

## Report

	contigs
# contigs ( $\geq 0$ bp)	100
# contigs ( $\geq 1000$ bp)	70
# contigs ( $\geq 5000$ bp)	52
# contigs ( $\geq 10000$ bp)	48
# contigs ( $\geq 25000$ bp)	42
# contigs ( $\geq 50000$ bp)	26
Total length ( $\geq 0$ bp)	4567737
Total length ( $\geq 1000$ bp)	4559124
Total length ( $\geq 5000$ bp)	4517445
Total length ( $\geq 10000$ bp)	4485753
Total length ( $\geq 25000$ bp)	4394571
Total length ( $\geq 50000$ bp)	3854834
# contigs	76
Largest contig	327064
Total length	4563469
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	174057
NG50	174057
N75	80764
NG75	78605
L50	10
LG50	10
L75	20
LG75	21
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.257
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	5.70
# indels per 100 kbp	0.42
Largest alignment	327064
NA50	172541
NGA50	172541
NA75	80764
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	2
# mismatches	260
# indels	19
# short indels	19
# long indels	0
Indels length	26

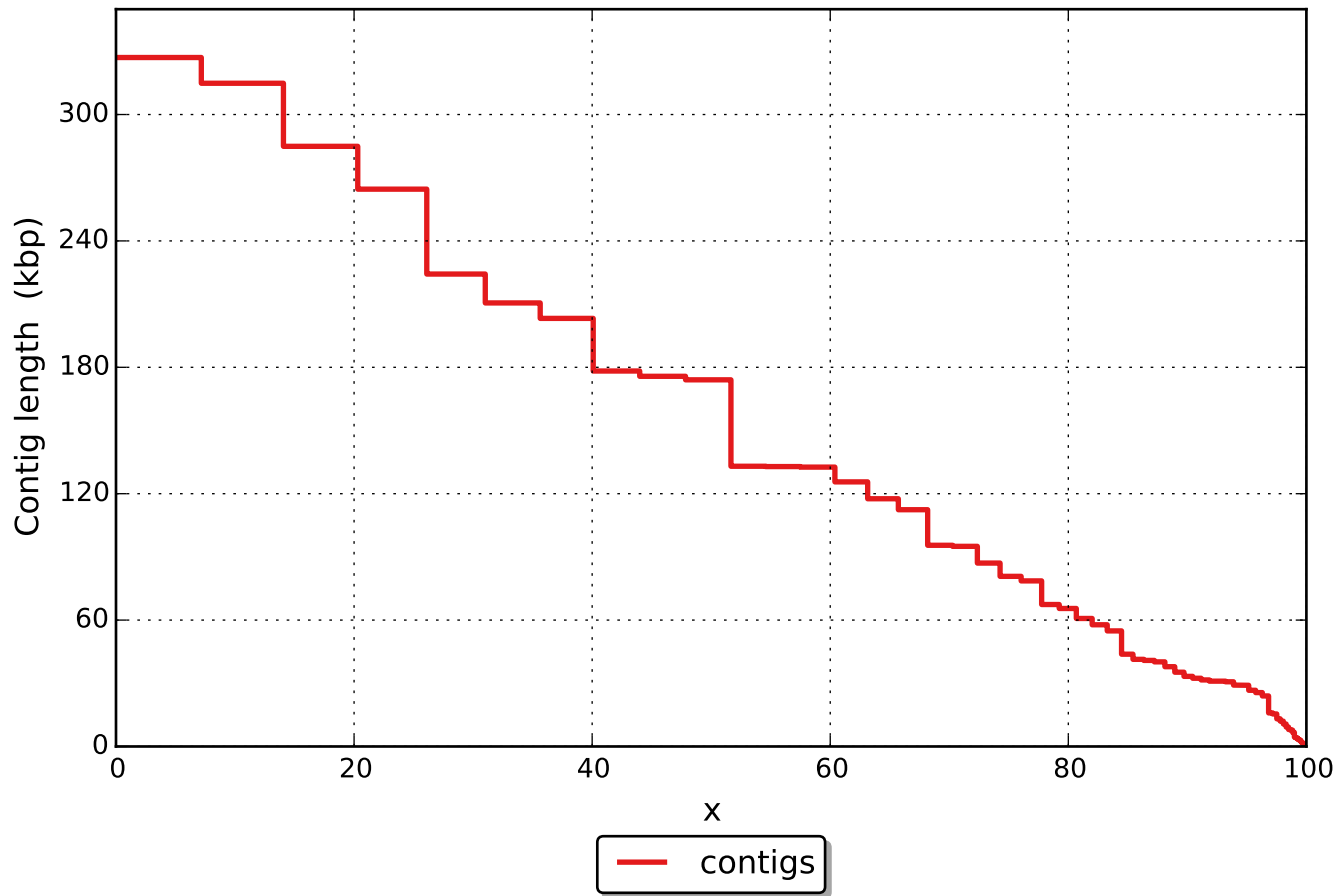
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

