

# Report

	final.contigs
# contigs ( $\geq 0$ bp)	172
# contigs ( $\geq 1000$ bp)	91
# contigs ( $\geq 5000$ bp)	68
# contigs ( $\geq 10000$ bp)	62
# contigs ( $\geq 25000$ bp)	48
# contigs ( $\geq 50000$ bp)	29
Total length ( $\geq 0$ bp)	4580691
Total length ( $\geq 1000$ bp)	4551768
Total length ( $\geq 5000$ bp)	4501613
Total length ( $\geq 10000$ bp)	4456000
Total length ( $\geq 25000$ bp)	4231109
Total length ( $\geq 50000$ bp)	3589993
# contigs	172
Largest contig	327151
Total length	4580691
Reference length	4641652
GC (%)	50.76
Reference GC (%)	50.79
N50	125651
NG50	125651
N75	58008
NG75	54946
L50	13
LG50	13
L75	27
LG75	28
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	163
Genome fraction (%)	98.548
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.48
# indels per 100 kbp	0.00
Largest alignment	327151
NA50	125651
NGA50	125651
NA75	58008
NGA75	54946
LA50	13
LGA50	13
LA75	27
LGA75	28

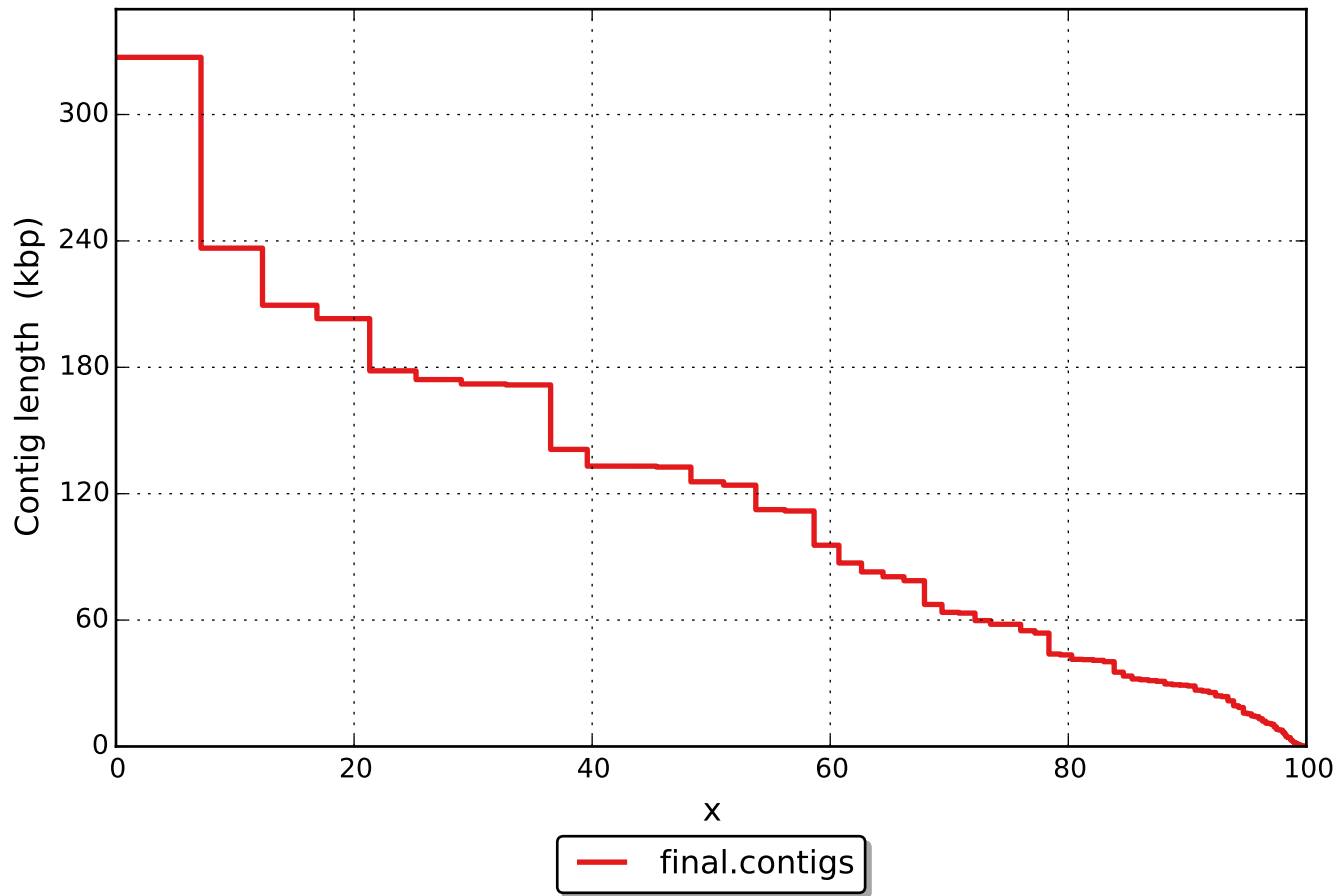
## Misassemblies report

	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	22
# indels	0
# short indels	0
# long indels	0
Indels length	0

