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):

- D.melanogaster_A4

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	8947	15350	N/A	8947	15350	N/A
median edge length	2	4	N/A	2	4	N/A
mean edge length	101.3	319.9	N/A	101.3	319.9	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)	410	489	512	267	398	354
# contigs ($\geq$ 1000 bp)	410	489	512	267	398	354
# contigs ($\geq$ 5000 bp)	361	446	478	242	374	341
# contigs ($\geq$ 10000 bp)	272	354	333	191	310	269
# contigs ($\geq$ 25000 bp)	168	247	180	106	216	134
# contigs ($\geq$ 50000 bp)	125	204	129	73	175	83

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)	134993783	358005105	136879265	131198691	358755769	137731063
Total length ($\geq$ 1000 bp)	134993783	358005105	136879265	131198691	358755769	137731063
Total length ($\geq$ 5000 bp)	134811773	357849603	136749755	131099252	358662984	137682874
Total length ($\geq$ 10000 bp)	134176588	357195290	135707179	130735124	358196529	137172875
Total length ($\geq$ 25000 bp)	132478125	355469285	133238137	129342679	356655467	134965478
Total length ($\geq$ 50000 bp)	130933959	353959905	131372801	128192526	355243155	133168501

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	398	476	506	263	393	351
Largest contig	9811937	16841047	9814815	21249486	19609847	27922500
Total length	134967528	357975430	136866322	131189688	358743788	137724585
Reference length	144125362	144125362	144125362	144125362	144125362	144125362
GC (%)	42.04	41.99	42.00	42.00	41.98	41.97
Reference GC (%)	41.87	41.87	41.87	41.87	41.87	41.87
N50	5136366	5874654	5135913	13095909	7598006	17049462
NG50	4588230	8727892	4590036	13095909	12000082	17049462
N75	1699462	3461124	1517205	5136361	4228353	5136273
NG75	952664	8031143	953677	2006217	9641247	5136273
L50	11	21	11	4	17	4
LG50	12	7	12	4	5	4
L75	22	41	23	8	34	7
LG75	27	11	27	11	9	7

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	136	245	143	156	263	164
# unique misassemblies	133	174	141	155	192	162
# misassembled contigs	48	85	53	40	83	50
Misassembled contigs length	31304300	95554553	29778303	77515712	130473454	100060063
# local misassemblies	278	618	323	318	645	331
# unique local misassemblies	273	414	317	314	439	325
# scaffold gap ext. mis.	0	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0	0
# possible TEs	6	12	8	6	8	8
# unaligned mis. contigs	39	39	58	39	40	65
# unaligned contigs	96+209p	98+290p	136+275p	73+158p	77+255p	98+218p
Unaligned length	4614706	6581364	5800378	5392360	7291393	6727571
Genome fraction (%)	90.039	90.654	90.319	86.862	90.604	90.331
Duplication ratio	1.005	2.690	1.007	1.005	2.691	1.006
# N's per 100 kbp	0.00	0.00	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	36.65	27.46	42.31	40.53	27.91	42.00
# indels per 100 kbp	71.78	64.65	76.08	72.97	64.44	75.84
Largest alignment	9796689	16809467	9797550	20614903	19537279	27861234
Total aligned length	130301459	351143419	130975865	125667867	351184686	130909347
EA50max	3428876	5360495	3826290	7233184	5609343	8262087
Strict EA50max	1703200	2255381	1741840	2245848	2267456	2417890
NGA50	3428876	8586980	3826290	7233184	9998805	8262087
EA75max	885559	1405948	953422	1097297	1942981	2255120
Strict EA75max	519110	926525	523290	507486	953025	926529
NGA75	885559	7665604	953422	1097297	8577992	2255120
LGA50	13	7	13	6	5	5
LGA75	33	11	31	17	9	12

