

Report

	final.contigs
# contigs (≥ 0 bp)	1211
# contigs (≥ 1000 bp)	357
# contigs (≥ 5000 bp)	258
# contigs (≥ 10000 bp)	174
# contigs (≥ 25000 bp)	39
# contigs (≥ 50000 bp)	7
Total length (≥ 0 bp)	4802171
Total length (≥ 1000 bp)	4524747
Total length (≥ 5000 bp)	4256780
Total length (≥ 10000 bp)	3644157
Total length (≥ 25000 bp)	1449341
Total length (≥ 50000 bp)	445743
# contigs	382
Largest contig	89368
Total length	4542961
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	19266
NG50	19068
N75	11576
NG75	11124
L50	77
LG50	80
L75	153
LG75	159
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	1 + 0 part
Unaligned length	512
Genome fraction (%)	97.589
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.97
# indels per 100 kbp	0.00
Largest alignment	89368
NA50	19266
NGA50	19068
NA75	11576
NGA75	11124
LA50	77
LGA50	80
LA75	153
LGA75	159

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

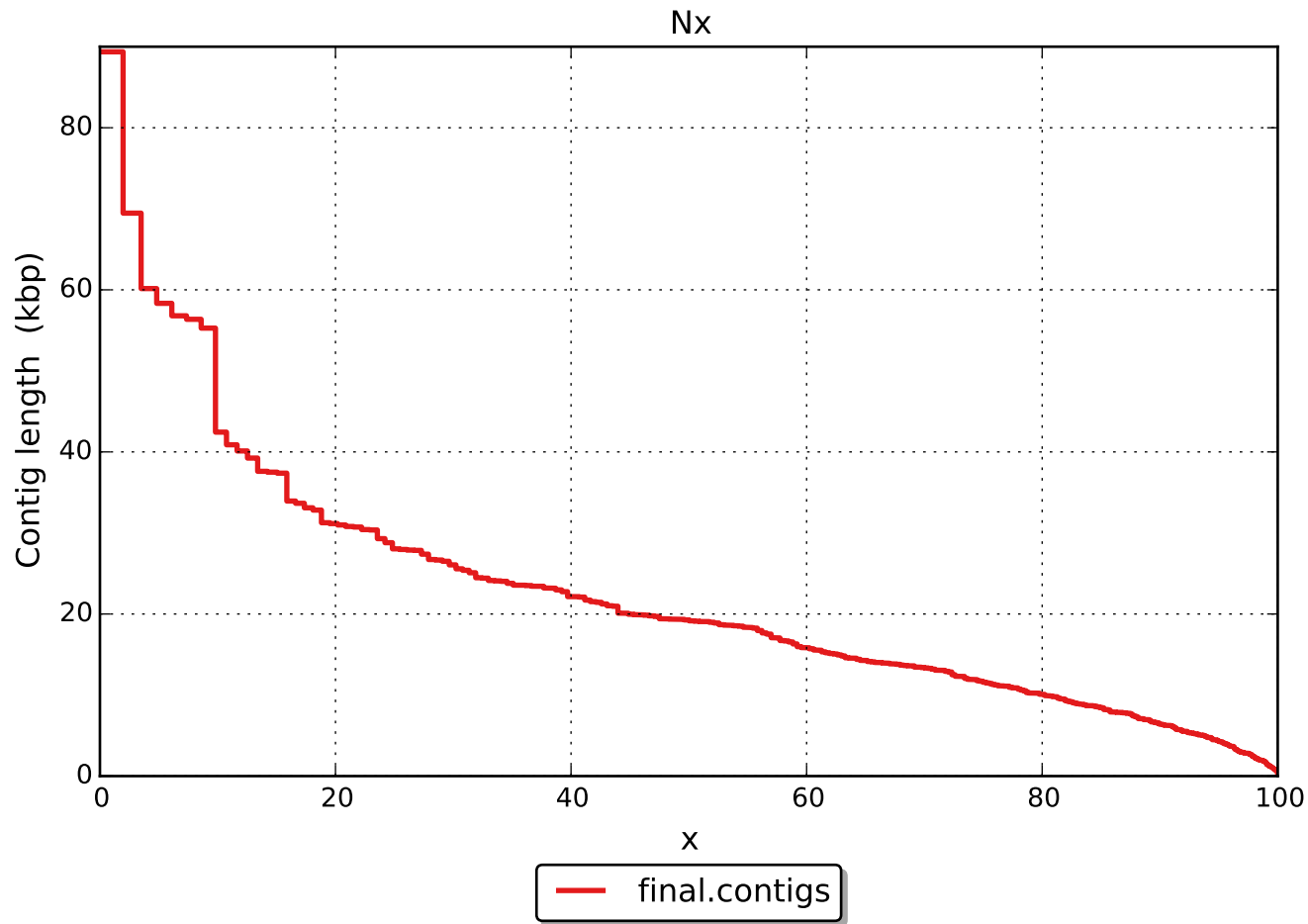
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	44
