

Report

	final.contigs
# contigs (>= 1000 bp)	98
# contigs (>= 5000 bp)	74
# contigs (>= 10000 bp)	68
# contigs (>= 25000 bp)	50
# contigs (>= 50000 bp)	31
Total length (>= 1000 bp)	4550464
Total length (>= 5000 bp)	4499084
Total length (>= 10000 bp)	4455584
Total length (>= 25000 bp)	4166960
Total length (>= 50000 bp)	3520935
# contigs	120
Largest contig	327151
Total length	4565389
Reference length	4641652
GC (℥)	50.75
Reference GC (℥)	50.79
N50	105736
NG50	105683
N75	53827
NG75	53820
L50	14
LG50	15
L75	30
LG75	31
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	8
# unaligned contigs	0 + 1 part
Unaligned length	53
Genome fraction (℥)	98.290
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.05
# indels per 100 kbp	0.09
Largest alignment	327151
NA50	105736
NGA50	105683
NA75	53827
NGA75	53820
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	48
# indels	4
# short indels	4
# long indels	0
Indels length	4

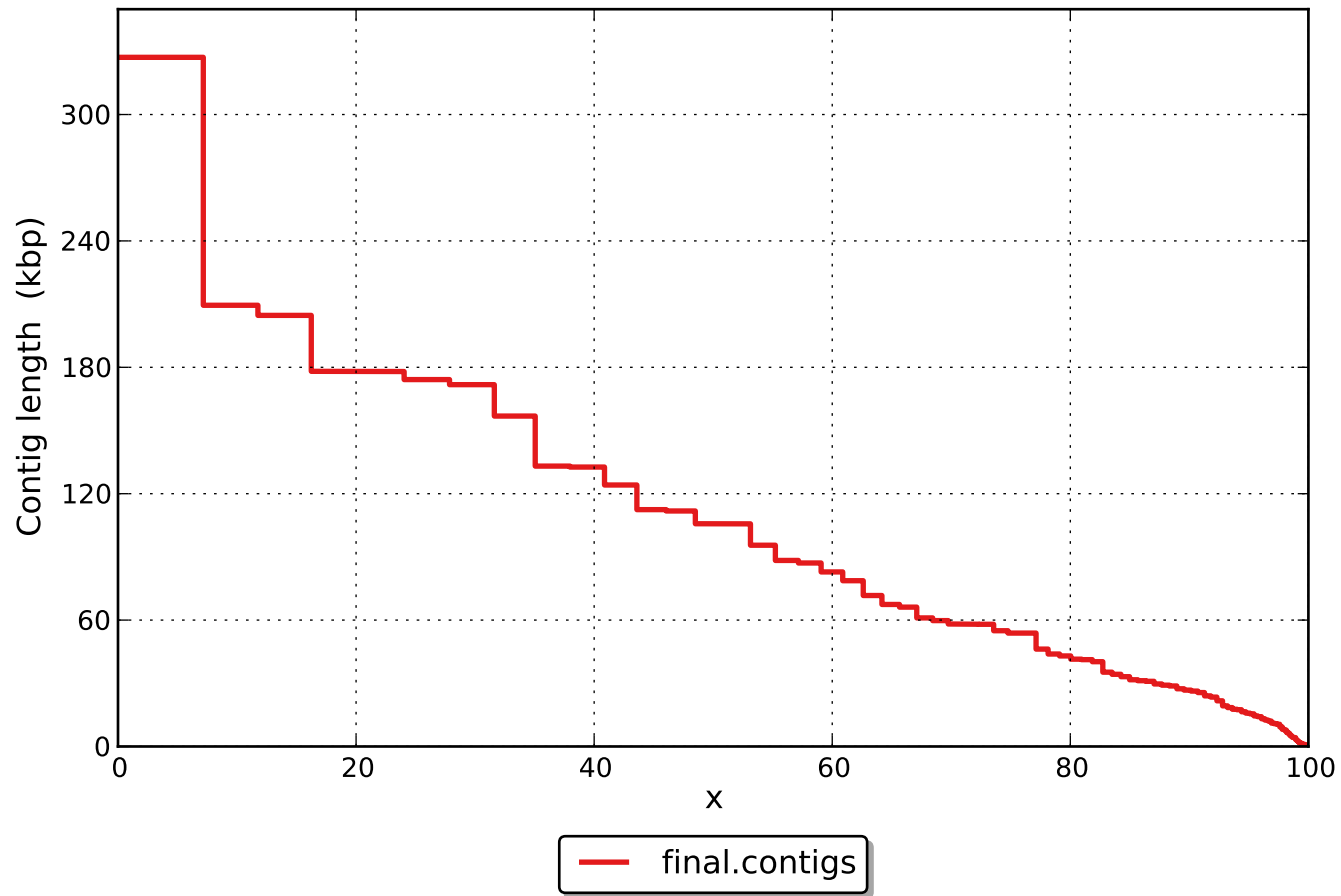
