

Report

	final.contigs
# contigs (>= 0 bp)	172
# contigs (>= 1000 bp)	91
# contigs (>= 5000 bp)	68
# contigs (>= 10000 bp)	62
# contigs (>= 25000 bp)	48
# contigs (>= 50000 bp)	29
Total length (>= 0 bp)	4580691
Total length (>= 1000 bp)	4551768
Total length (>= 5000 bp)	4501613
Total length (>= 10000 bp)	4456000
Total length (>= 25000 bp)	4231109
Total length (>= 50000 bp)	3589993
# contigs	108
Largest contig	327151
Total length	4563300
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	125651
NG50	125651
N75	58023
NG75	54946
L50	13
LG50	13
L75	26
LG75	28
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	163
Genome fraction (%)	98.257
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.48
# indels per 100 kbp	0.00
Largest alignment	327151
NA50	125651
NGA50	125651
NA75	58023
NGA75	54946
LA50	13
LGA50	13
LA75	26
LGA75	28

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	0
# mismatches	22
# indels	0
# short indels	0
# long indels	0
Indels length	0

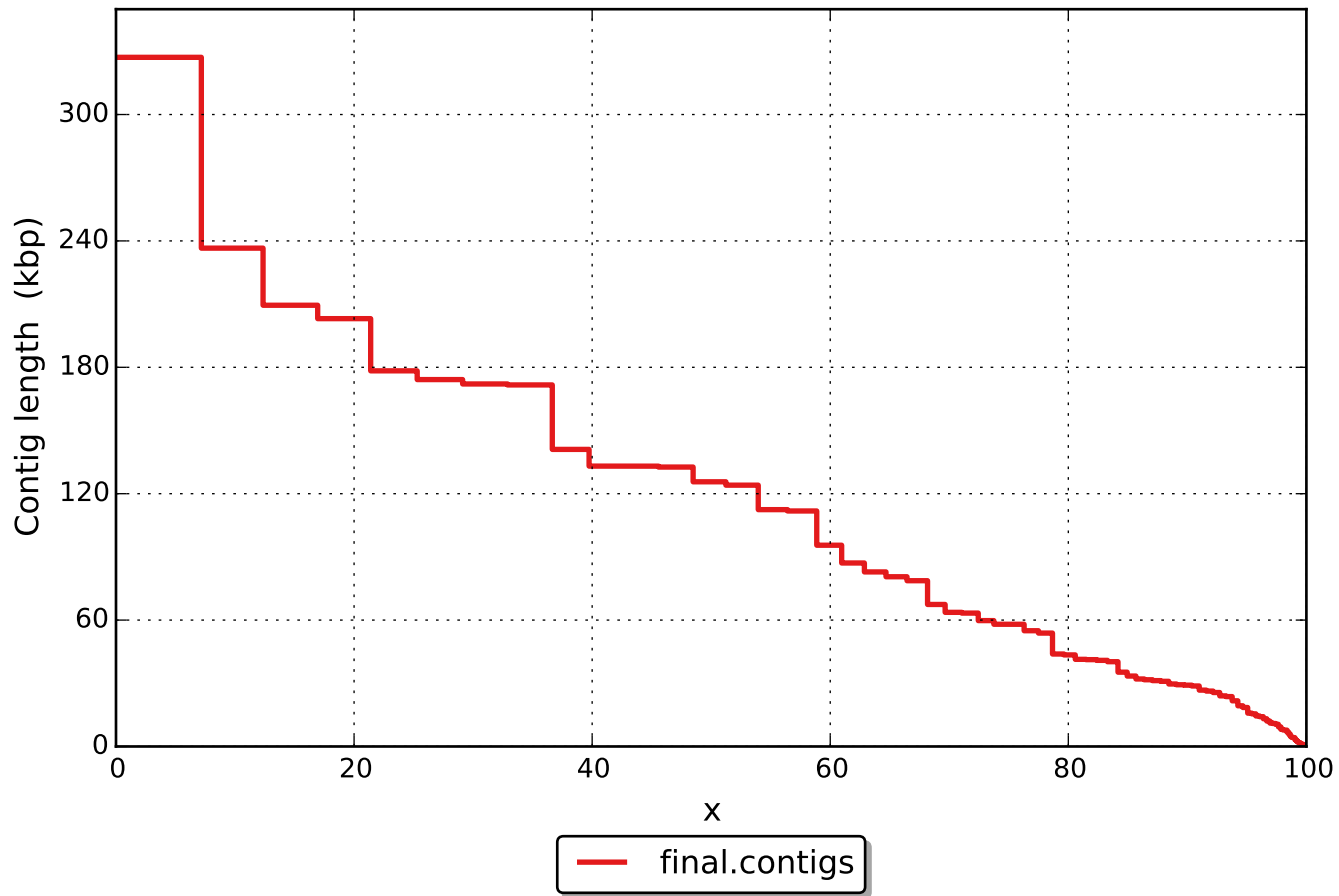
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

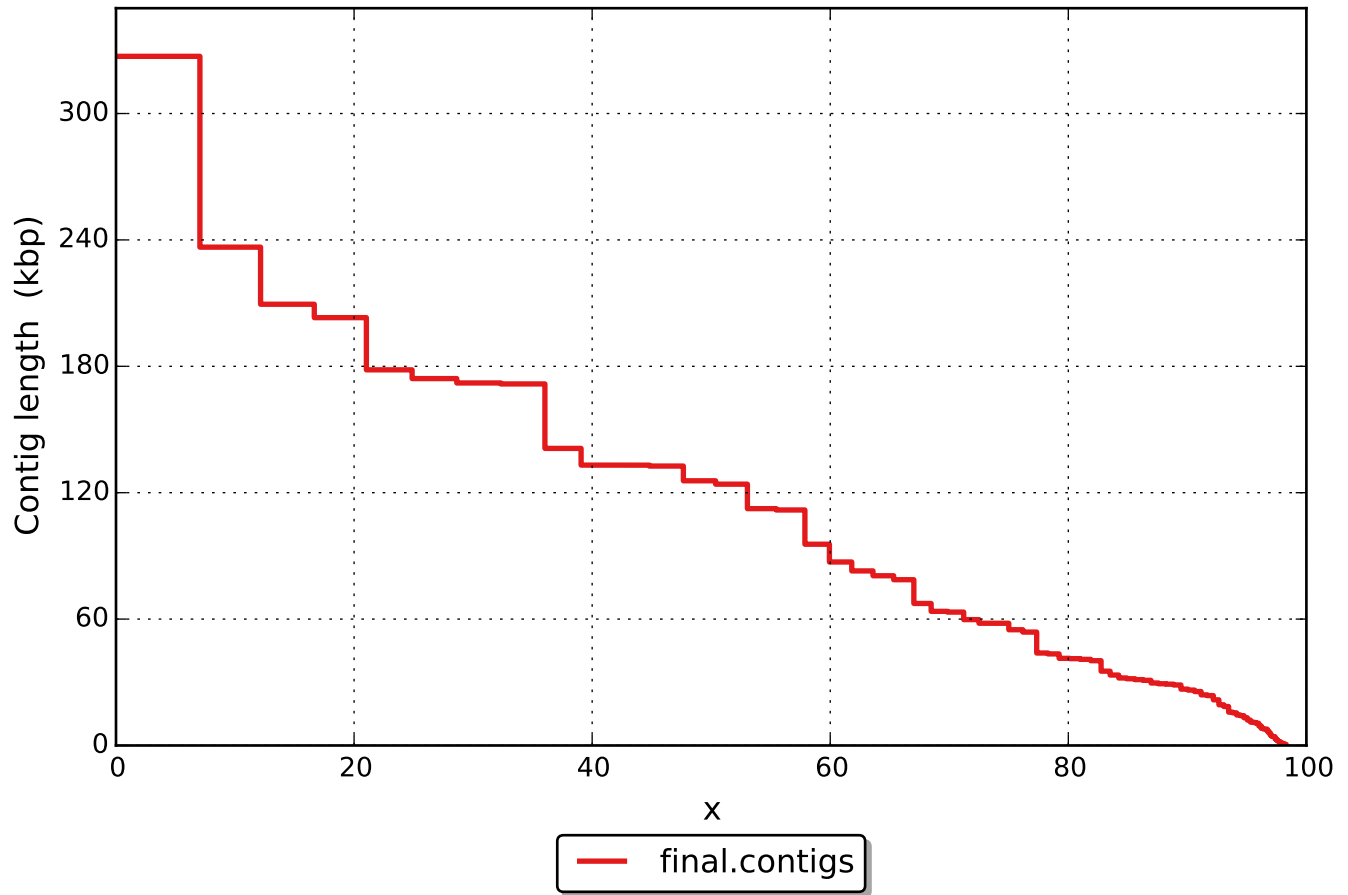
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	163
# N's	0

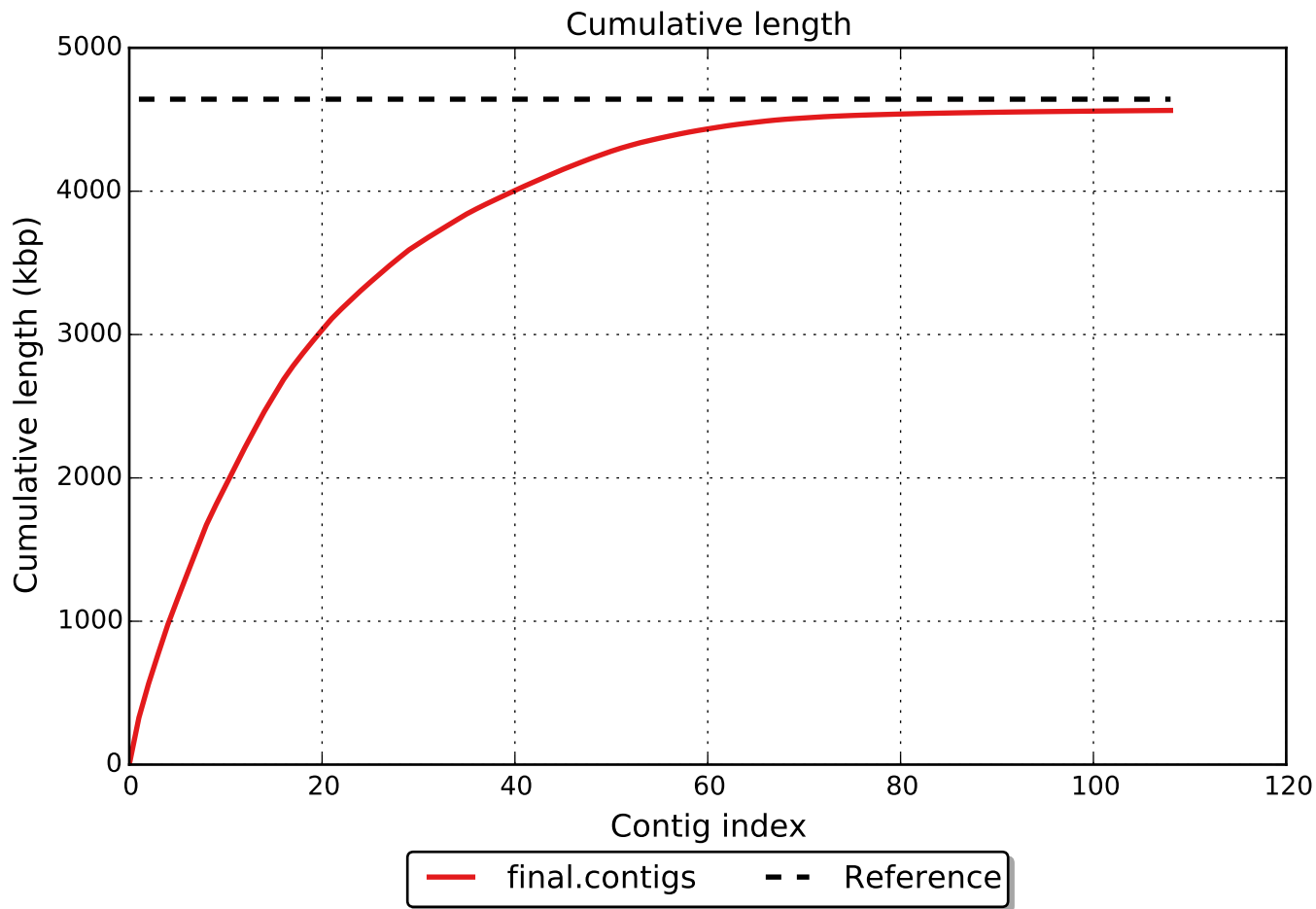
