

Report

	final.contigs
# contigs (>= 0 bp)	127
# contigs (>= 1000 bp)	86
# contigs (>= 5000 bp)	61
# contigs (>= 10000 bp)	56
# contigs (>= 25000 bp)	47
# contigs (>= 50000 bp)	30
Total length (>= 0 bp)	4585247
Total length (>= 1000 bp)	4567435
Total length (>= 5000 bp)	4510444
Total length (>= 10000 bp)	4473687
Total length (>= 25000 bp)	4331927
Total length (>= 50000 bp)	3763387
# contigs	99
Largest contig	327235
Total length	4576390
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	132708
NG50	117769
N75	61269
NG75	58799
L50	12
LG50	13
L75	25
LG75	26
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	4
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.487
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2.12
# indels per 100 kbp	0.09
Largest alignment	327235
NA50	132708
NGA50	117769
NA75	61269
NGA75	58799
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	4
# mismatches	97
# indels	4
# short indels	4
# long indels	0
Indels length	4

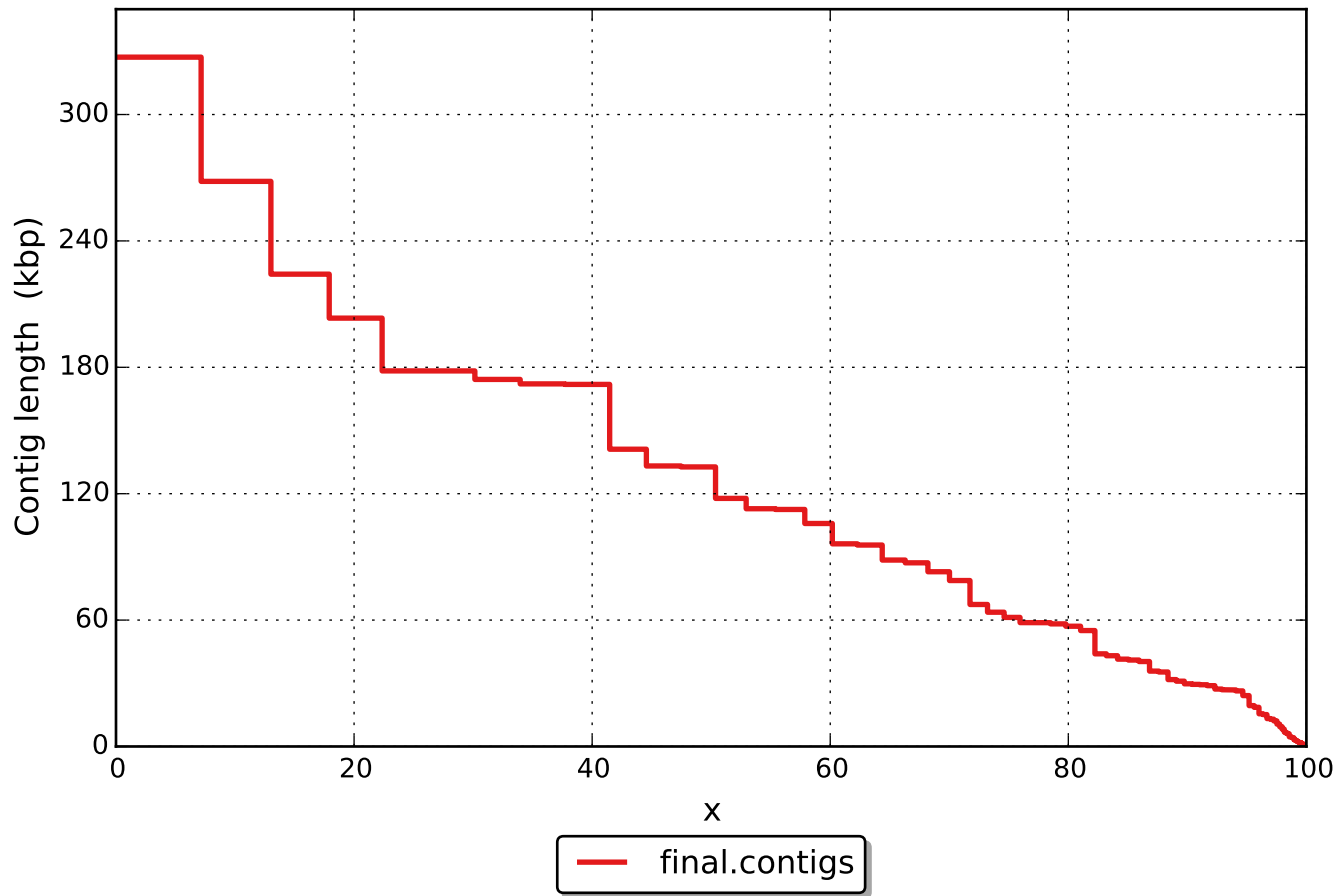
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

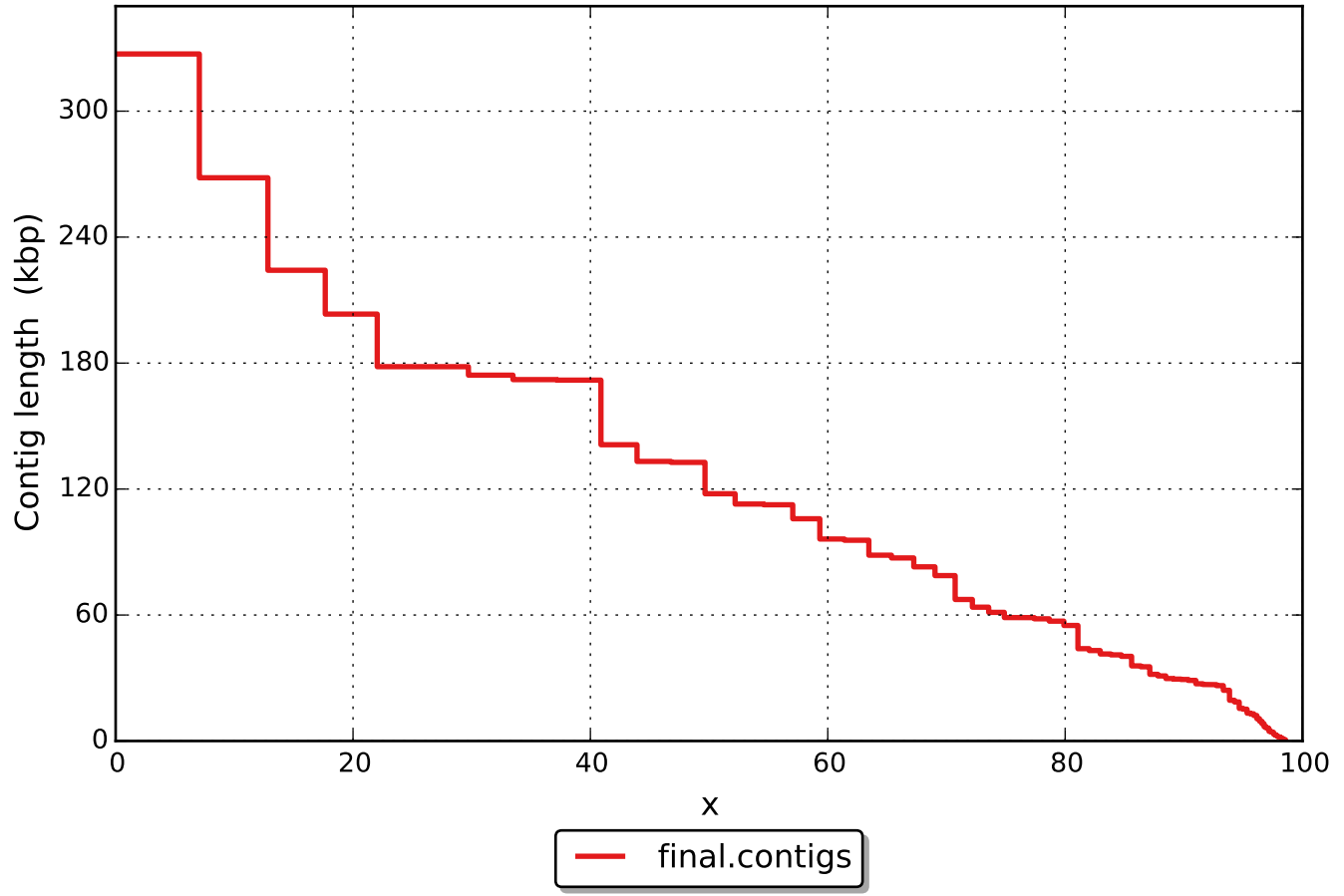
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

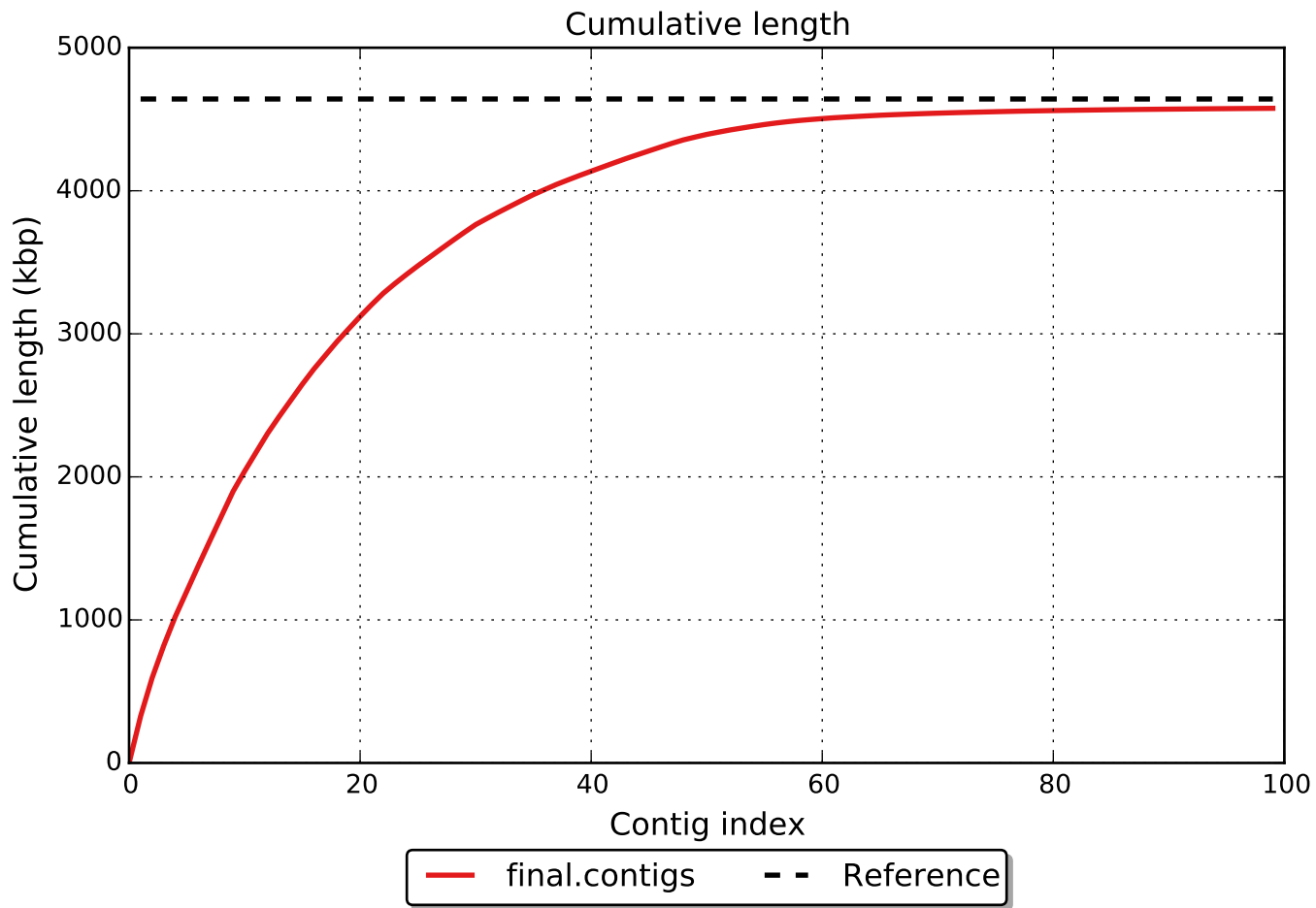
