

## Report

	contigs
# contigs ( $\geq 0$ bp)	123
# contigs ( $\geq 1000$ bp)	75
# contigs ( $\geq 5000$ bp)	58
# contigs ( $\geq 10000$ bp)	51
# contigs ( $\geq 25000$ bp)	44
# contigs ( $\geq 50000$ bp)	27
Total length ( $\geq 0$ bp)	4573957
Total length ( $\geq 1000$ bp)	4564325
Total length ( $\geq 5000$ bp)	4525527
Total length ( $\geq 10000$ bp)	4472509
Total length ( $\geq 25000$ bp)	4359749
Total length ( $\geq 50000$ bp)	3758277
# contigs	79
Largest contig	327064
Total length	4567522
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	133027
NG50	133027
N75	67340
NG75	65511
L50	11
LG50	11
L75	22
LG75	23
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.341
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	8.30
# indels per 100 kbp	0.39
Largest alignment	327064
NA50	133027
NGA50	133027
NA75	67340
NGA75	65511
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	3
# mismatches	379
# indels	18
# short indels	18
# long indels	0
Indels length	19

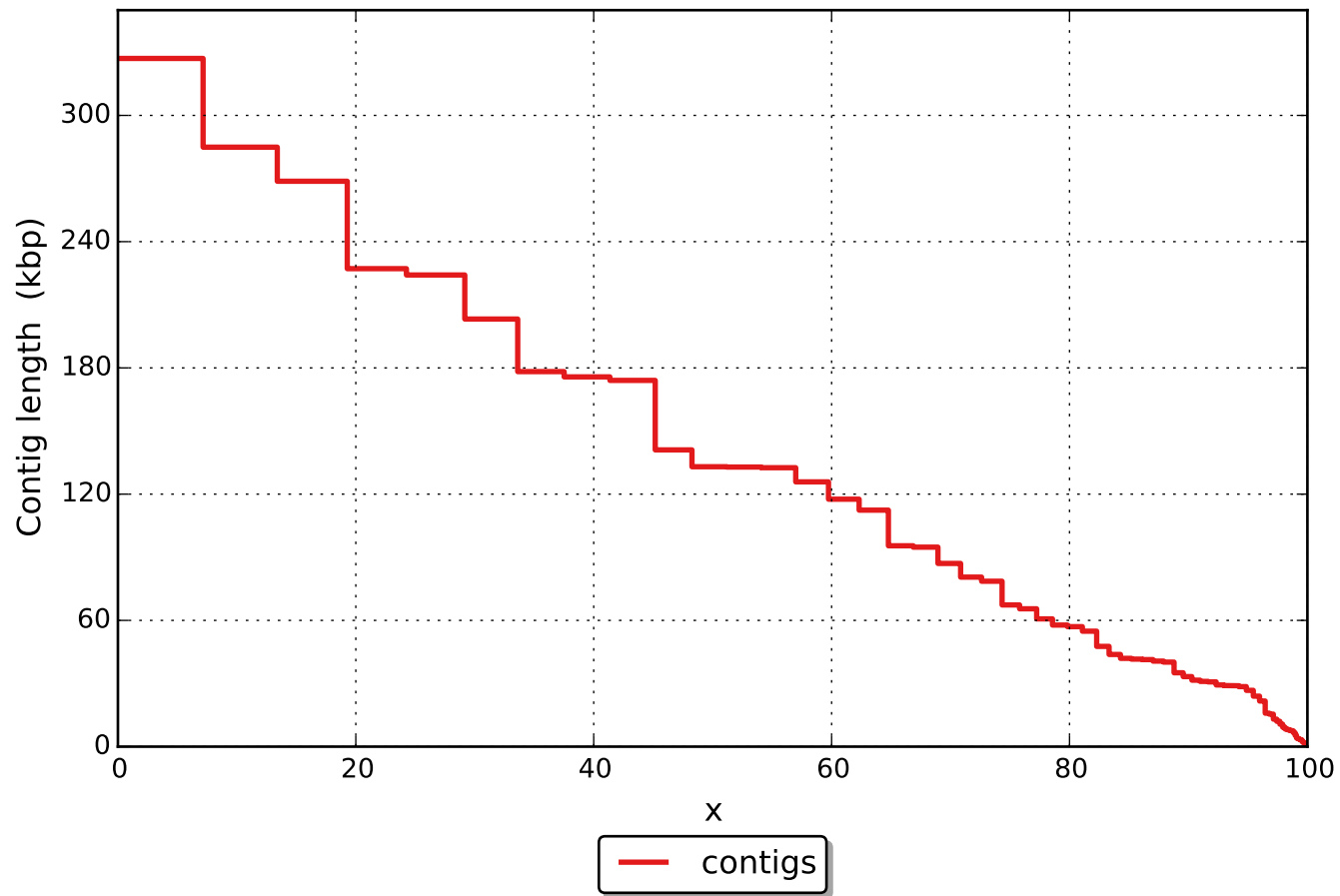
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

