

## Report

	contigs
# contigs ( $\geq 0$ bp)	108
# contigs ( $\geq 1000$ bp)	76
# contigs ( $\geq 5000$ bp)	56
# contigs ( $\geq 10000$ bp)	52
# contigs ( $\geq 25000$ bp)	45
# contigs ( $\geq 50000$ bp)	28
Total length ( $\geq 0$ bp)	4566691
Total length ( $\geq 1000$ bp)	4556280
Total length ( $\geq 5000$ bp)	4505862
Total length ( $\geq 10000$ bp)	4476470
Total length ( $\geq 25000$ bp)	4374405
Total length ( $\geq 50000$ bp)	3809079
# contigs	83
Largest contig	327064
Total length	4561809
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	133024
NG50	133024
N75	65511
NG75	60768
L50	11
LG50	11
L75	22
LG75	23
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	5
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.216
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3.44
# indels per 100 kbp	0.31
Largest alignment	327064
NA50	133024
NGA50	133024
NA75	65511
NGA75	60768
LA50	11
LGA50	11
LA75	22
LGA75	23

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	5
# mismatches	157
# indels	14
# short indels	14
# long indels	0
Indels length	16

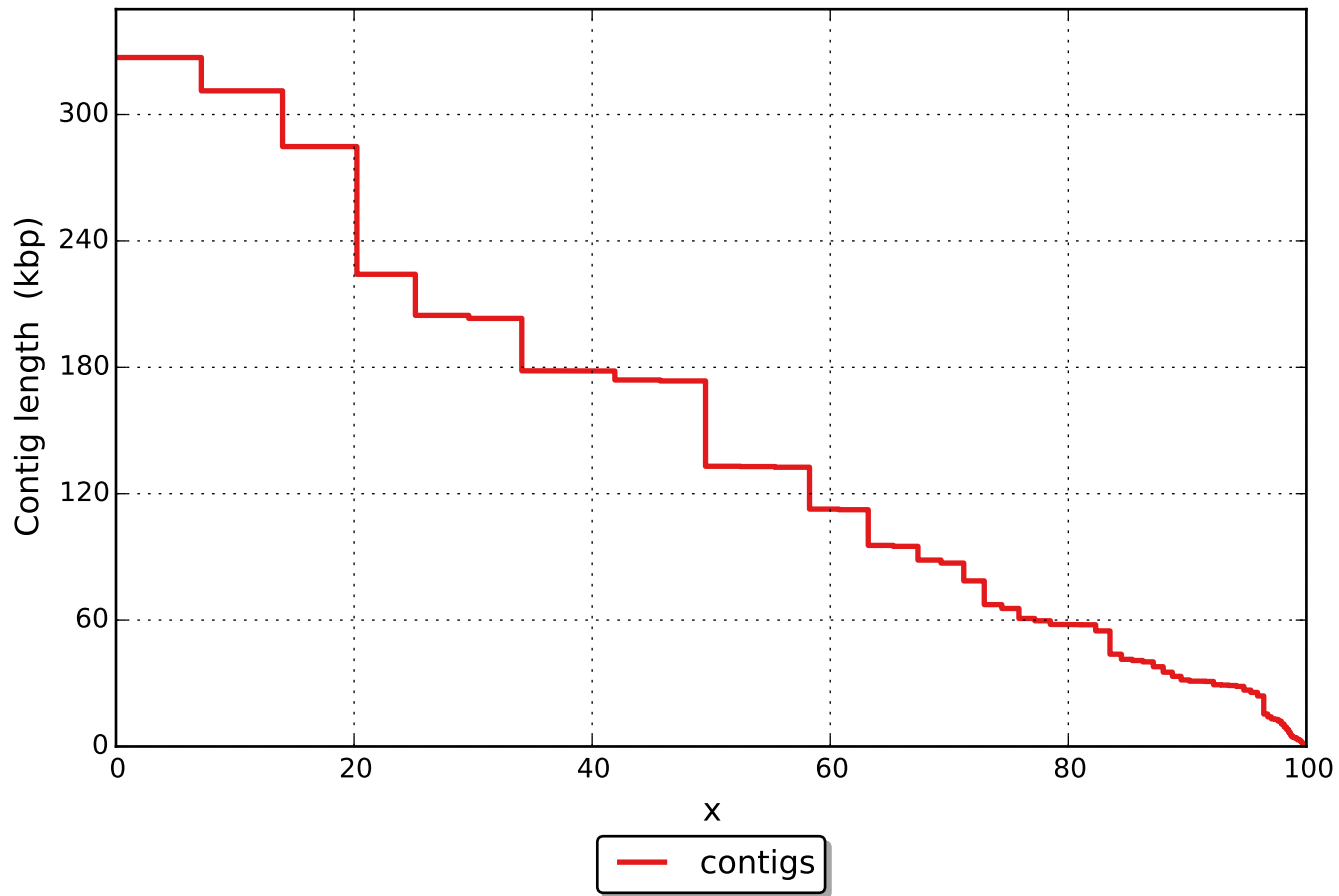
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

