

## Report

	contigs
# contigs ( $\geq 1000$ bp)	62
# contigs ( $\geq 5000$ bp)	48
# contigs ( $\geq 10000$ bp)	44
# contigs ( $\geq 25000$ bp)	39
# contigs ( $\geq 50000$ bp)	27
Total length ( $\geq 1000$ bp)	4510277
Total length ( $\geq 5000$ bp)	4488206
Total length ( $\geq 10000$ bp)	4455421
Total length ( $\geq 25000$ bp)	4374190
Total length ( $\geq 50000$ bp)	3975624
# contigs	88
Largest contig	333181
Total length	4527412
Reference length	4641652
GC (%)	50.77
Reference GC (%)	50.79
N50	165569
NG50	165569
N75	88482
NG75	82473
L50	11
LG50	11
L75	20
LG75	21
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	20404
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.505
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	356.69
# indels per 100 kbp	0.62
Largest alignment	333181
NA50	165569
NGA50	165569
NA75	88482
NGA75	82473
LA50	11
LGA50	11
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	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	20404
# local misassemblies	0
# mismatches	16143
# indels	28
# short indels	28
# long indels	0
Indels length	28

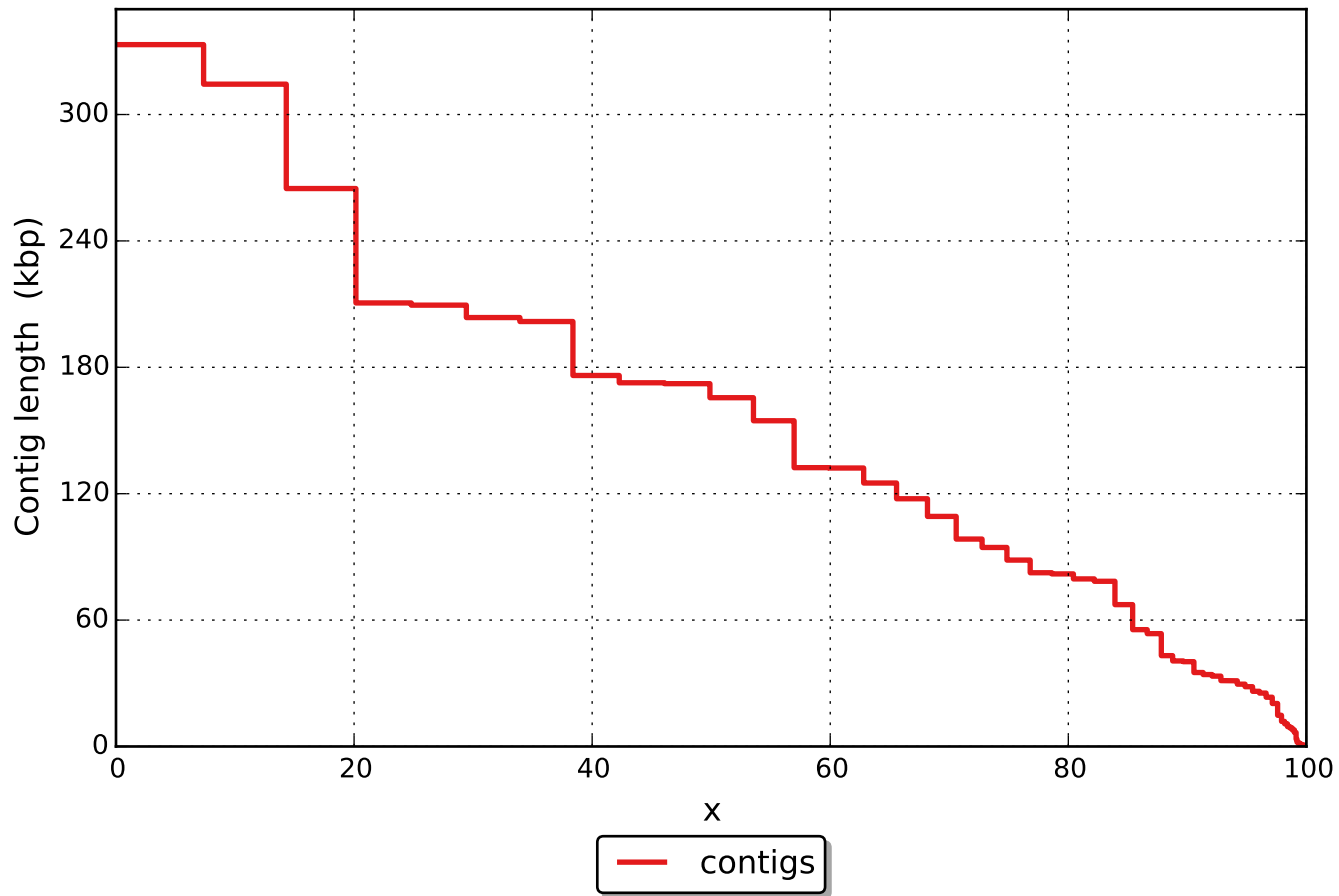
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

