

## Report

	contigs
# contigs ( $\geq 1000$ bp)	59
# contigs ( $\geq 5000$ bp)	47
# contigs ( $\geq 10000$ bp)	44
# contigs ( $\geq 25000$ bp)	41
# contigs ( $\geq 50000$ bp)	29
Total length ( $\geq 1000$ bp)	4829654
Total length ( $\geq 5000$ bp)	4807080
Total length ( $\geq 10000$ bp)	4784053
Total length ( $\geq 25000$ bp)	4745103
Total length ( $\geq 50000$ bp)	4336260
# contigs	69
Largest contig	401996
Total length	4836752
Reference length	4641652
GC (%)	50.78
Reference GC (%)	50.79
N50	174787
NG50	174787
N75	94470
NG75	109022
L50	10
LG50	10
L75	19
LG75	18
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	69931
# local misassemblies	2
# unaligned contigs	0 + 1 part
Unaligned length	290386
Genome fraction (%)	97.771
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	308.19
# indels per 100 kbp	0.77
Largest alignment	315025
NA50	154629
NGA50	165140
NA75	79549
NGA75	82473
LA50	12
LGA50	11
LA75	23
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	2
# relocations	2
# translocations	0
# inversions	0
# possibly misassembled contigs	1
# misassembled contigs	2
Misassembled contigs length	69931
# local misassemblies	2
# mismatches	13986
# indels	35
# short indels	35
# long indels	0
Indels length	41

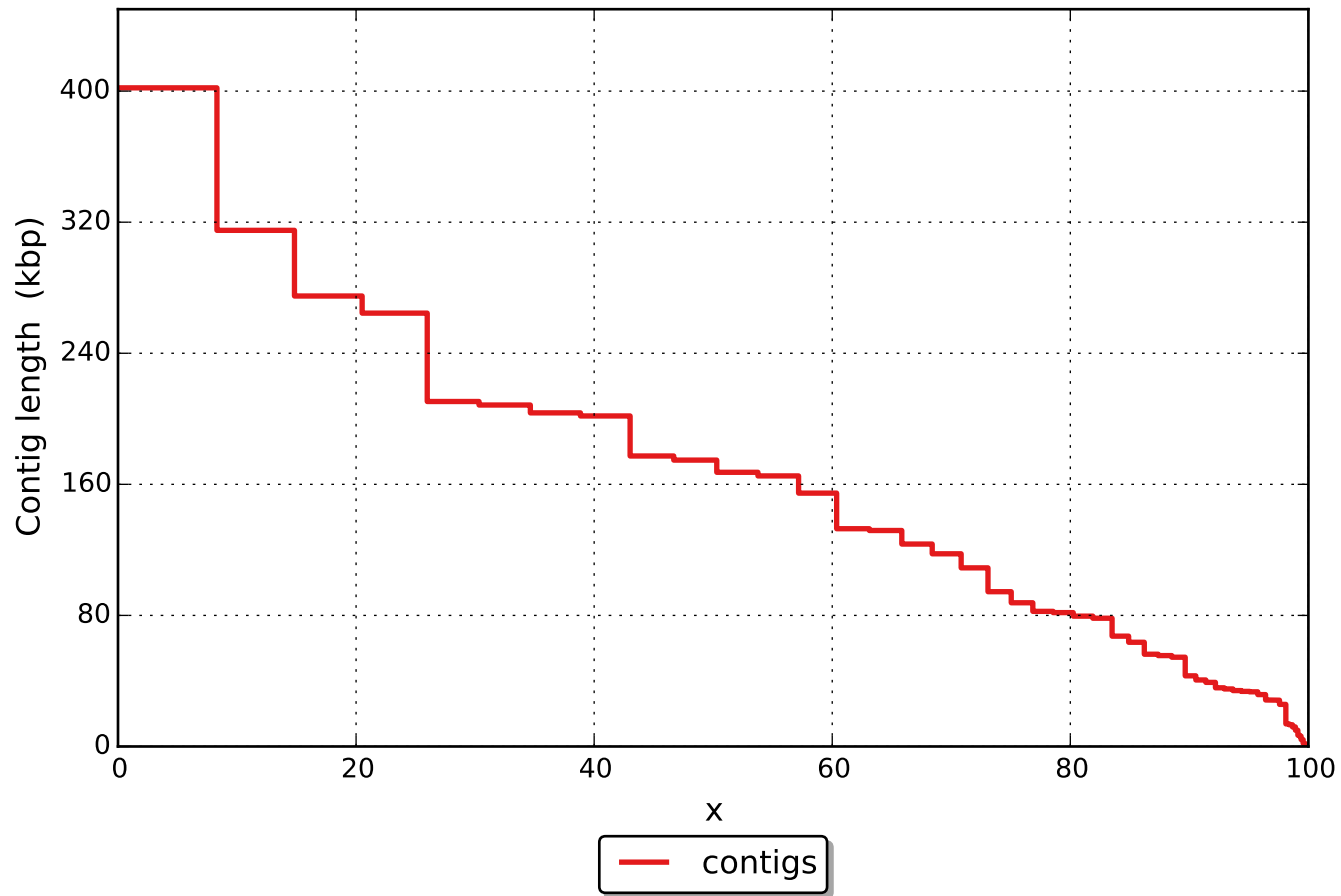
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

