

## Report

	final.contigs
# contigs (>= 0 bp)	390
# contigs (>= 1000 bp)	87
# contigs (>= 5000 bp)	66
# contigs (>= 10000 bp)	59
# contigs (>= 25000 bp)	47
# contigs (>= 50000 bp)	31
Total length (>= 0 bp)	4688494
Total length (>= 1000 bp)	4564439
Total length (>= 5000 bp)	4514581
Total length (>= 10000 bp)	4461457
Total length (>= 25000 bp)	4271965
Total length (>= 50000 bp)	3720481
# contigs	138
Largest contig	327242
Total length	4596412
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	117784
NG50	117784
N75	61451
NG75	61451
L50	14
LG50	14
L75	27
LG75	27
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	22973
# local misassemblies	8
# unaligned contigs	0 + 2 part
Unaligned length	369
Genome fraction (%)	98.631
Duplication ratio	1.004
# N's per 100 kbp	0.00
# mismatches per 100 kbp	11.16
# indels per 100 kbp	0.59
Largest alignment	327242
NA50	117784
NGA50	117784
NA75	61451
NGA75	61451
LA50	14
LGA50	14
LA75	27
LGA75	27

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	1
# relocations	1
# translocations	0
# inversions	0
# misassembled contigs	1
Misassembled contigs length	22973
# local misassemblies	8
# mismatches	511
# indels	27
# short indels	23
# long indels	4
Indels length	102

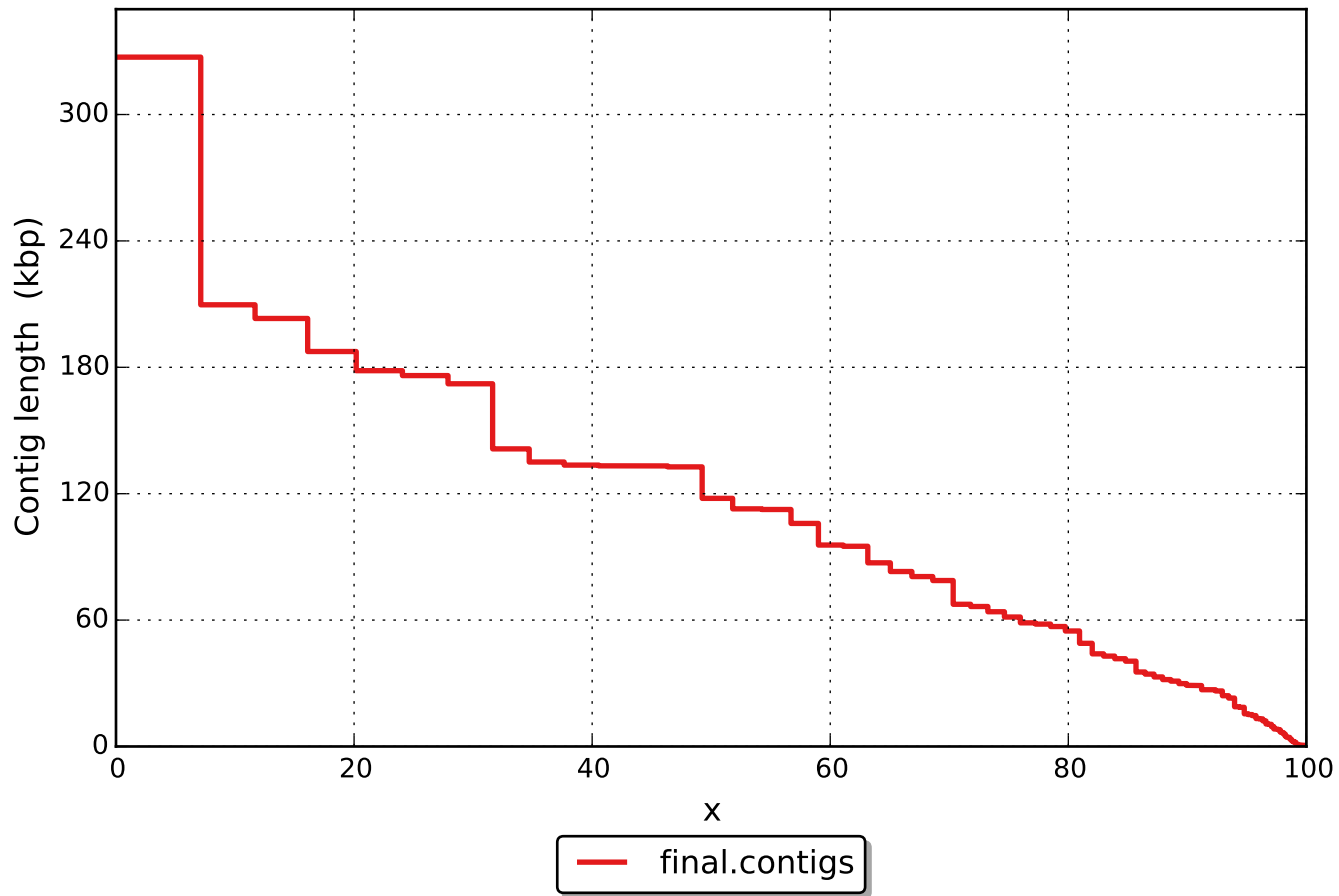
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

