

# Report

	contigs
# contigs ( $\geq 0$ bp)	100
# contigs ( $\geq 1000$ bp)	1
# contigs ( $\geq 5000$ bp)	0
# contigs ( $\geq 10000$ bp)	0
# contigs ( $\geq 25000$ bp)	0
# contigs ( $\geq 50000$ bp)	0
Total length ( $\geq 0$ bp)	28478
Total length ( $\geq 1000$ bp)	1374
Total length ( $\geq 5000$ bp)	0
Total length ( $\geq 10000$ bp)	0
Total length ( $\geq 25000$ bp)	0
Total length ( $\geq 50000$ bp)	0
# contigs	5
Largest contig	1374
Total length	3904
Reference length	4641652
GC (%)	53.43
Reference GC (%)	50.79
N50	791
N75	575
L50	2
L75	4
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	1374
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	0.084
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1617.46
# indels per 100 kbp	0.00
Largest alignment	1304
NA50	791
NGA50	-
NA75	567
LA50	2
LA75	4

All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Misassemblies report

	contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# misassembled contigs	1
Misassembled contigs length	1374
# local misassemblies	0
# mismatches	63
# indels	0
# short indels	0
# long indels	0
Indels length	0

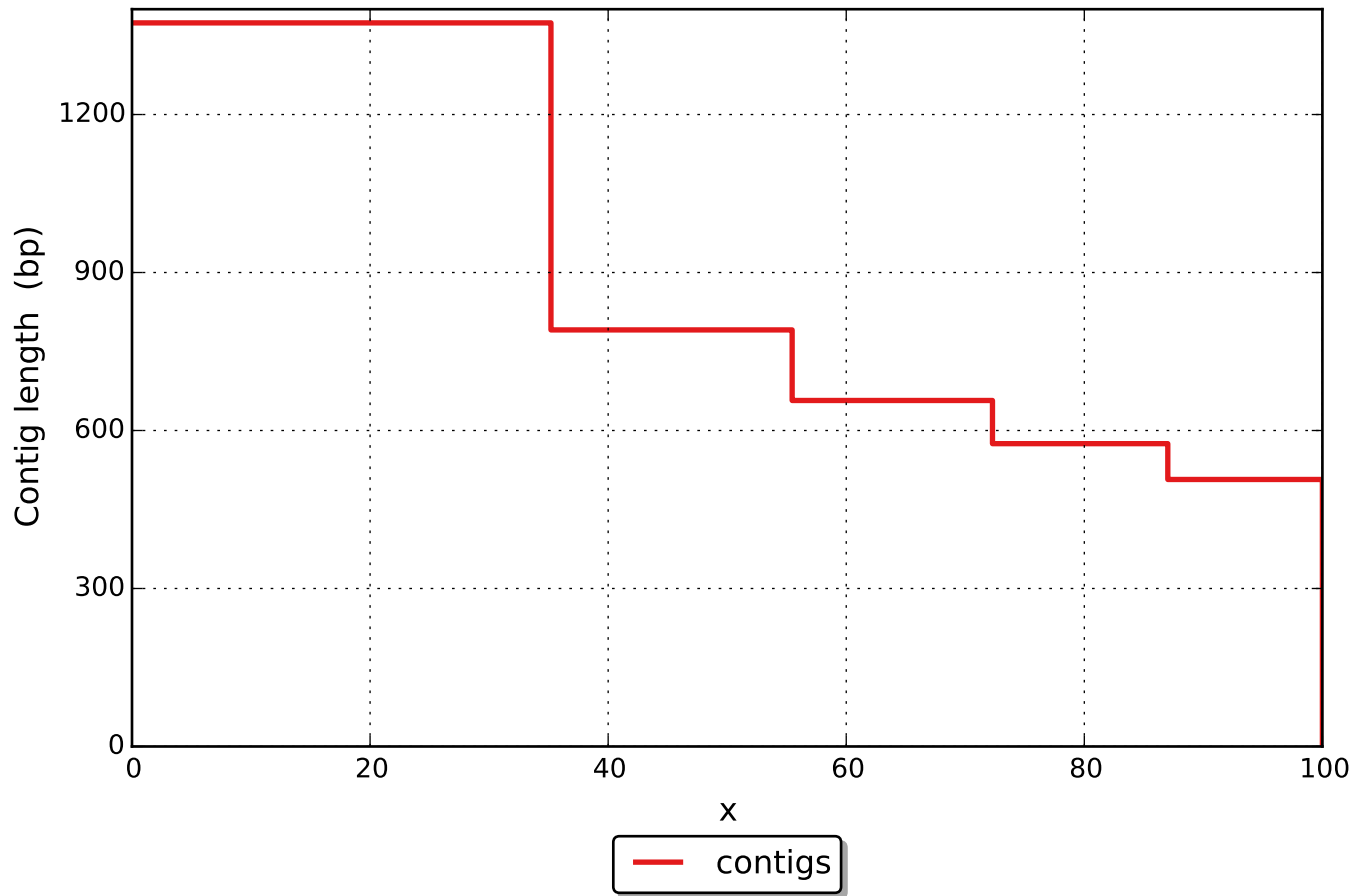
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

