

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	142
# contigs ( $\geq 1000$ bp)	85
# contigs ( $\geq 5000$ bp)	60
# contigs ( $\geq 10000$ bp)	55
# contigs ( $\geq 25000$ bp)	46
# contigs ( $\geq 50000$ bp)	29
Total length ( $\geq 0$ bp)	4588517
Total length ( $\geq 1000$ bp)	4567676
Total length ( $\geq 5000$ bp)	4510094
Total length ( $\geq 10000$ bp)	4473317
Total length ( $\geq 25000$ bp)	4329836
Total length ( $\geq 50000$ bp)	3760478
# contigs	95
Largest contig	327235
Total length	4574732
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	132728
NG50	132728
N75	63760
NG75	61429
L50	12
LG50	12
L75	24
LG75	25
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	4
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.468
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.01
# indels per 100 kbp	0.04
Largest alignment	327235
NA50	132728
NGA50	132728
NA75	63760
NGA75	61429
LA50	12
LGA50	12
LA75	24
LGA75	25

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

	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	4
# mismatches	46
# indels	2
# short indels	2
# long indels	0
Indels length	2

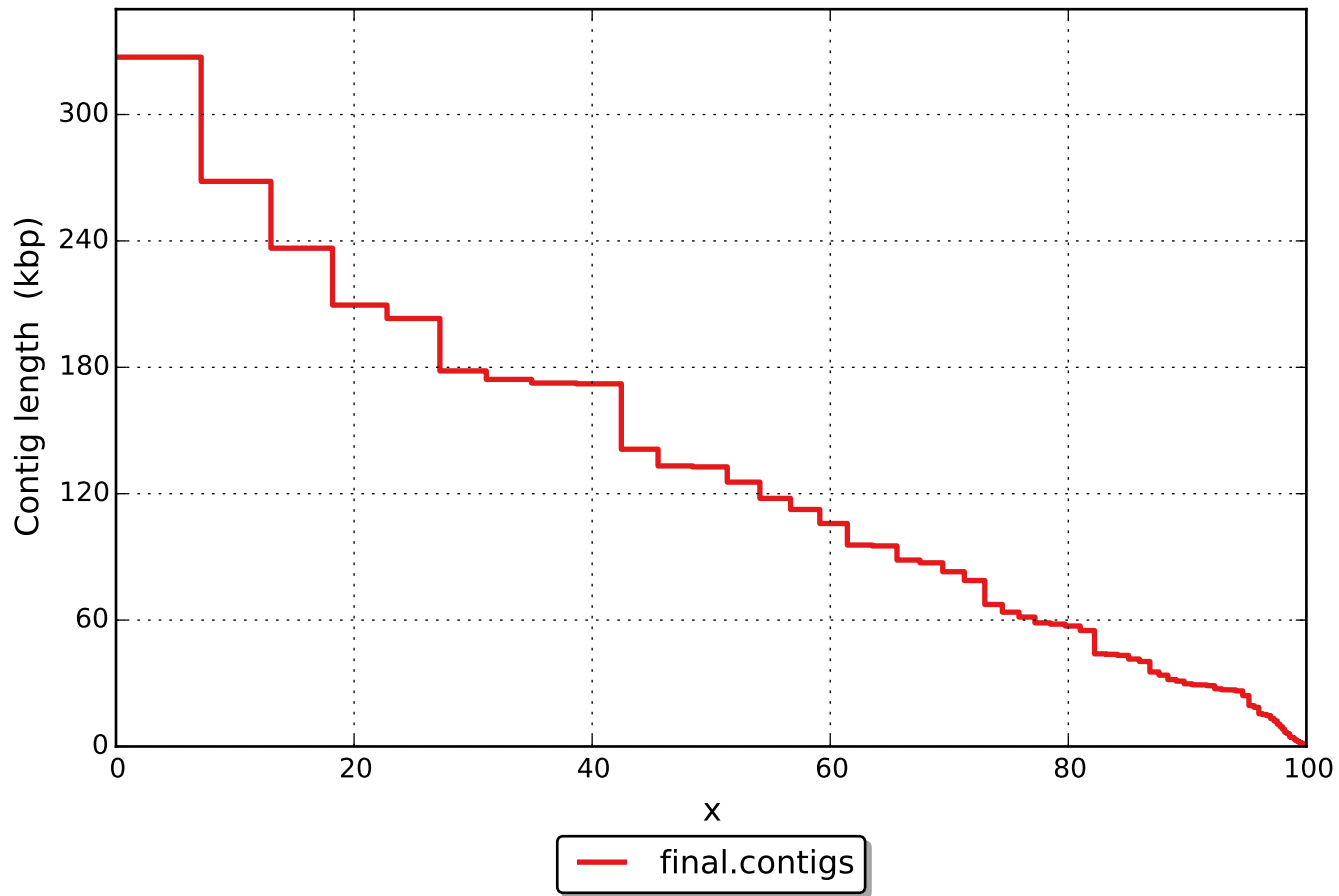
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