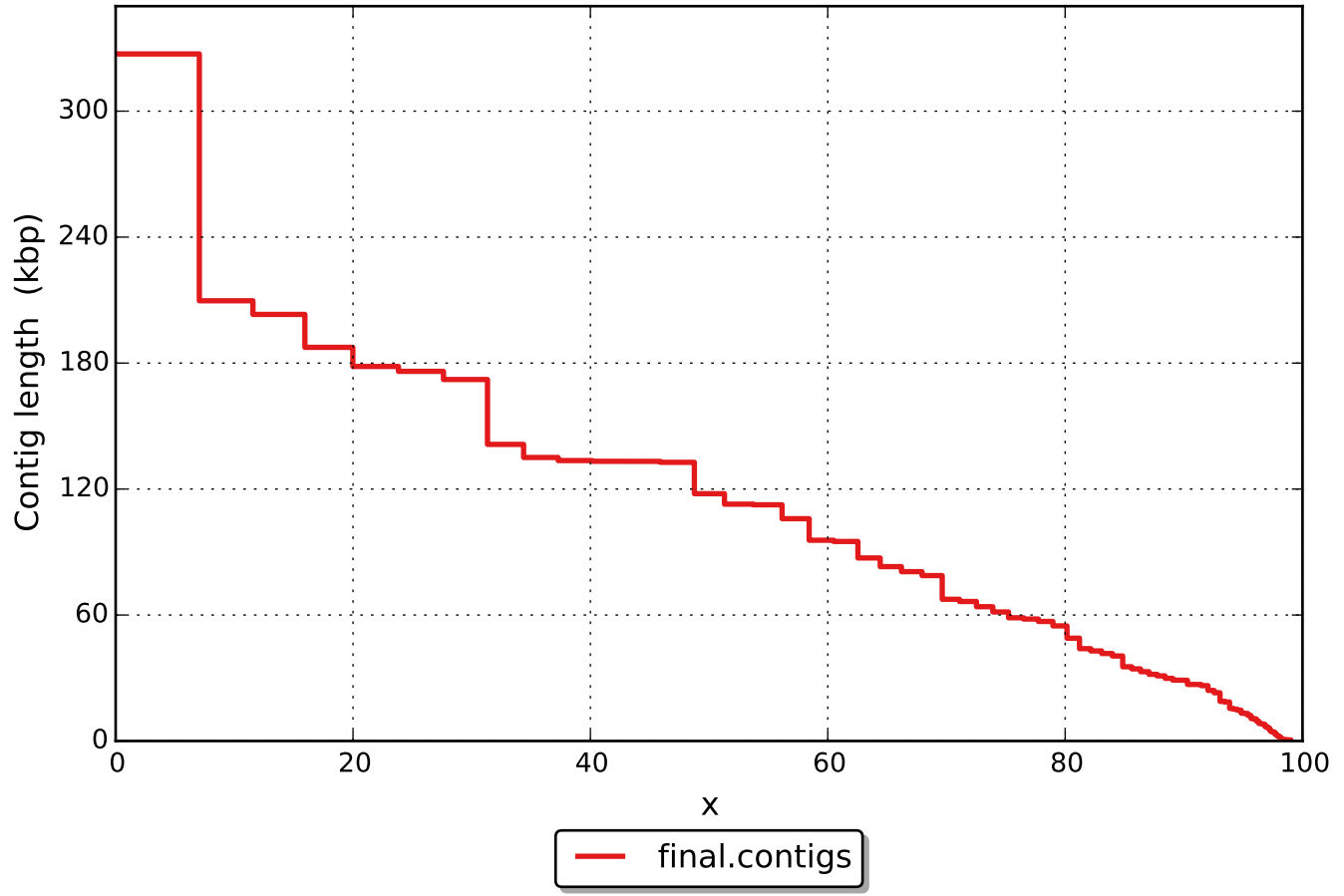
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	369
# N's	0

