

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

Revision: b'bigraph-v0.2.0-313-g0a90677'

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

- C.elegans C.elegans "genome":"C.elegans","assembler":"wtDBG2","cli_arguments":{"-x":"rs","-s":0.05

Table 1: Genome Graph Statistics

Table 2: Algorithm Statistics

Parameter	Y-to-V sfa	wtDBG2 sfa	Y-to-V frg	Y-to-V wtDBG2
min non-trivial omnitigs per macrotig	N/A	N/A	N/A	N/A
max non-trivial omnitigs per macrotig	N/A	N/A	N/A	N/A
median non-trivial omnitigs per macrotig	N/A	N/A	N/A	N/A
mean non-trivial omnitigs per macrotig	N/A	N/A	N/A	N/A
min edge length	1	N/A	1	N/A
max edge length	5552	N/A	5552	N/A
median edge length	31	N/A	31	N/A
mean edge length	397.0	N/A	397.0	N/A

Table 3: ContigValidator

Parameter	Y-to-V sfa	wtDBG2 sfa	Y-to-V frg	Y-to-V wtDBG2
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Table 4: QUAST: # of contigs

Parameter	Y-to-V sfa	wtdbg2 sfa	Y-to-V	frg Y-to-V	wtdbg2
# contigs (≥ 0 bp)	315	262	278	189	192
# contigs (≥ 1000 bp)	313	262	277	188	192
# contigs (≥ 5000 bp)	298	252	268	182	187
# contigs (≥ 10000 bp)	240	206	217	147	148
# contigs (≥ 25000 bp)	191	154	170	104	104
# contigs (≥ 50000 bp)	161	134	147	90	89

Table 5: QUAST: total length of contigs

Parameter	Y-to-V sfa	wtdbg2 sfa	Y-to-V	frg Y-to-V	wtdbg2
Total length (≥ 0 bp)	152635973	100859930	152292810	112550789	100489169
Total length (≥ 1000 bp)	152634418	100859930	152292088	112550067	100489169
Total length (≥ 5000 bp)	152578531	100822277	152256427	112527653	100473405
Total length (≥ 10000 bp)	152168071	100499140	151885172	112268891	100192109
Total length (≥ 25000 bp)	151379727	99687283	151130320	111613724	99524323
Total length (≥ 50000 bp)	150334887	98992409	150361160	111129122	99007534

Table 6: QUAST: statistics for contigs ≥ 500 bp (or 3000bp for QUAST-LG)

Parameter	Y-to-V sfa	wtdbg2 sfa	Y-to-V	frg Y-to-V	wtdbg2
# contigs	310	259	276	187	189
Largest contig	6178931	6180070	6178933	6178931	6180070
Total length	152628903	100853287	152290662	112548641	100482526
Reference length	104169699	104169699	104169699	104169699	104169699
GC (%)	35.70	35.61	35.70	35.66	35.61
Reference GC (%)	35.67	35.67	35.67	35.67	35.67
N50	1428633	1208751	1620942	2051248	2010311
NG50	2039971	1205835	2546796	2242410	1906099
N75	763900	720918	841540	1025595	998289
NG75	1425820	640359	1524798	1420592	939694
L50	31	24	27	19	18
LG50	17	25	16	17	19
L75	68	51	60	37	36
LG75	32	55	29	32	39

Table 7: QUAST: alignment statistics for contigs ≥ 500 bp (or 3000bp for QUAST-LG)