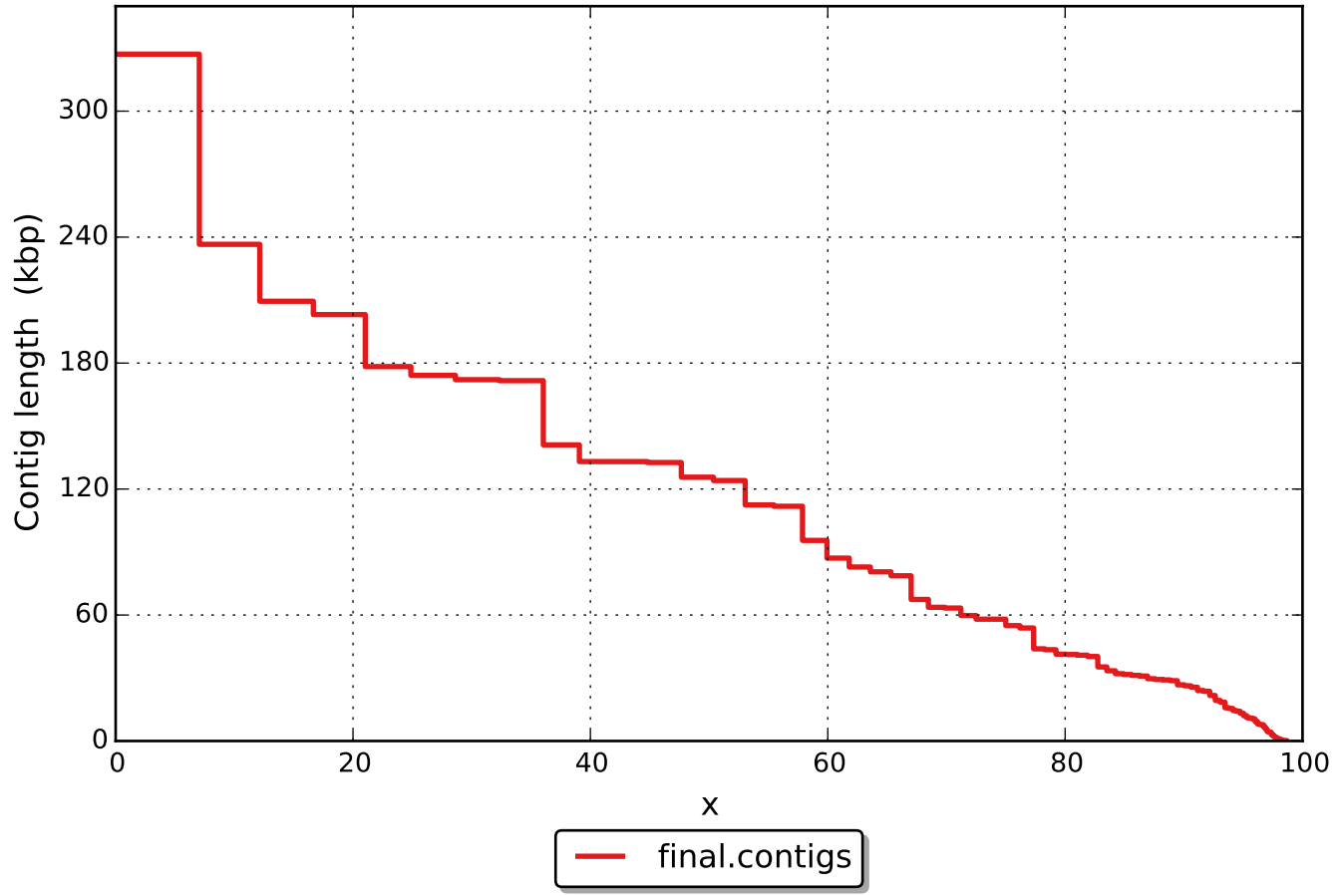
## Unaligned report

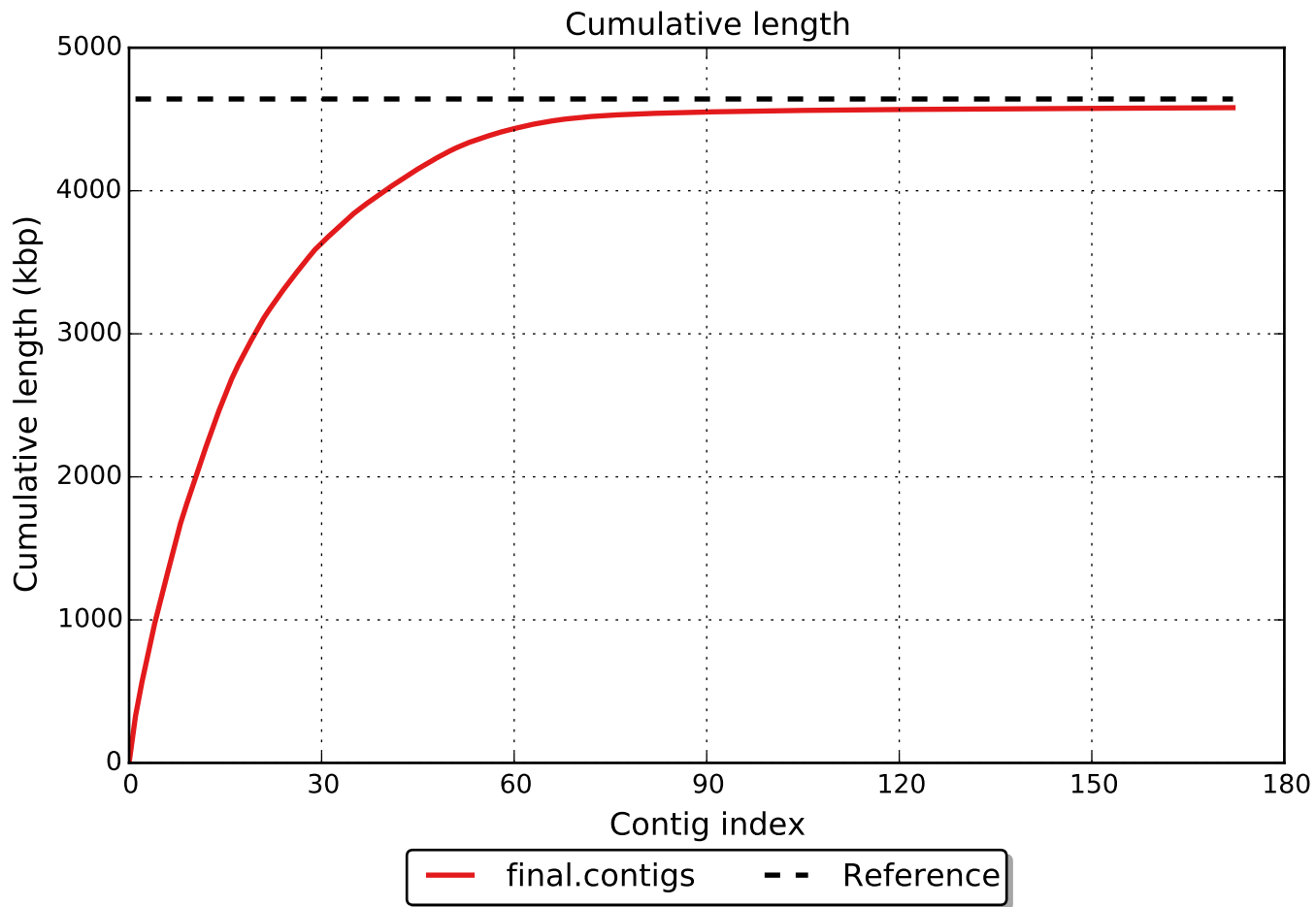
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	1
Partially unaligned length	163
# N's	0

