

## Report

	final.contigs
# contigs (>= 0 bp)	255
# contigs (>= 1000 bp)	78
# contigs (>= 5000 bp)	61
# contigs (>= 10000 bp)	56
# contigs (>= 25000 bp)	47
# contigs (>= 50000 bp)	29
Total length (>= 0 bp)	4637221
Total length (>= 1000 bp)	4564268
Total length (>= 5000 bp)	4514045
Total length (>= 10000 bp)	4474516
Total length (>= 25000 bp)	4334535
Total length (>= 50000 bp)	3708515
# contigs	112
Largest contig	327201
Total length	4586630
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	125650
NG50	125650
N75	67461
NG75	58357
L50	13
LG50	13
L75	25
LG75	26
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	3663
# local misassemblies	9
# unaligned contigs	1 + 0 part
Unaligned length	615
Genome fraction (%)	98.604
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	9.98
# indels per 100 kbp	0.15
Largest alignment	327201
NA50	125650
NGA50	125650
NA75	67461
NGA75	58323
LA50	13
LGA50	13
LA75	25
LGA75	26

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	2
# relocations	2
# translocations	0
# inversions	0
# misassembled contigs	2
Misassembled contigs length	3663
# local misassemblies	9
# mismatches	457
# indels	7
# short indels	7
# long indels	0
Indels length	9

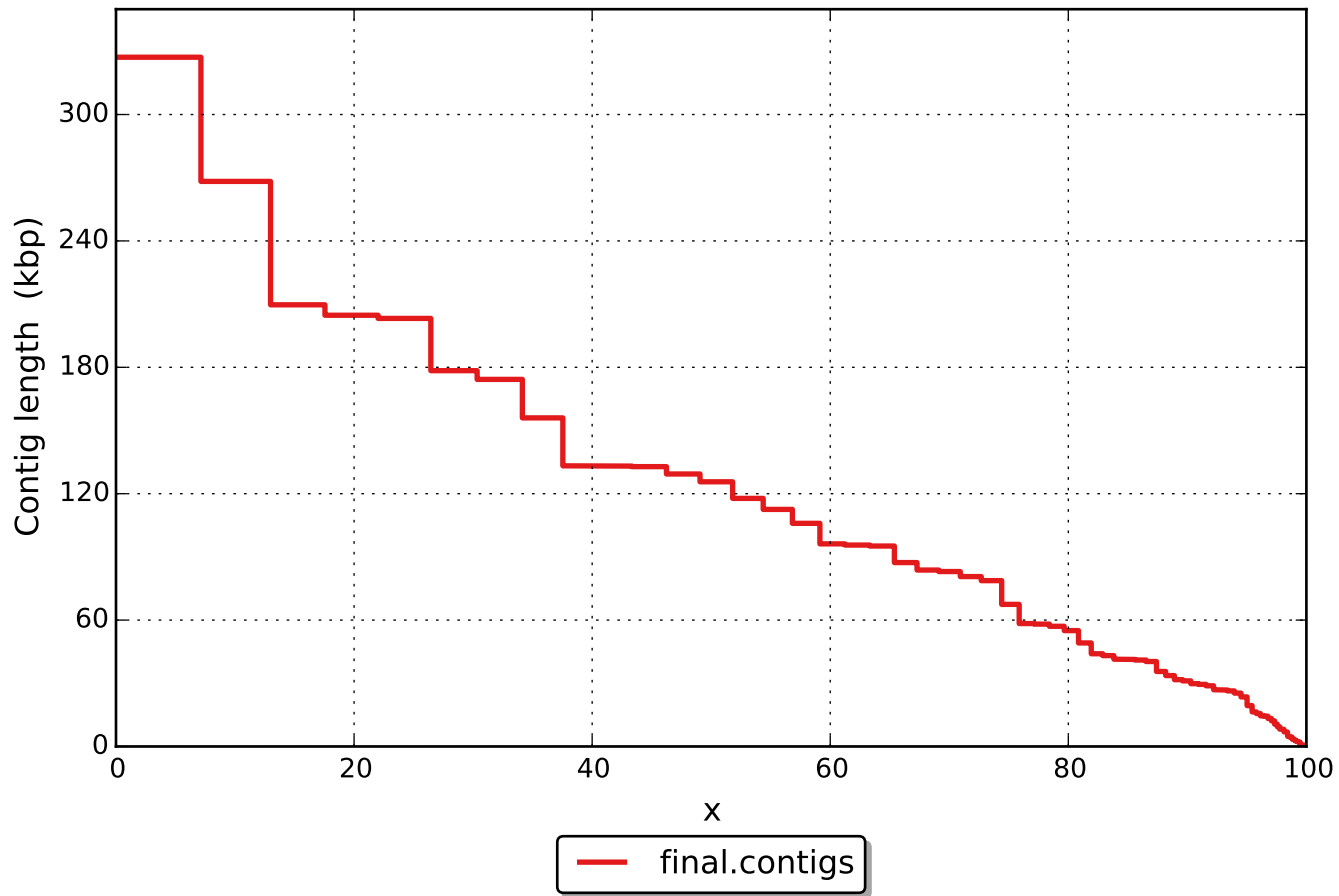
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