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

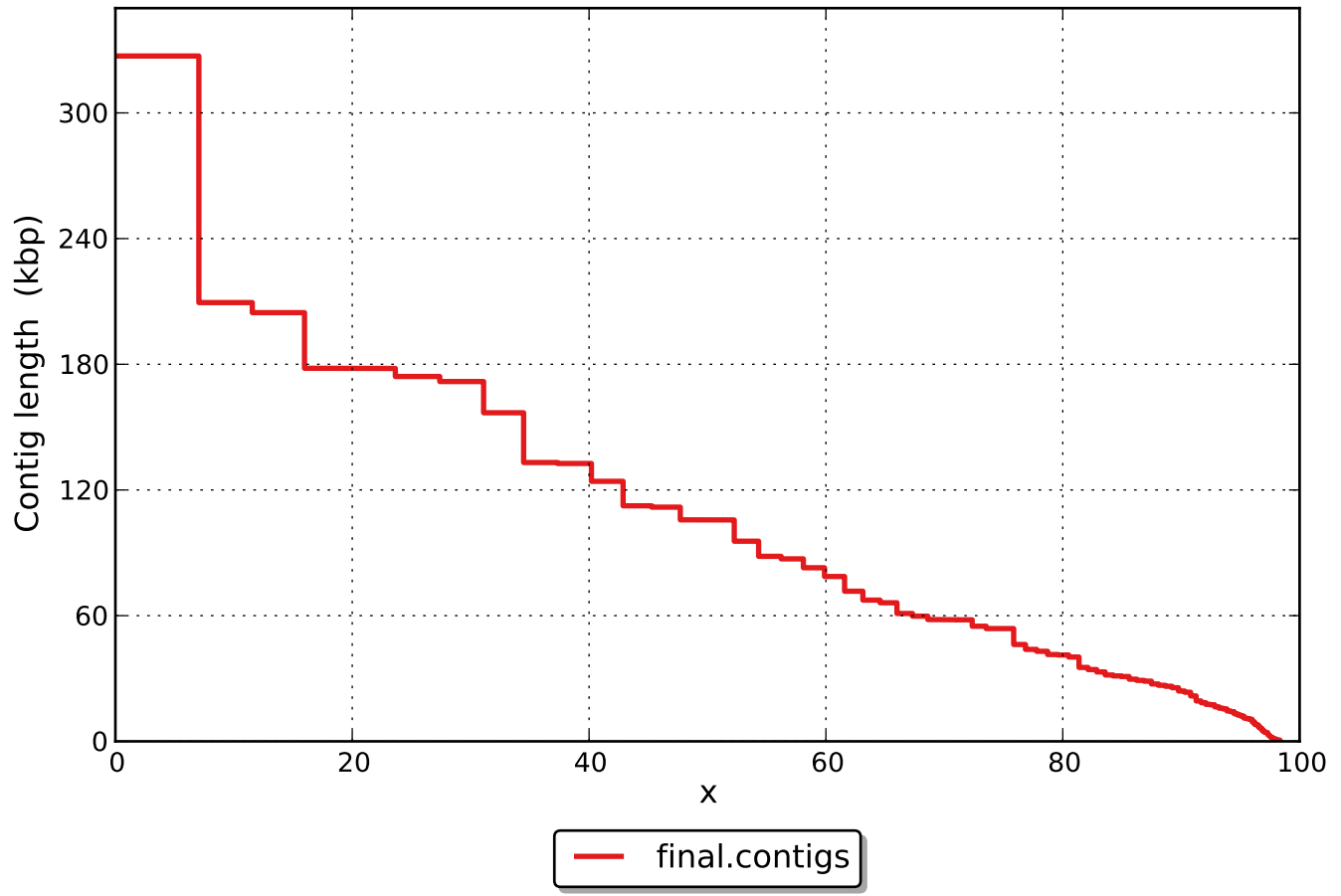
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	53
# N's	0

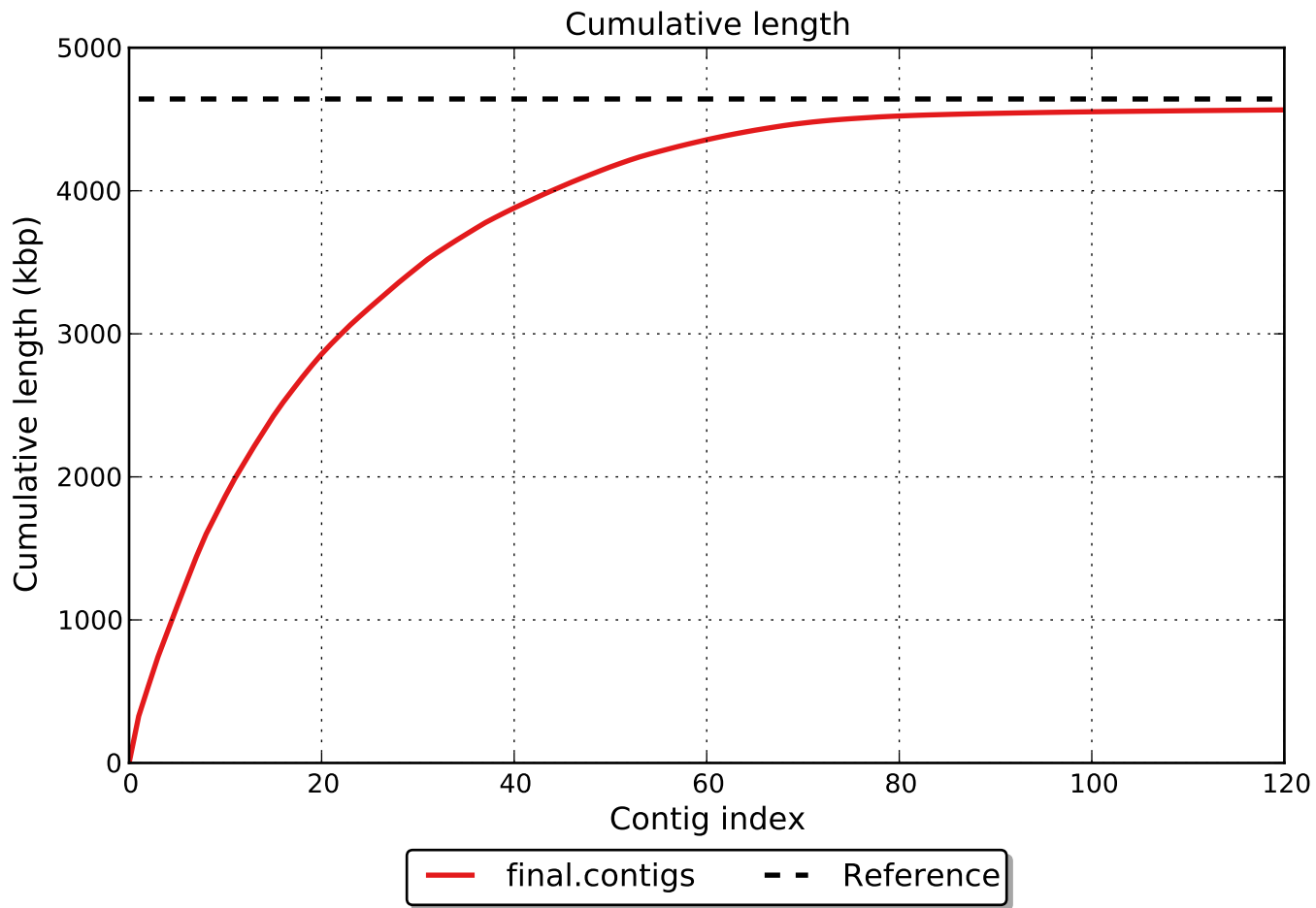