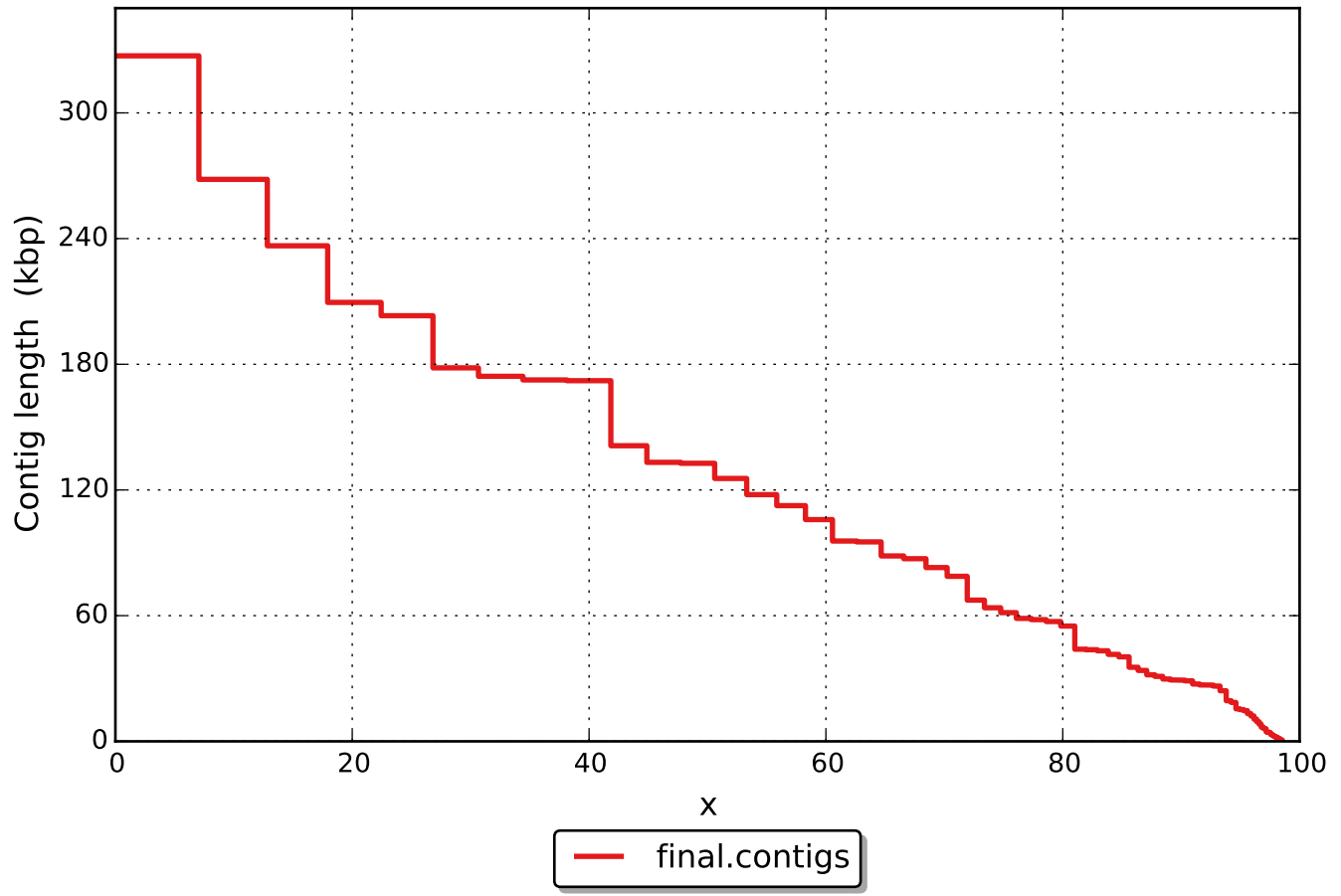
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