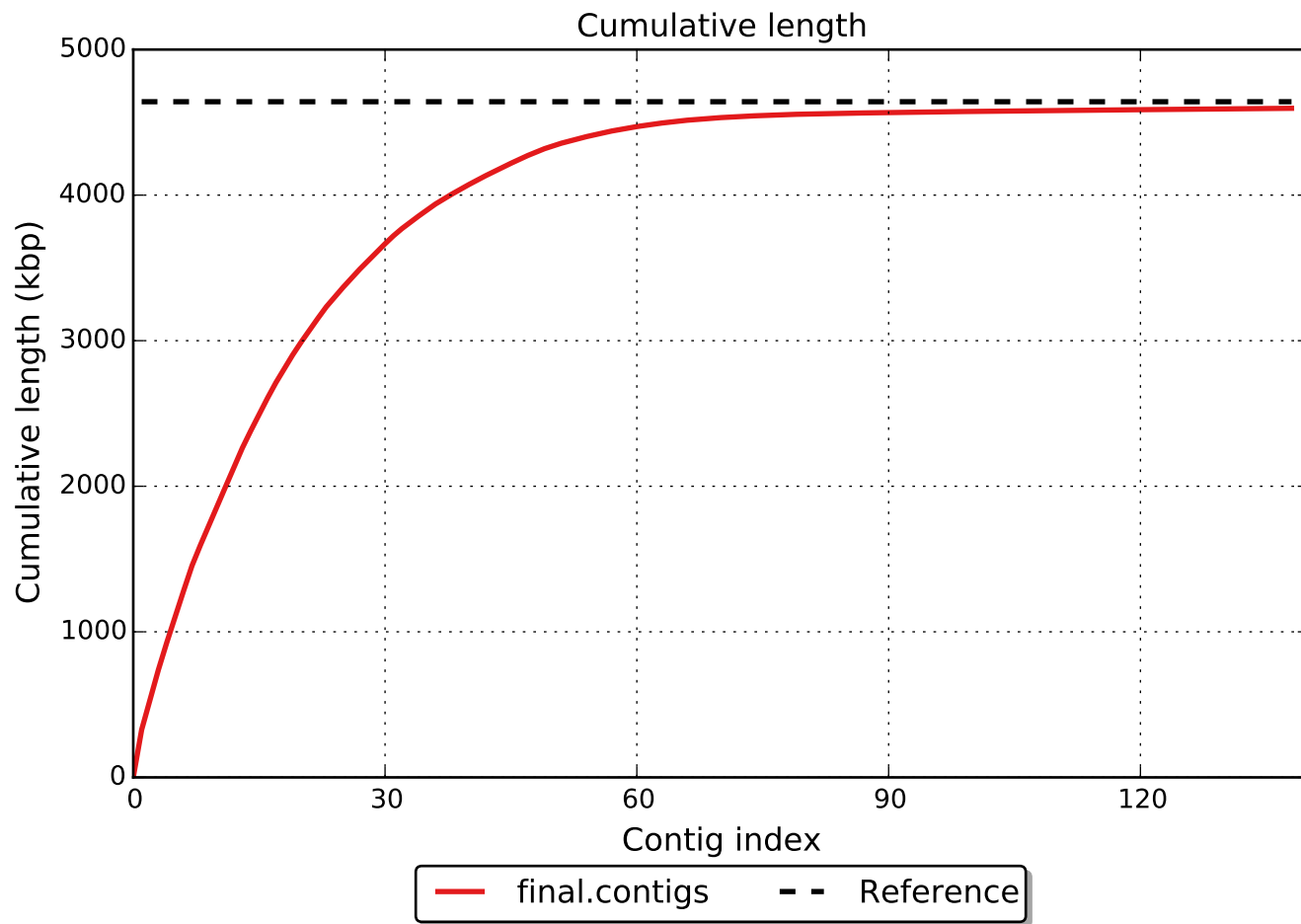
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

