

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):

- Flye_comparison C.elegans "genome":"C.elegans","assembler":"wtDBG2":"cli_arguments":"-x":"rs"

Table 1: Genome Graph Statistics

Table 2: Algorithm Statistics

Parameter	wtDBG2 sfa	Y-to-V sfa	Y-to-V	wtDBG2	flye raw	flye corr
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	N/A	N/A	N/A
max edge length	5552	5552	N/A	N/A	N/A	N/A
median edge length	30	30	N/A	N/A	N/A	N/A
mean edge length	394.7	394.7	N/A	N/A	N/A	N/A

Table 3: ContigValidator

Parameter	wtDBG2 sfa	Y-to-V sfa	Y-to-V	wtDBG2	flye raw	flye corr
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Table 4: QUASt: # of contigs

Parameter	wtdbg2 sfa	Y-to-V sfa	Y-to-V	wtdbg2	flye raw	flye corr
# contigs (≥ 0 bp)	261	314	275	192	91	124
# contigs (≥ 1000 bp)	261	312	274	192	91	124
# contigs (≥ 5000 bp)	252	298	267	189	88	118
# contigs (≥ 10000 bp)	206	240	217	150	86	115
# contigs (≥ 25000 bp)	154	191	170	105	80	111
# contigs (≥ 50000 bp)	134	161	147	90	68	97

Table 5: QUASt: total length of contigs

Parameter	wtdbg2 sfa	Y-to-V sfa	Y-to-V	wtdbg2	flye raw	flye corr
Total length (≥ 0 bp)	100859688	152632834	152282179	98782647	101440945	101726343
Total length (≥ 1000 bp)	100859688	152631279	152281457	98782647	101440945	101726343
Total length (≥ 5000 bp)	100825051	152579748	152253245	98773465	101432411	101709629
Total length (≥ 10000 bp)	100501684	152169058	151886811	98491939	101418263	101691774
Total length (≥ 25000 bp)	99689827	151380714	151131959	97805986	101297339	101605461
Total length (≥ 50000 bp)	98991259	150333341	150360266	97285503	100882932	101104316

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

Parameter	wtdbg2 sfa	Y-to-V sfa	Y-to-V	wtdbg2	flye raw	flye corr
# contigs	259	309	273	190	89	120
Largest contig	6180070	6178933	6178932	6180070	5065916	4102934
Total length	100855254	152625764	152280031	98778213	101436280	101716725
Reference length	104169699	104169699	104169699	104169699	104169699	104169699
GC (%)	35.61	35.70	35.70	35.63	35.53	35.52
Reference GC (%)	35.67	35.67	35.67	35.67	35.67	35.67
N50	1208751	1428633	1620942	1906099	2309765	1917212
NG50	1205835	2039971	2546796	1854232	2279155	1889879
N75	720918	763900	841540	949752	1455397	1027660
NG75	640359	1425820	1524798	895623	1431538	1000927
L50	24	31	27	19	15	20
LG50	25	17	16	20	16	21
L75	51	68	60	37	29	38
LG75	55	32	29	41	30	40