Parameter	Y-to-V sfa	wtdbg2 sfa	Y-to-V	frg Y-to-V	wtdbg2
# misassemblies	137	65	145	96	78
# unique misassemblies	112	64	120	85	77
# misassembled contigs	89	45	87	53	46
Misassembled contigs length	94616158	50810998	102620341	83829363	67453564
# local misassemblies	304	158	297	182	156
# unique local misassemblies	215	157	214	167	155
# scaffold gap ext. mis.	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0
# possible TEs	20	6	20	16	6
# unaligned mis. contigs	1	1	1	0	0
# unaligned contigs	13+165p	14+111p	12+150p	12+85p	10+85p
Unaligned length	1071998	680705	1099148	789265	703993
Genome fraction (%)	96.693	96.185	96.705	96.496	95.797
Duplication ratio	1.505	1.000	1.501	1.112	1.000
# N's per 100 kbp	0.00	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	36.84	30.98	36.79	31.02	30.88
# indels per 100 kbp	50.39	49.37	50.34	49.94	49.76
Largest alignment	3148846	3150502	3148999	3148846	3150502
Total aligned length	151272359	100063374	150913275	111597180	99672912
EA50max	978031	846349	986630	1011711	949214
Strict EA50max	604113	590484	621916	624411	650482
NGA50	1359914	846349	1524225	1112601	949214
EA75max	536678	418864	536678	582967	534820
Strict EA75max	308970	245444	309257	310064	310064
NGA75	851548	416035	855158	650645	534820
LGA50	25	36	24	27	30
LGA75	50	79	48	58	66

Table 8: QUAST: misassembly statistics for contigs $\geq 500\text{bp}$ (or 3000bp for QUAST-LG)

Parameter	Y-to-V sfa	wtdbg2 sfa	Y-to-V	frg Y-to-V	wtdbg2
# misassemblies	137	65	145	96	78
# contig misassemblies	137	65	145	96	78
# c. relocations	32	15	33	22	18
# c. translocations	102	49	110	74	60
# c. inversions	3	1	2	0	0
# scaffold misassemblies	0	0	0	0	0
# s. relocations	0	0	0	0	0
# s. translocations	0	0	0	0	0
# s. inversions	0	0	0	0	0
# misassembled contigs	89	45	87	53	46
Misassembled contigs length	94616158	50810998	102620341	83829363	67453564
# local misassemblies	304	158	297	182	156
# scaffold gap ext. mis.	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0
# mis. caused by frag. ref.	0	0	0	0	0
# possible TEs	20	6	20	16	6
# unaligned mis. contigs	1	1	1	0	0
# mismatches	55725	30999	55524	34612	30782
# indels	76223	49397	75971	55728	49594
# indels (≤ 5 bp)	74381	48329	74139	54507	48509
# indels (> 5 bp)	1842	1068	1832	1221	1085
Indels length	229794	158611	238193	171187	156526

