

**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\_contigbreaker Minghui63 "genome":"Minghui63","assembler":"wtDBG2","cli\_arguments":"-x":"ccs"

Table 1: Genome Graph Statistics

Table 2: Algorithm Statistics

Parameter	Y-to-V sfa	wtDBG2 sfa	Y-to-V	frg Y-to-V	wtDBG2	Y-to-V sfa brk	wtDBG2 sfa brk	Y-to-V brk	frg Y-to-V
min non-trivial omnitigs per macrotig	N/A	N/A	N/A	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	N/A	N/A	N/A
median non-trivial omnitigs per macrotig	N/A	N/A	N/A	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	N/A	N/A	N/A
min edge length	1	N/A	1	N/A	N/A	N/A	N/A	N/A	N/A
max edge length	3737	N/A	3737	N/A	N/A	N/A	N/A	N/A	N/A
median edge length	115	N/A	115	N/A	N/A	N/A	N/A	N/A	N/A
mean edge length	231.8	N/A	231.8	N/A	N/A	N/A	N/A	N/A	N/A

Table 3: ContigValidator

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

Parameter	Y-to-V sfa	wtdbg2 sfa	Y-to-V frg	Y-to-V wtdbg2	Y-to-V sfa brk	wtdbg2 sfa brk	Y-to-V brk	Y-to-V frg	Y-to-V wtdbg2
# contigs ( $\geq 0$ bp)	4078	2815	3696	1302	1613	4075	2810	1609	1304
# contigs ( $\geq 1000$ bp)	4078	2815	3696	1302	1613	4075	2810	1609	1304
# contigs ( $\geq 5000$ bp)	4056	2806	3681	1293	1605	4023	2797	1597	1295
# contigs ( $\geq 10000$ bp)	3784	2549	3478	1224	1478	3742	2541	1472	1226
# contigs ( $\geq 25000$ bp)	3394	2075	3142	1113	1239	3357	2070	1243	1116
# contigs ( $\geq 50000$ bp)	3009	1610	2829	1033	1020	2973	1602	1019	1029

Table 5: QUASt: total length of contigs

Parameter	Y-to-V sfa	wtdbg2 sfa	Y-to-V frg	Y-to-V wtdbg2	Y-to-V sfa brk	wtdbg2 sfa brk	Y-to-V brk	Y-to-V frg	Y-to-V wtdbg2
Total length ( $\geq 0$ bp)	1109862364	367923144	1106634859	1006952303	349666720	1093454720	365902211	342518872	950103959
Total length ( $\geq 1000$ bp)	1109862364	367923144	1106634859	1006952303	349666720	1093454720	365902211	342518872	950103959
Total length ( $\geq 5000$ bp)	1109775037	367889896	1106573143	1006917812	349638349	1093292617	365860227	342484773	950069468
Total length ( $\geq 10000$ bp)	1107746346	366054219	1105038757	1006417891	348736932	1091206672	364030547	341593539	949569547
Total length ( $\geq 25000$ bp)	1101317485	358177408	1099457564	1004643508	344757350	1084863086	356206451	337829094	947808623
Total length ( $\geq 50000$ bp)	1087080247	341158821	1087861966	1001706283	336699990	1070661909	339096568	329541619	944599814

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

Parameter	Y-to-V sfa	wtdbg2 sfa	Y-to-V frg	Y-to-V wtdbg2	Y-to-V sfa brk	wtdbg2 sfa brk	Y-to-V brk	Y-to-V frg	Y-to-V wtdbg2
# contigs	4074	2811	3694	1300	1609	4052	2803	1601	1302
Largest contig	3870585	3258382	3870585	6167046	4273861	3870585	3258382	4273861	6167046
Total length	1109853157	367913124	1106629186	1006946530	349656700	1093409398	365886751	342503124	950098186
Reference length	387424359	387424359	387424359	387424359	387424359	387424359	387424359	387424359	387424359
GC (%)	43.51	43.43	43.50	43.55	43.51	43.50	43.43	43.49	43.55
Reference GC (%)	43.61	43.61	43.61	43.61	43.61	43.61	43.61	43.61	43.61
N50	558991	279184	596180	1558267	527590	554742	278341	510848	1541702
NG50	1092649	261895	1139889	2855000	462314	1085246	257930	426656	2695471
N75	286561	133922	310071	924390	254146	285553	133590	249099	871296
NG75	921633	113191	964986	2326814	169941	903290	111395	149824	2207837
L50	602	371	568	203	182	599	369	186	195
LG50	131	407	125	53	220	133	409	234	54
L75	1288	845	1204	411	421	1278	842	425	402
LG75	228	963	217	90	559	231	974	601	94