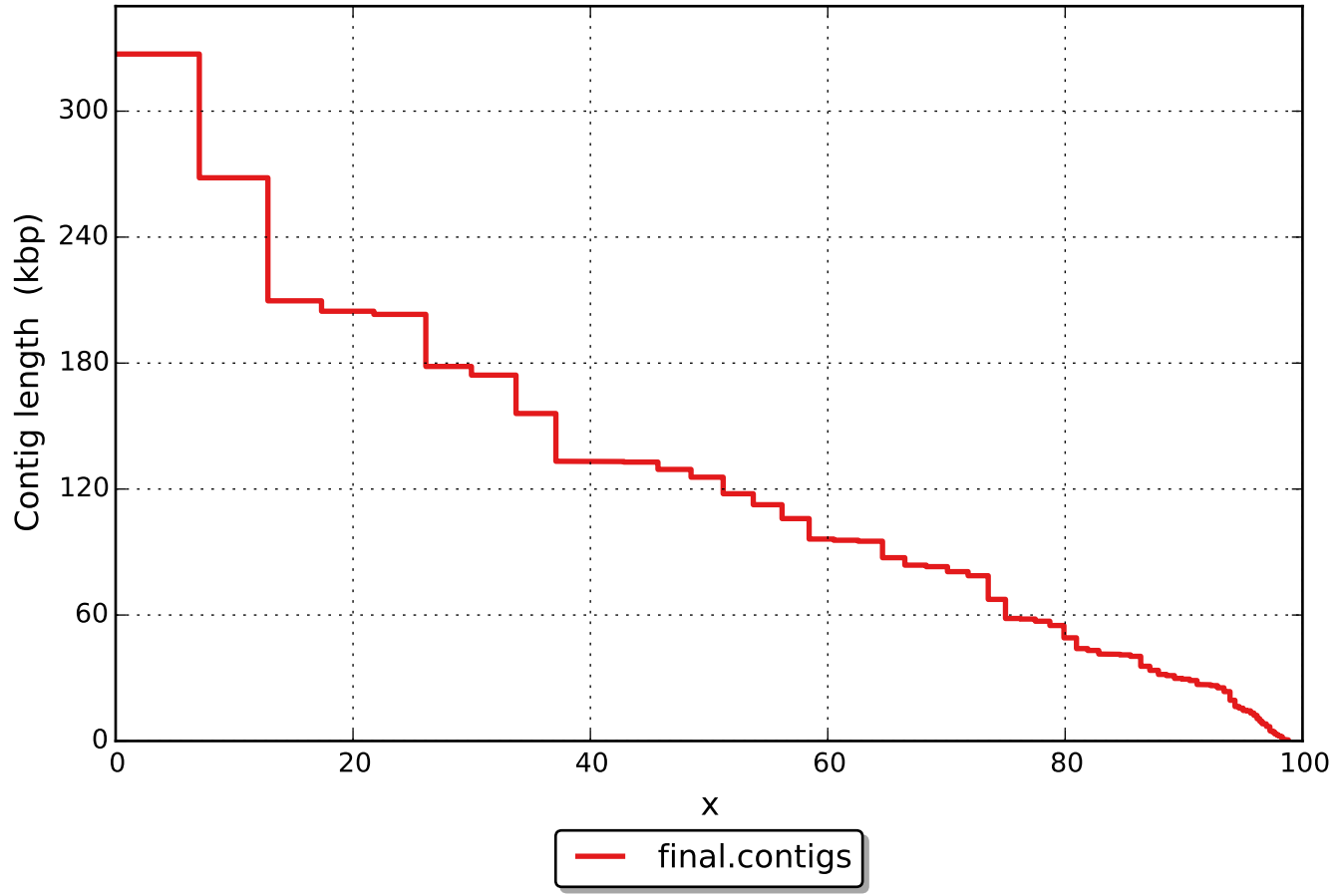
	final.contigs
# fully unaligned contigs	1
Fully unaligned length	615
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