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

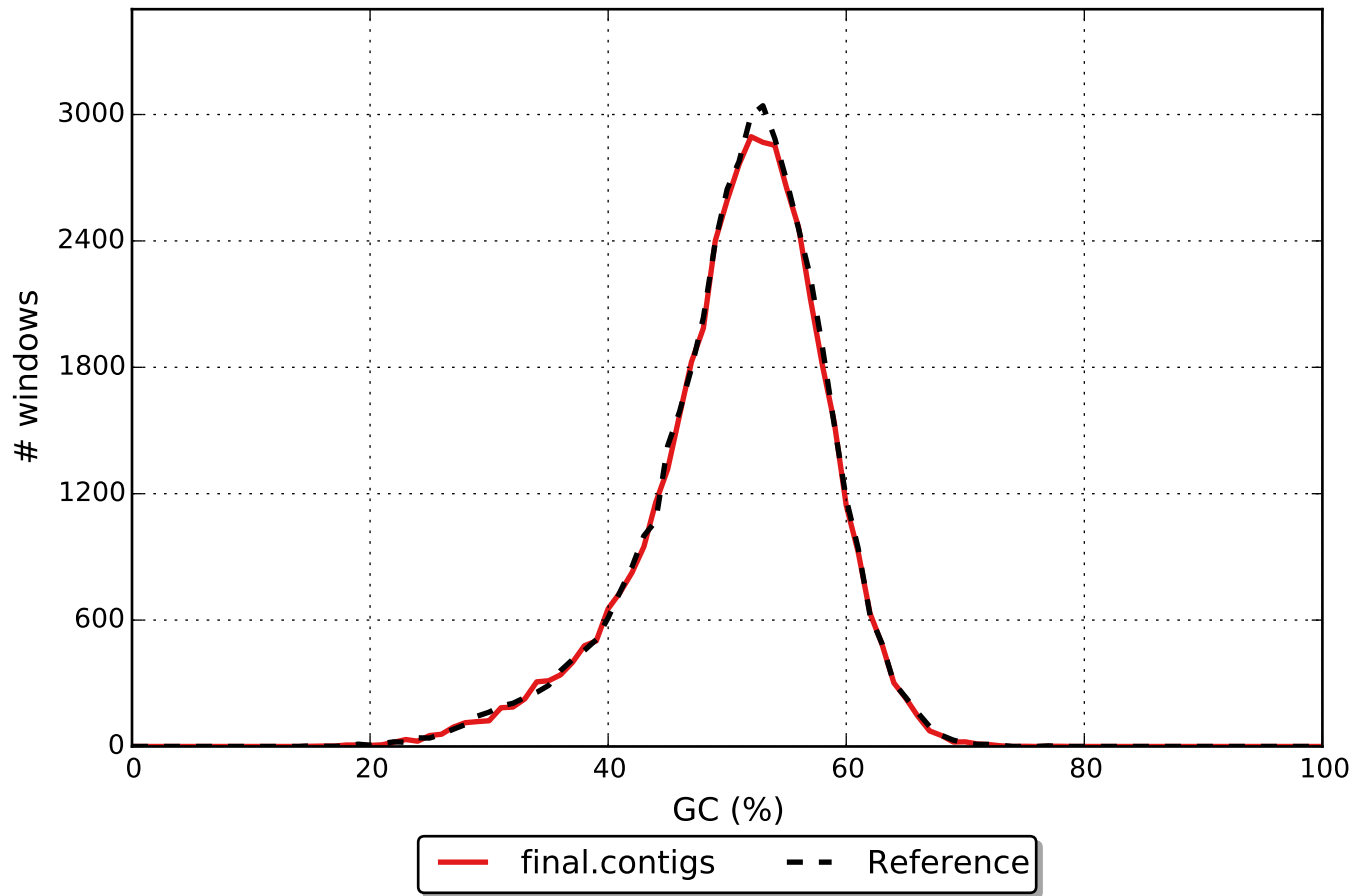


NGx





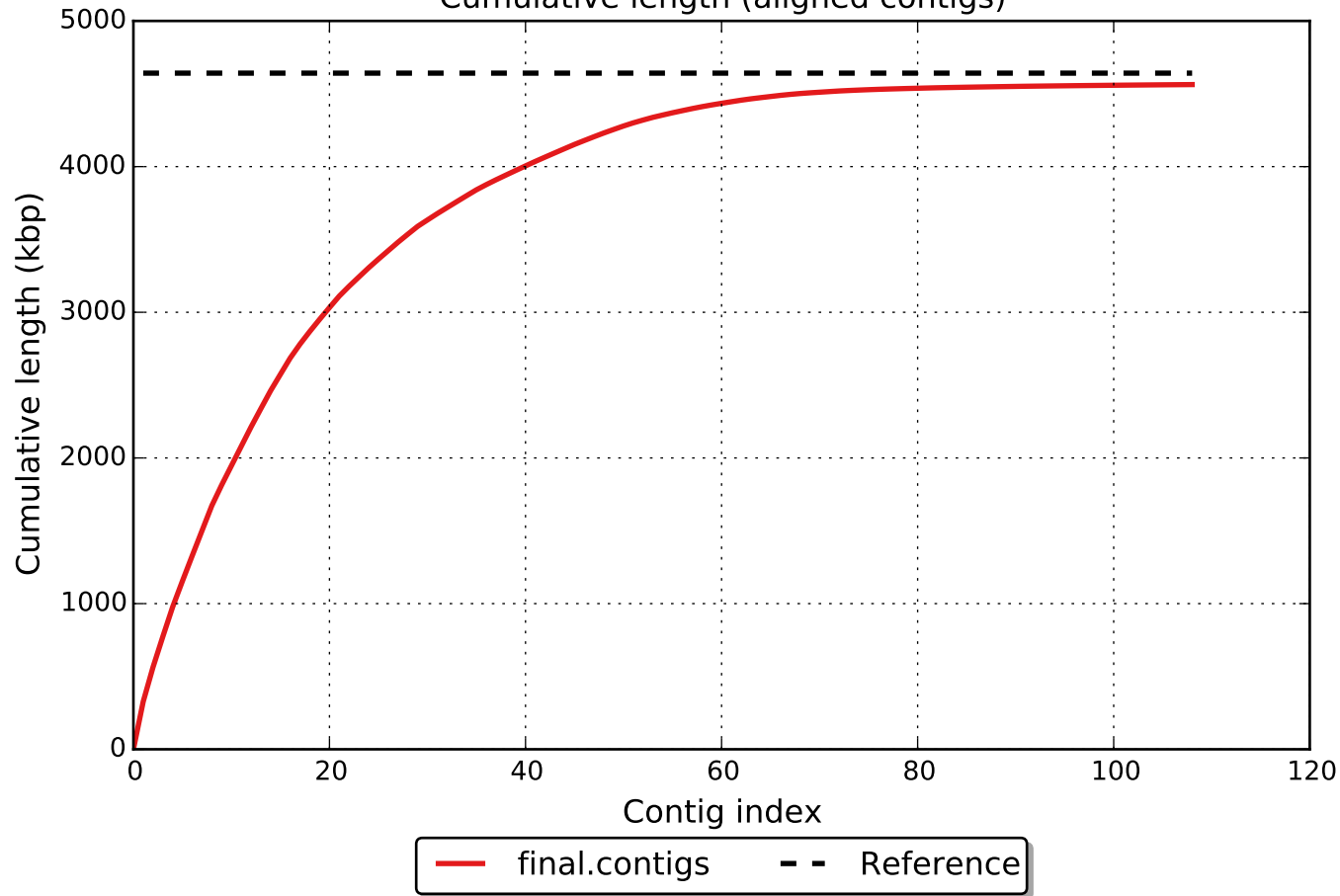
GC content



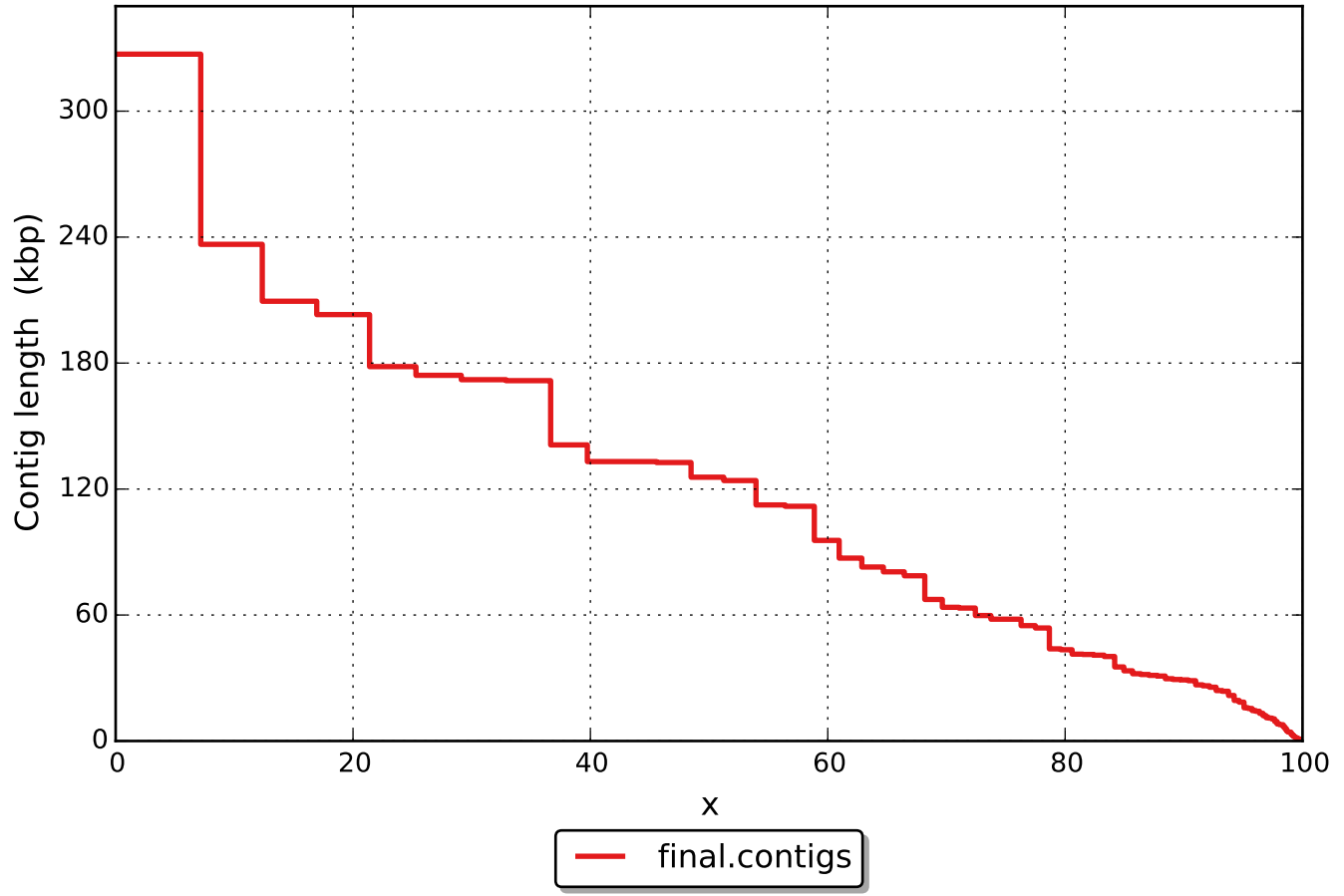
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