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

Parameter	wtdbg2 sfa	Y-to-V sfa	Y-to-V	wtdbg2	flye raw	flye corr
# misassemblies	66	137	145	76	80	61
# unique misassemblies	65	112	120	75	83	63
# misassembled contigs	45	89	87	47	39	38
Misassembled contigs length	50809767	94614612	102619447	63840733	66488044	48898321
# local misassemblies	157	304	296	162	57	50
# unique local misassemblies	156	215	213	158	59	52
# scaffold gap ext. mis.	0	0	0	0	3	2
# scaffold gap loc. mis.	0	0	0	0	2	2
# possible TEs	6	20	20	6	0	2
# unaligned mis. contigs	1	1	1	0	0	0
# unaligned contigs	14+111p	12+165p	10+149p	9+87p	0+58p	0+84p
Unaligned length	682639	1068689	1095501	712079	501272	715144
Genome fraction (%)	96.184	96.693	96.701	94.149	96.847	96.785
Duplication ratio	1.000	1.505	1.501	1.000	1.000	1.002
# N's per 100 kbp	0.00	0.00	0.00	0.00	1.77	1.38
# mismatches per 100 kbp	31.01	36.91	36.68	32.01	7.08	7.16
# indels per 100 kbp	49.37	50.39	50.28	50.11	39.60	39.58
Largest alignment	3150502	3148999	3148846	3150502	3164784	3164733
Total aligned length	100063381	151272529	150906291	97960020	100881958	100844681
EA50max	846349	978031	986630	945038	1177105	1081685
Strict EA50max	590484	604113	621916	631804	980578	960423
NGA50	846349	1359914	1524225	945038	1177105	1081685
EA75max	418864	536678	536678	510912	677296	678280
Strict EA75max	245444	308970	309257	292317	518885	535705
NGA75	416035	851548	855158	510912	677296	678280
LGA50	36	25	24	30	27	28
LGA75	79	50	48	67	55	58

Table 8: QUASt: misassembly statistics for contigs ≥ 500 bp (or 3000bp for QUASt-LG)

Parameter	wtdbg2 sfa	Y-to-V sfa	Y-to-V	wtdbg2	flye raw	flye corr
# misassemblies	66	137	145	76	80	61
# contig misassemblies	66	137	145	76	76	55
# c. relocations	16	32	34	18	9	12
# c. translocations	49	102	109	58	65	43
# c. inversions	1	3	2	0	2	0
# scaffold misassemblies	0	0	0	0	4	6
# s. relocations	0	0	0	0	2	3
# s. translocations	0	0	0	0	2	3
# s. inversions	0	0	0	0	0	0
# misassembled contigs	45	89	87	47	39	38
Misassembled contigs length	50809767	94614612	102619447	63840733	66488044	48898321
# local misassemblies	157	304	296	162	57	50
# scaffold gap ext. mis.	0	0	0	0	3	2
# scaffold gap loc. mis.	0	0	0	0	2	2
# mis. caused by frag. ref.	0	0	0	0	0	2
# possible TEs	6	20	20	6	0	2
# unaligned mis. contigs	1	1	1	0	0	0
# mismatches	31025	55833	55356	31353	7138	7221
# indels	49398	76228	75869	49091	39954	39912
# indels (≤ 5 bp)	48331	74382	74036	48025	38850	38827
# indels (> 5 bp)	1067	1846	1833	1066	1104	1085
Indels length	158388	229862	238061	153973	174242	136500

