

Report

	contigs_1	contigs_2
s (>= 0 bp)	3	4
s (>= 1000 bp)	3	2
gth (>= 0 bp)	6710	5870
gth (>= 1000 bp)	6710	5460
s	3	2
contig	3980	3360
gth	6710	5460
e length	10000	10000
	51.28	52.44
e GC (%)	52.07	52.07
	3980	3360
	1610	2100
	1610	2100
	1	1
	2	2
	2	2
semblies	1	2
sembled contigs	1	1
nbled contigs length	3980	3360
nisassemblies	0	0
ned contigs	0 + 0 part	0 + 0 part
d length	0	0
fraction (%)	67.120	54.610
on ratio	1.000	1.000
r 100 kbp	0.00	0.00
tches per 100 kbp	0.00	0.00
per 100 kbp	0.00	0.00
	5 + 4 part	1 + 6 part
s	1 + 1 part	0 + 2 part
ted genes (unique)	7	6
ted genes (>= 0 bp)	7	6
ted genes (>= 300 bp)	6	5
ted genes (>= 1500 bp)	1	1
ted genes (>= 3000 bp)	0	0
alignment	2030	2100
	1950	1470
	1610	700
	1610	1190
	2	2
	3	4
	3	3

Statistics are based on contigs of size >= 500 bp, unless otherwise specified. The labels "Total contigs (>= 0 bp)" and "Total length (>= 0 bp)" include

Misassemblies report

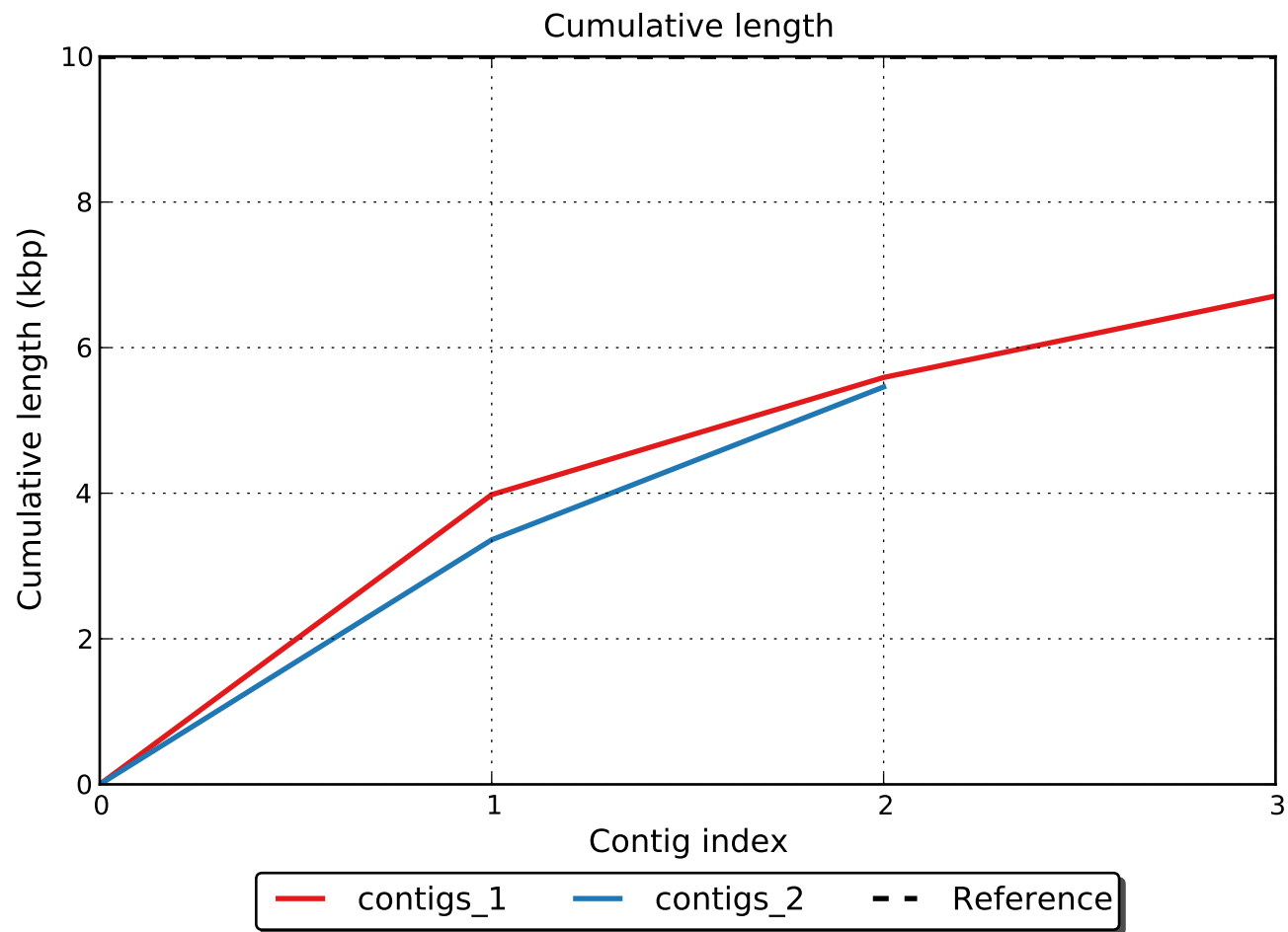
	contigs_1	contigs_2
assemblies	1	2
elocations	1	2
anslocations	0	0
versions	0	0
assembled contigs	1	1
sembled contigs length	3980	3360
l misassemblies	0	0
matches	0	0
ls	0	0
hort indels	0	0
ng indels	0	0
length	0	0

