

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	620
# contigs ( $\geq 1000$ bp)	417
Total length ( $\geq 0$ bp)	2563171
Total length ( $\geq 1000$ bp)	2429371
# contigs	620
Largest contig	34557
Total length	2563171
Reference length	5478683
GC (%)	50.33
Reference GC (%)	50.49
N50	8140
N75	4234
L50	93
L75	196
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	46.462
Duplication ratio	1.007
# N's per 100 kbp	0.00
# mismatches per 100 kbp	429.93
# indels per 100 kbp	0.04
Largest alignment	34557
NA50	8140
NA75	4234
LA50	93
LA75	196

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

## Misassemblies report

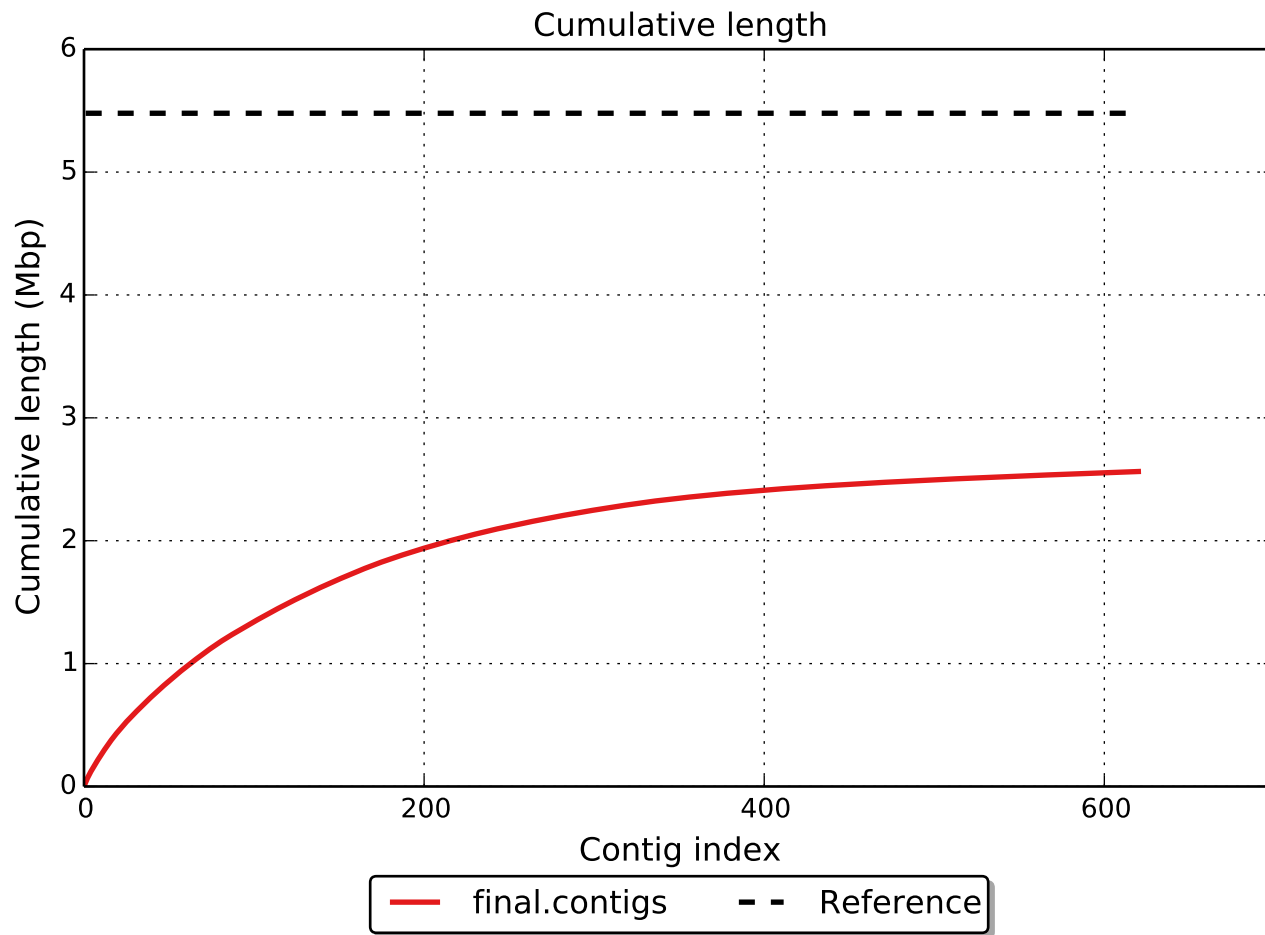
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	10944
# indels	1
# short indels	0
# long indels	1
Indels length	18