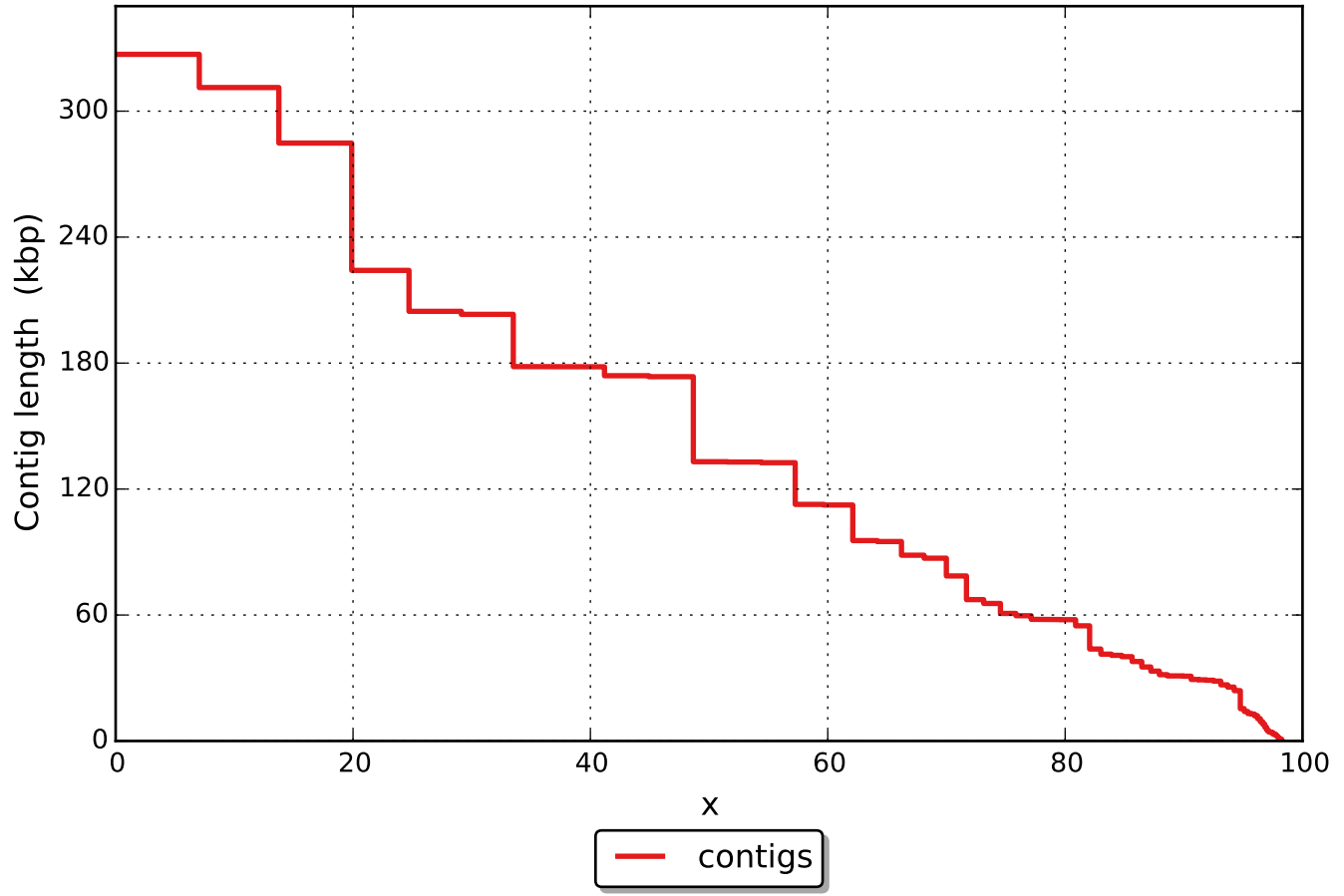
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