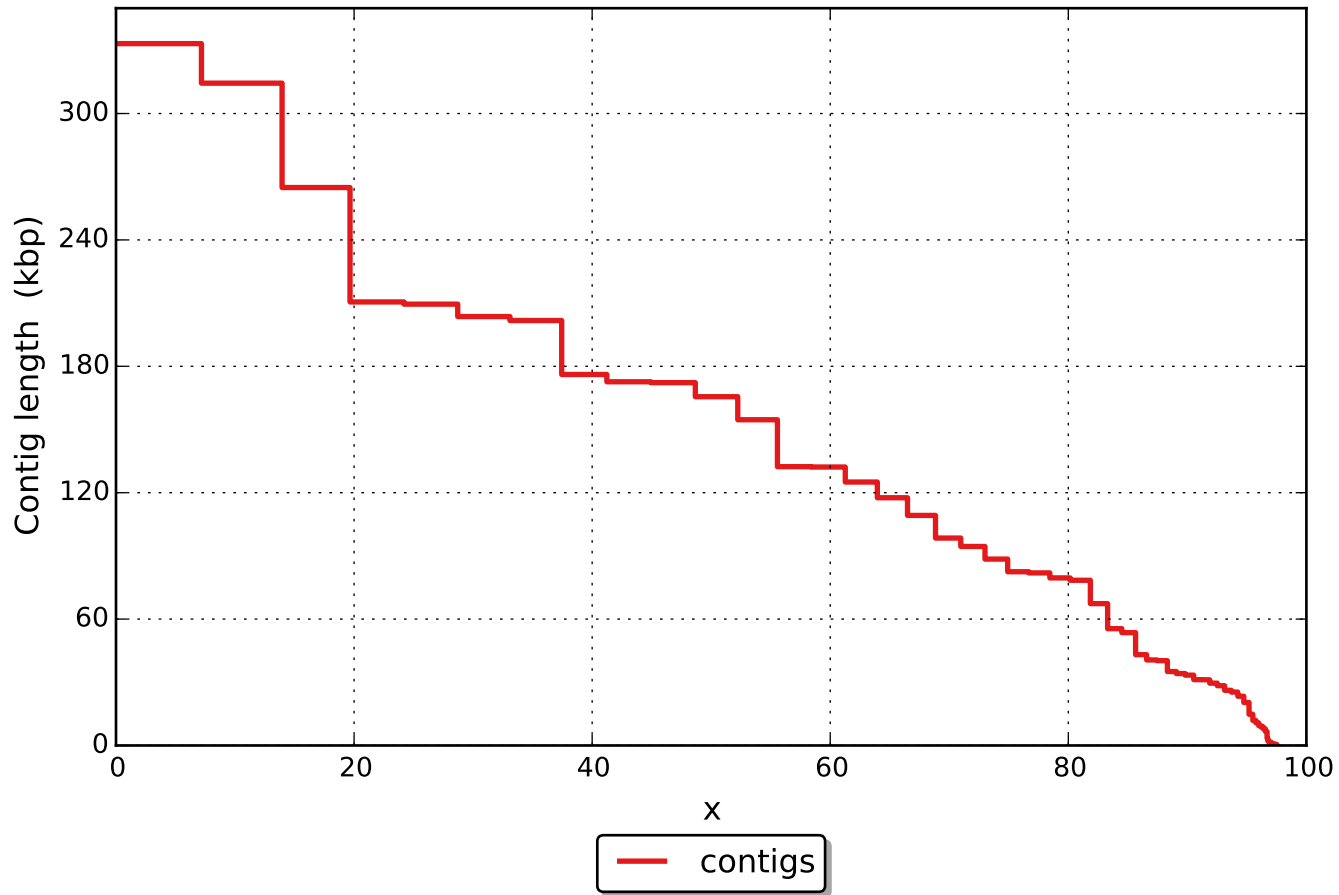
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

