

Report

	final.contigs
# contigs (>= 1000 bp)	95
# contigs (>= 5000 bp)	71
# contigs (>= 10000 bp)	66
# contigs (>= 25000 bp)	49
# contigs (>= 50000 bp)	32
Total length (>= 1000 bp)	4553116
Total length (>= 5000 bp)	4499119
Total length (>= 10000 bp)	4463368
Total length (>= 25000 bp)	4193515
Total length (>= 50000 bp)	3603122
# contigs	110
Largest contig	327143
Total length	4562904
Reference length	4641652
GC (℥)	50.74
Reference GC (℥)	50.79
N50	110840
NG50	105790
N75	56864
NG75	55080
L50	14
LG50	15
L75	29
LG75	30
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	10
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (℥)	98.246
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	57.26
# indels per 100 kbp	8.79
Largest alignment	327143
NA50	110840
NGA50	105790
NA75	56864
NGA75	55080
LA50	14
LGA50	15
LA75	29
LGA75	30

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	10
# mismatches	2611
# indels	401
# short indels	400
# long indels	1
Indels length	667

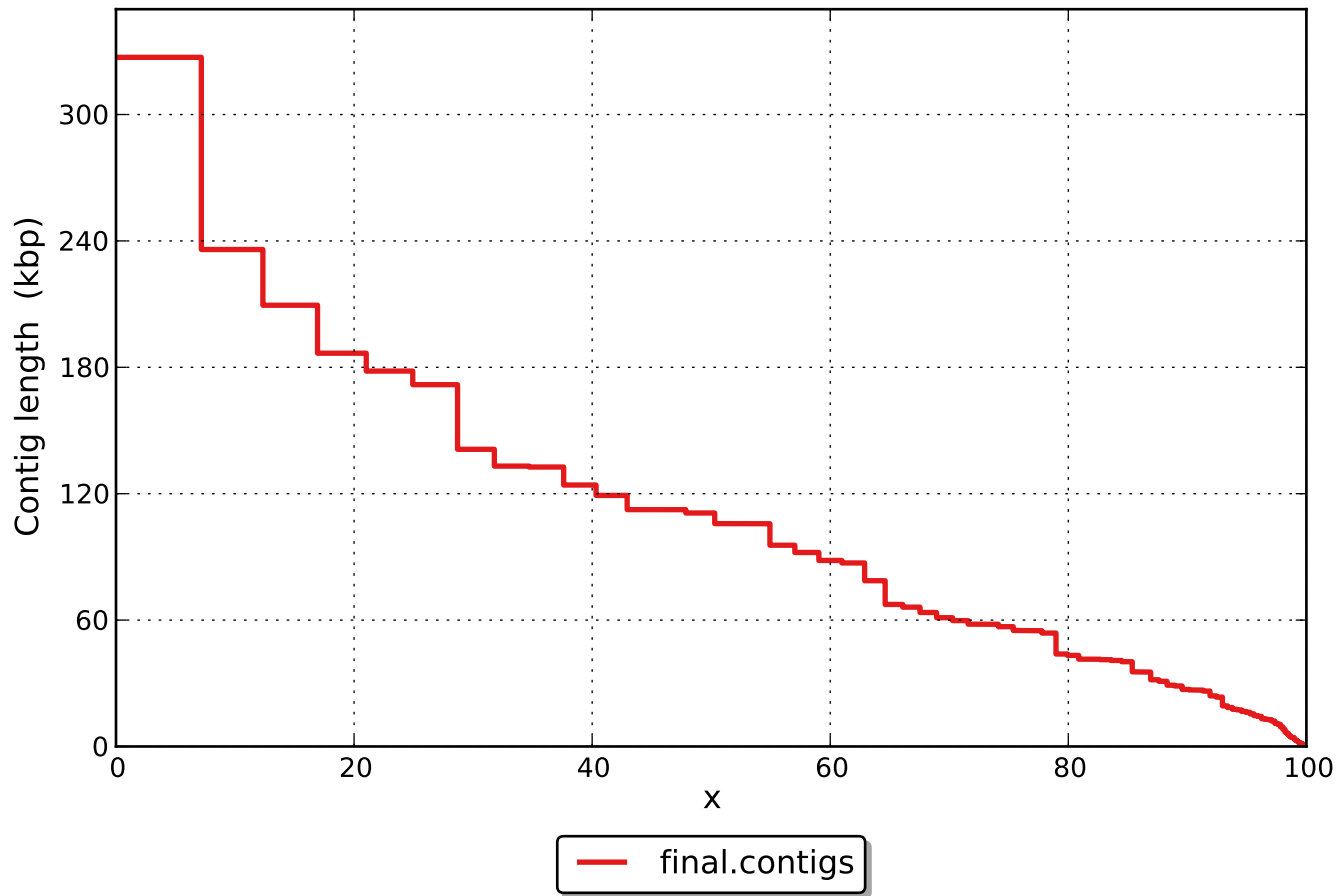
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

