

## Report

	contigs
# contigs ( $\geq 0$ bp)	106
# contigs ( $\geq 1000$ bp)	70
# contigs ( $\geq 5000$ bp)	51
# contigs ( $\geq 10000$ bp)	48
# contigs ( $\geq 25000$ bp)	41
# contigs ( $\geq 50000$ bp)	27
Total length ( $\geq 0$ bp)	4566719
Total length ( $\geq 1000$ bp)	4557145
Total length ( $\geq 5000$ bp)	4515022
Total length ( $\geq 10000$ bp)	4491071
Total length ( $\geq 25000$ bp)	4385406
Total length ( $\geq 50000$ bp)	3902504
# contigs	75
Largest contig	327064
Total length	4560560
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	174013
NG50	174013
N75	87014
NG75	78605
L50	10
LG50	10
L75	20
LG75	21
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.198
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4.41
# indels per 100 kbp	0.42
Largest alignment	327064
NA50	172843
NGA50	172843
NA75	87014
NGA75	78605
LA50	10
LGA50	10
LA75	20
LGA75	21

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	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# mismatches	201
# indels	19
# short indels	19
# long indels	0
Indels length	25

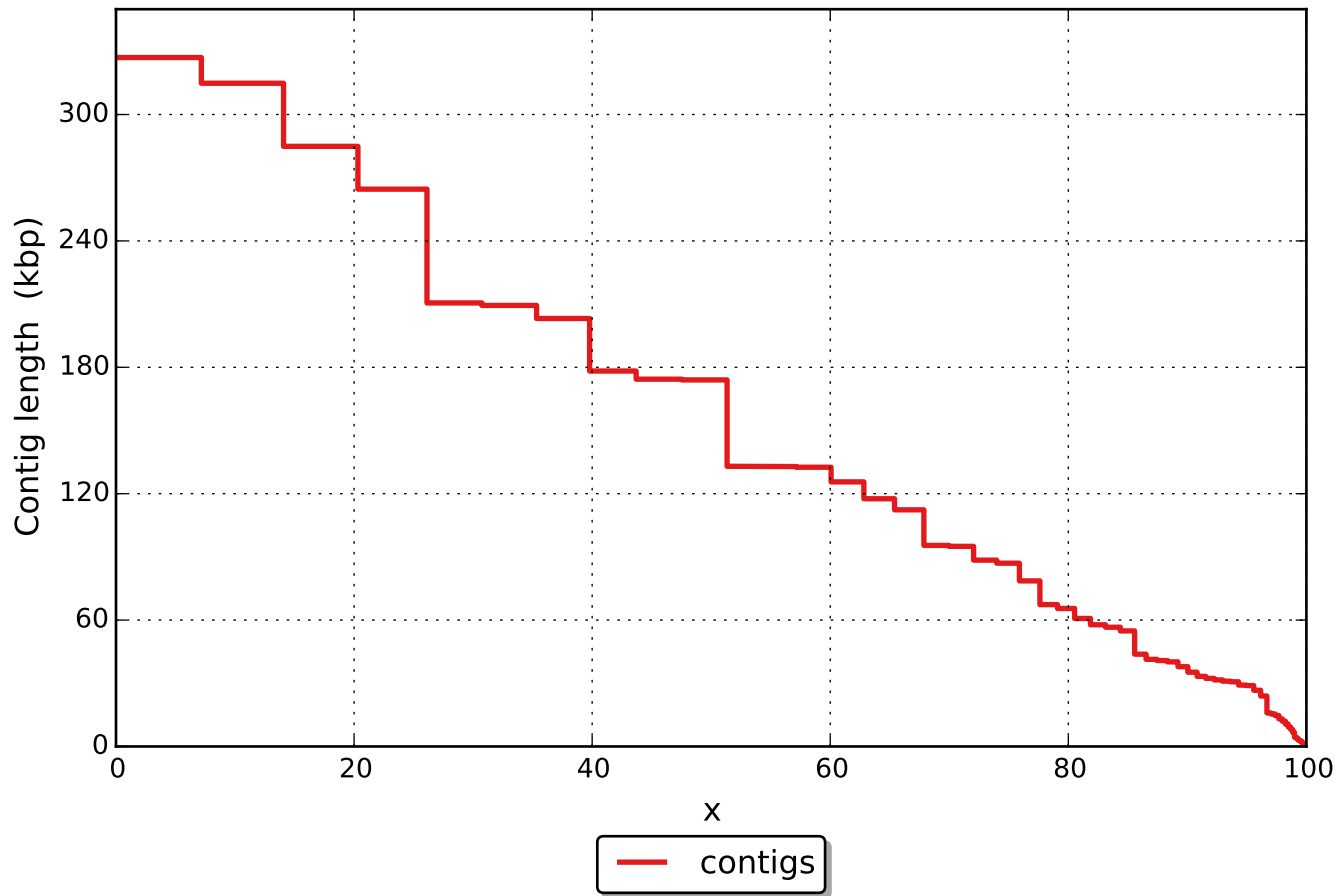
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