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	136	245	143	156	263	164
# contig misassemblies	136	245	143	156	263	164
# c. relocations	64	112	66	82	126	79
# c. translocations	72	131	77	74	135	85
# c. inversions	0	2	0	0	2	0
# 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	85	53	40	83	50
Misassembled contigs length	31304300	95554553	29778303	77515712	130473454	100060063
# local misassemblies	278	618	323	318	645	331
# 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	6	12	8	6	8	8
# unaligned mis. contigs	39	39	58	39	40	65
# mismatches	47750	96434	55411	50927	98011	54982
# indels	93526	226999	99647	91700	226291	99280
# indels (≤ 5 bp)	93012	226063	99076	91195	225363	98702
# indels (> 5 bp)	514	936	571	505	928	578
Indels length	132755	310735	144217	132791	307918	147178
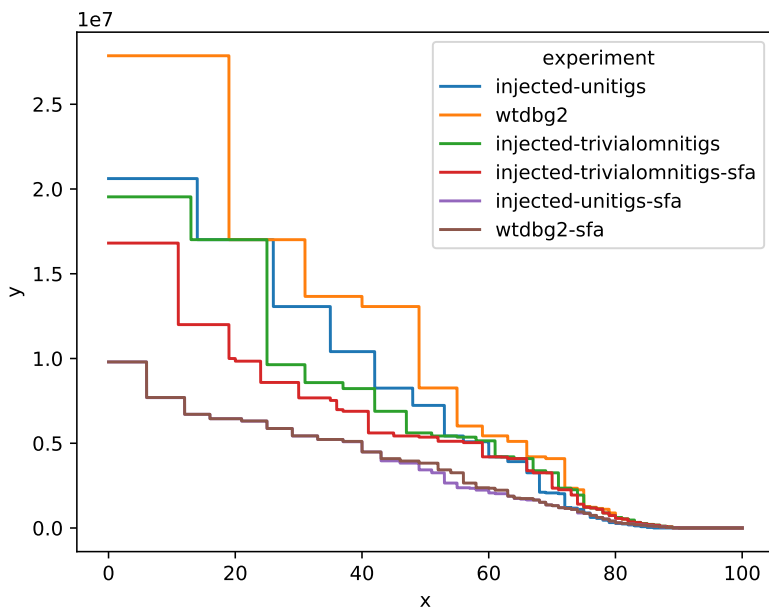
Figure 1: EAxmax
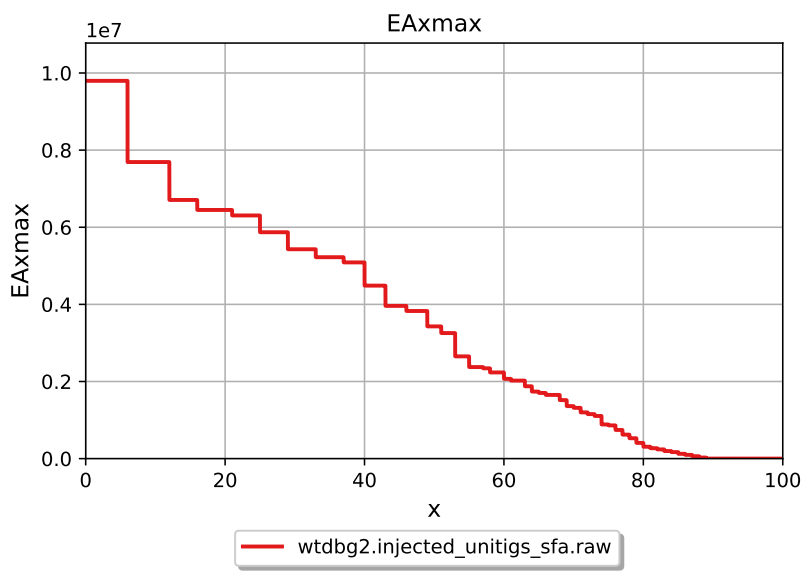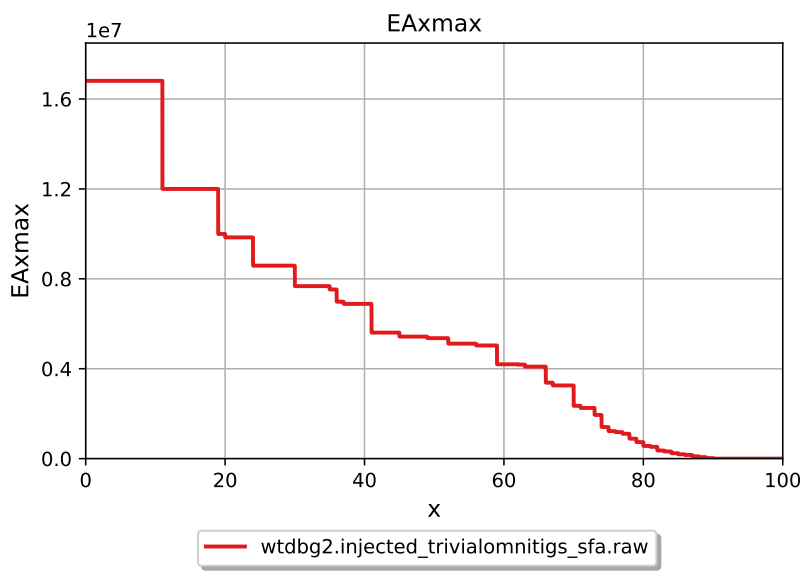
Figure 2: QUAST EAxmax graph for inj uni sfa

