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):

- Minghui63 Minghui63 "genome":"Minghui63","assembler":"wtdbg2":"cli_arguments":"-x":"ccs","-s":0.5,"flye":"cli_arguments":"–pacbio-hifi":true

Table 1: Genome Graph Statistics

Table 2: Algorithm Statistics

Parameter	Y-to-V sfa	wtdbg2 sfa	Y-to-V	frg Y-to-V	wtdbg2	flye
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	N/A	1	N/A	N/A	N/A
max edge length	3737	N/A	3737	N/A	N/A	N/A
median edge length	115	N/A	115	N/A	N/A	N/A
mean edge length	230.7	N/A	230.7	N/A	N/A	N/A

Table 3: ContigValidator

Parameter	Y-to-V sfa	wtdbg2 sfa	Y-to-V	frg Y-to-V	wtdbg2	flye

Table 4: QUAST: # of contigs

Parameter	Y-to-V sfa	wtdbg2 sfa	Y-to-V	frg Y-to-V	wtdbg2	flye
# contigs ($\geq$ 0 bp)	4076	2809	3689	1304	1618	235
# contigs ($\geq$ 1000 bp)	4076	2809	3689	1304	1618	209
# contigs ($\geq$ 5000 bp)	4054	2800	3673	1295	1610	170
# contigs ($\geq$ 10000 bp)	3782	2547	3472	1226	1486	145
# contigs ($\geq$ 25000 bp)	3392	2072	3136	1103	1245	97
# contigs ($\geq$ 50000 bp)	3007	1609	2825	1023	1025	72

Table 5: QUAST: total length of contigs

Parameter	Y-to-V sfa	wtdbg2 sfa	Y-to-V	frg Y-to-V	wtdbg2	flye
Total length ($\geq$ 0 bp)	1104688914	367928013	1101094237	1041765667	350651409	396223273
Total length ($\geq$ 1000 bp)	1104688914	367928013	1101094237	1041765667	350651409	396206125
Total length ($\geq$ 5000 bp)	1104601587	367894765	1101027524	1041731176	350623038	396098835
Total length ($\geq$ 10000 bp)	1102564374	366079787	1099501434	1041234605	349735354	395922220
Total length ($\geq$ 25000 bp)	1096142826	358192827	1093954209	1039273790	345728829	395085992
Total length ($\geq$ 50000 bp)	1081902909	341289841	1082429289	1036338685	337544611	394227488

Table 6: QUAST: statistics for contigs $\geq$ 500bp (or 3000bp for QUAST-LG)

Parameter	Y-to-V sfa	wtdbg2 sfa	Y-to-V	frg Y-to-V	wtdbg2	flye
# contigs	4072	2805	3687	1302	1614	185
Largest contig	3870585	3258382	3870585	6167045	4273861	39839004
Total length	1104679707	367917993	1101088564	1041759894	350641389	396160265
Reference length	387424359	387424359	387424359	387424359	387424359	387424359
GC (%)	43.51	43.43	43.51	43.54	43.50	43.66
Reference GC (%)	43.61	43.61	43.61	43.61	43.61	43.61
N50	555497	279334	590194	1599311	522547	11759902
NG50	1085246	262375	1128568	3049783	462977	13659039
N75	285520	133922	308412	966911	254656	7785702
NG75	914750	113191	943999	2419656	173143	8348051
L50	605	369	571	202	186	11
LG50	133	405	126	49	224	10
L75	1292	842	1209	408	424	21
LG75	231	960	220	85	556	20