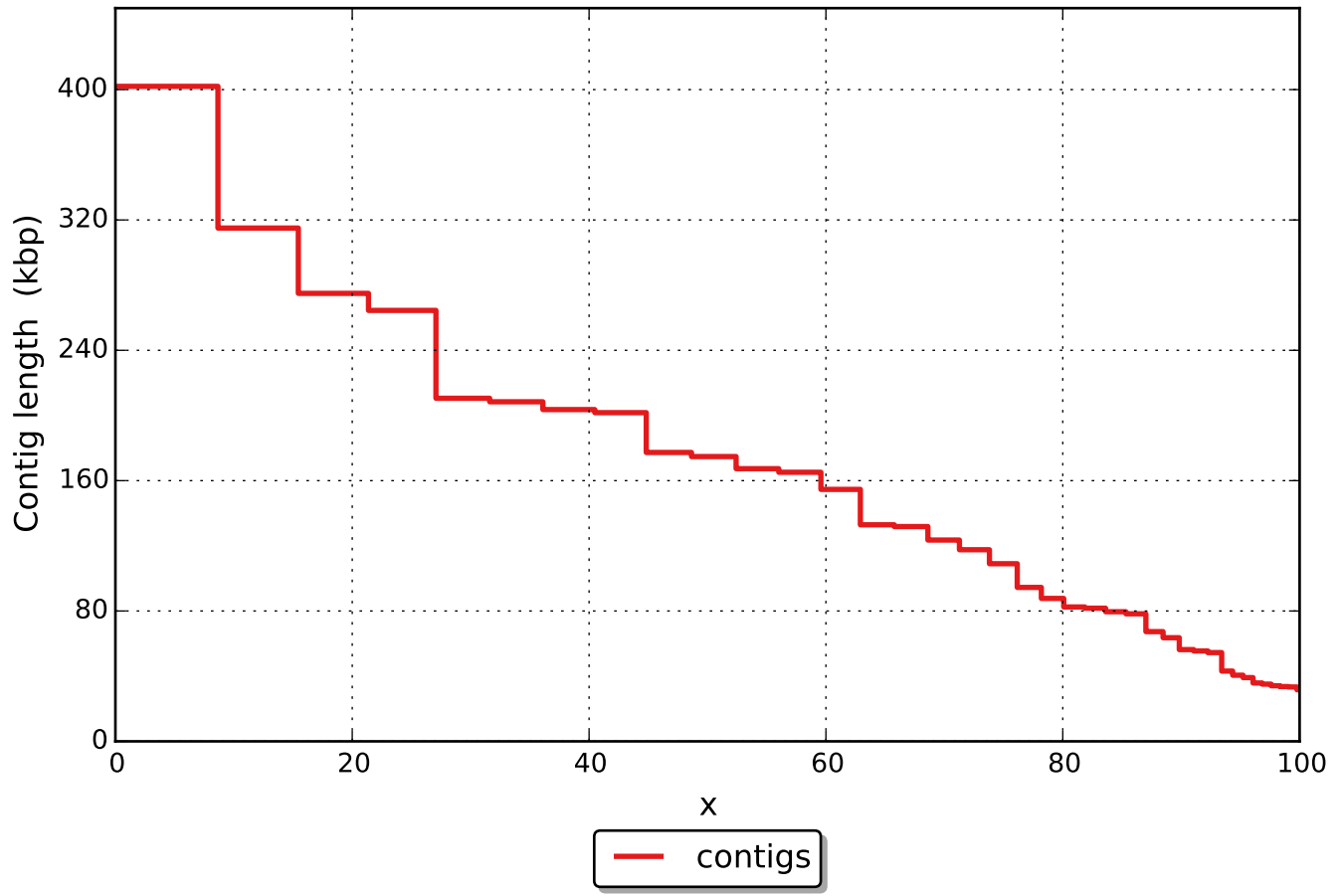
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	1
# both parts are significant	1
Partially unaligned length	290386
# N's	0

