

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	388
# contigs ( $\geq 1000$ bp)	375
Total length ( $\geq 0$ bp)	5616825
Total length ( $\geq 1000$ bp)	5607843
# contigs	388
Largest contig	83434
Total length	5616825
Reference length	5547323
GC (%)	50.48
Reference GC (%)	50.49
N50	23420
NG50	23589
N75	13021
NG75	13457
L50	78
LG50	76
L75	160
LG75	156
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	34780
Genome fraction (%)	99.978
Duplication ratio	1.006
# N's per 100 kbp	0.00
# mismatches per 100 kbp	5.01
# indels per 100 kbp	0.04
Largest alignment	83434
NA50	22967
NGA50	23420
NA75	12957
NGA75	13164
LA50	79
LGA50	77
LA75	162
LGA75	158

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

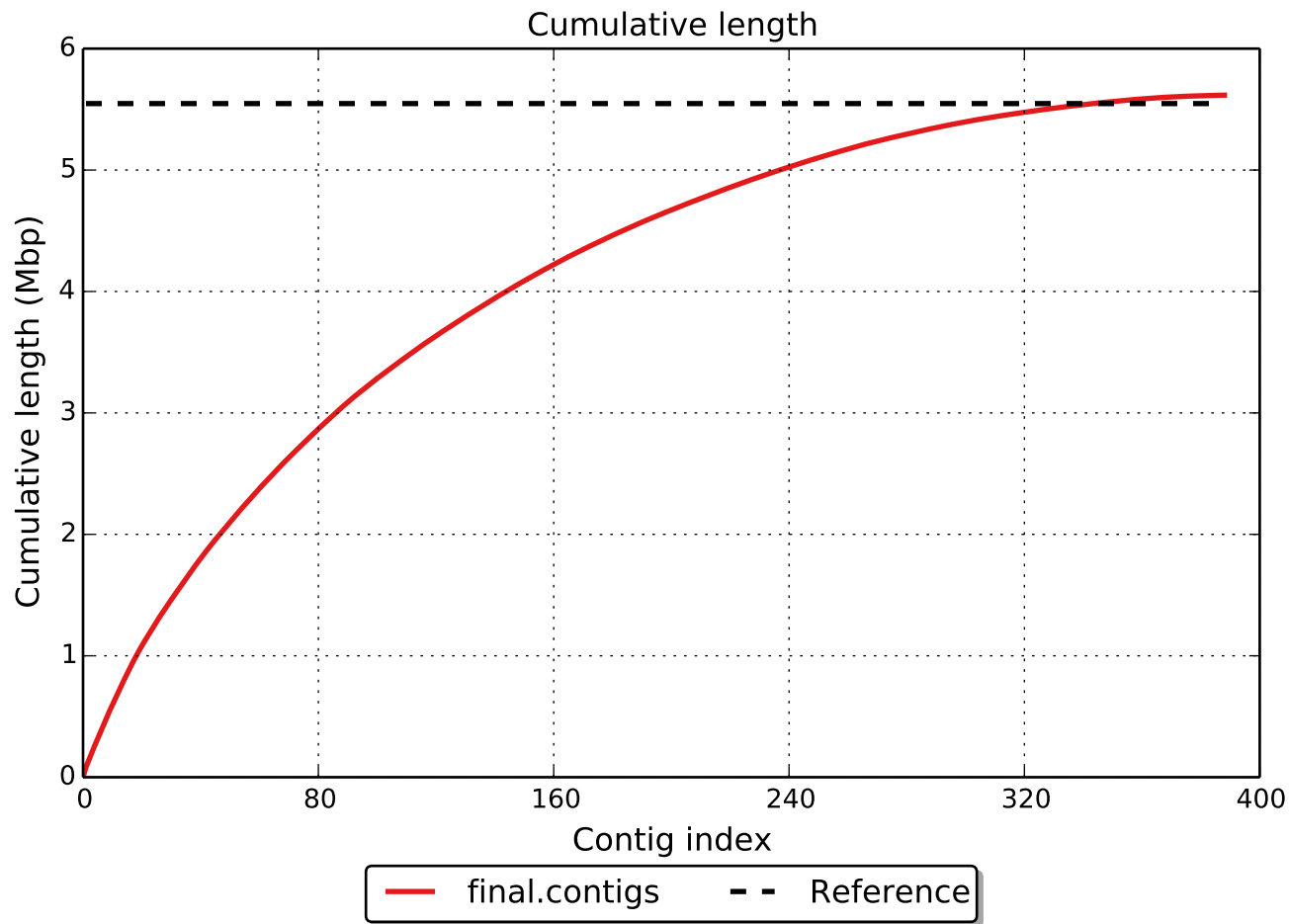
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	1
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	278
# indels	2
# short indels	2
# long indels	0
Indels length	2