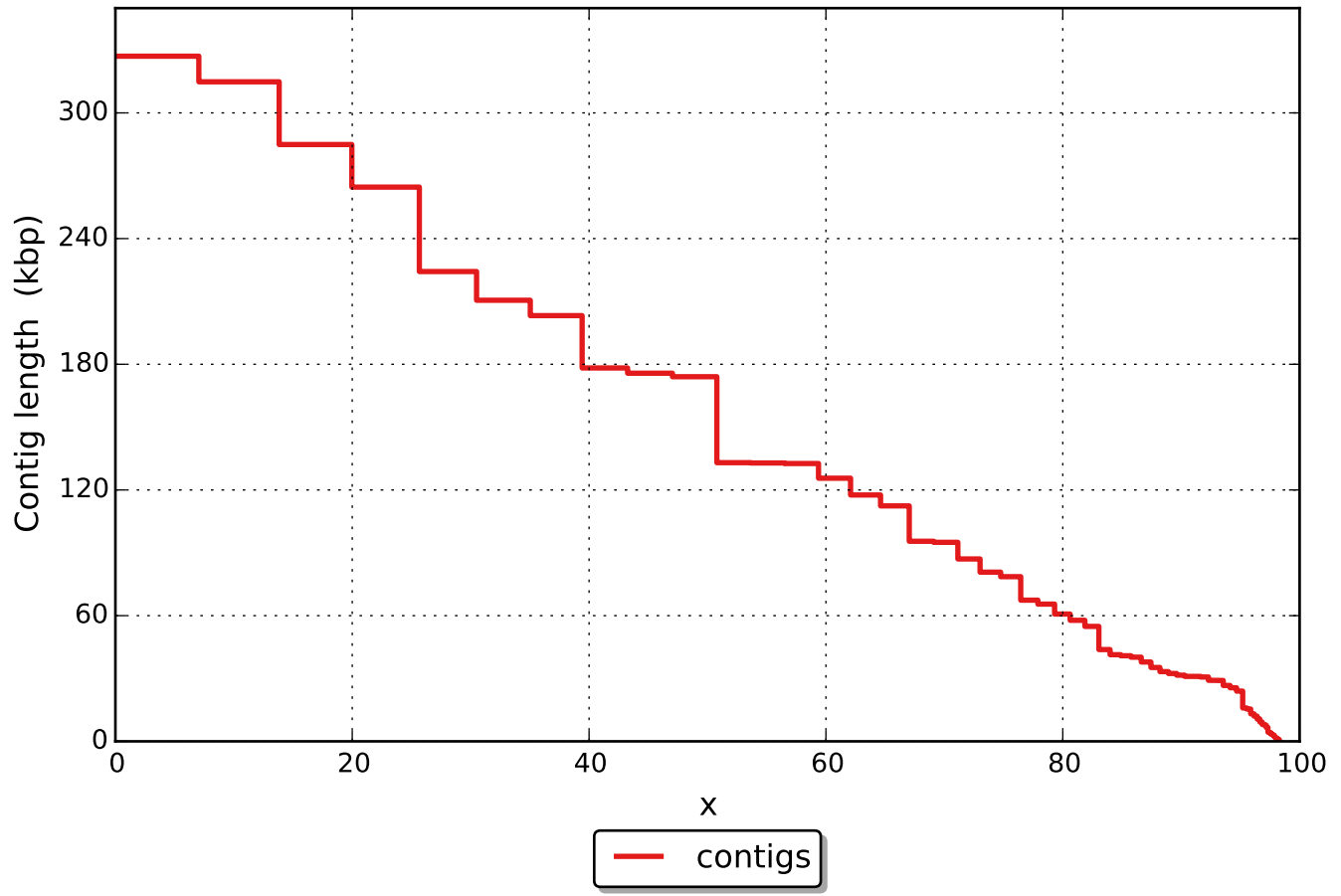
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