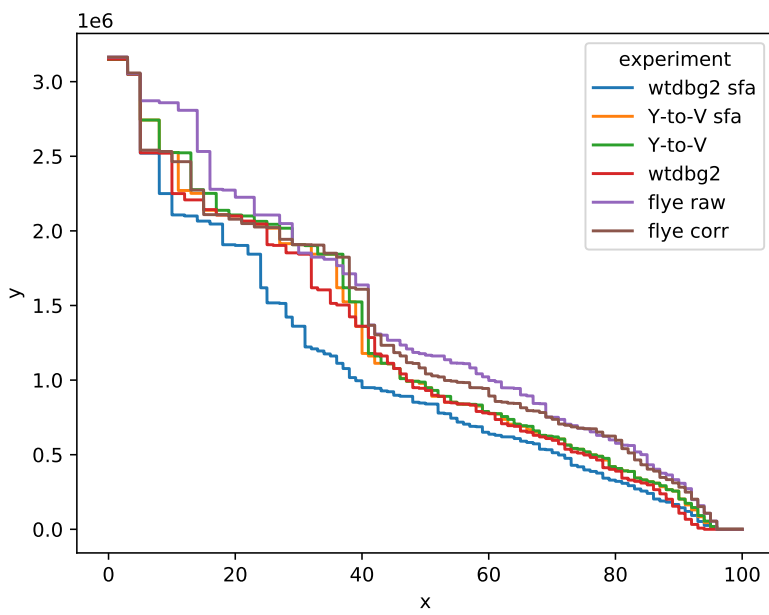


Figure 1: EAxmax

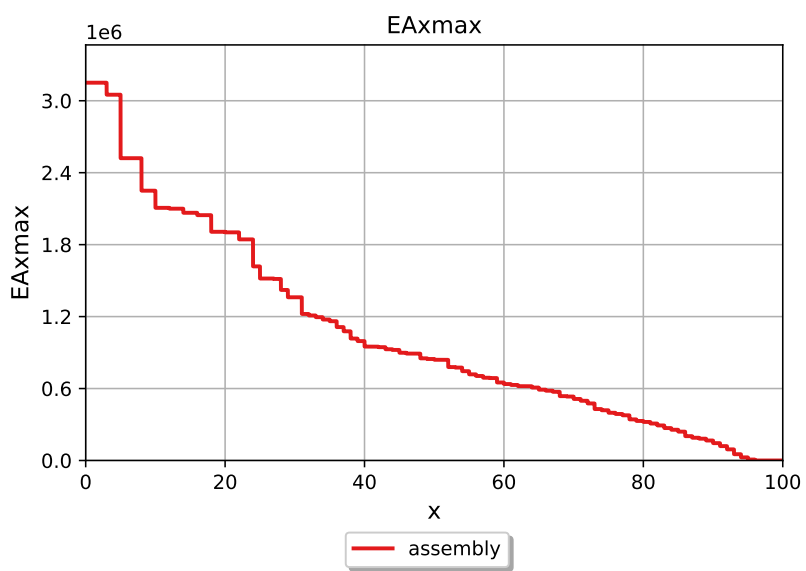


Figure 2: QUAST EAxmax graph for wtdbg2 sfa

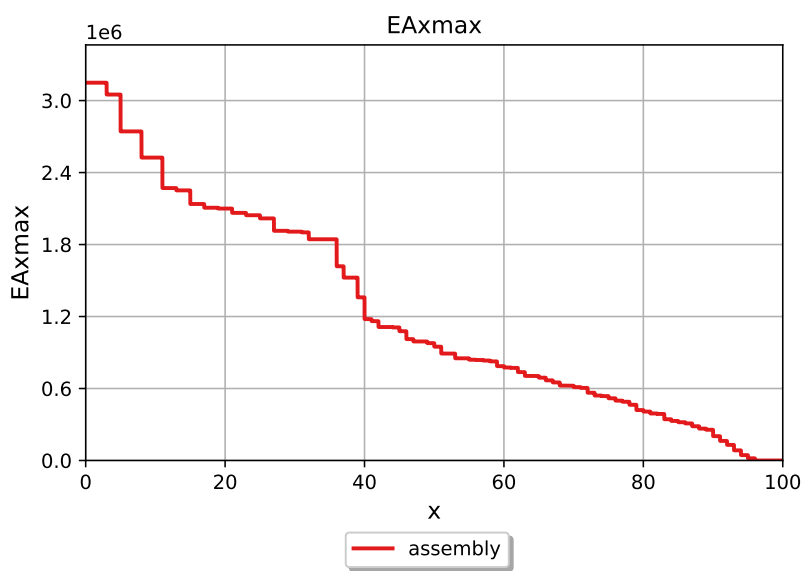


Figure 3: QUAST EAxmax graph for Y-to-V sfa