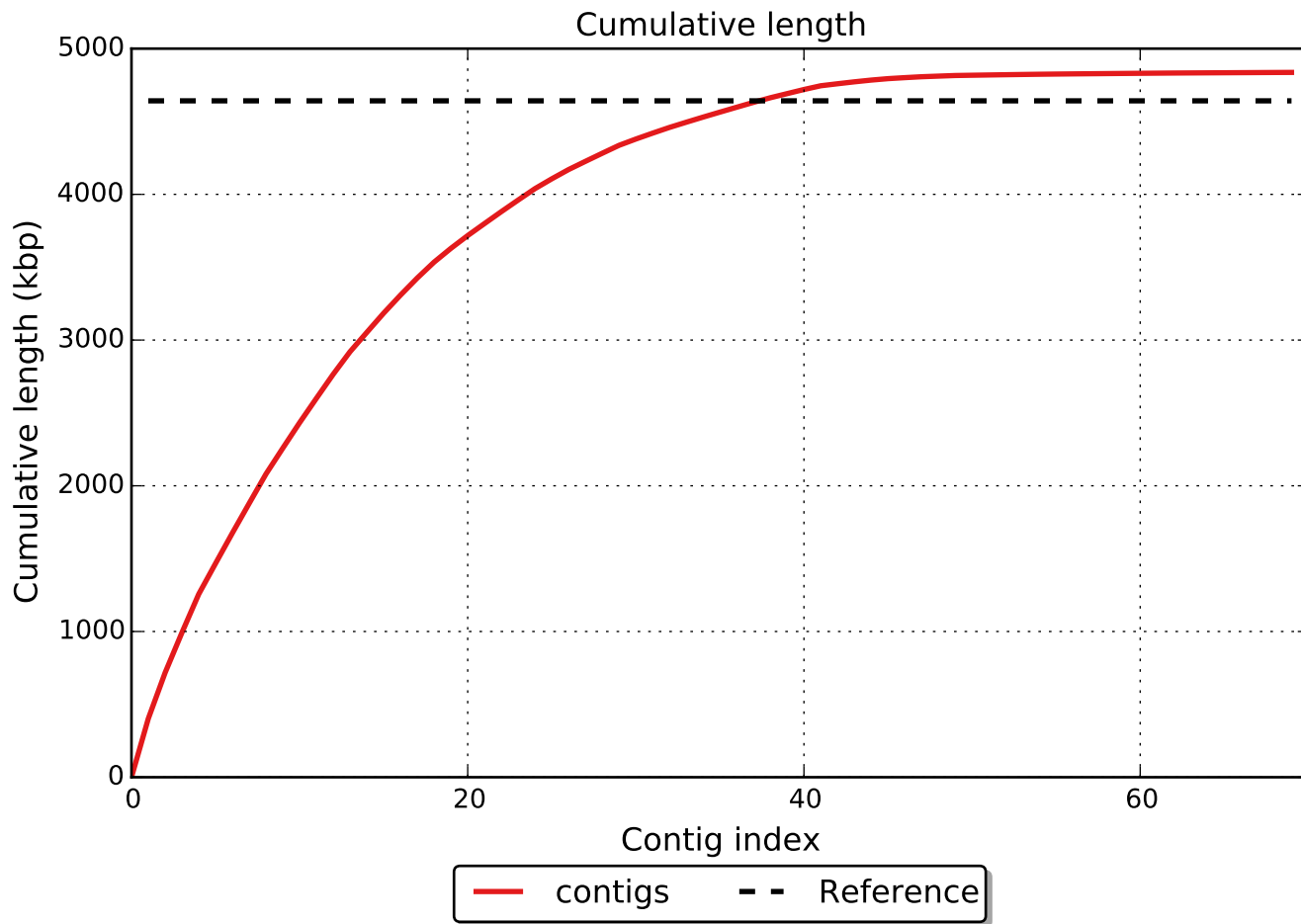
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