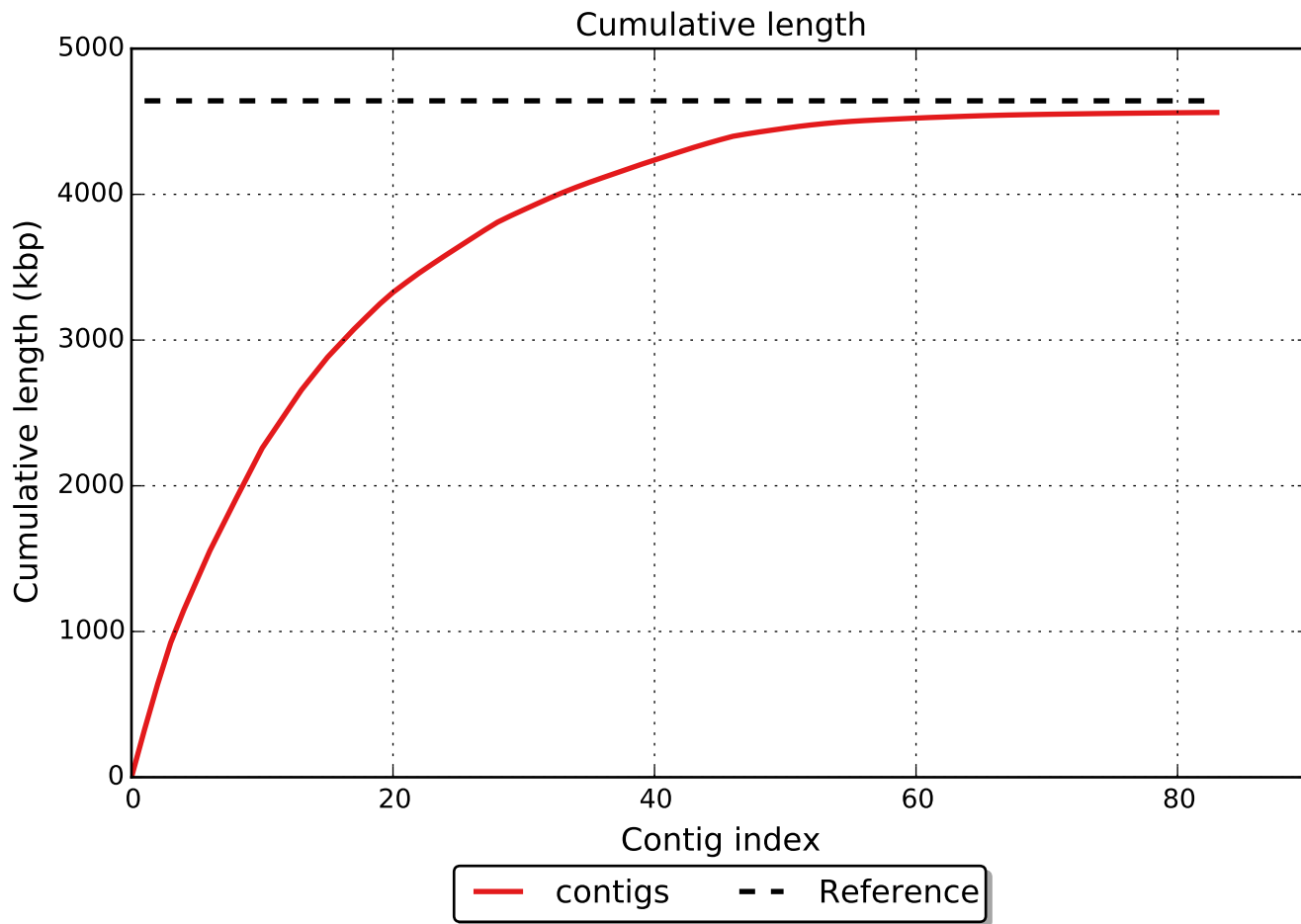
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

