

Report

	final.contigs
# contigs (>= 1000 bp)	96
# contigs (>= 5000 bp)	73
# contigs (>= 10000 bp)	67
# contigs (>= 25000 bp)	52
# contigs (>= 50000 bp)	32
Total length (>= 1000 bp)	4553175
Total length (>= 5000 bp)	4508428
Total length (>= 10000 bp)	4462114
Total length (>= 25000 bp)	4218044
Total length (>= 50000 bp)	3521899
# contigs	111
Largest contig	327137
Total length	4563905
Reference length	4641652
GC (℥)	50.74
Reference GC (℥)	50.79
N50	105688
NG50	105688
N75	52804
NG75	51558
L50	14
LG50	14
L75	31
LG75	32
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	12
# unaligned contigs	0 + 3 part
Unaligned length	153
Genome fraction (℥)	98.270
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	58.84
# indels per 100 kbp	9.27
Largest alignment	327137
NA50	105688
NGA50	105688
NA75	52804
NGA75	51558
LA50	14
LGA50	14
LA75	31
LGA75	32

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	12
# mismatches	2684
# indels	423
# short indels	422
# long indels	1
Indels length	660

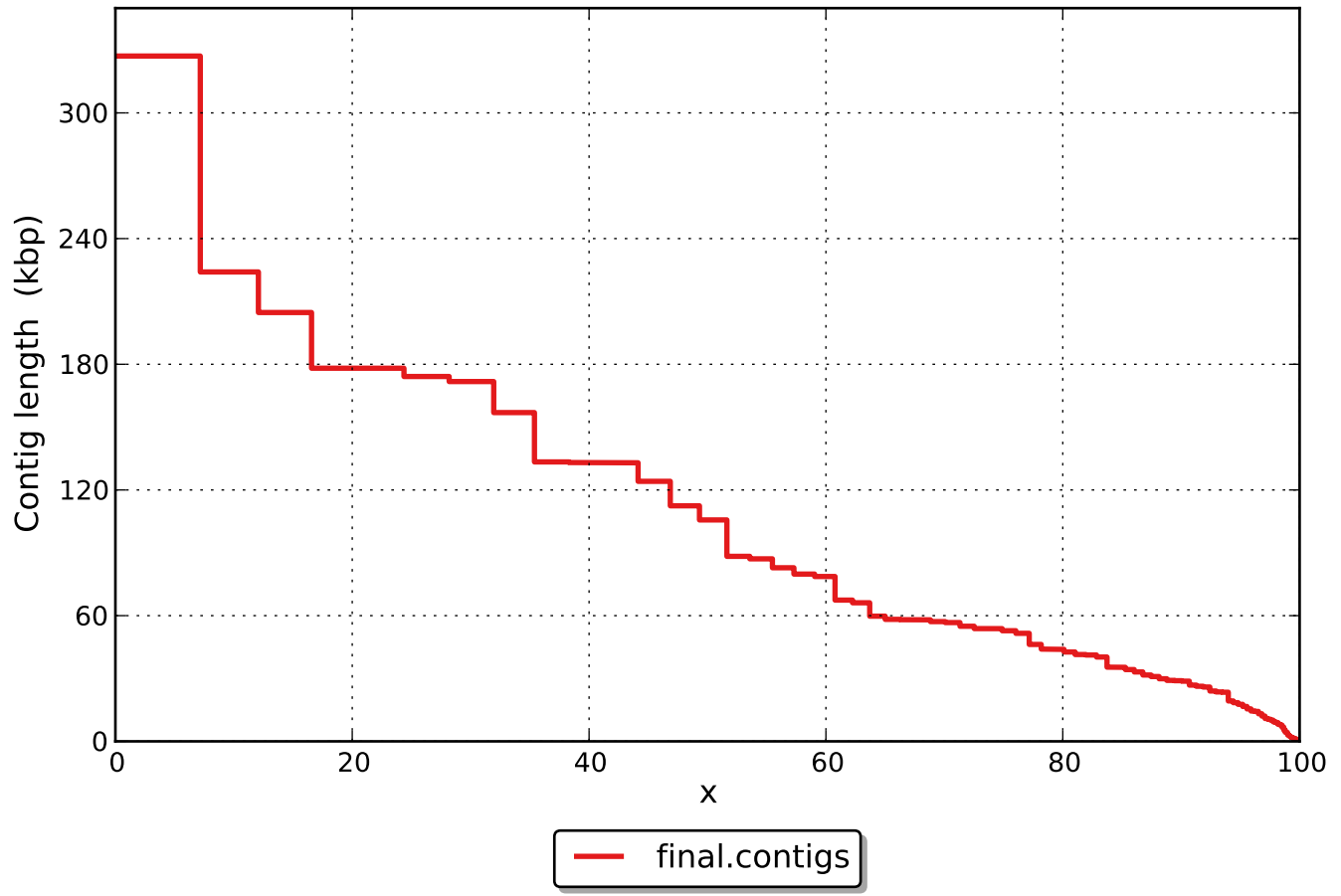