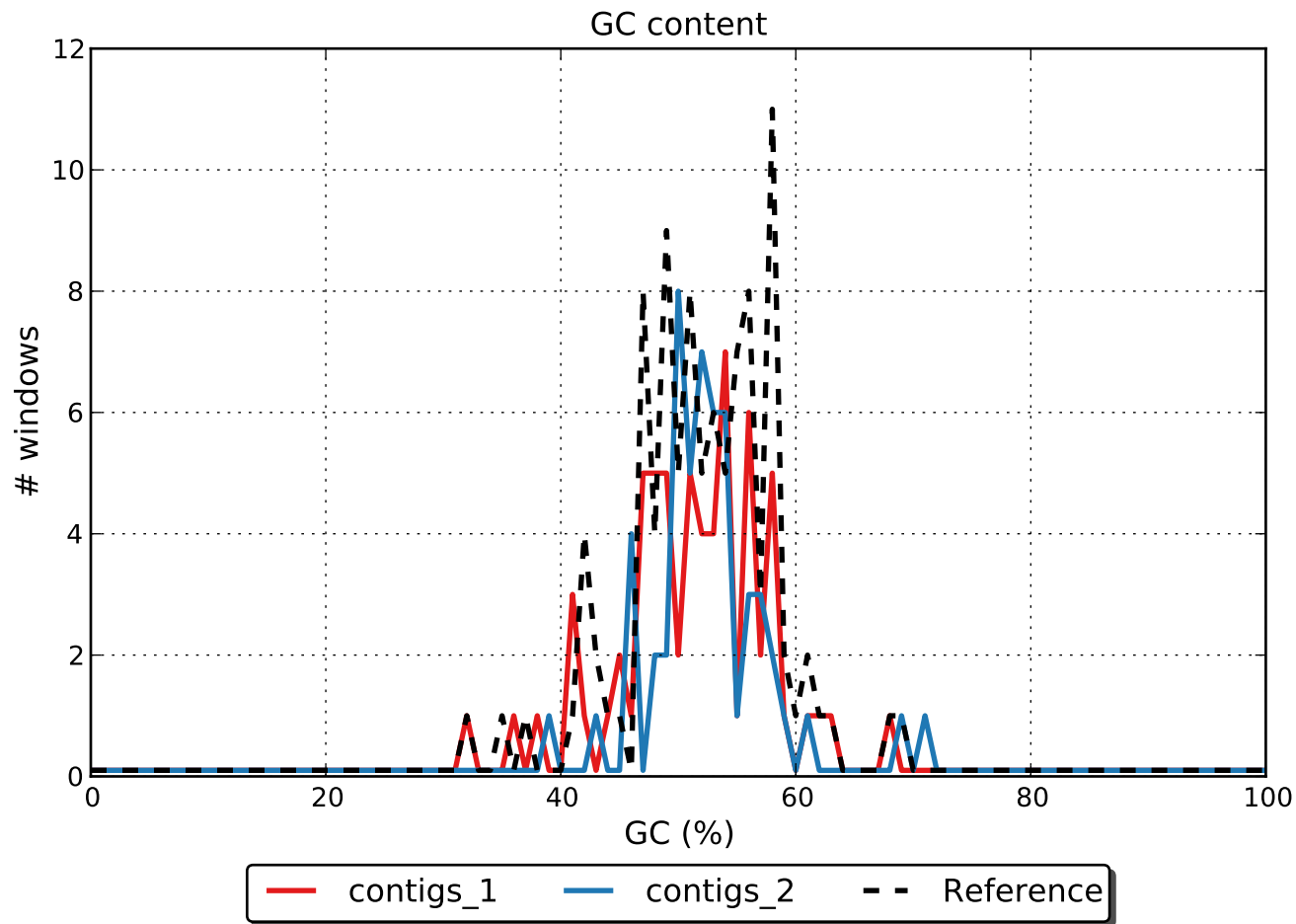
istics are based on contigs of size ≥ 500 bp, using
 # contigs (≥ 0 bp)" and "Total length (≥ 0 bp)

