

Report

	final.contigs
# contigs (≥ 0 bp)	414
# contigs (≥ 1000 bp)	323
Total length (≥ 0 bp)	5202965
Total length (≥ 1000 bp)	5141435
# contigs	414
Largest contig	137783
Total length	5202965
Reference length	5547323
GC (%)	50.30
Reference GC (%)	50.48
N50	34189
NG50	30418
N75	17658
NG75	13958
L50	48
LG50	53
L75	102
LG75	119
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	16523
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	93.293
Duplication ratio	1.005
# N's per 100 kbp	0.00
# mismatches per 100 kbp	10.63
# indels per 100 kbp	0.44
Largest alignment	137783
NA50	34189
NGA50	30418
NA75	17658
NGA75	13958
LA50	48
LGA50	53
LA75	102
LGA75	119

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

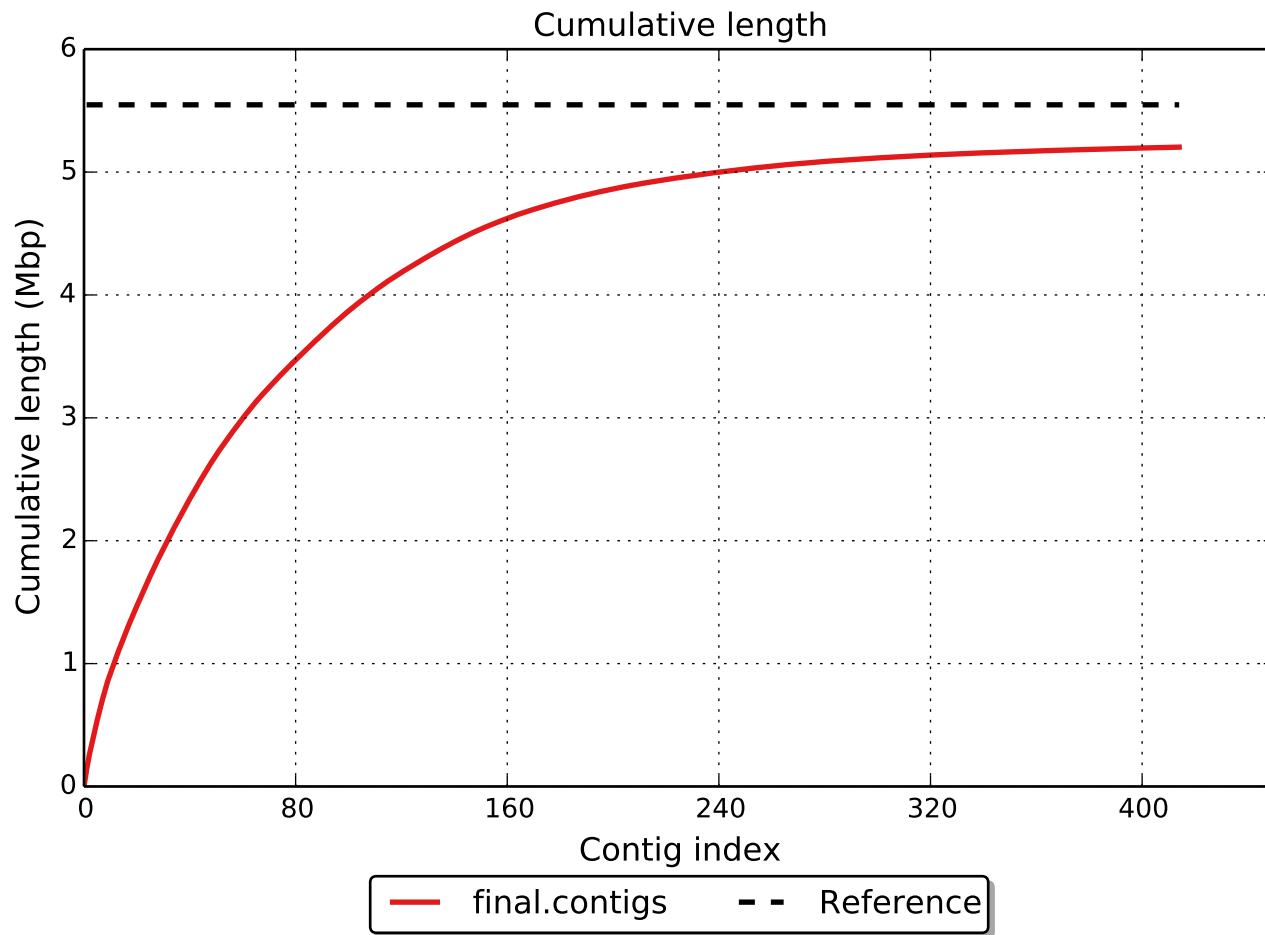
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	16523
# local misassemblies	3
# mismatches	550
# indels	23
# short indels	21
# long indels	2
Indels length	35