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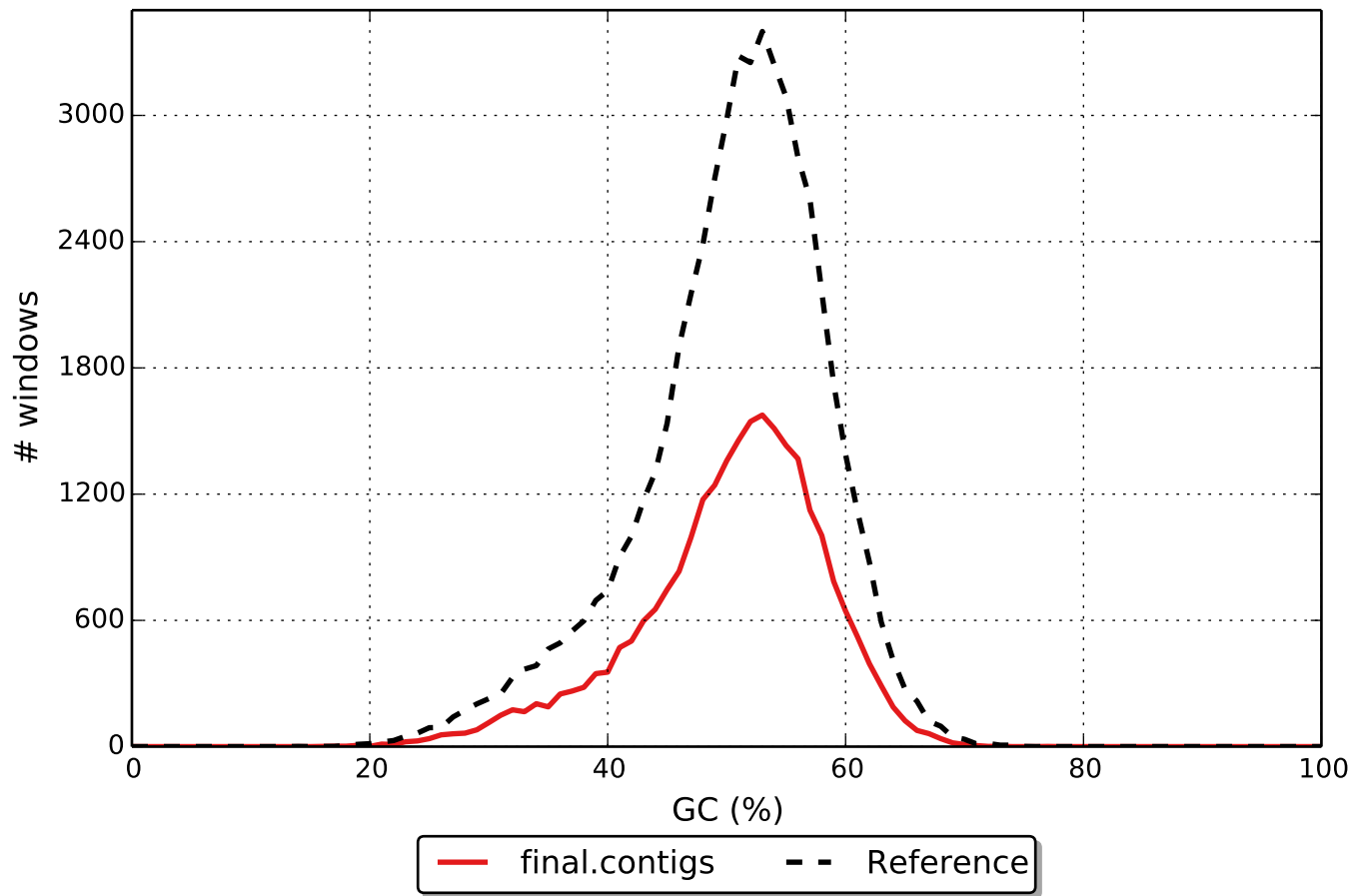
## Unaligned report