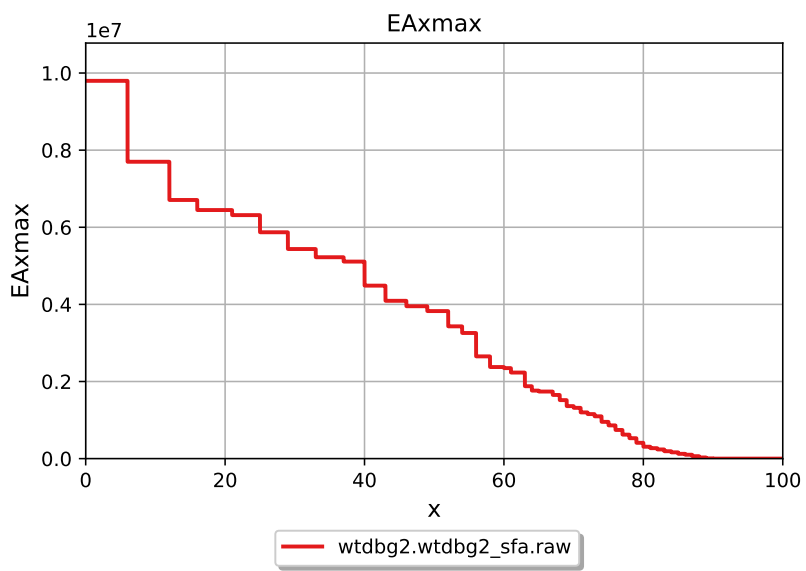Figure 3: QUAST EAxmax graph for inj Y-to-V sfa

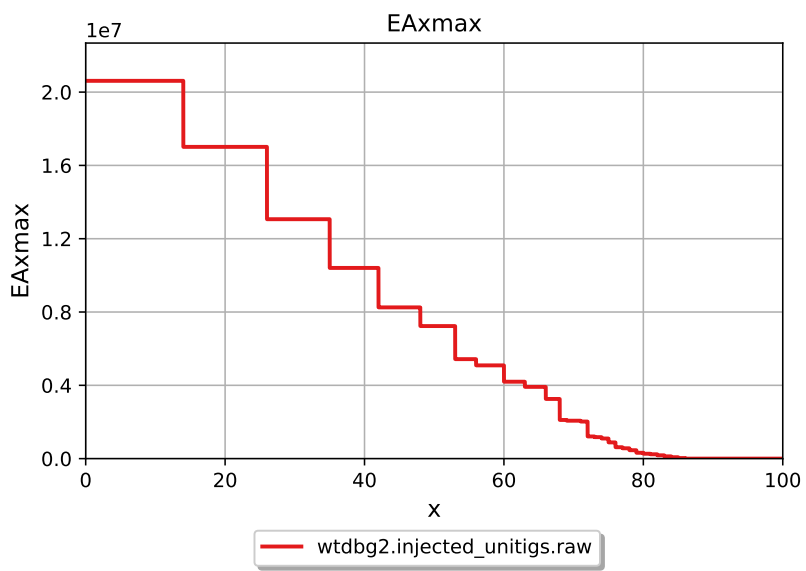Figure 4: QUAST EAxmax graph for wtdbg2 sfa