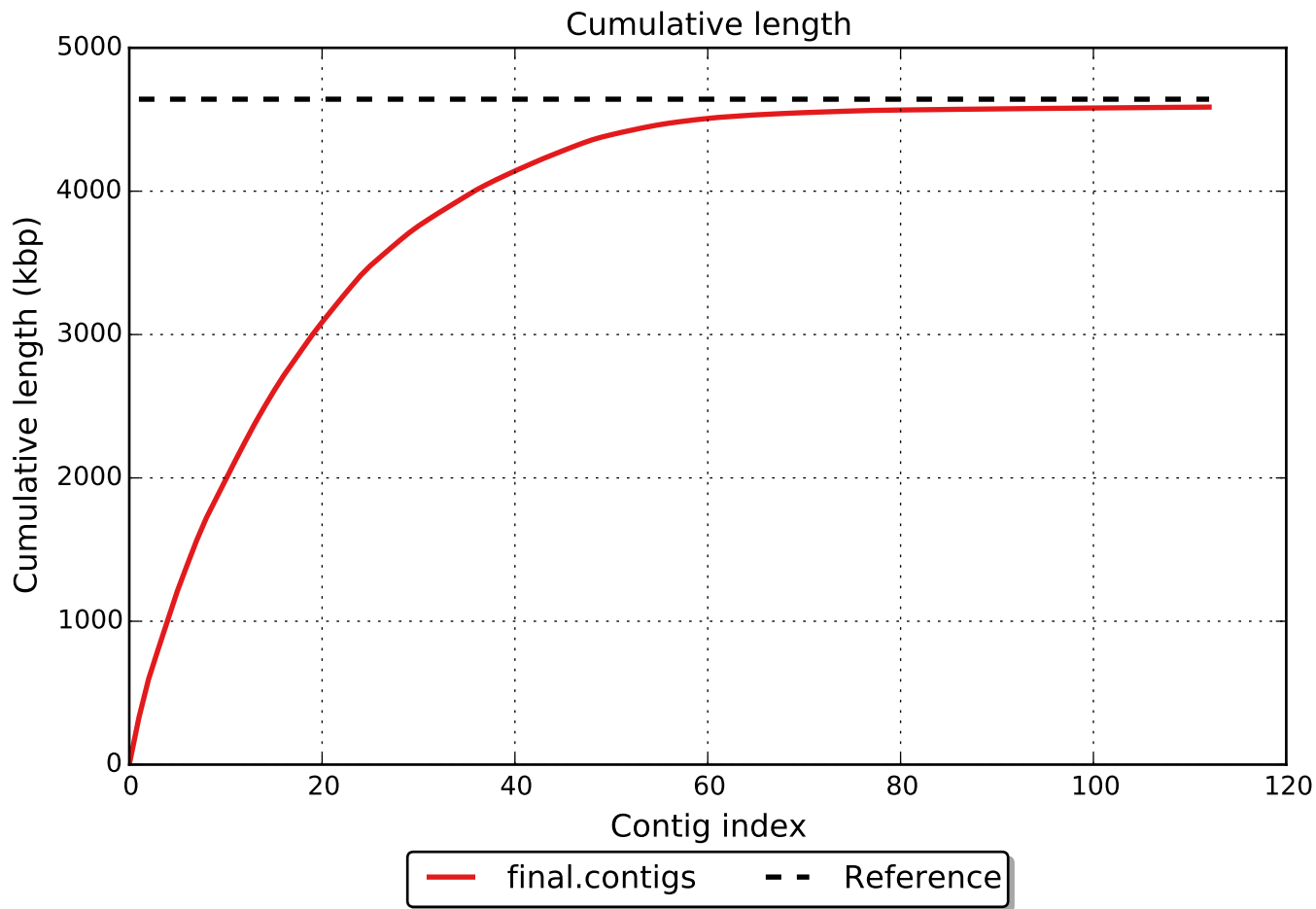
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