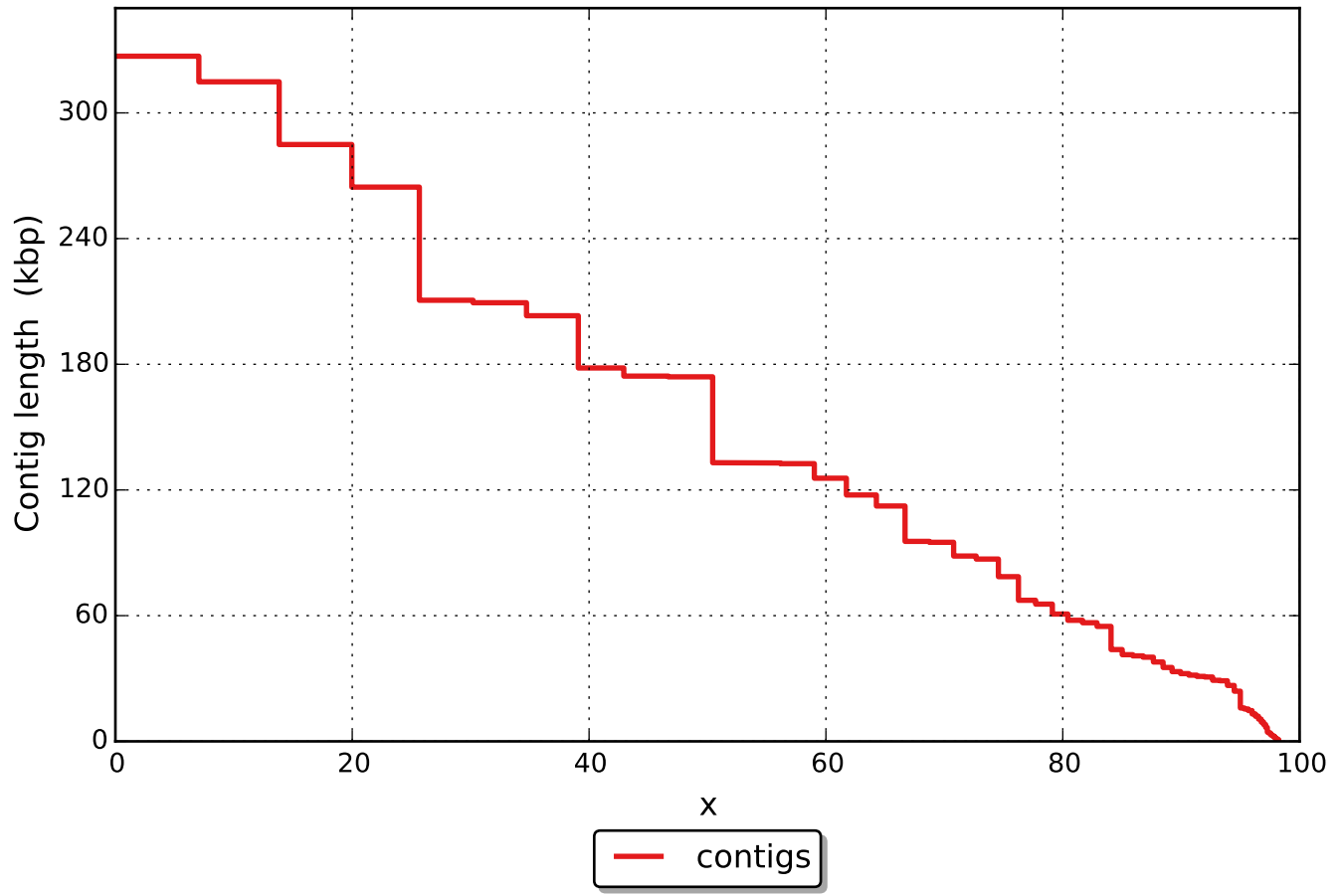
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