# indels	0
# short indels	0
# long indels	0
Indels length	0

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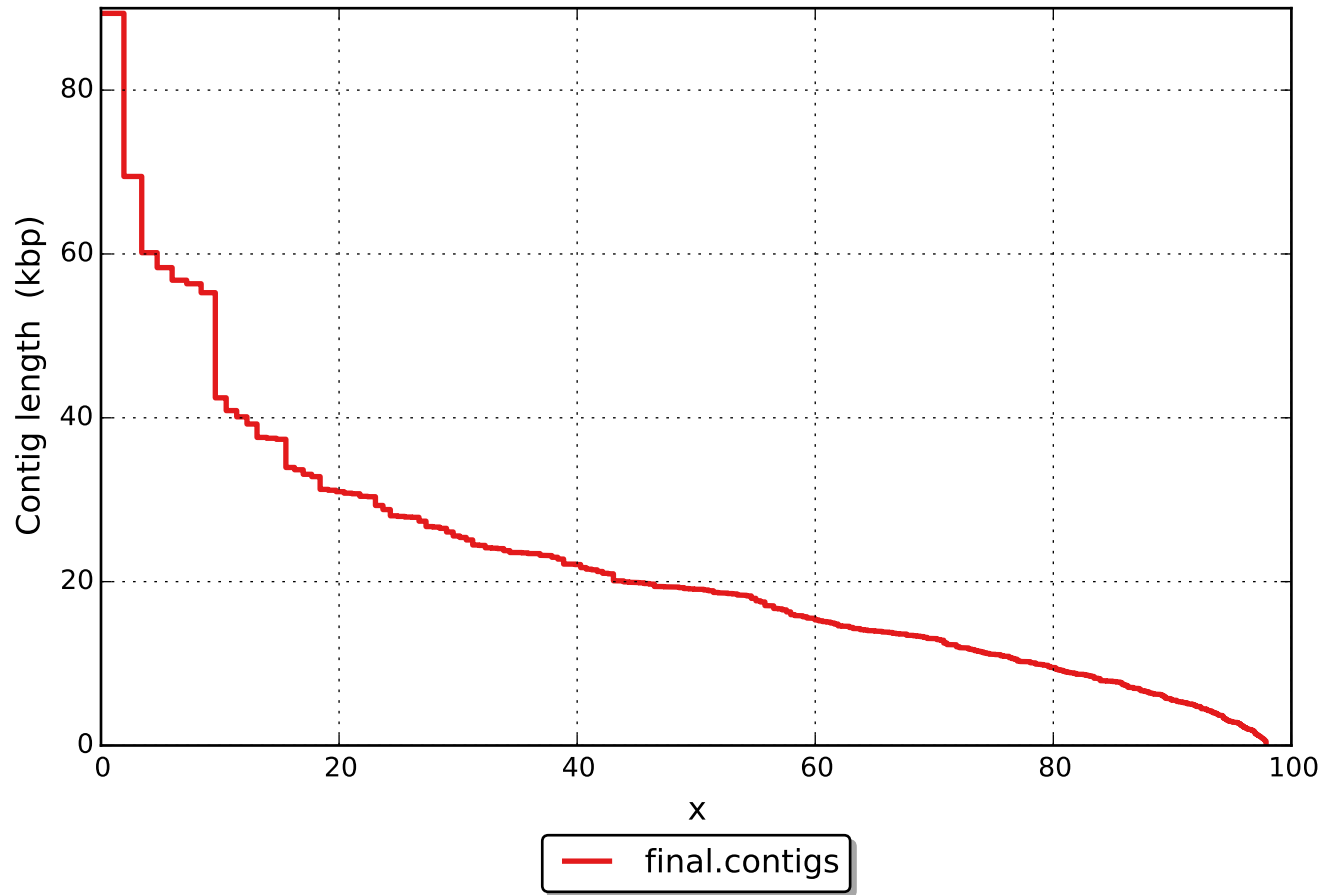
Unaligned report

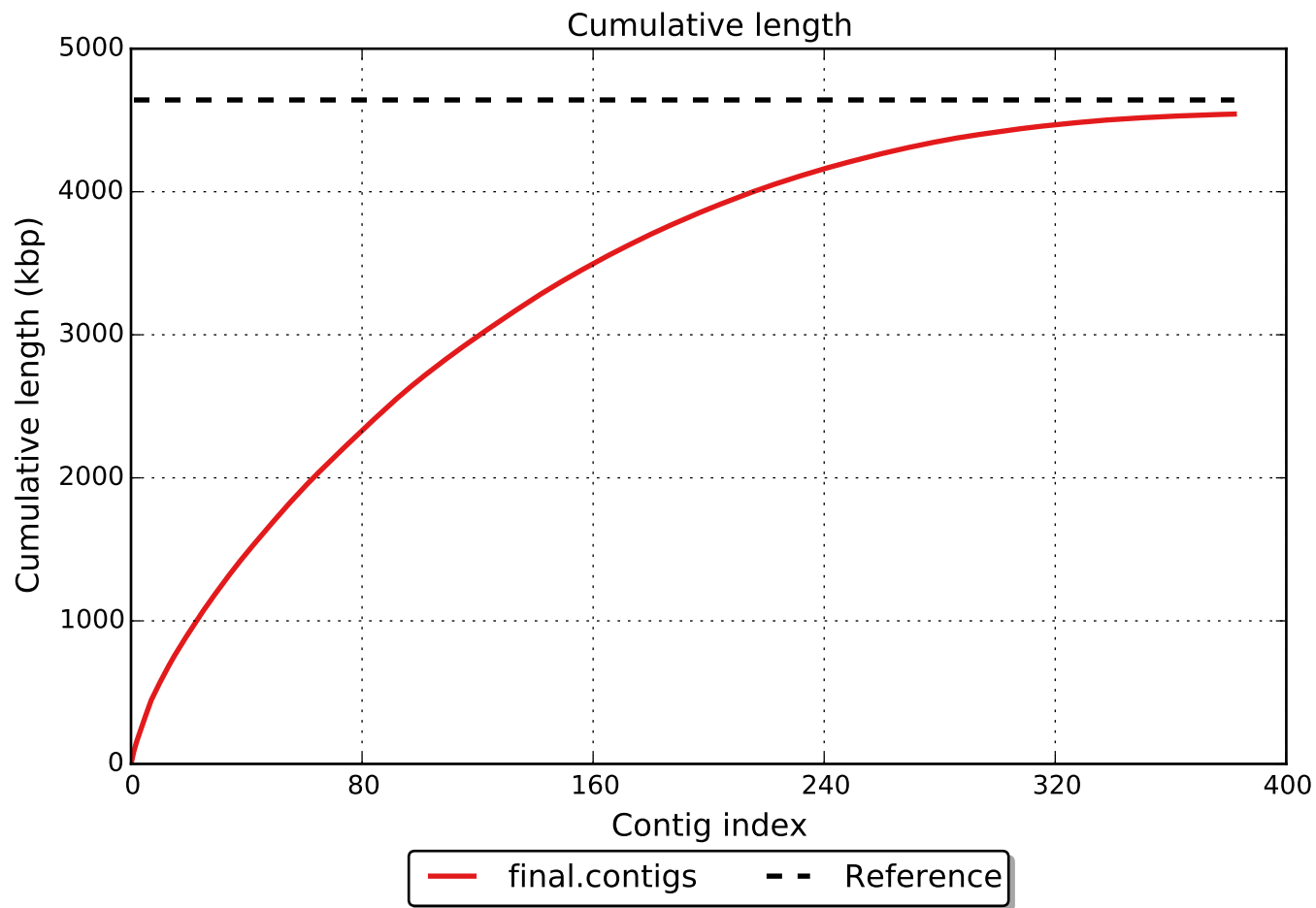
	final.contigs
# fully unaligned contigs	1
Fully unaligned length	512