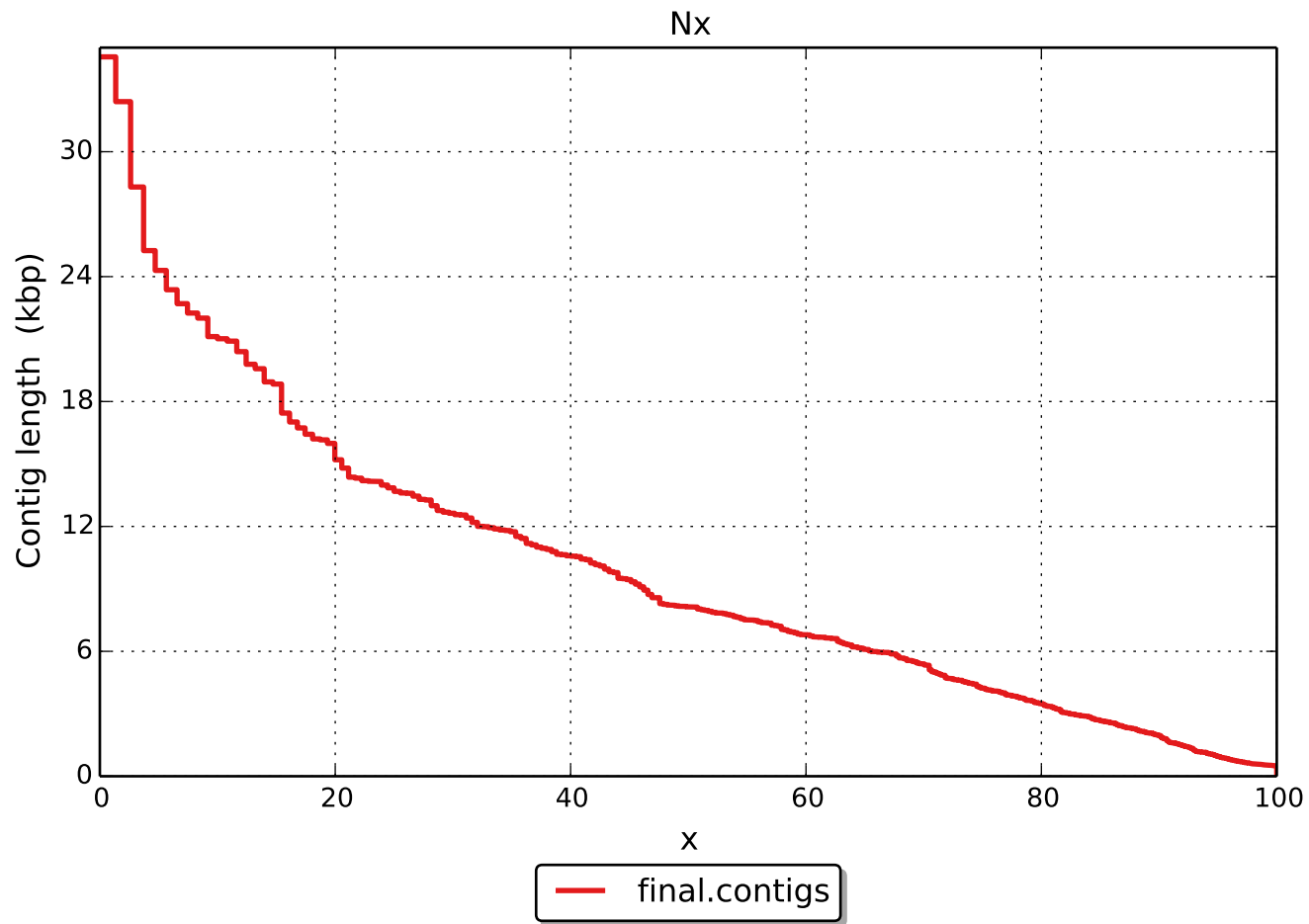
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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