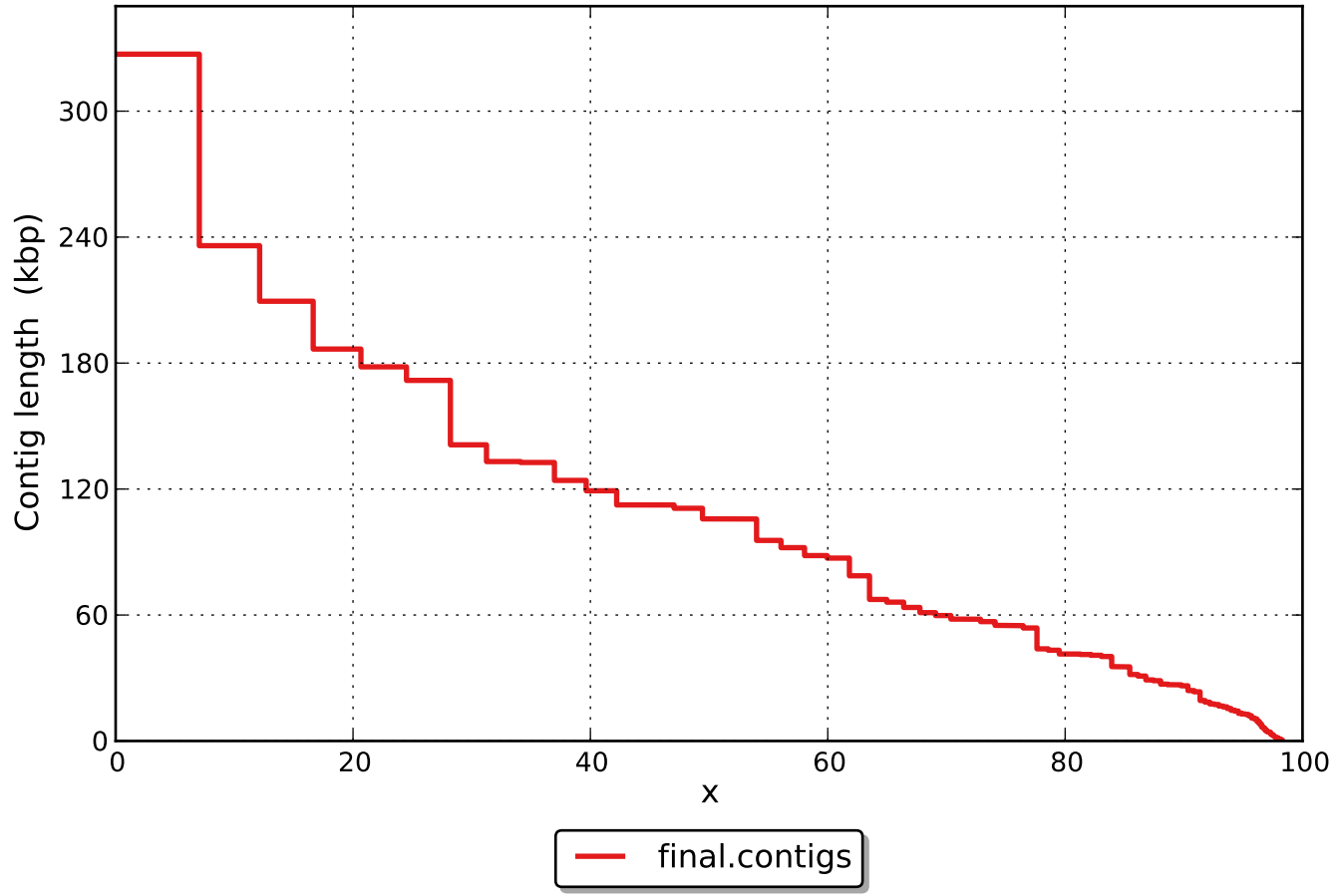
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