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

Parameter	Y-to-V sfa	wtdbg2 sfa	Y-to-V frg	Y-to-V wtdbg2	Y-to-V sfa brk	wtdbg2 sfa brk	Y-to-V brk	Y-to-V frg	Y-to-V wtdbg2
# misassemblies	3477	661	3552	2604	769	3321	636	711	236
# unique misassemblies	2398	637	2446	1555	742	2299	614	688	143
# misassembled contigs	1709	221	1696	794	237	1646	213	222	73
Misassembled contigs length	578445545	27301242	625174961	818140471	74428609	564801389	26228399	68891946	74838653
# local misassemblies	1430	416	1401	1171	399	1363	397	360	108
# unique local misassemblies	691	351	677	515	330	652	344	307	48
# scaffold gap ext. mis.	0	0	0	0	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0	0	0	0	0
# possible TEs	182	58	186	164	64	170	56	58	15
# unaligned mis. contigs	37	24	31	14	15	37	23	15	7
# unaligned contigs	6+778p	2+254p	5+750p	2+382p	1+214p	5+744p	2+244p	1+204p	2+349p
Unaligned length	6210531	2355891	6245170	5805217	2340421	6019069	2212477	2200176	525538
Genome fraction (%)	98.156	93.713	98.163	97.305	88.964	97.409	93.248	87.195	95.36
Duplication ratio	2.902	1.007	2.893	2.656	1.008	2.881	1.007	1.007	2.55
# N's per 100 kbp	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	54.26	36.36	54.08	41.32	41.14	53.40	35.47	38.70	40.8
# indels per 100 kbp	30.16	28.98	30.26	30.22	30.10	30.05	28.88	29.82	30.1
Largest alignment	3870585	3258382	3870585	4904198	4273861	3870585	3258382	4273861	4904198
Total aligned length	1102126729	365409918	1098781118	999231018	347092199	1085903289	363531583	340100618	94309342
EA50max	565115	254805	582511	1072258	409611	558951	253218	385433	100413
Strict EA50max	542468	241578	560200	958263	380586	539491	239964	365622	90789
NGA50	897982	254805	916378	1826605	409611	887697	253218	385433	17469
EA75max	297054	106649	318929	537989	142297	293093	104661	130745	46872
Strict EA75max	277366	101677	293455	467154	136119	271944	99605	120128	42763
NGA75	708355	106725	728379	1421771	142297	699915	104661	130745	137172
LGA50	162	421	157	78	250	163	424	262	8
LGA75	284	1009	276	141	640	288	1020	681	14

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

Parameter	Y-to-V sfa	wtdbg2 sfa	Y-to-V	frg Y-to-V	wtdbg2	Y-to-V sfa brk	wtdbg2 sfa brk	Y-to-V brk	frg Y-to-V brk
# misassemblies	3477	661	3552	2604	769	3321	636	711	2368
# contig misassemblies	3477	661	3552	2604	769	3321	636	711	2368
# c. relocations	897	181	925	835	233	843	175	207	737
# c. translocations	2556	473	2602	1753	529	2458	455	497	1619
# c. inversions	24	7	25	16	7	20	6	7	12
# scaffold misassemblies	0	0	0	0	0	0	0	0	0
# s. relocations	0	0	0	0	0	0	0	0	0
# s. translocations	0	0	0	0	0	0	0	0	0
# s. inversions	0	0	0	0	0	0	0	0	0
# misassembled contigs	1709	221	1696	794	237	1646	213	222	755
Misassembled contigs length	578445545	27301242	625174961	818140471	74428609	564801389	26228399	68891946	748386584
# local misassemblies	1430	416	1401	1171	399	1363	397	360	1089
# scaffold gap ext. mis.	0	0	0	0	0	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0	0	0	0	0	0
# mis. caused by frag. ref.	0	0	0	0	0	0	0	0	0
# possible TEs	182	58	186	164	64	170	56	58	152
# unaligned mis. contigs	37	24	31	14	15	37	23	15	14
# mismatches	597973	132874	594224	412851	142790	579904	128934	131623	382549
# indels	332362	105888	332506	301950	104462	326306	104988	101434	283941
# indels ( $\leq 5$ bp)	326006	104620	326172	297740	103177	320087	103748	100193	280011
# indels ( $> 5$ bp)	6356	1268	6334	4210	1285	6219	1240	1241	3930
Indels length	1427153	365057	1474643	1541001	412749	1352225	346824	384169	1140063

