

Report

	final.contigs
# contigs (>= 1000 bp)	96
# contigs (>= 5000 bp)	71
# contigs (>= 10000 bp)	65
# contigs (>= 25000 bp)	48
# contigs (>= 50000 bp)	30
Total length (>= 1000 bp)	4555364
Total length (>= 5000 bp)	4499789
Total length (>= 10000 bp)	4456499
Total length (>= 25000 bp)	4182272
Total length (>= 50000 bp)	3555196
# contigs	108
Largest contig	327145
Total length	4563479
Reference length	4641652
GC (℥)	50.74
Reference GC (℥)	50.79
N50	112493
NG50	112493
N75	54947
NG75	54110
L50	14
LG50	14
L75	28
LG75	29
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	12
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (℥)	98.255
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	60.06
# indels per 100 kbp	9.93
Largest alignment	327145
NA50	112493
NGA50	112493
NA75	54947
NGA75	54110
LA50	14
LGA50	14
LA75	28
LGA75	29

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

## Misassemblies report

	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	12
# mismatches	2739
# indels	453
# short indels	447
# long indels	6
Indels length	804

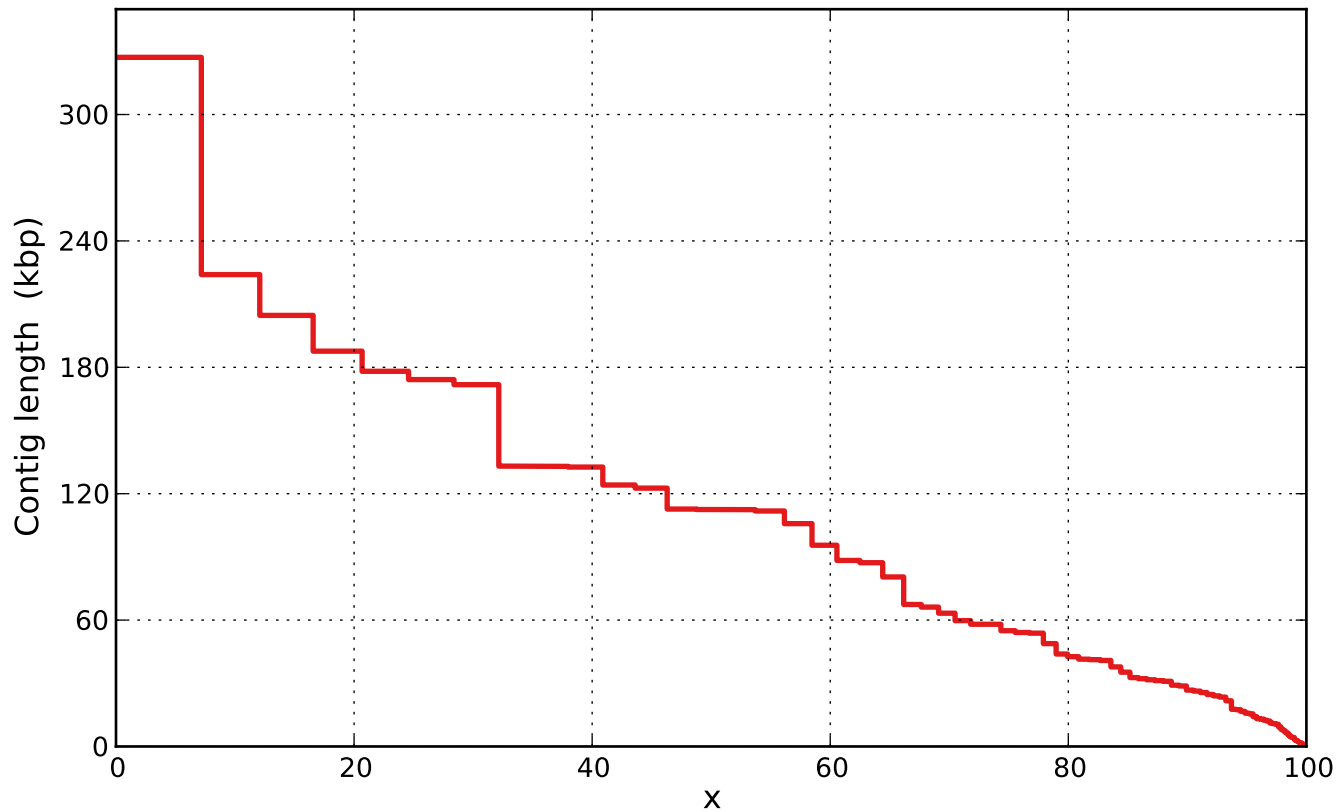
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