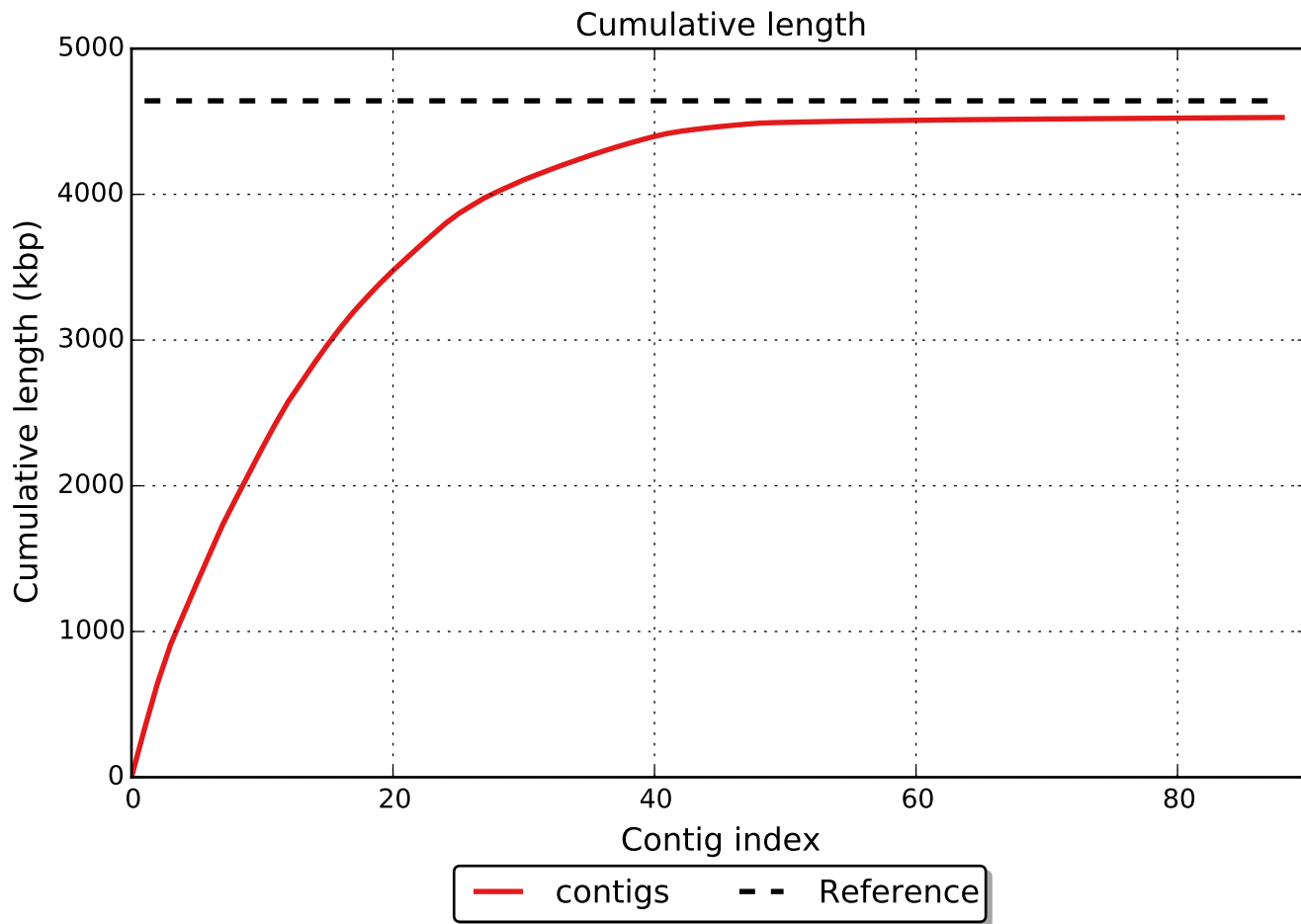
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

