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

Revision: b'bigraph-v0.1.0-rc.1-325-g38b23f8'

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

- C.elegans

Table 1: Genome Graph Statistics

Table 2: Algorithm Statistics

Parameter	uni	Y-to-V	inj uni	inj Y-to-V	wtdbg2
min non-trivial omnitigs per macrotig	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
median non-trivial omnitigs per macrotig	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
min edge length	1	1	1	1	N/A
max edge length	5552	5552	5552	5552	N/A
median edge length	6	30	6	30	N/A
mean edge length	197.6	395.8	197.6	395.8	N/A

Table 3: ContigValidator

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

NGAx

NGAx

NGAx

Contig length (kbp) vs x

Legend: wtdbg2.injected_unitigs.raw

NGAx

NGAx
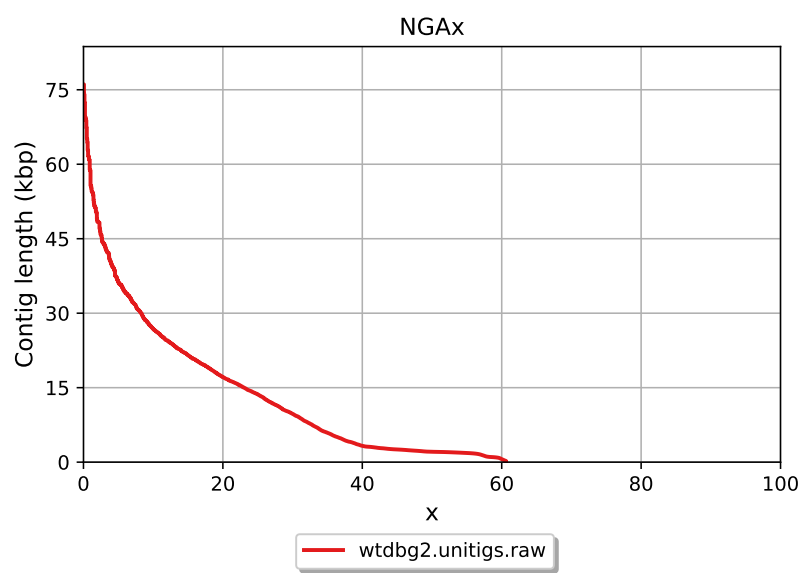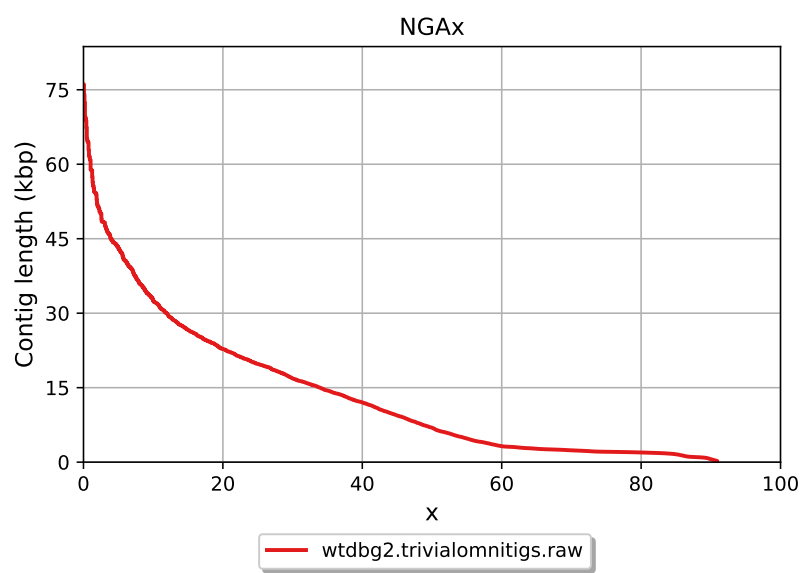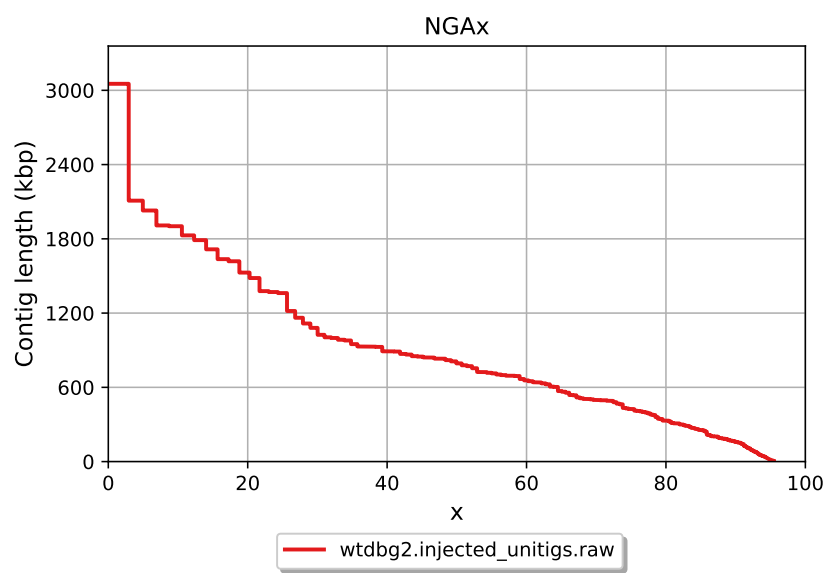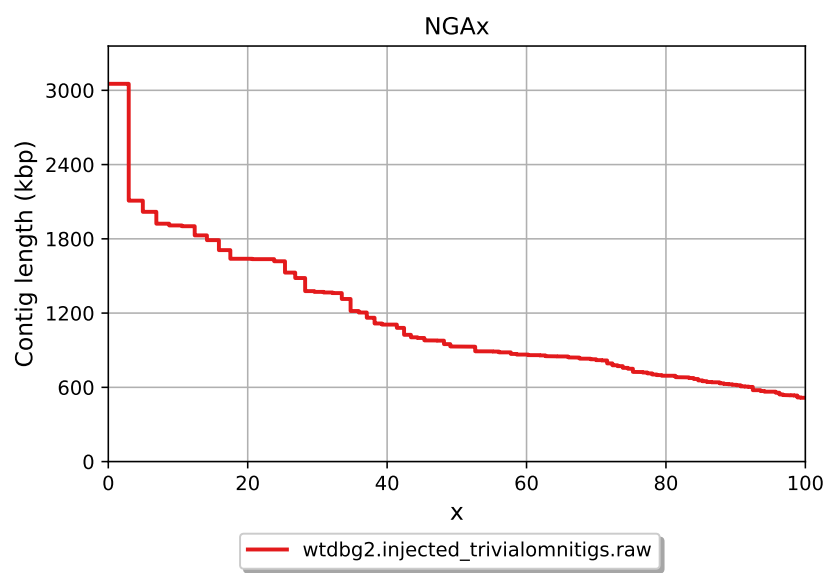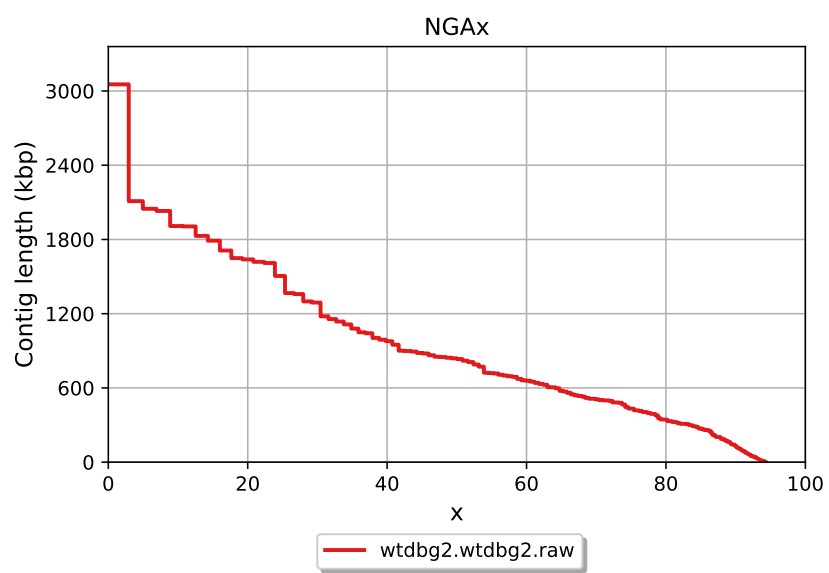
Table 4: QUAST: # of contigs

