

Report

	final.contigs
# contigs (>= 0 bp)	143
# contigs (>= 1000 bp)	84
# contigs (>= 5000 bp)	59
# contigs (>= 10000 bp)	54
# contigs (>= 25000 bp)	45
# contigs (>= 50000 bp)	29
Total length (>= 0 bp)	4587667
Total length (>= 1000 bp)	4564828
Total length (>= 5000 bp)	4508447
Total length (>= 10000 bp)	4471675
Total length (>= 25000 bp)	4329022
Total length (>= 50000 bp)	3787408
# contigs	97
Largest contig	327235
Total length	4573824
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	133109
NG50	133109
N75	67406
NG75	63760
L50	12
LG50	12
L75	23
LG75	24
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	4
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.450
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.99
# indels per 100 kbp	0.02
Largest alignment	327235
NA50	133109
NGA50	133109
NA75	67406
NGA75	63760
LA50	12
LGA50	12
LA75	23
LGA75	24

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	4
# mismatches	91
# indels	1
# short indels	1
# long indels	0
Indels length	1

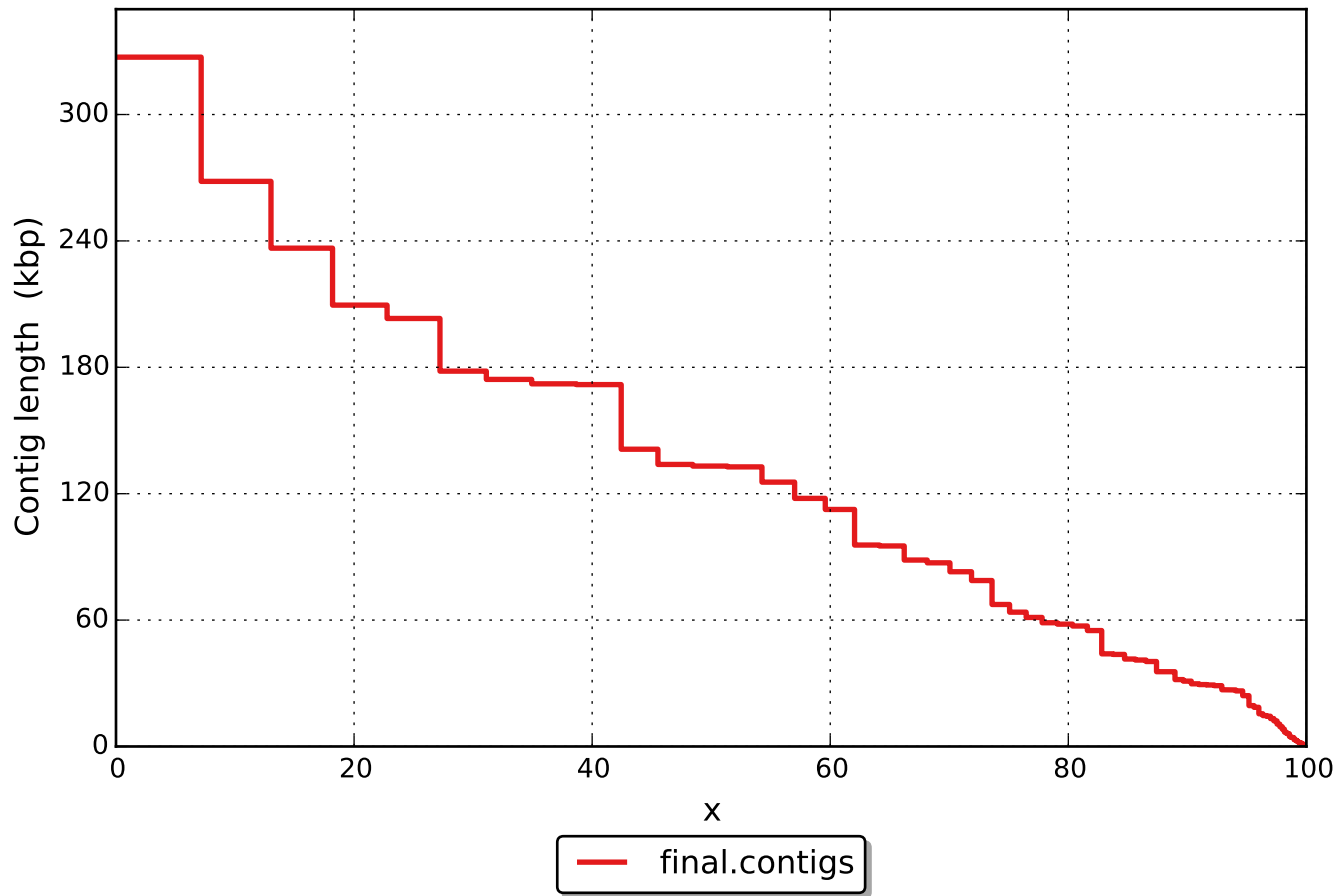
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

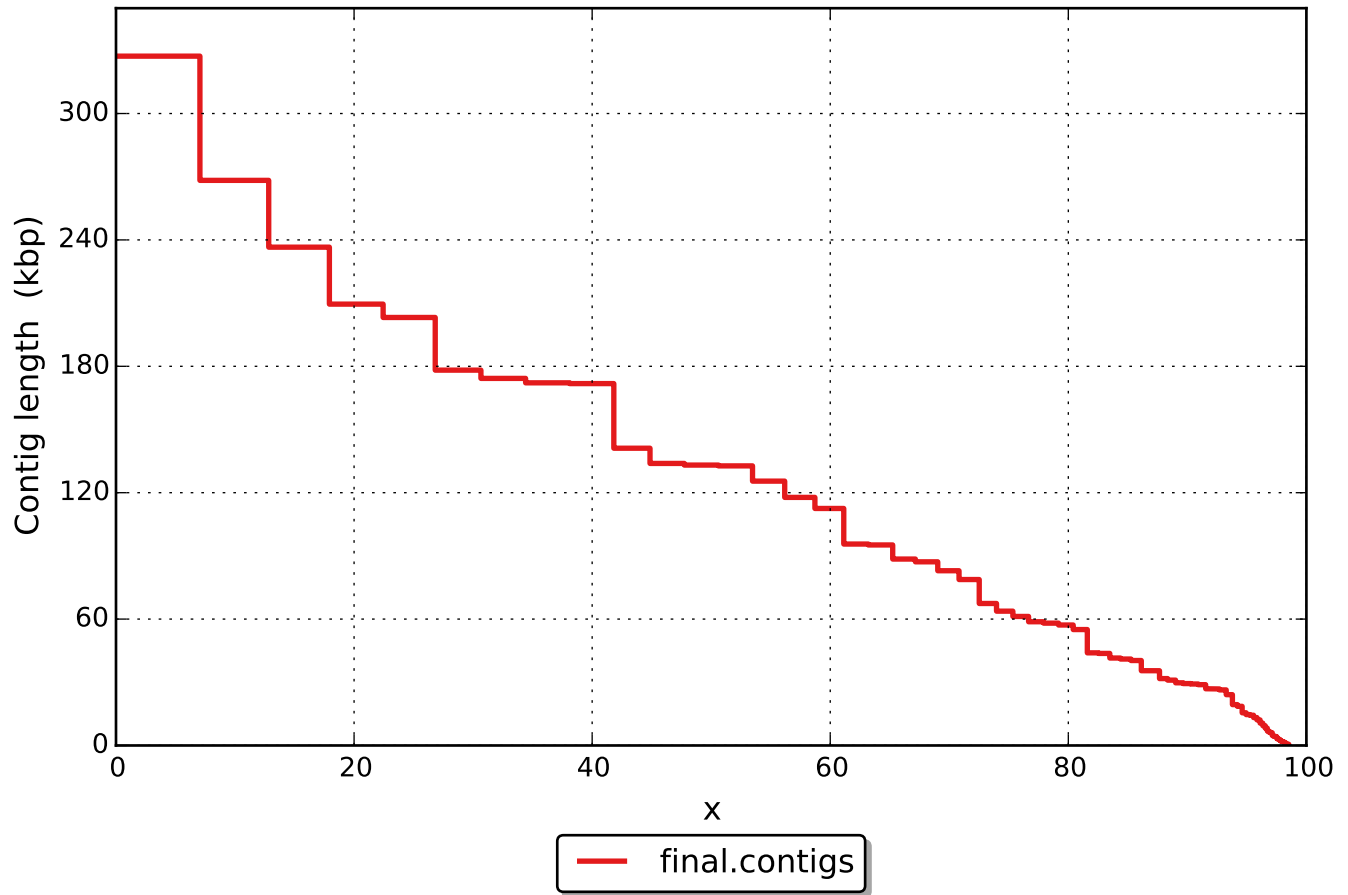
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

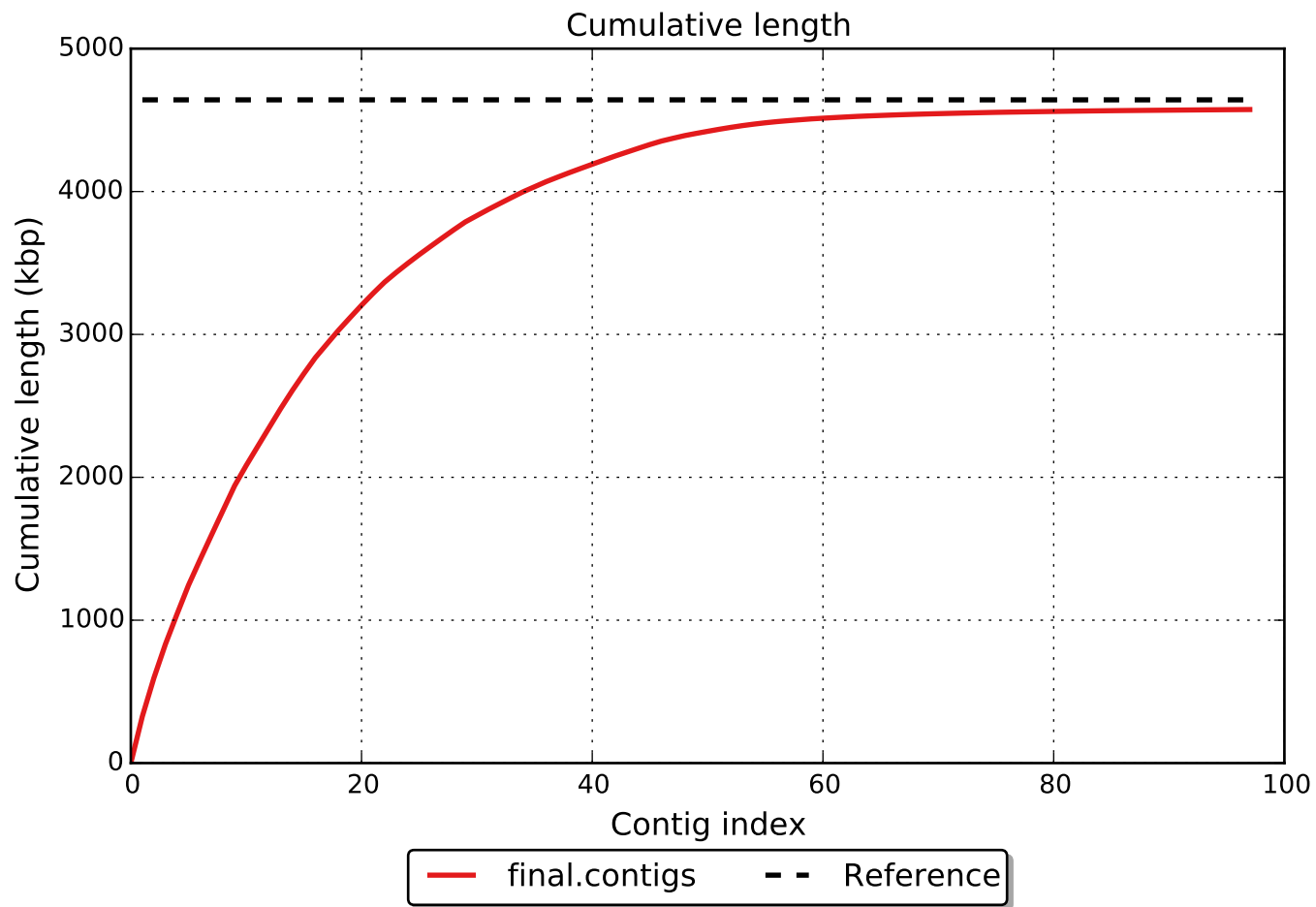
