

Report

	final.contigs
# contigs (≥ 0 bp)	238
# contigs (≥ 1000 bp)	127
# contigs (≥ 5000 bp)	100
# contigs (≥ 10000 bp)	87
# contigs (≥ 25000 bp)	63
# contigs (≥ 50000 bp)	32
Total length (≥ 0 bp)	4597283
Total length (≥ 1000 bp)	4556951
Total length (≥ 5000 bp)	4495313
Total length (≥ 10000 bp)	4396217
Total length (≥ 25000 bp)	3992149
Total length (≥ 50000 bp)	2877275
# contigs	238
Largest contig	309478
Total length	4597283
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	71793
NG50	71793
N75	37774
NG75	35546
L50	23
LG50	23
L75	46
LG75	47
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# unaligned contigs	35 + 0 part
Unaligned length	11862
Genome fraction (%)	98.497
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	7.28
# indels per 100 kbp	0.04
Largest alignment	309478
NA50	71793
NGA50	71793
NA75	37774
NGA75	35546
LA50	23
LGA50	23
LA75	46
LGA75	47

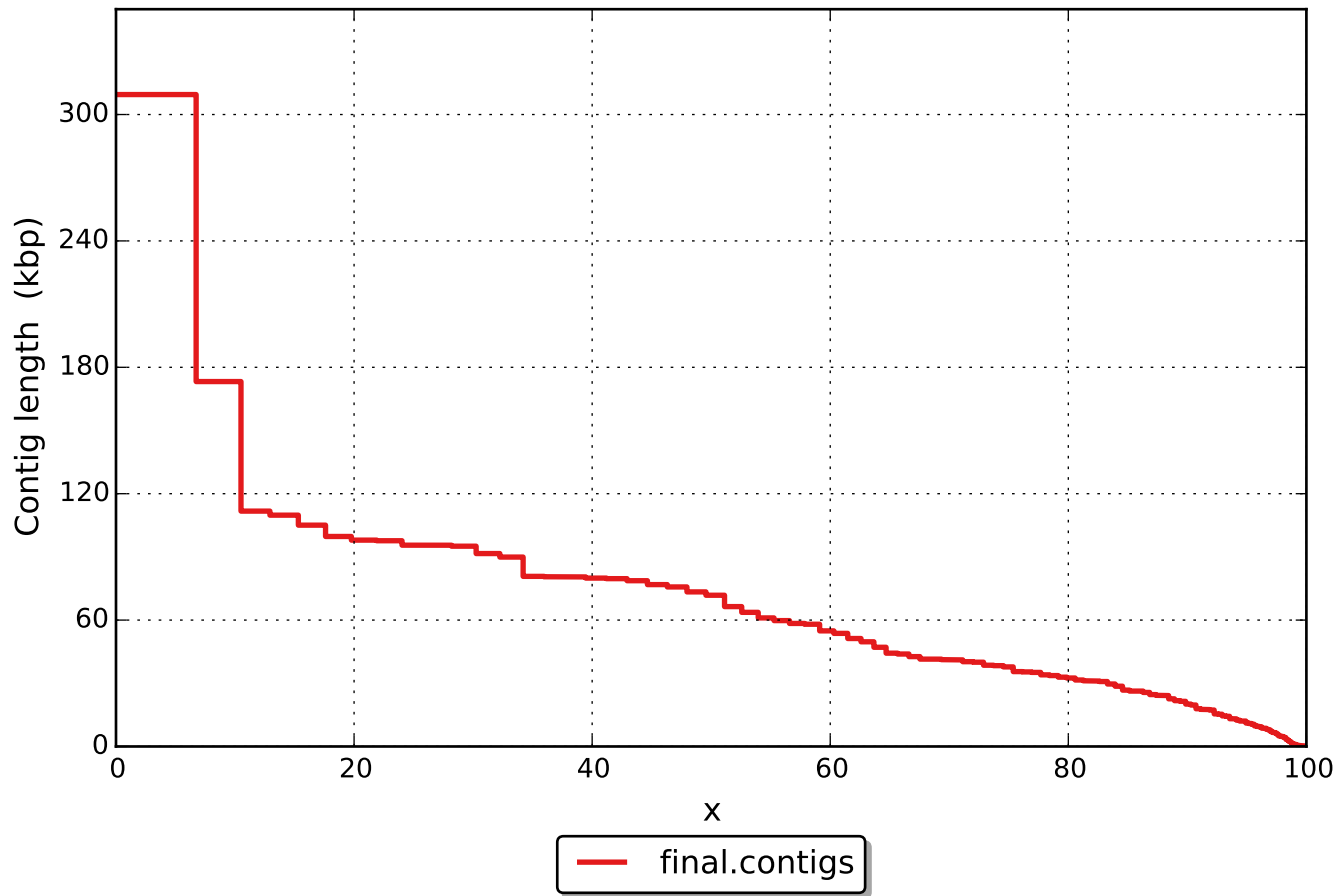
Misassemblies report

	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# mismatches	333
# indels	2
# short indels	2
# long indels	0
Indels length	3