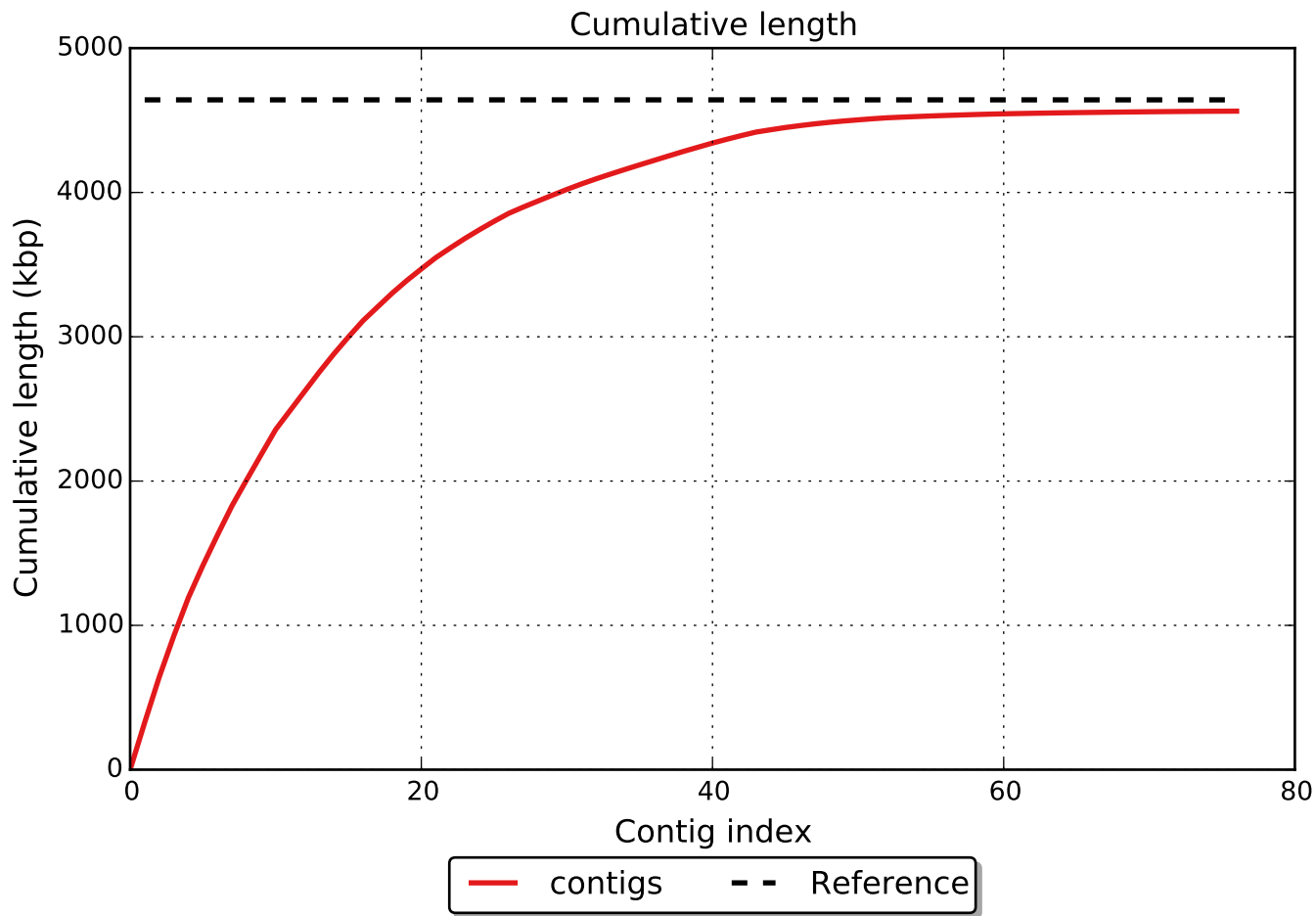
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