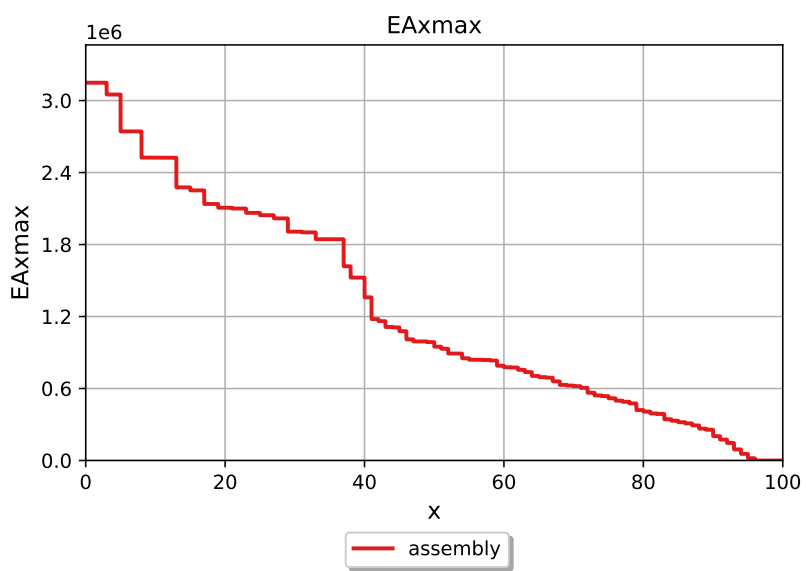


Figure 4: QUAST EAxmax graph for Y-to-V

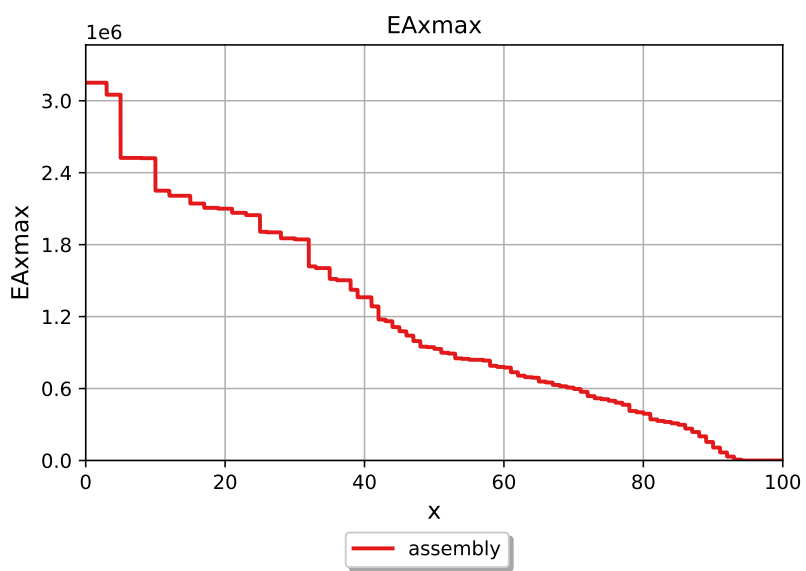


Figure 5: QUAST EAxmax graph for wtdbg2

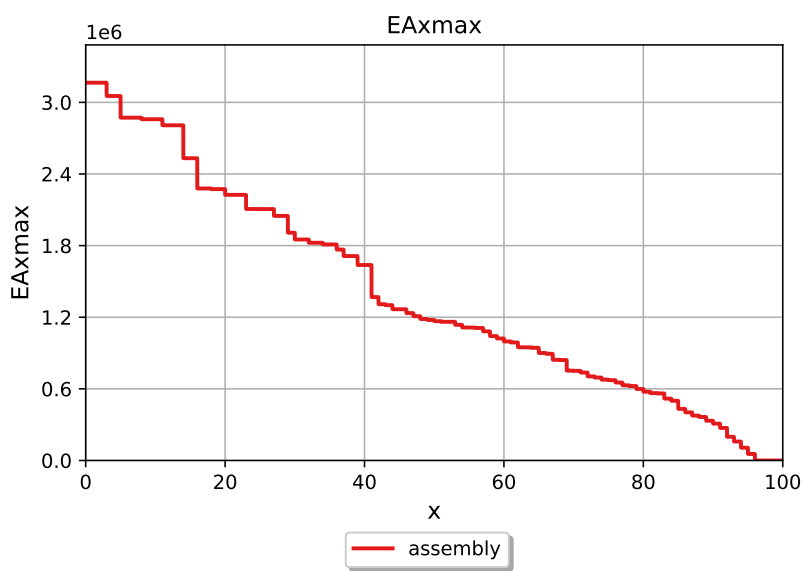


