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):

- D.melanogaster_ISO1

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	10763	25340	N/A	10763	25340	N/A
median edge length	2	3	N/A	2	3	N/A
mean edge length	48.2	101.7	N/A	48.2	101.7	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)	712	852	1606	481	665	631
# contigs ($\geq$ 1000 bp)	710	850	1606	481	665	631
# contigs ($\geq$ 5000 bp)	601	753	1373	438	624	543
# contigs ($\geq$ 10000 bp)	421	567	834	336	510	397
# contigs ($\geq$ 25000 bp)	229	348	489	200	340	210
# contigs ($\geq$ 50000 bp)	130	229	352	110	206	111

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)	131586152	241701283	136079270	133289830	240831854	136350527
Total length ($\geq$ 1000 bp)	131585069	241700200	136079270	133289830	240831854	136350527
Total length ($\geq$ 5000 bp)	131203207	241354539	135130092	133129941	240682860	136045968
Total length ($\geq$ 10000 bp)	129891257	239993363	131405094	132377323	239828456	134977581
Total length ($\geq$ 25000 bp)	126775548	236410213	125989755	130134258	237029224	131952778
Total length ($\geq$ 50000 bp)	123207010	232050872	121107996	126969128	232192840	128515634

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	677	822	1563	472	656	601
Largest contig	13509618	31980344	2258349	23175650	31980154	23175131
Total length	131513928	241638111	135975954	133269443	240811467	136282519
Reference length	143726002	143726002	143726002	143726002	143726002	143726002
GC (%)	41.70	41.67	41.70	41.63	41.65	41.50
Reference GC (%)	42.01	42.01	42.01	42.01	42.01	42.01
N50	4907997	6538874	541557	15689039	11543110	12018667
NG50	4172948	11940250	513089	15689039	18124697	10619744
N75	1567697	2136704	205230	2409157	3651422	1979116
NG75	813718	10702598	155295	1760335	11935975	1344727
L50	8	9	68	4	7	4
LG50	9	4	75	4	3	5
L75	20	23	169	9	16	11
LG75	29	7	201	13	6	14

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	
# misassemblies	86	233	57	103	253	
# unique misassemblies	86	164	56	103	185	
# misassembled contigs	48	115	47	44	110	
Misassembled contigs length	68776314	180734836	17482926	107265574	198052173	
# local misassemblies	1181	2225	3600	1213	2242	
# unique local misassemblies	1179	1505	3596	1213	1524	
# scaffold gap ext. mis.	0	0	0	0	0	
# scaffold gap loc. mis.	0	0	0	0	0	
# possible TEs	16	34	10	18	34	
# unaligned mis. contigs	71	92	116	65	90	
# unaligned contigs	299 + 311 part	321 + 443 part	808 + 730 part	221 + 219 part	244 + 372 part	370
Unaligned length	11194584	17970132	25915334	12781078	19344416	
Genome fraction (%)	85.352	86.182	77.931	85.474	85.892	
Duplication ratio	0.989	1.820	0.991	0.989	1.809	
# N's per 100 kbp	0.00	0.00	0.00	0.00	0.00	
# mismatches per 100 kbp	450.18	434.82	756.42	448.36	435.50	
# indels per 100 kbp	1175.81	1166.36	1238.98	1177.11	1167.90	
Largest alignment	8934361	11804160	2082608	12220857	12215999	
Total aligned length	120277493	223550117	110055416	120420224	221352930	
EA50max	2252874	2639528	350648	2721422	4198022	
Strict EA50max	221985	231390	41033	230593	235920	
NGA50	2010037	5068310	347227	2721422	6049770	
EA75max	321980	404860	28367	613638	555423	
Strict EA75max	52222	55801	4509	55802	55619	
NGA75	285006	4522615	15093	538044	4528670	
LGA50	17	10	98	13	9	
LGA75	55	17	445	41	16	