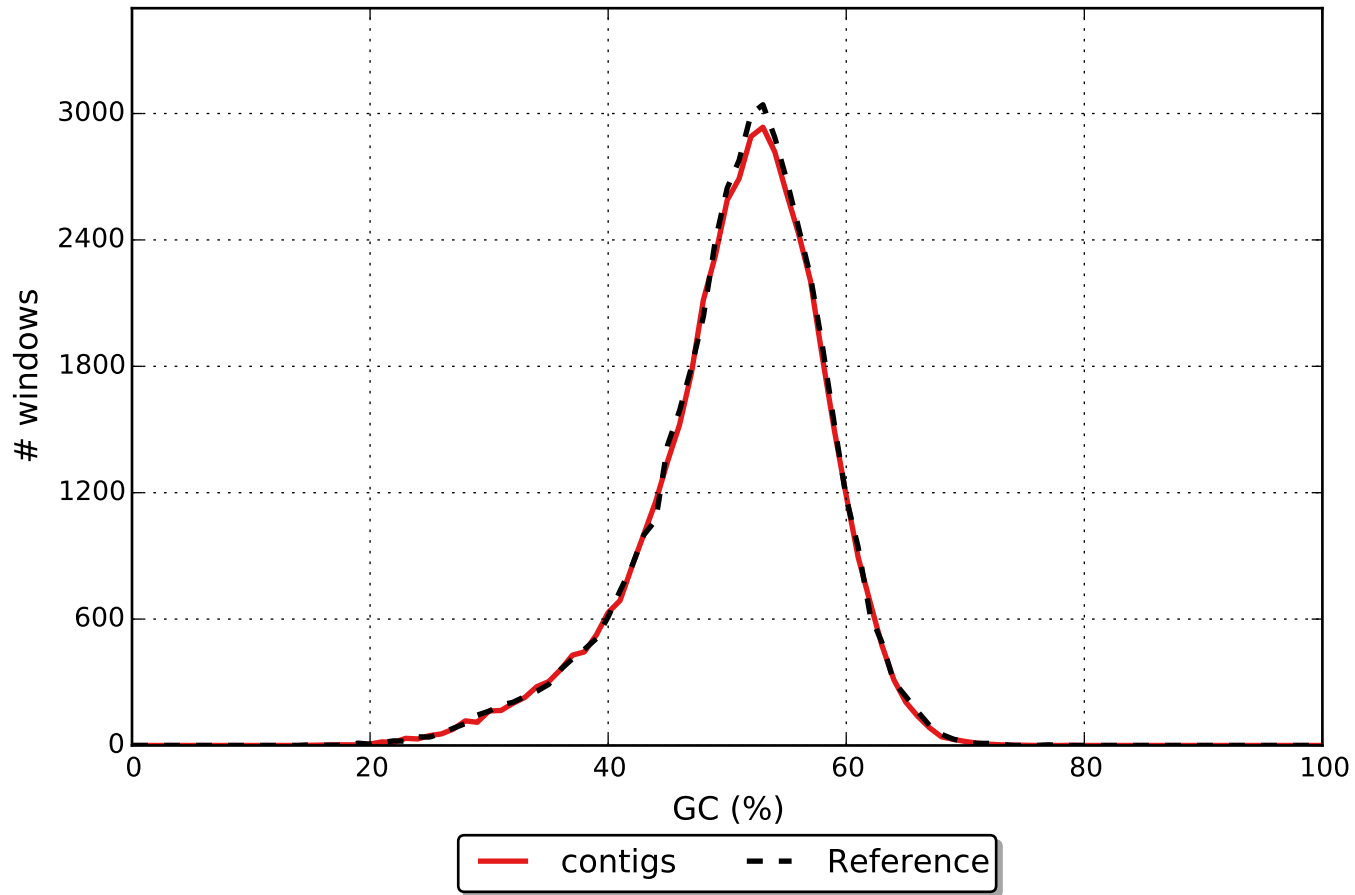


NGx





GC content