Figure 6: QUAST EAxmax graph for flye raw

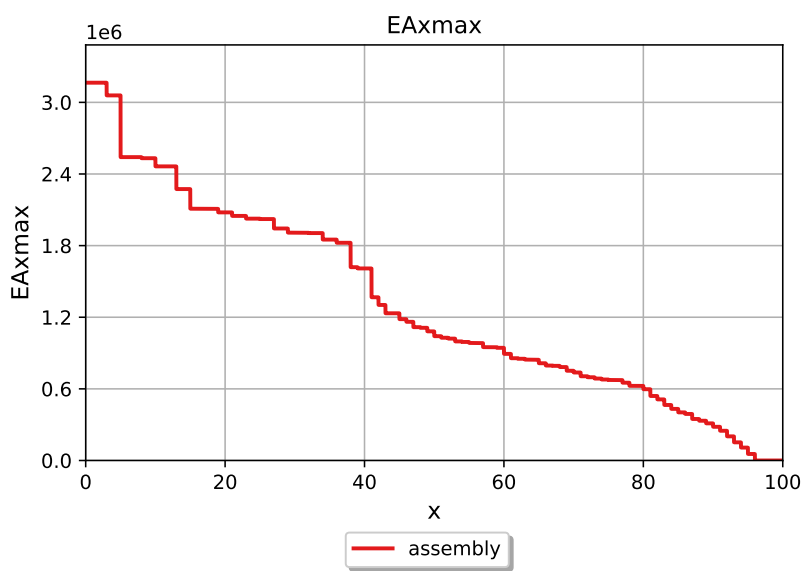


Figure 7: QUAST EAxmax graph for flye corr

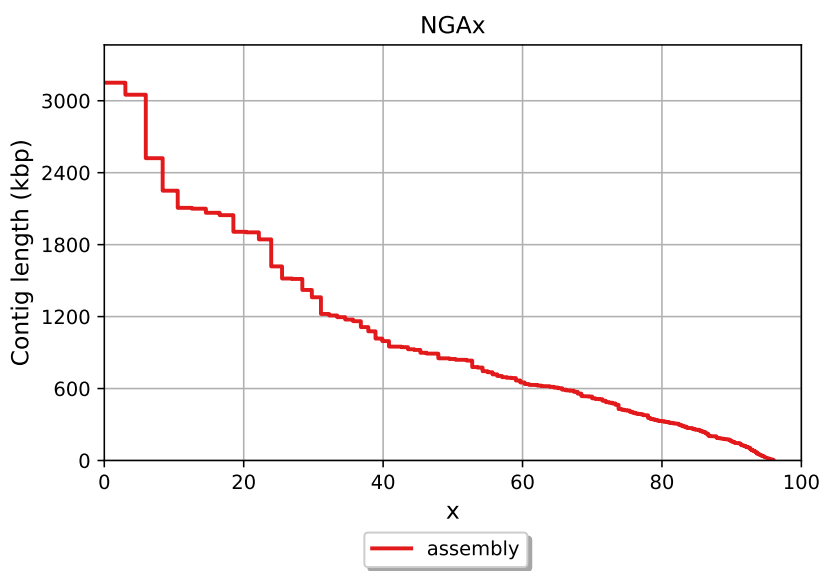


Figure 8: QUAST NGAx graph for wtdbg2 sfa