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	86	233	57	103	253	113
# contig misassemblies	86	233	57	103	253	113
# c. relocations	55	166	45	80	172	87
# c. translocations	31	63	12	22	76	25
# c. inversions	0	4	0	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	48	115	47	44	110	40
Misassembled contigs length	68776314	180734836	17482926	107265574	198052173	107805107
# local misassemblies	1181	2225	3600	1213	2242	1209
# 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	16	34	10	18	34	24
# unaligned mis. contigs	71	92	116	65	90	69
# mismatches	541467	972036	832486	539912	963994	541189
# indels	1414240	2607410	1363568	1417483	2585179	1422479
# indels (≤ 5 bp)	1407858	2595991	1356611	1411091	2573886	1416037
# indels (> 5 bp)	6382	11419	6957	6392	11293	6442
Indels length	1758026	3253102	1706375	1764629	3225905	1782774
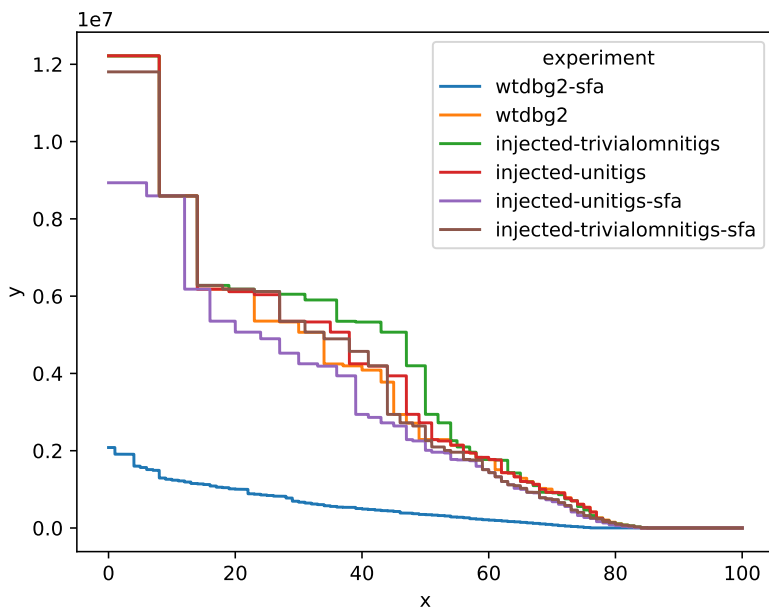
Figure 1: EAxmax
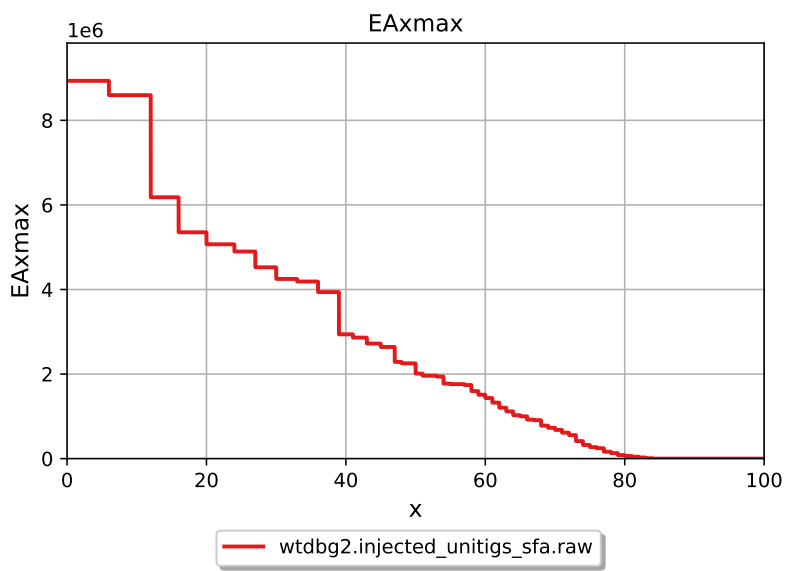
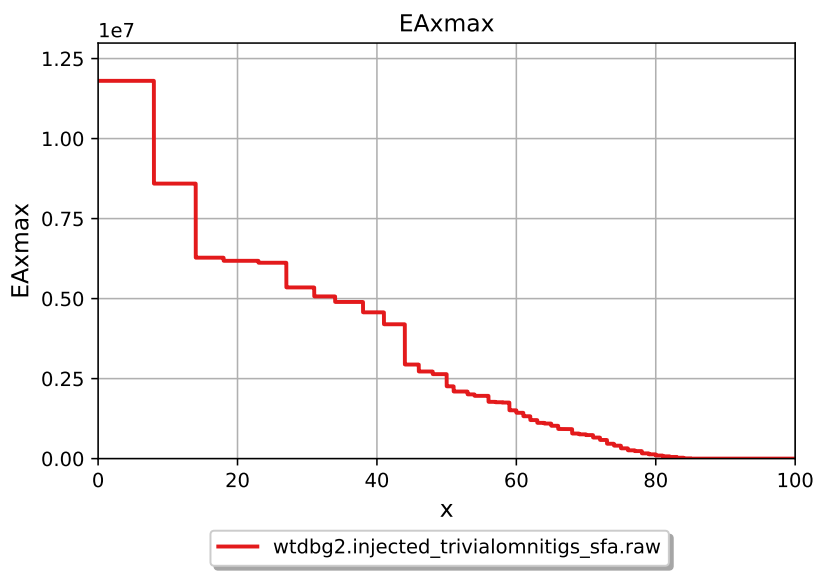Figure 2: QUAST EAxmax graph for inj uni sfa