Parameter	uni	Y-to-V	inj uni	inj Y-to-V	wtdbg2
# contigs ($\geq$ 0 bp)	254	292	179	238	191
# contigs ($\geq$ 1000 bp)	250	289	179	238	191
# contigs ($\geq$ 5000 bp)	234	270	176	235	188
# contigs ($\geq$ 10000 bp)	195	228	146	202	151
# contigs ($\geq$ 25000 bp)	150	185	106	160	106
# contigs ($\geq$ 50000 bp)	132	160	94	142	91

Table 5: QUAST: total length of contigs

Parameter	uni	Y-to-V	inj uni	inj Y-to-V	wtdbg2
Total length ($\geq$ 0 bp)	78707478	118012984	99985787	151807827	98734207
Total length ($\geq$ 1000 bp)	78706652	118012245	99985787	151807827	98734207
Total length ($\geq$ 5000 bp)	78655990	117948916	99971914	151793866	98725025
Total length ($\geq$ 10000 bp)	78359781	117643950	99753953	151562943	98459597
Total length ($\geq$ 25000 bp)	77619563	116915087	99118667	150885755	97785394
Total length ($\geq$ 50000 bp)	76975017	116044527	98691127	150247433	97268912

Table 6: QUAST: statistics for contigs $\geq$ 500bp

Parameter	uni	Y-to-V	inj uni	inj Y-to-V	wtdbg2
# contigs	251	290	179	238	191
Largest contig	4927882	4927882	6177007	6177007	6180070
Total length	78707226	118012819	99985787	151807827	98734207
Reference length	104169699	104169699	104169699	104169699	104169699
GC (%)	35.02	35.16	35.58	35.67	35.62
Reference GC (%)	35.67	35.67	35.67	35.67	35.67
N50	960954	1035709	2049090	1618829	1906099
NG50	638149	1271615	1901869	2268406	1854232
N75	529140	581631	945991	946537	949752
NG75	14703	727131	926774	1601409	854990
L50	24	32	17	28	19
LG50	41	26	18	16	20
L75	53	70	35	59	37
LG75	177	54	38	29	42

Table 7: QUAST: alignment statistics for contigs ≥ 500bp

Parameter	uni	Y-to-V	inj uni	inj Y-to-V	wtdbg2
# misassemblies	15809	24114	136	235	136
# misassembled contigs	191	227	56	103	62
Misassembled contigs length	78182956	117466986	79319537	118923275	74449288
# local misassemblies	4662	7050	189	326	308
# scaffold gap ext. mis.	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0
# unaligned mis. contigs	7	11	1	2	3
# unaligned contigs	6 + 204 part	6 + 248 part	1 + 45 part	1 + 77 part	8 + 62 part
Unaligned length	15505803	23189727	232621	357312	325373
Genome fraction (%)	54.709	59.785	95.736	96.716	94.398
Duplication ratio	1.109	1.523	1.000	1.503	1.001
# N's per 100 kbp	0.00	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	292.39	412.25	25.52	42.85	30.02
# indels per 100 kbp	368.02	512.03	61.31	93.15	64.93
Largest alignment	76087	76087	3052603	3052603	3053768
Total aligned length	63141026	94685726	99498482	150980868	98214293
NA50	4252	4149	831508	778233	851988
NGA50	2089	6933	793547	929224	839440
NA75	1626	1591	490451	468154	499384
LA50	2823	2085	425209	750204	432434
LGA50	7525	4324	40	64	36
LA75	11138	3022	43	37	39