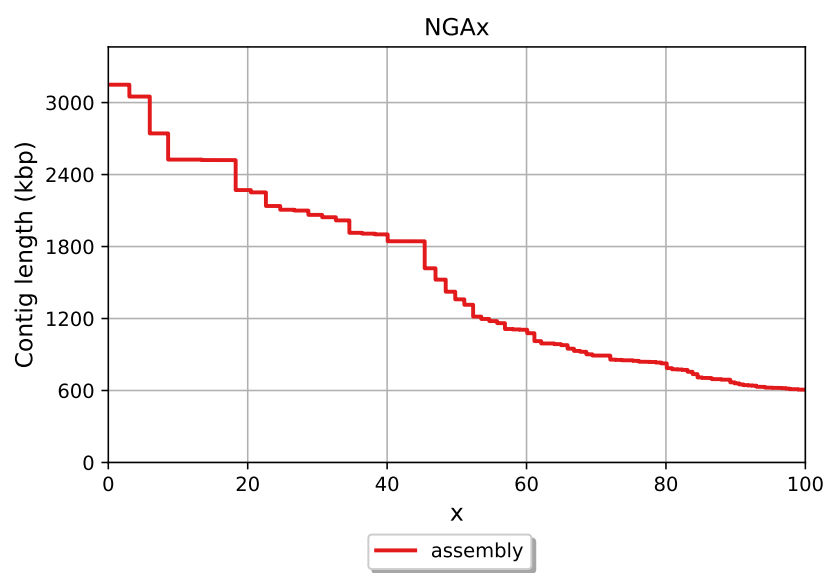


Figure 9: QUAST NGAx graph for Y-to-V sfa

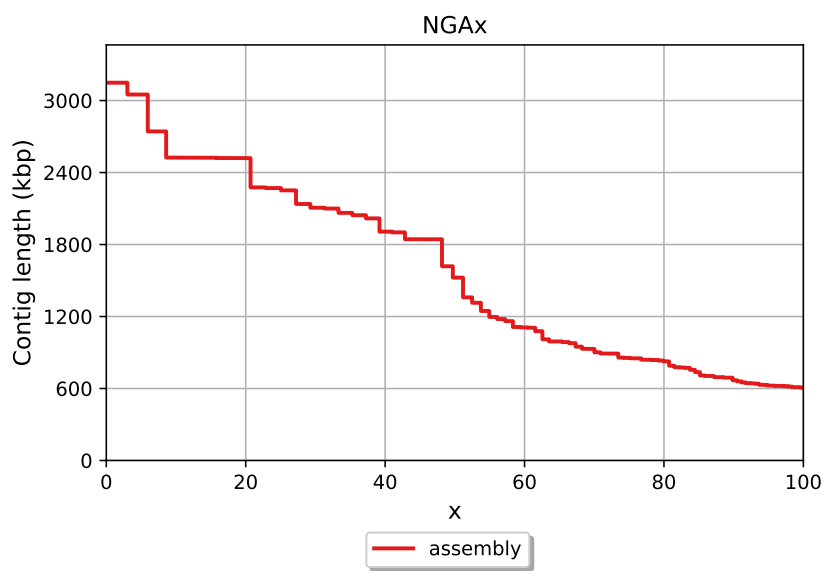


Figure 10: QUAST NGAx graph for Y-to-V

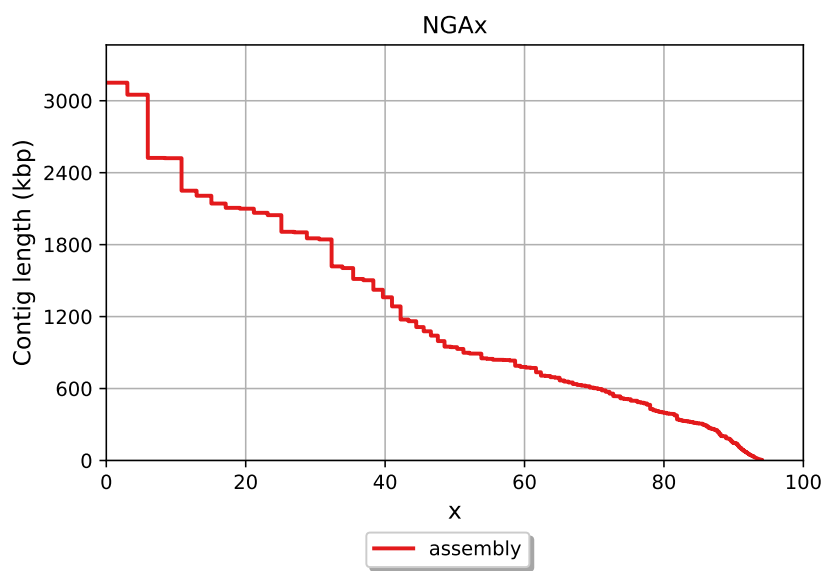


