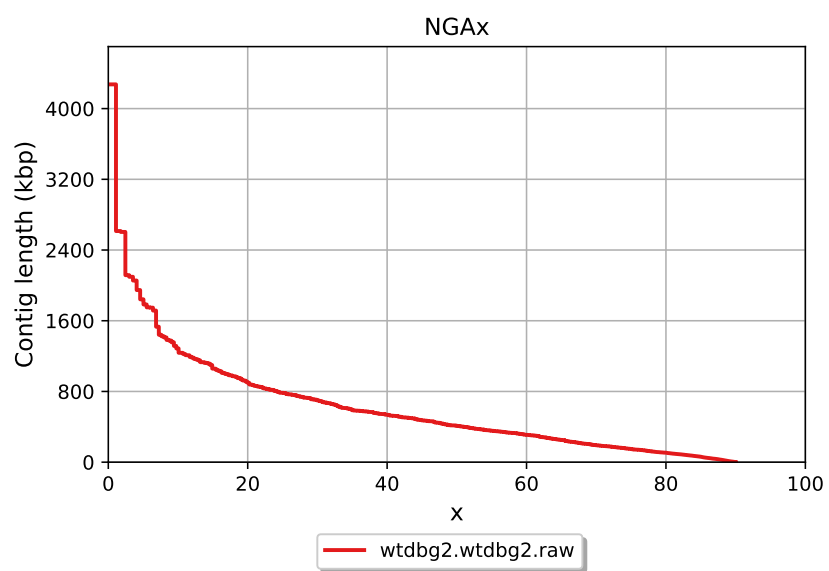
Figure 11: QUAST NGAx graph for inj uni

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

Figure 13: QUAST NGAx graph for wtdbg2