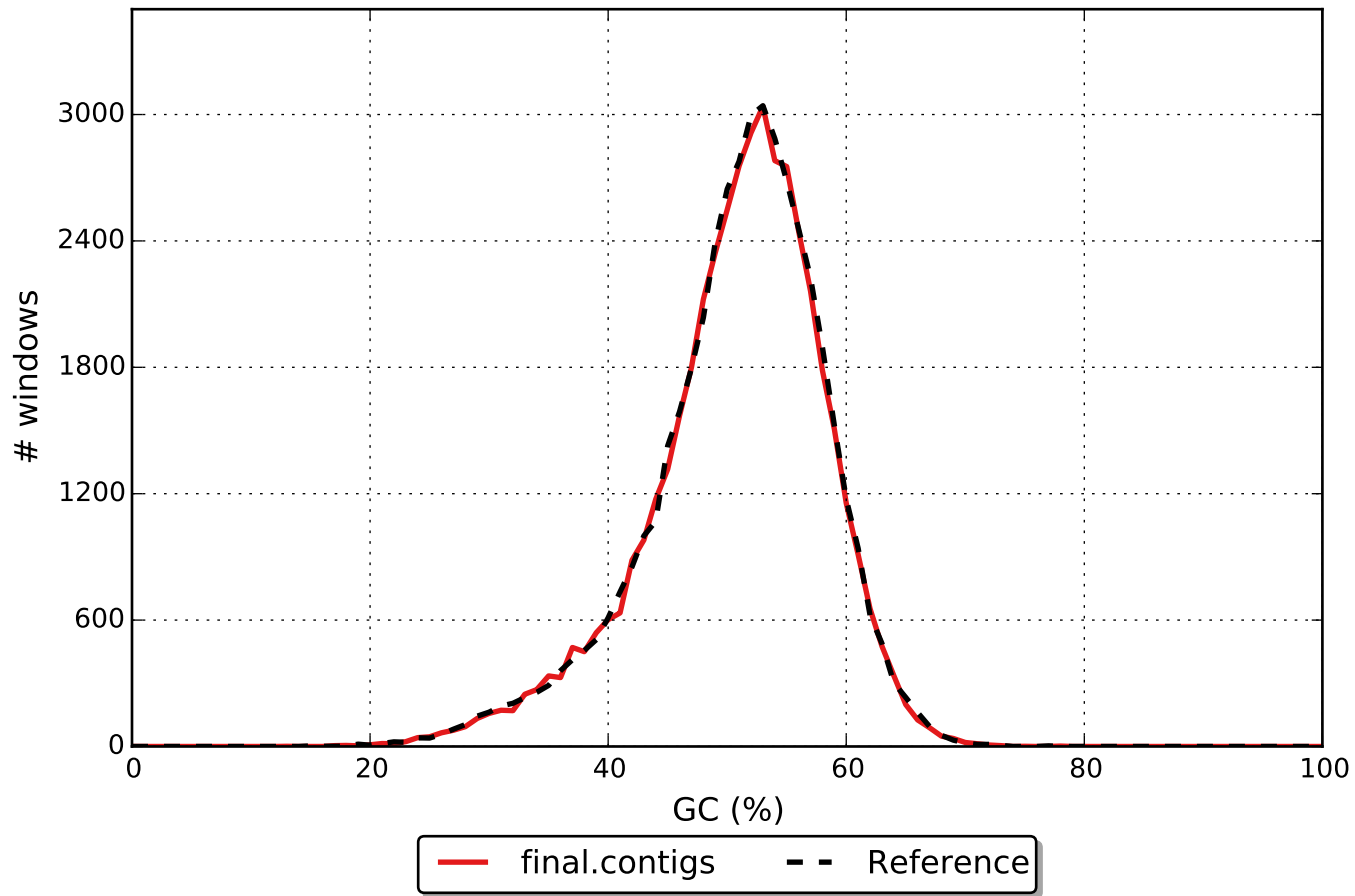


NGx