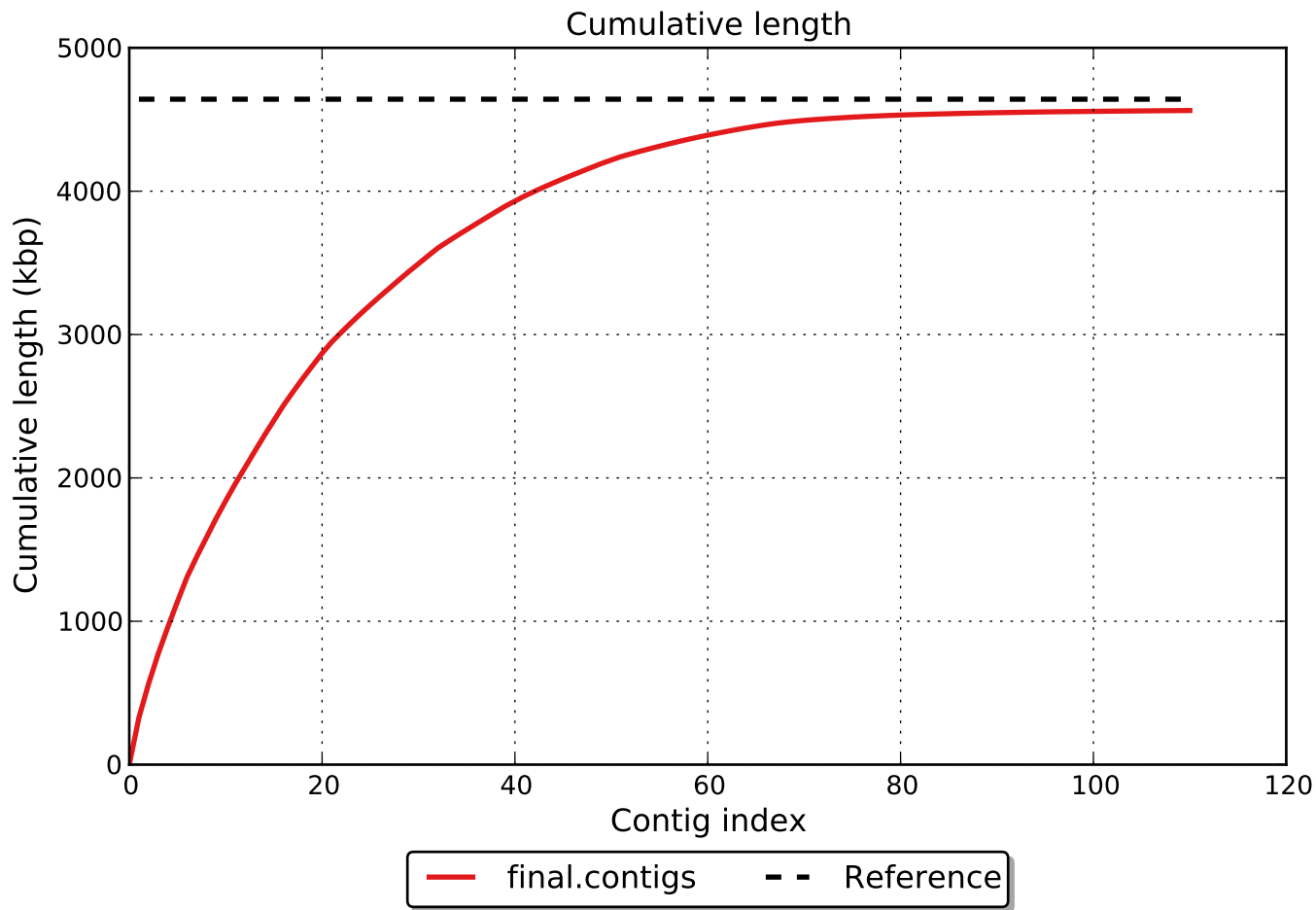
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

