

## Report

	final.contigs
# contigs (>= 0 bp)	157
# contigs (>= 1000 bp)	87
# contigs (>= 5000 bp)	62
# contigs (>= 10000 bp)	56
# contigs (>= 25000 bp)	47
# contigs (>= 50000 bp)	30
Total length (>= 0 bp)	4591188
Total length (>= 1000 bp)	4564712
Total length (>= 5000 bp)	4507354
Total length (>= 10000 bp)	4462645
Total length (>= 25000 bp)	4319949
Total length (>= 50000 bp)	3754056
# contigs	99
Largest contig	327235
Total length	4573623
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	132728
NG50	125735
N75	63361
NG75	58691
L50	12
LG50	13
L75	25
LG75	26
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.442
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.74
# indels per 100 kbp	0.02
Largest alignment	327235
NA50	132728
NGA50	125735
NA75	63361
NGA75	58691
LA50	12
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	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# mismatches	34
# indels	1
# short indels	1
# long indels	0
Indels length	1

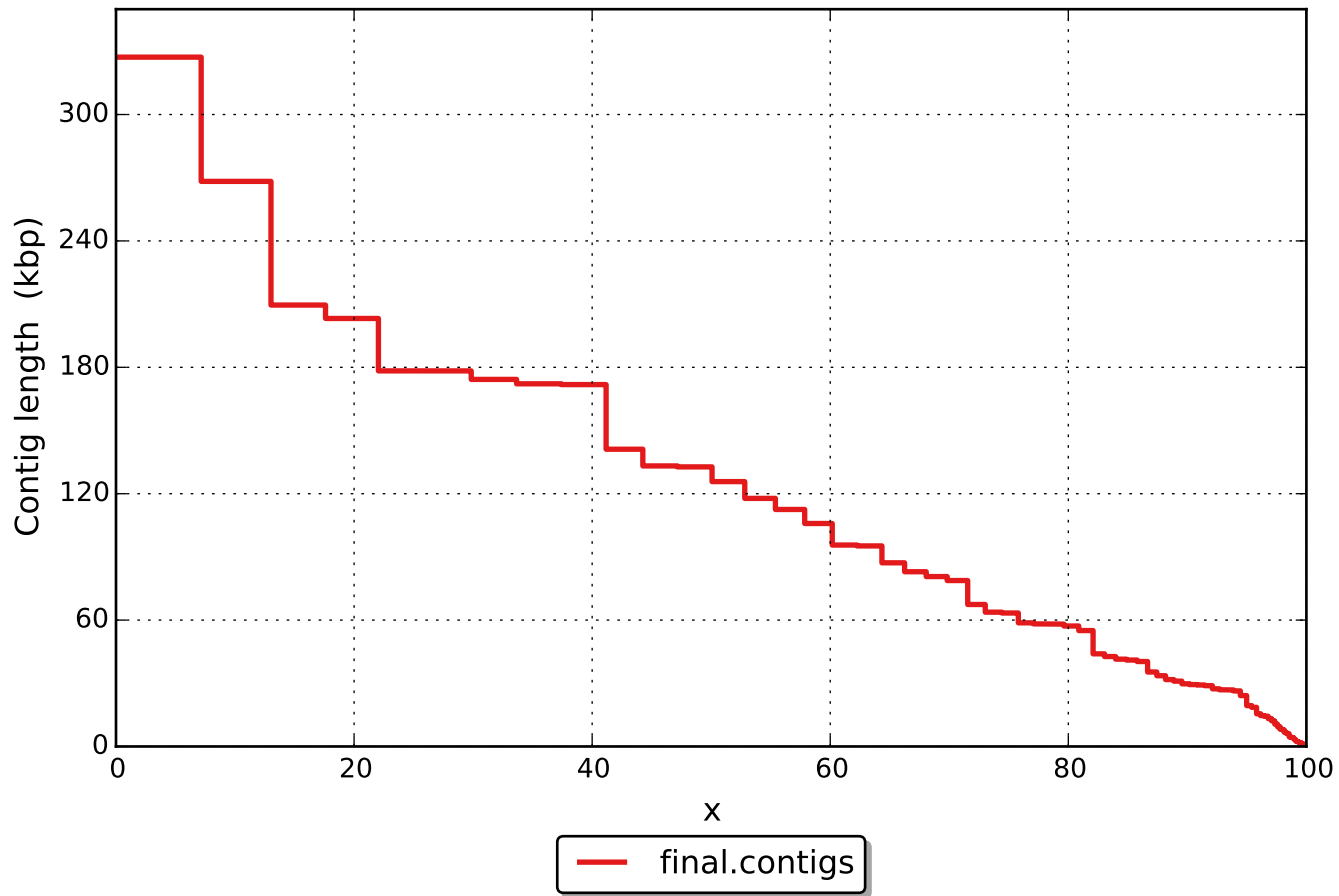
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