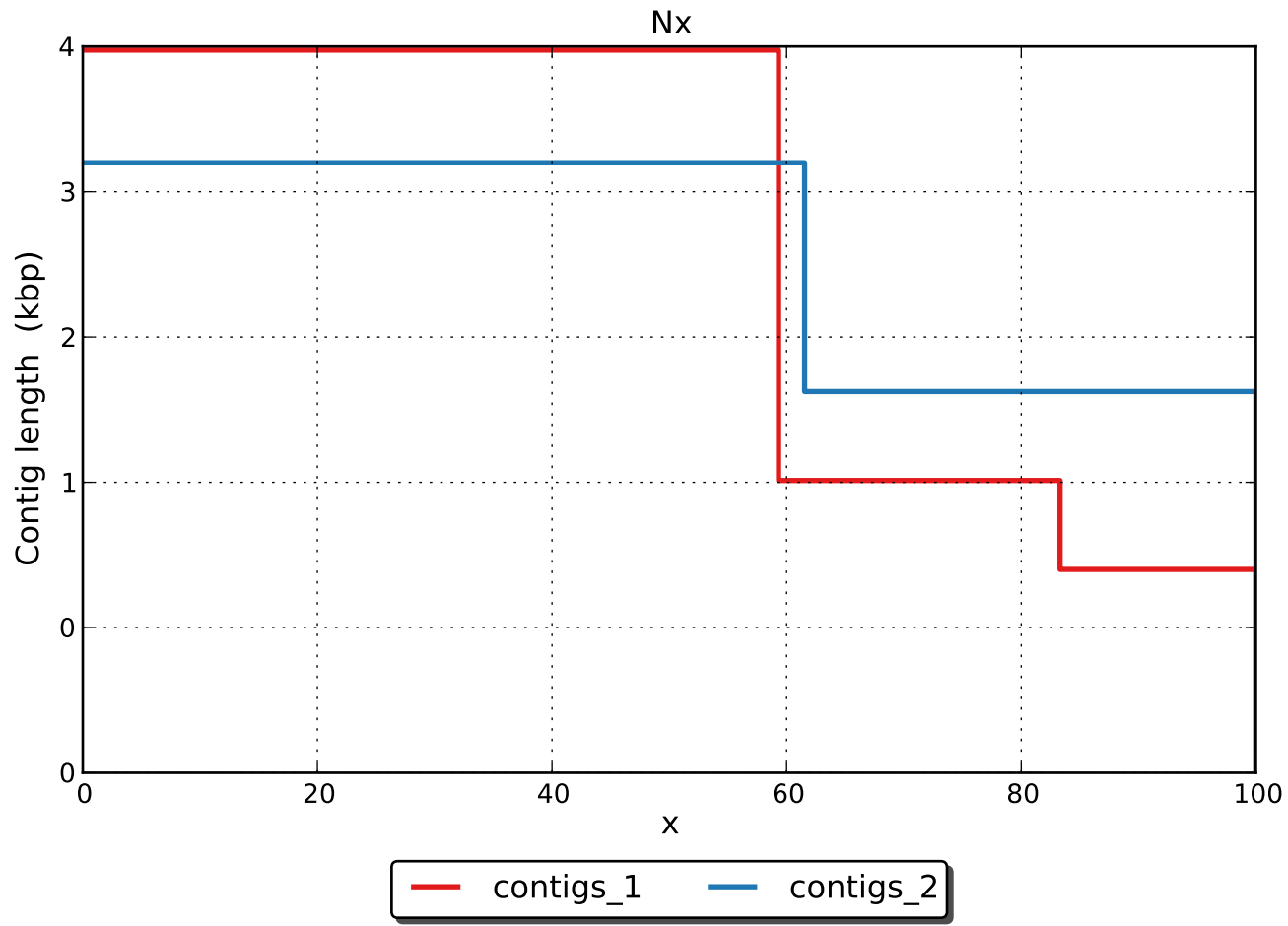
Unaligned report

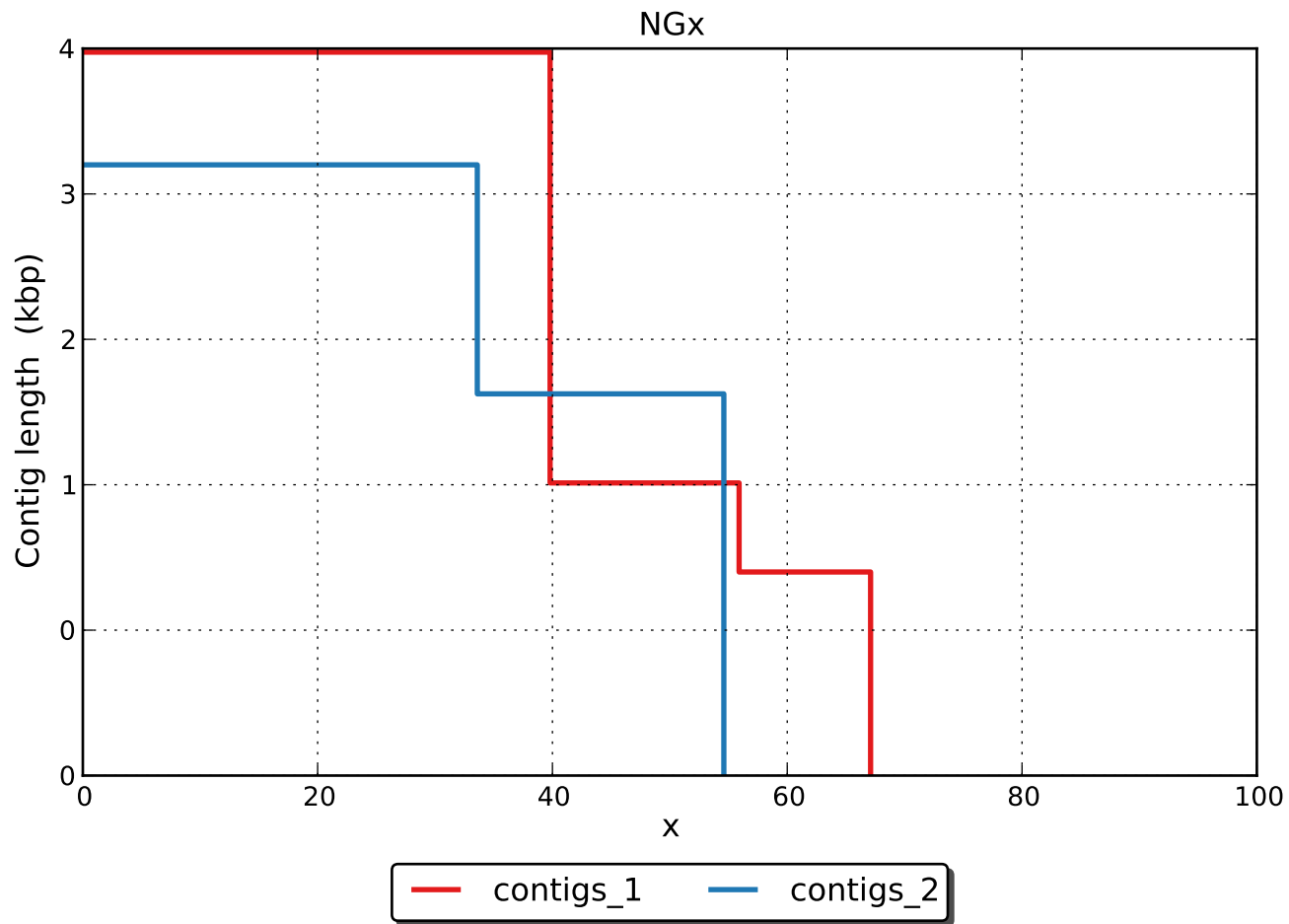
	contigs_1	contigs_2
fully unaligned contigs	0	0
fully unaligned length	0	0
partially unaligned contigs	0	0
partially unaligned length with misassembly	0	0
contigs where both parts are significant	0	0
contigs where both parts are significant length	0	0
contigs where both parts are significant	0	0