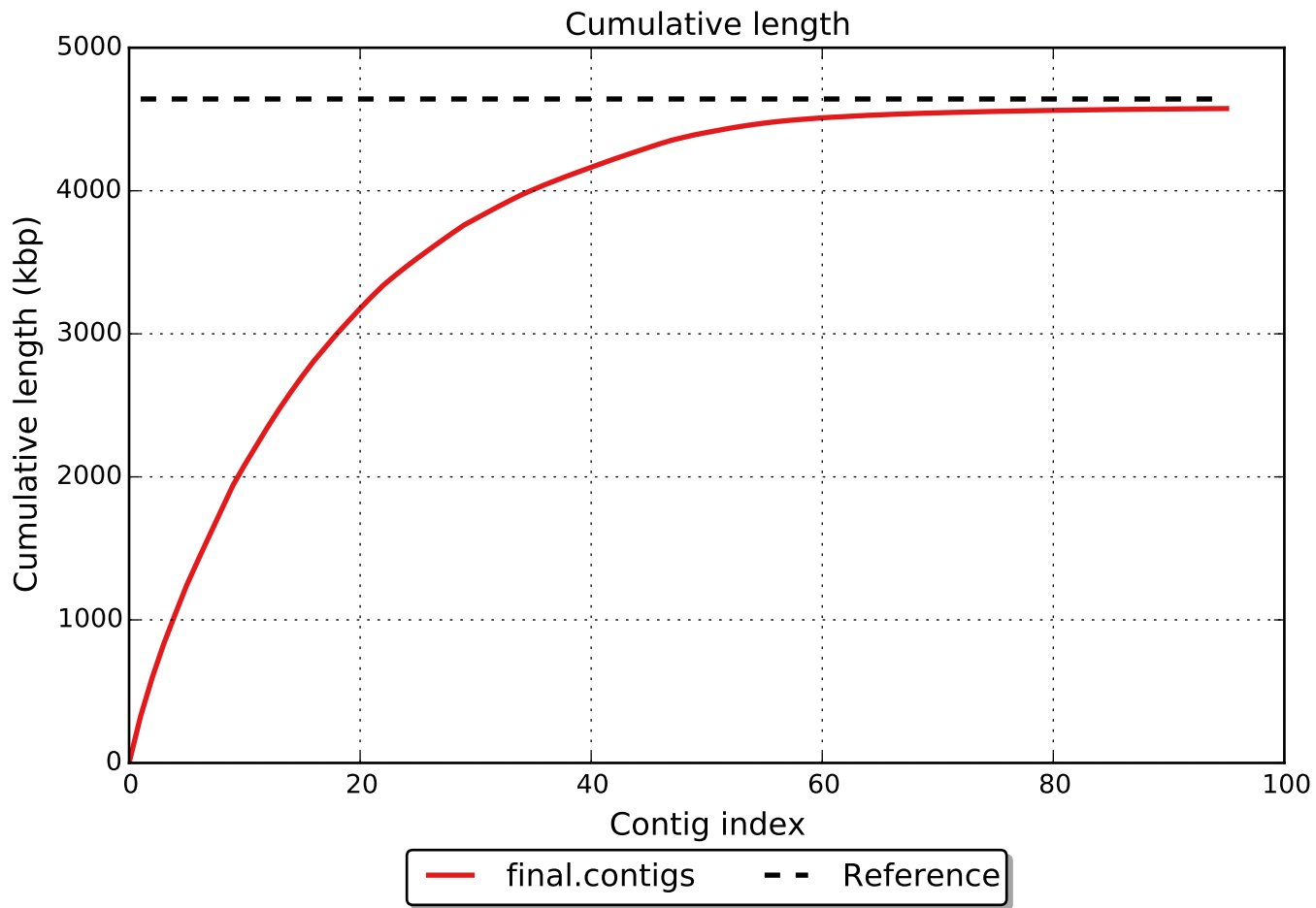
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