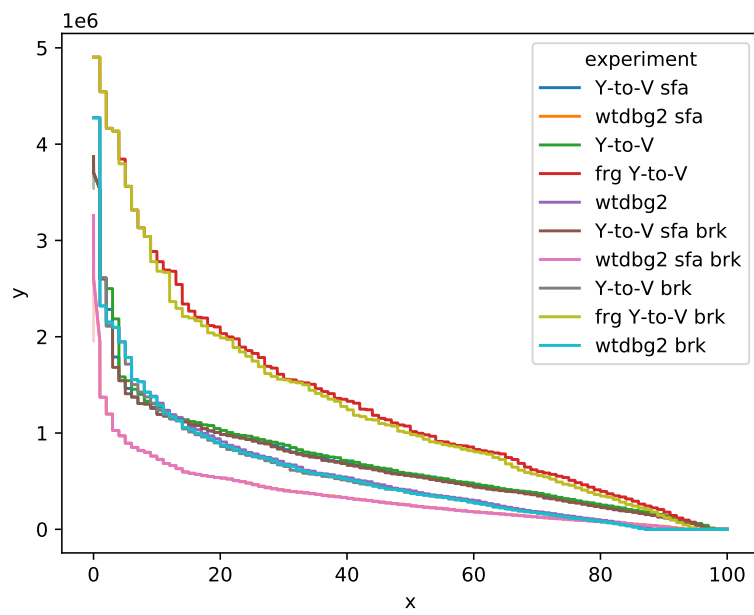


Figure 1: EAxmax

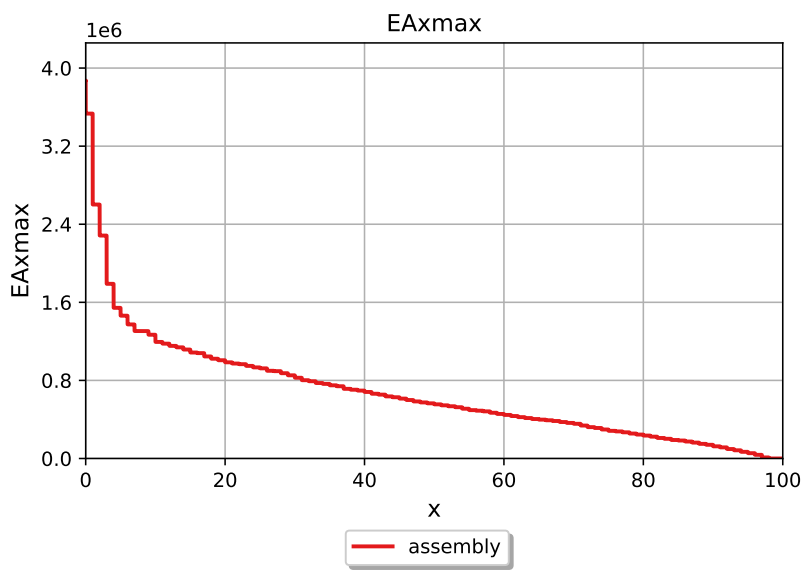


Figure 2: QUAST EAxmax graph for Y-to-V sfa

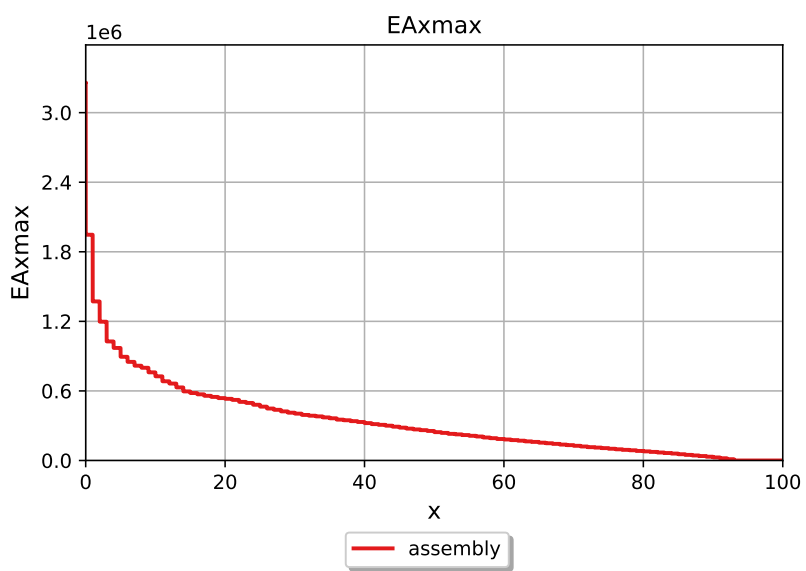


Figure 3: QUAST EAxmax graph for wtdbg2 sfa

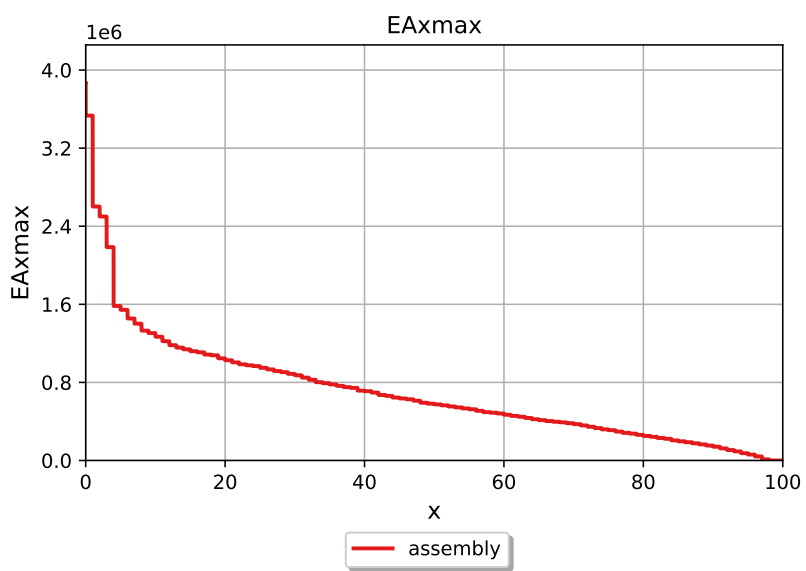


Figure 4: QUAST EAXmax graph for Y-to-V