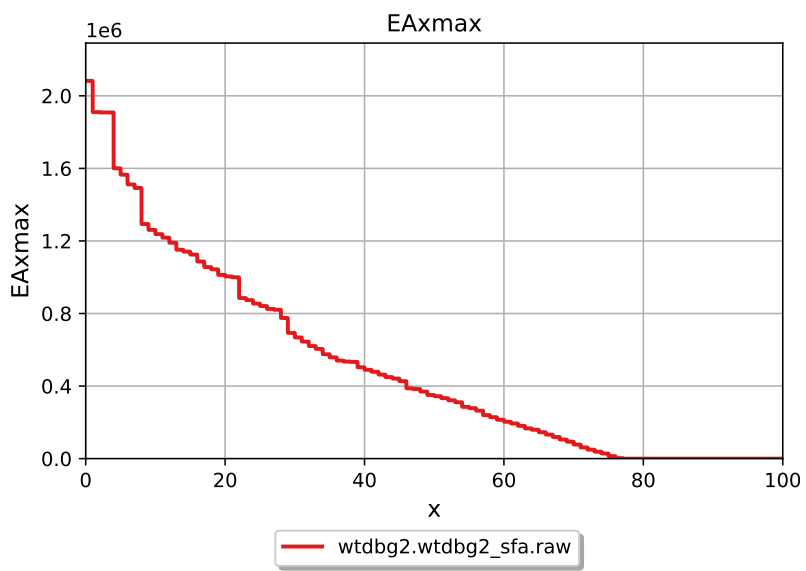Figure 3: QUAST EAxmax graph for inj Y-to-V sfa

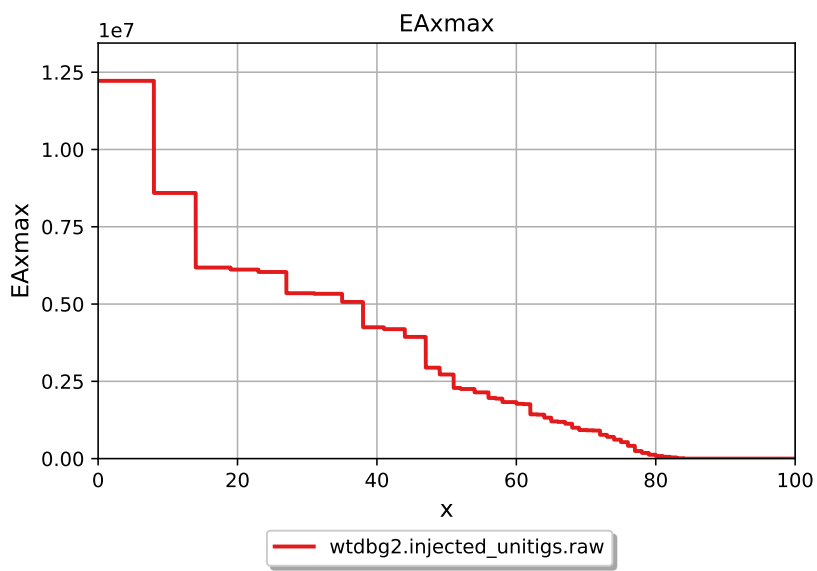Figure 4: QUAST EAxmax graph for wtdbg2 sfa
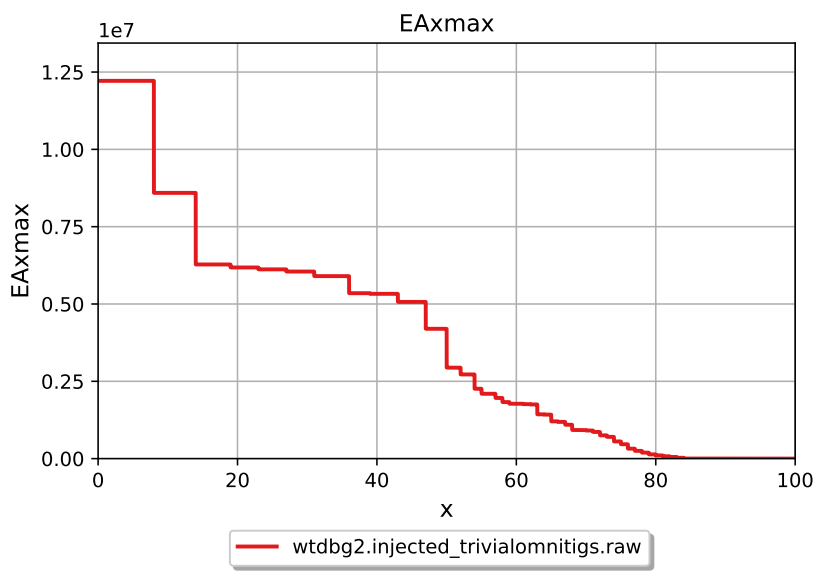
Figure 5: QUAST EAxmax graph for inj uni

