

Report

	final.contigs
# contigs (>= 1000 bp)	98
# contigs (>= 5000 bp)	74
# contigs (>= 10000 bp)	67
# contigs (>= 25000 bp)	51
# contigs (>= 50000 bp)	31
Total length (>= 1000 bp)	4551580
Total length (>= 5000 bp)	4499796
Total length (>= 10000 bp)	4448404
Total length (>= 25000 bp)	4197218
Total length (>= 50000 bp)	3492331
# contigs	118
Largest contig	327151
Total length	4564749
Reference length	4641652
GC (℥)	50.75
Reference GC (℥)	50.79
N50	105683
NG50	95537
N75	53827
NG75	53804
L50	14
LG50	15
L75	30
LG75	31
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	8
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (℥)	98.275
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.51
# indels per 100 kbp	0.04
Largest alignment	327151
NA50	105683
NGA50	95537
NA75	53827
NGA75	53804
LA50	14
LGA50	15
LA75	30
LGA75	31

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	8
# mismatches	69
# indels	2
# short indels	2
# long indels	0
Indels length	3

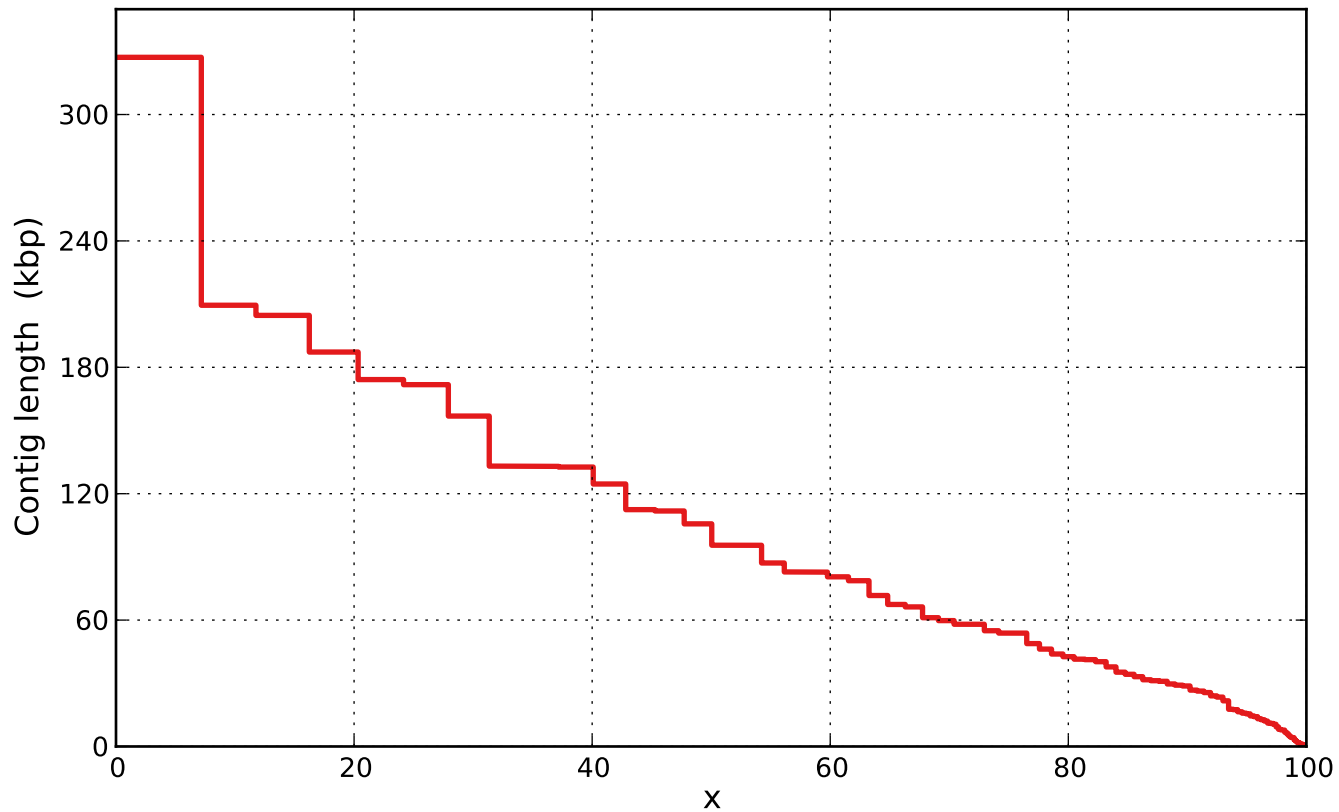
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