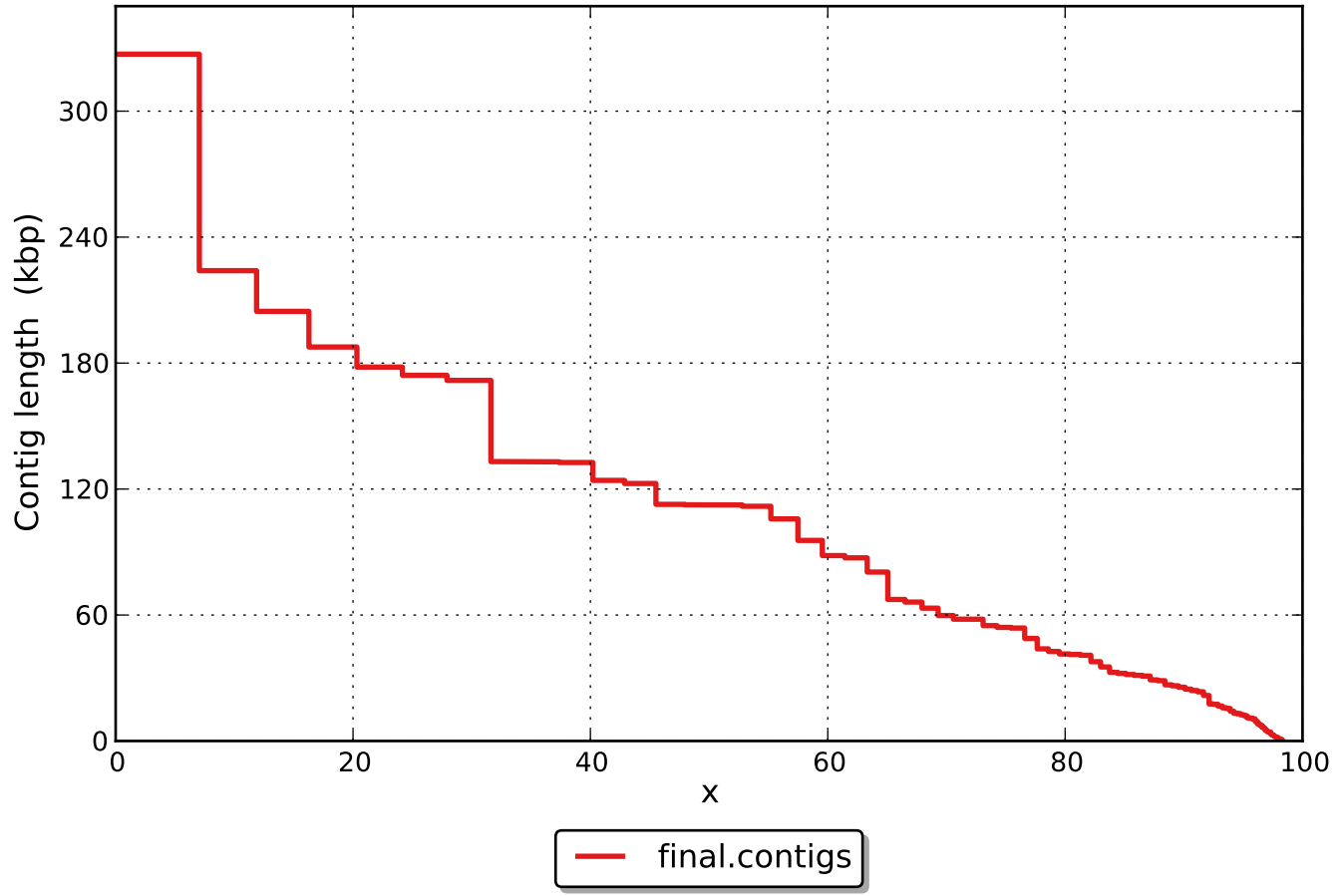
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