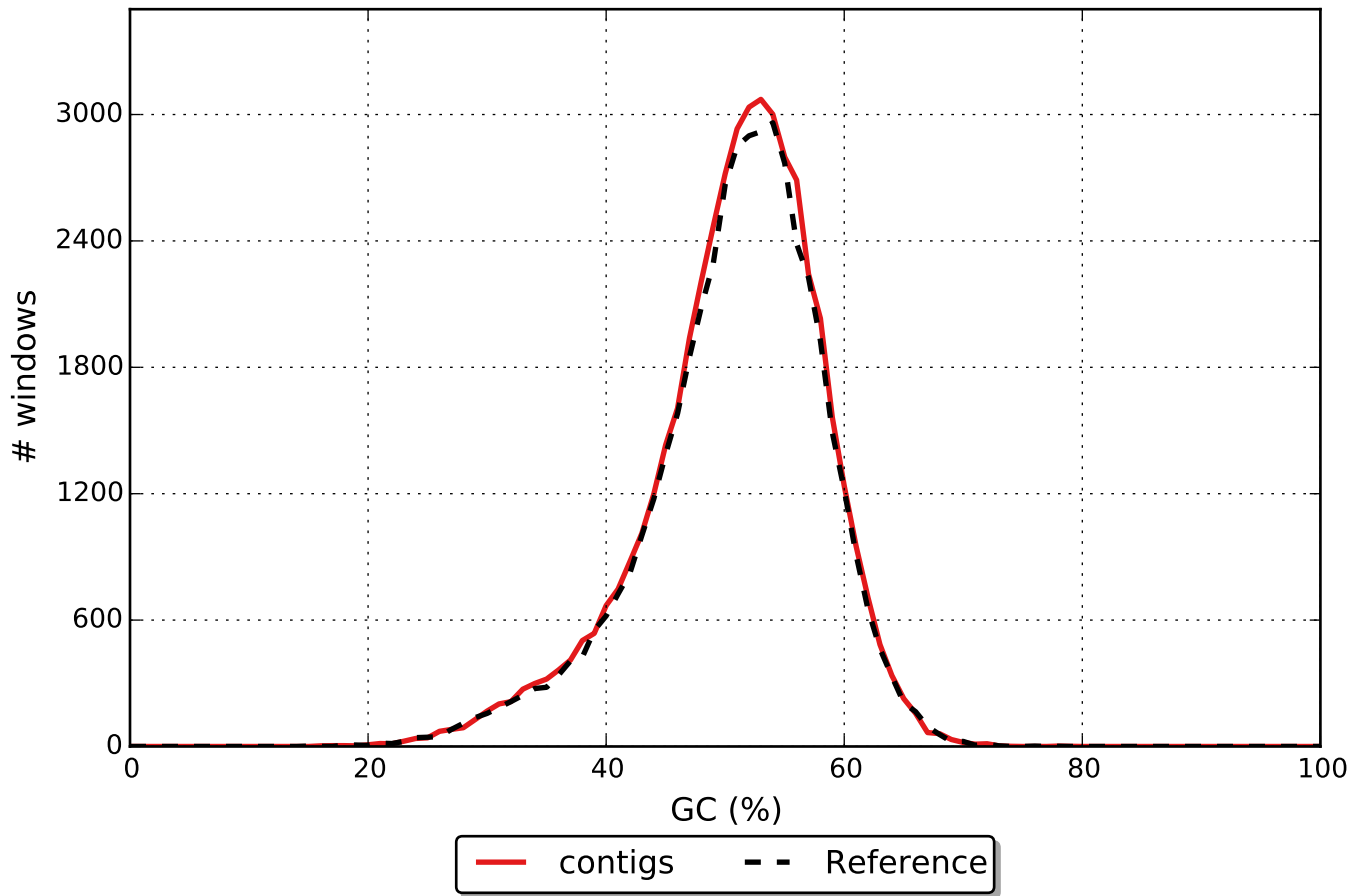


NGx