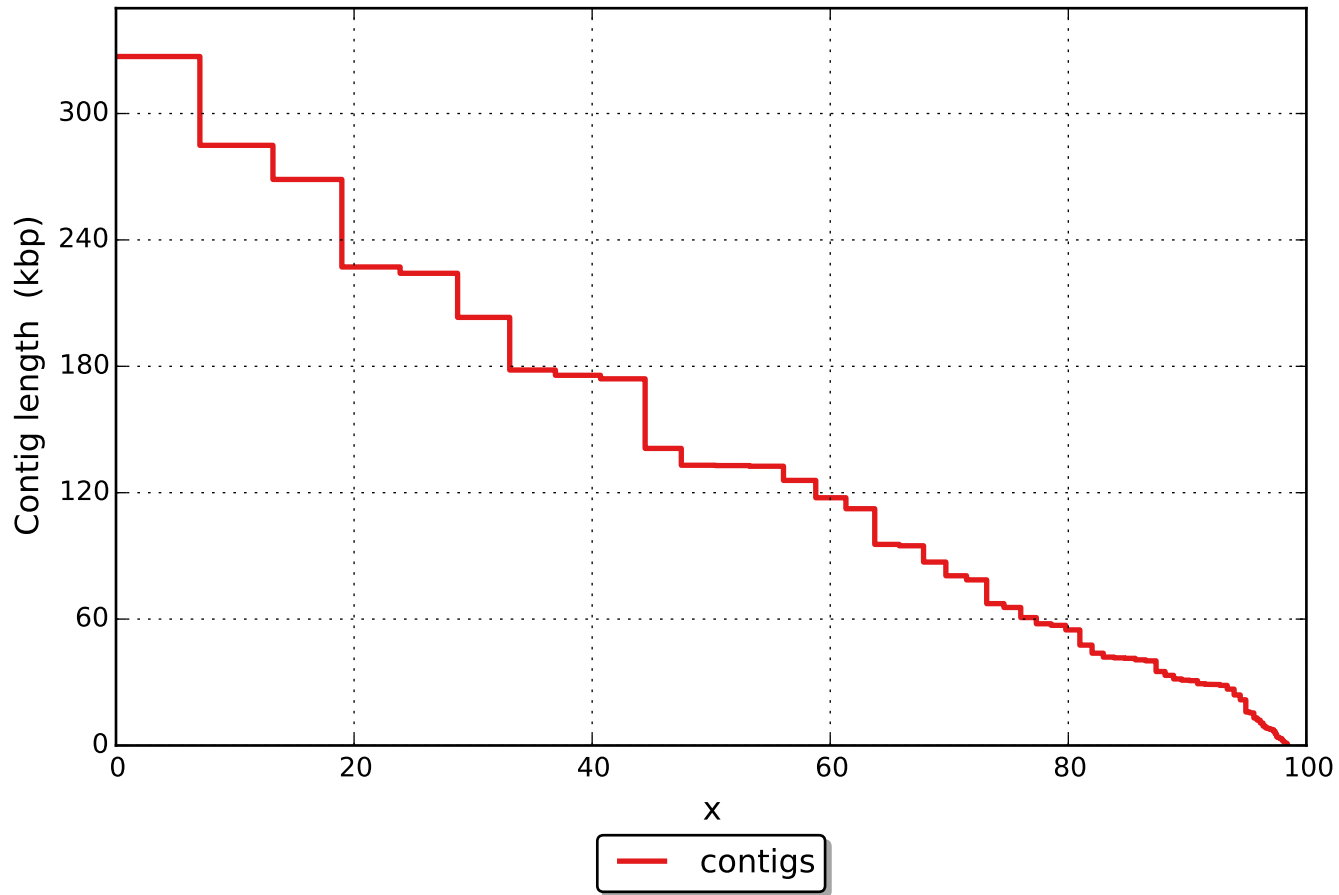
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