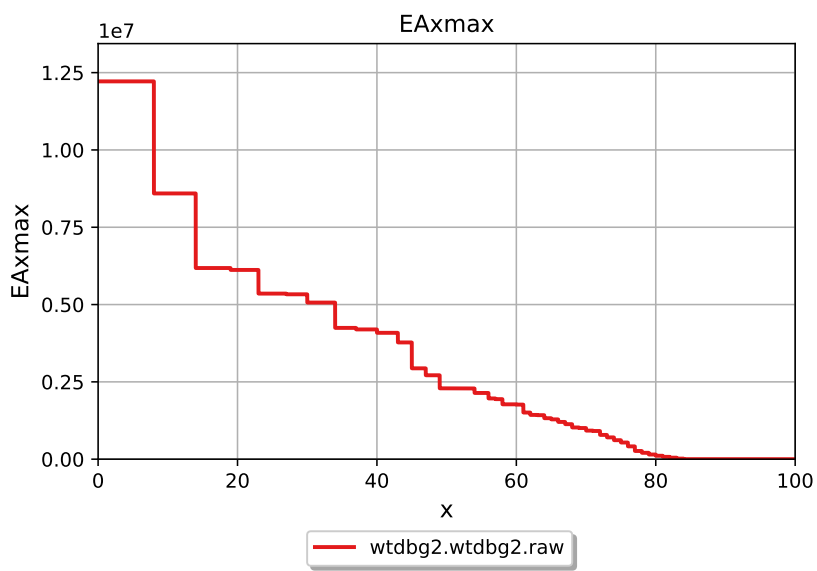Figure 6: QUAST EAxmax graph for inj Y-to-V