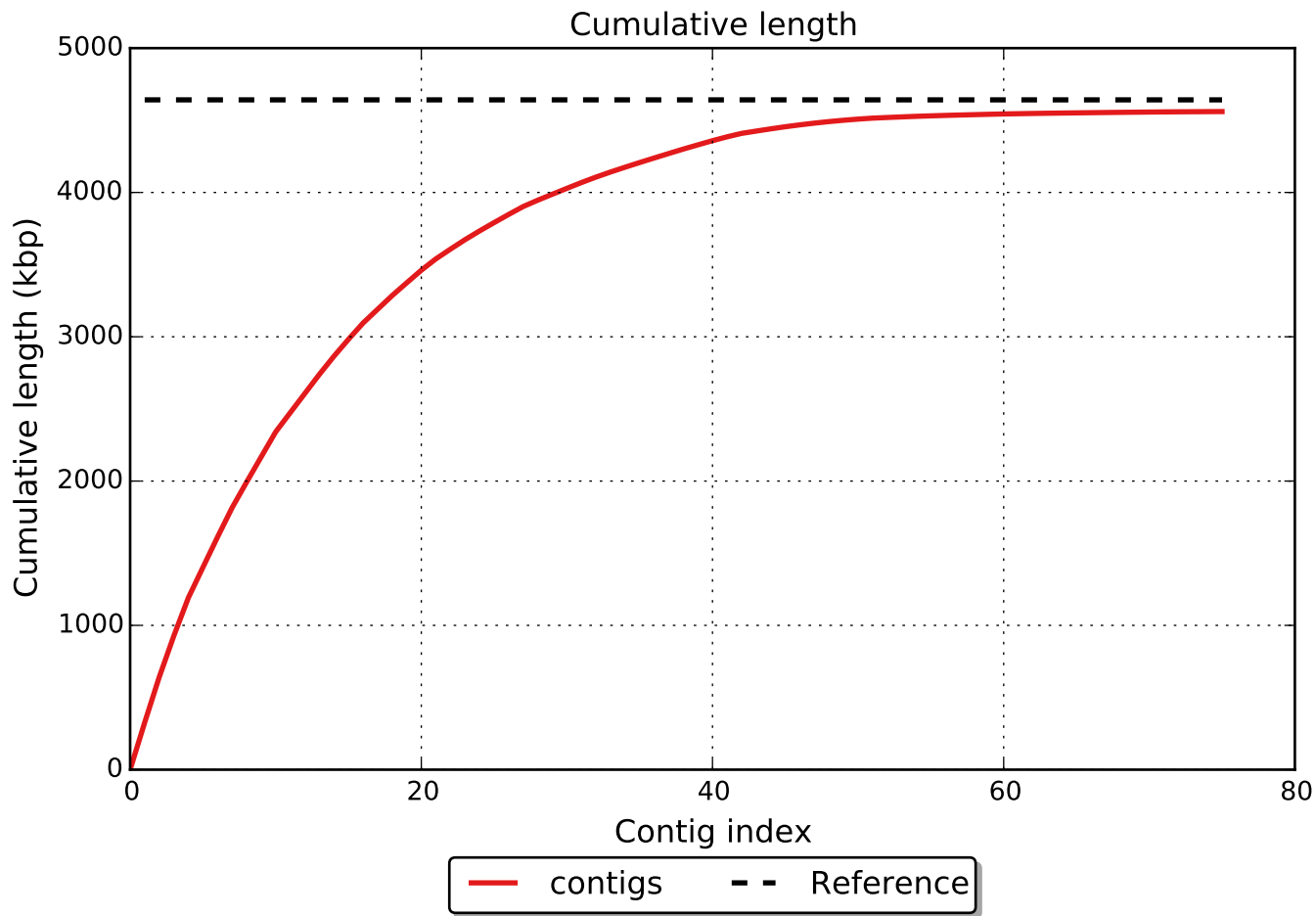
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