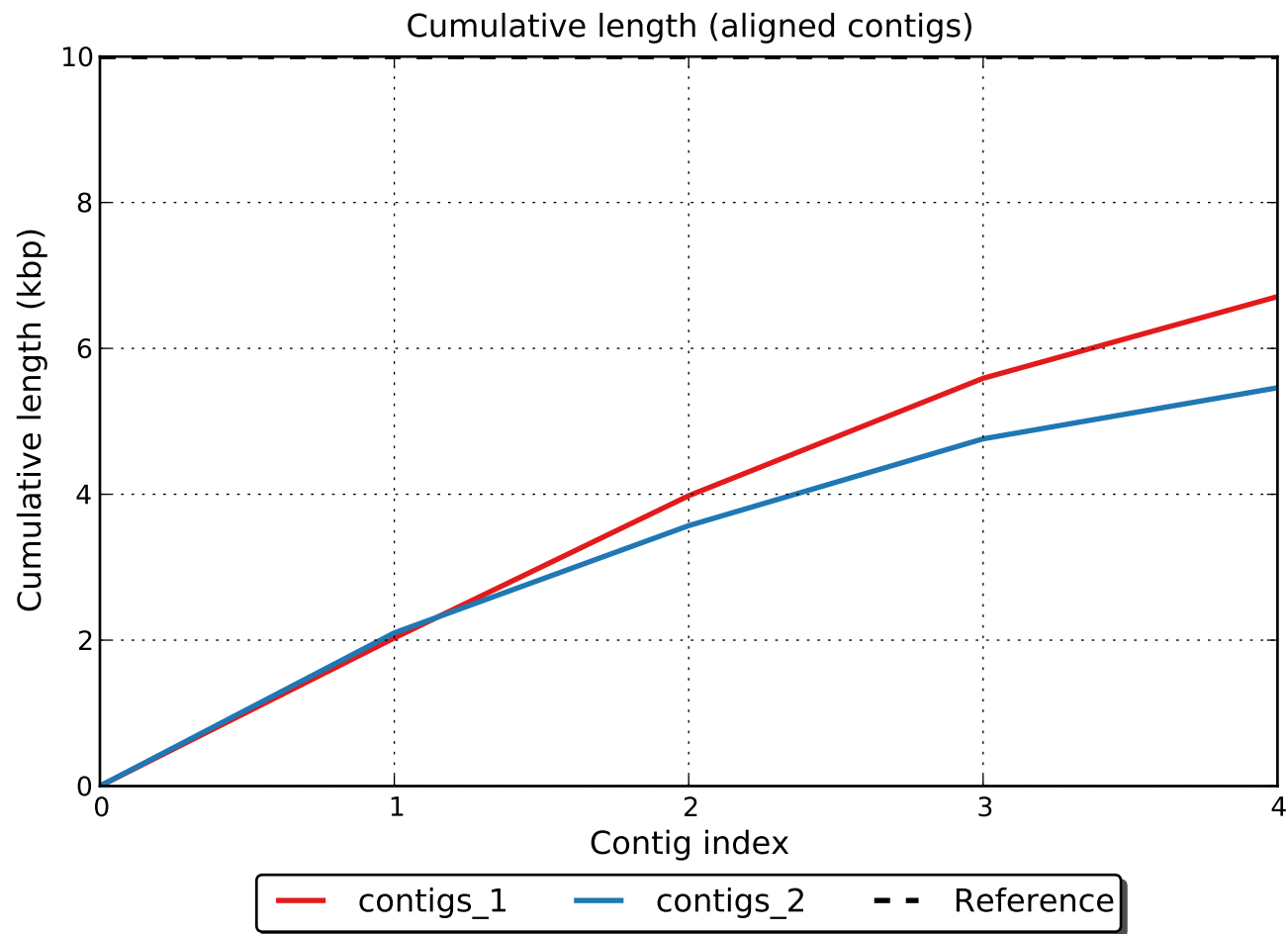
Statistics are based on contigs of size ≥ 500 bp, unless otherwise specified. "Total length (≥ 0 bp)" and "Total length (≥ 0 bp)" include