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

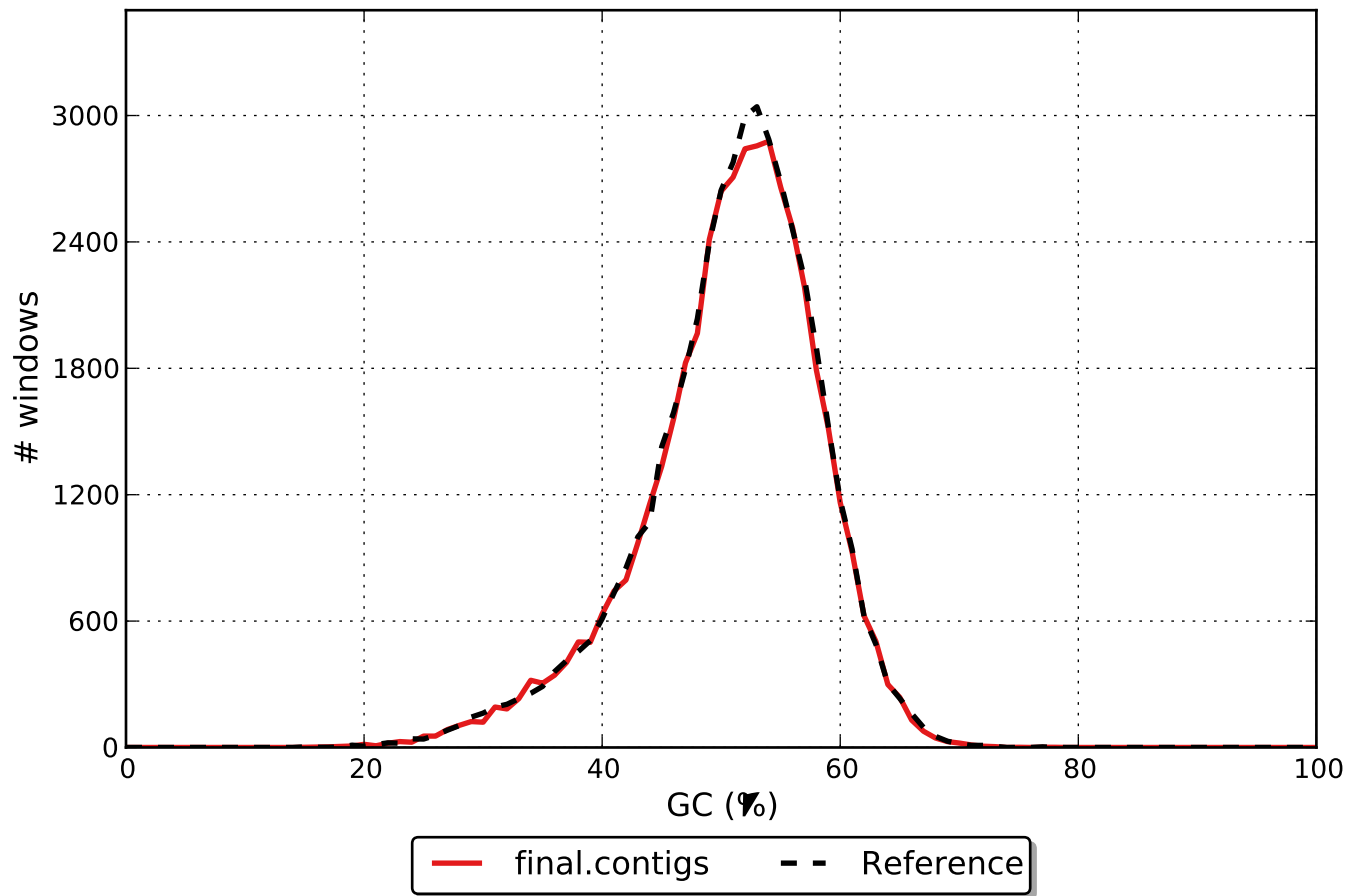


NGx





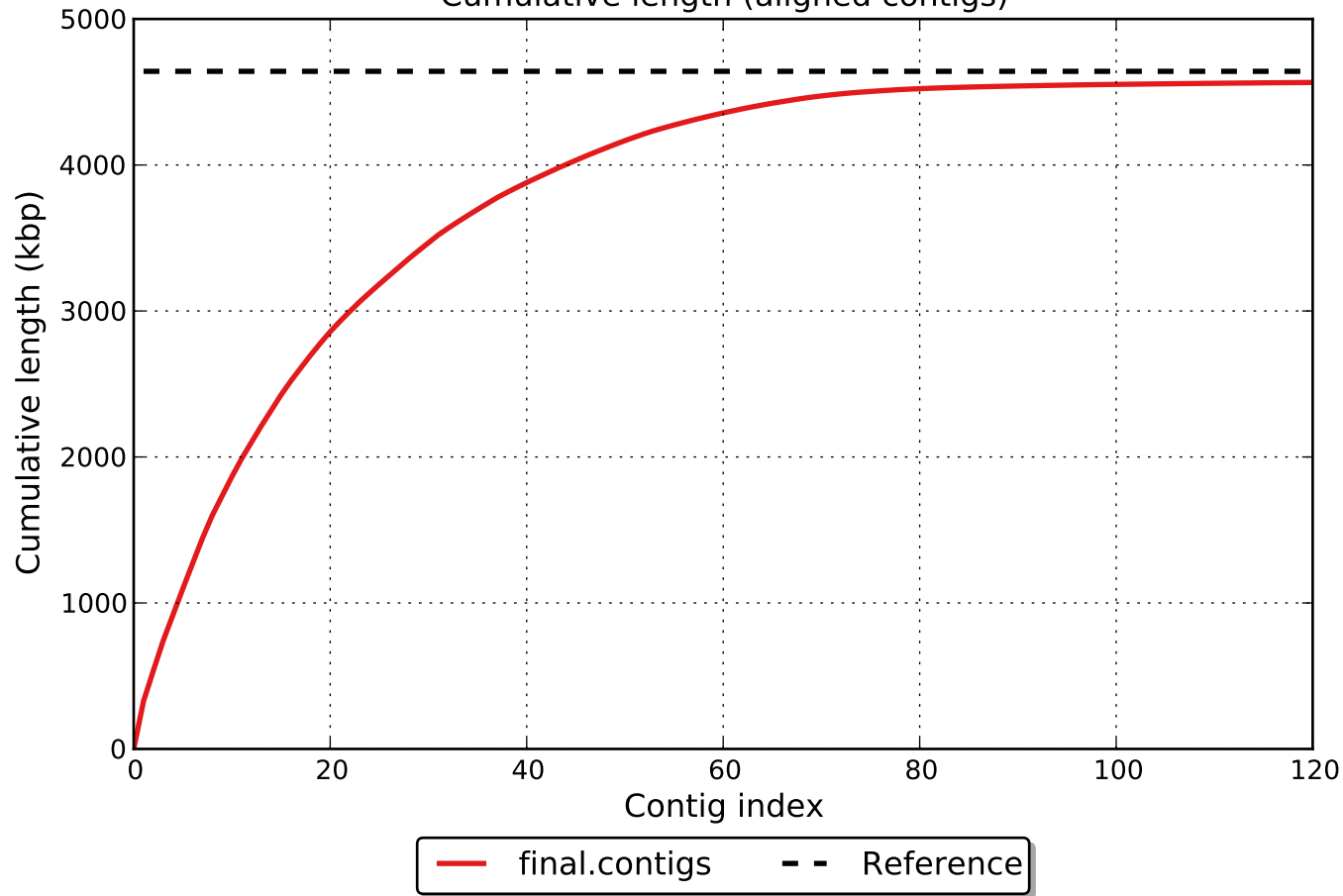
GC content



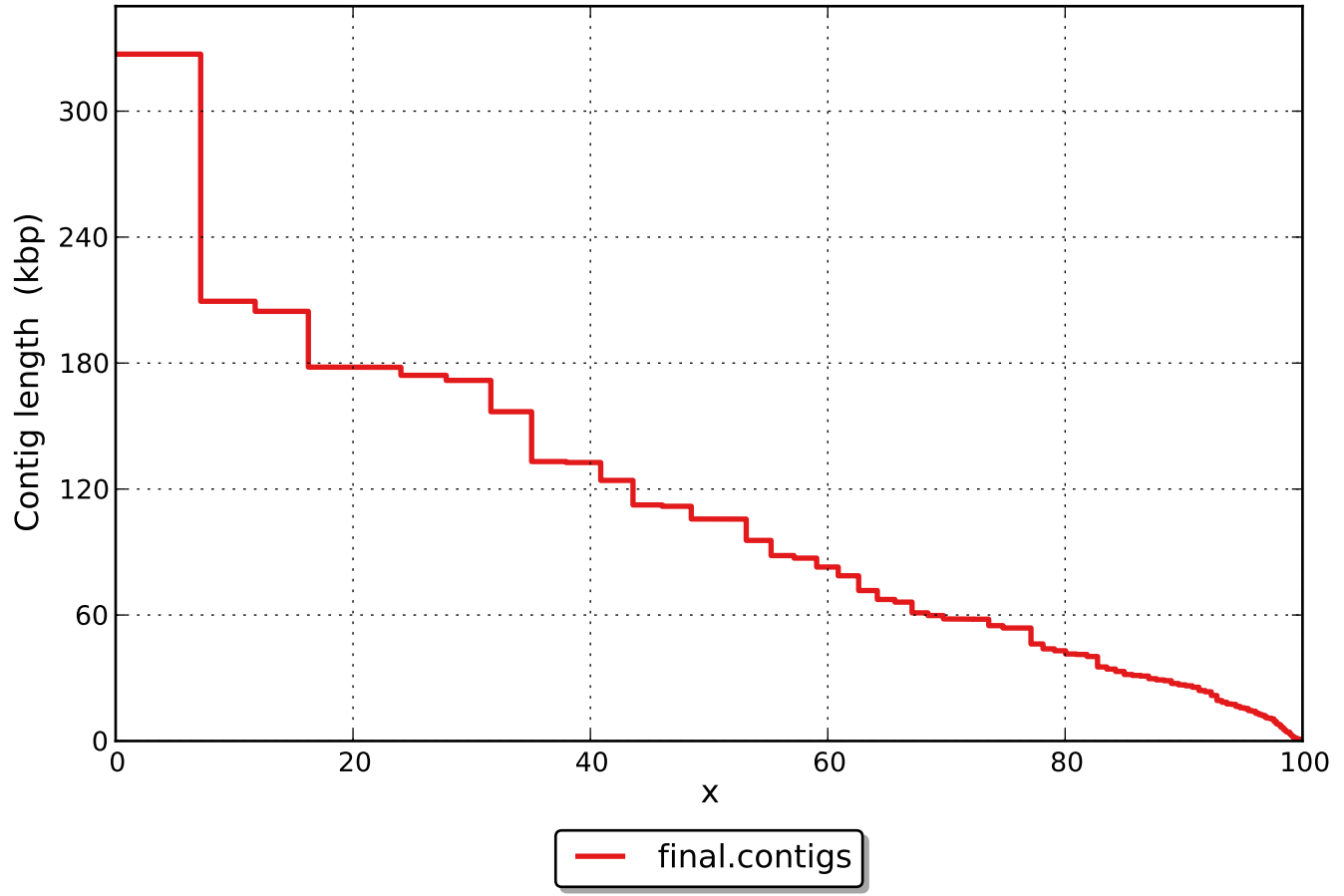
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