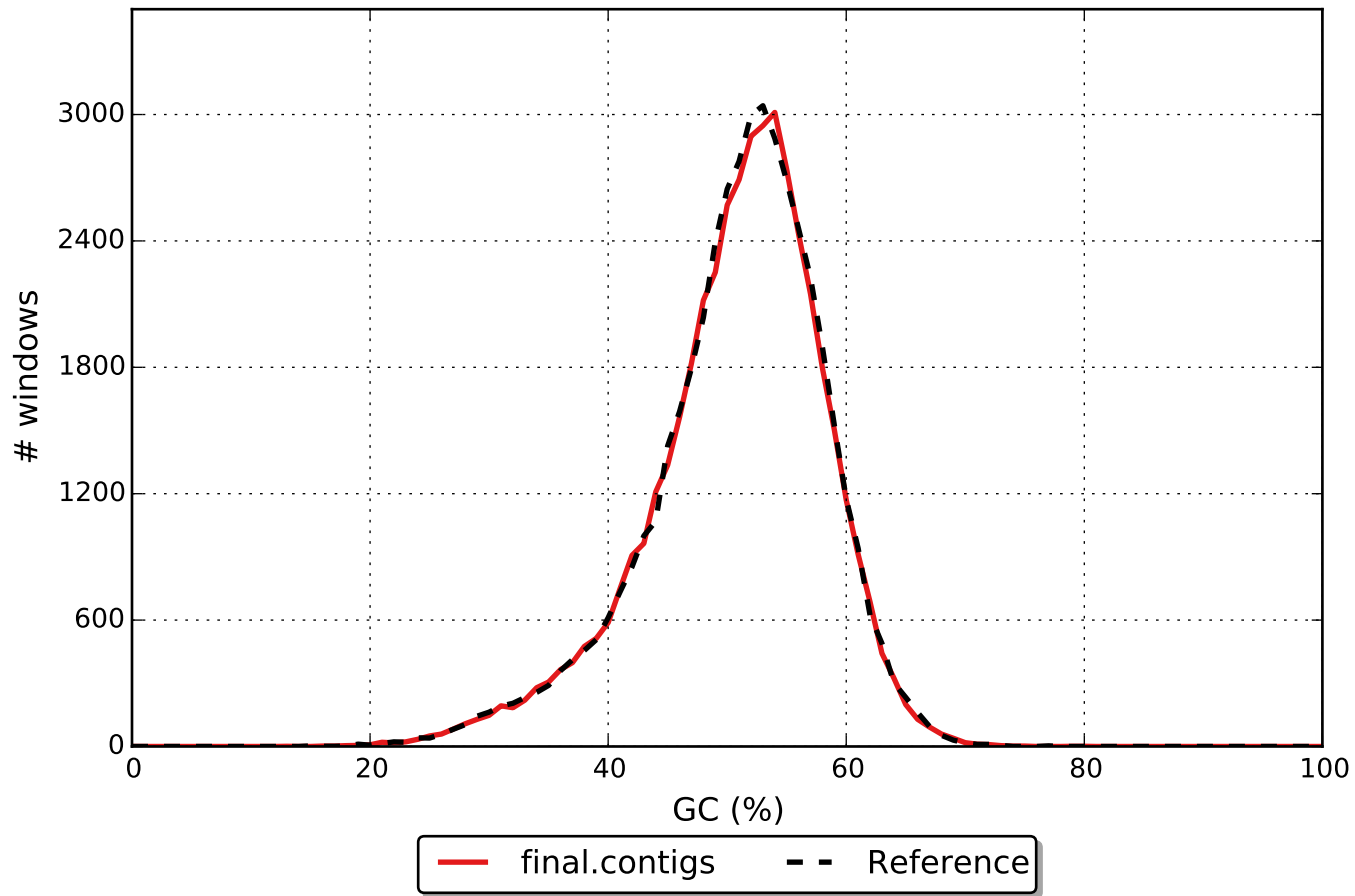


NGx