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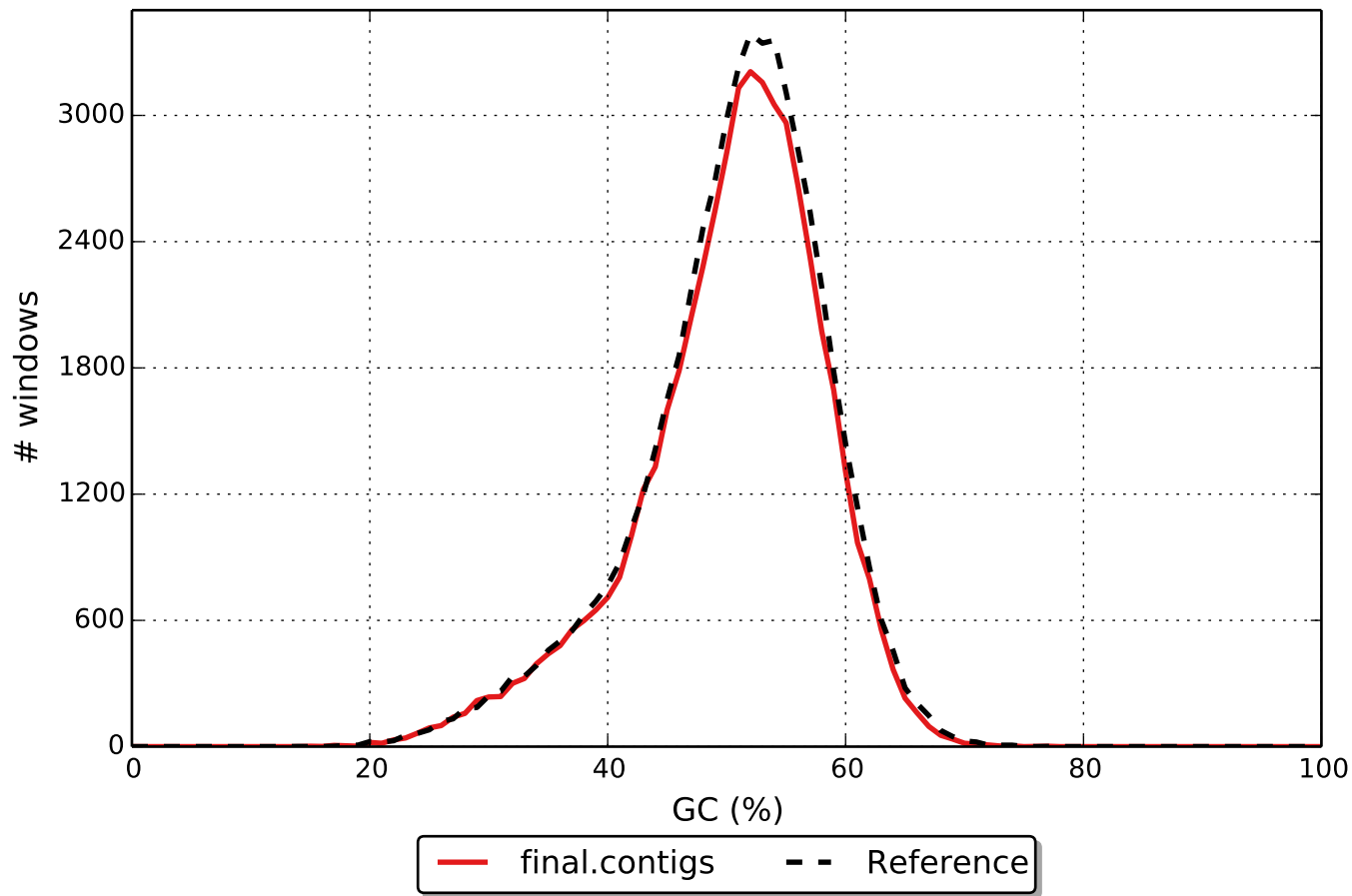
Unaligned report