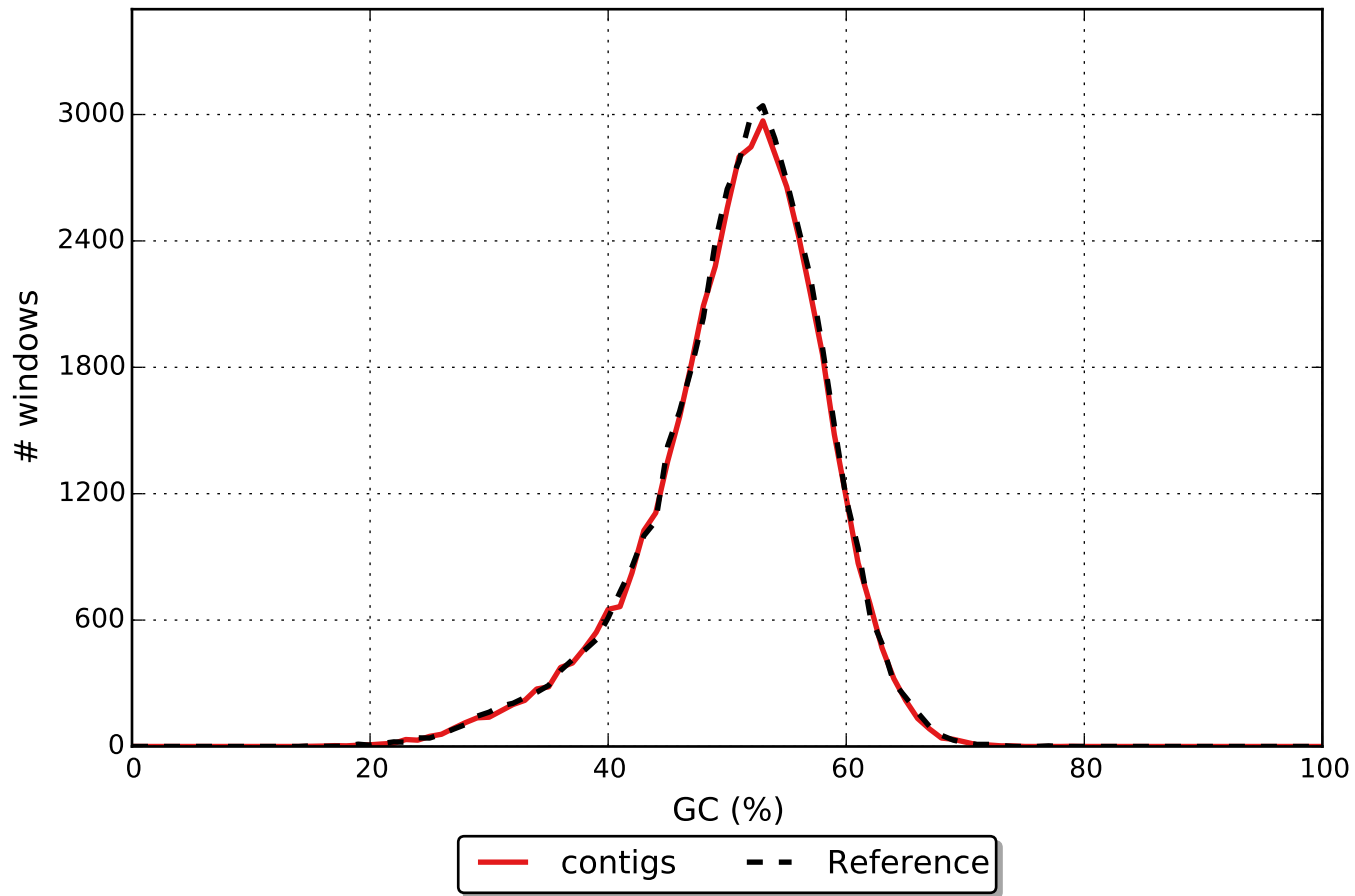


NGx





GC content