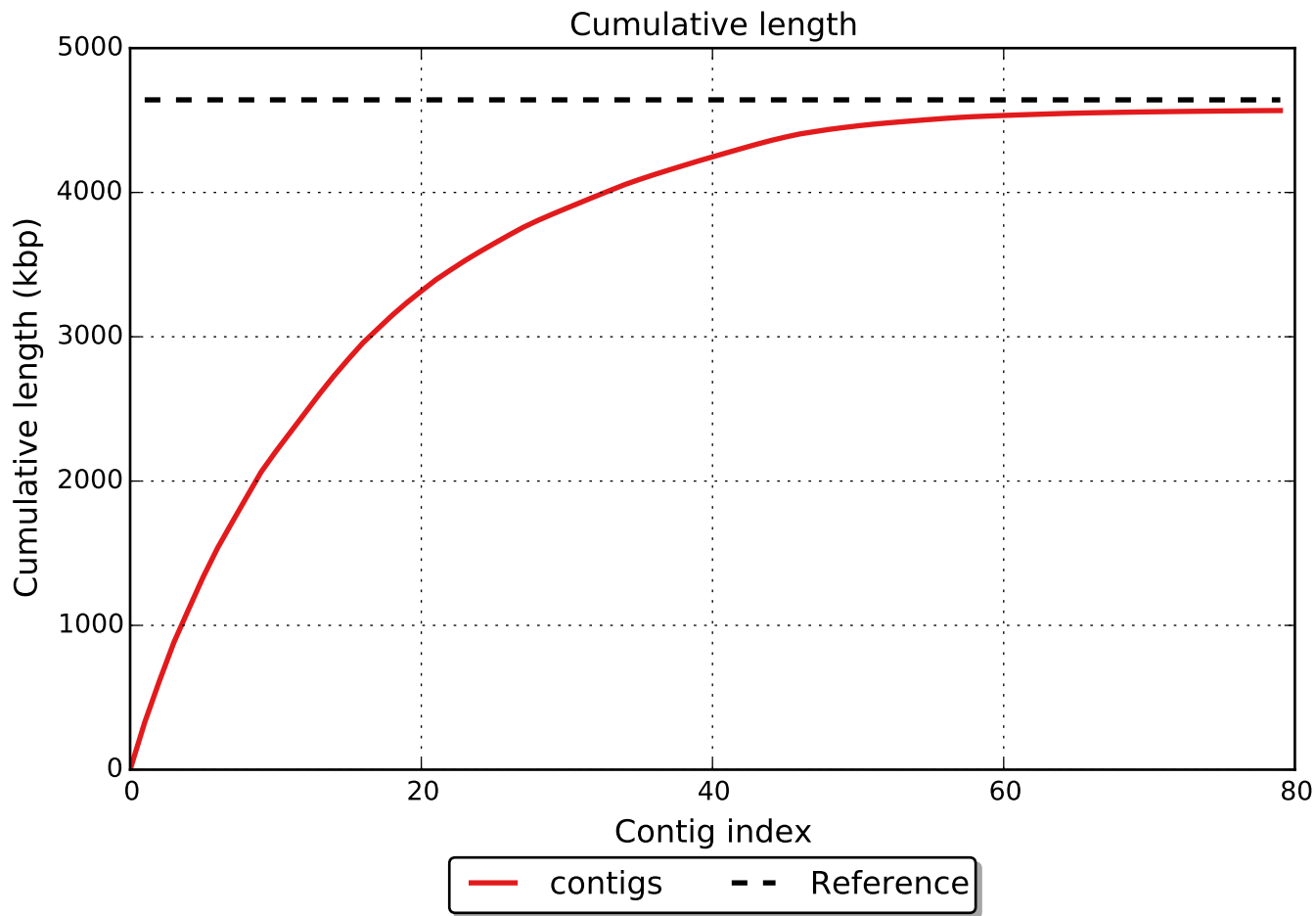
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