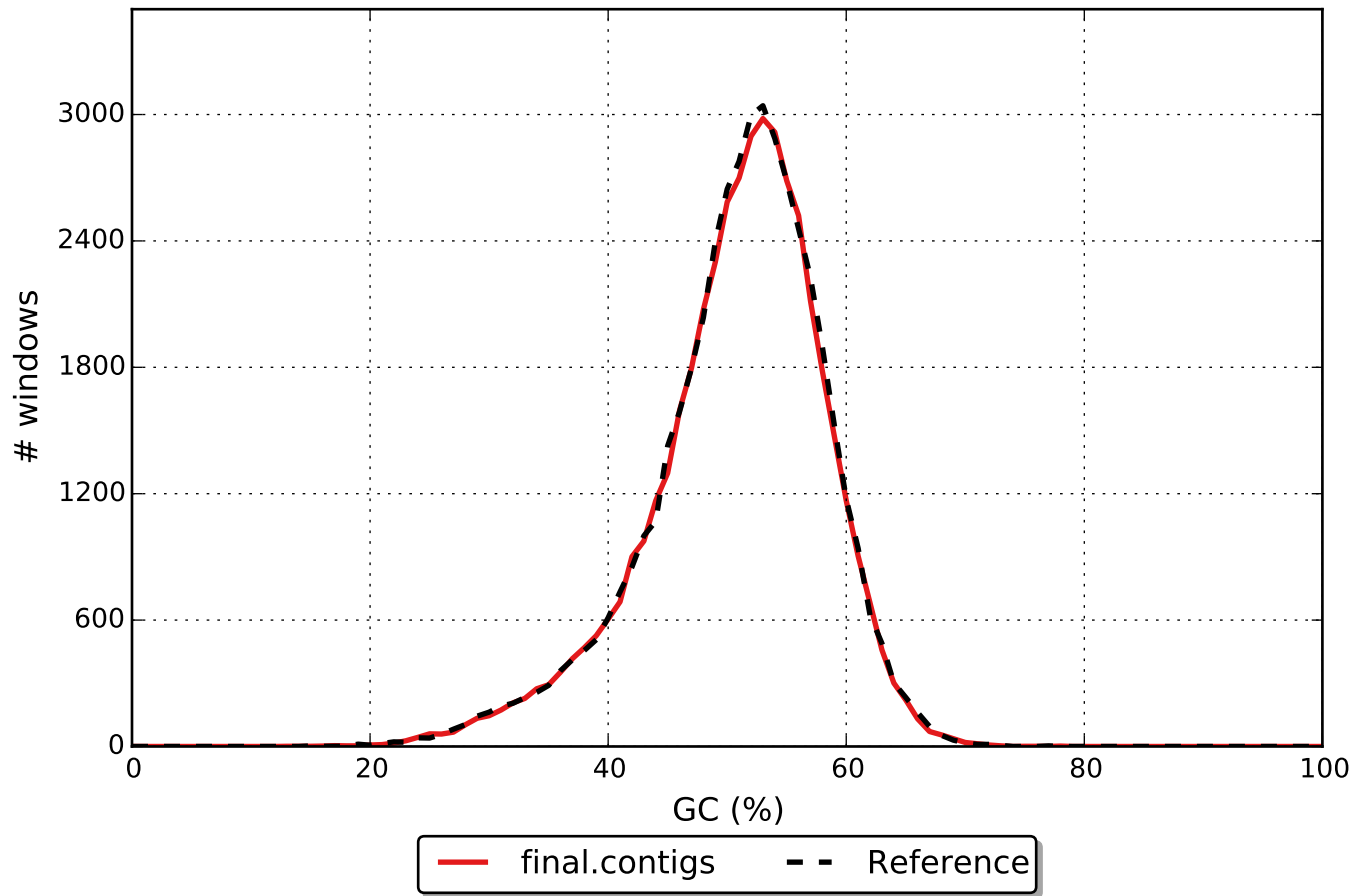


NGx





GC content