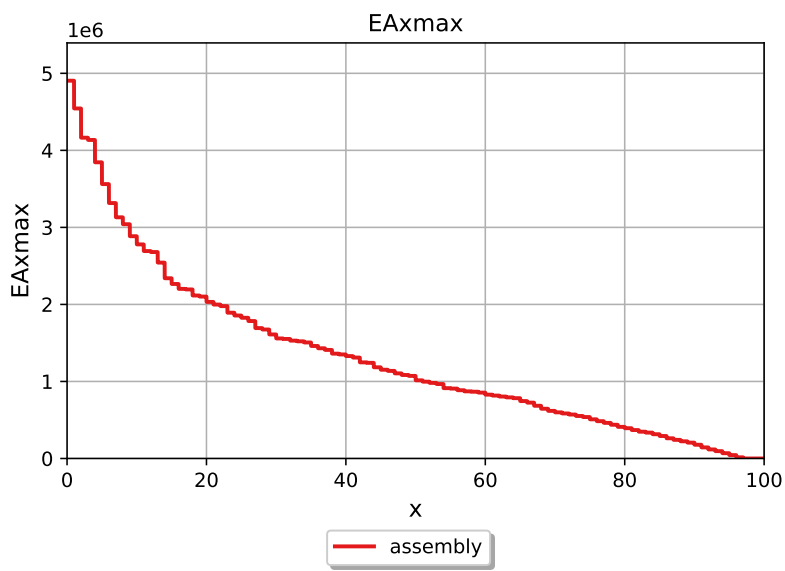


Figure 5: QUAST EAxmax graph for frg Y-to-V



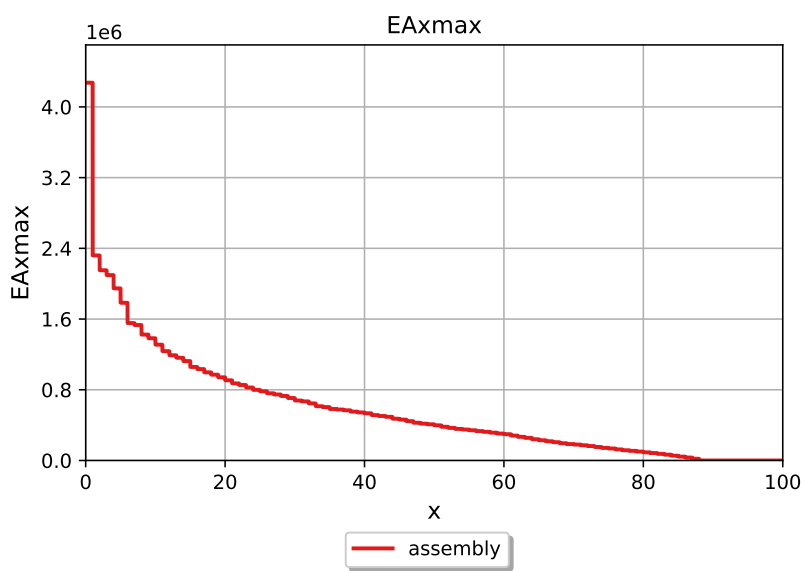


Figure 6: QUAST EAxmax graph for wtdbg2

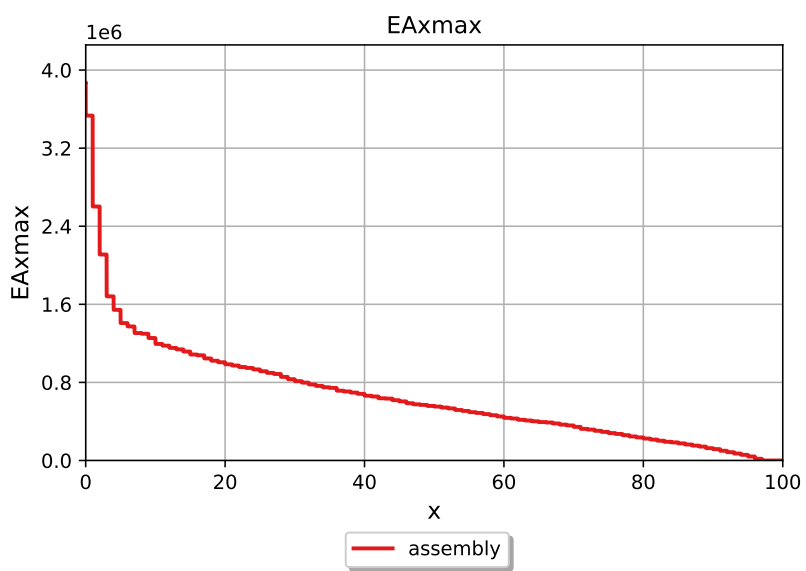


Figure 7: QUAST EAxmax graph for Y-to-V sfa brk