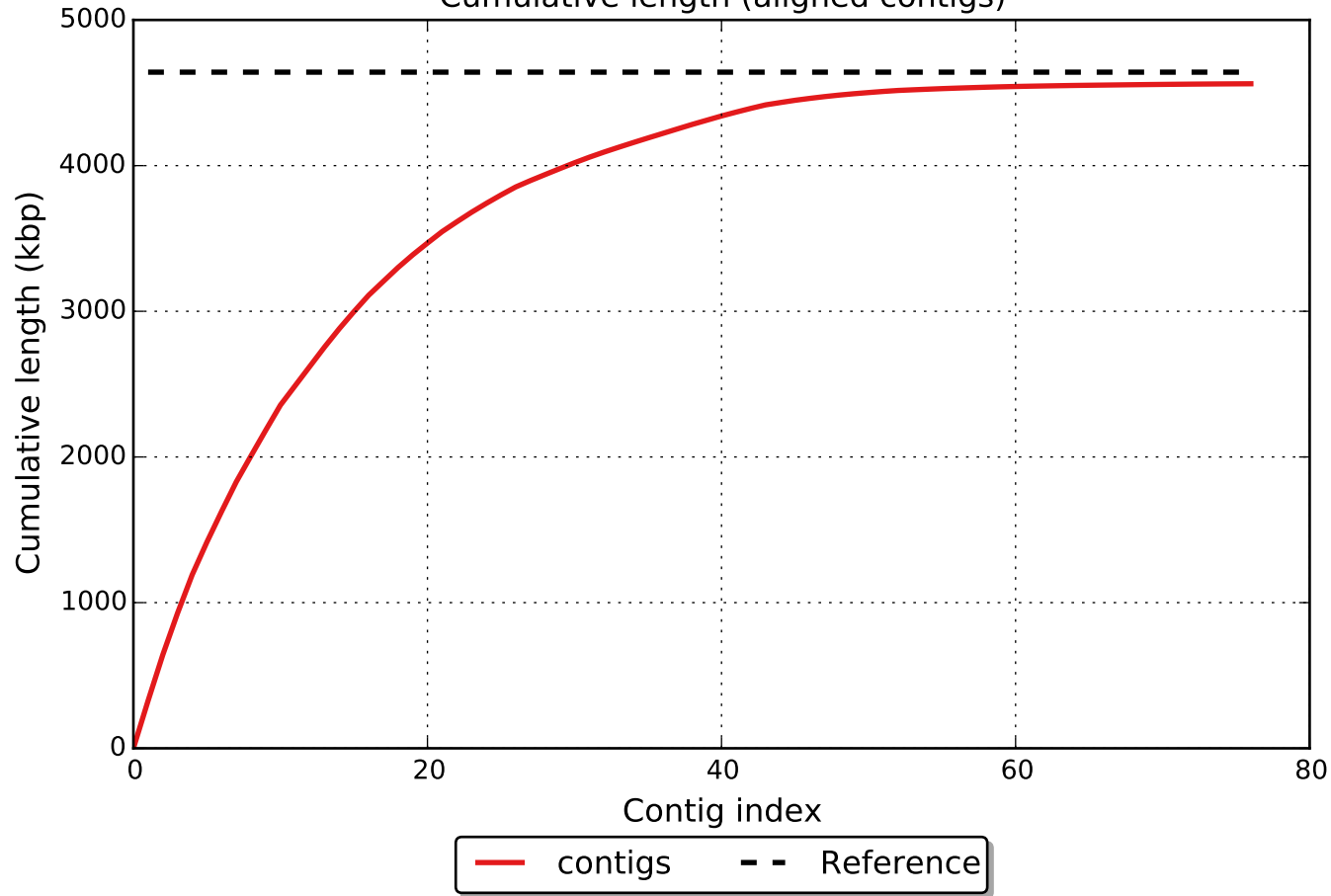


# Misassemblies

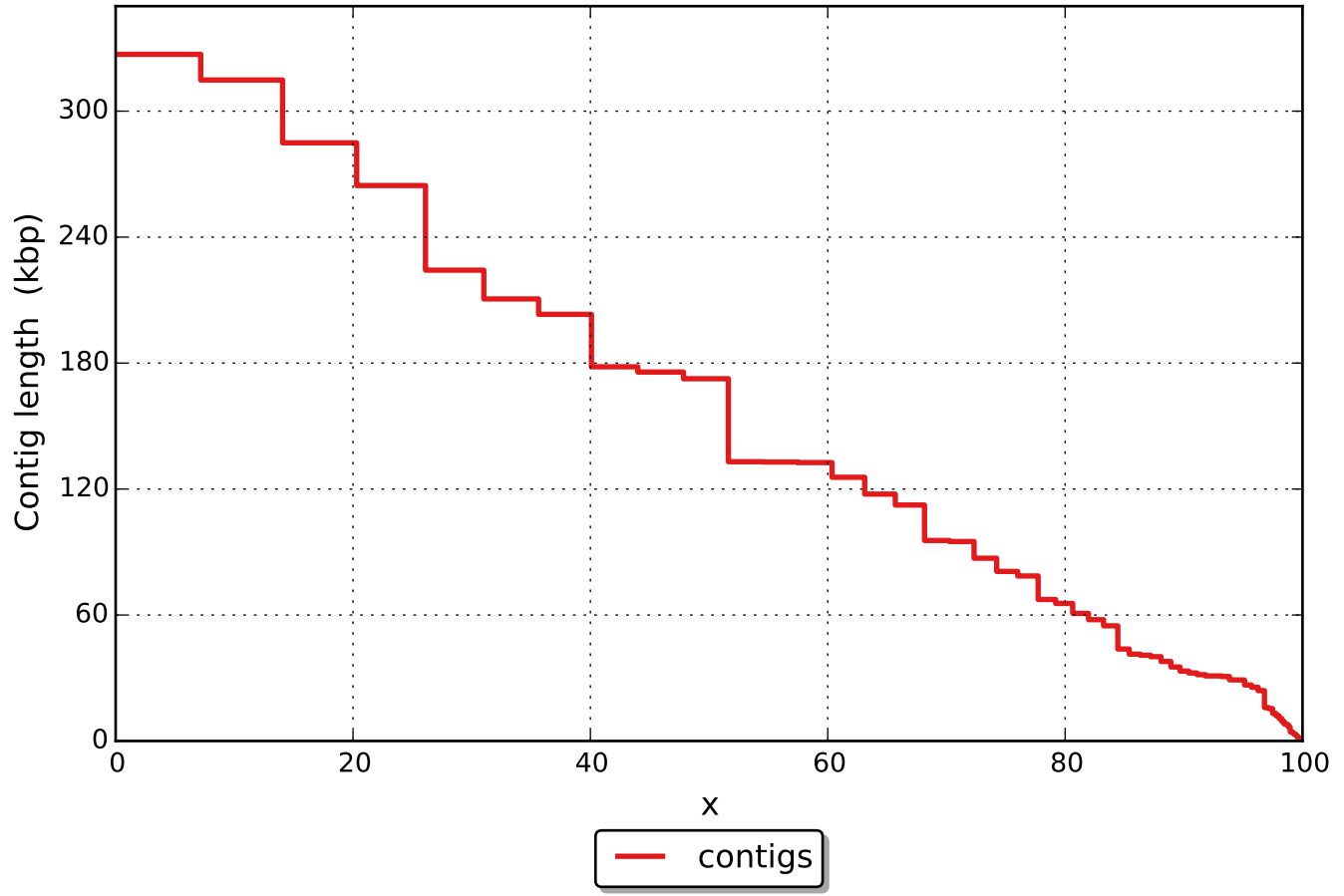




Cumulative length (aligned contigs)



NAx



# NGAx