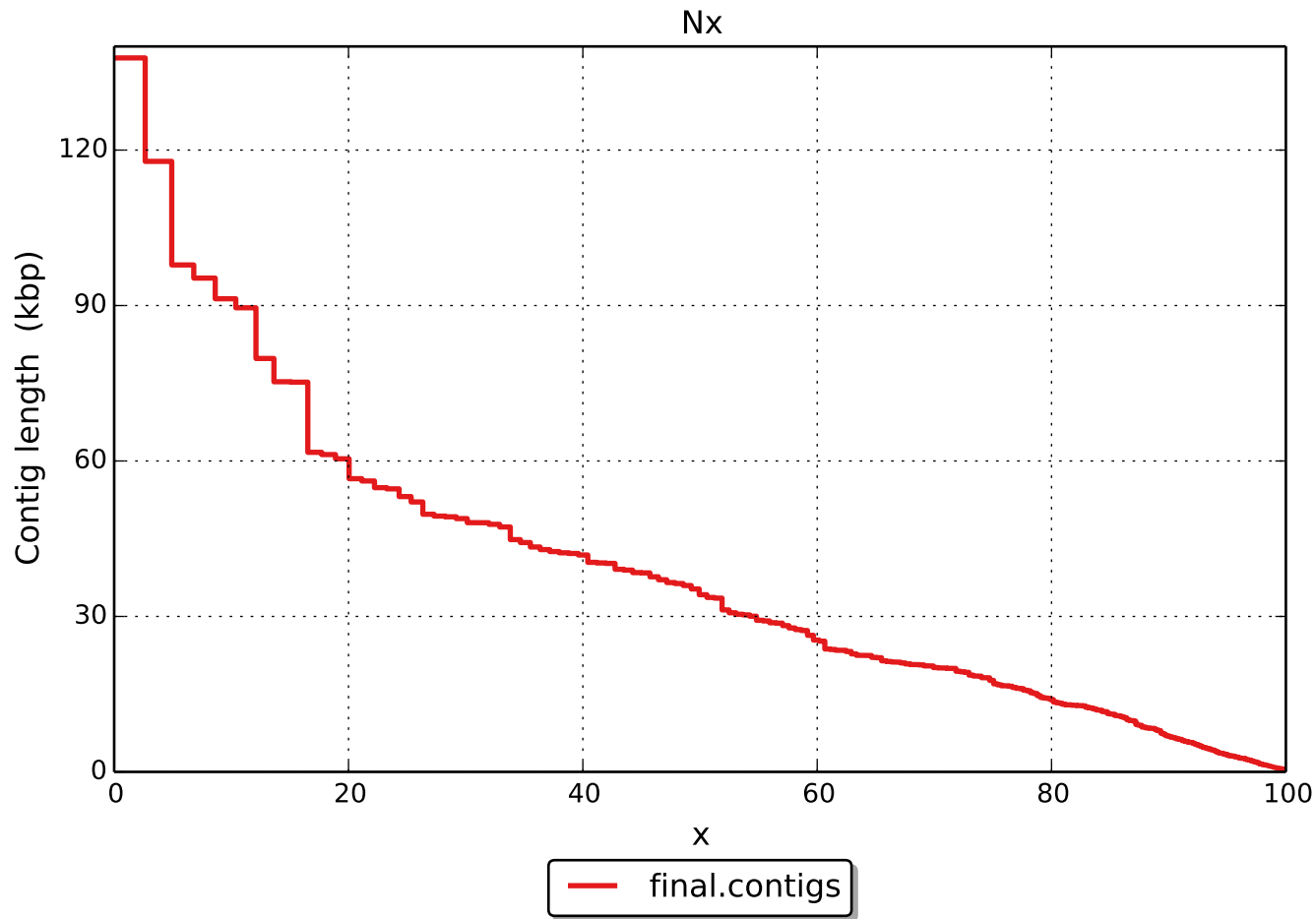
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