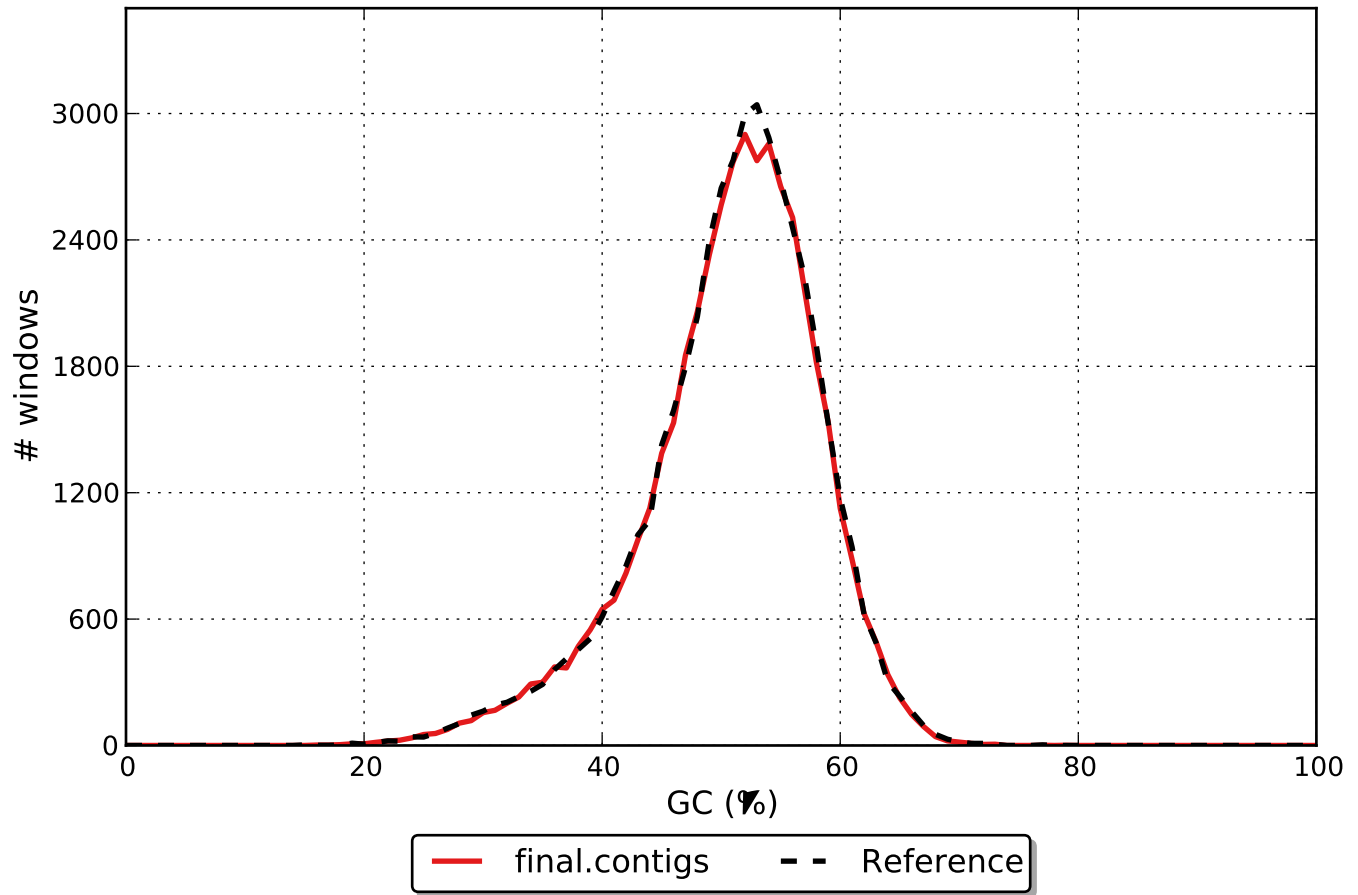


NGx





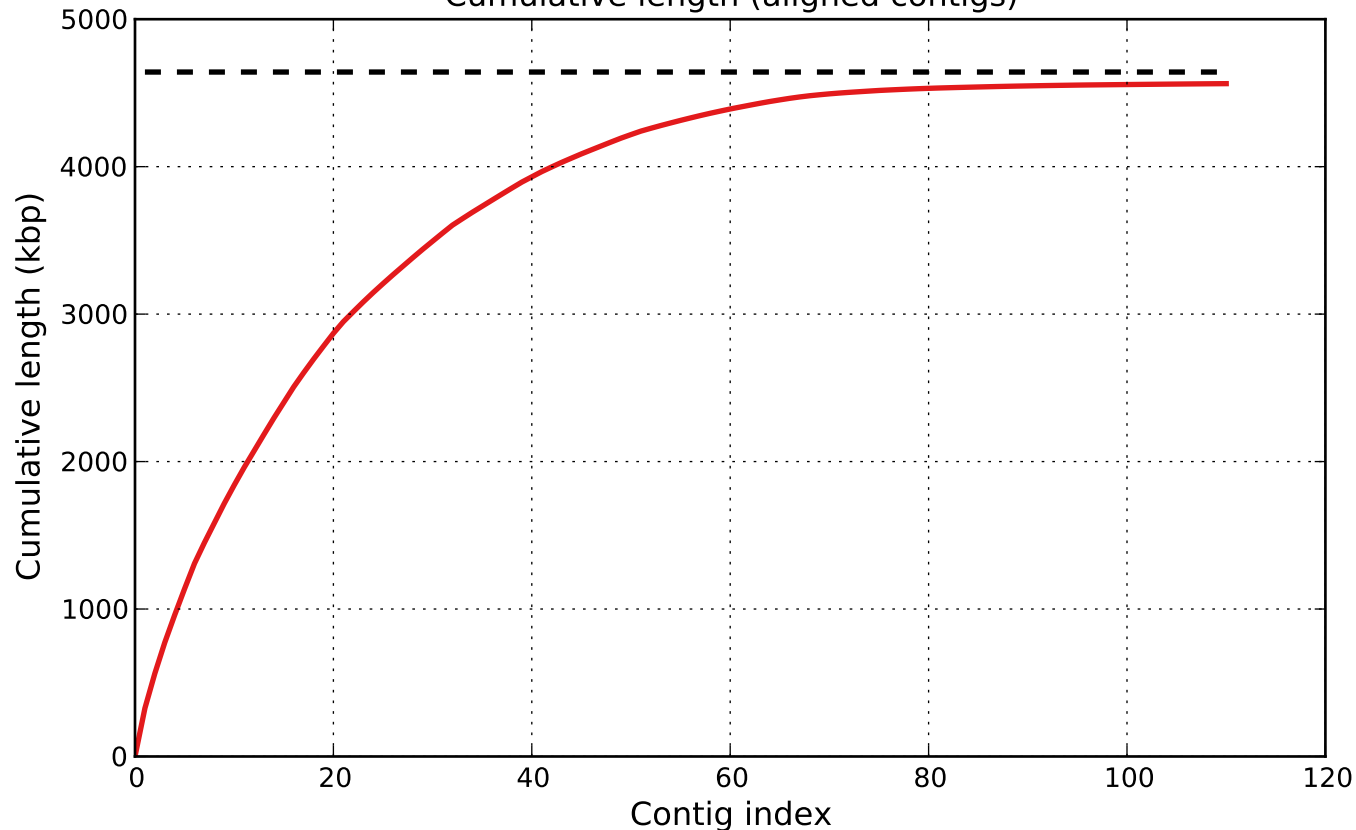