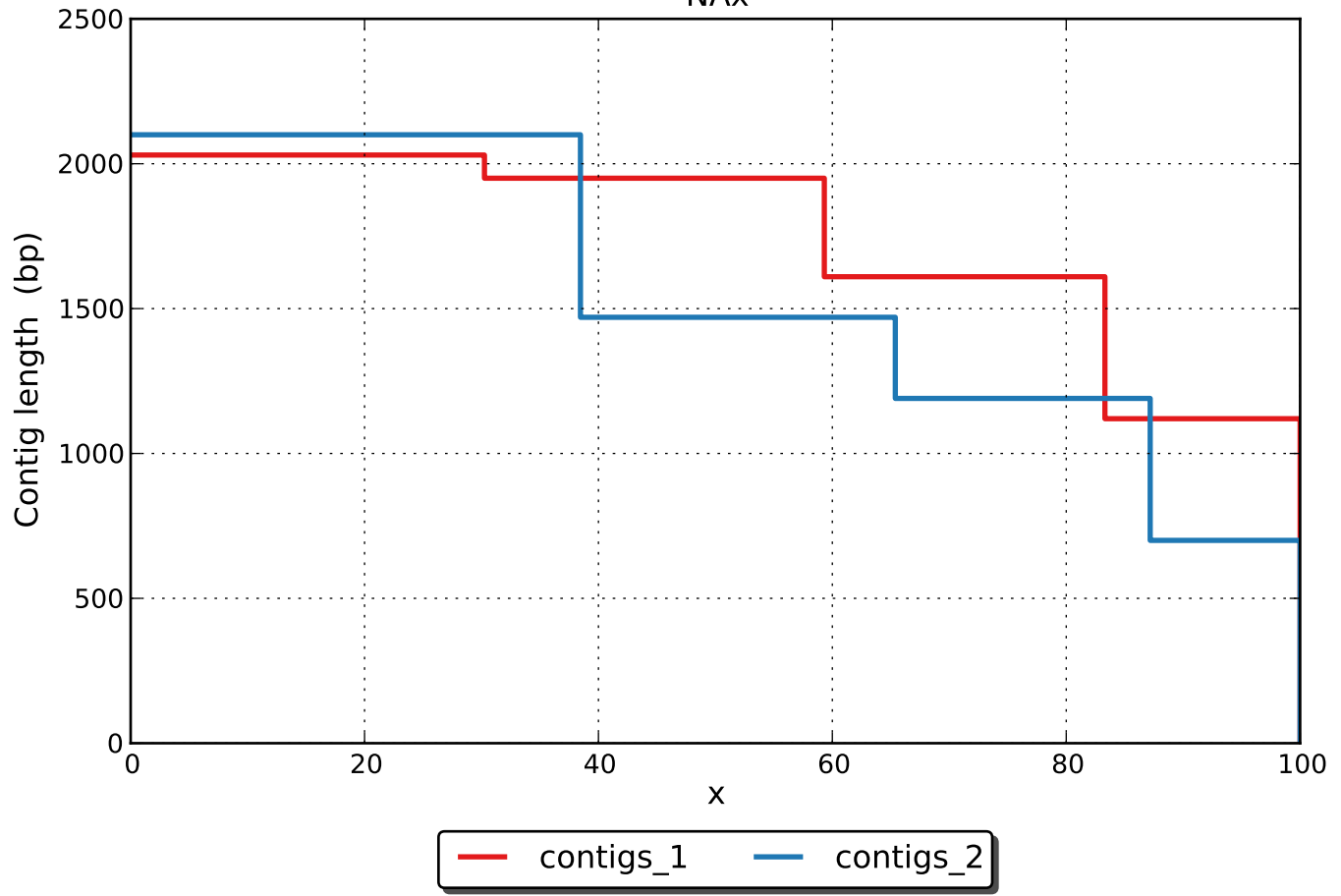