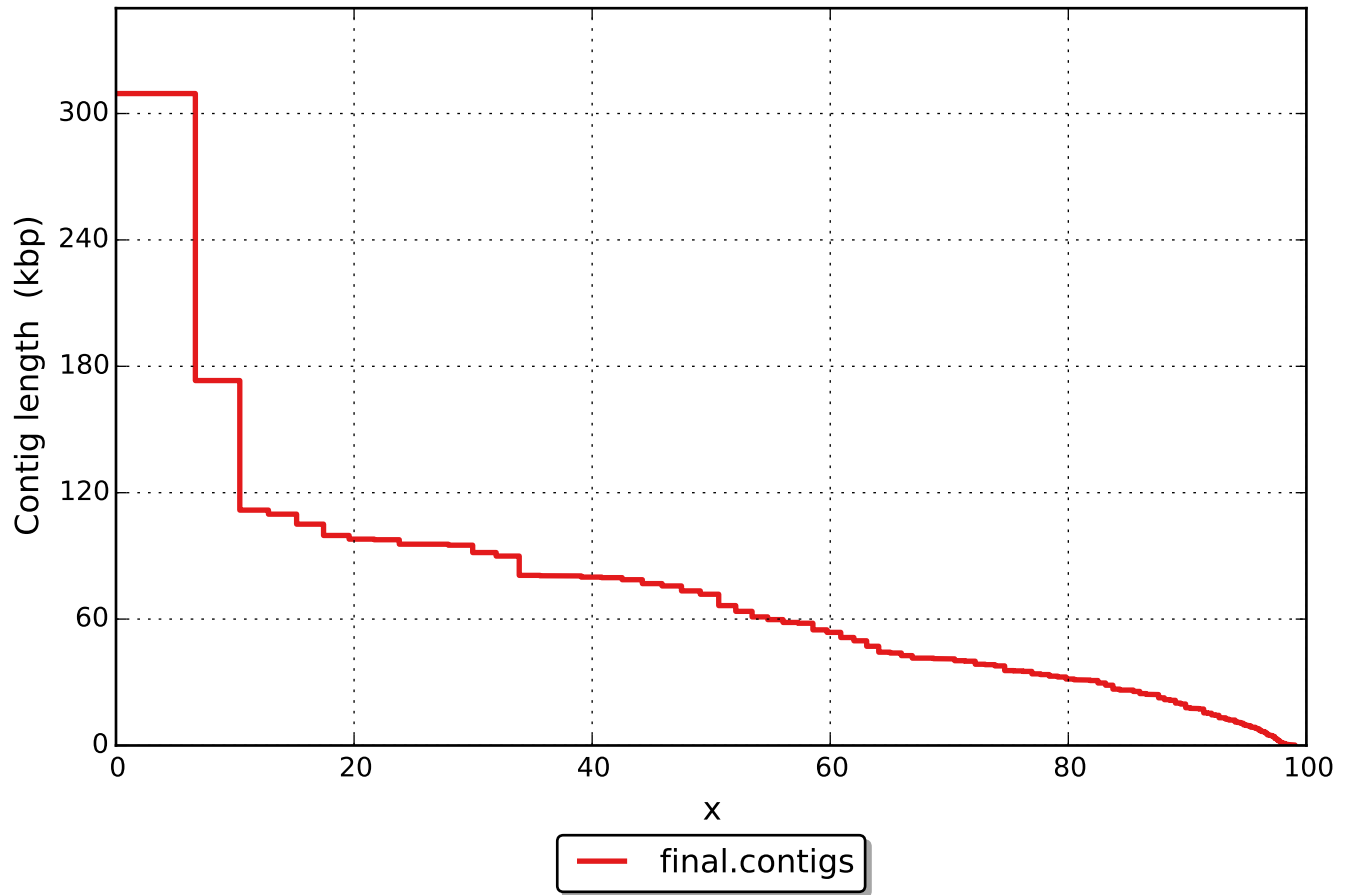
Unaligned report

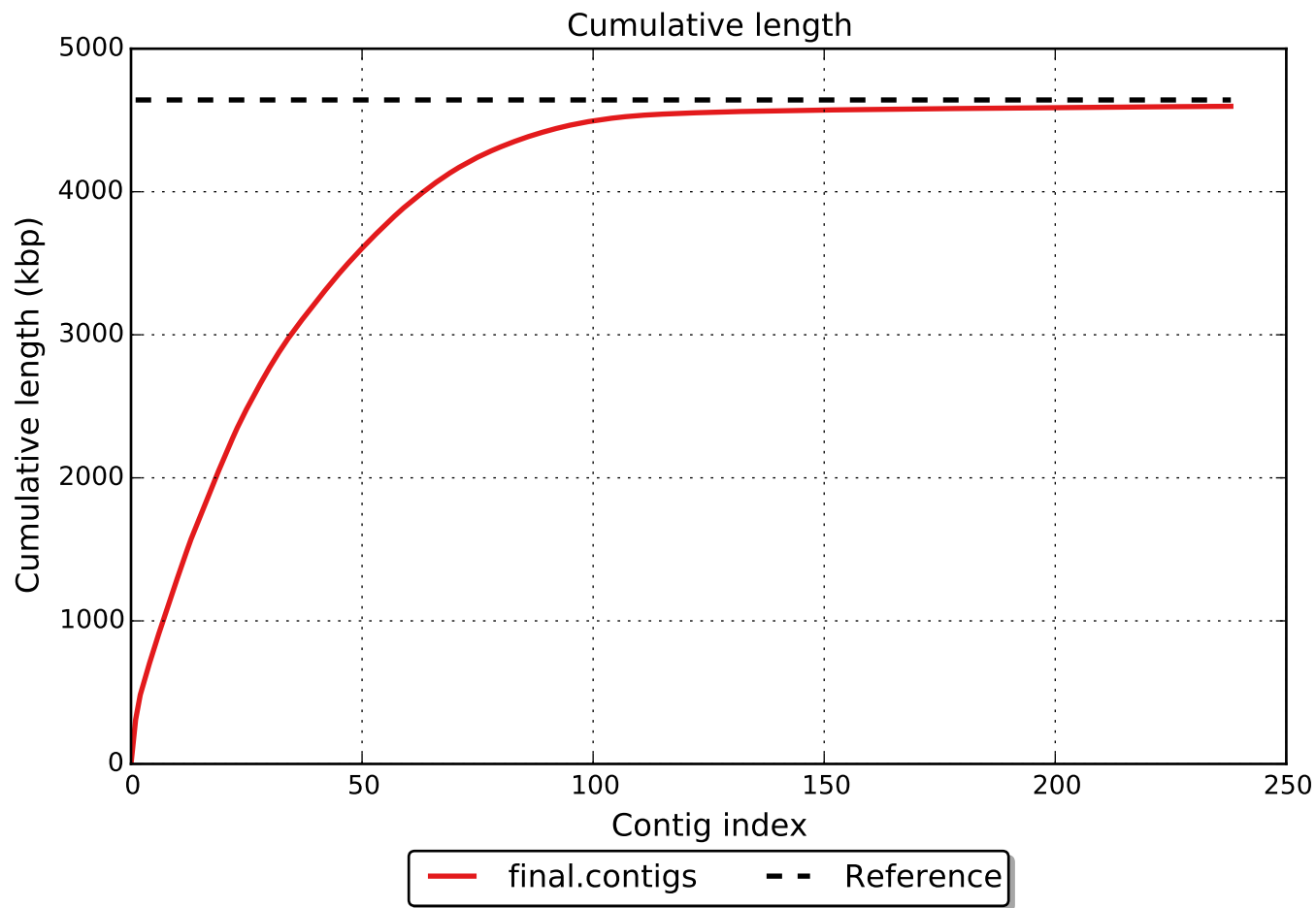
	final.contigs
# fully unaligned contigs	35
Fully unaligned length	11862
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