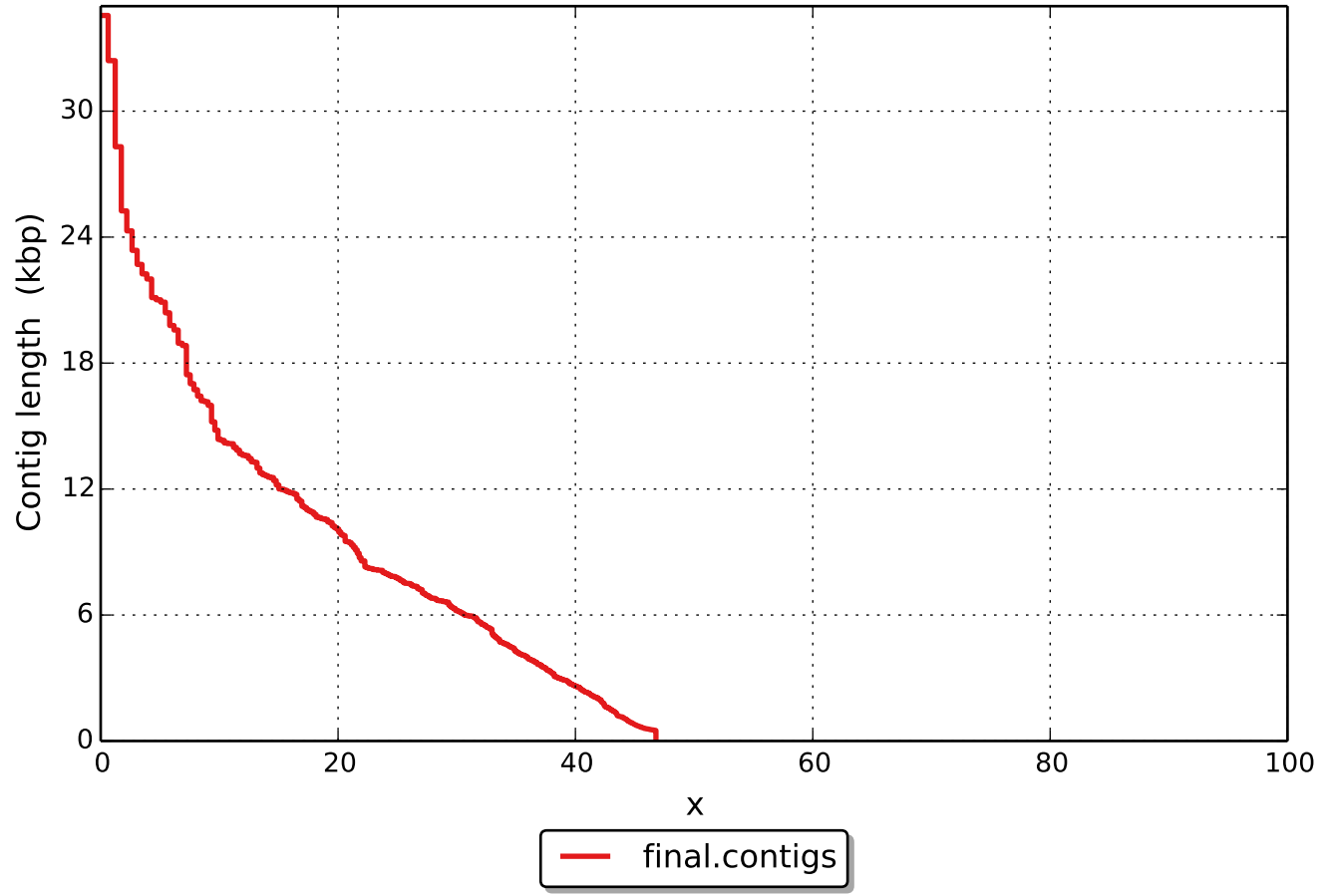


GC content