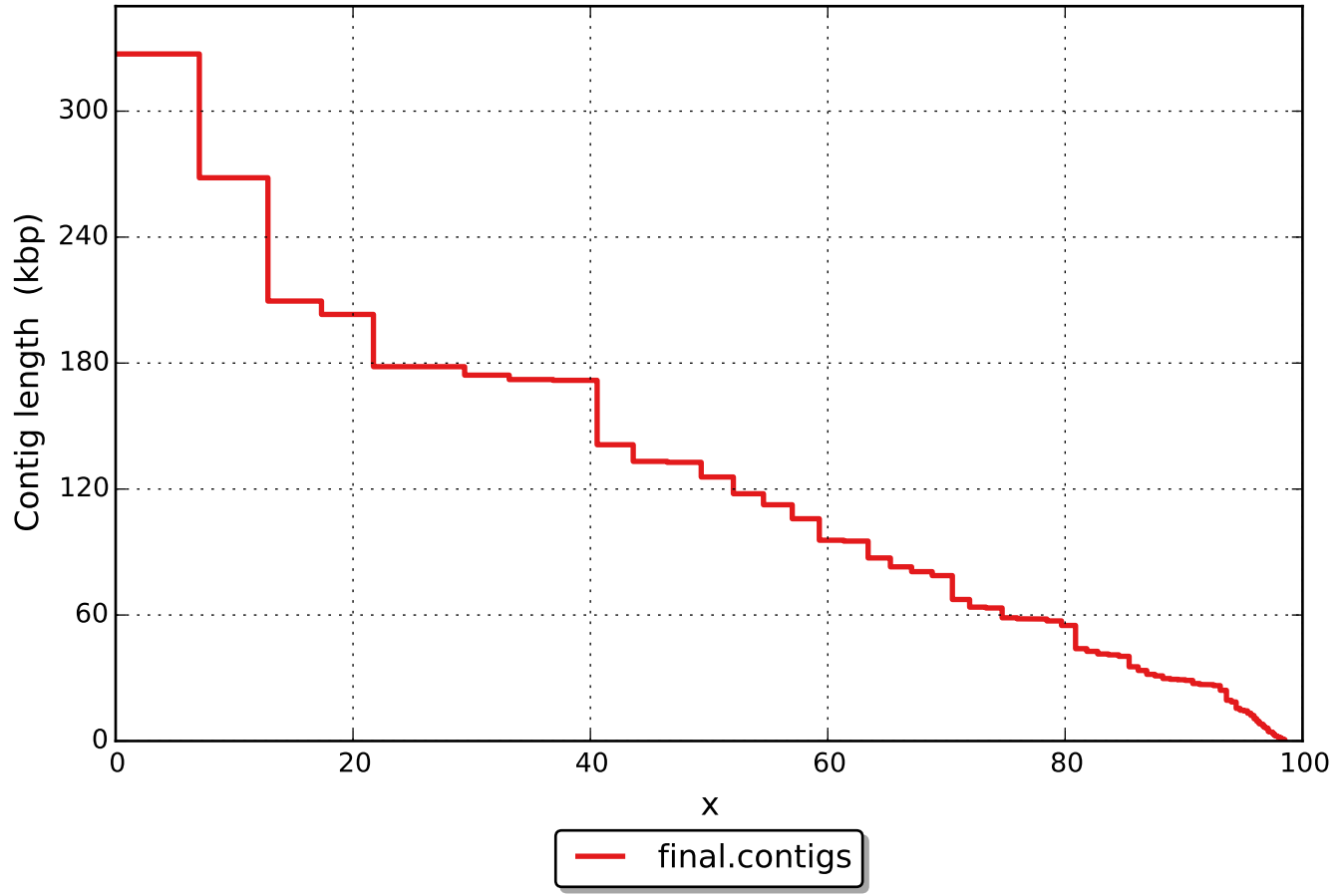
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