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

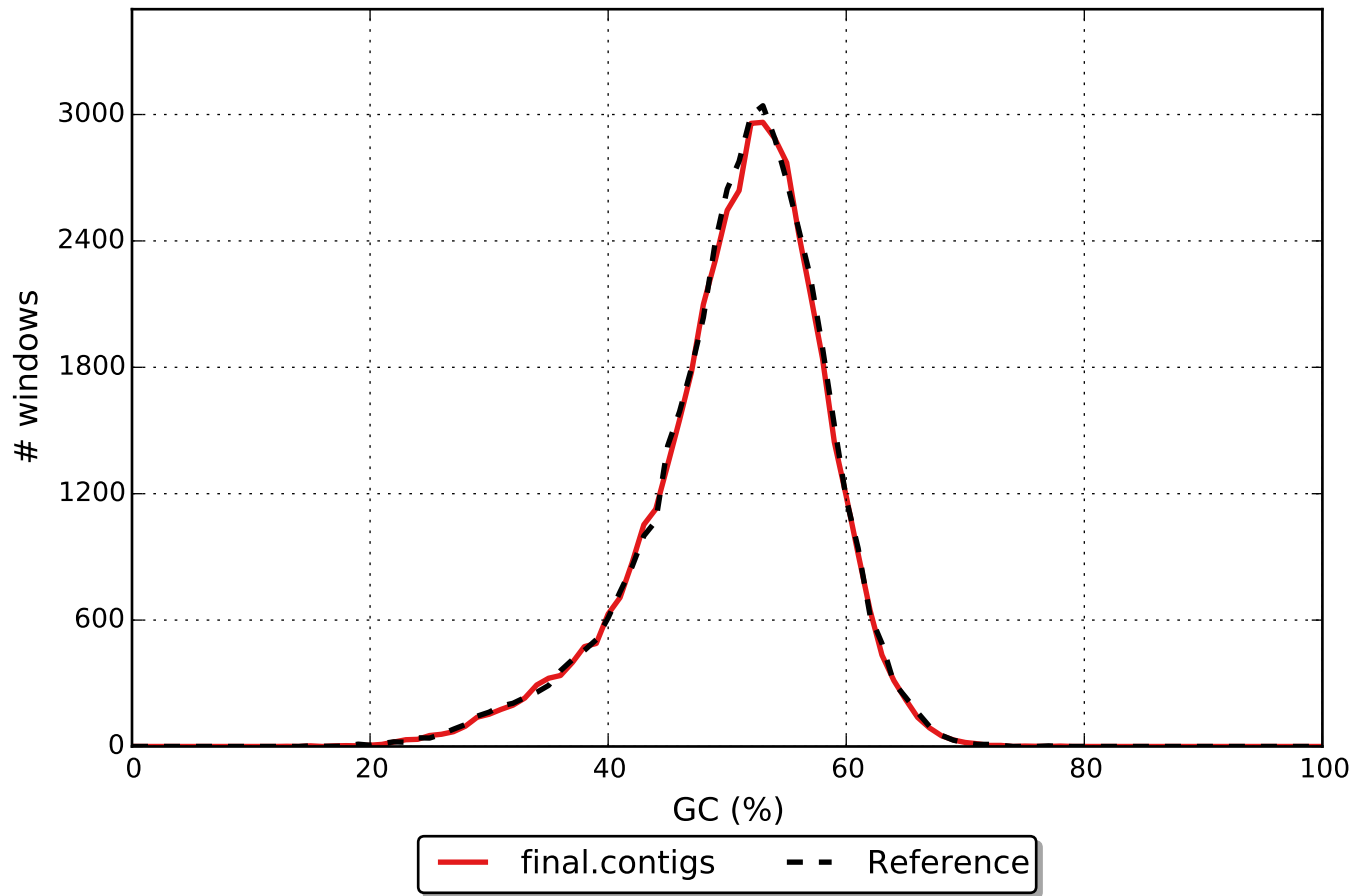


NGx





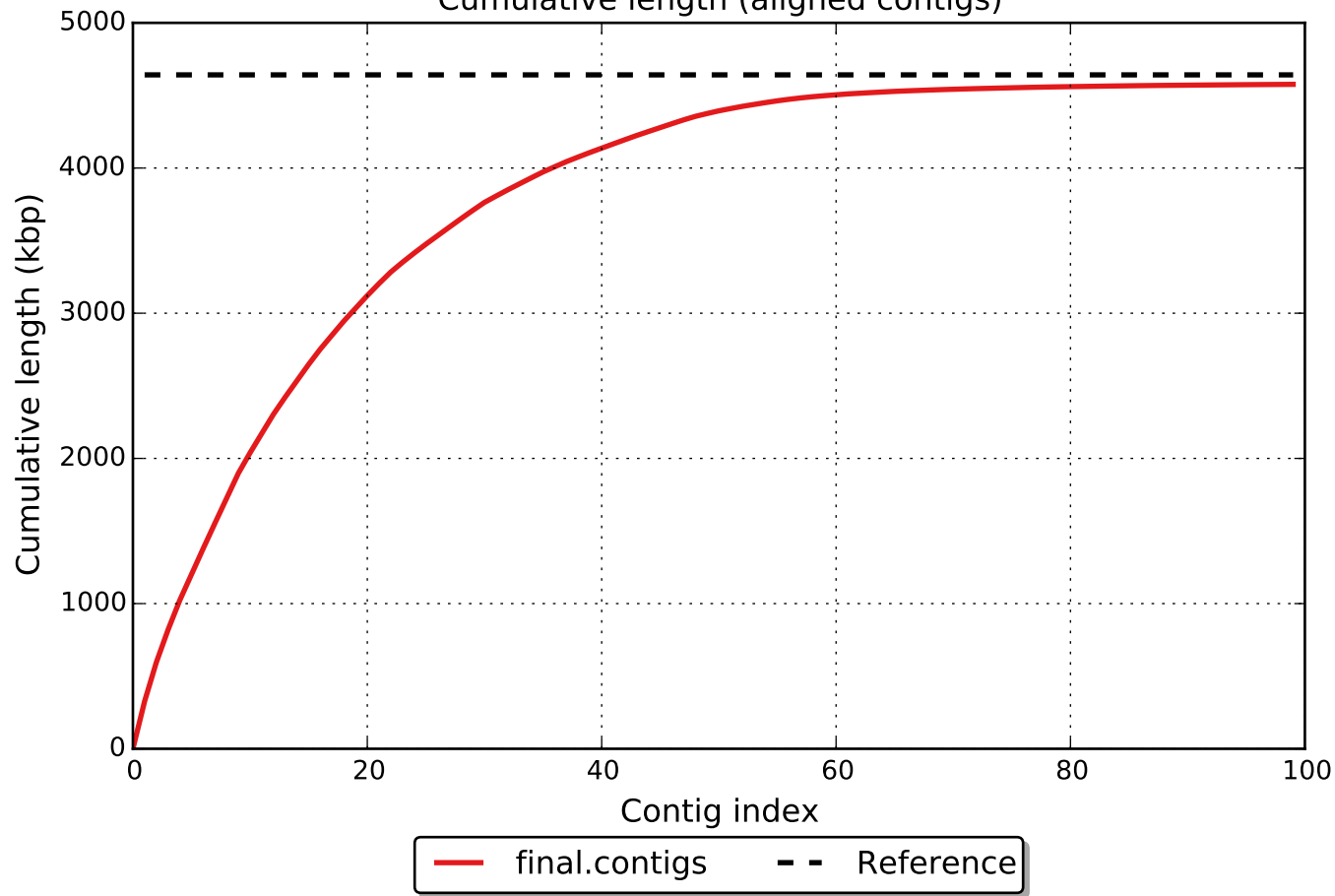
GC content



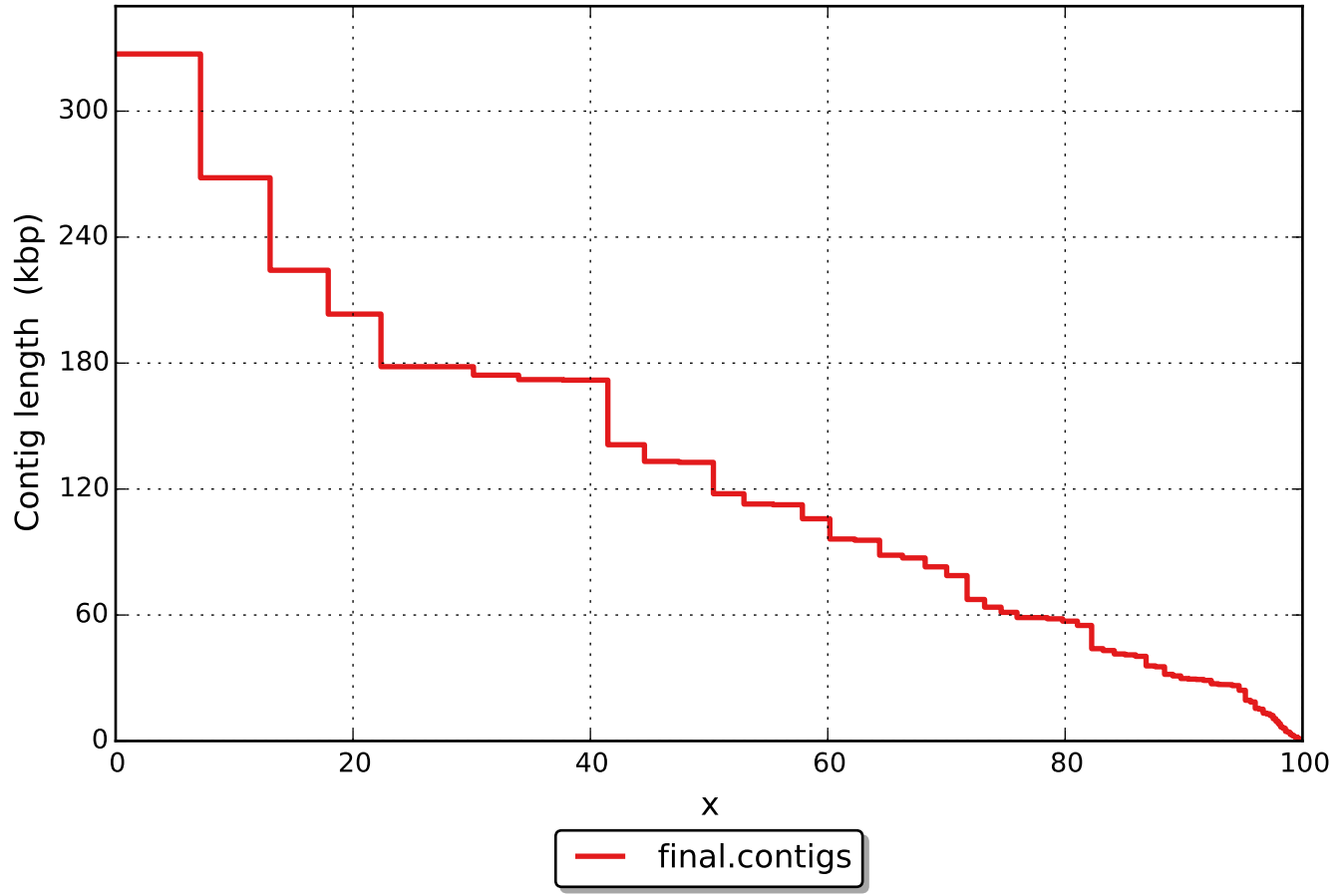
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