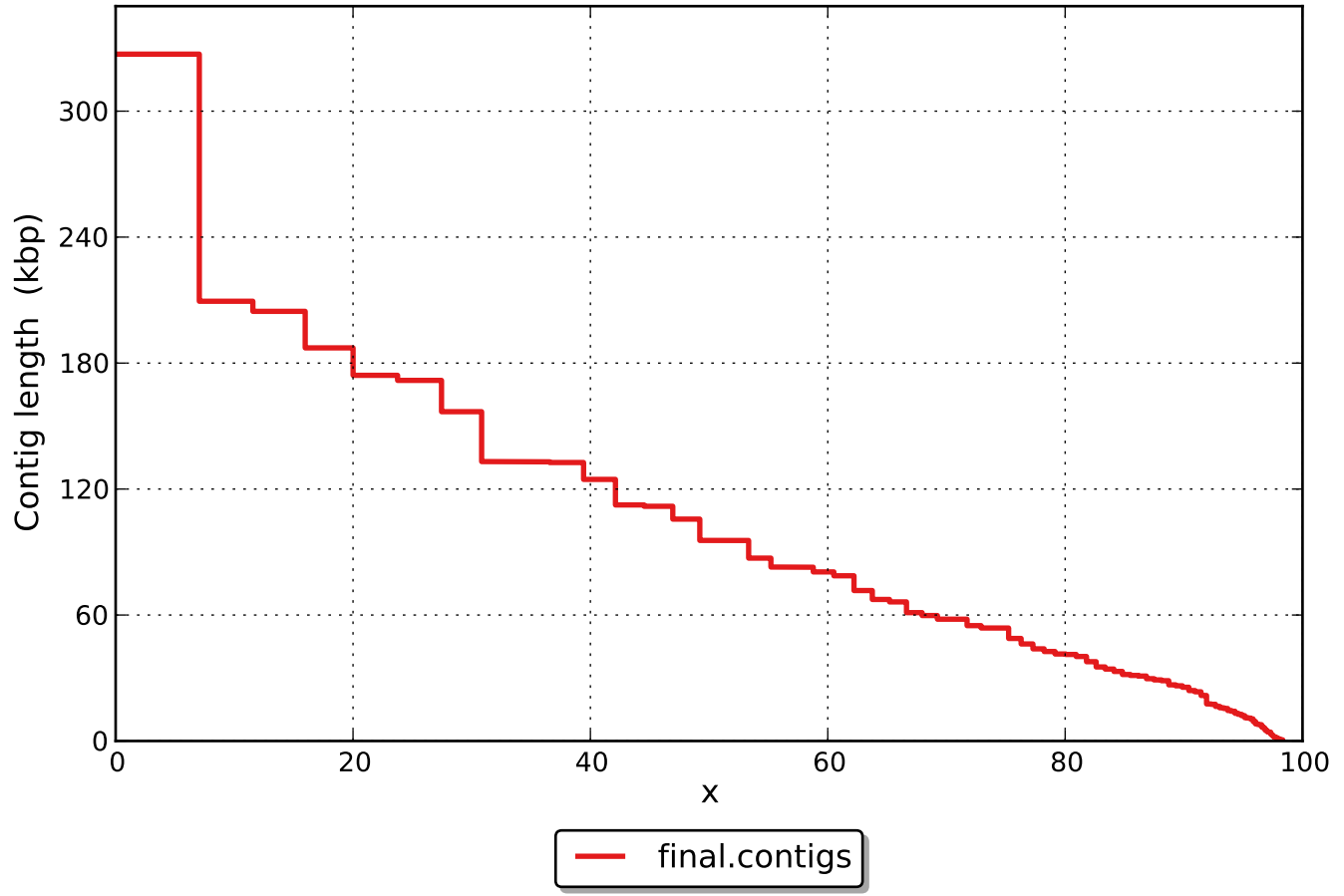
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