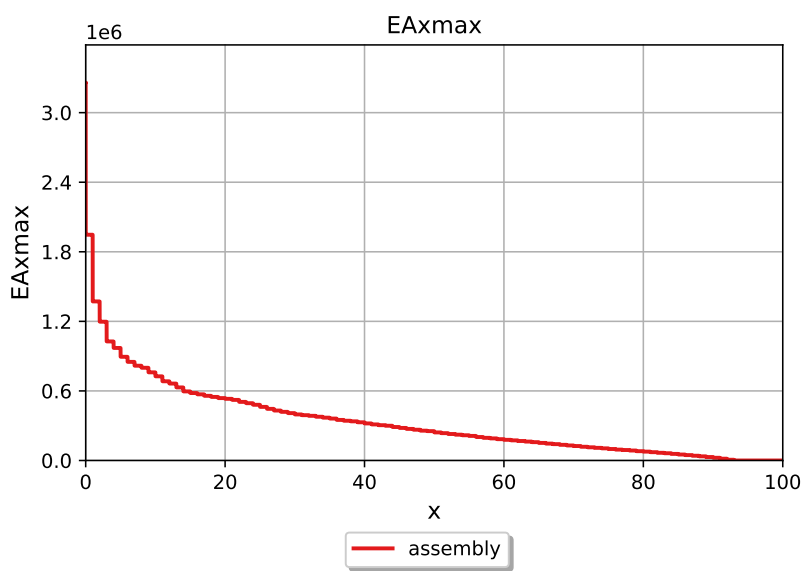


Figure 8: QUAST EAxmax graph for wtdbg2 sfa brk

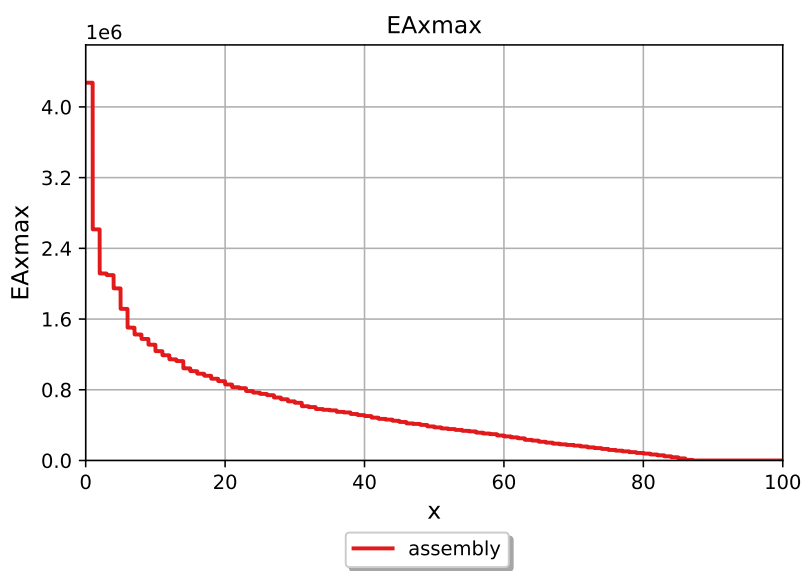


Figure 9: QUAST EAxmax graph for Y-to-V brk

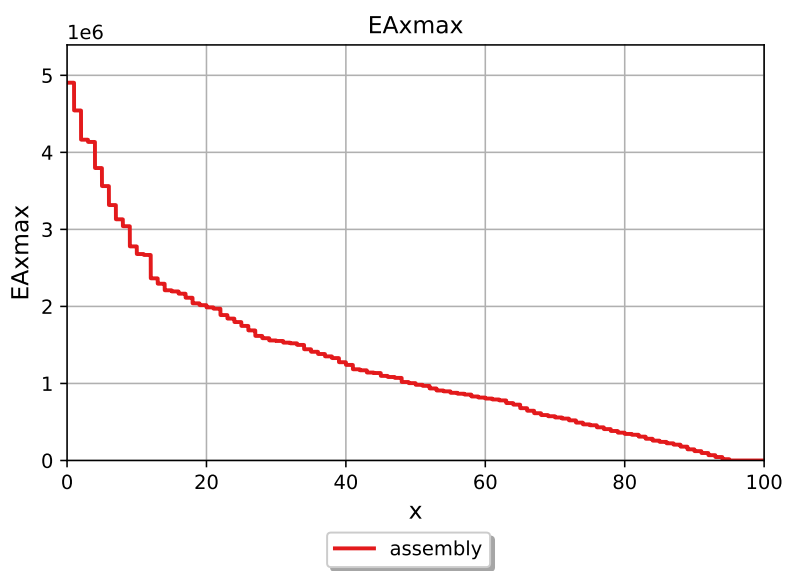


Figure 10: QUAST EAxmax graph for frg Y-to-V brk

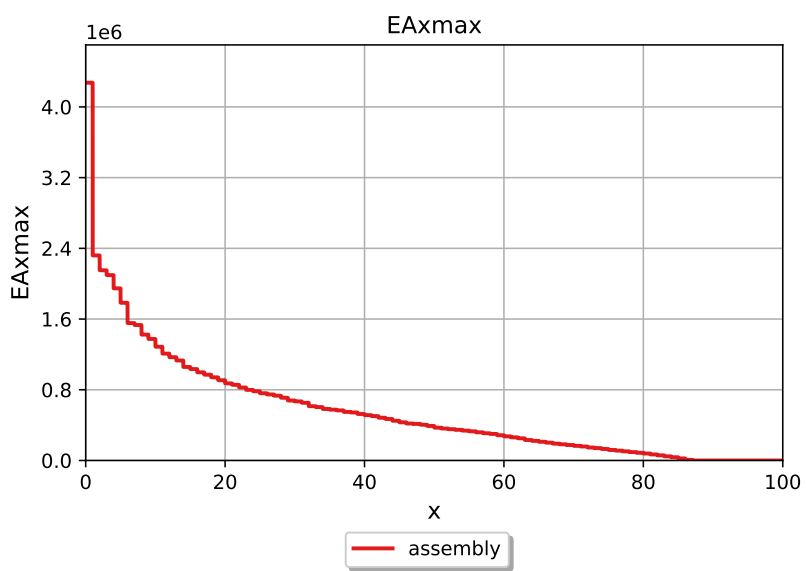