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

Parameter	Y-to-V sfa	wtdbg2 sfa	Y-to-V	frg Y-to-V	wtdbg2	flye
# misassemblies	3396	662	3473	2562	765	1099
# unique misassemblies	2386	636	2439	1551	736	966
# misassembled contigs	1702	221	1691	786	236	84
Misassembled contigs length	570047733	27335829	617574189	841161460	72494983	372367625
# local misassemblies	1367	415	1337	1117	403	695
# unique local misassemblies	681	350	667	517	337	408
# scaffold gap ext. mis.	0	0	0	0	0	5
# scaffold gap loc. mis.	0	0	0	0	0	27
# possible TEs	176	58	178	148	64	76
# unaligned mis. contigs	37	24	31	14	15	6
# unaligned contigs	6+771p	2+254p	5+746p	2+393p	1+216p	0+80p
Unaligned length	5754991	2351697	5793094	5531814	2301253	4045539
Genome fraction (%)	98.153	93.715	98.157	97.232	89.233	99.619
Duplication ratio	2.890	1.007	2.880	2.751	1.008	1.016
# N's per 100 kbp	0.00	0.00	0.00	0.00	0.00	1.54
# mismatches per 100 kbp	52.55	36.03	52.48	38.30	40.59	51.20
# indels per 100 kbp	30.07	28.97	30.22	30.04	30.07	28.85
Largest alignment	3870585	3258382	3870585	4737669	4273861	17585194
Total aligned length	1097411042	365417153	1093687161	1034275355	348099938	391612437
EA50max	565895	255636	584068	1080592	415403	5046799
Strict EA50max	542468	242084	558743	966550	385433	3834054
NGA50	899848	255636	919719	1975425	415403	5046799
EA75max	297054	106868	318842	551728	146830	2748327
Strict EA75max	277366	102135	293455	484879	139318	1875140
NGA75	710138	106918	733334	1509729	146830	2748327
LGA50	161	420	156	71	251	23
LGA75	282	1004	275	129	633	49

