

Report

	final.contigs
# contigs (≥ 0 bp)	178
# contigs (≥ 1000 bp)	93
# contigs (≥ 5000 bp)	69
# contigs (≥ 10000 bp)	63
# contigs (≥ 25000 bp)	49
# contigs (≥ 50000 bp)	30
Total length (≥ 0 bp)	4581338
Total length (≥ 1000 bp)	4550640
Total length (≥ 5000 bp)	4498283
Total length (≥ 10000 bp)	4452670
Total length (≥ 25000 bp)	4227784
Total length (≥ 50000 bp)	3587644
# contigs	178
Largest contig	327151
Total length	4581338
Reference length	4641652
GC (%)	50.76
Reference GC (%)	50.79
N50	112430
NG50	112430
N75	58008
NG75	54946
L50	14
LG50	14
L75	28
LG75	29
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 2 part
Unaligned length	177
Genome fraction (%)	98.553
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.37
# indels per 100 kbp	0.00
Largest alignment	327151
NA50	112430
NGA50	112430
NA75	58008
NGA75	54946
LA50	14
LGA50	14
LA75	28
LGA75	29

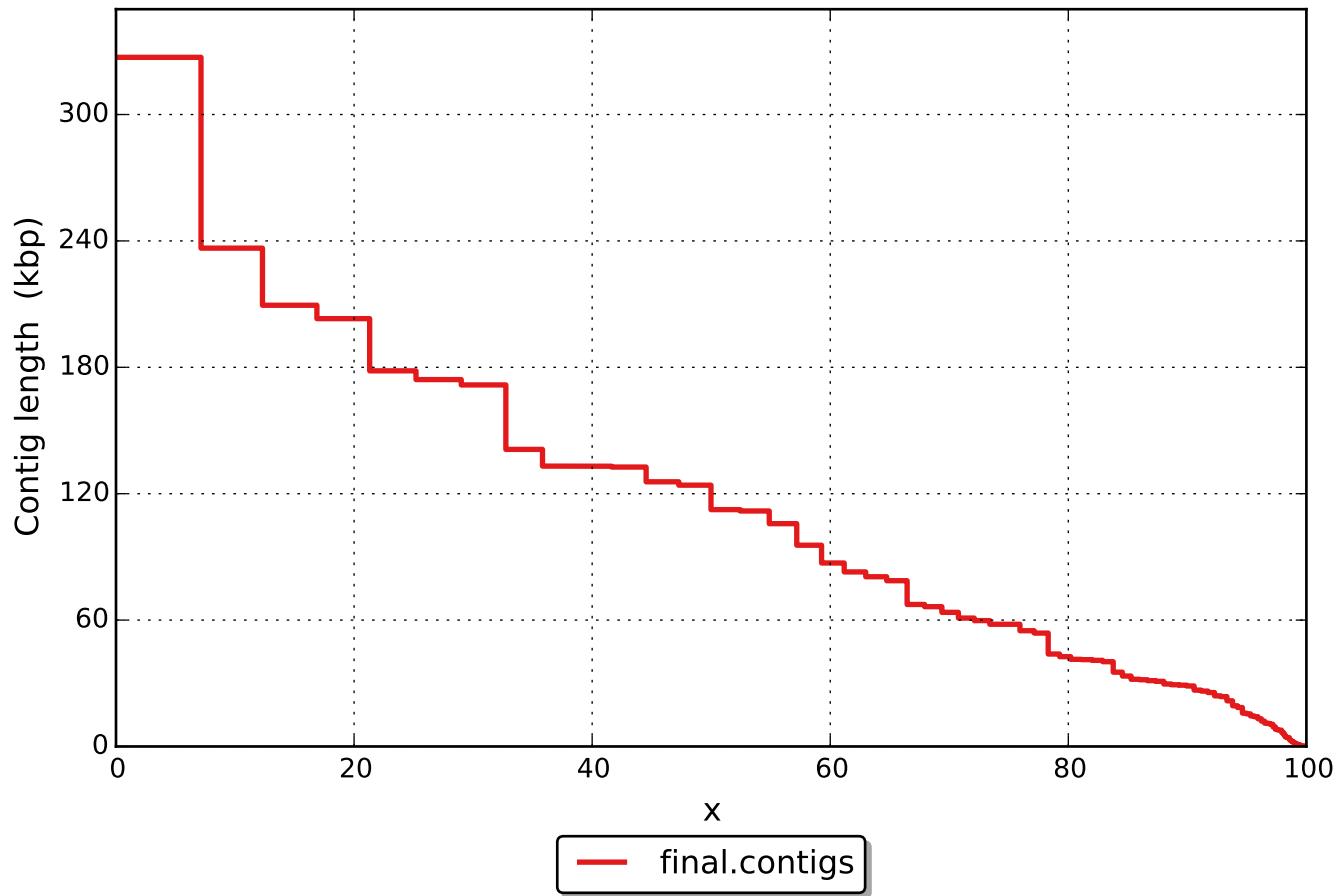
Misassemblies report

	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	17
# indels	0
# short indels	0
# long indels	0
Indels length	0