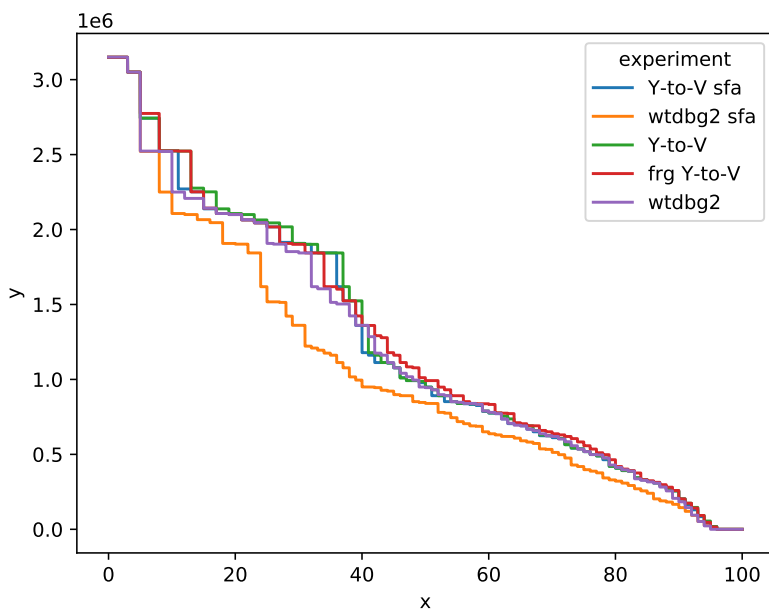


Figure 1: EAxmax

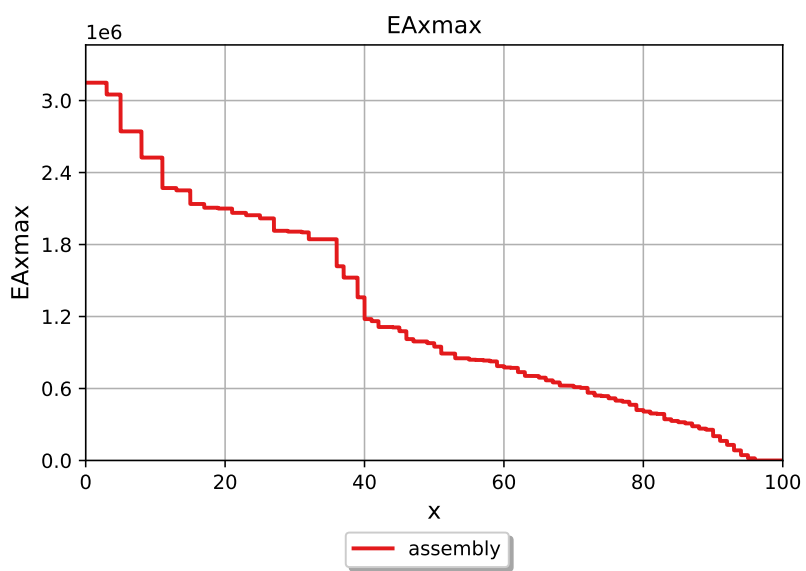


Figure 2: QUAST EAxmax graph for Y-to-V sfa

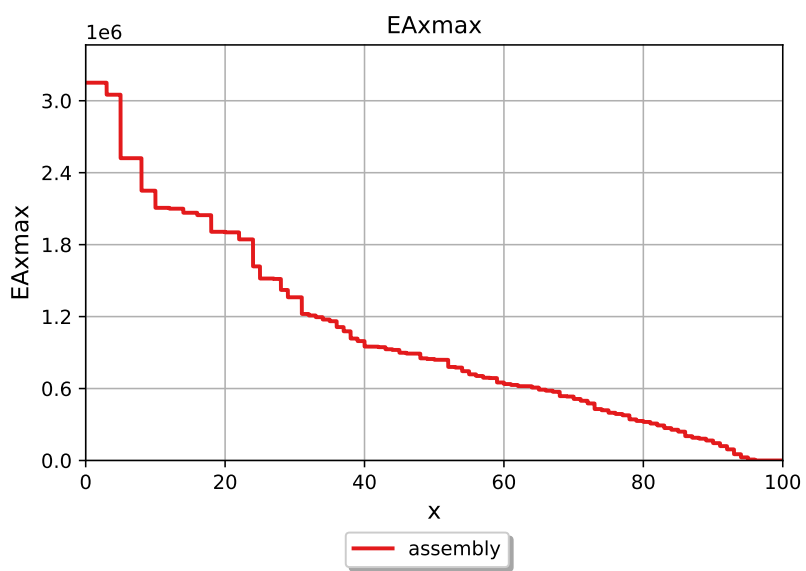


Figure 3: QUAST EAxmax graph for wtdbg2 sfa