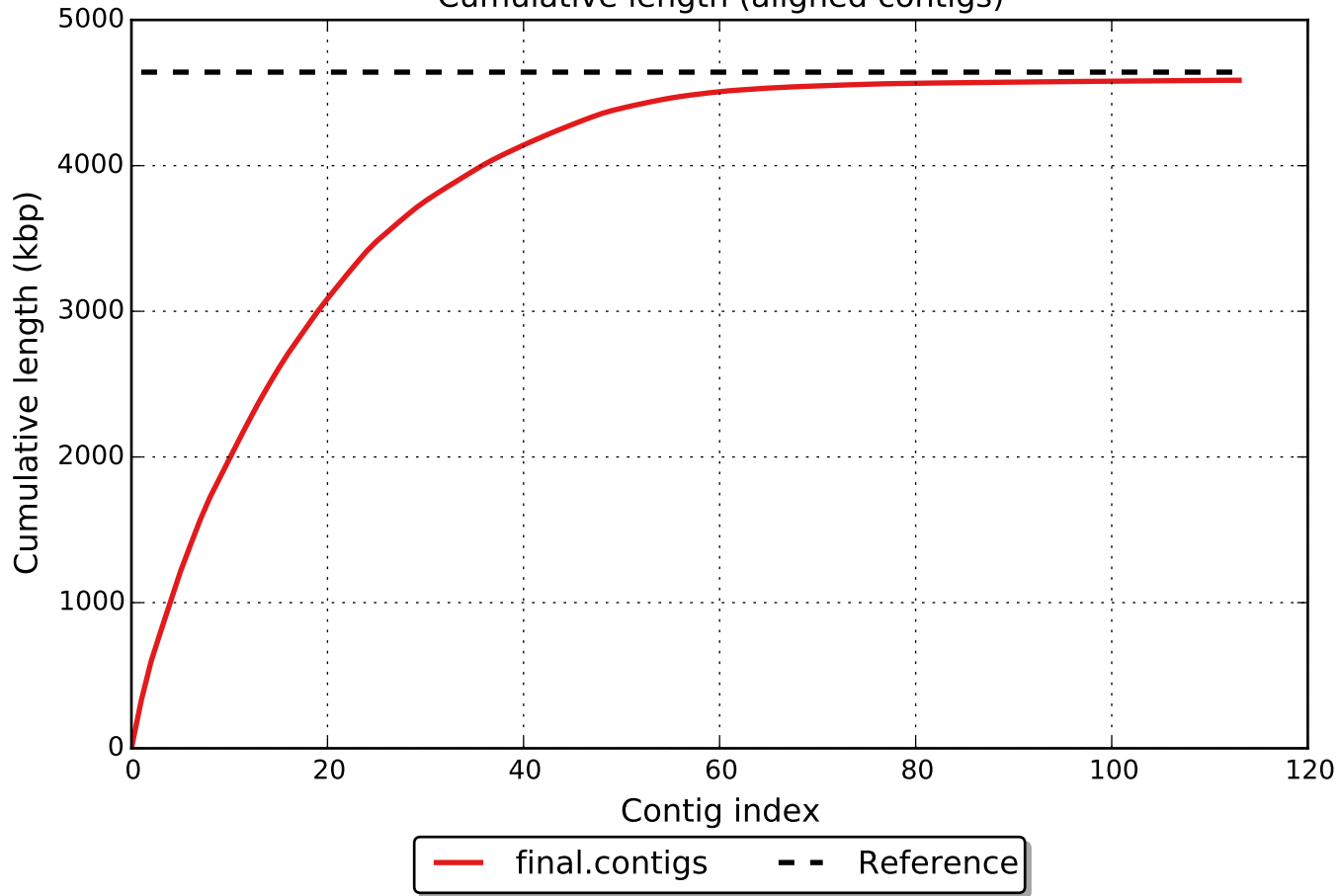
GC content



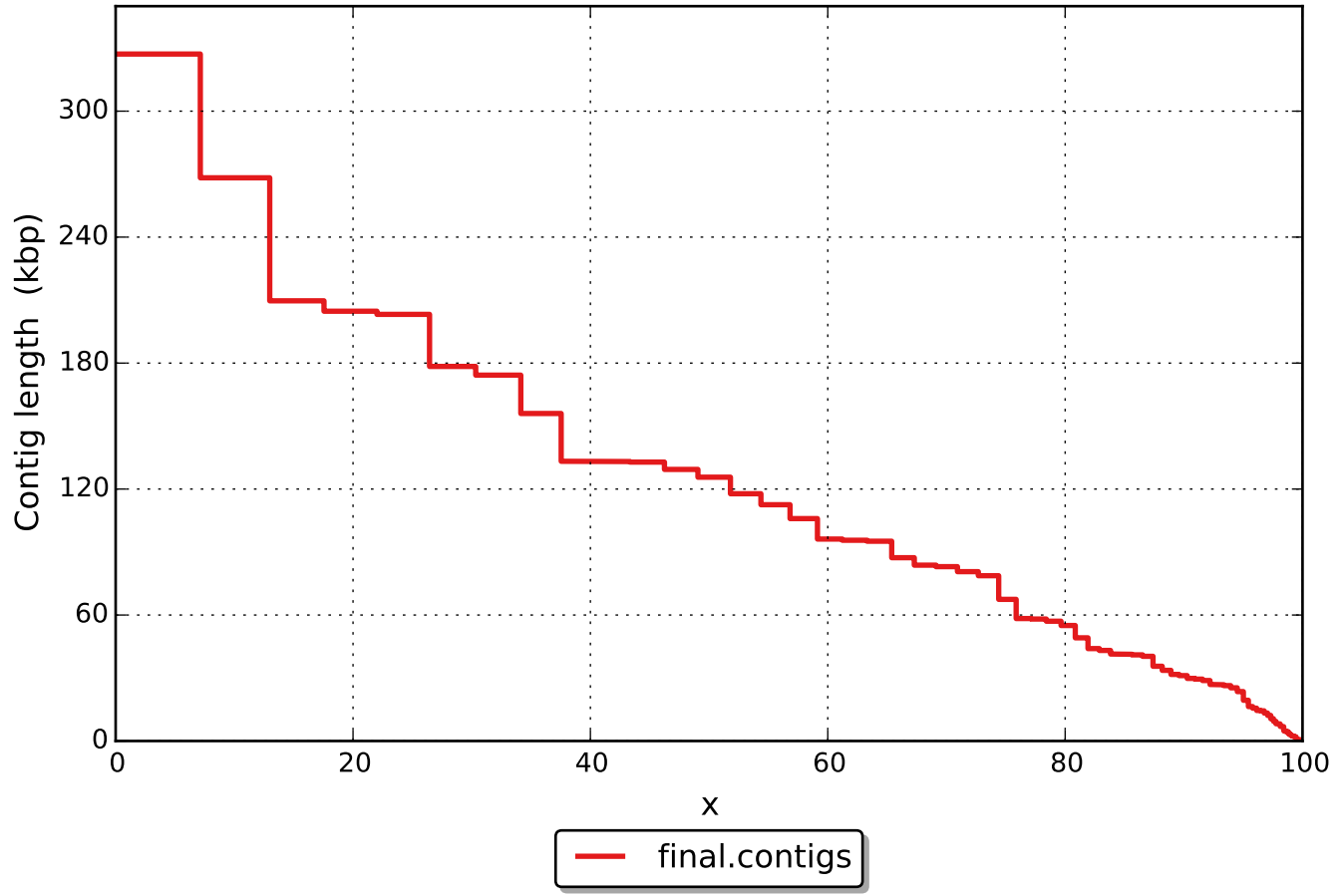




Cumulative length (aligned contigs)



NAx



NGAx