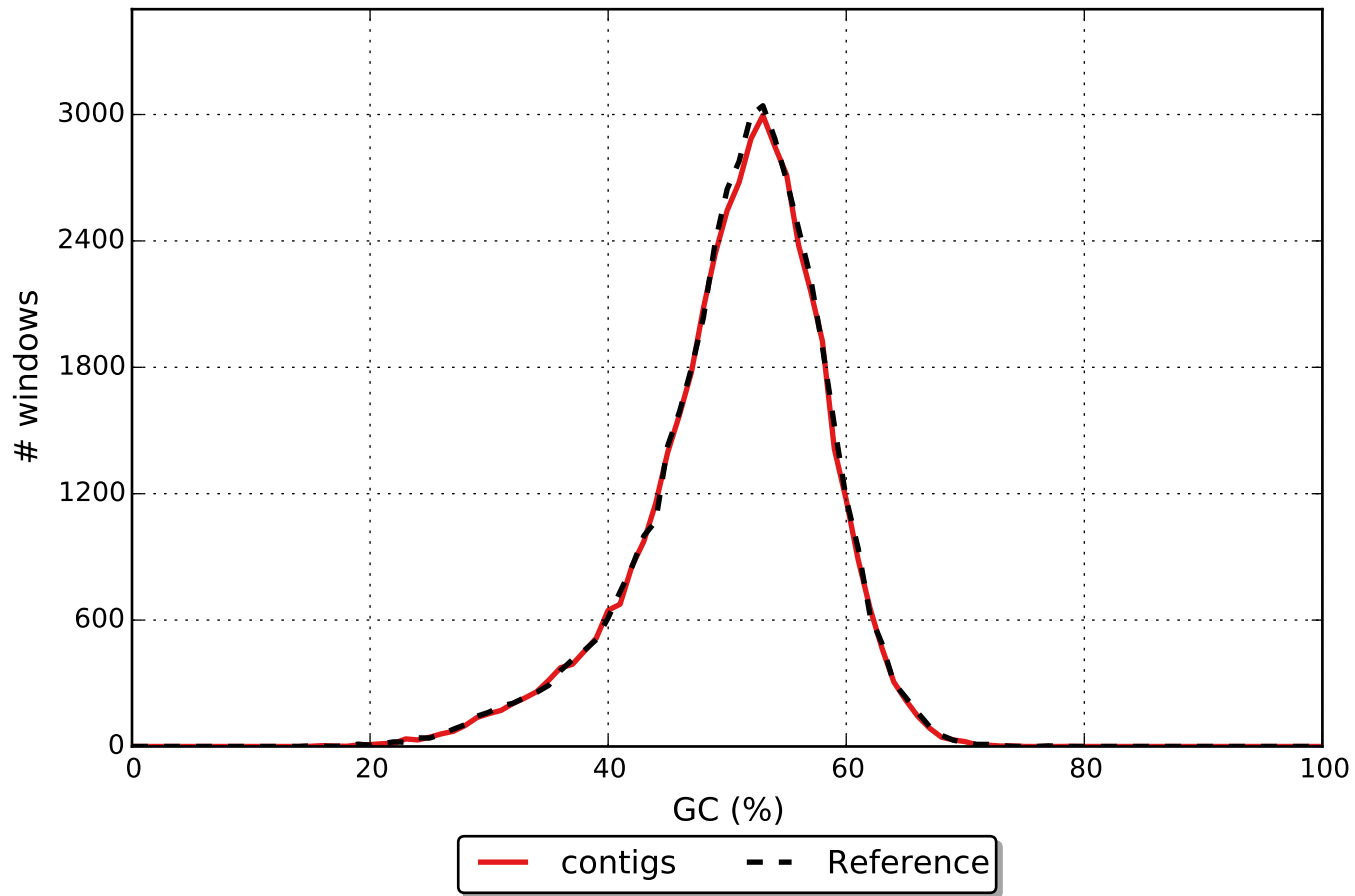


NGx





GC content