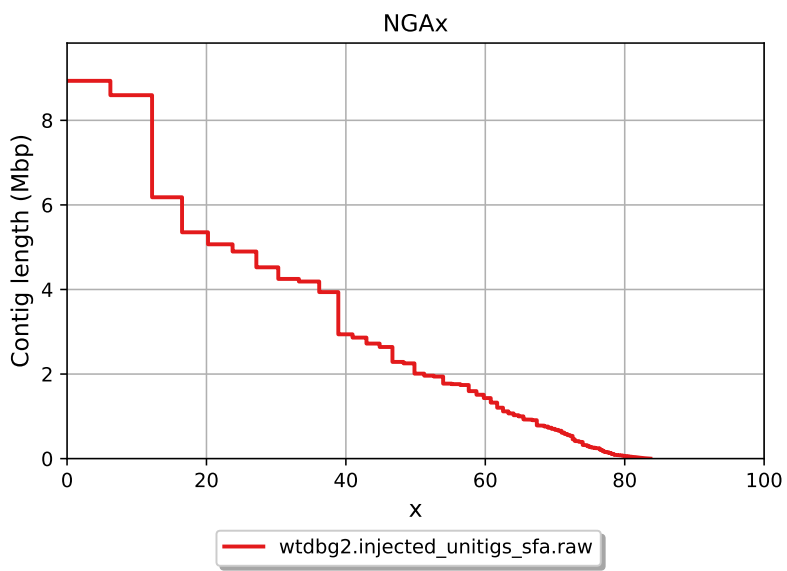Figure 7: QUAST EAxmax graph for wtdbg2
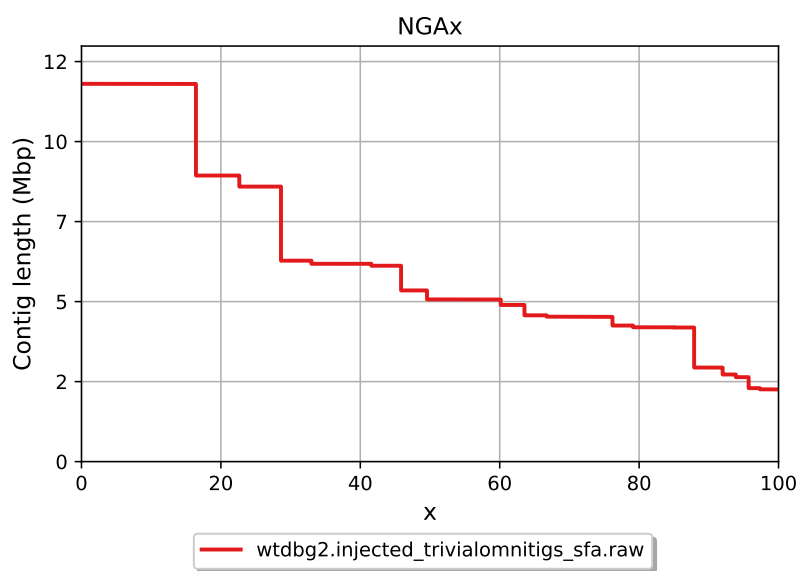
Figure 8: QUAST NGAx graph for inj uni sfa