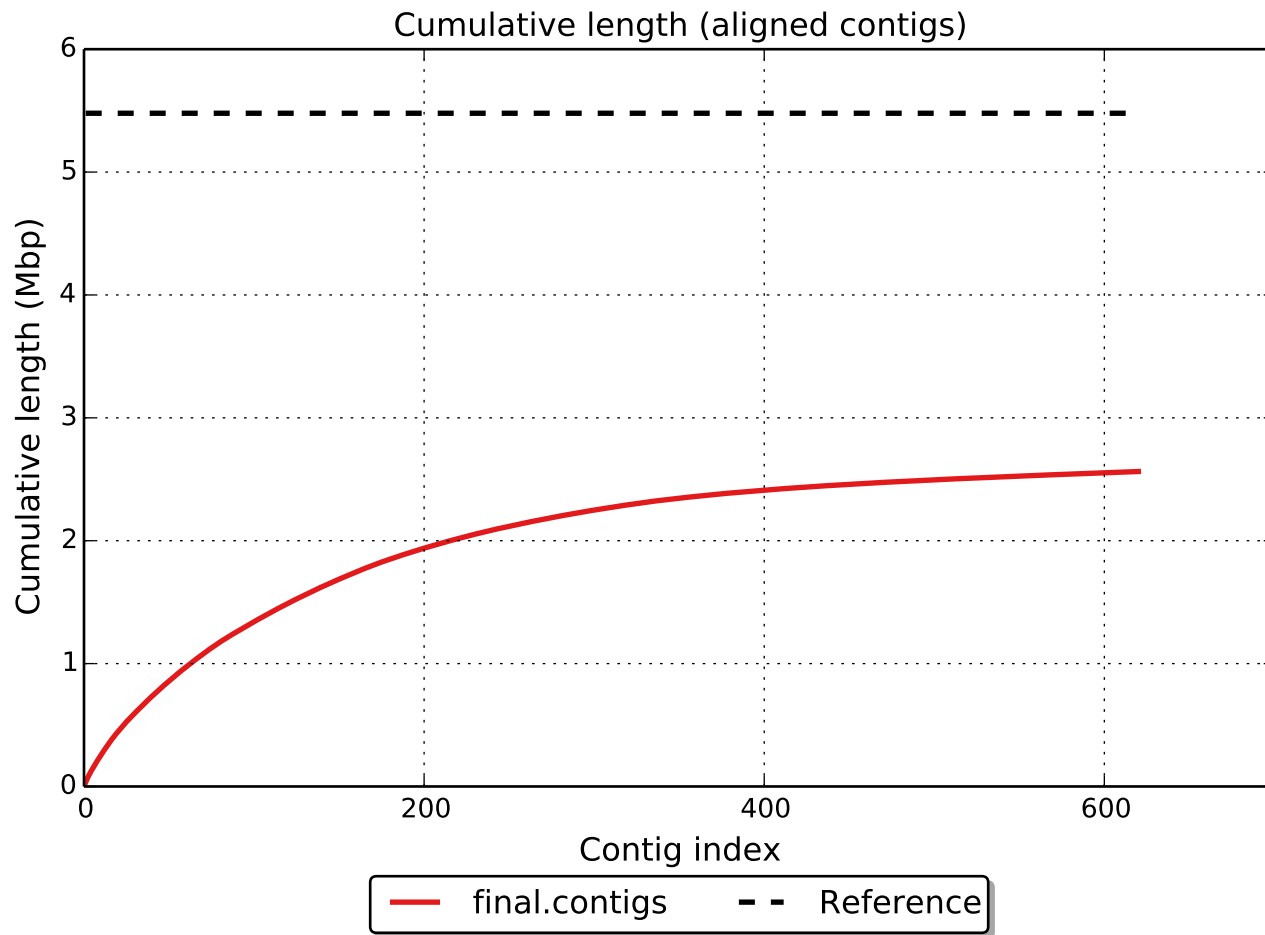
NGx