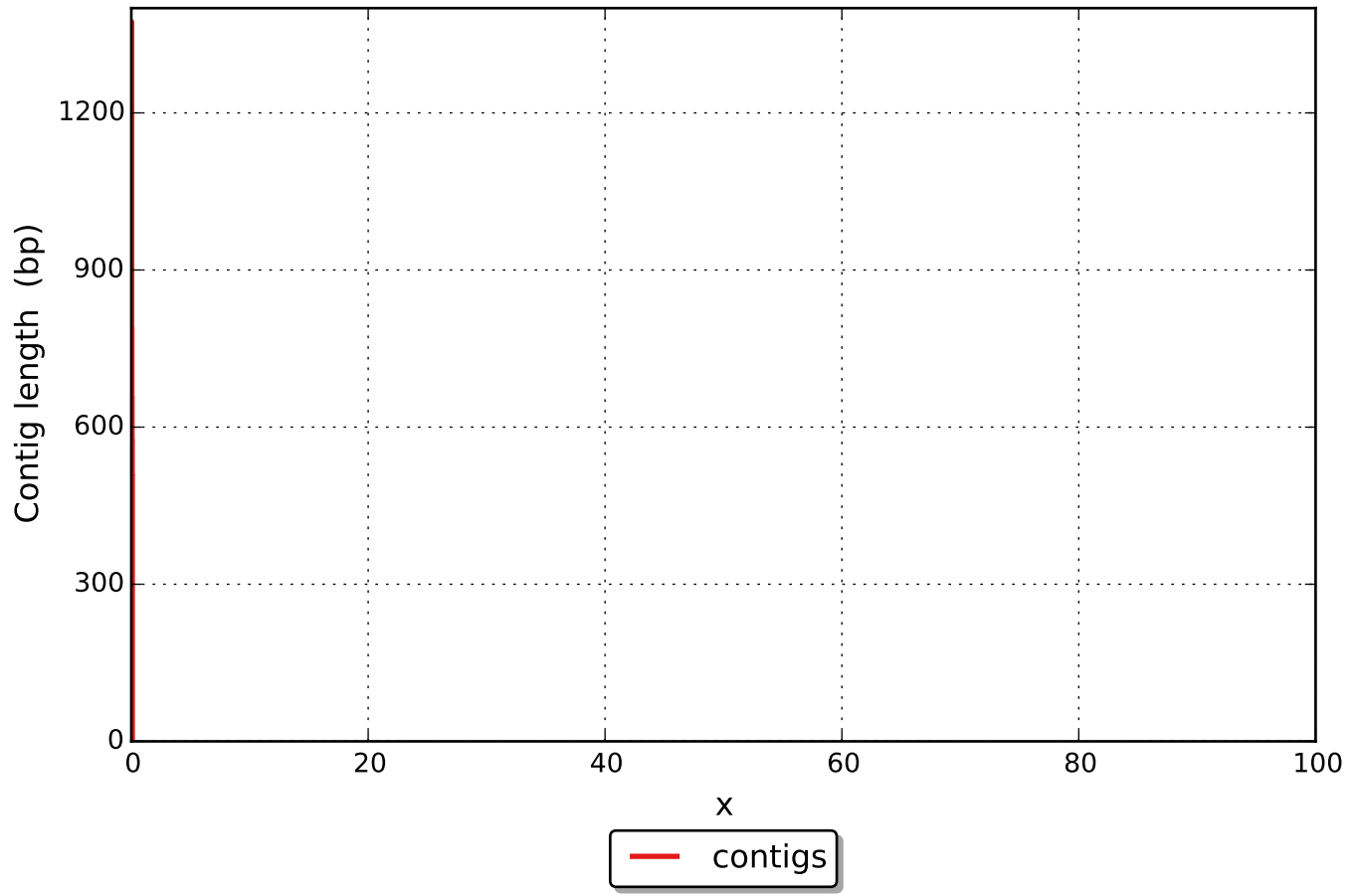
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