Figure 11: QUAST EAxmax graph for wtdbg2 brk

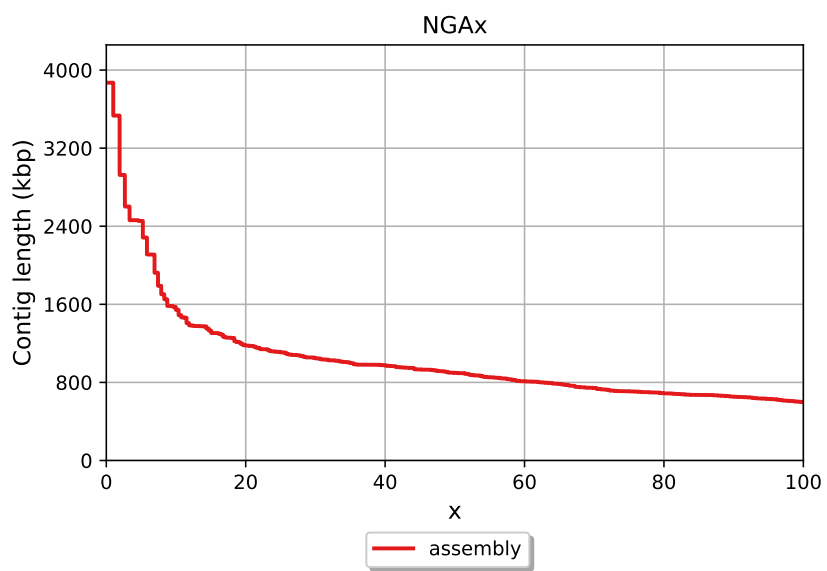


Figure 12: QUAST NGAx graph for Y-to-V sfa

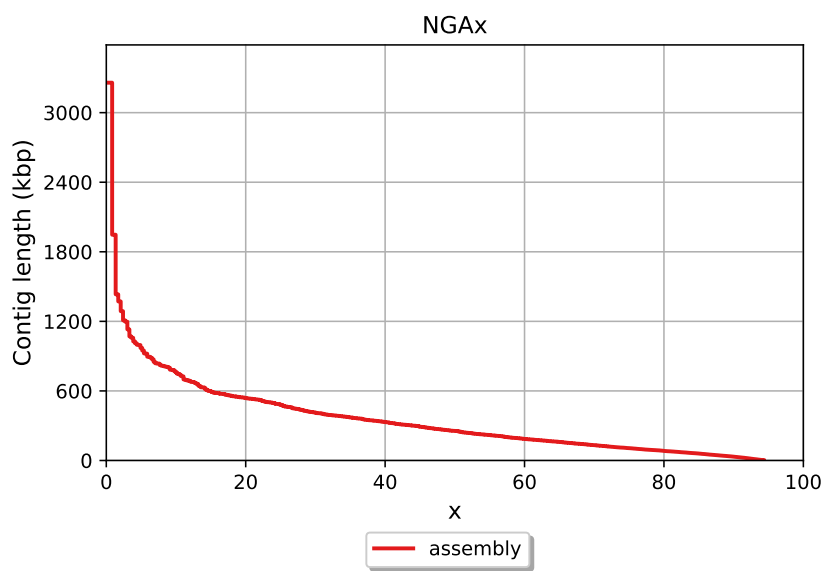


Figure 13: QUAST NGAx graph for wtdbg2 sfa



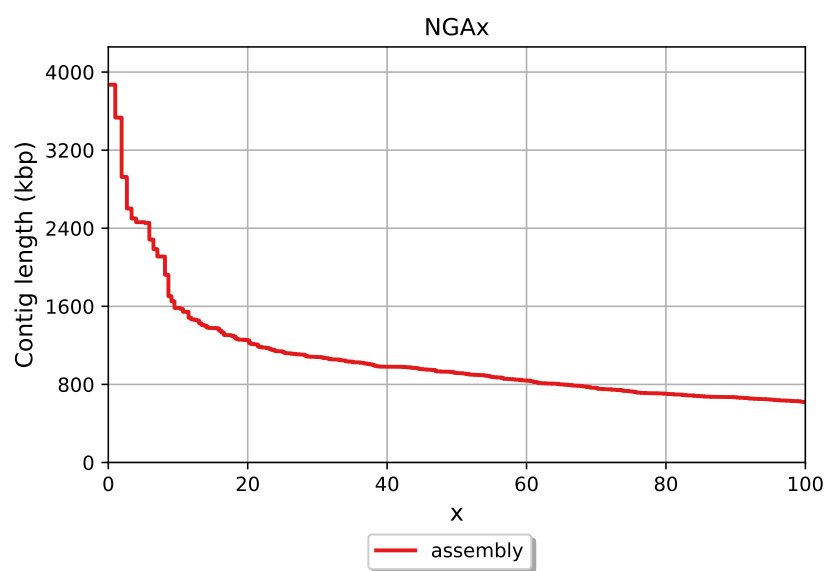


Figure 14: QUASt NGAx graph for Y-to-V