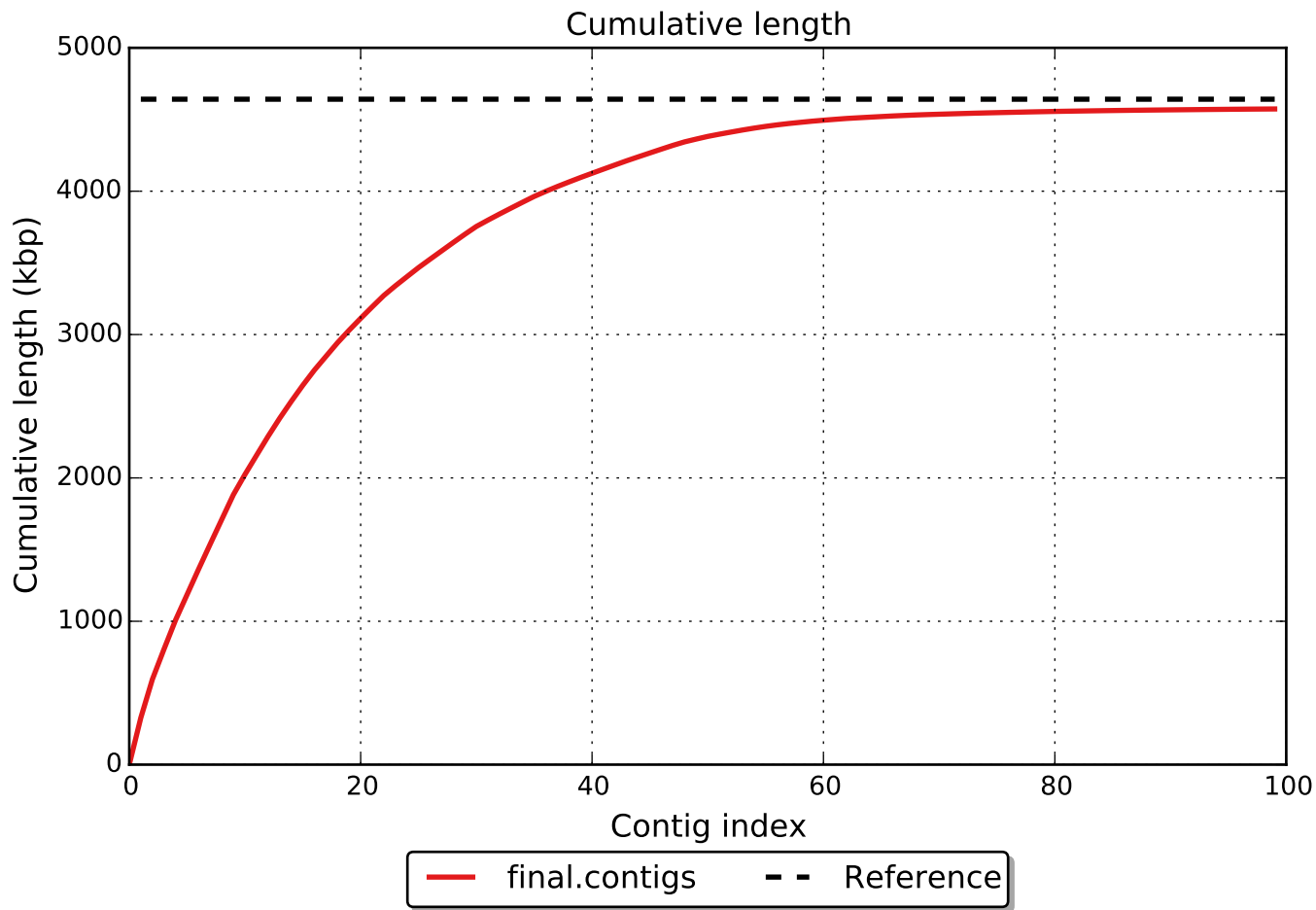
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