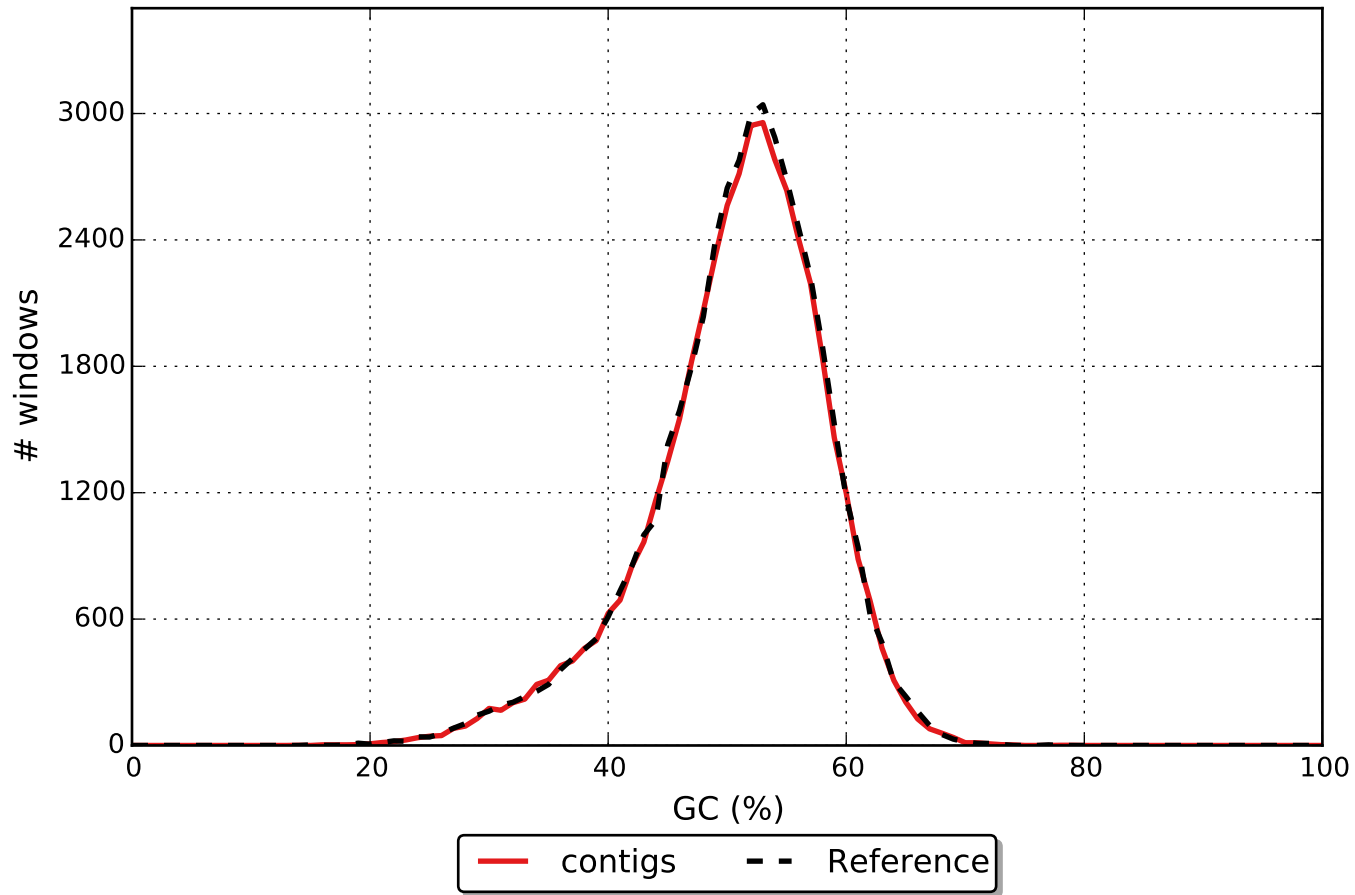


NGx





# GC content