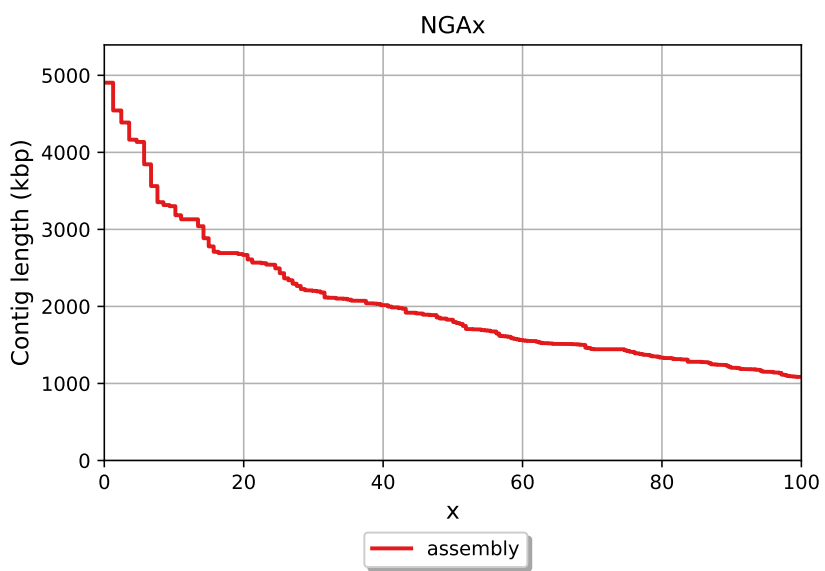


Figure 15: QUAST NGAx graph for frg Y-to-V

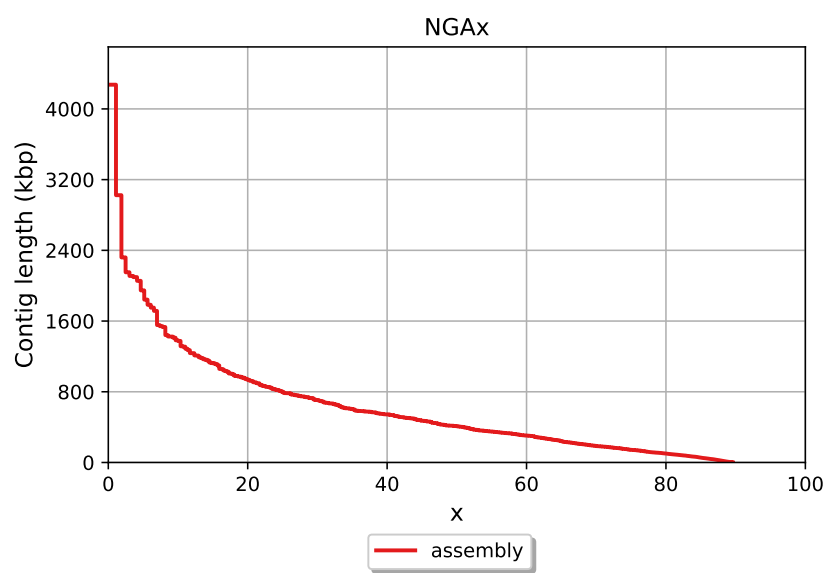


Figure 16: QUAST NGAx graph for wtdbg2

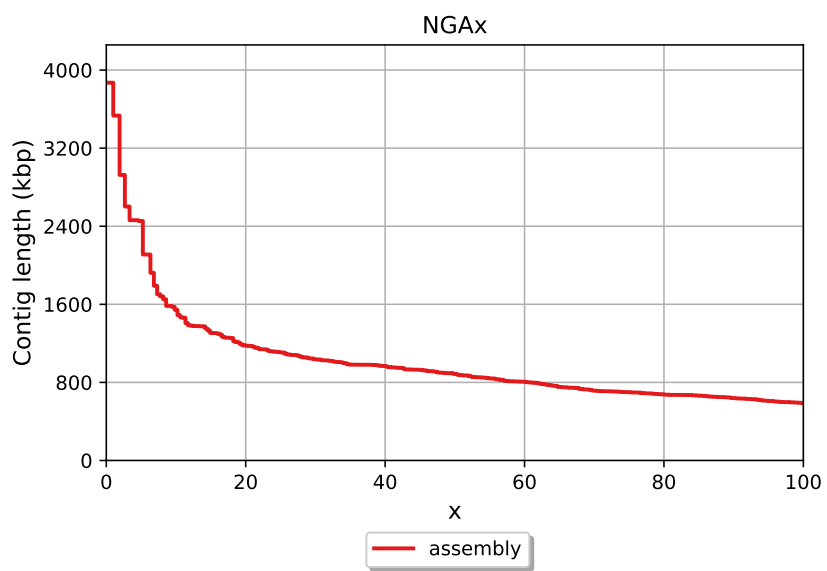


Figure 17: QUASt NGAx graph for Y-to-V sfa brk

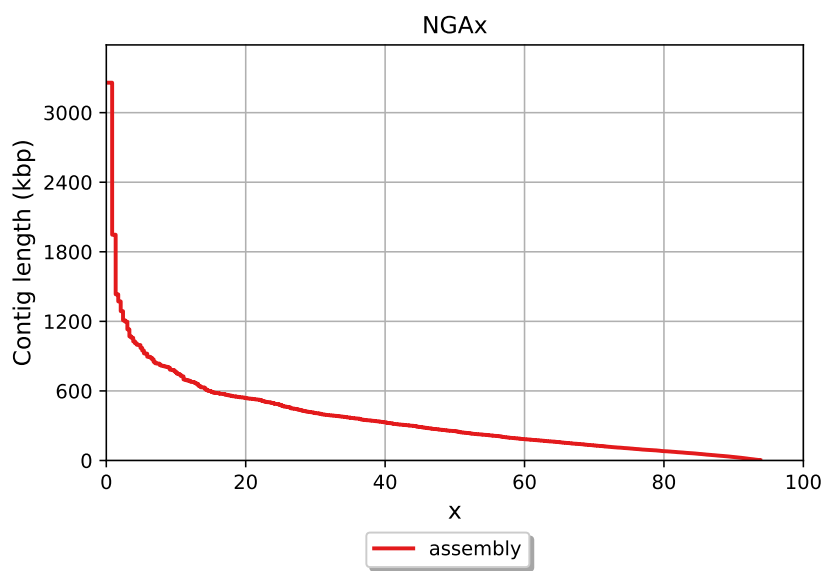