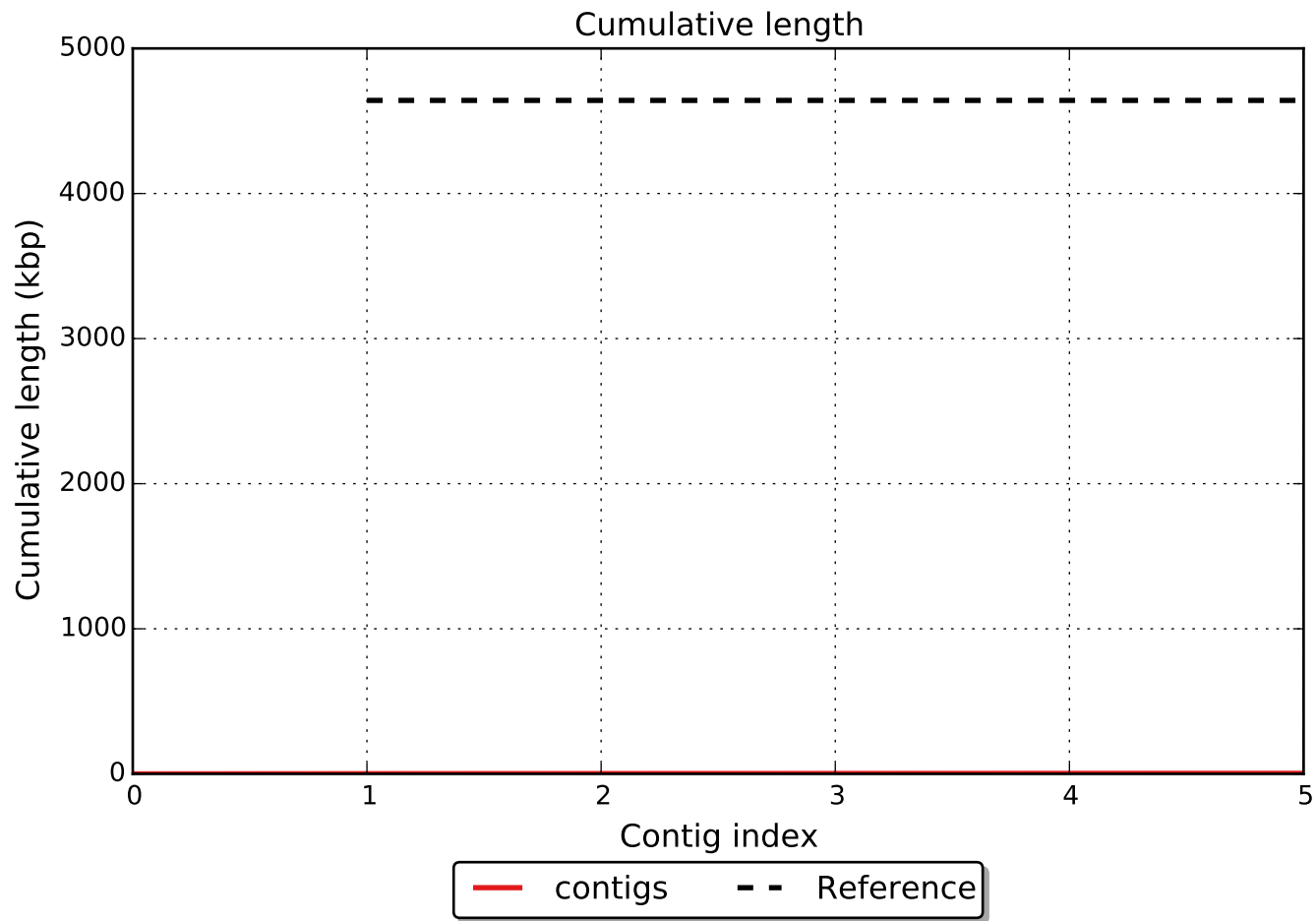
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