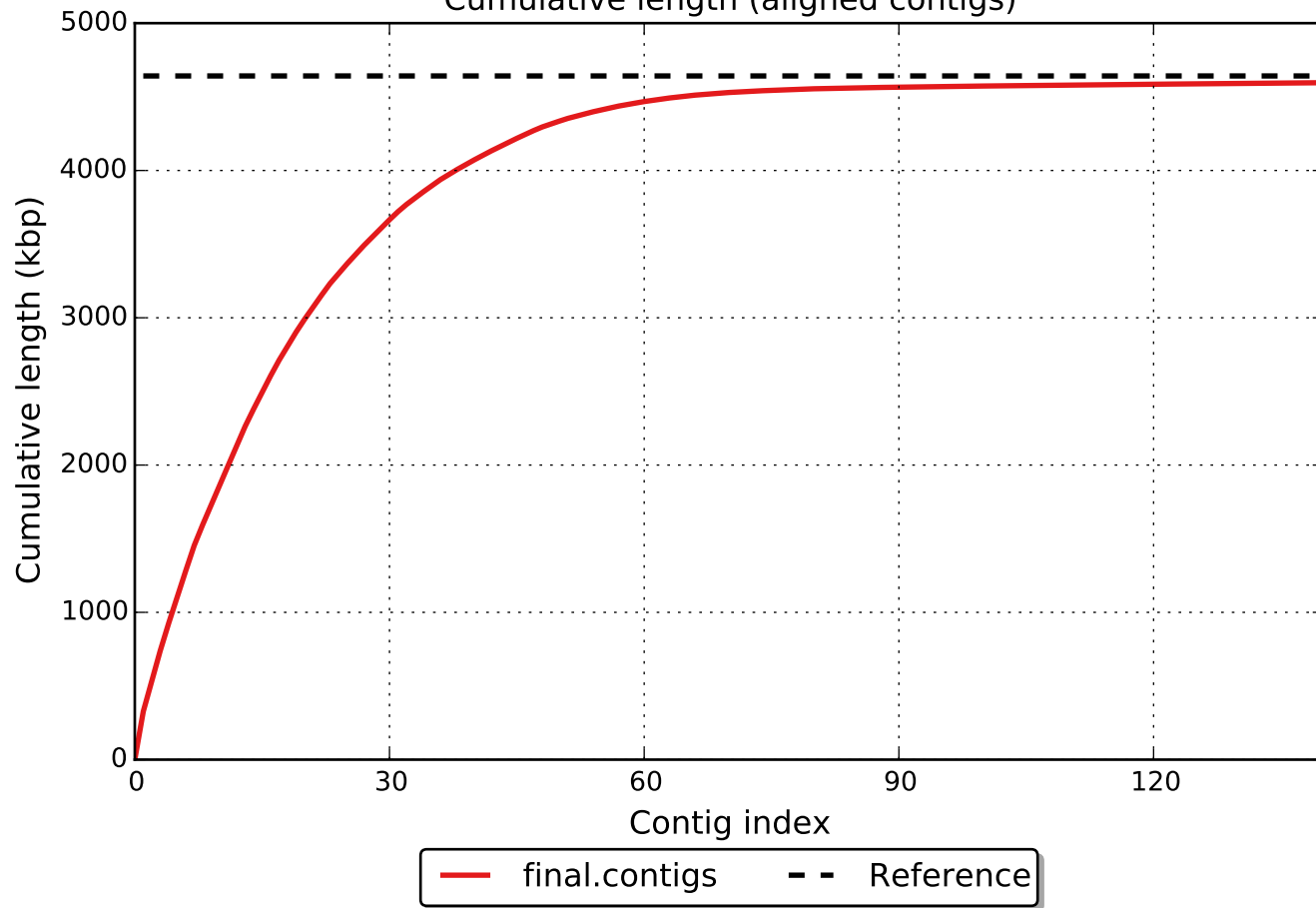
GC content



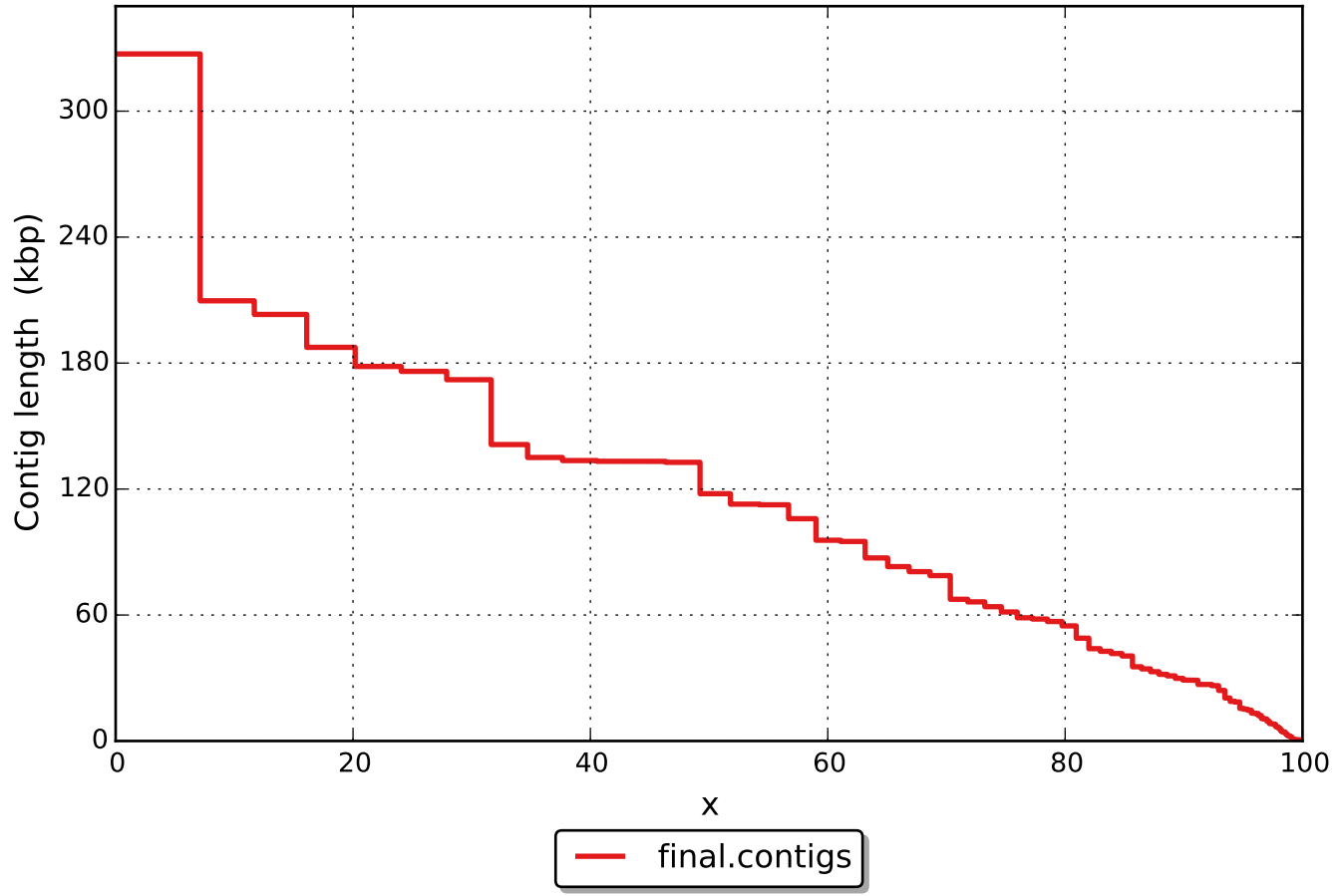




Cumulative length (aligned contigs)



NAx



# NGAx