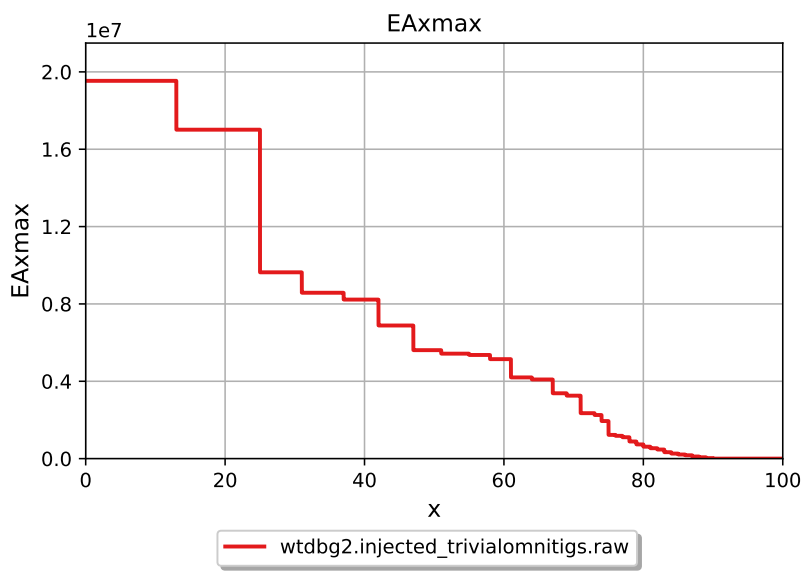Figure 5: QUAST EAxmax graph for inj uni
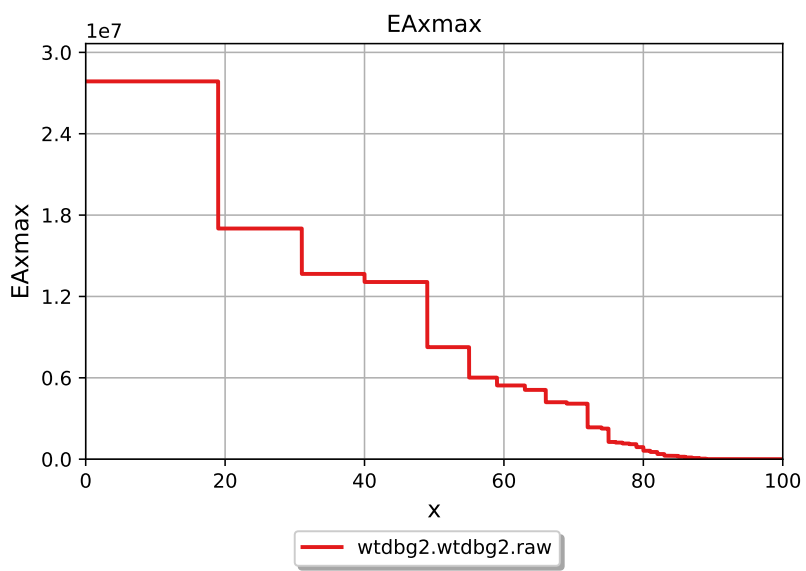
Figure 6: QUAST EAxmax graph for inj Y-to-V