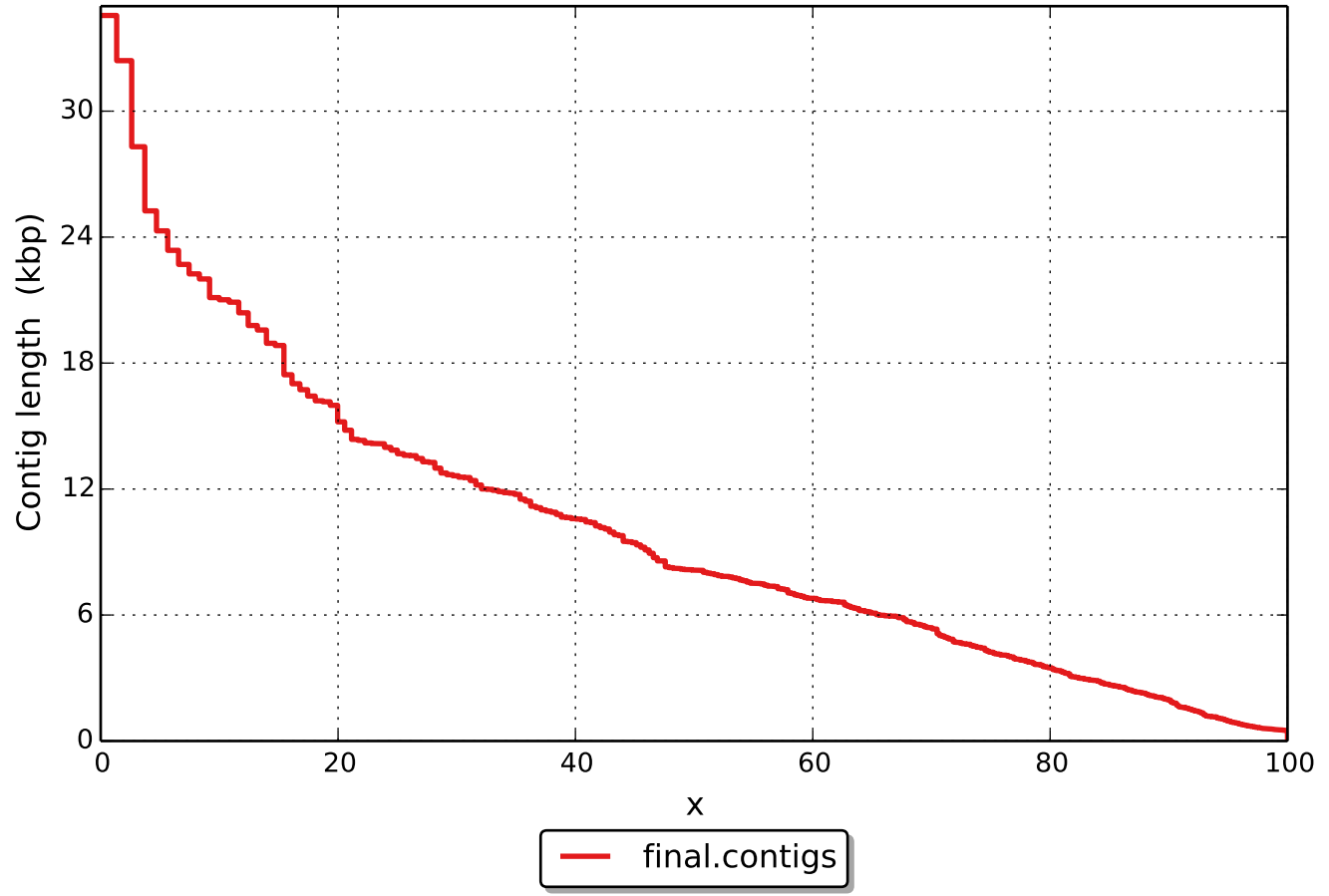
# Misassemblies







NAx



NGAx