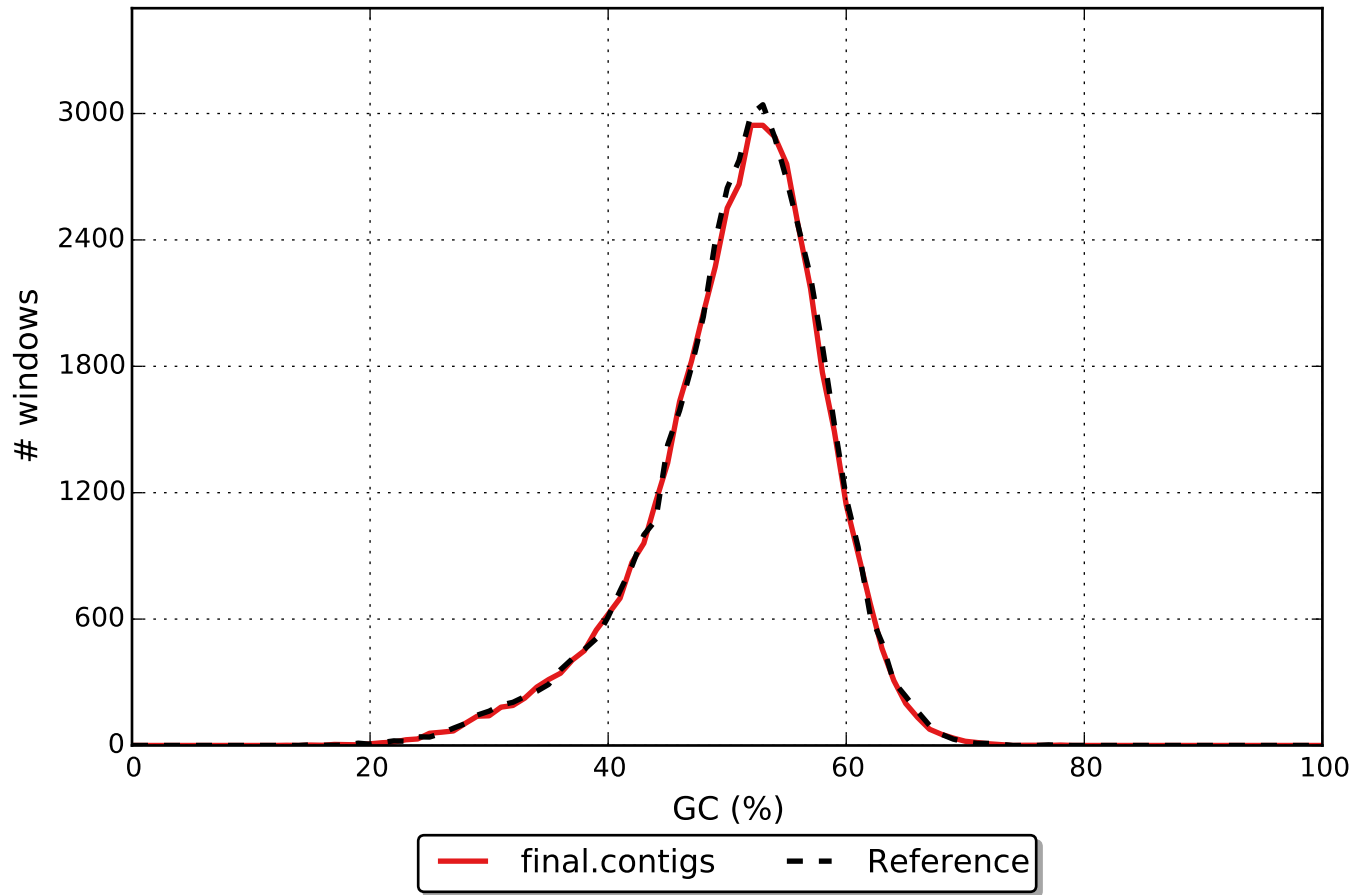


NGx





GC content