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

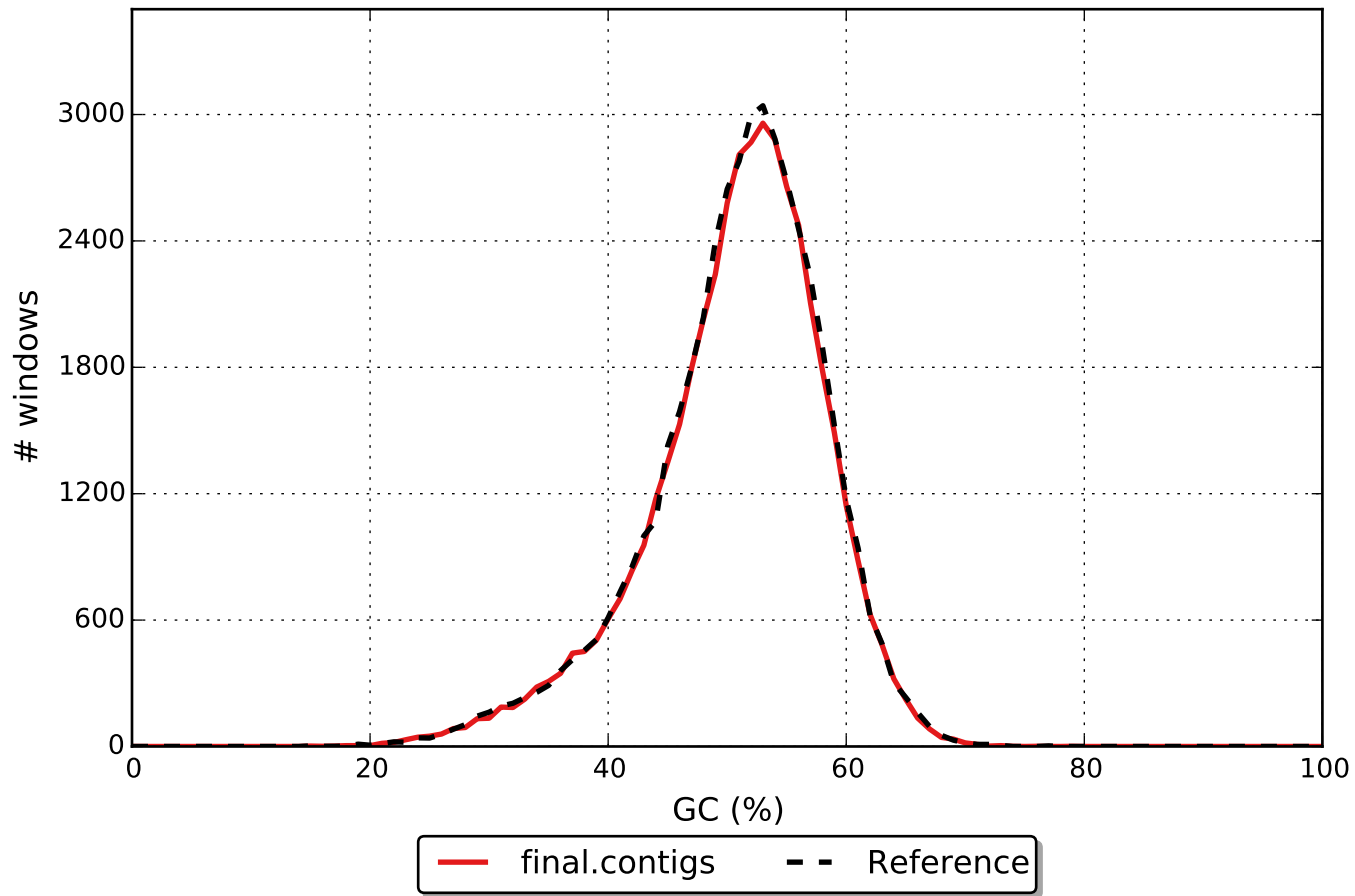


NGx





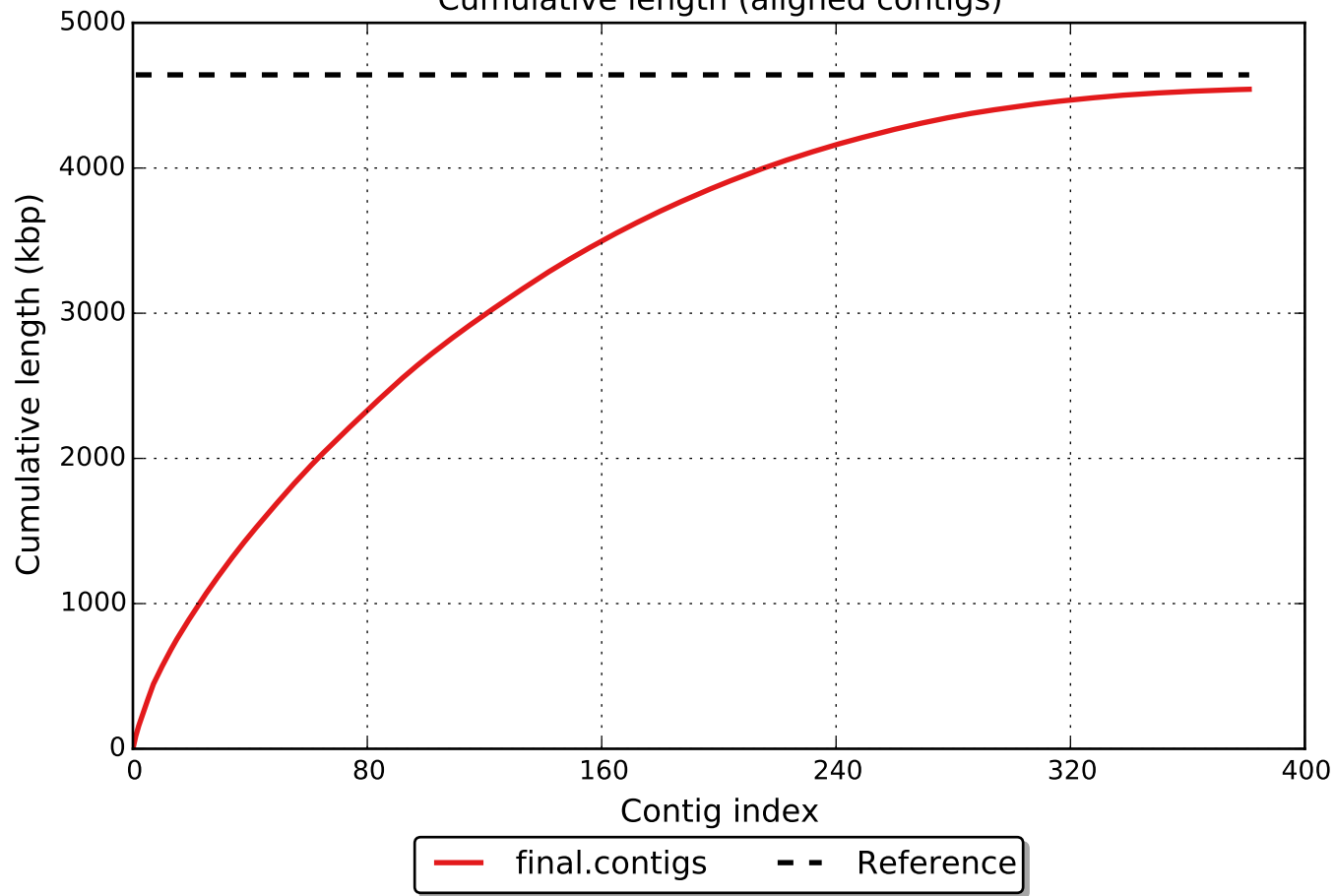
GC content



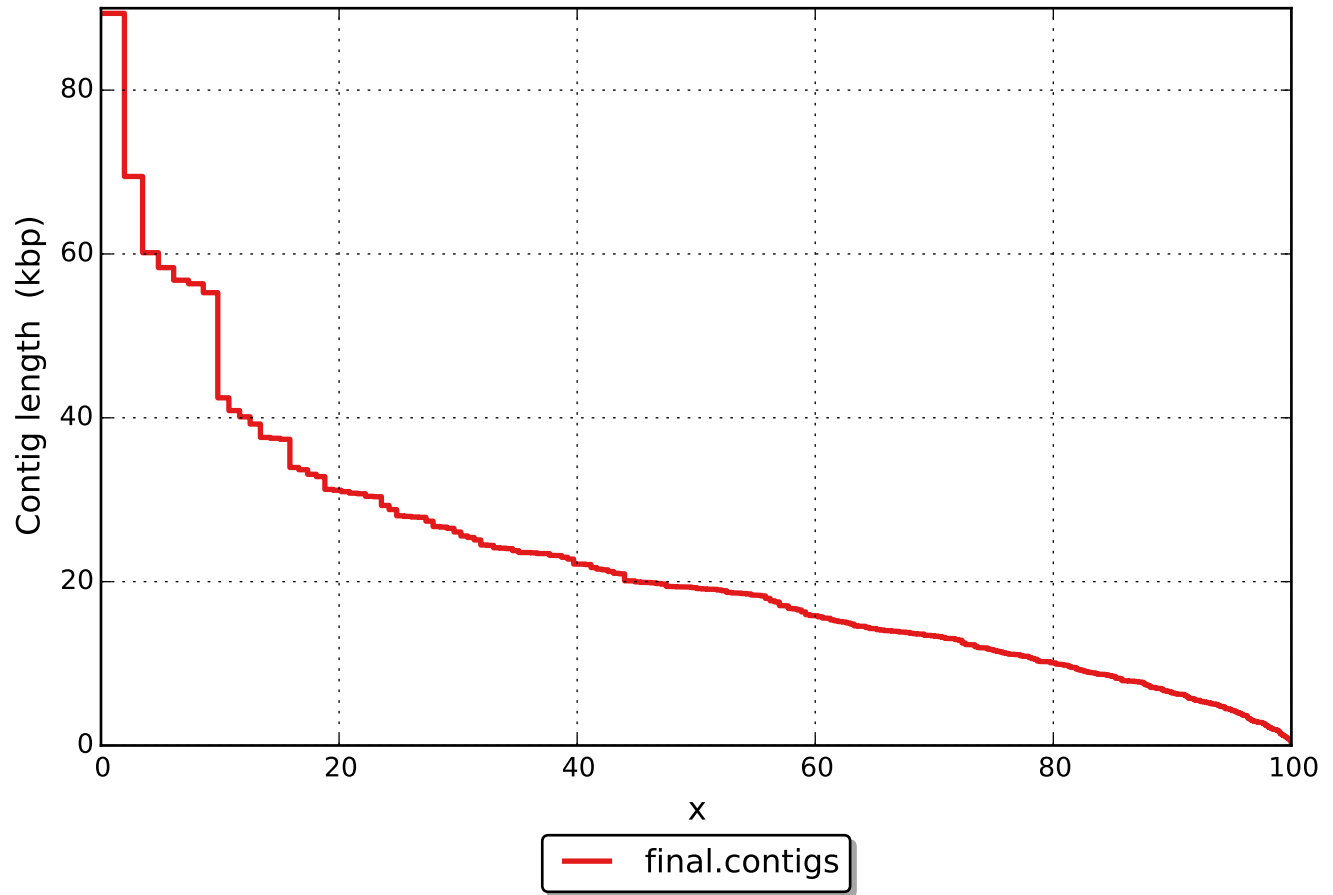
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