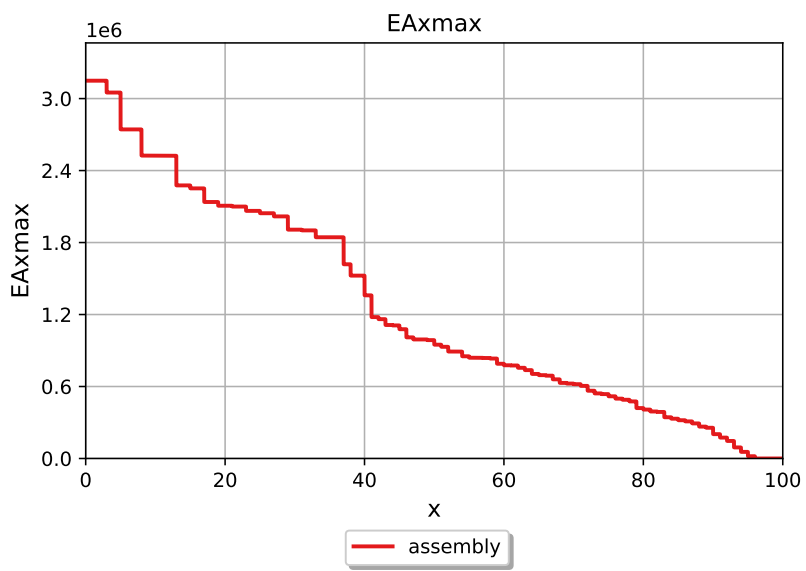


Figure 4: QUAST EAxmax graph for Y-to-V

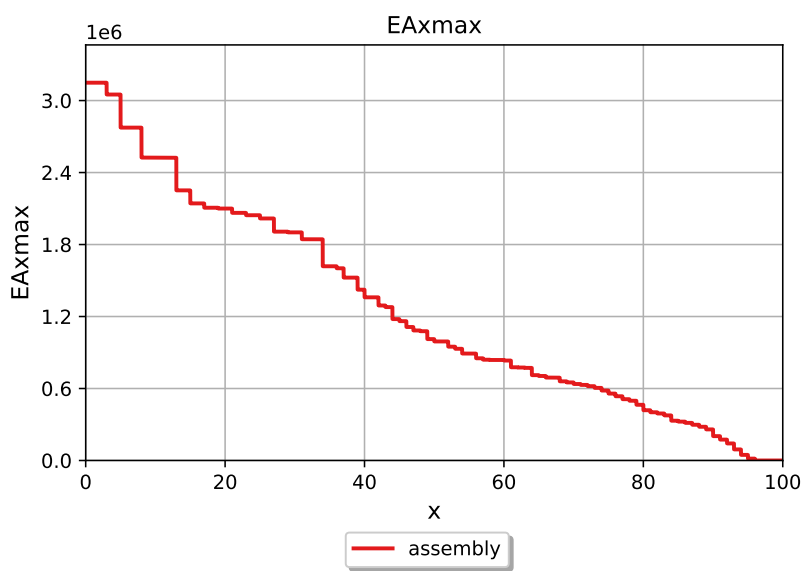


Figure 5: QUAST EAxmax graph for frg Y-to-V

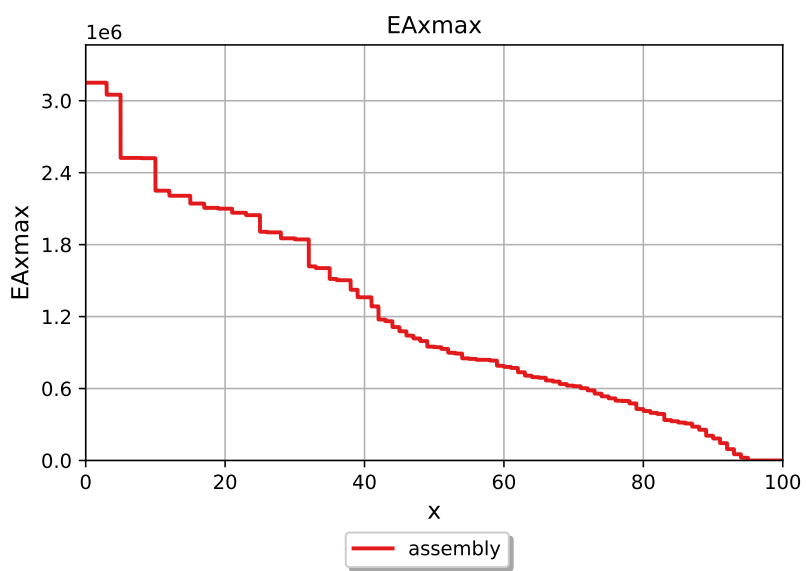