GC content



Misassemblies

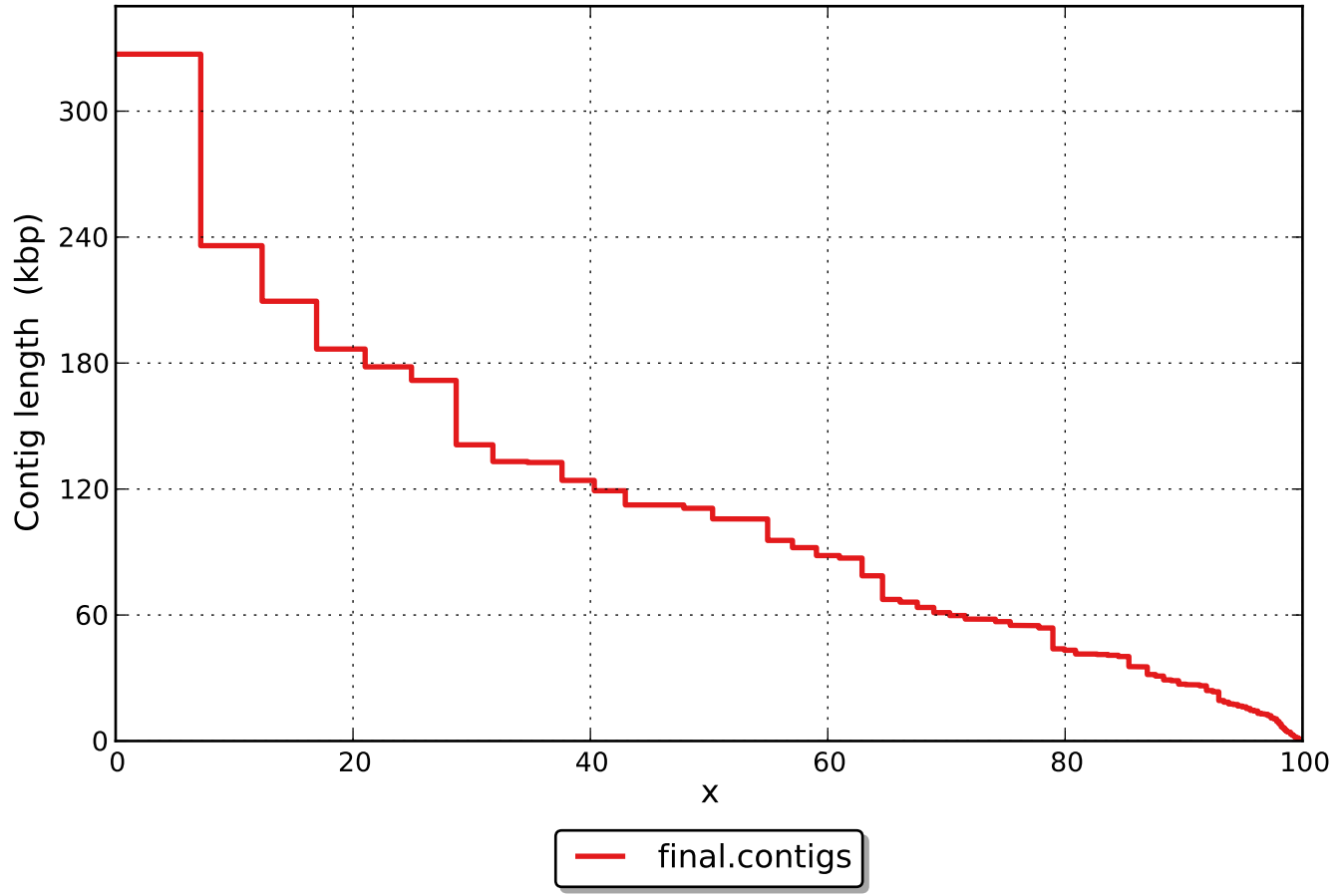


Cumulative length (aligned contigs)



— final.contigs - - Reference

NAx



NGAx