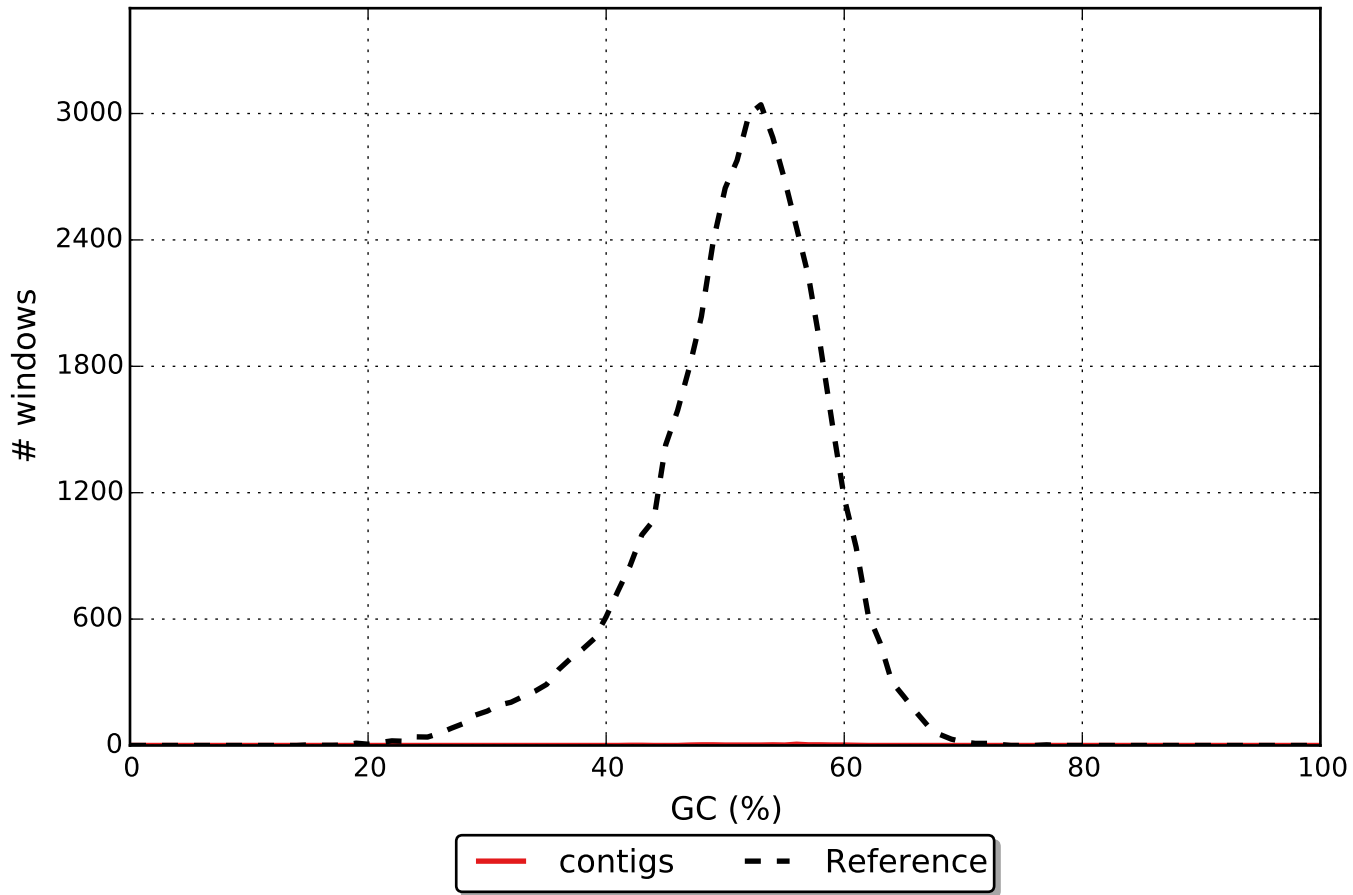


NGx





# GC content