Figure 6: QUAST EAxmax graph for wtdbg2

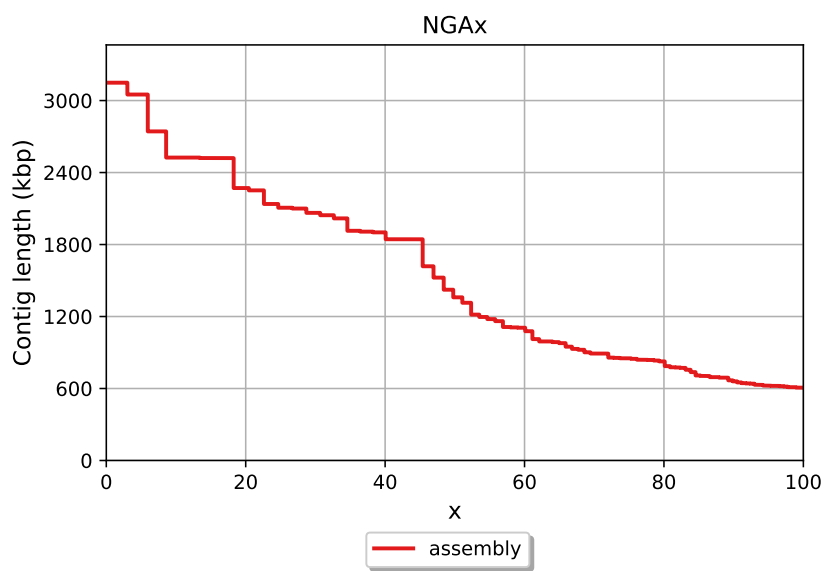


Figure 7: QUAST NGAx graph for Y-to-V sfa

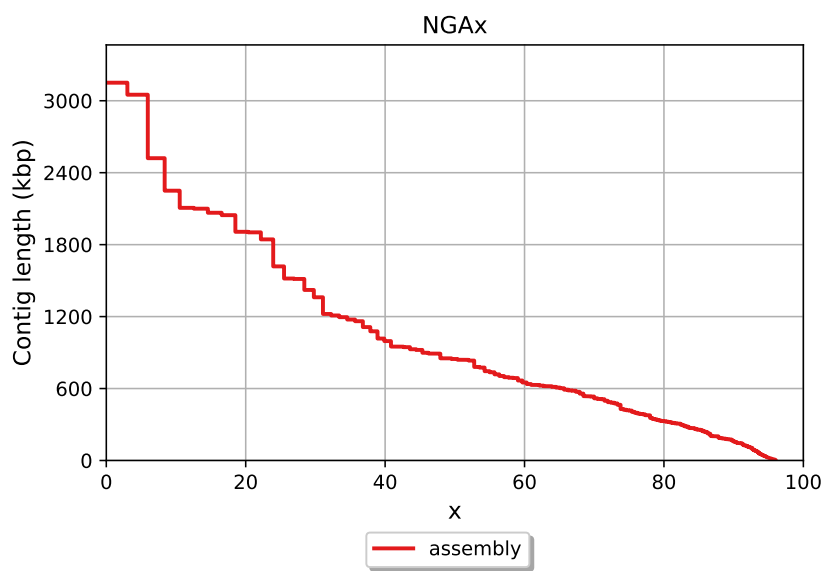


Figure 8: QUASt NGAx graph for wtdbg2 sfa