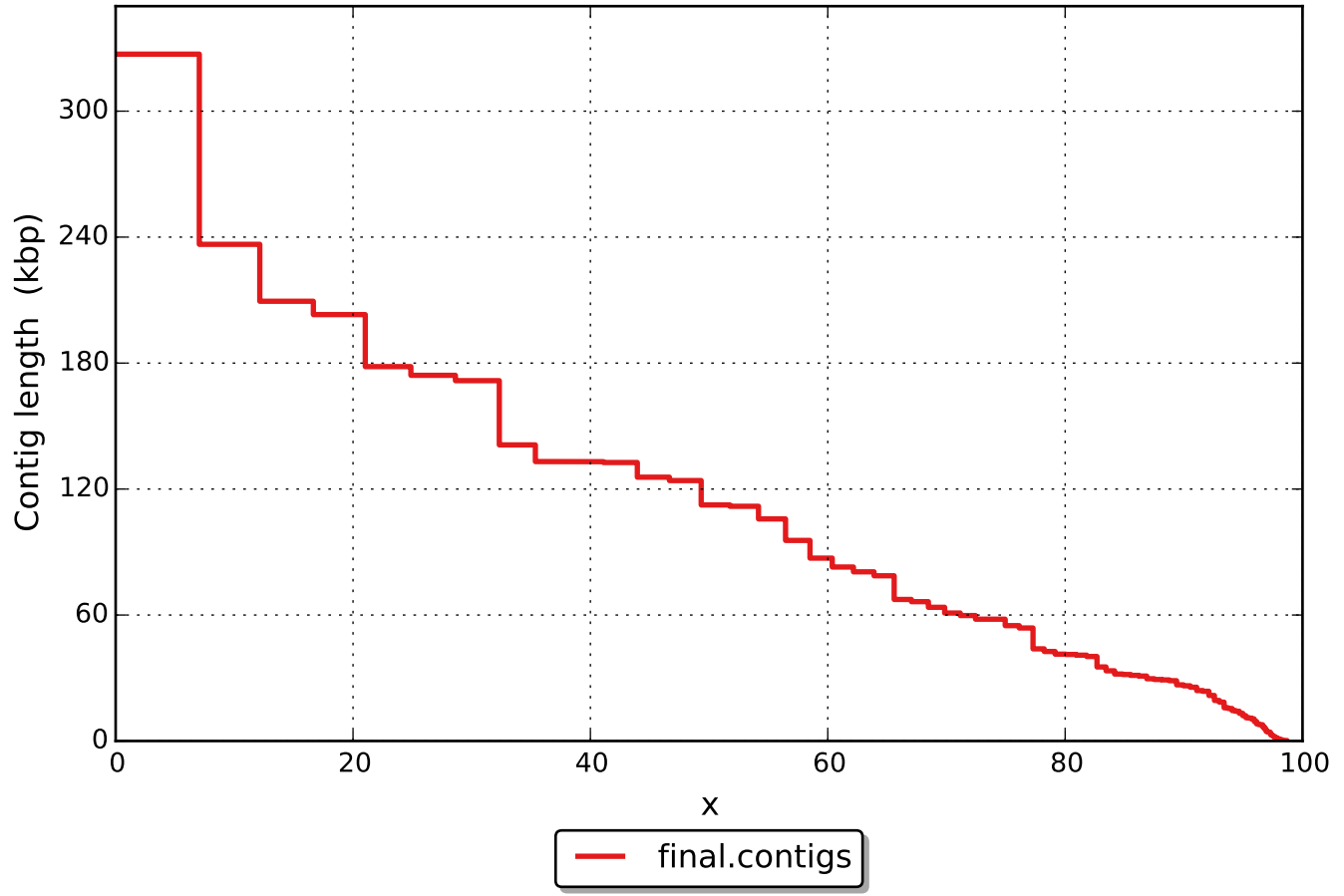
Unaligned report

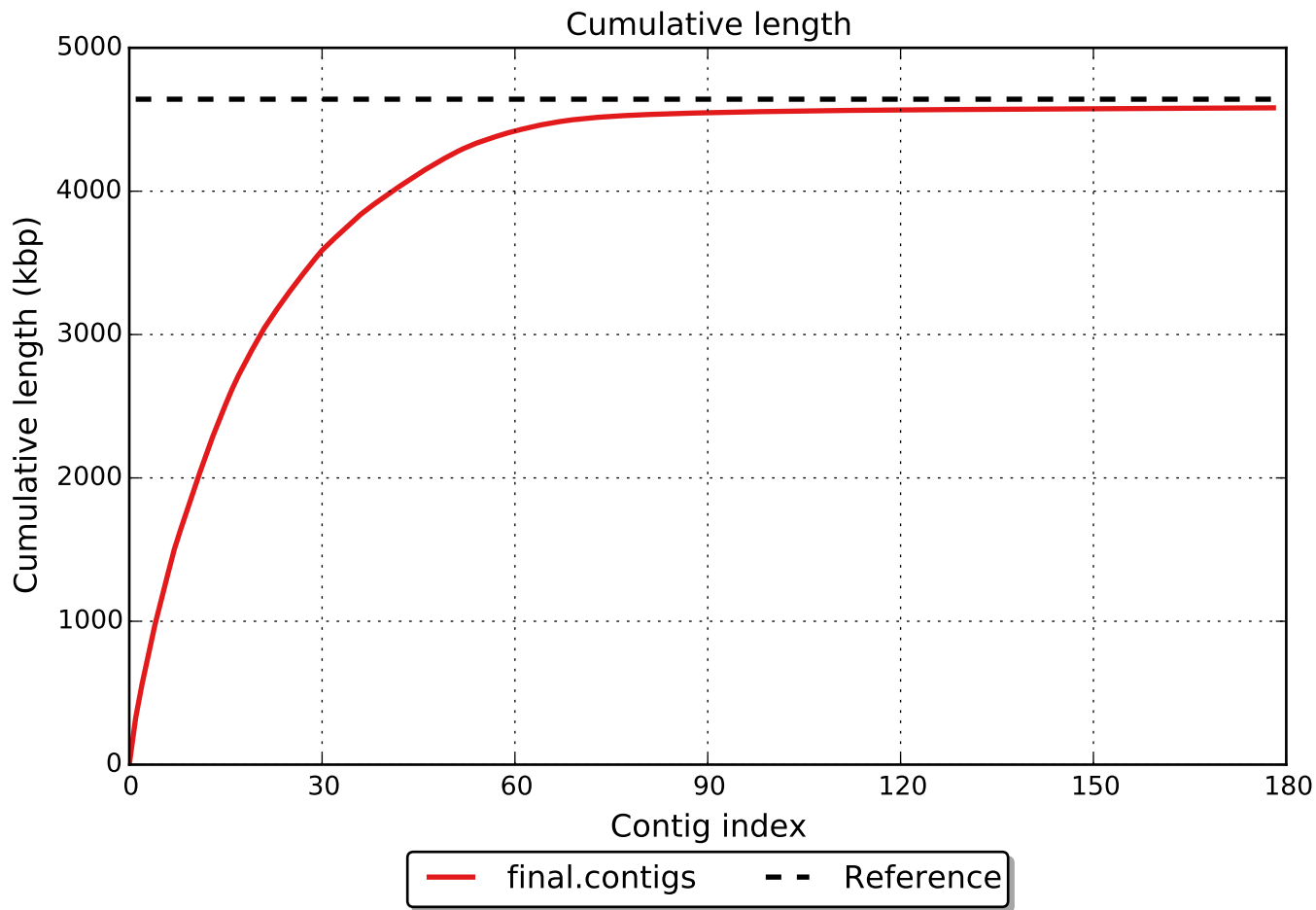
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	2
Partially unaligned length	177
# N's	0