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

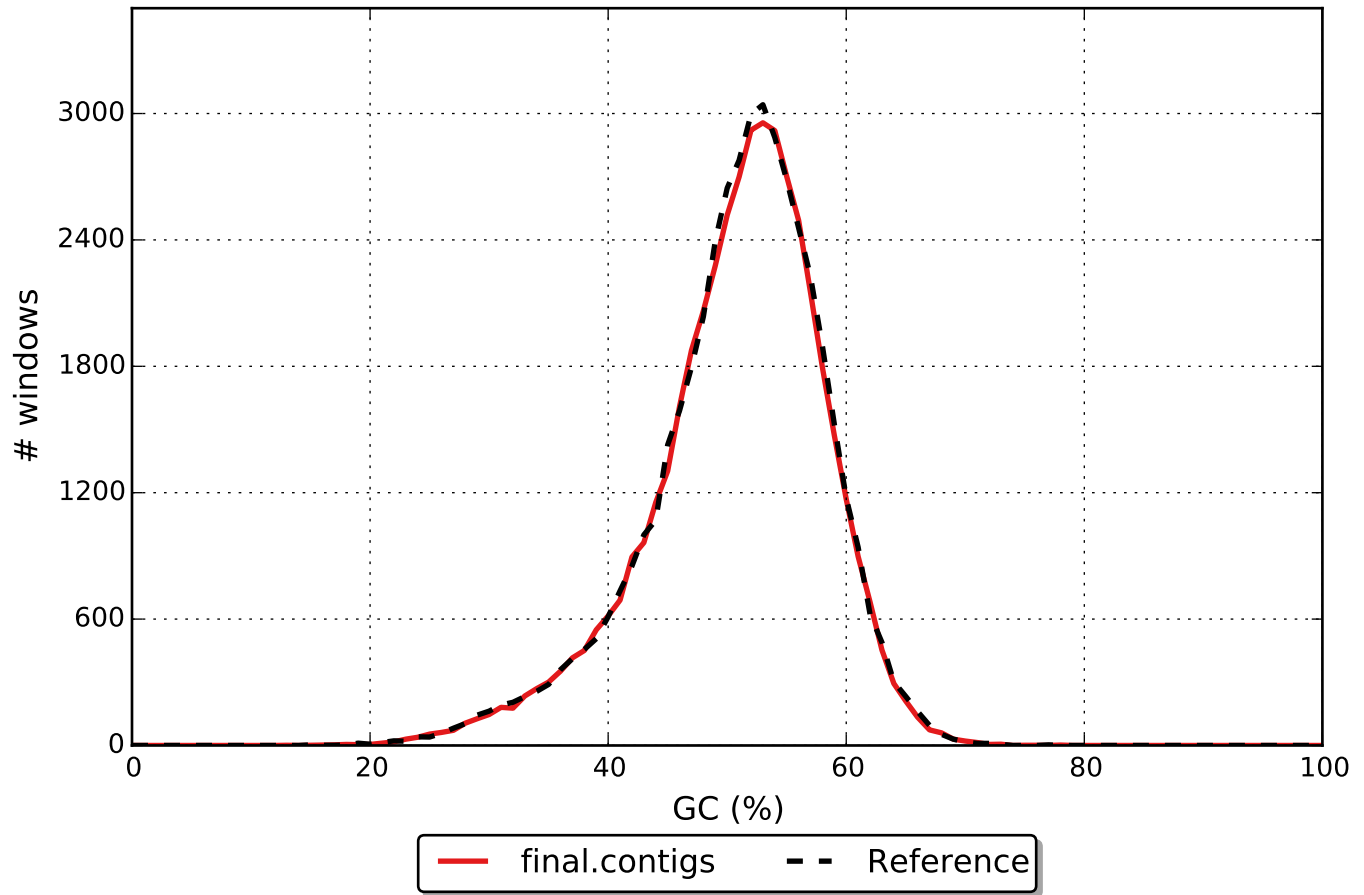


NGx





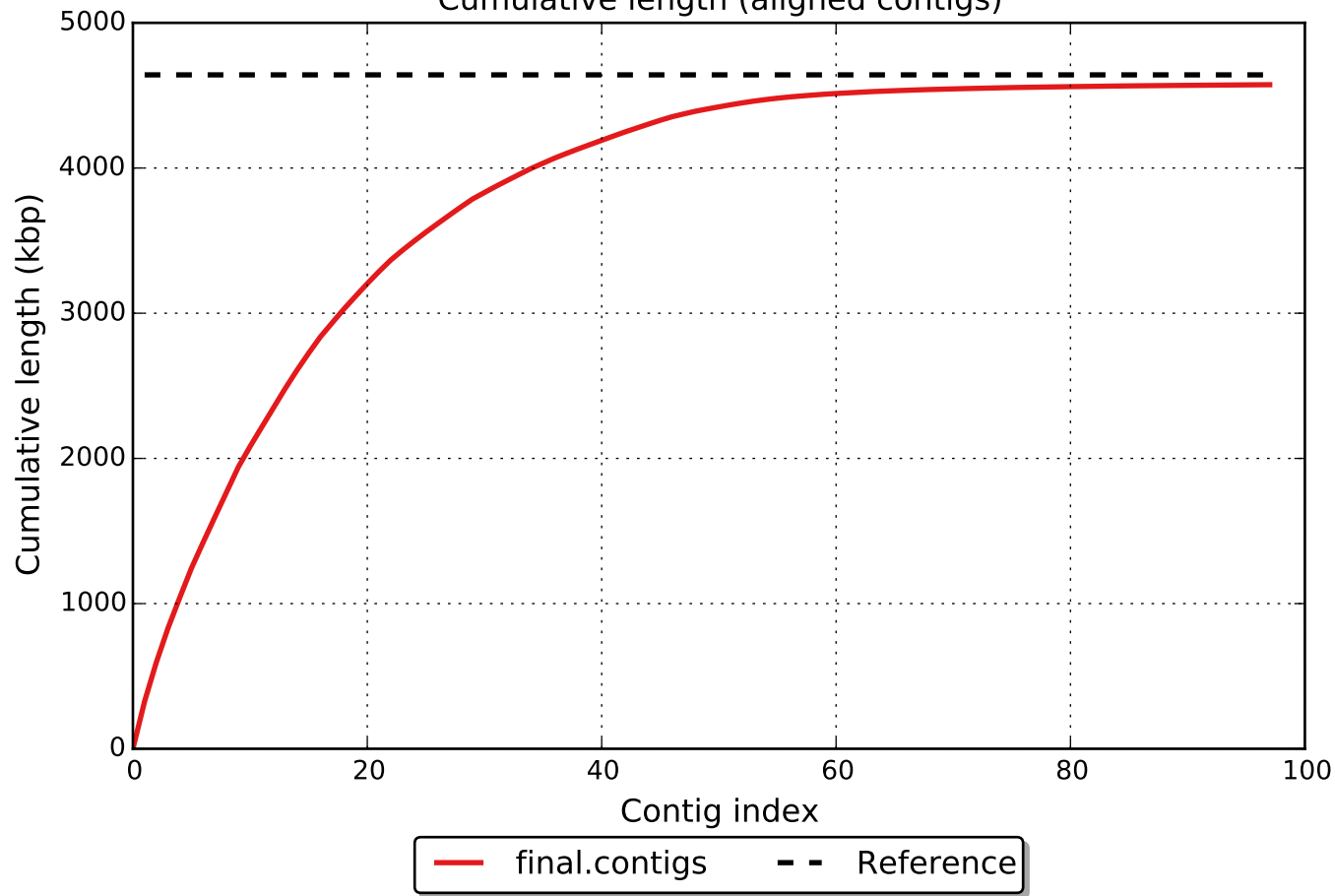
GC content



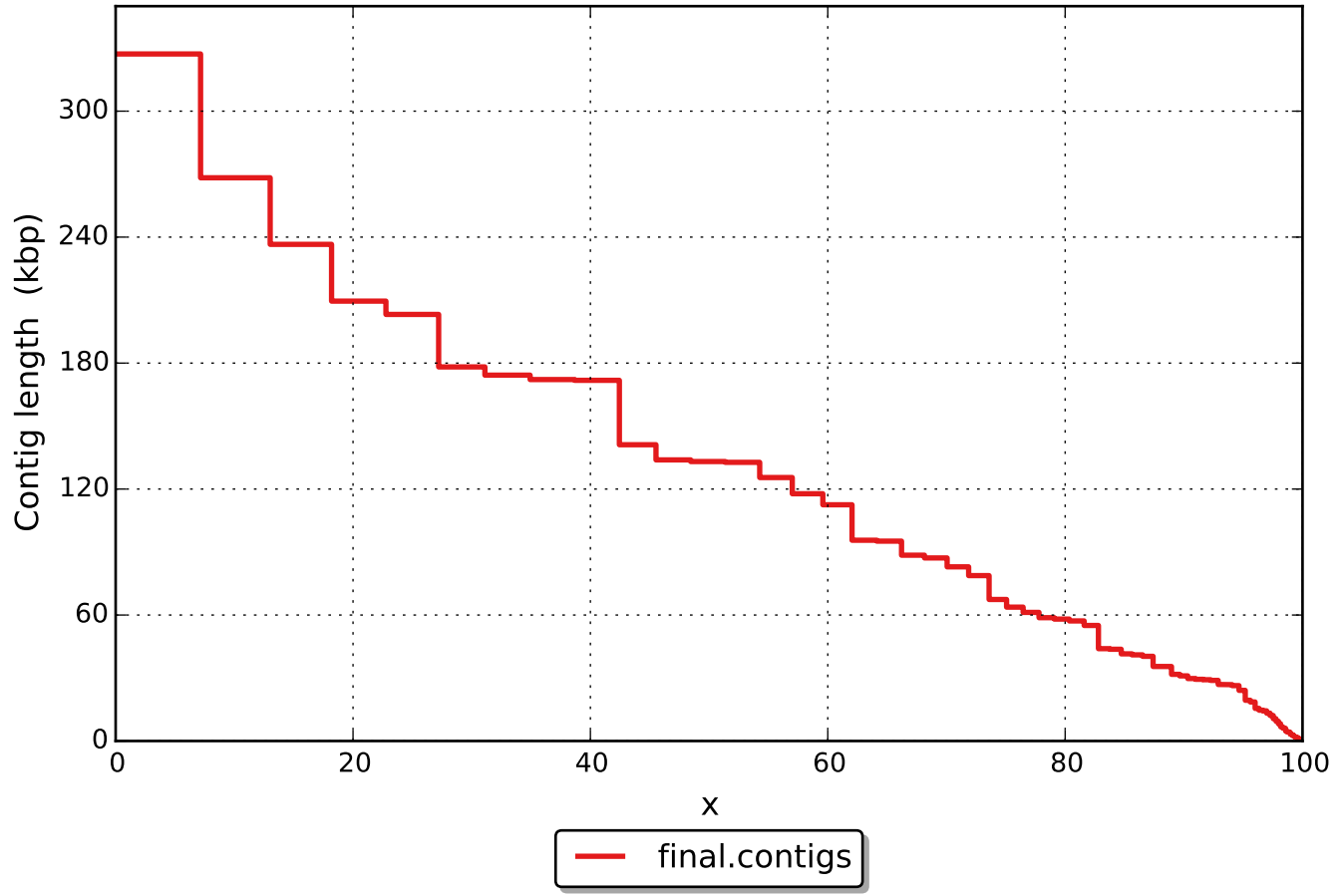
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