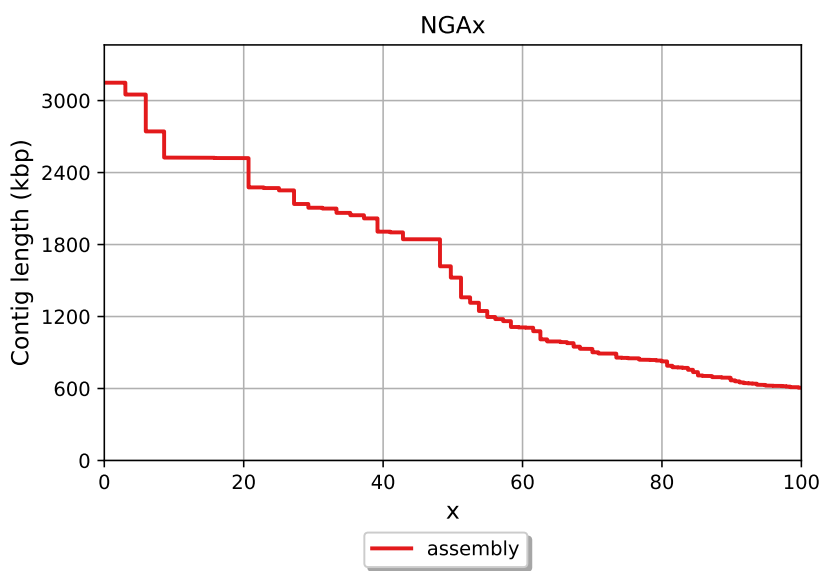


Figure 9: QUAST NGAx graph for Y-to-V

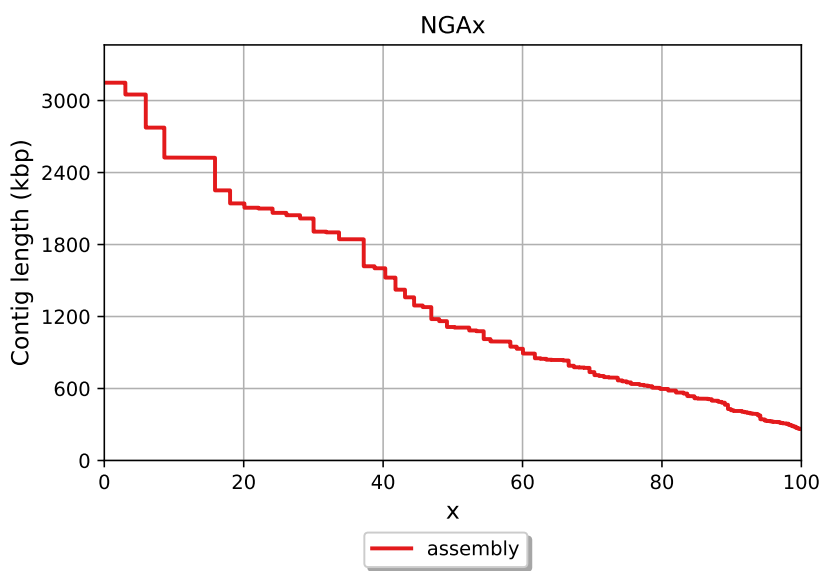


Figure 10: QUAST NGAx graph for frg Y-to-V

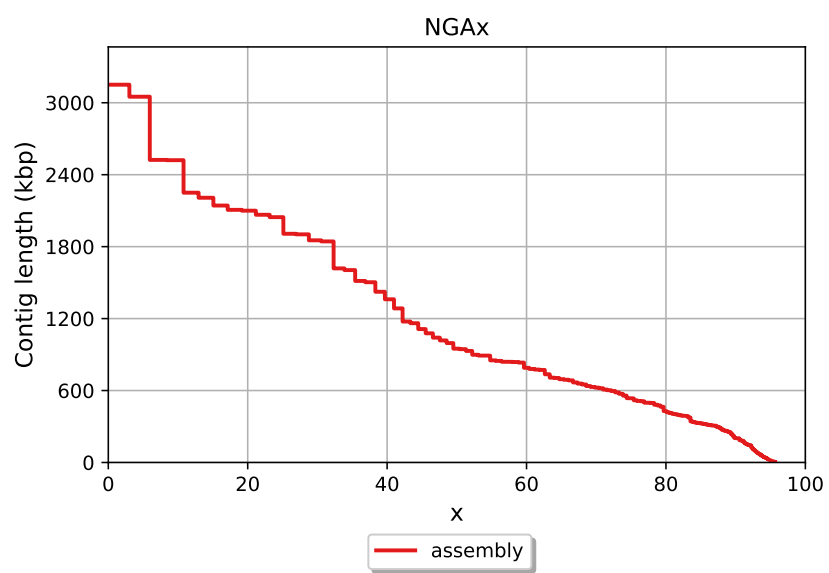


Figure 11: QUAST NGAx graph for wtdbg2