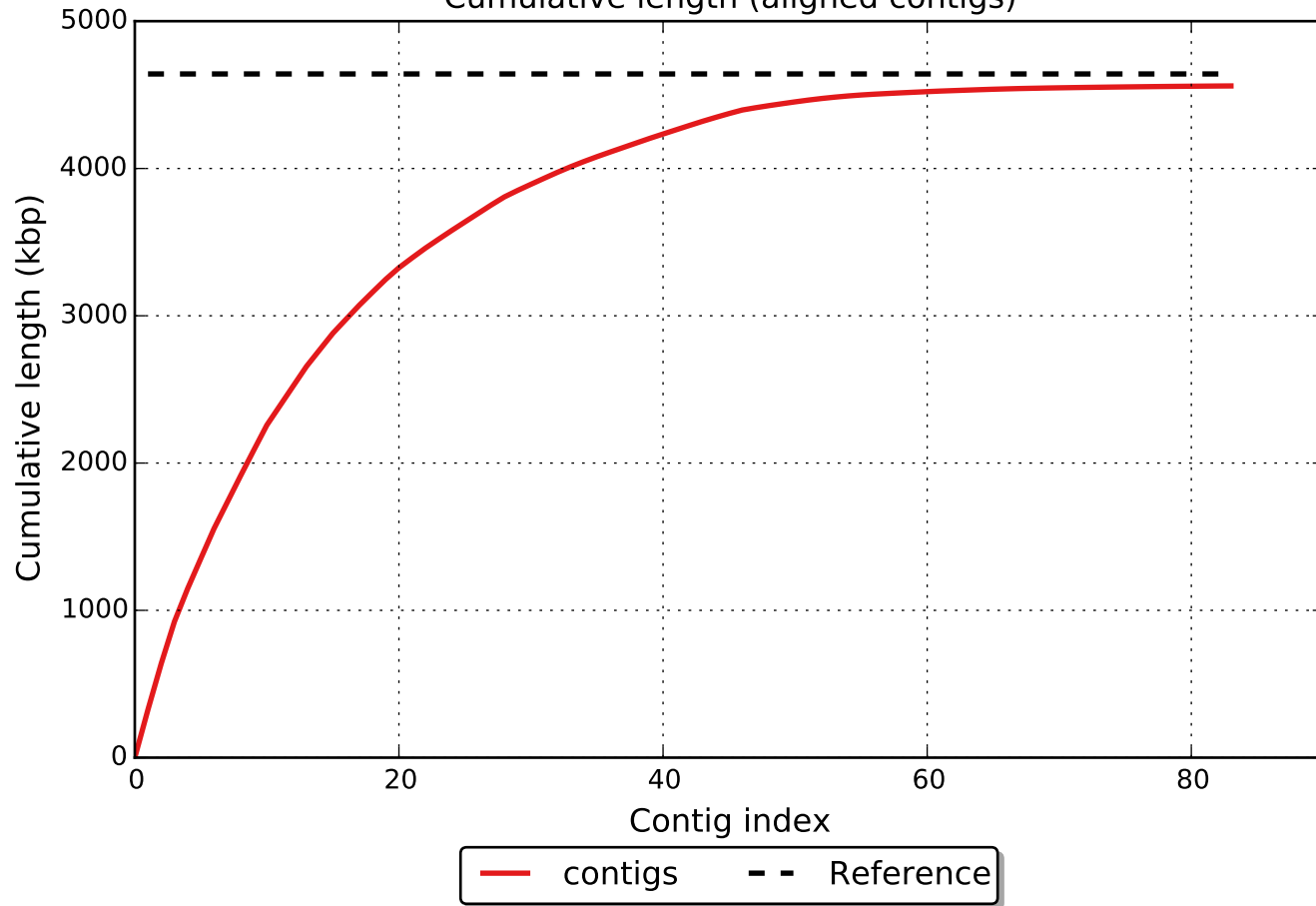


# Misassemblies

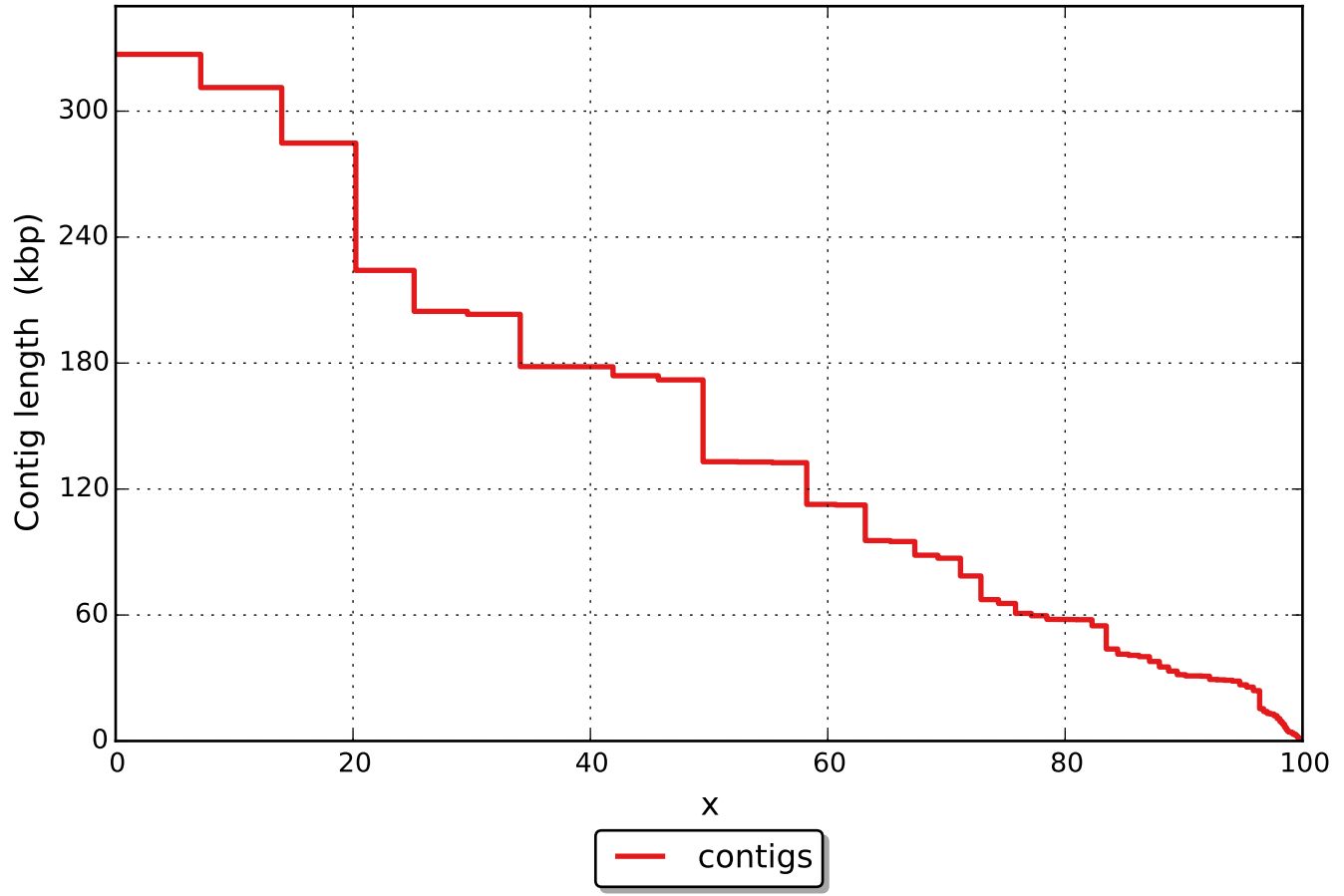




Cumulative length (aligned contigs)



NAx



# NGAx