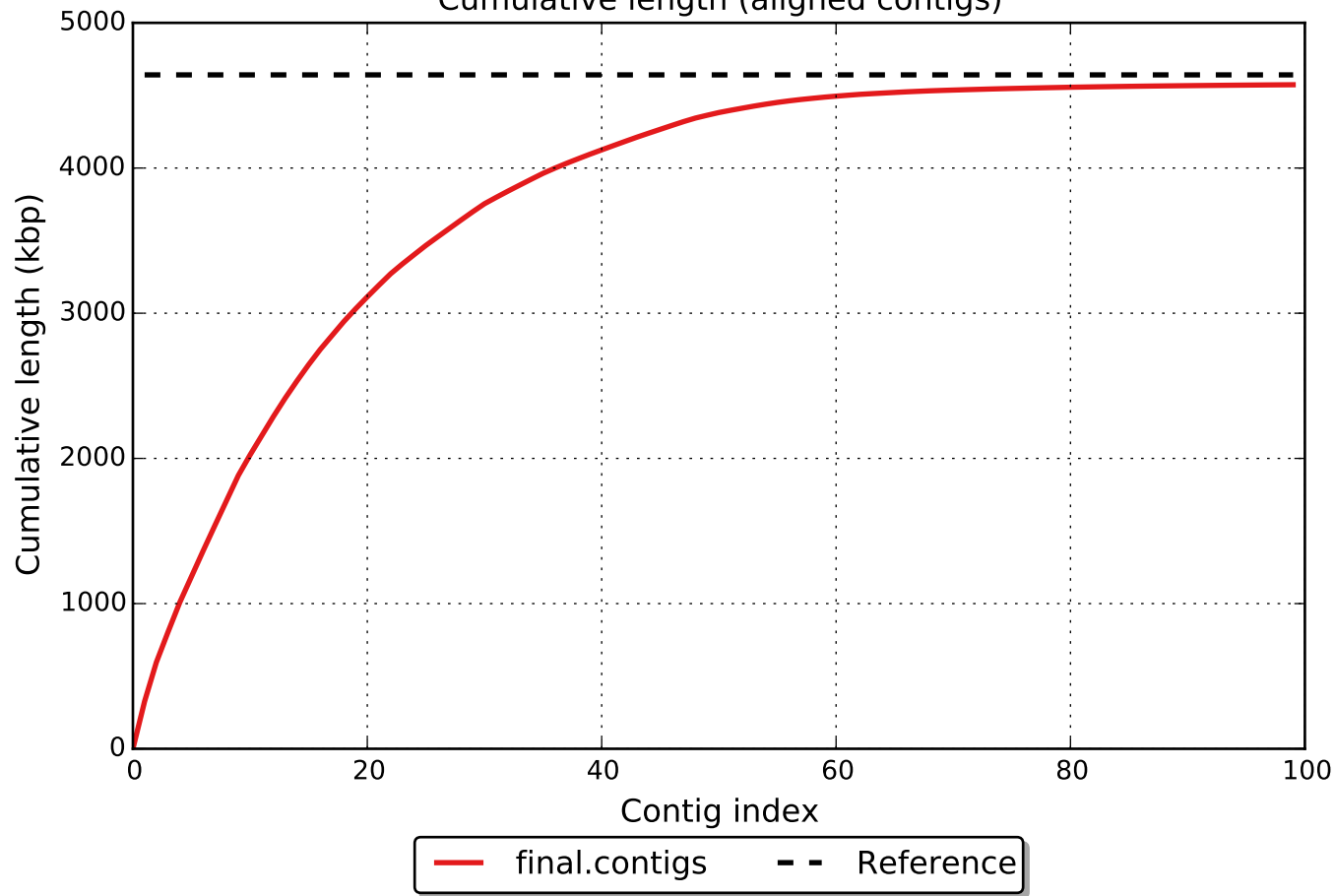


# Misassemblies

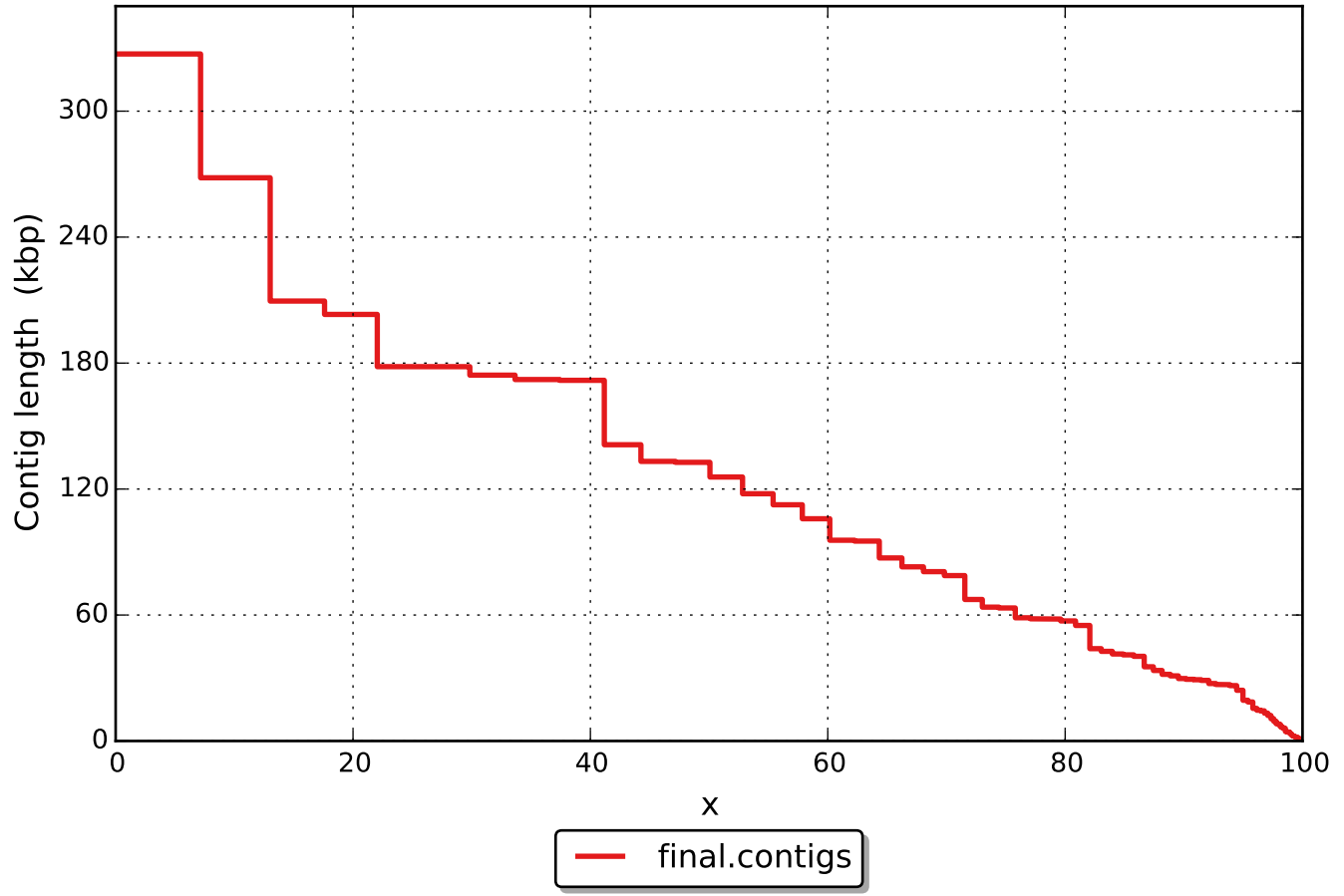




Cumulative length (aligned contigs)



NAx



NGAx