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

Parameter	Y-to-V sfa	wtdbg2 sfa	Y-to-V	frg Y-to-V	wtdbg2	flye
# misassemblies	3396	662	3473	2562	765	1099
# contig misassemblies	3396	662	3473	2562	765	1081
# c. relocations	864	180	898	823	231	290
# c. translocations	2508	475	2550	1726	527	783
# c. inversions	24	7	25	13	7	8
# scaffold misassemblies	0	0	0	0	0	18
# s. relocations	0	0	0	0	0	15
# s. translocations	0	0	0	0	0	2
# s. inversions	0	0	0	0	0	1
# misassembled contigs	1702	221	1691	786	236	84
Misassembled contigs length	570047733	27335829	617574189	841161460	72494983	372367625
# local misassemblies	1367	415	1337	1117	403	695
# scaffold gap ext. mis.	0	0	0	0	0	5
# scaffold gap loc. mis.	0	0	0	0	0	27
# mis. caused by frag. ref.	0	0	0	0	0	0
# possible TEs	176	58	178	148	64	76
# unaligned mis. contigs	37	24	31	14	15	6
# mismatches	576720	131651	573996	396126	141294	200488
# indels	330042	105874	330503	310715	104672	112991
# indels (≤ 5 bp)	323743	104599	324216	306506	103380	111678
# indels (> 5 bp)	6299	1275	6287	4209	1292	1313
Indels length	1318415	381478	1366688	1539909	438246	395868
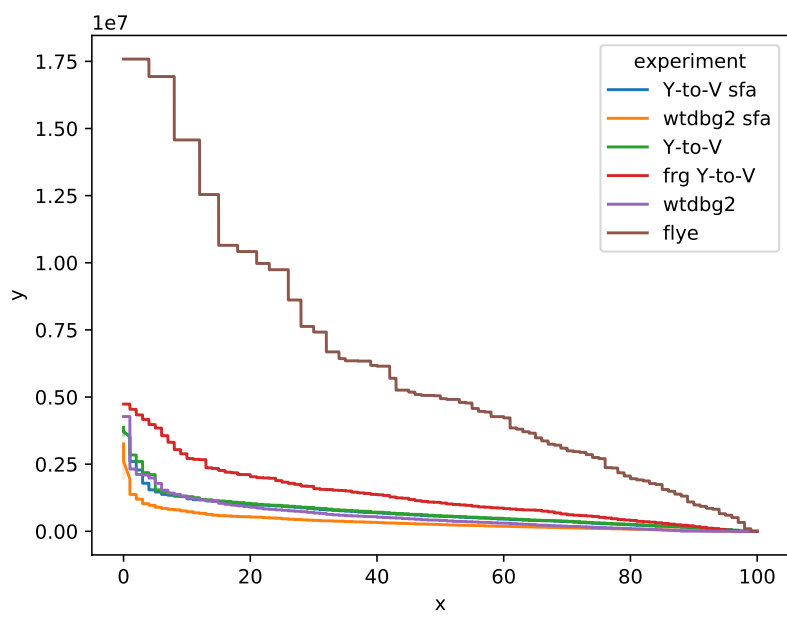
Figure 1: EAxmax
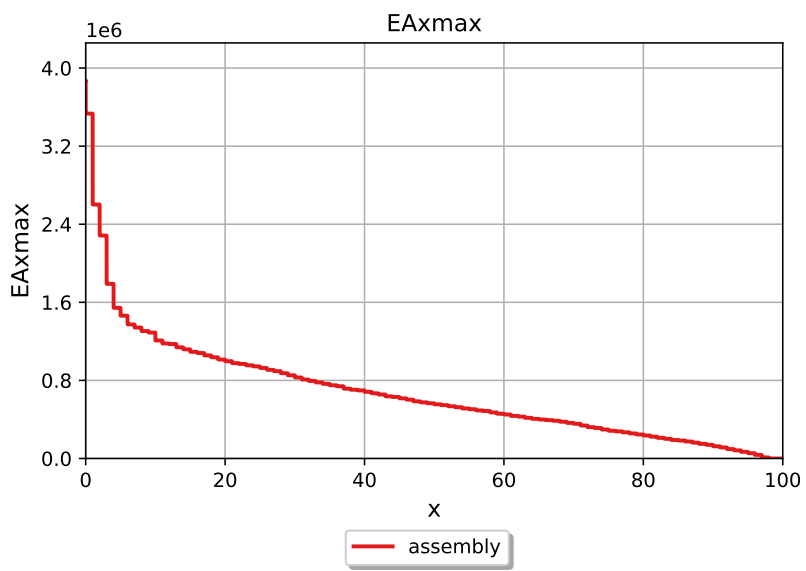
Figure 2: QUAST EAxmax graph for Y-to-V sfa
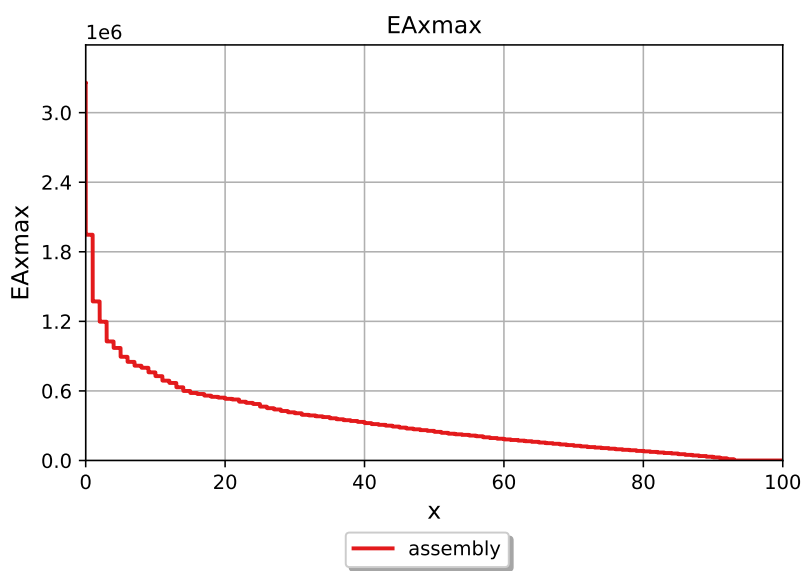
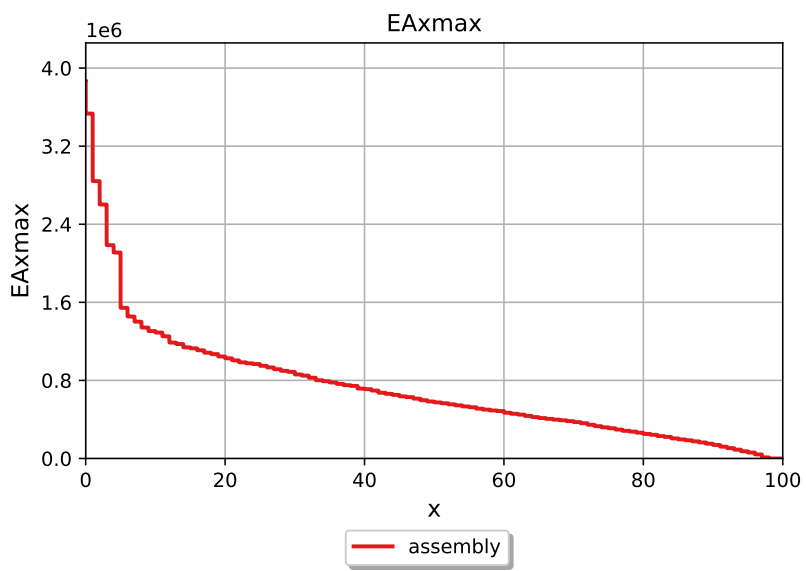Figure 3: QUAST EAxmax graph for wtdbg2 sfa
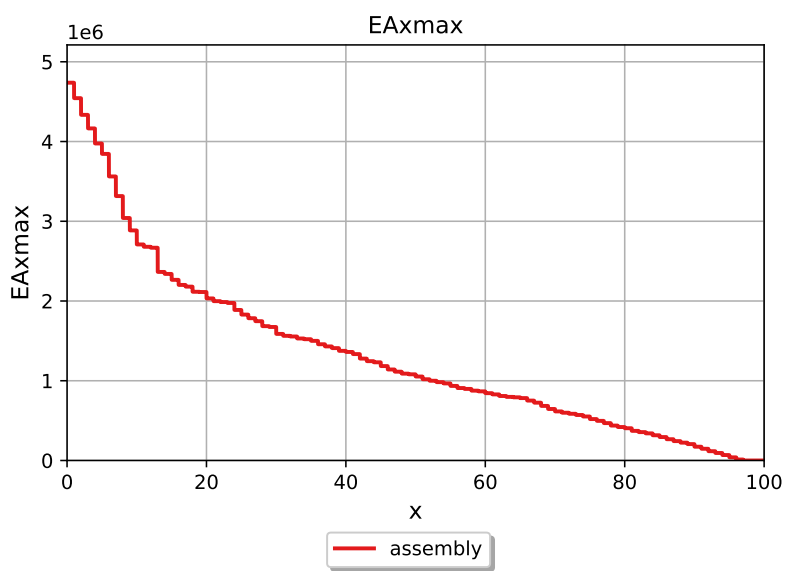
Figure 4: QUAST EAxmax graph for Y-to-V