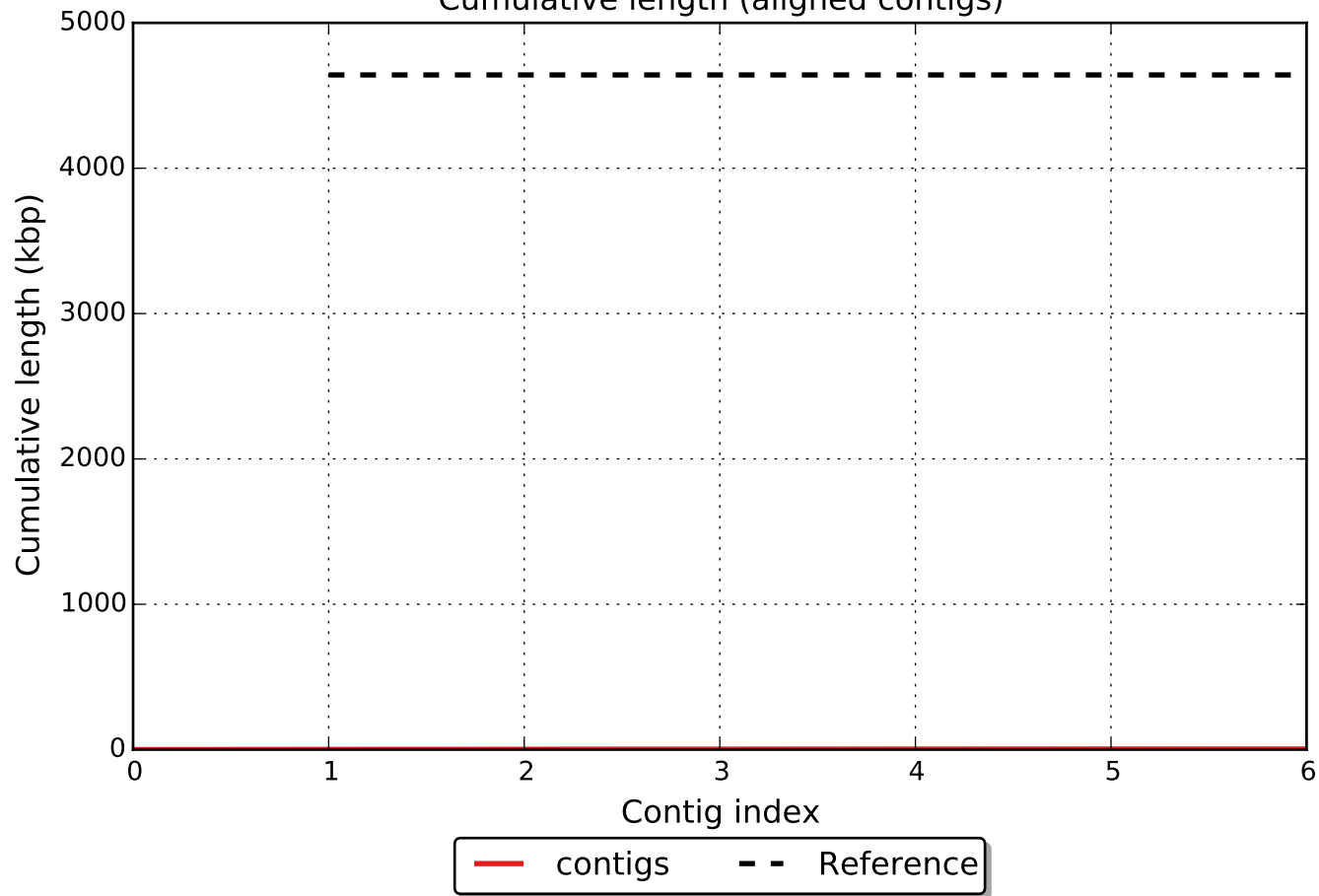
# Misassemblies



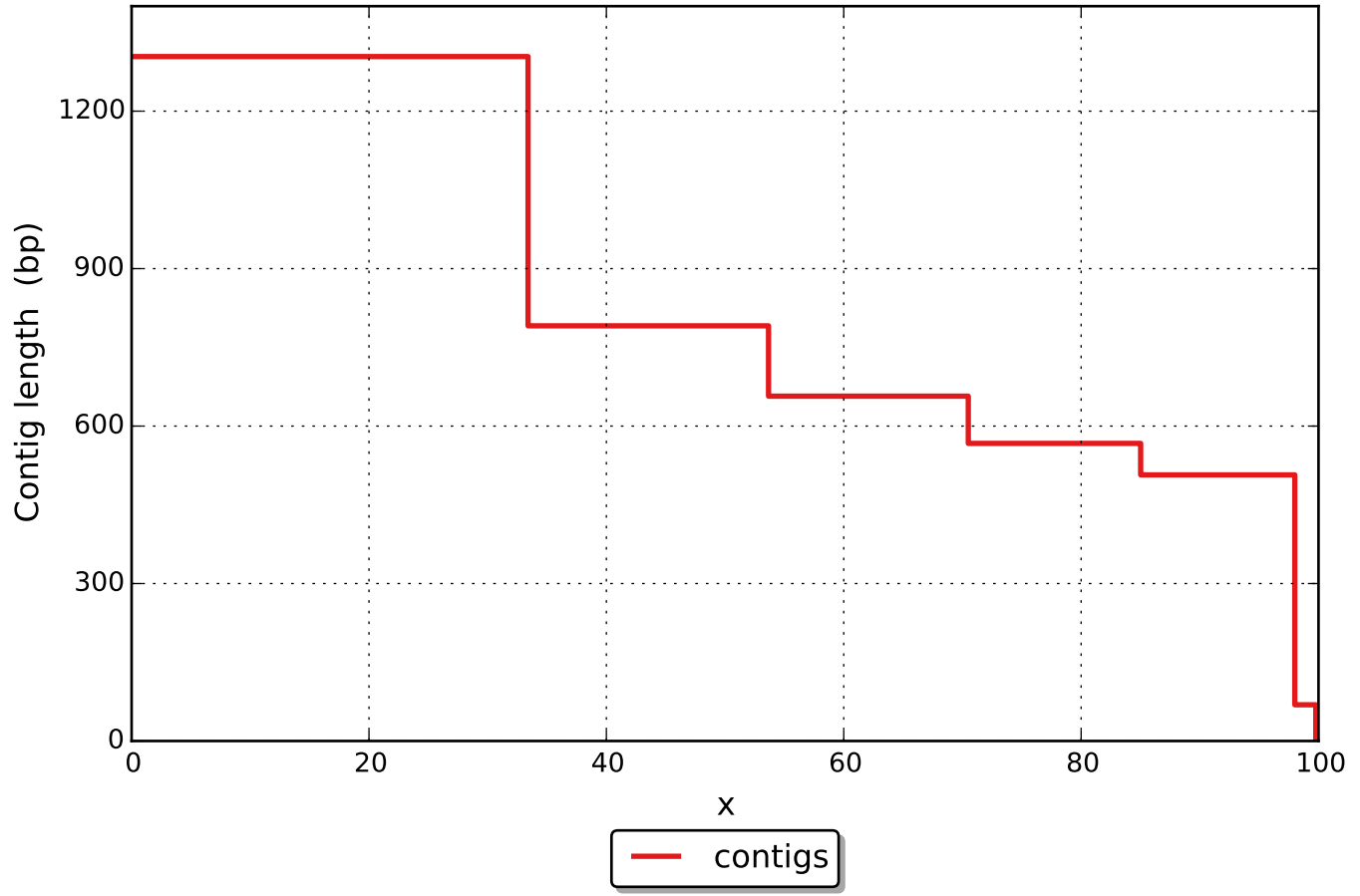
 # relocations



Cumulative length (aligned contigs)



NAx



NGAx