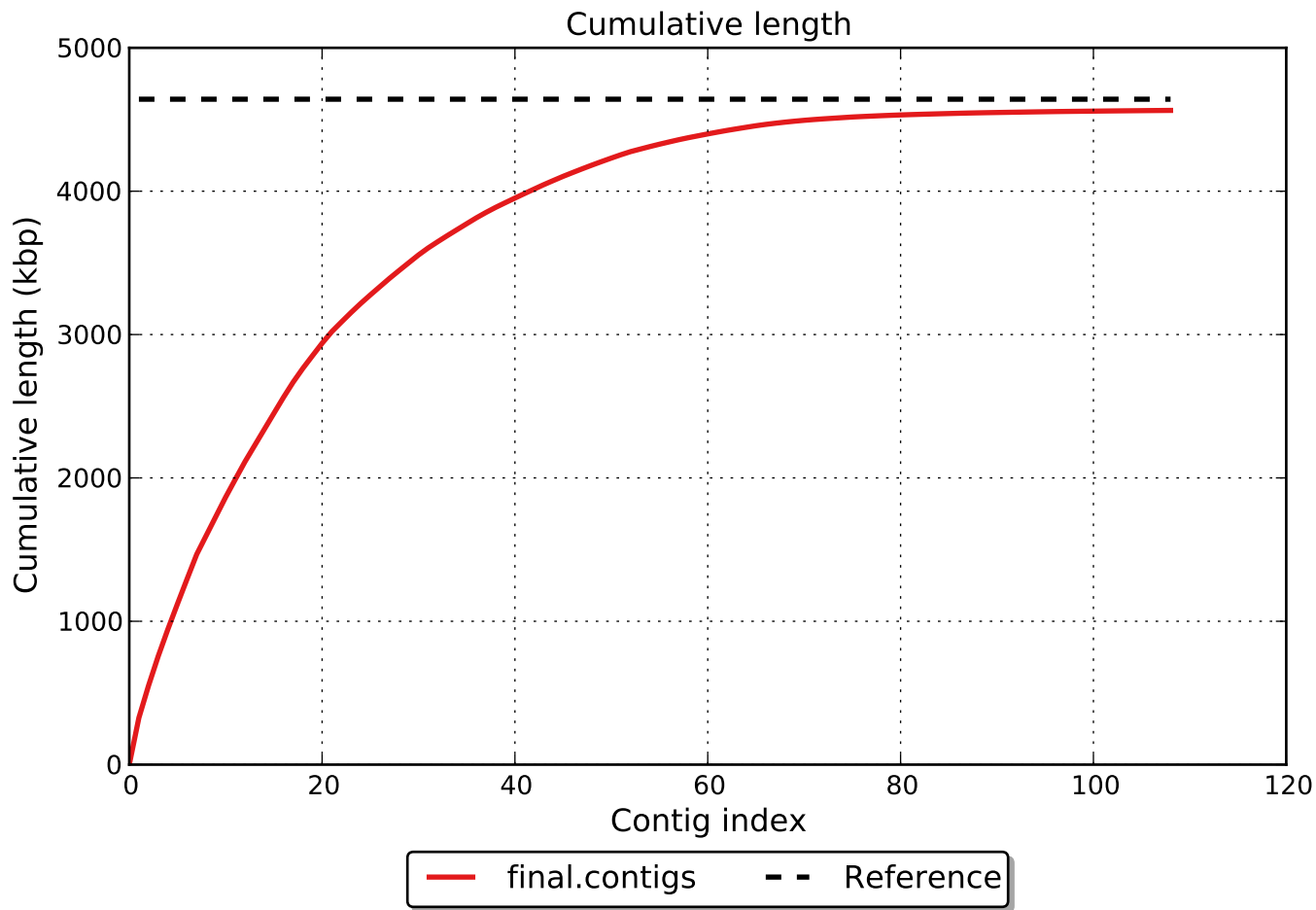
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