Nx

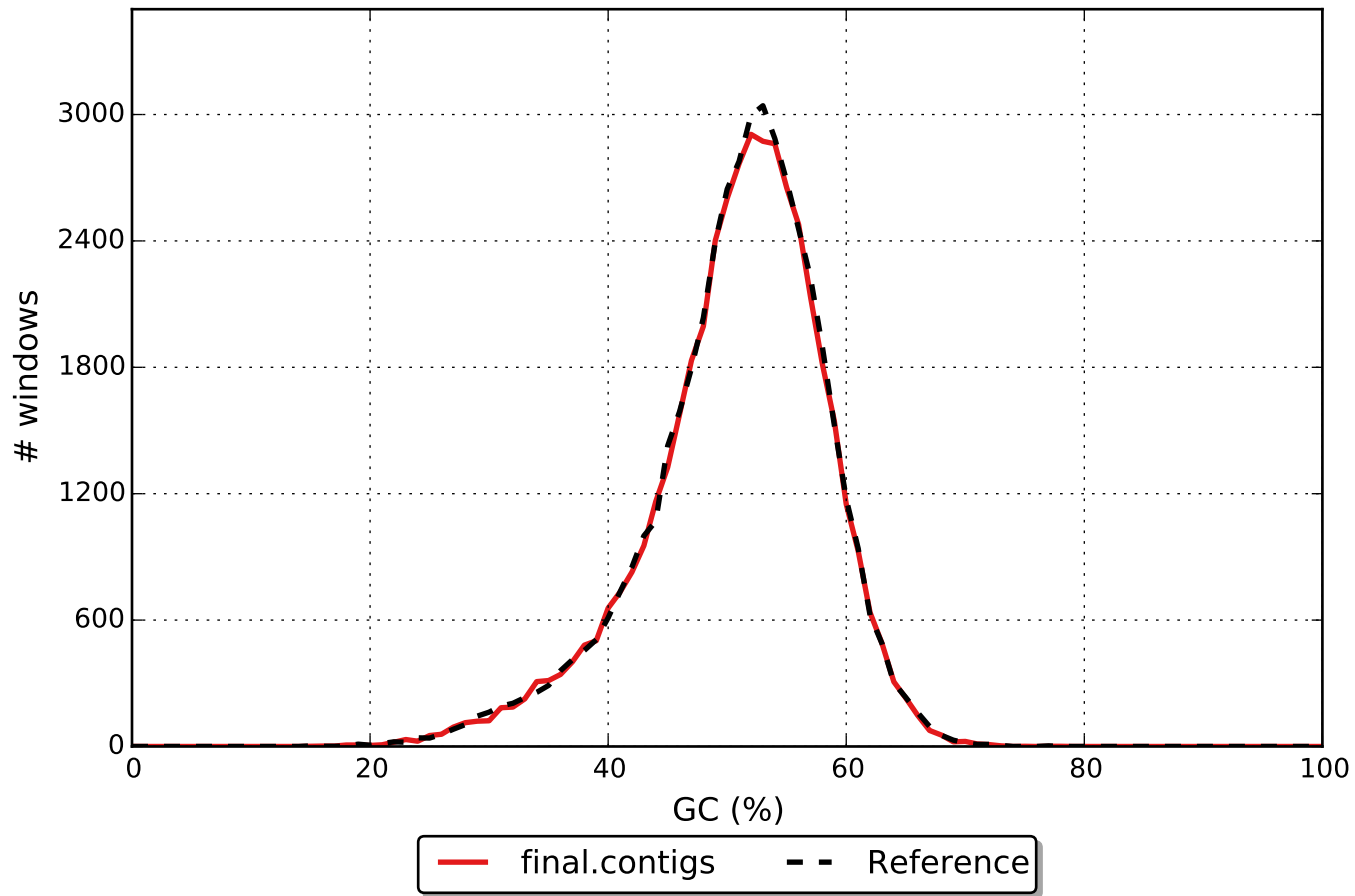


NGx





# GC content