Nx

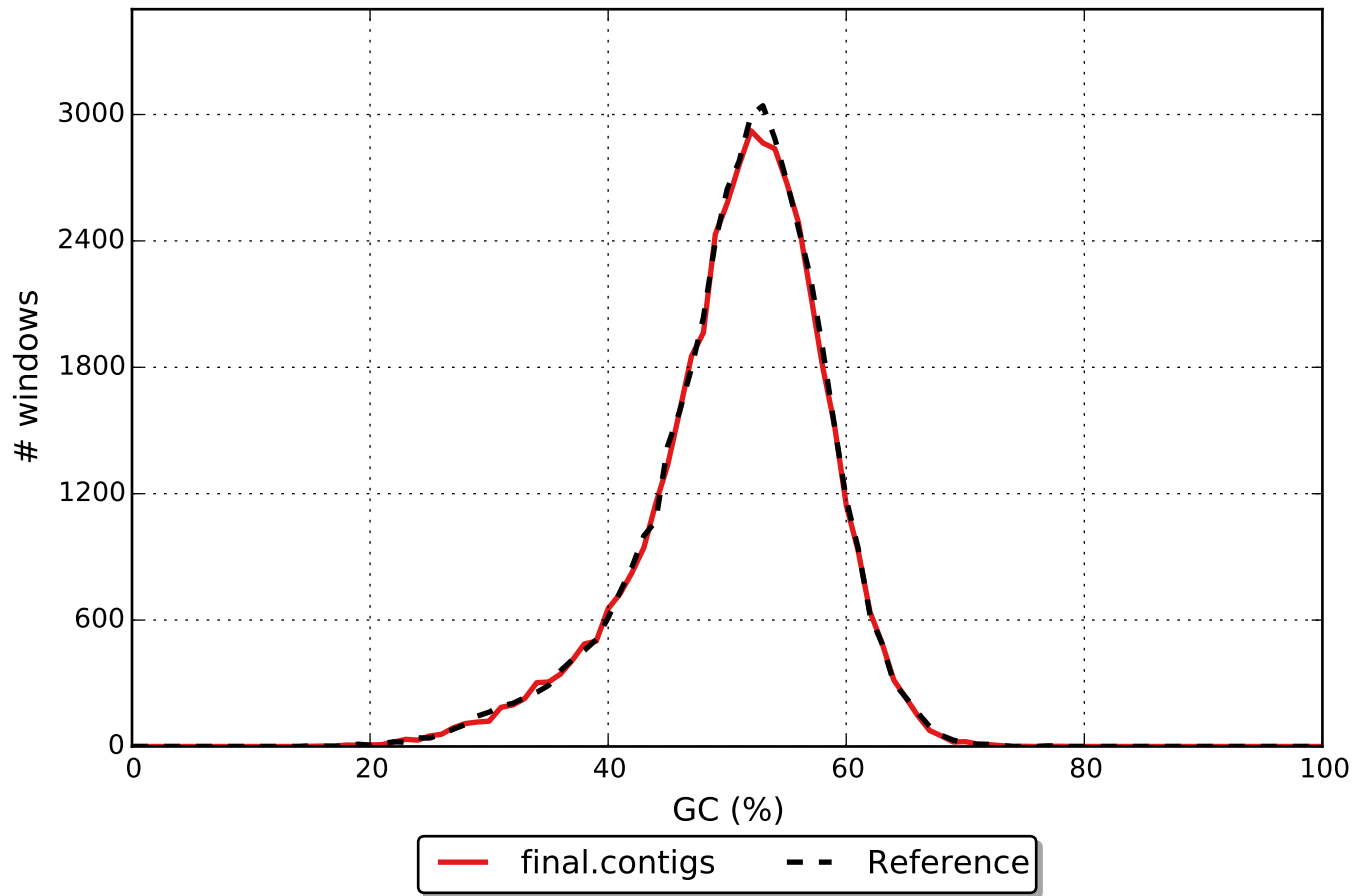


NGx