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

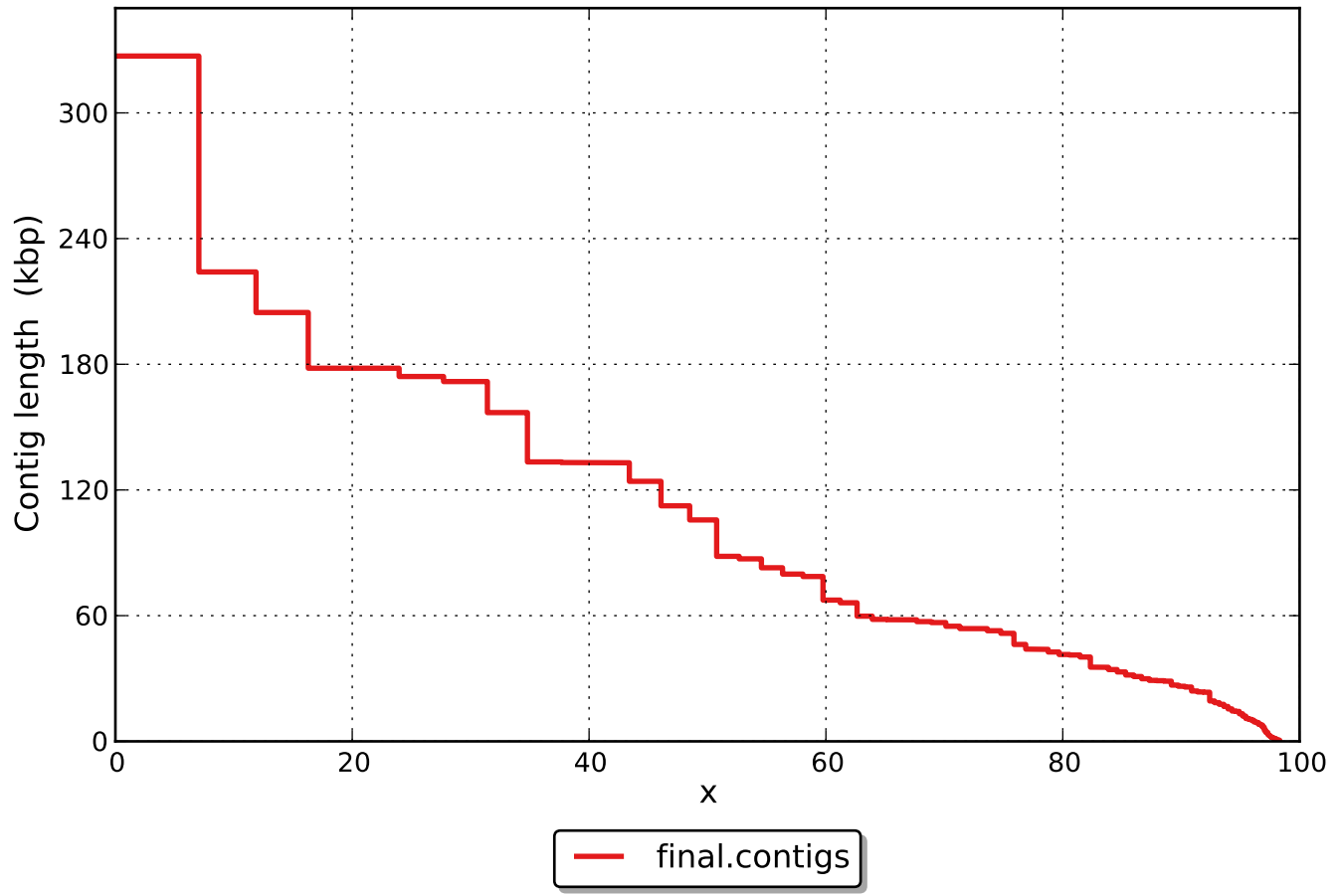
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	3
# with misassembly	0
# both parts are significant	0
Partially unaligned length	153
# N's	0

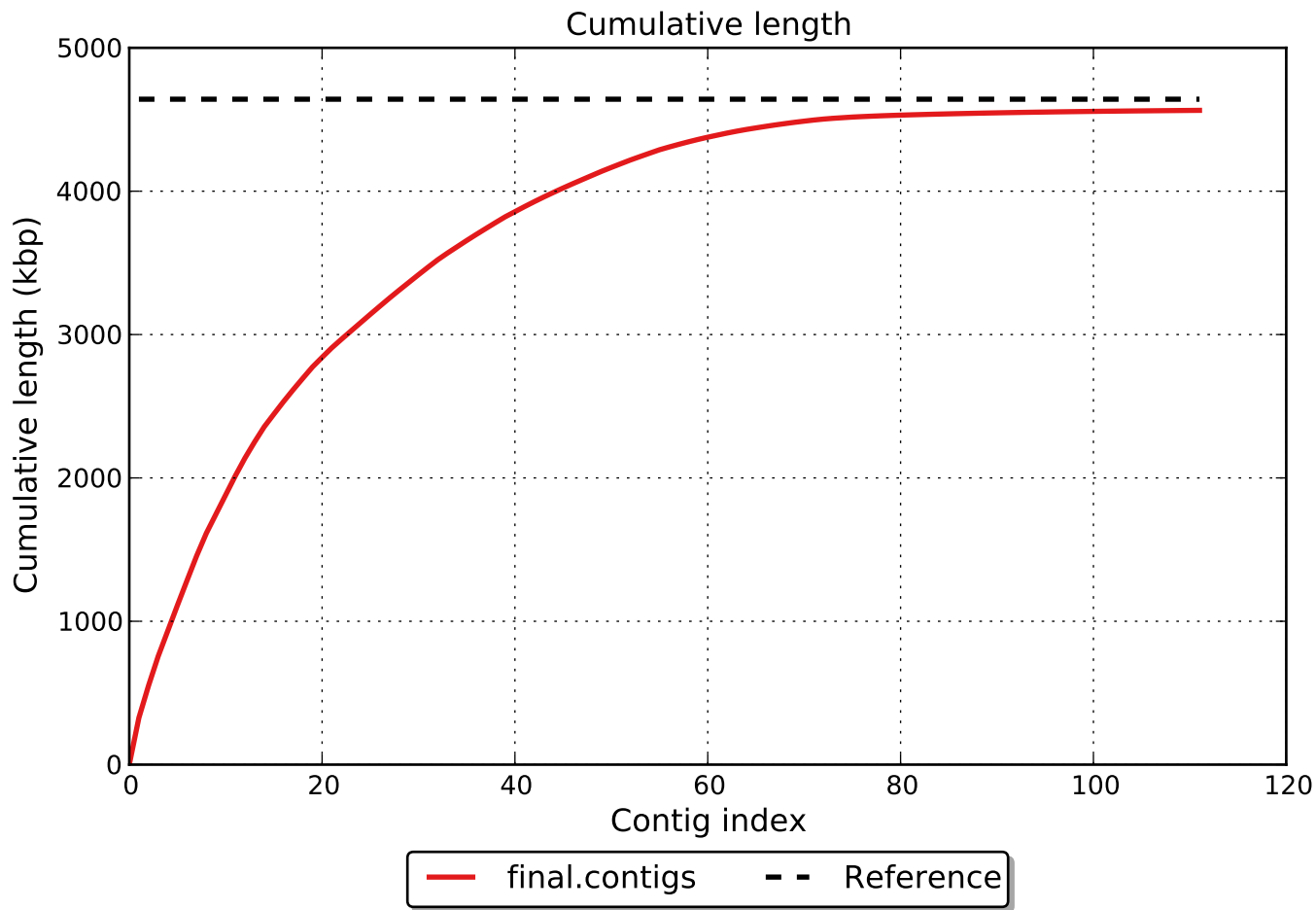