Figure 18: QUAST NGAx graph for wtdbg2 sfa brk

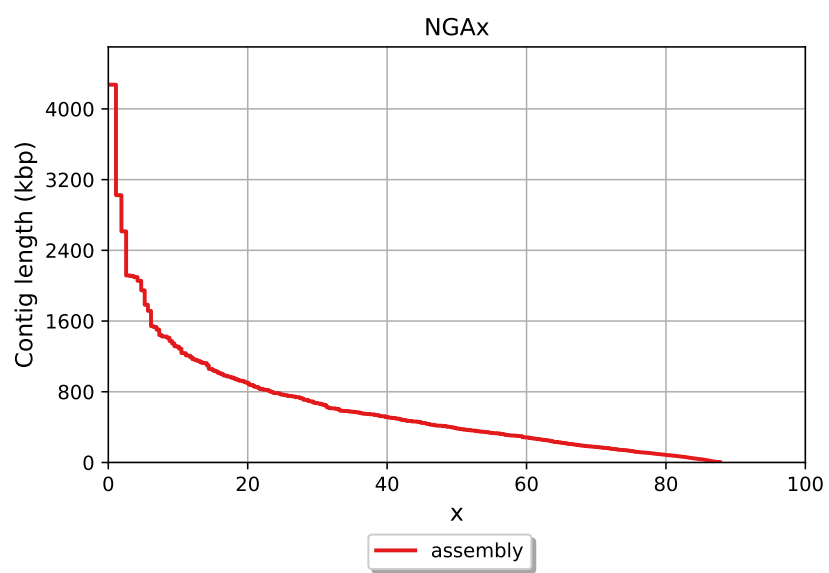


Figure 19: QUAST NGAx graph for Y-to-V brk

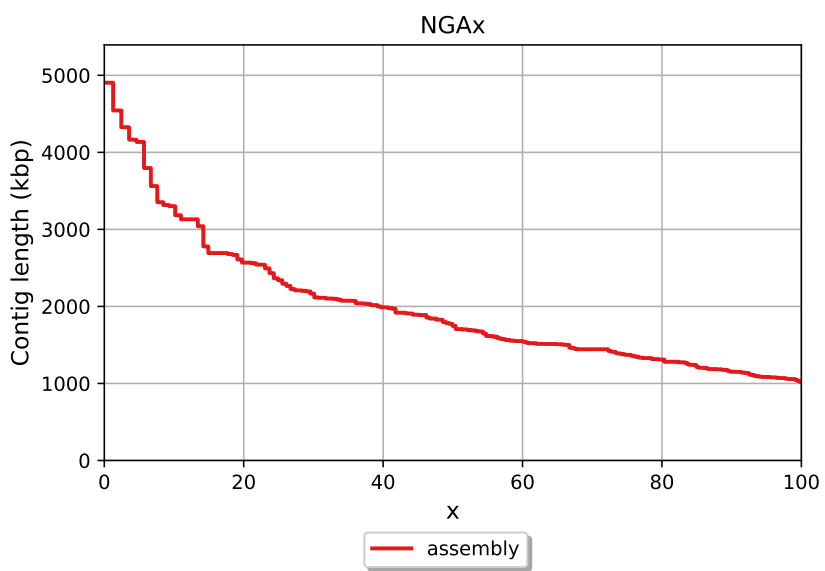


Figure 20: QUAST NGAx graph for frg Y-to-V brk

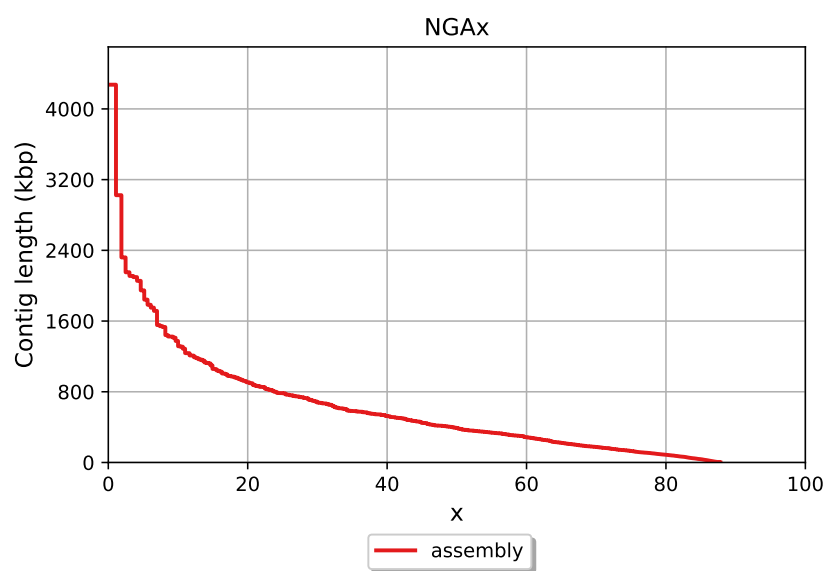


Figure 21: QUAST NGAx graph for wtdbg2 brk