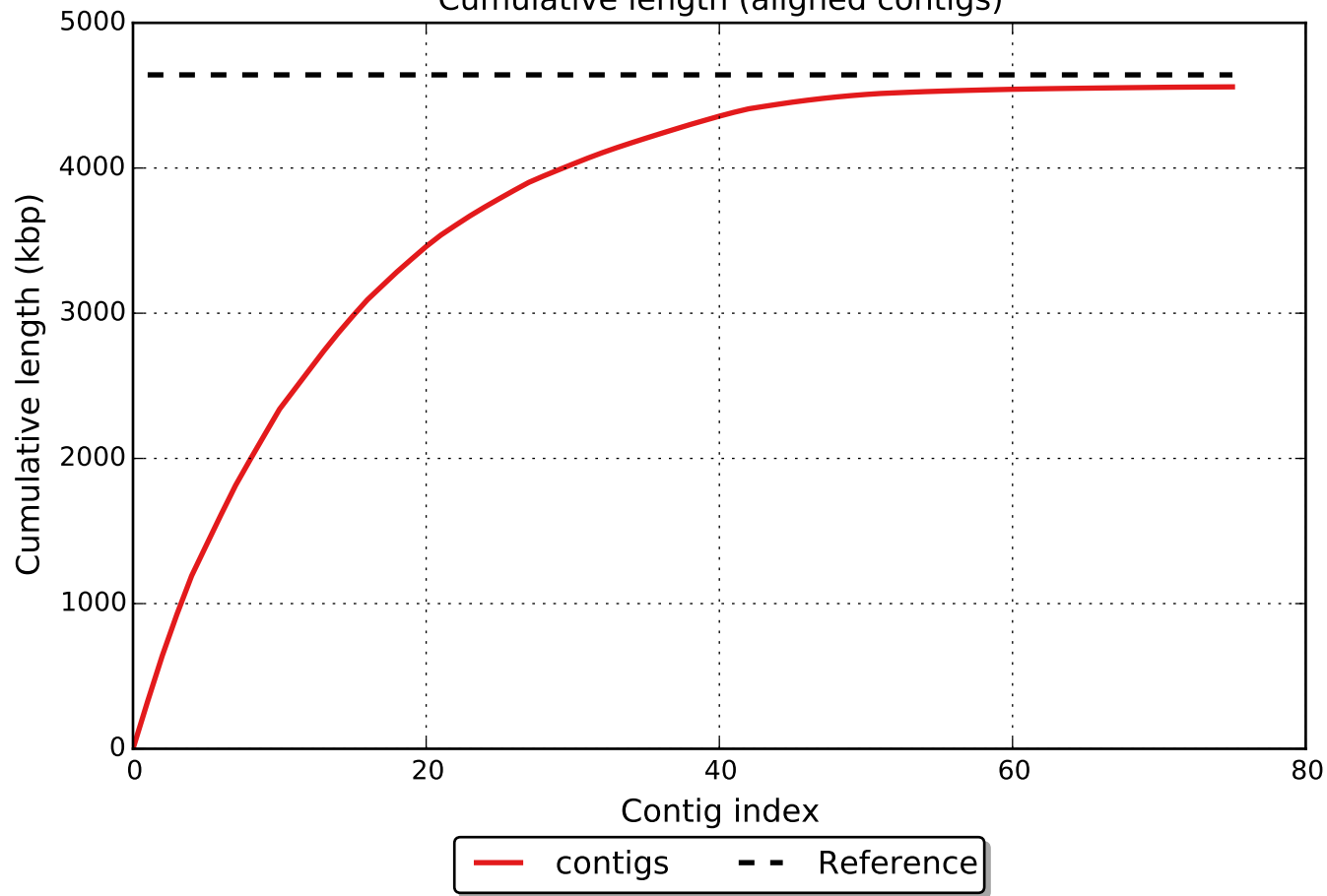


# Misassemblies

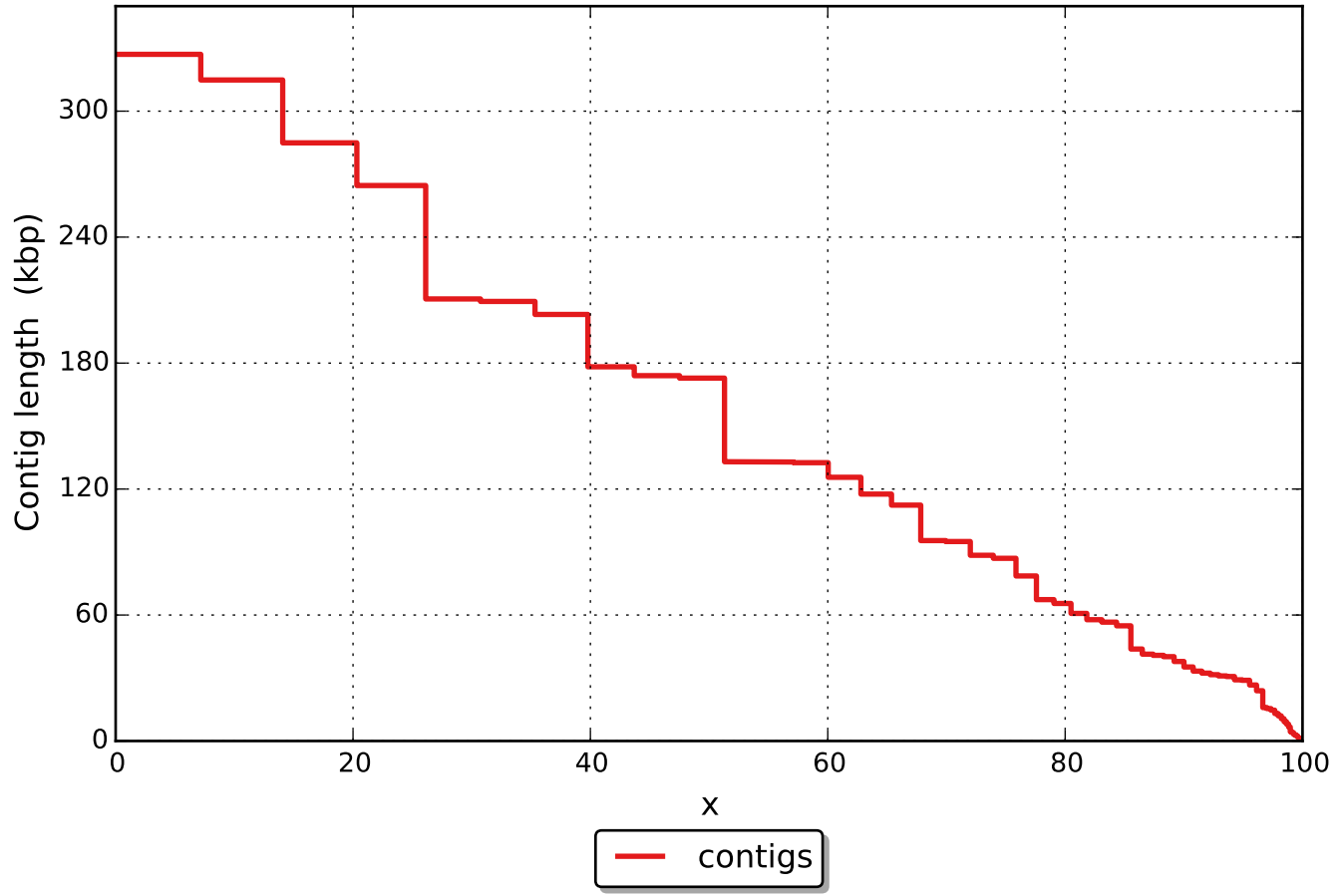




Cumulative length (aligned contigs)



NAx



# NGAx