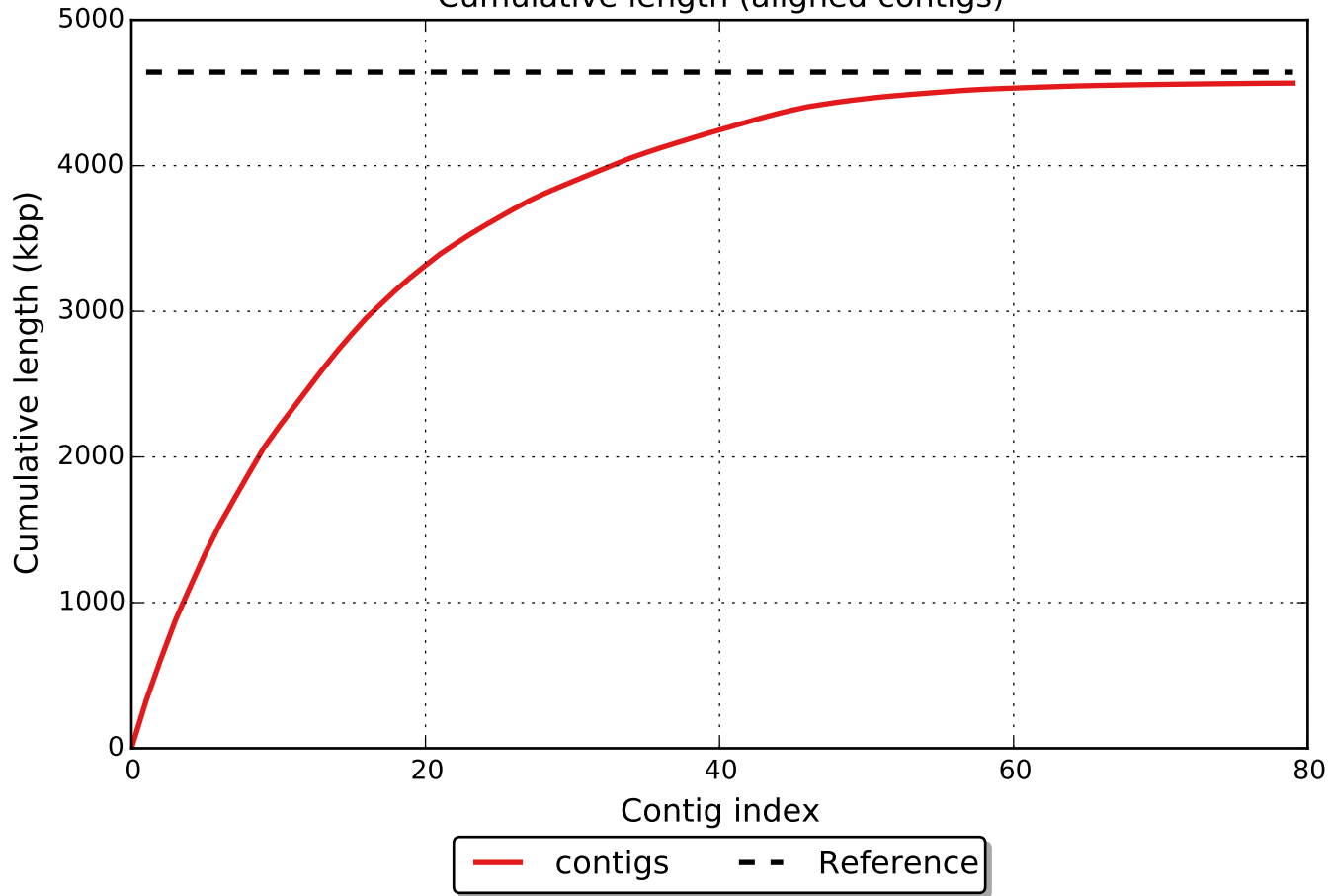


# Misassemblies

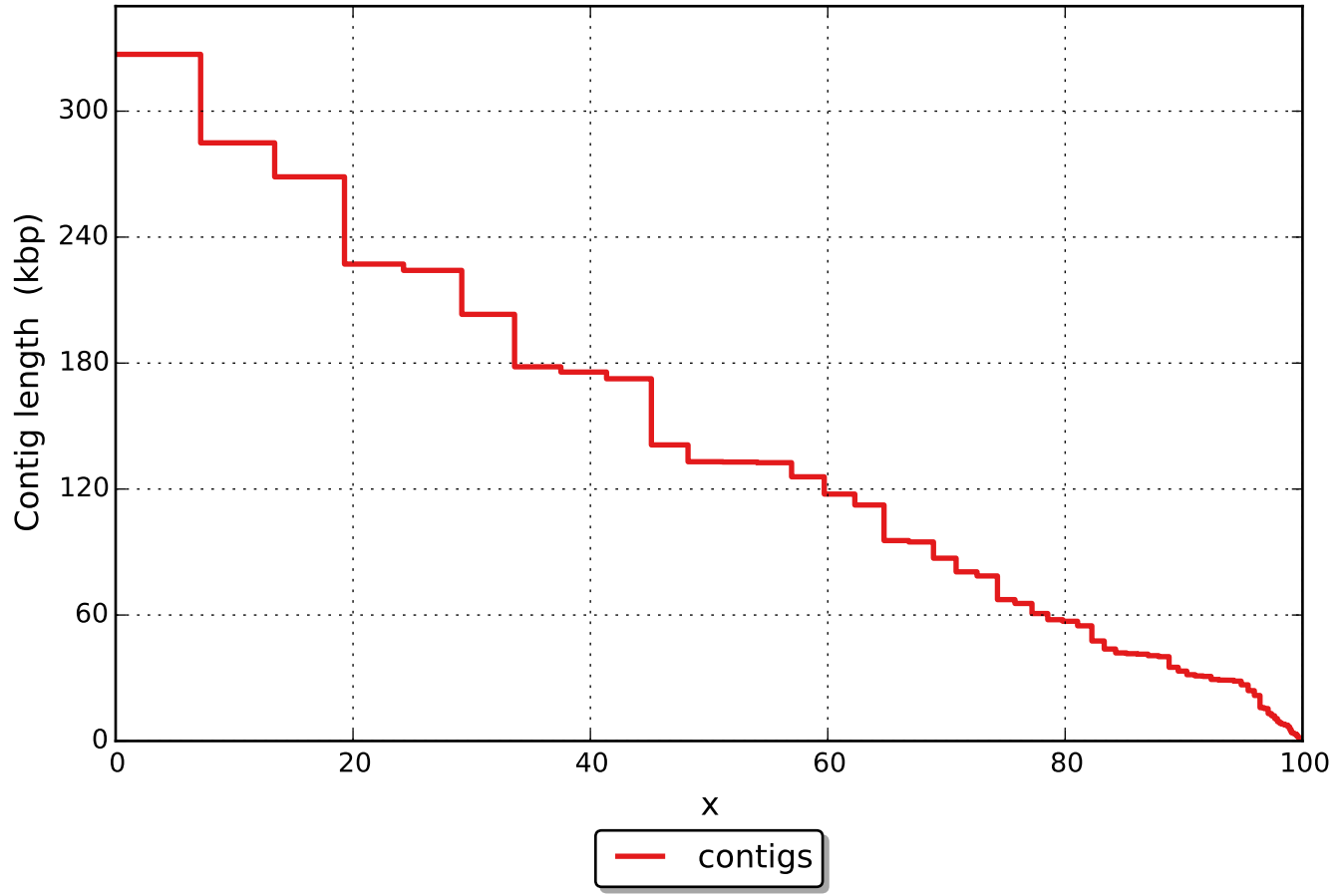




Cumulative length (aligned contigs)



NAx



# NGAx