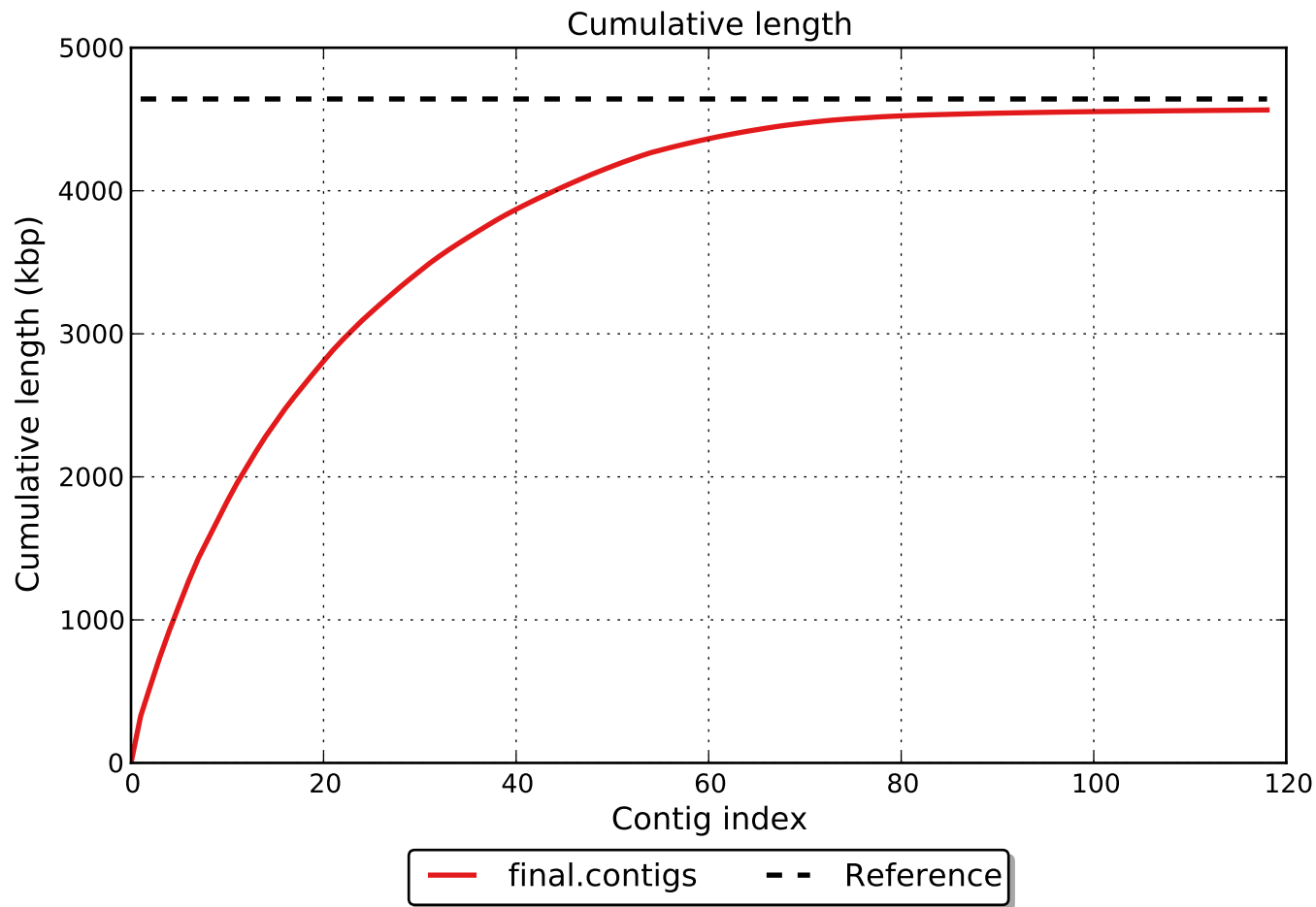
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