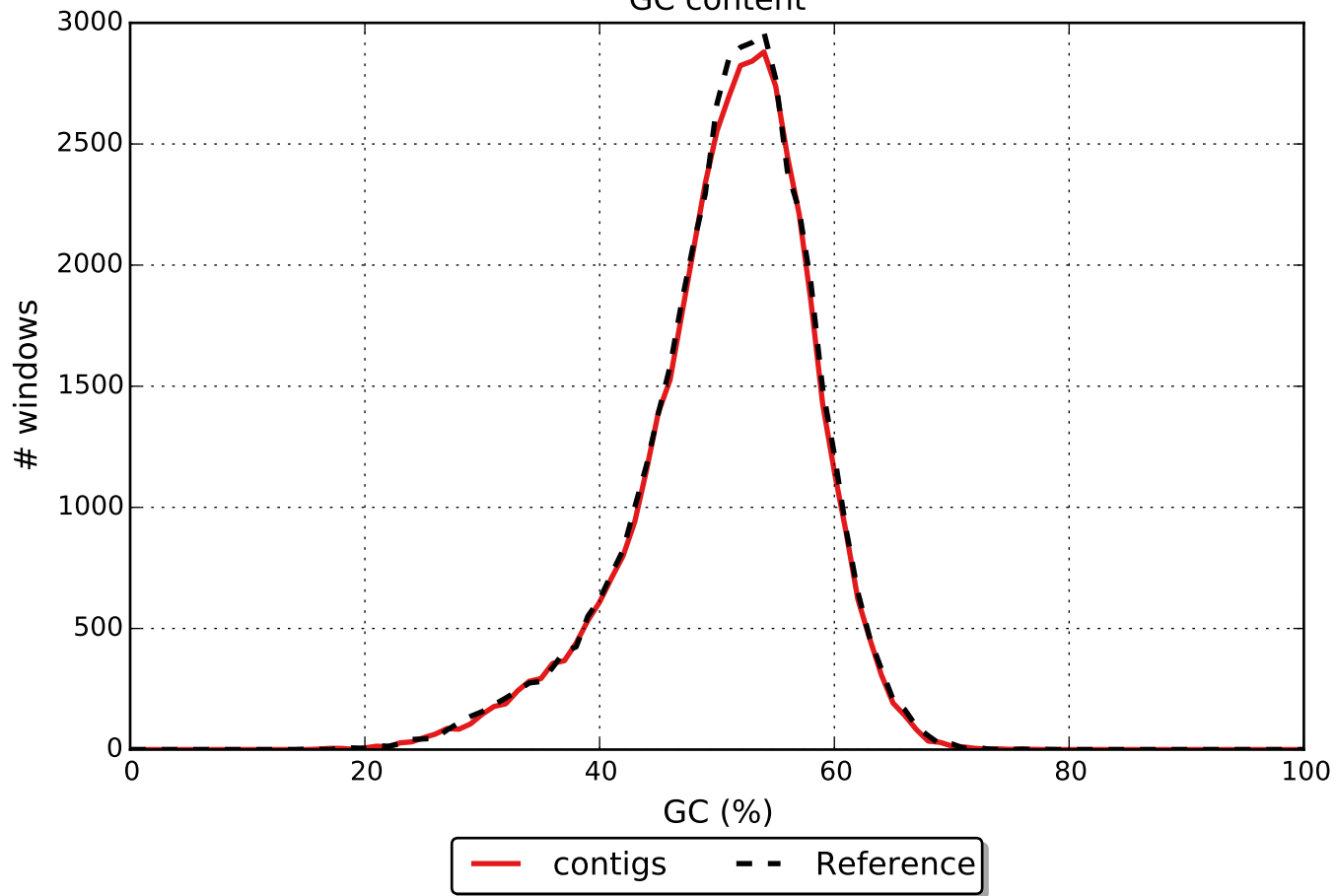


NGx





GC content