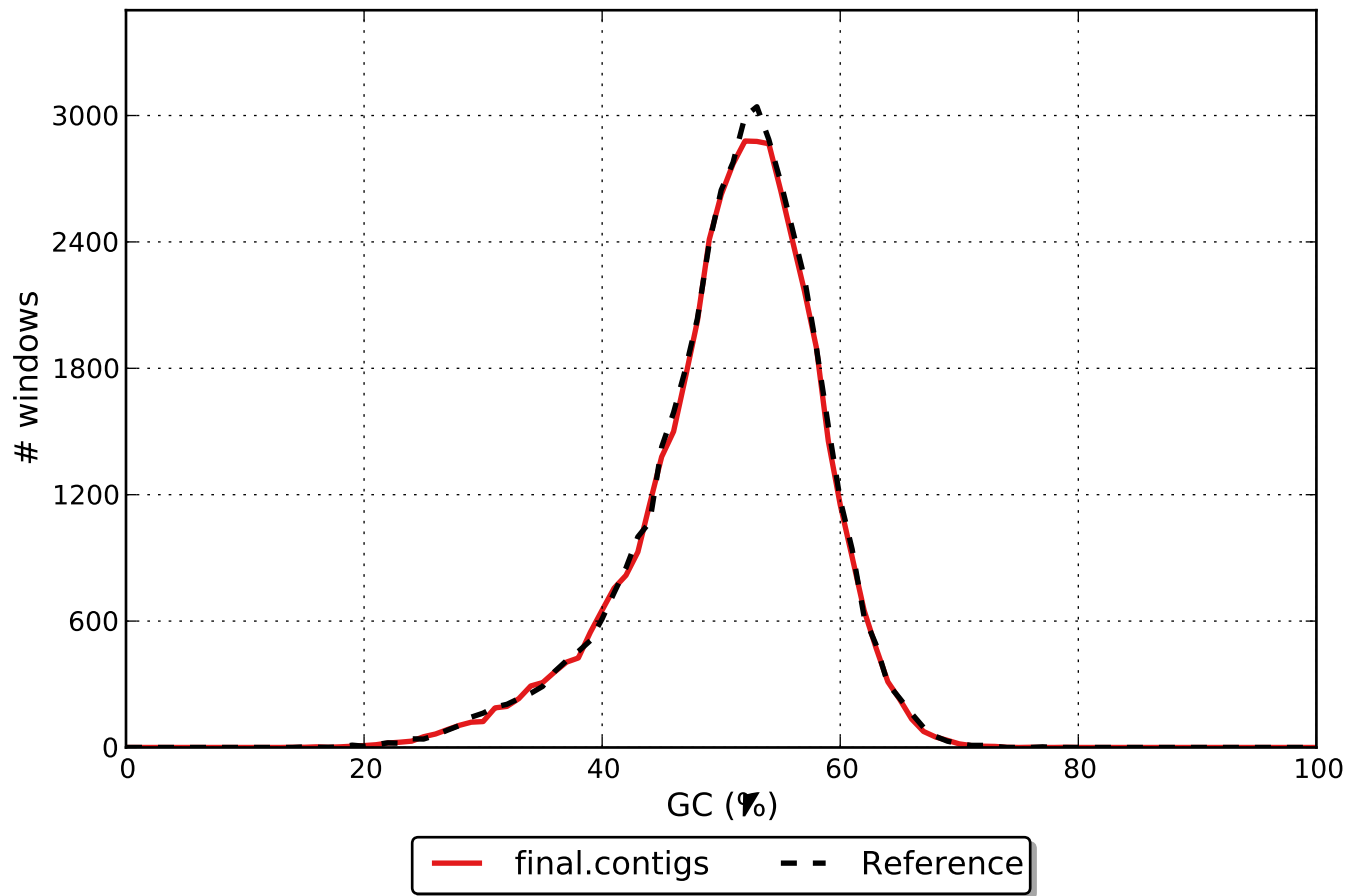


NGx





GC content