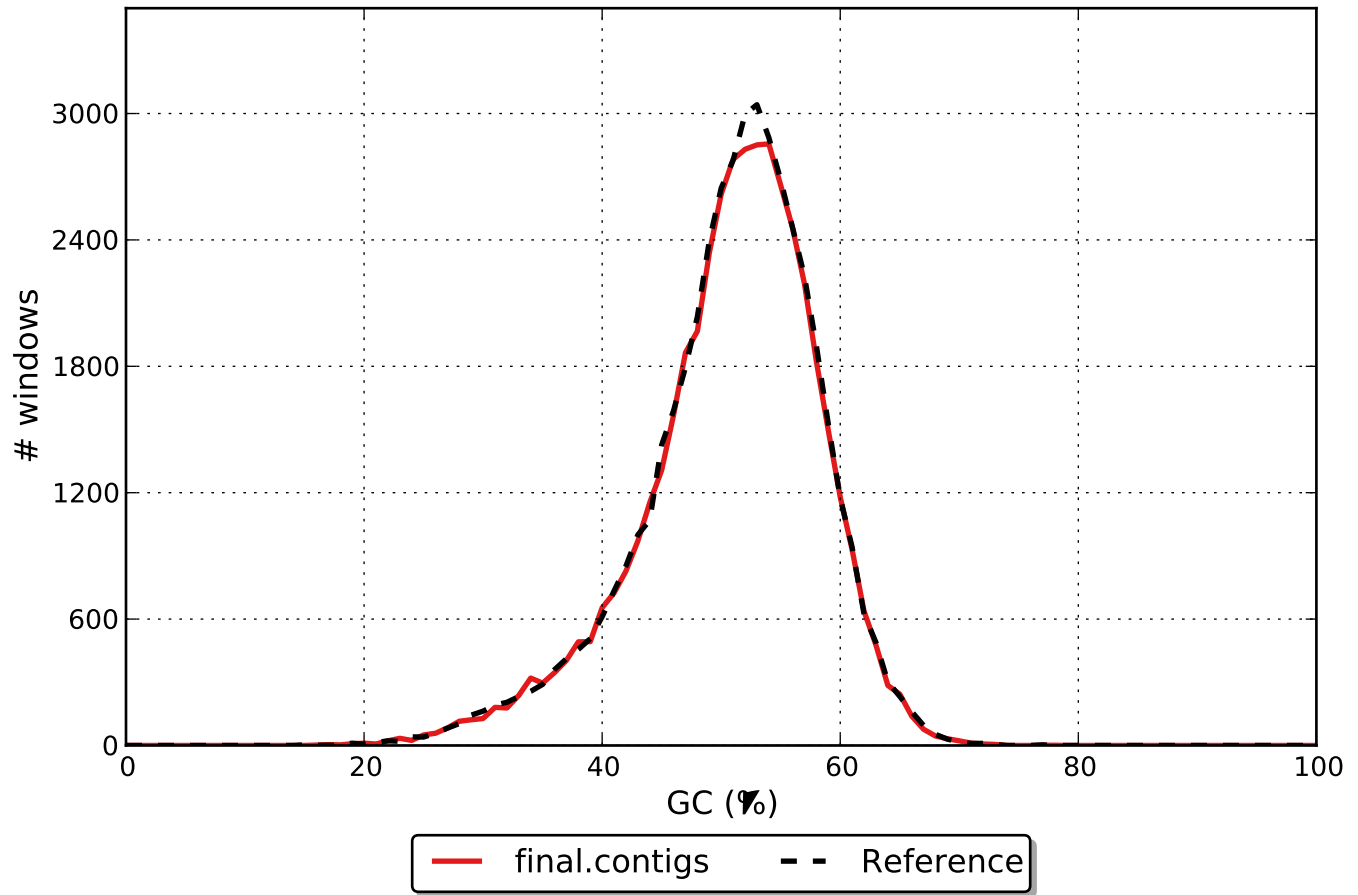


NGx





GC content

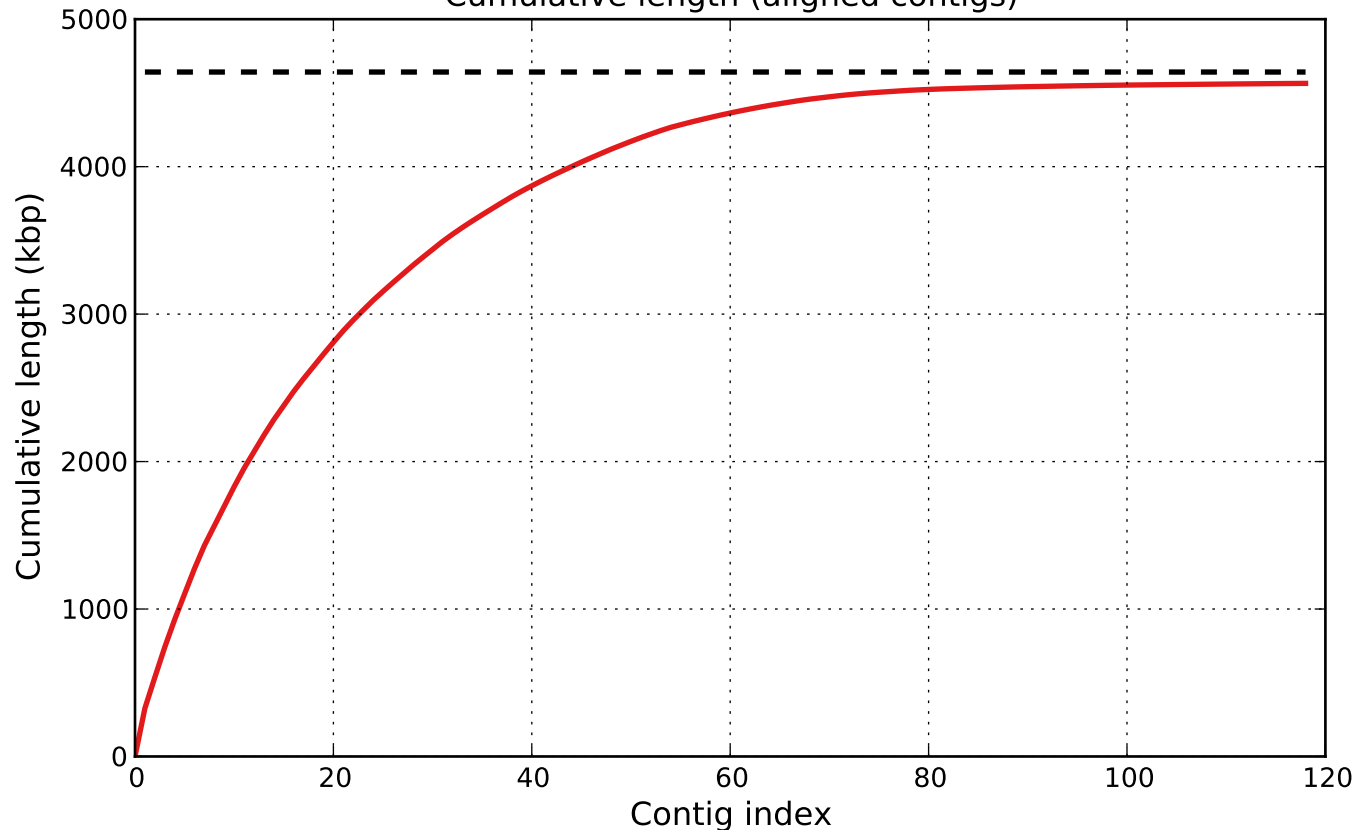