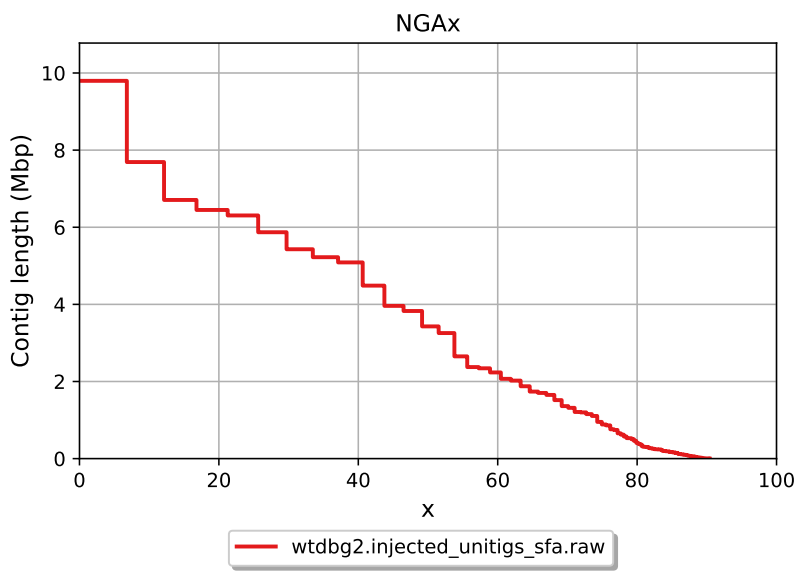Figure 7: QUAST EAxmax graph for wtdbg2

Figure 8: QUAST NGAx graph for inj uni sfa

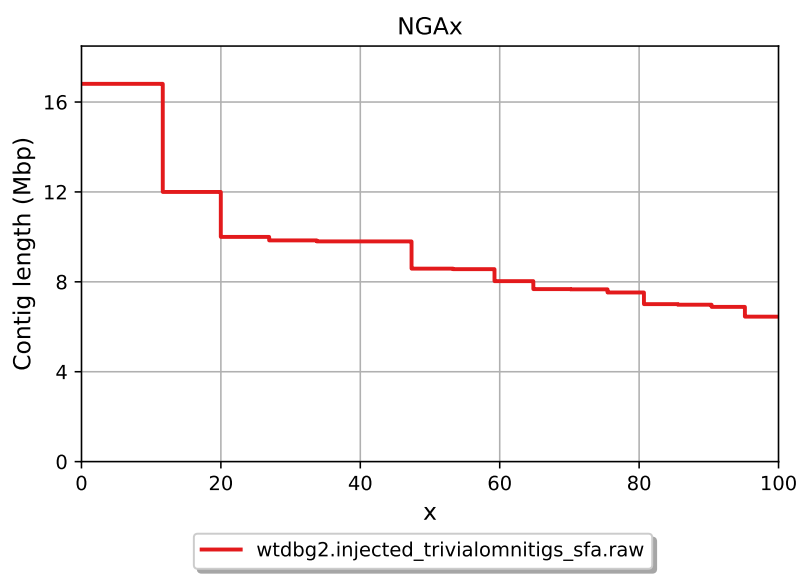Figure 9: QUAST NGAx graph for inj Y-to-V sfa