Nx

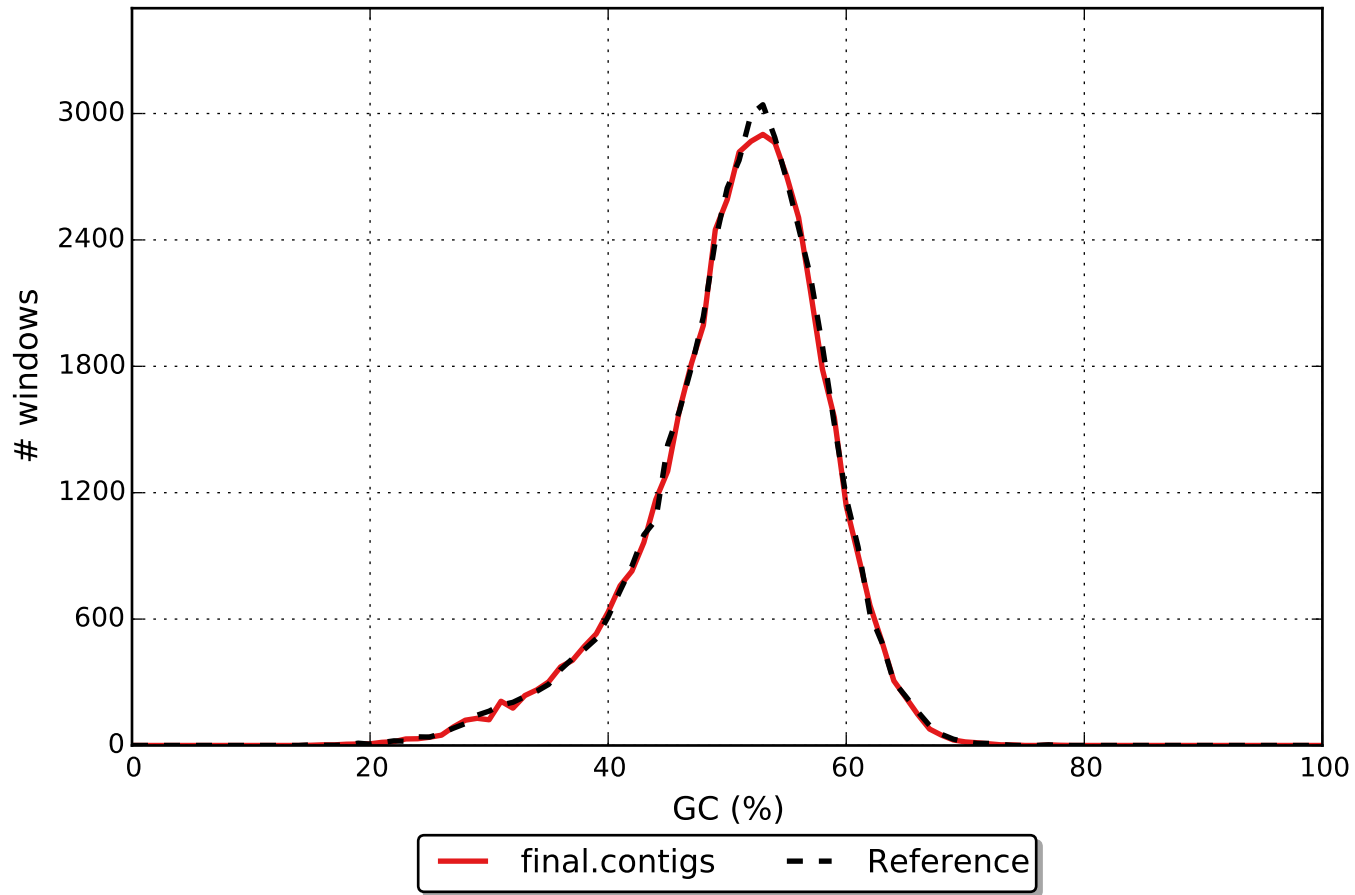


NGx