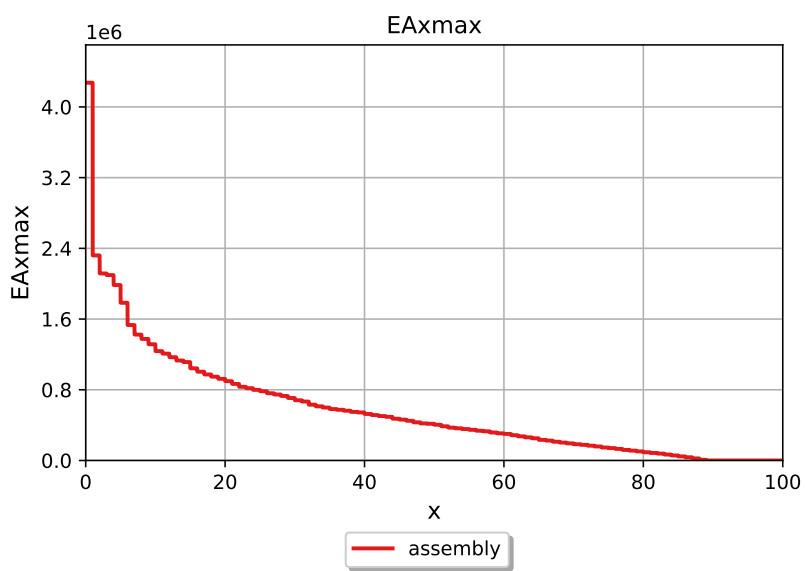Figure 5: QUAST EAxmax graph for frg Y-to-V