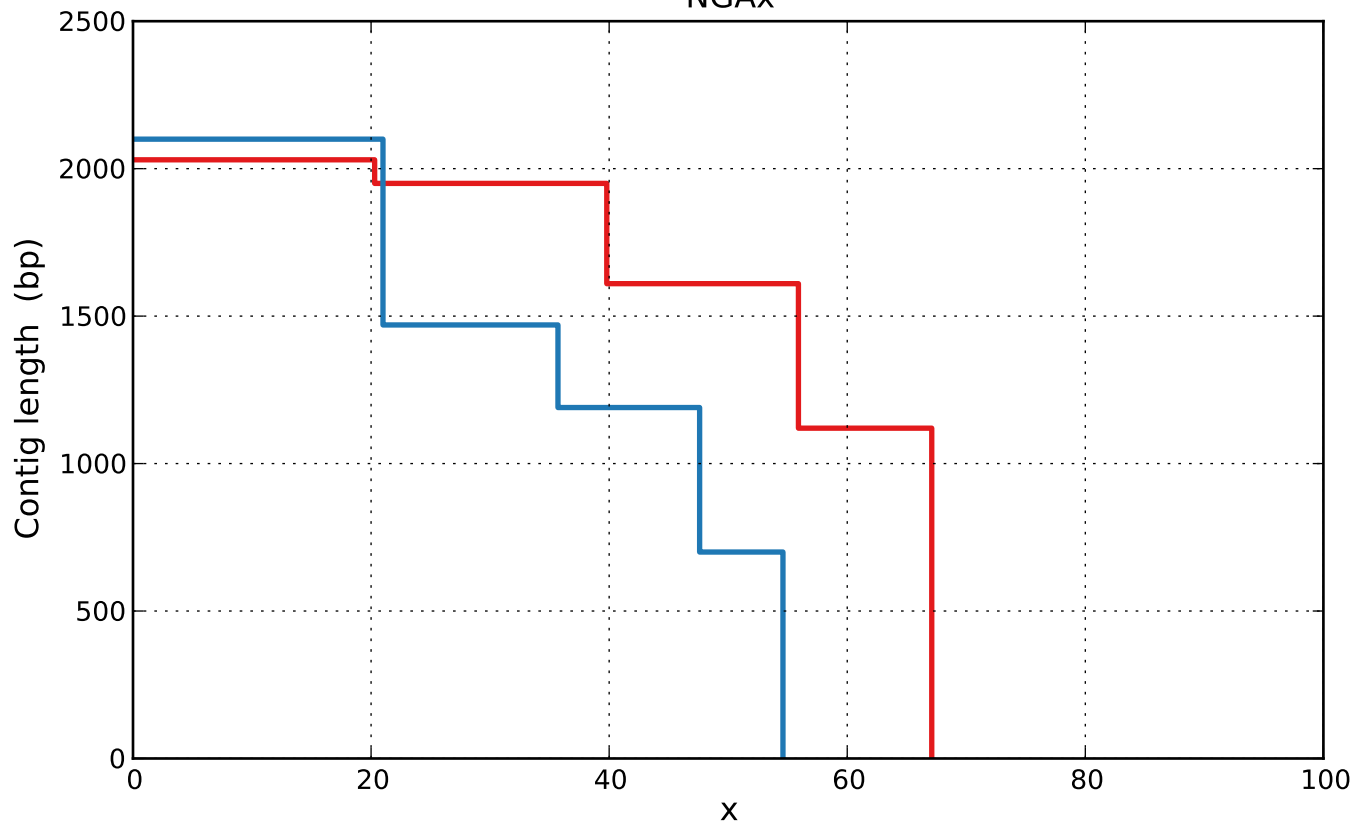




NAx



NGAx



— contigs_1 — contigs_2