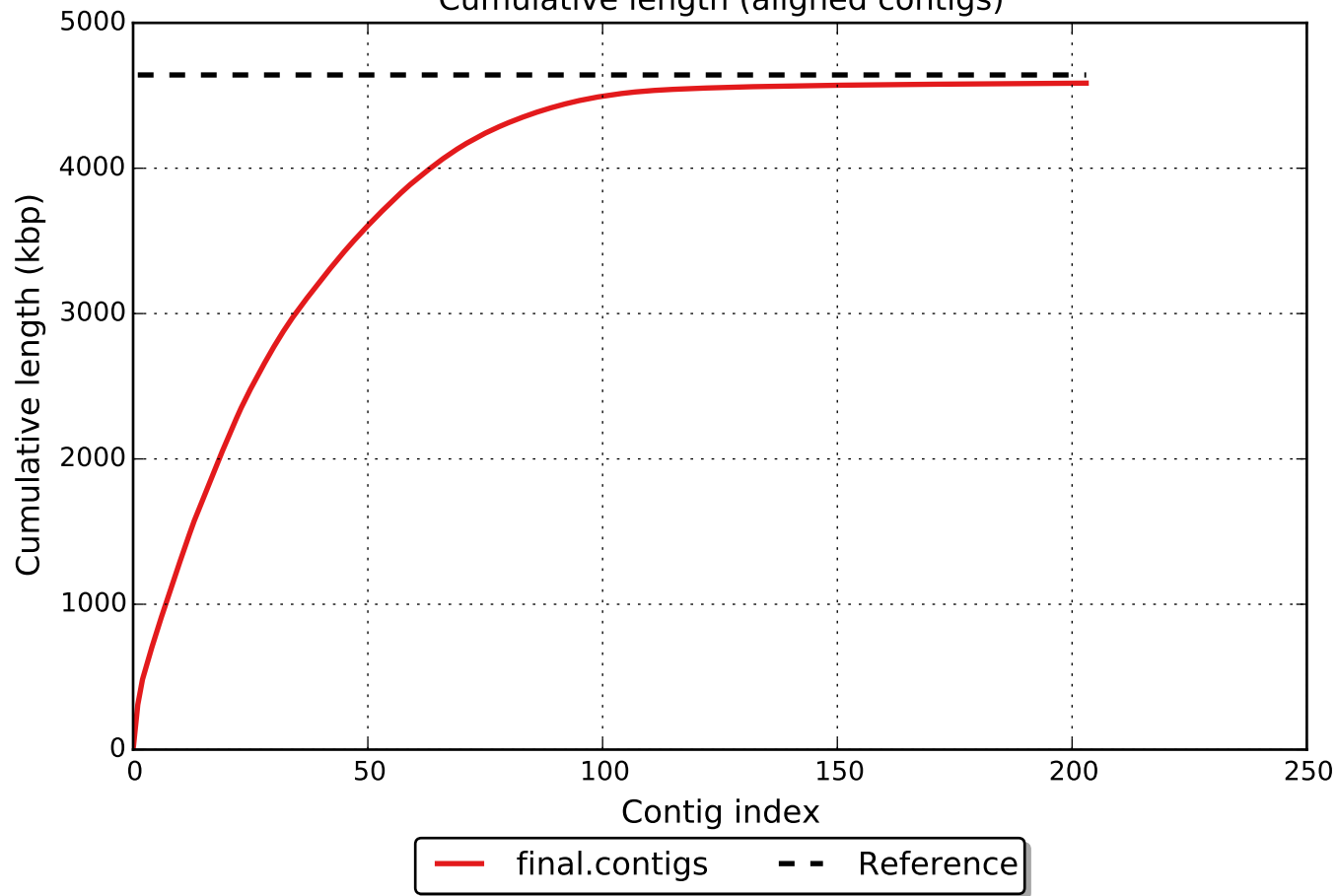
GC content



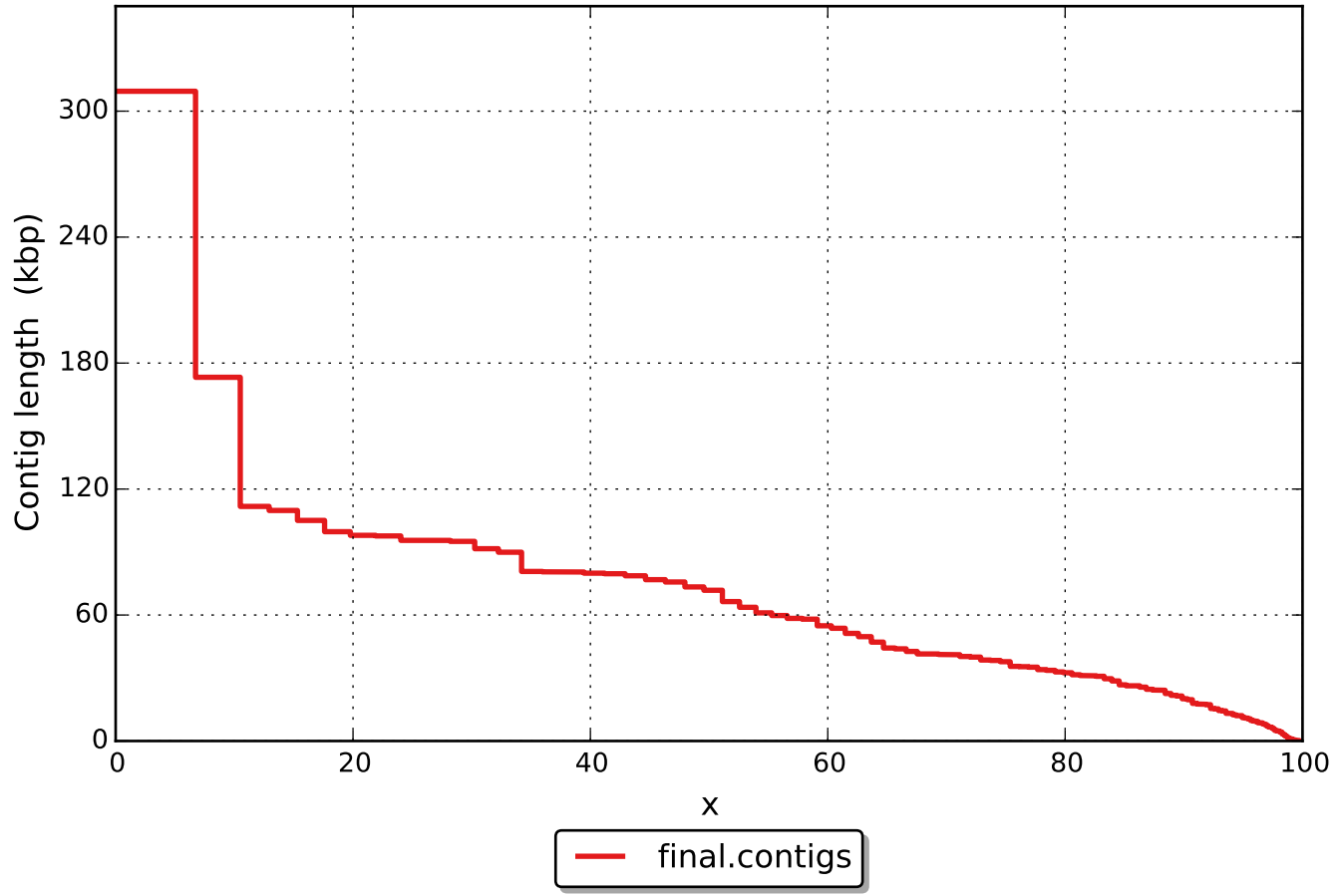
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