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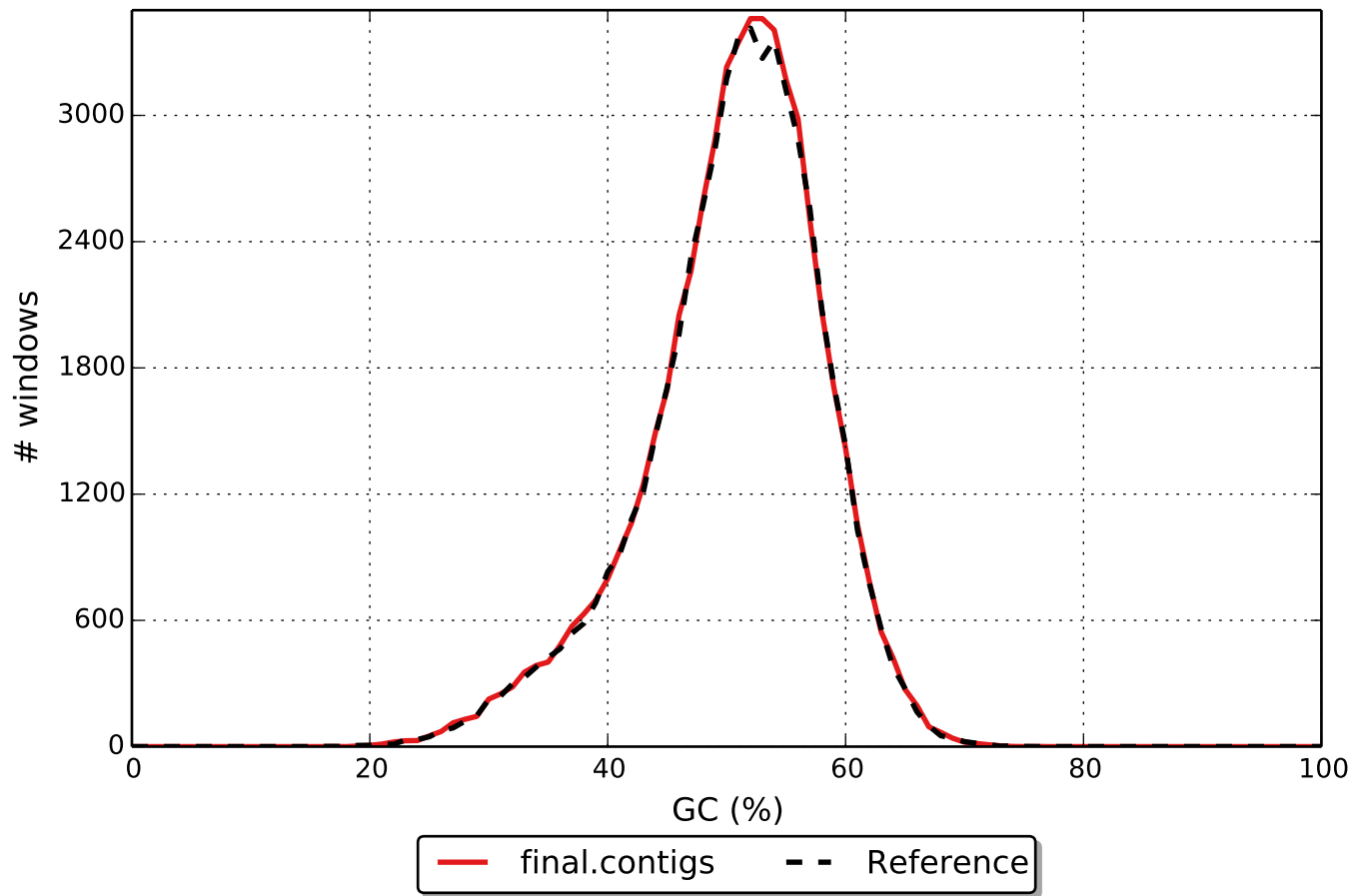
## Unaligned report

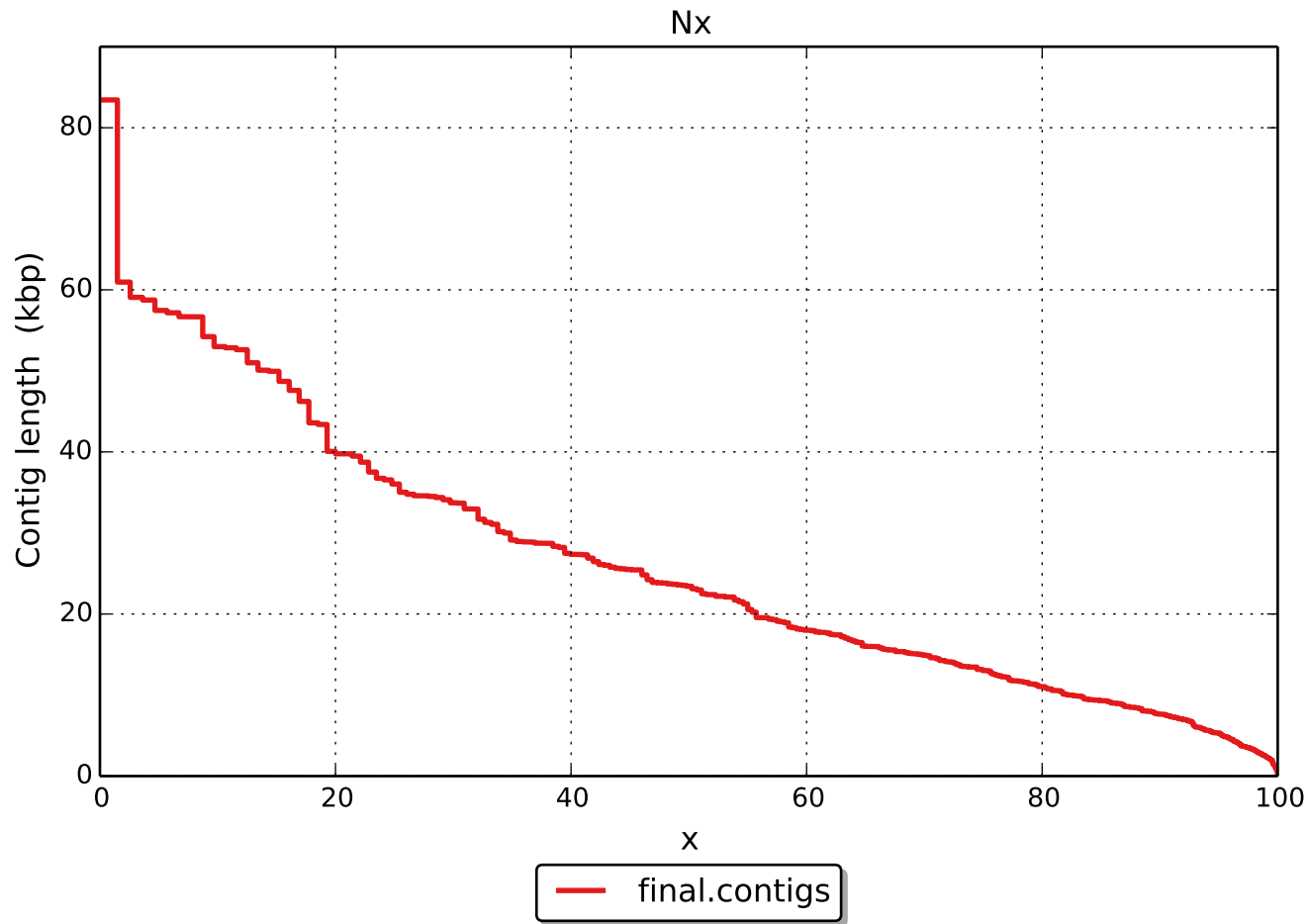
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	1