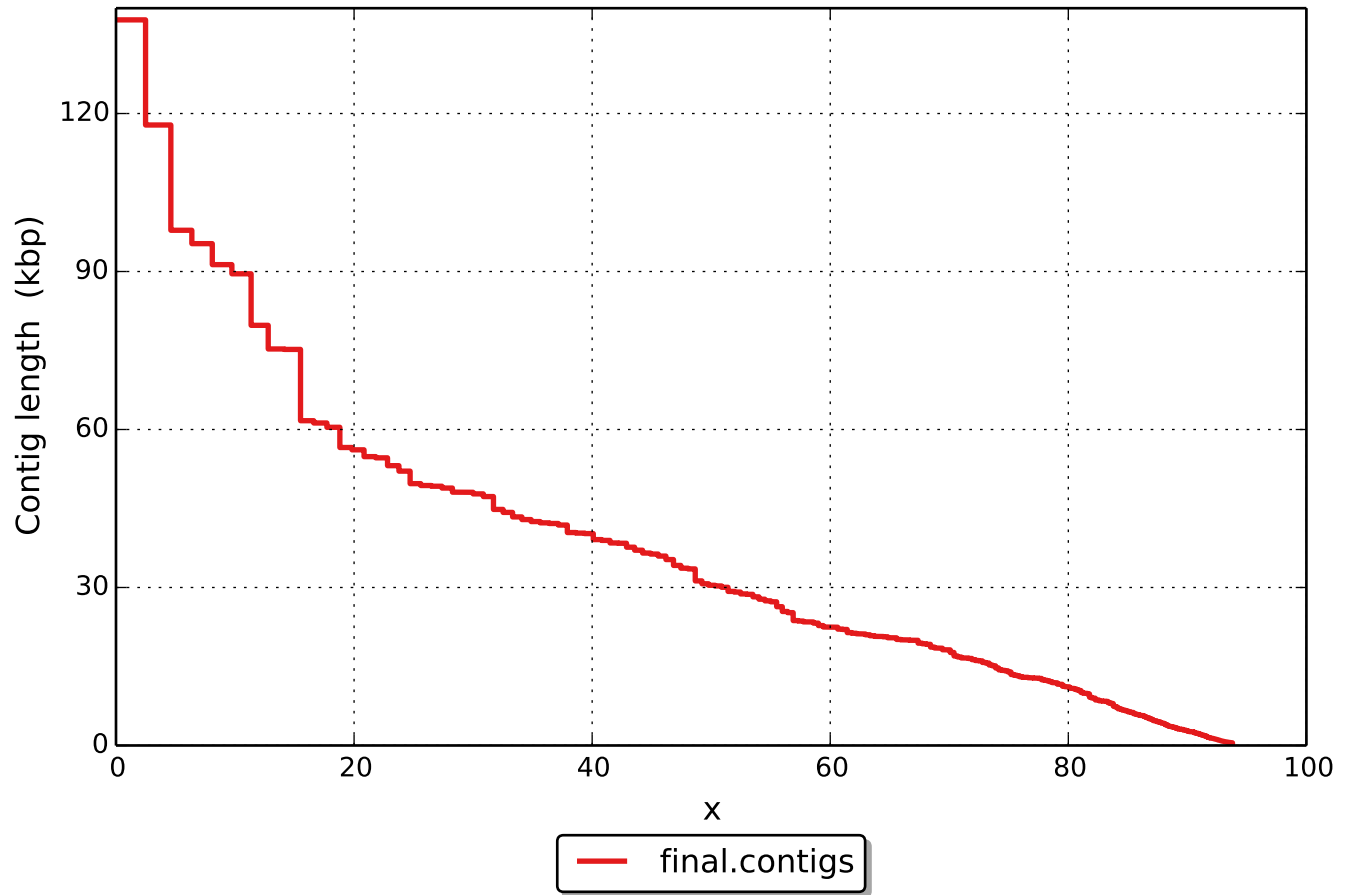


GC content