Figure 11: QUAST NGAx graph for wtdbg2

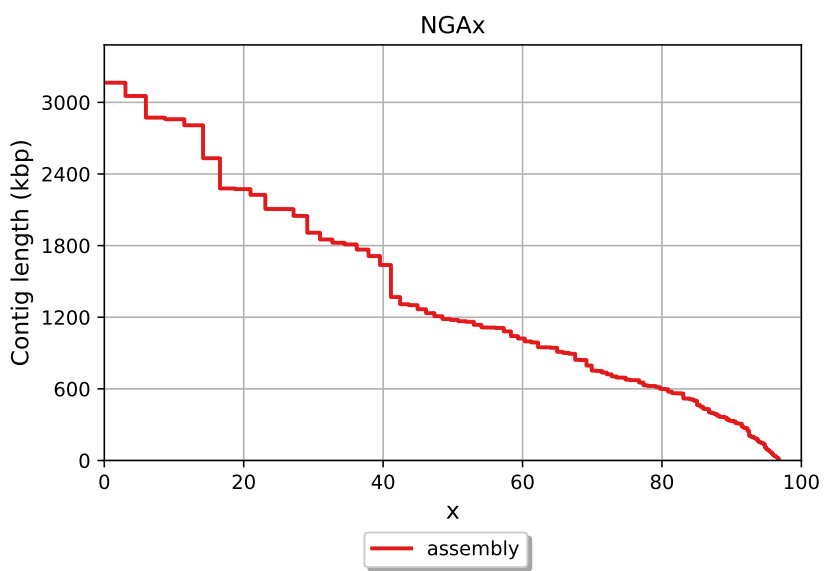


Figure 12: QUAST NGAx graph for flye raw

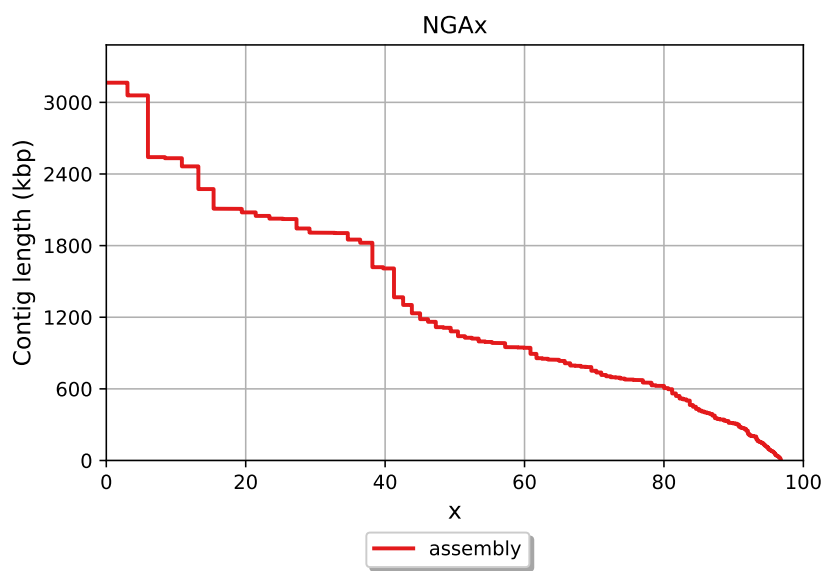


Figure 13: QUAST NGAx graph for flye corr