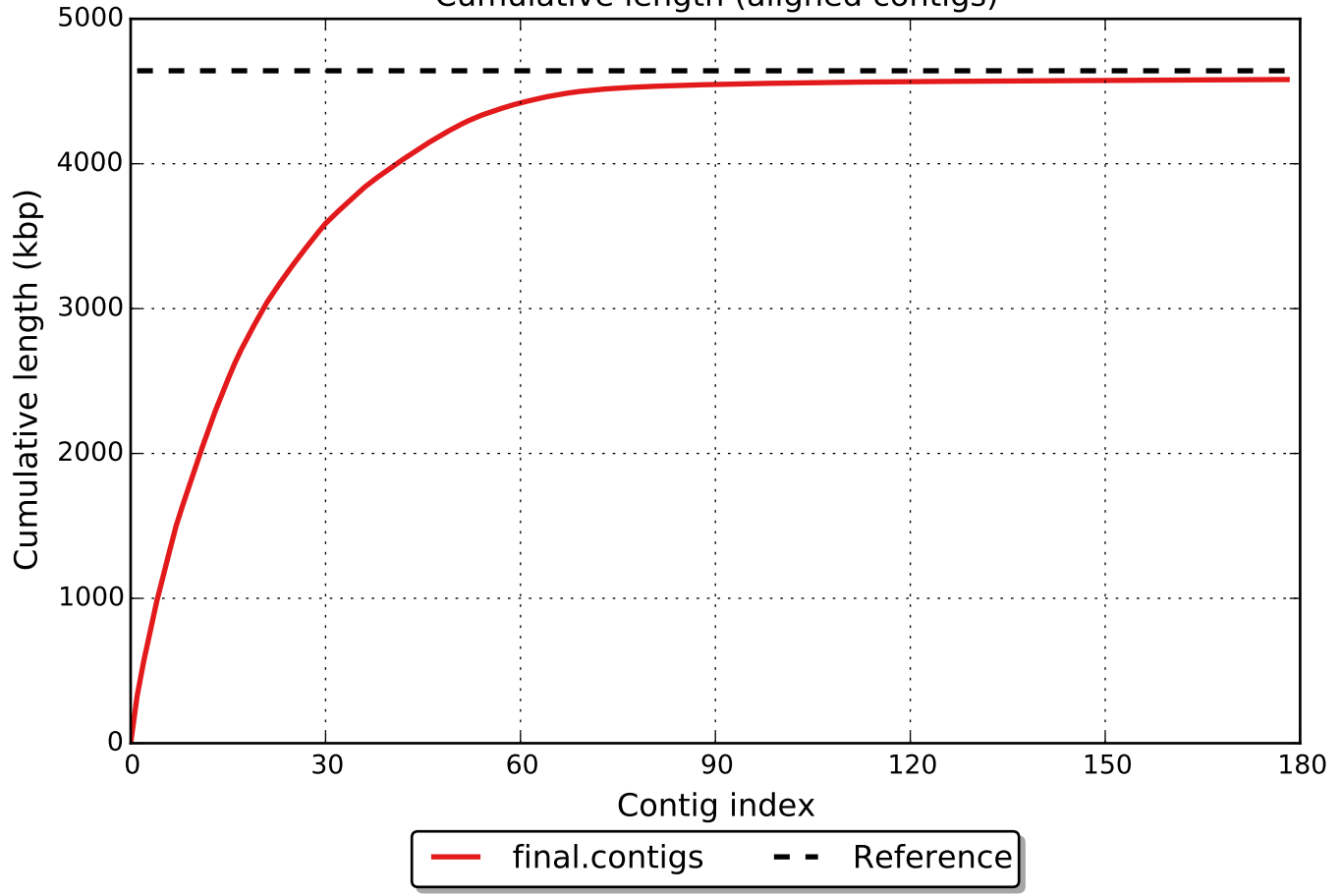
GC content



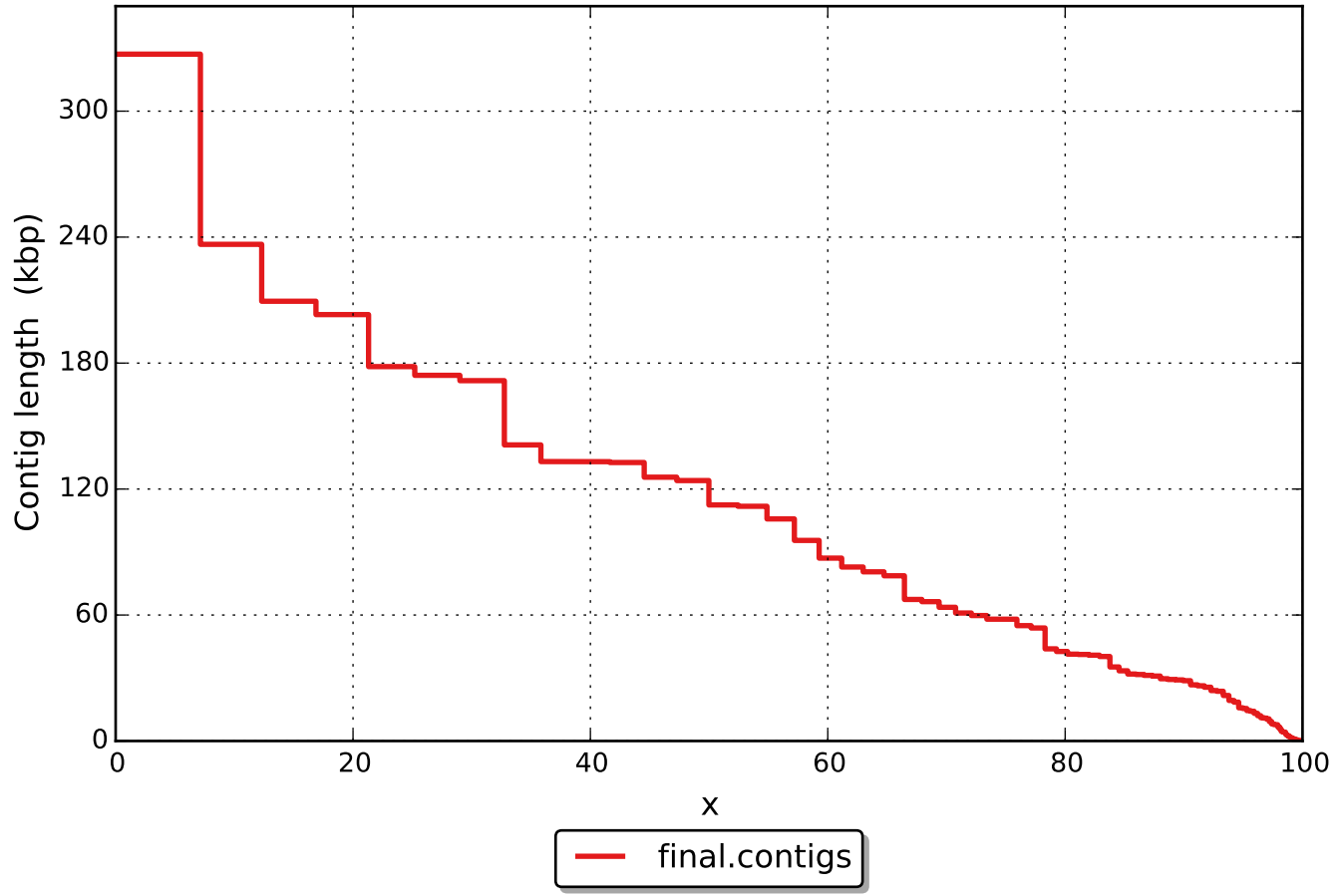
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