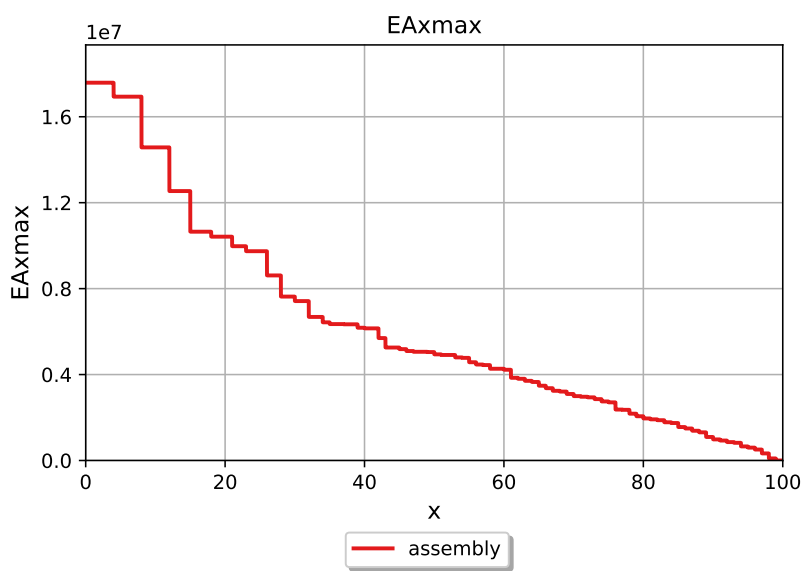Figure 6: QUAST EAxmax graph for wtdbg2
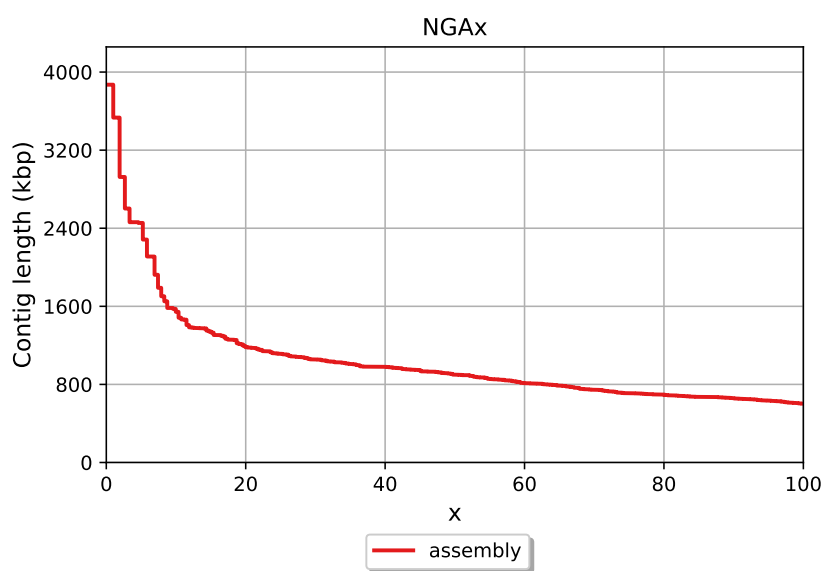
Figure 7: QUAST EAxmax graph for flye
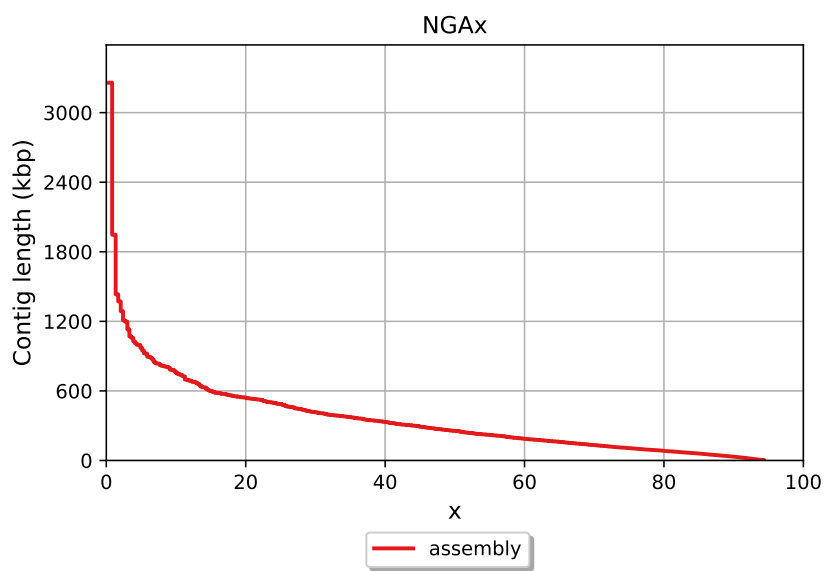
Figure 8: QUAST NGAx graph for Y-to-V sfa