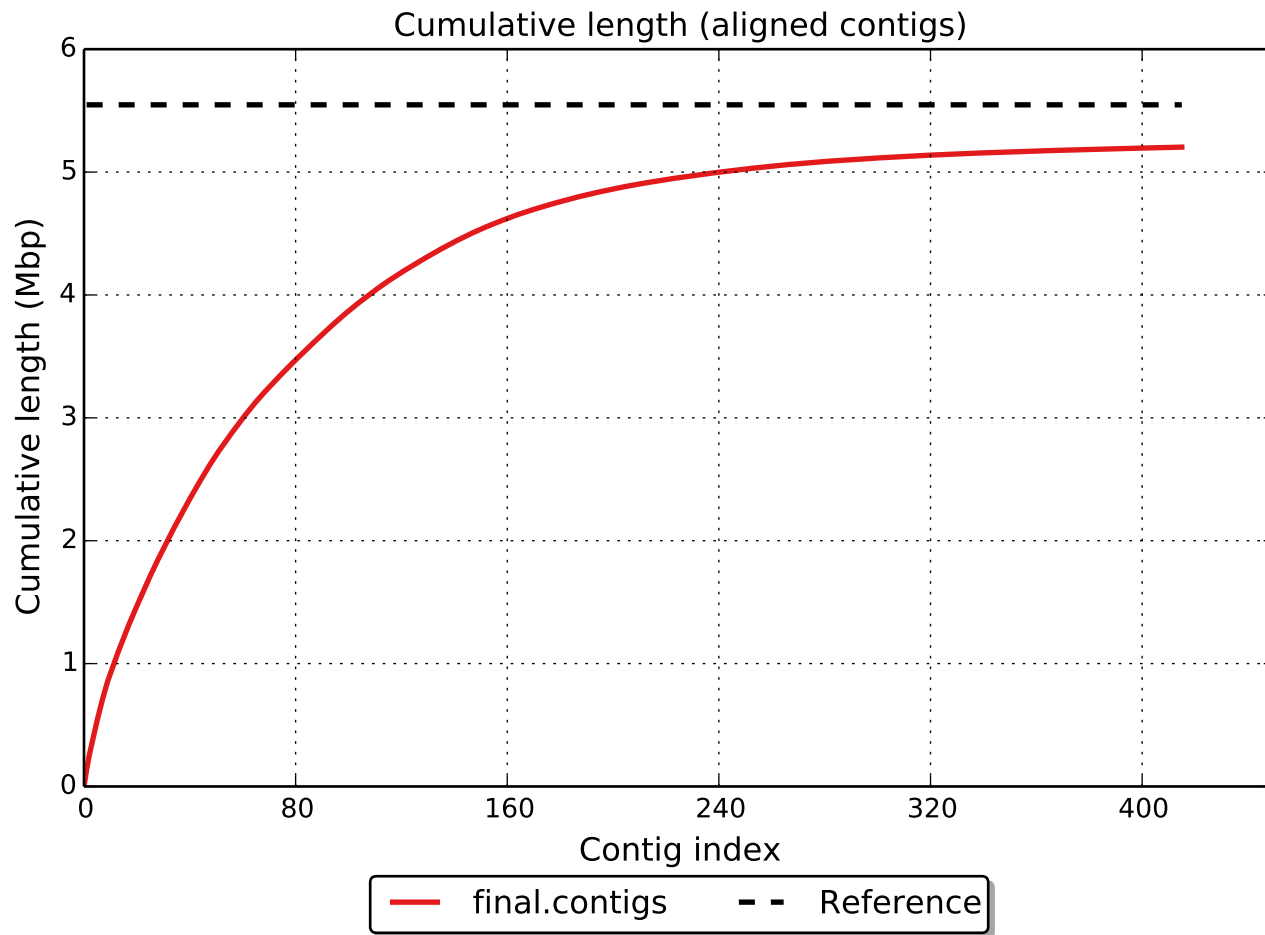
NGx



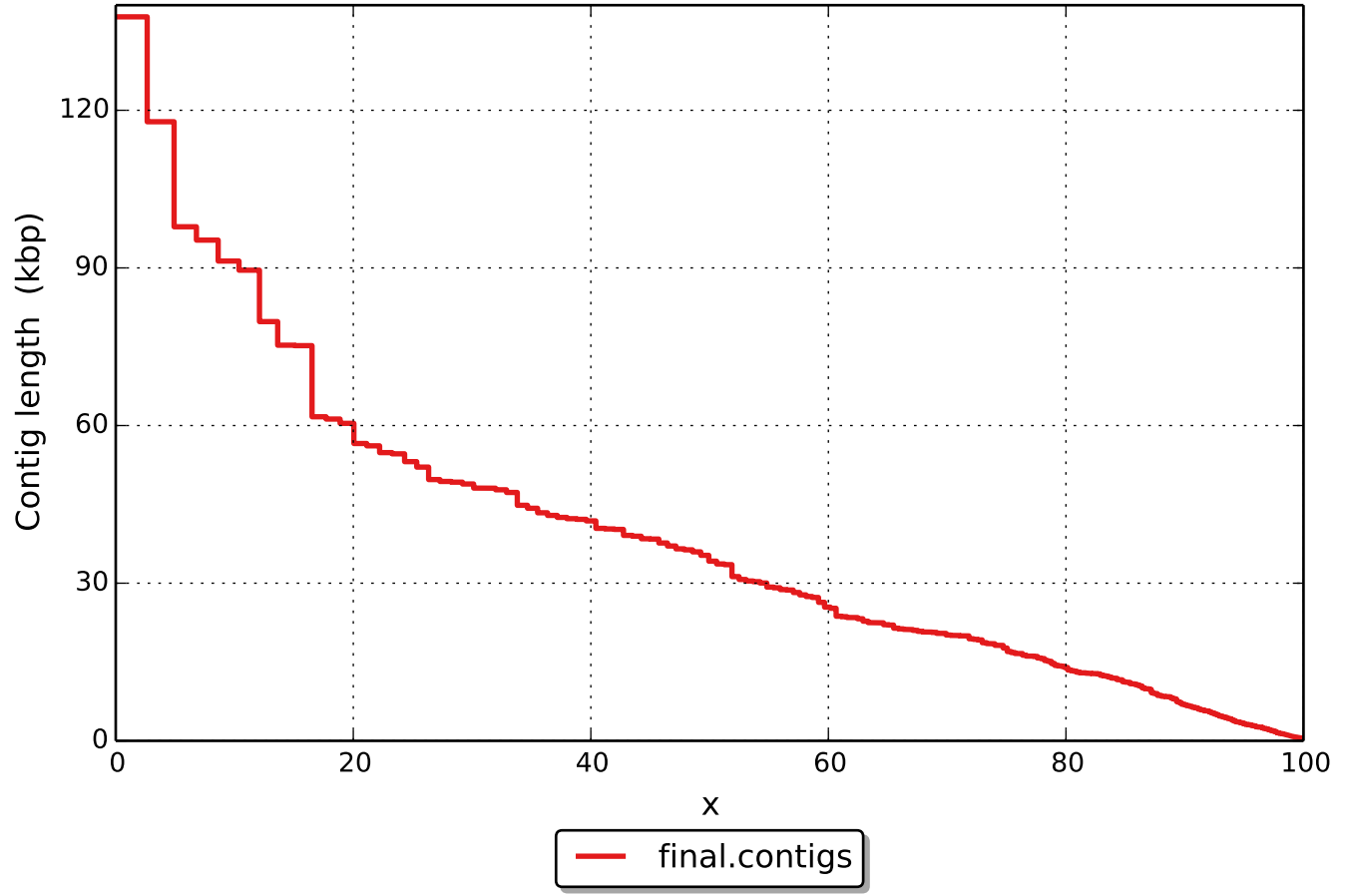
Misassemblies



 # relocations



NAx



NGAx