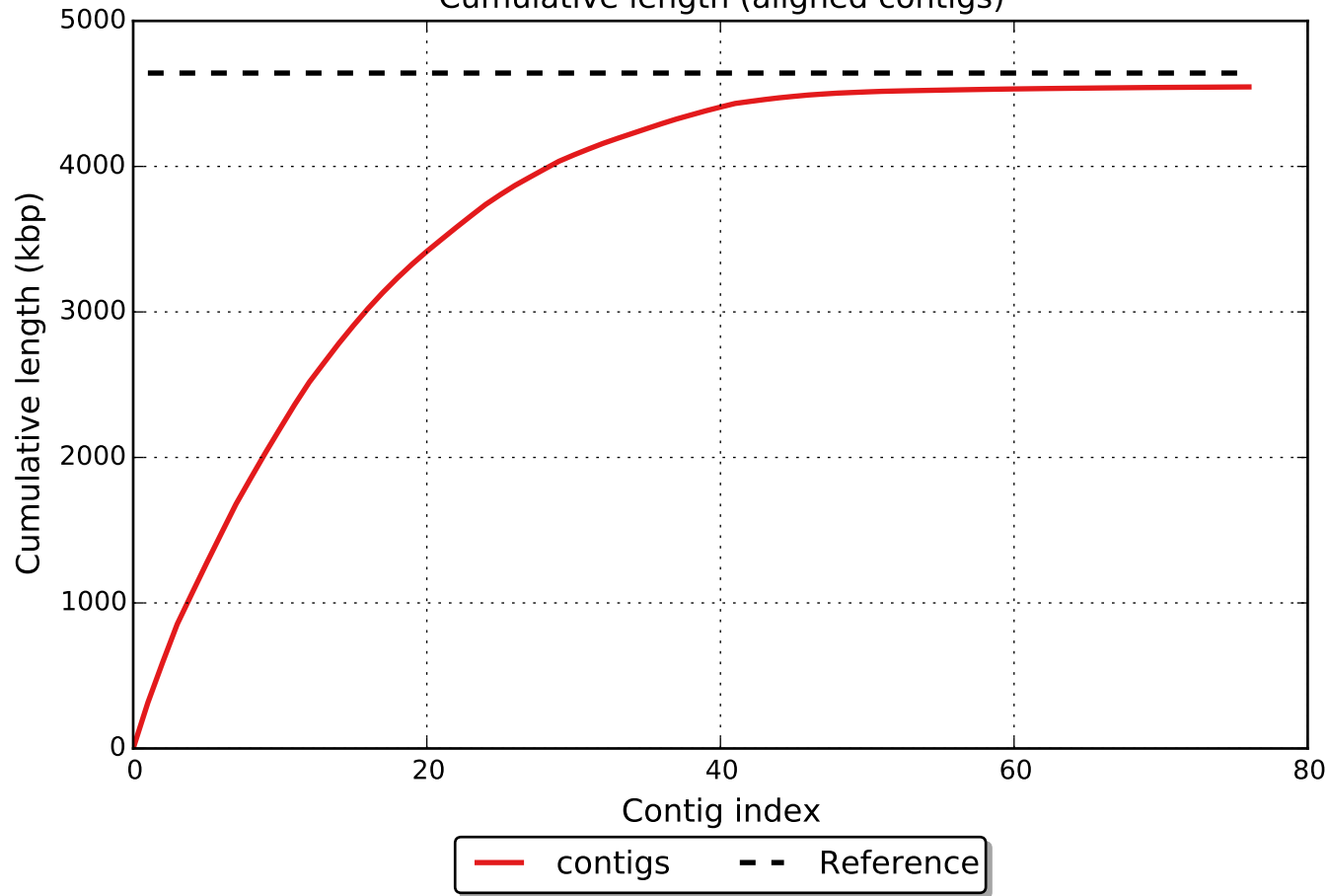
# GC content



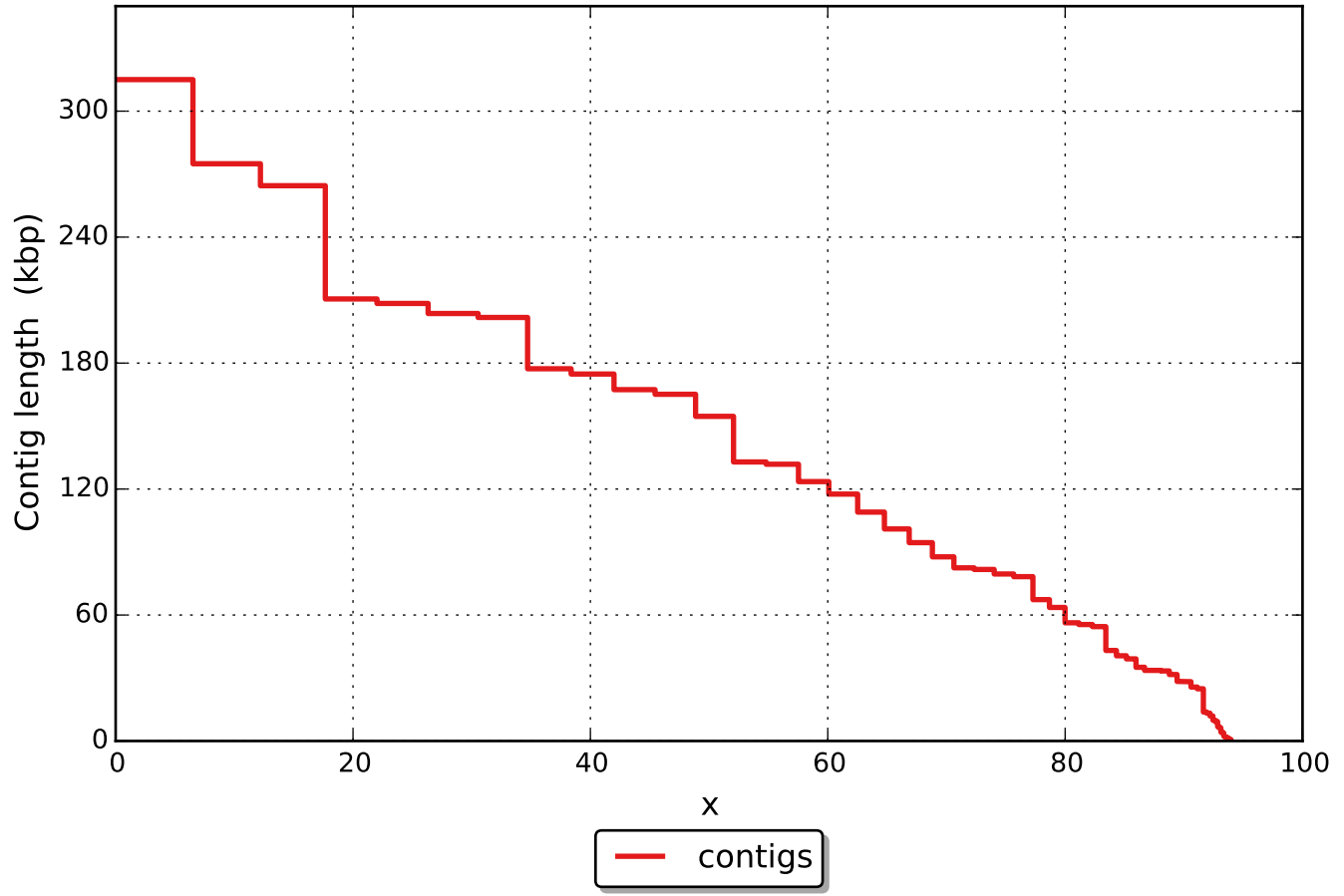




Cumulative length (aligned contigs)



NAx



# NGAx