Figure 9: QUAST NGAx graph for wtdbg2 sfa

Figure 10: QUAST NGAx graph for Y-to-V
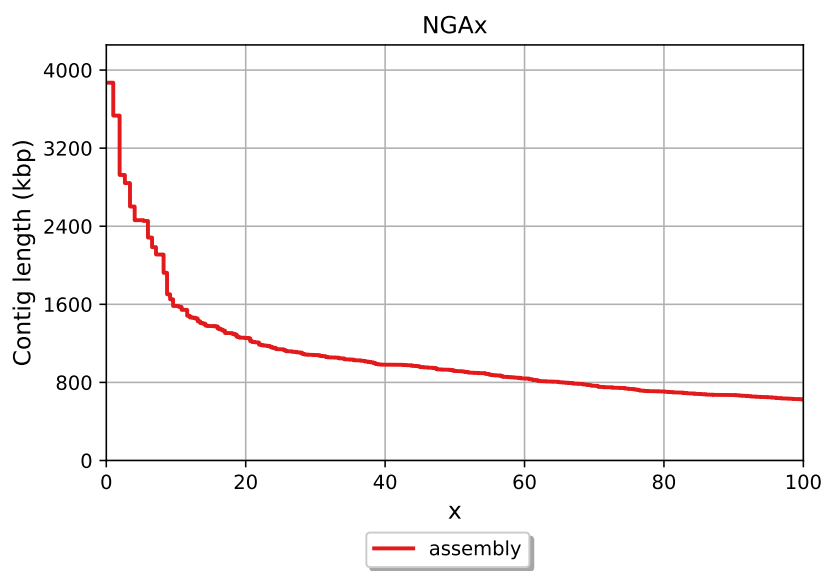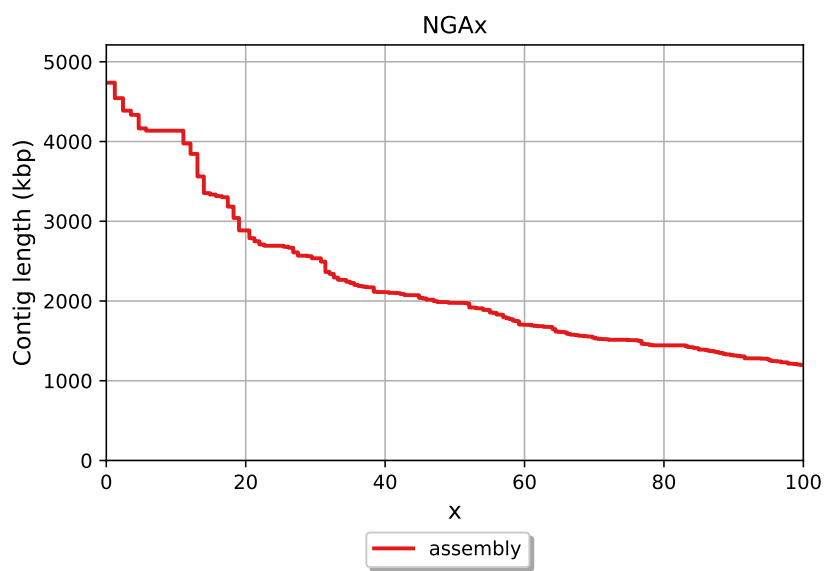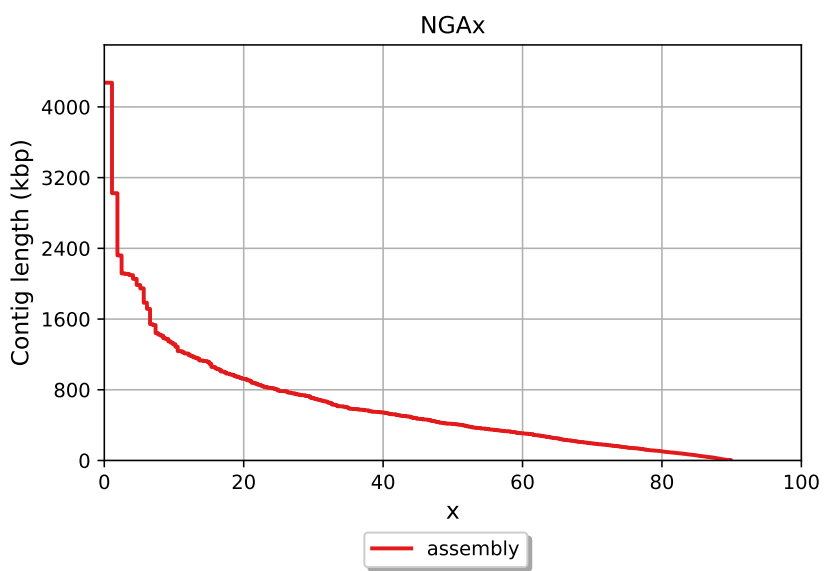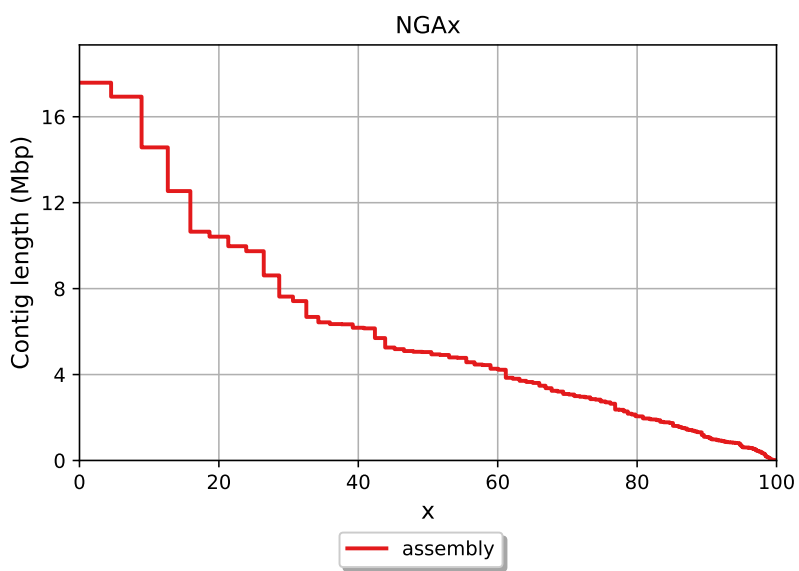
Figure 11: QUAST NGAx graph for frg Y-to-V

Figure 12: QUAST NGAx graph for wtdbg2

Figure 13: QUAST NGAx graph for flye