# Misassemblies



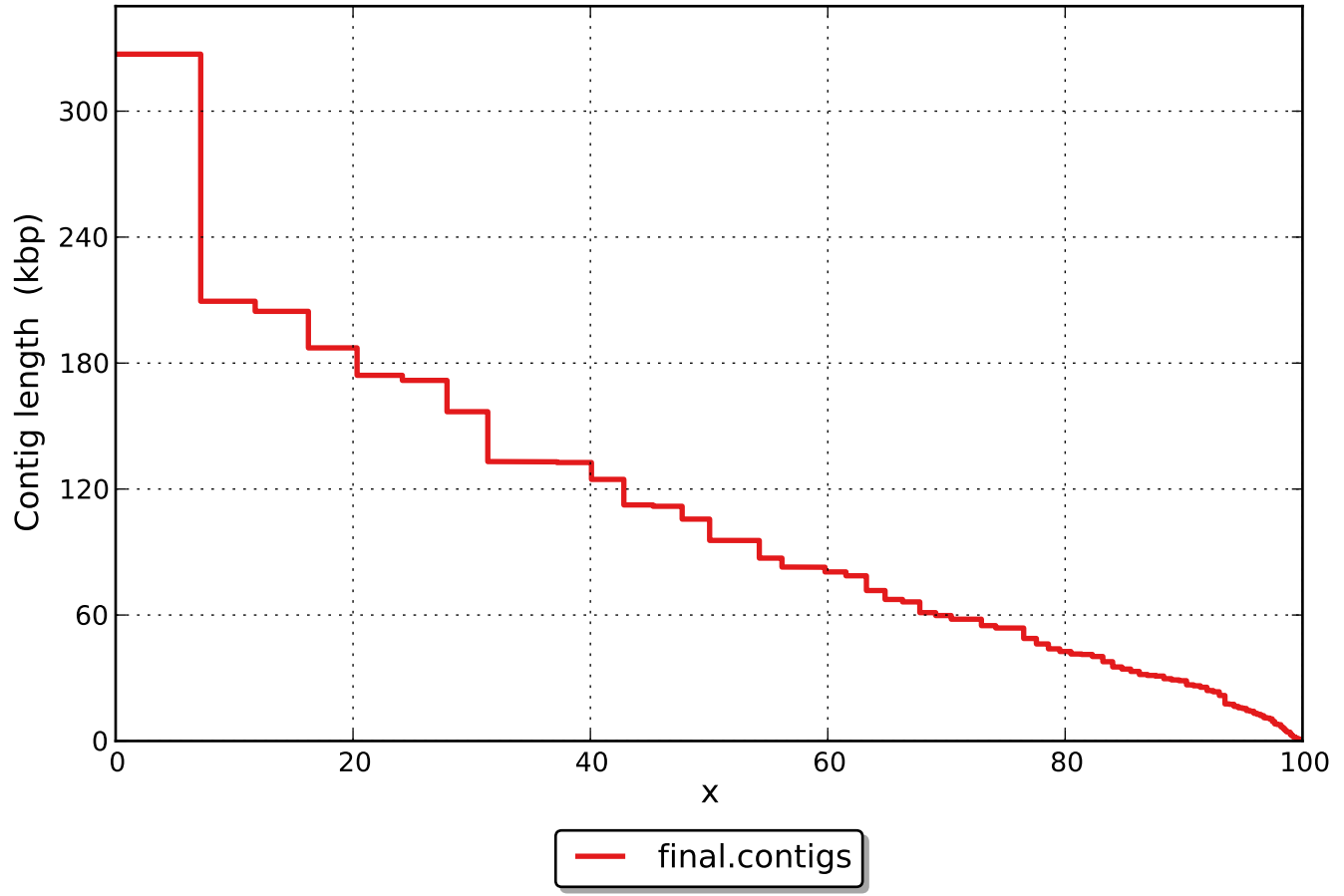


Cumulative length (aligned contigs)



— final.contigs      - - Reference

NAx



# NGAx