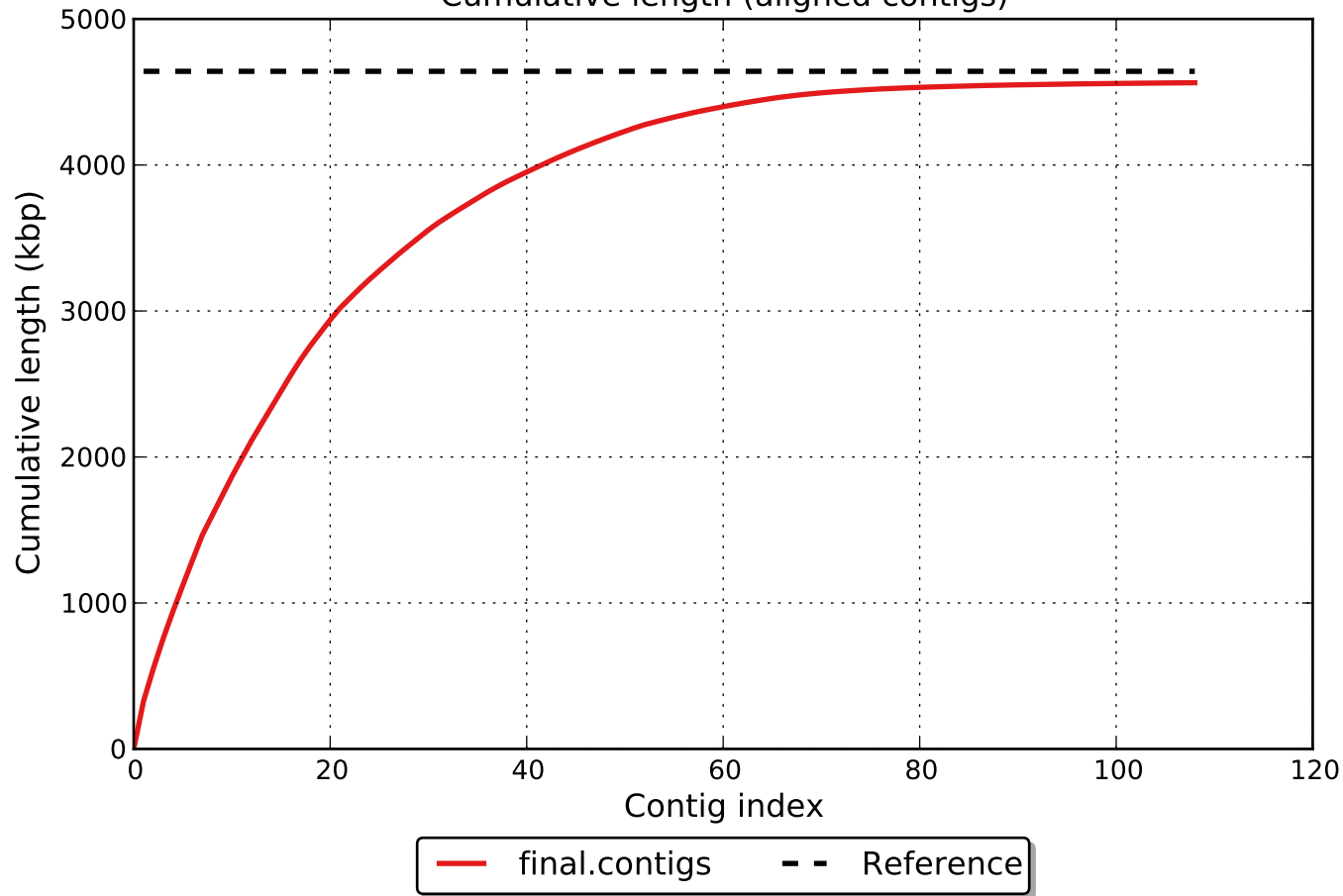


# Misassemblies

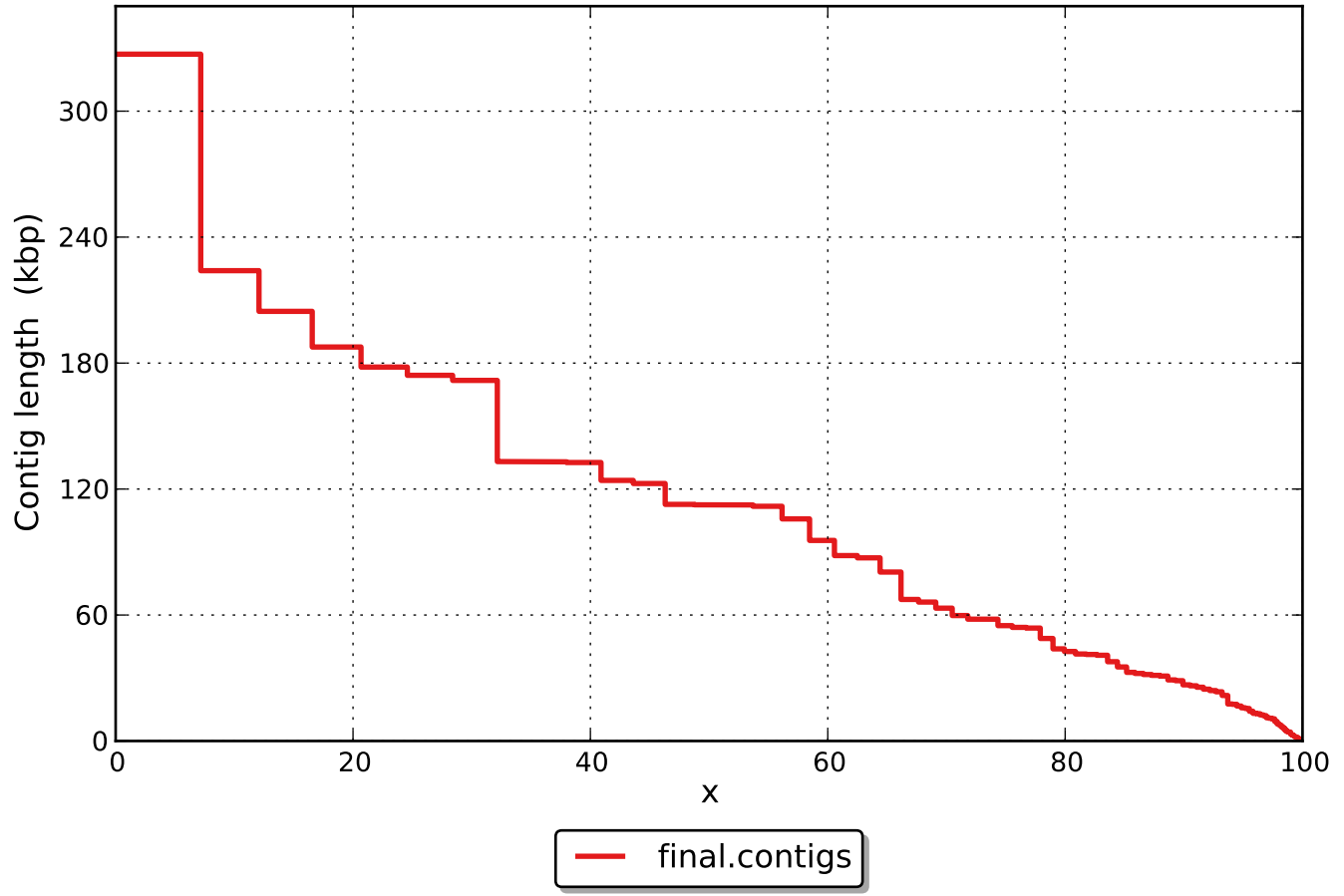




Cumulative length (aligned contigs)



NAx



# NGAx