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

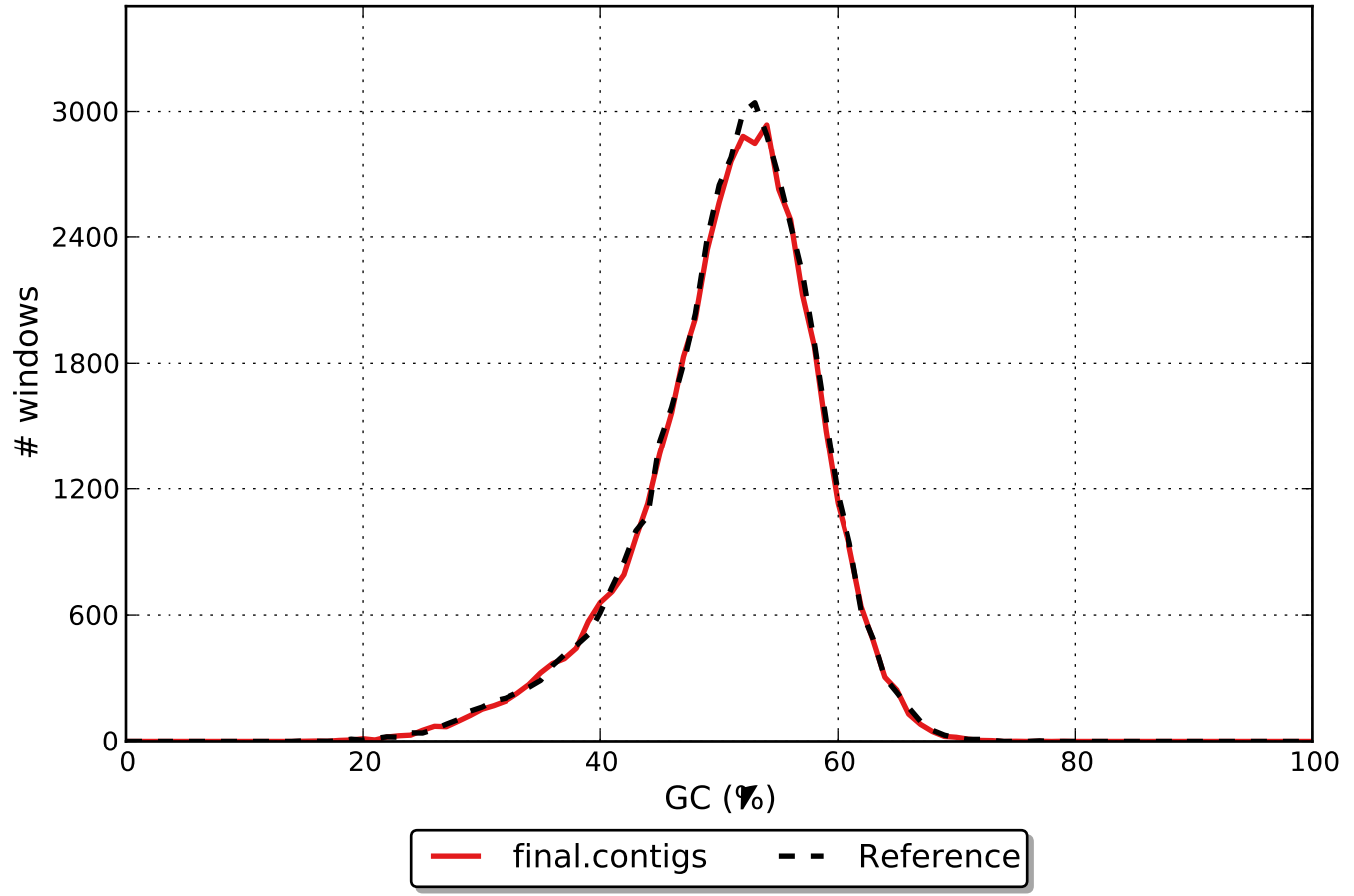


NGx





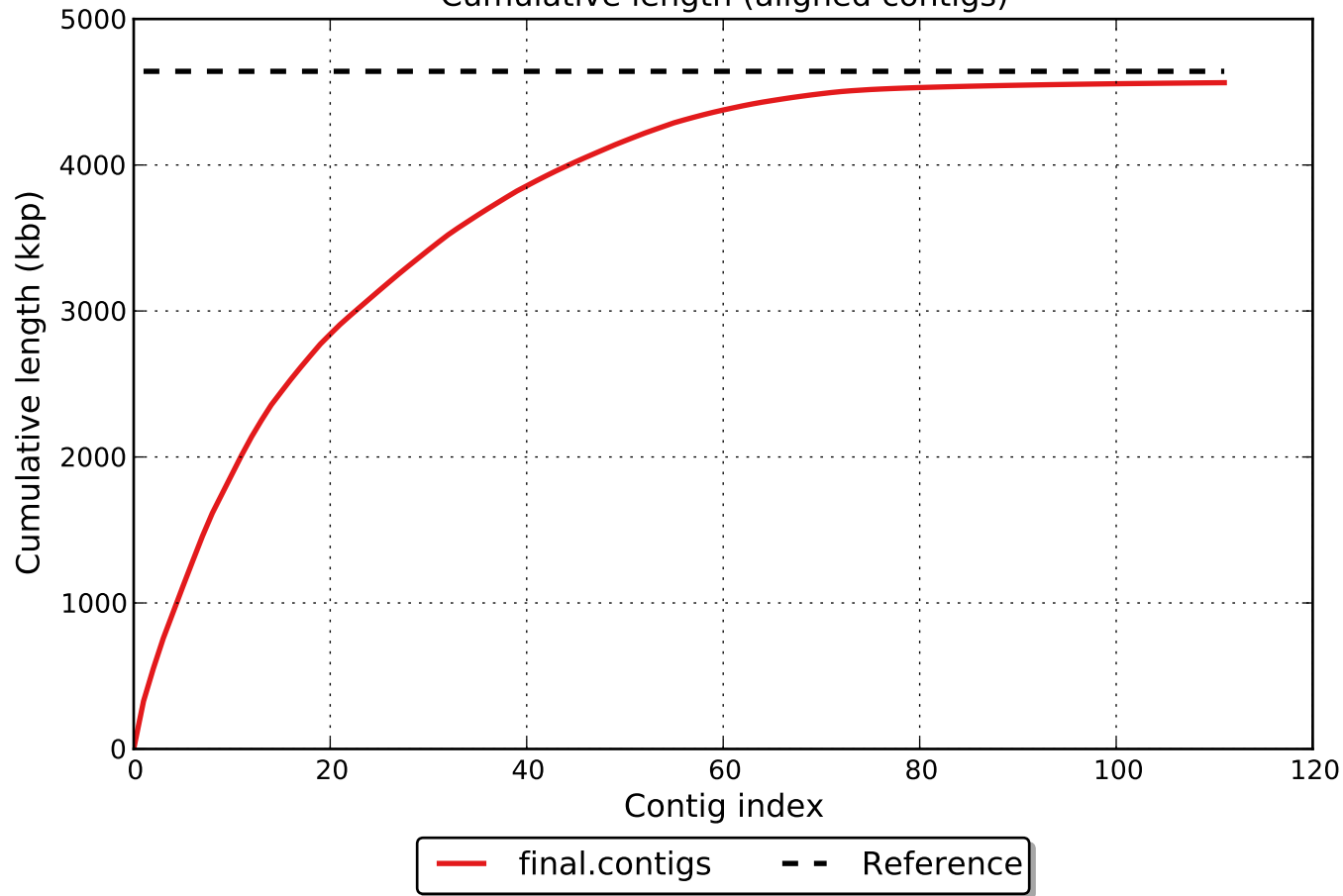
GC content



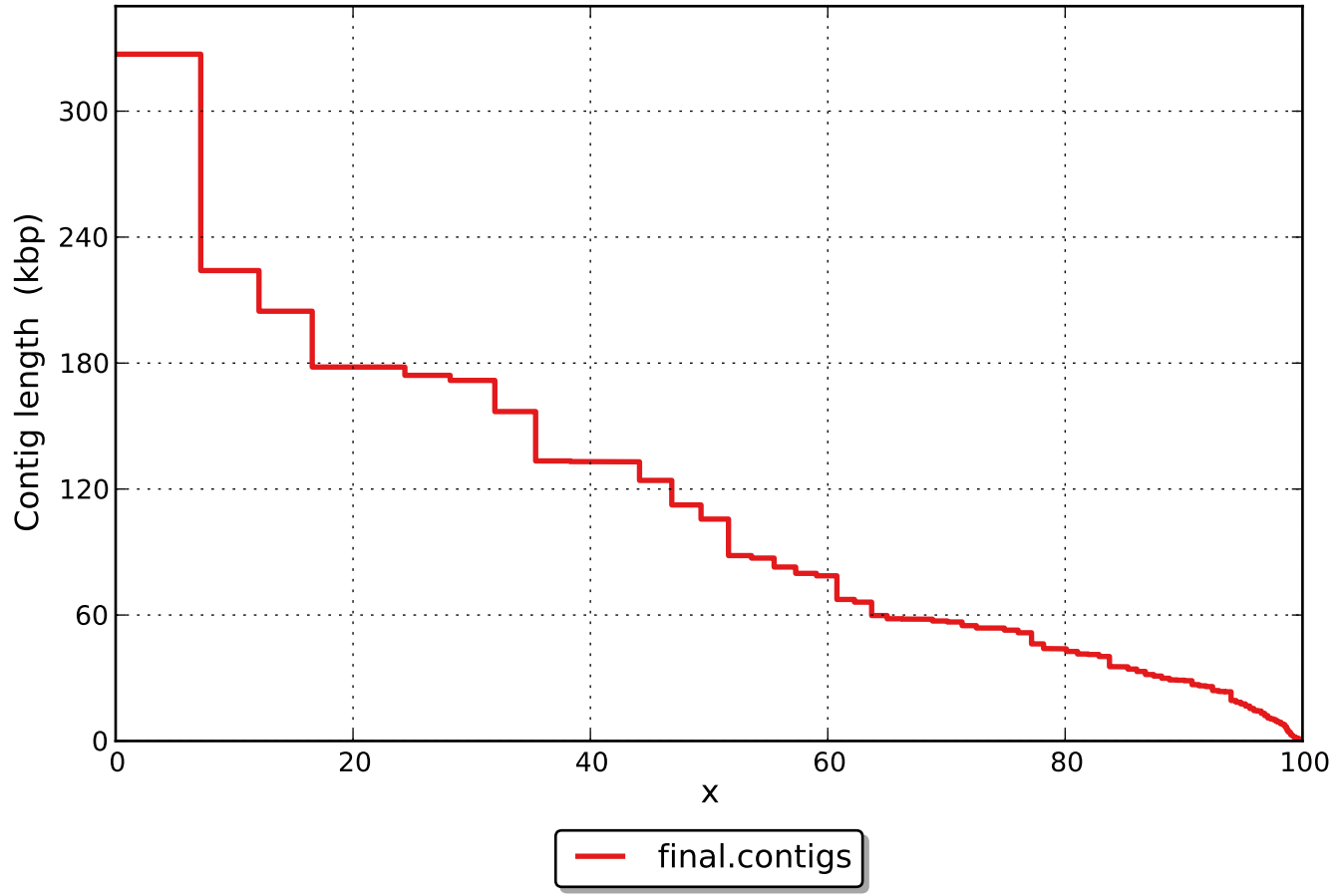
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