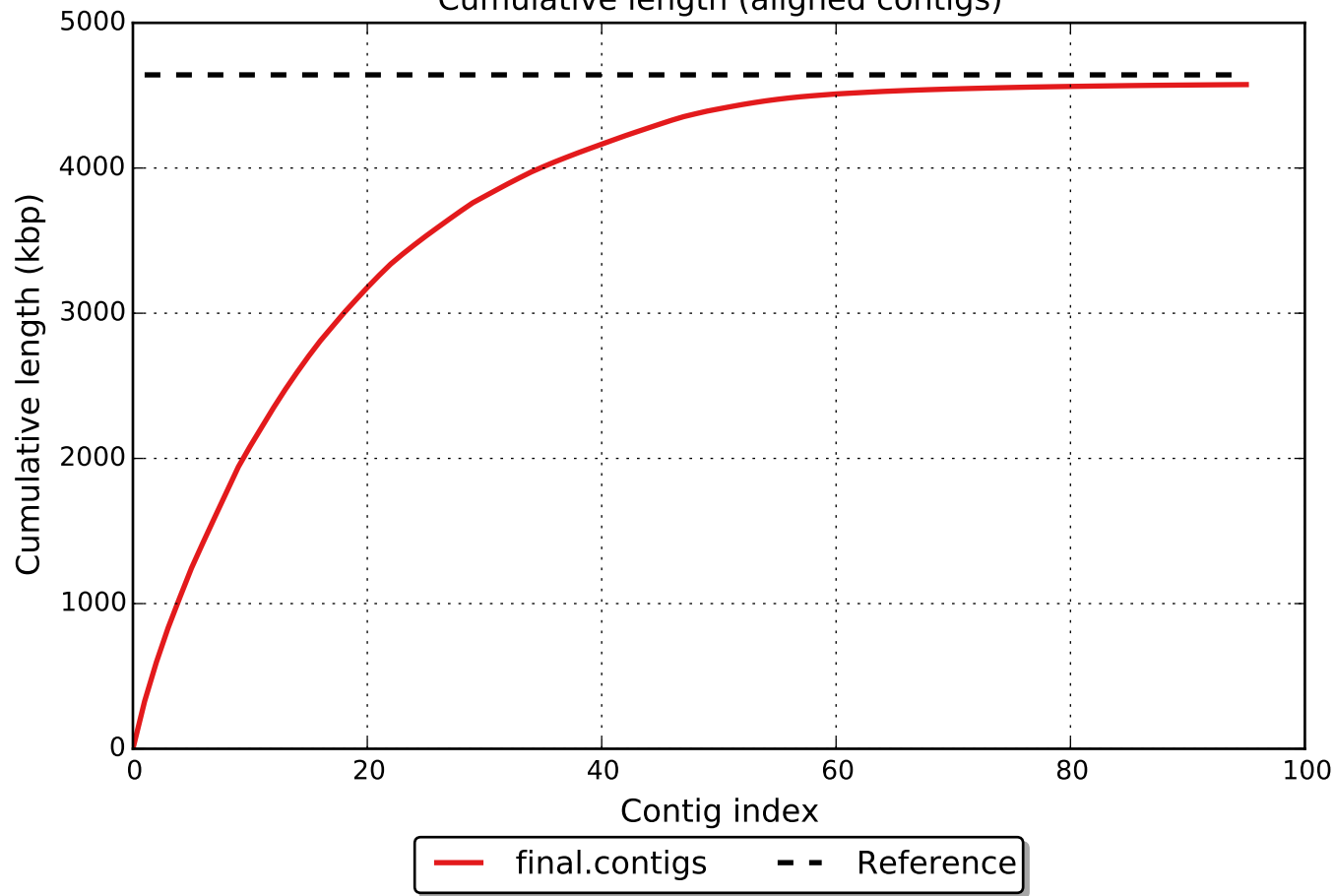


# Misassemblies

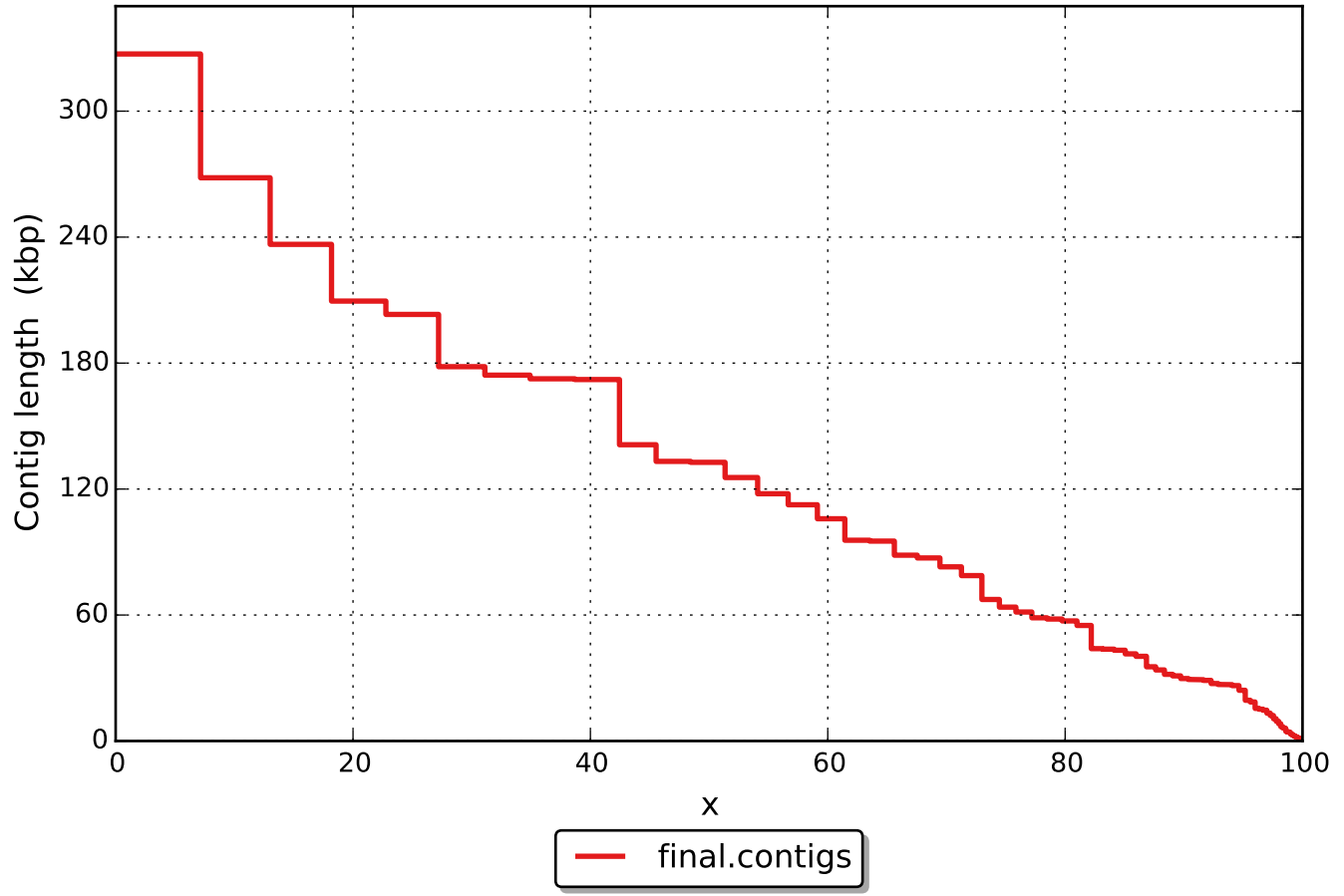




Cumulative length (aligned contigs)



NAx



# NGAx