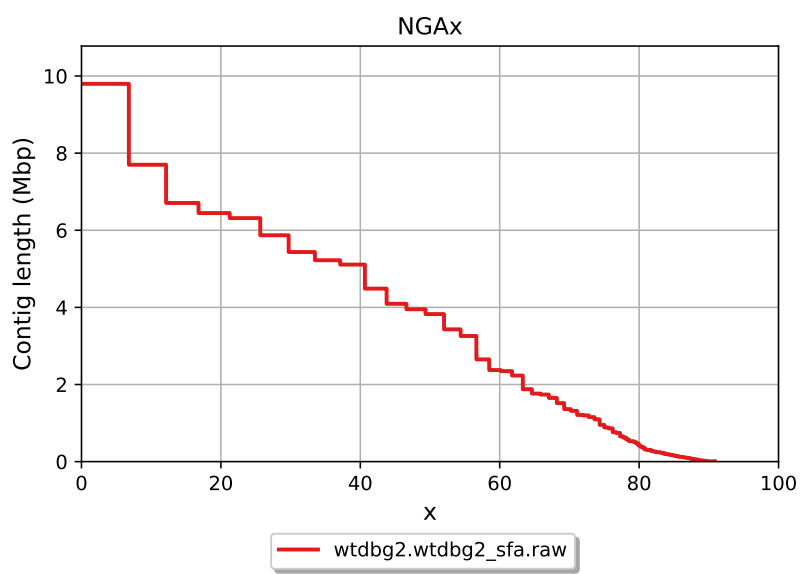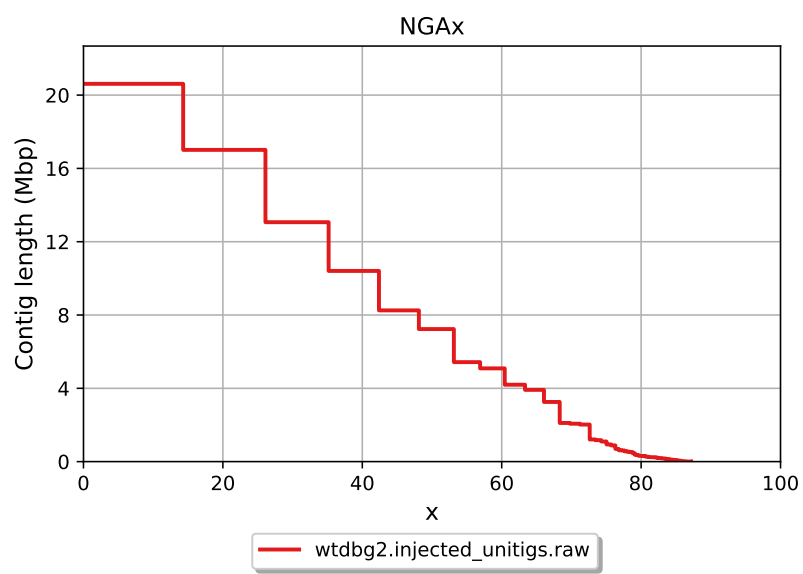Figure 10: QUAST NGAx graph for wtdbg2 sfa
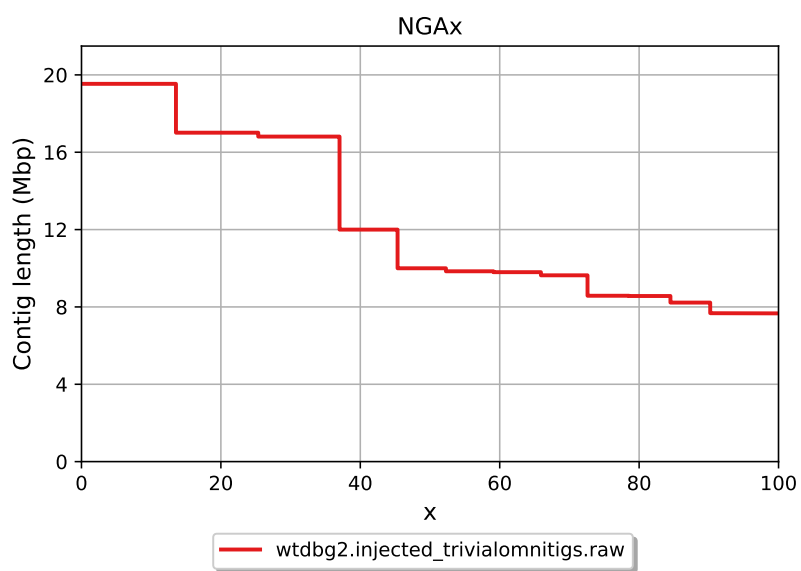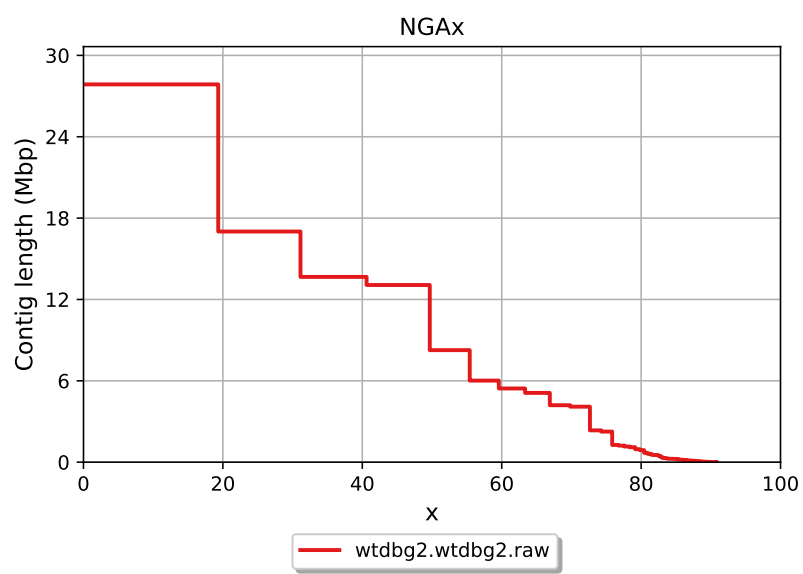
Figure 11: QUAST NGAx graph for inj uni

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

Figure 13: QUAST NGAx graph for wtdbg2