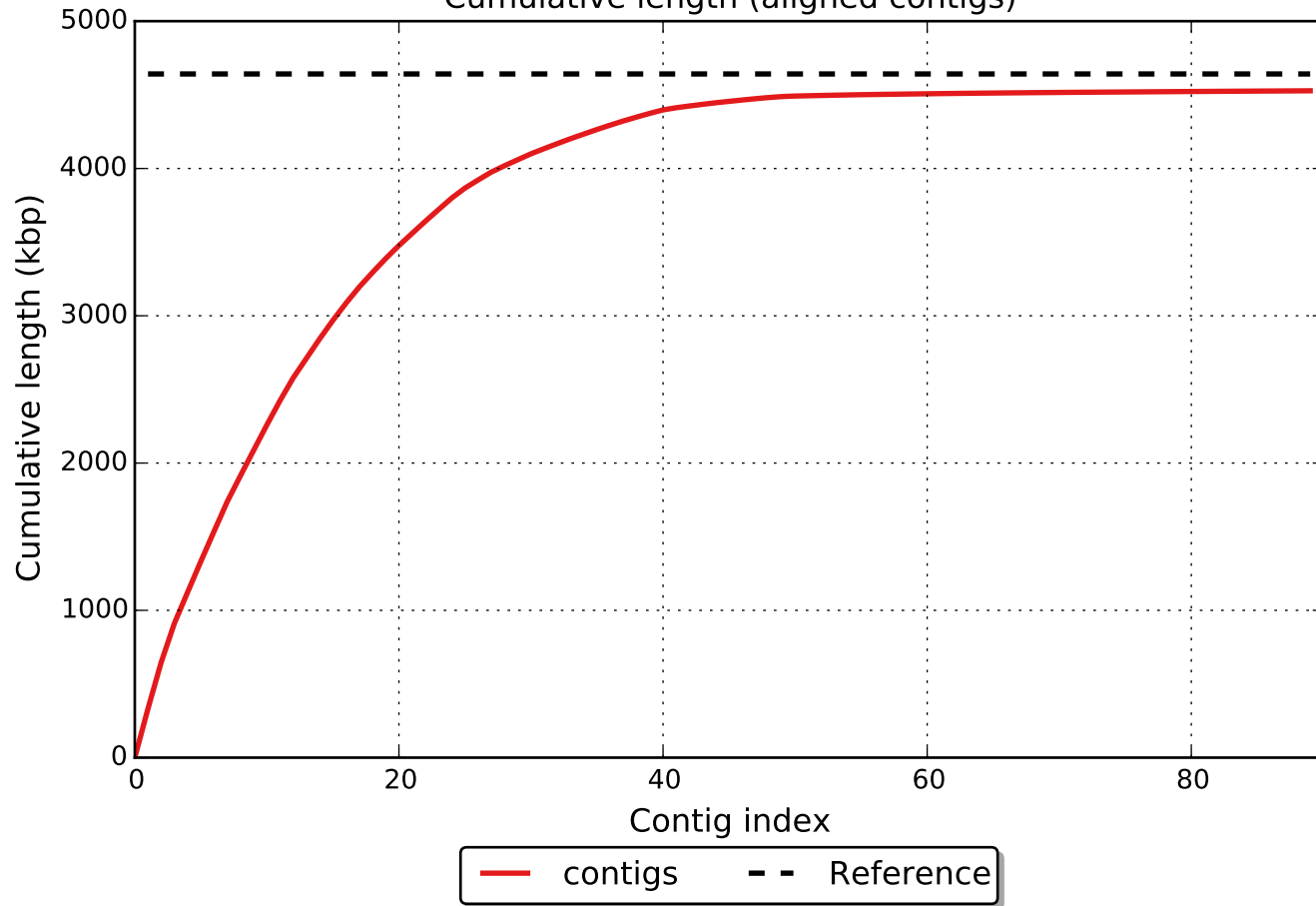


# Misassemblies

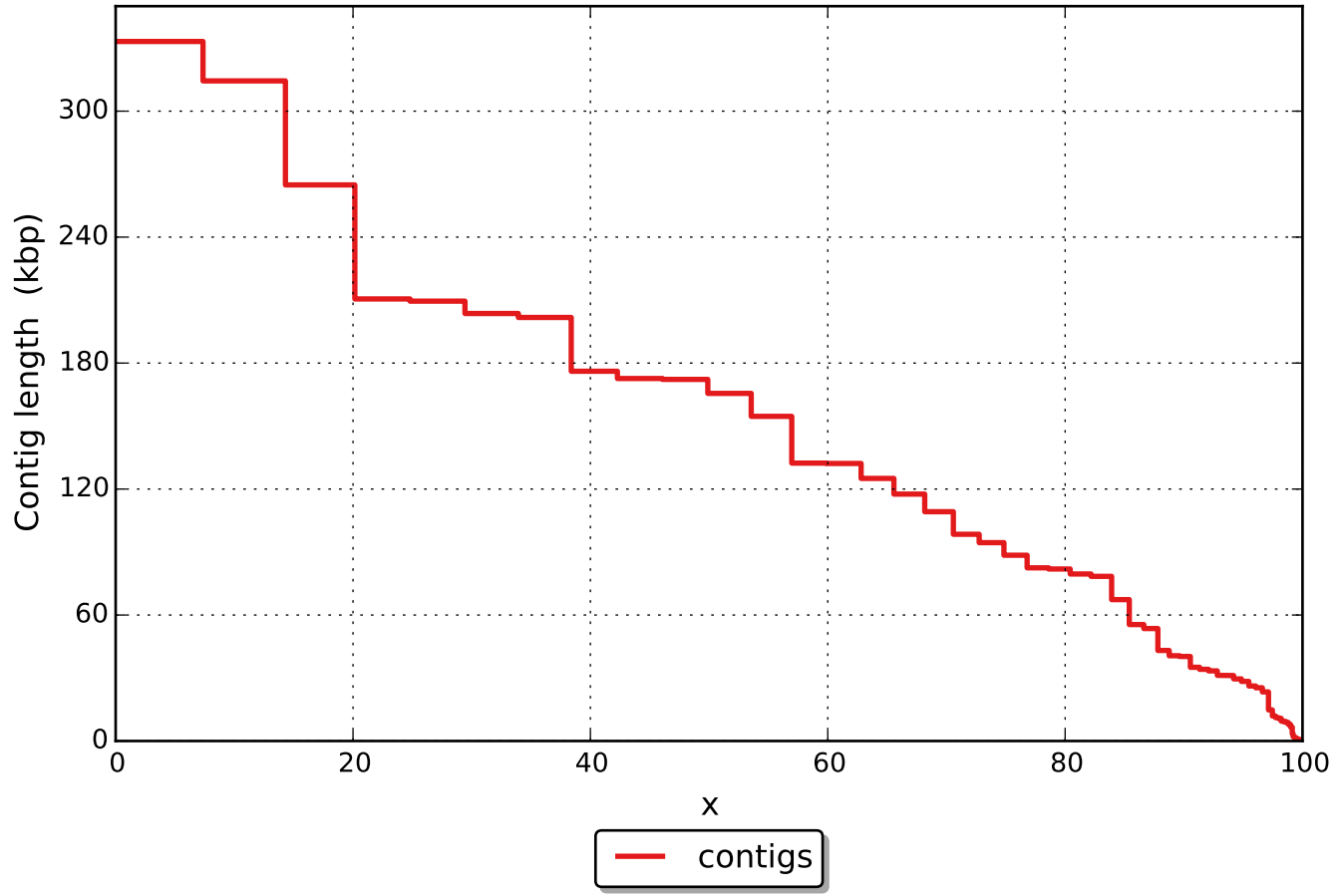




Cumulative length (aligned contigs)



NAx



# NGAx