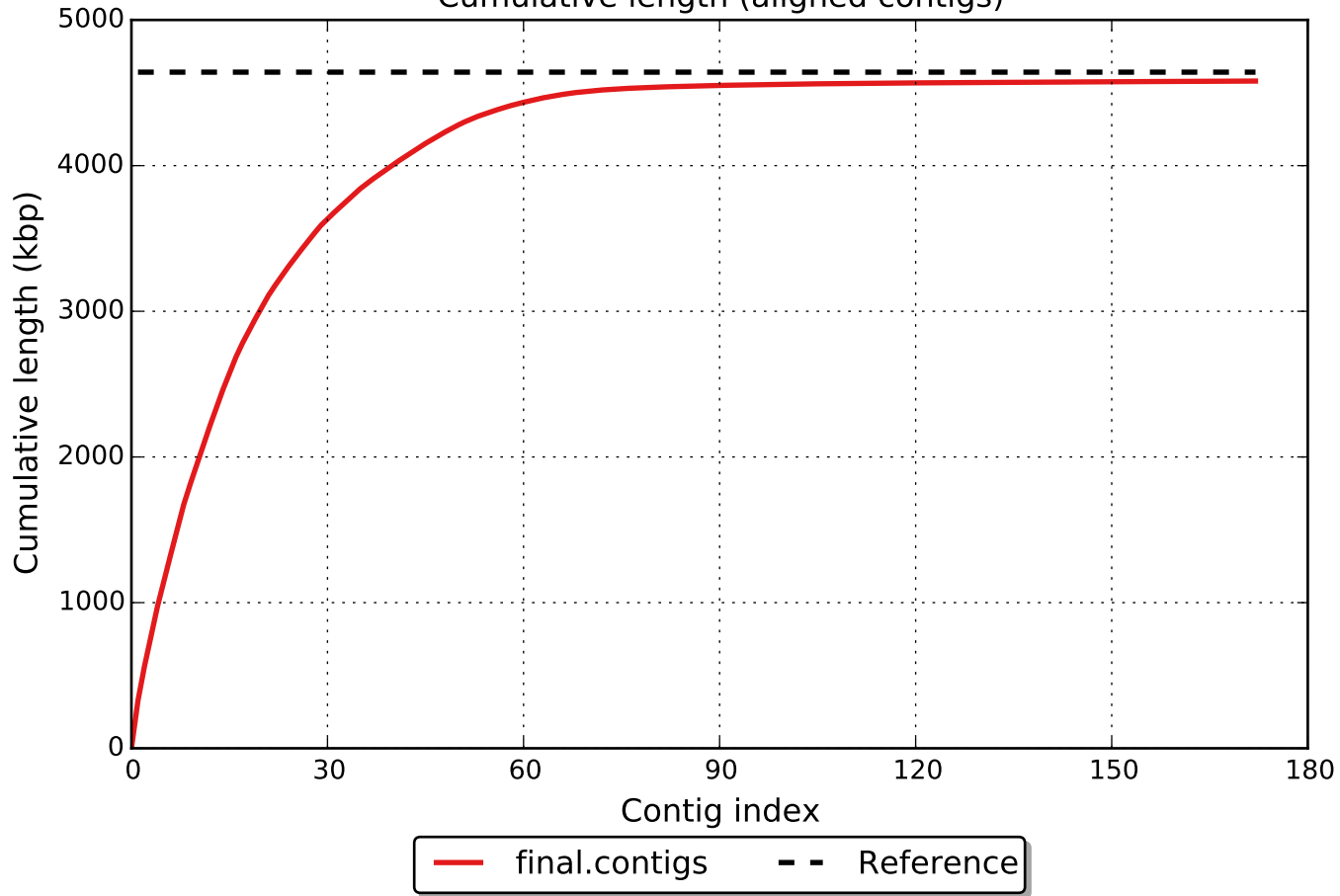


# Misassemblies

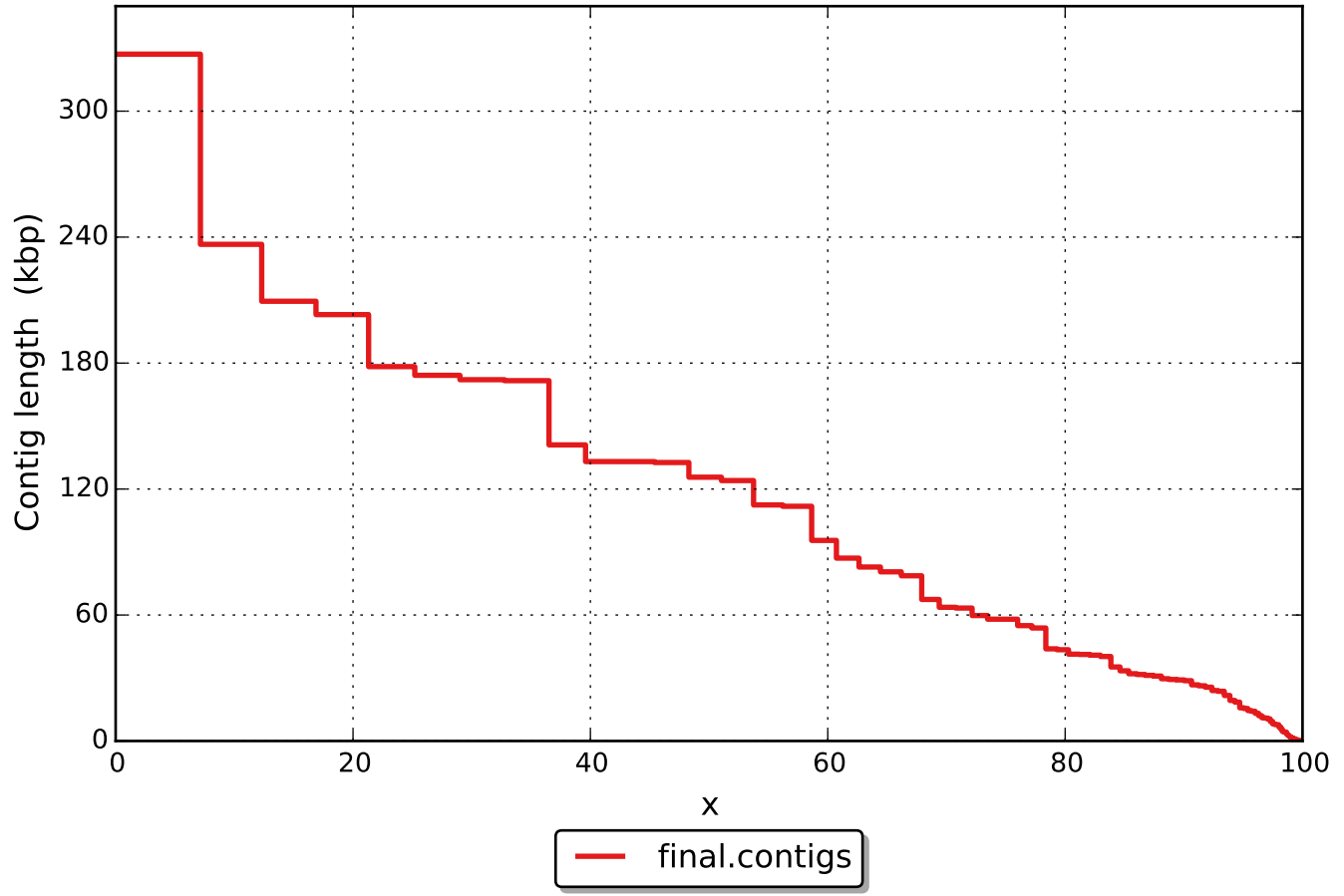




Cumulative length (aligned contigs)



NAx



# NGAx