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

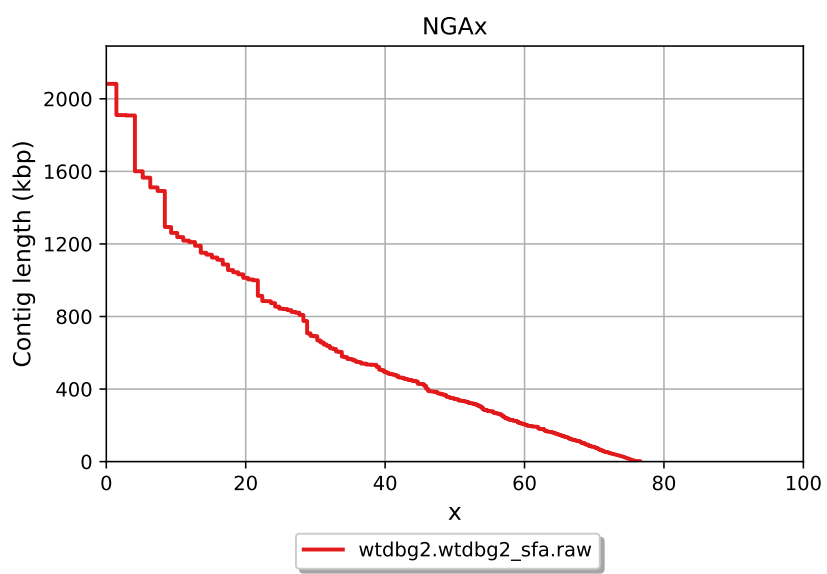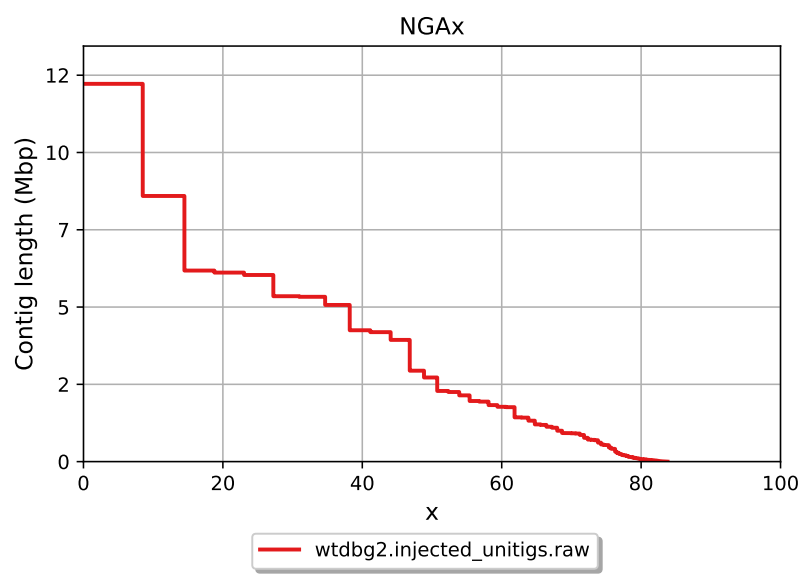Figure 10: QUAST NGAx graph for wtdbg2 sfa
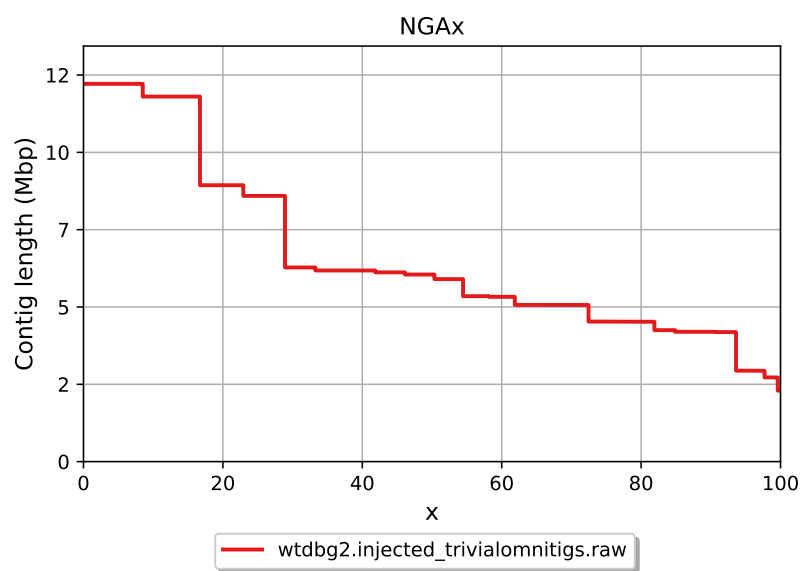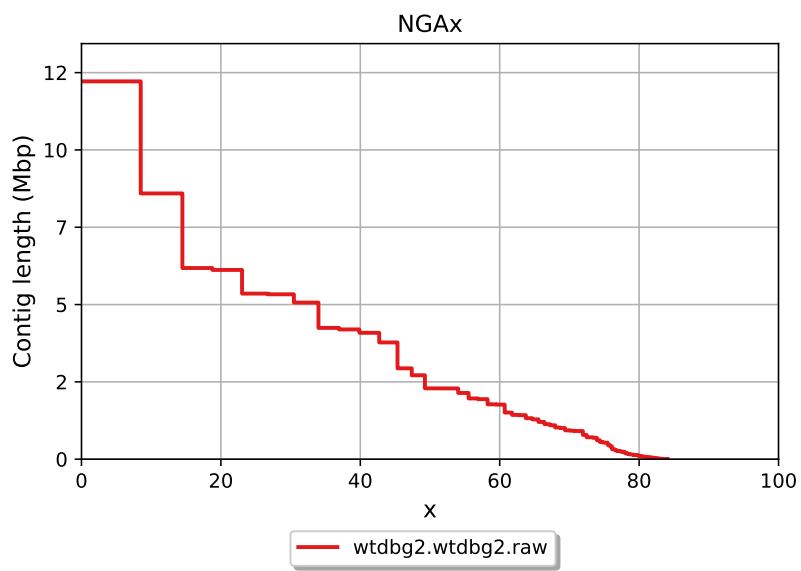
Figure 11: QUAST NGAx graph for inj uni

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

Figure 13: QUAST NGAx graph for wtdbg2