Partially unaligned length	34780
# N's	0

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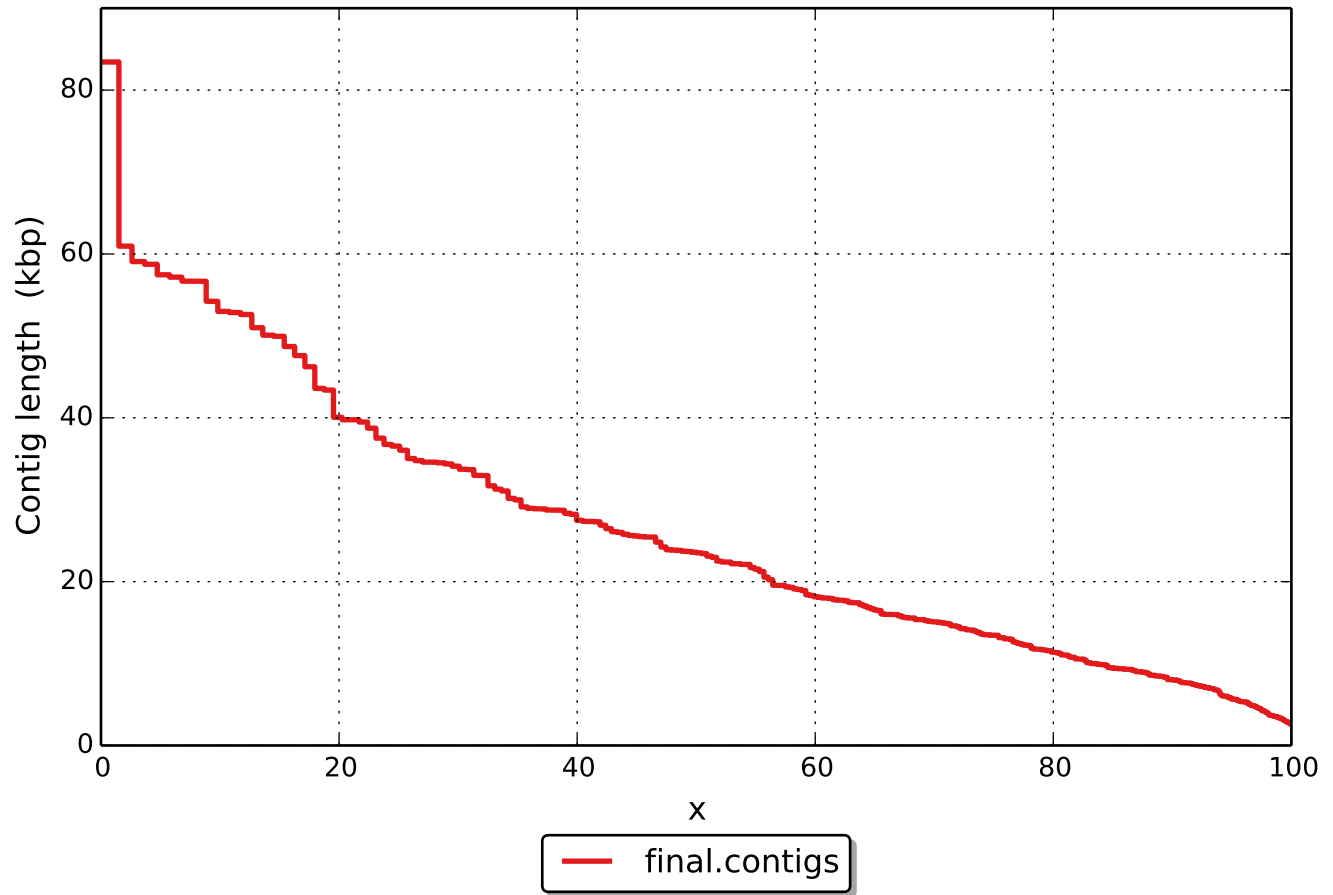


GC content

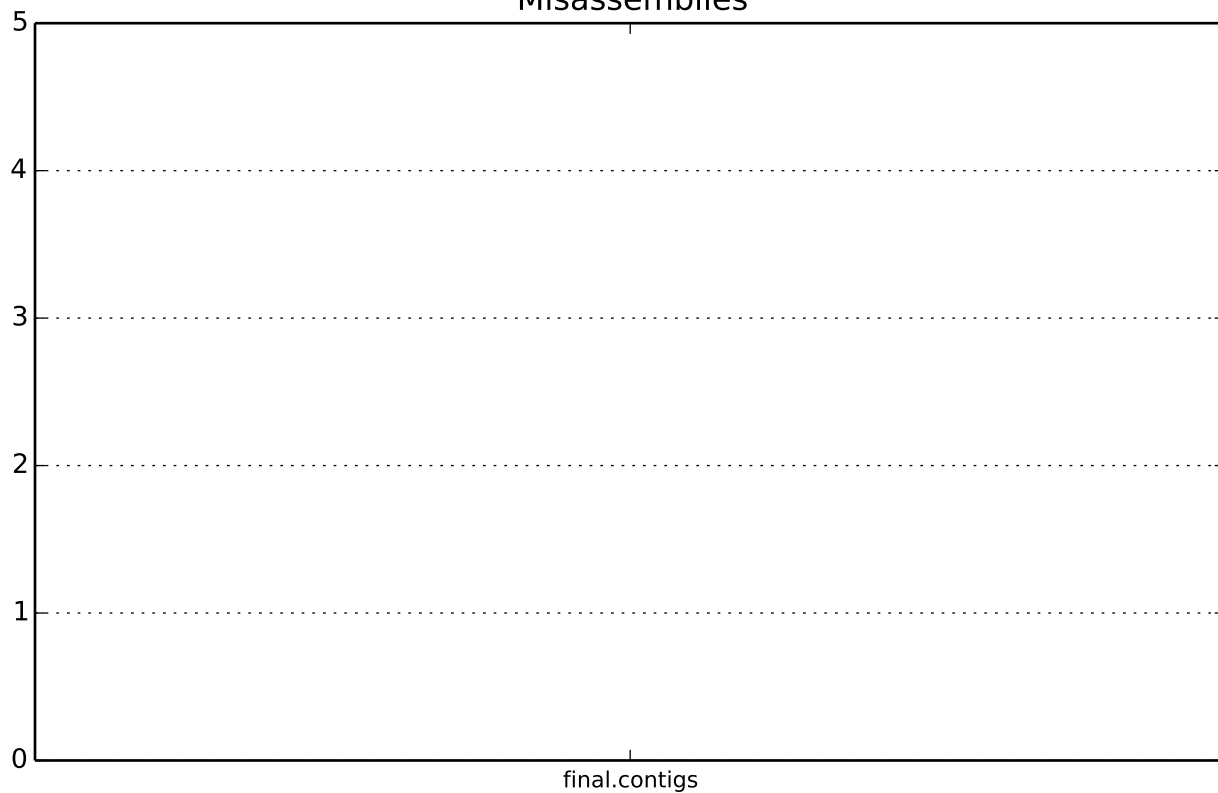




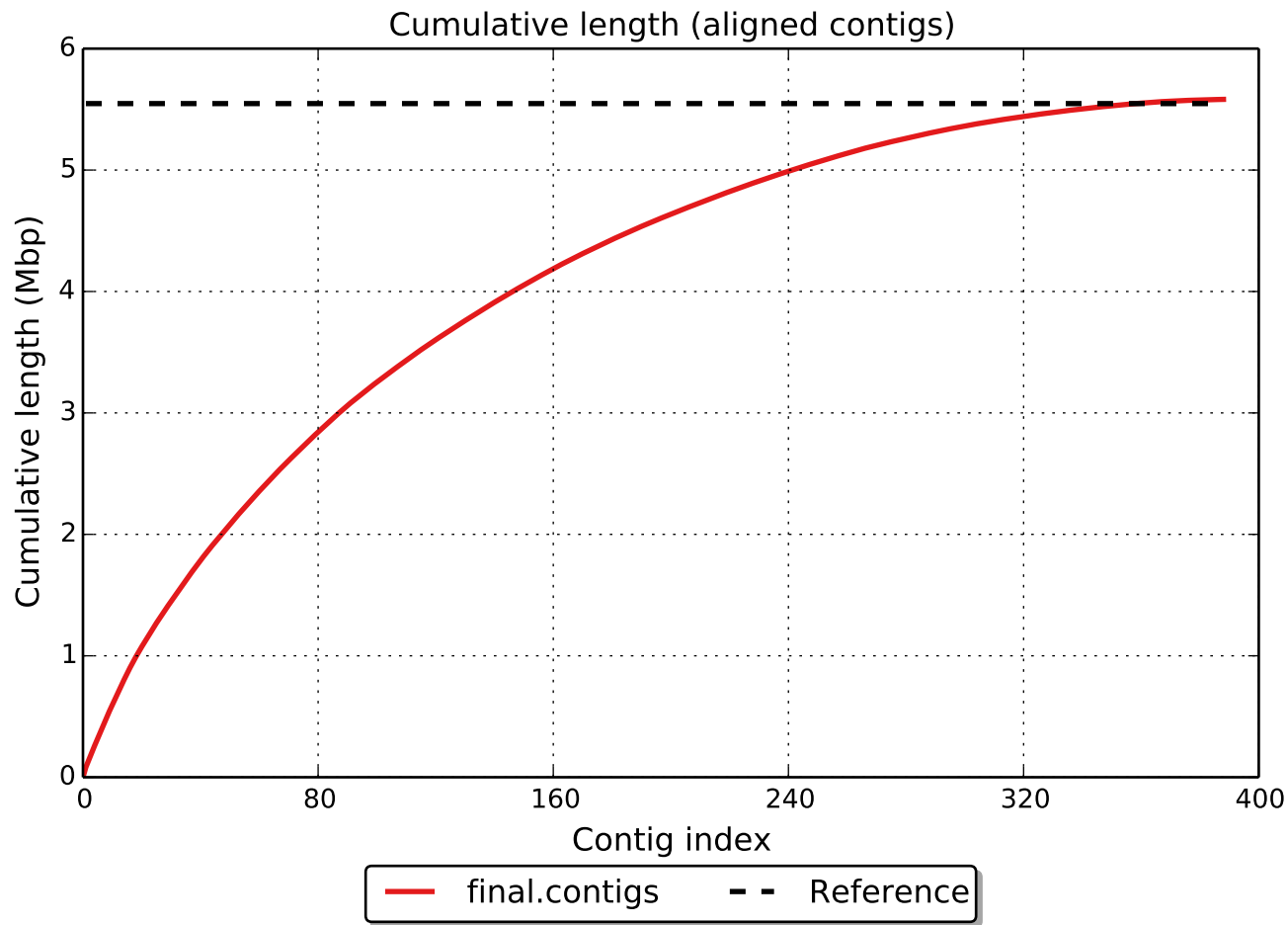
NGx



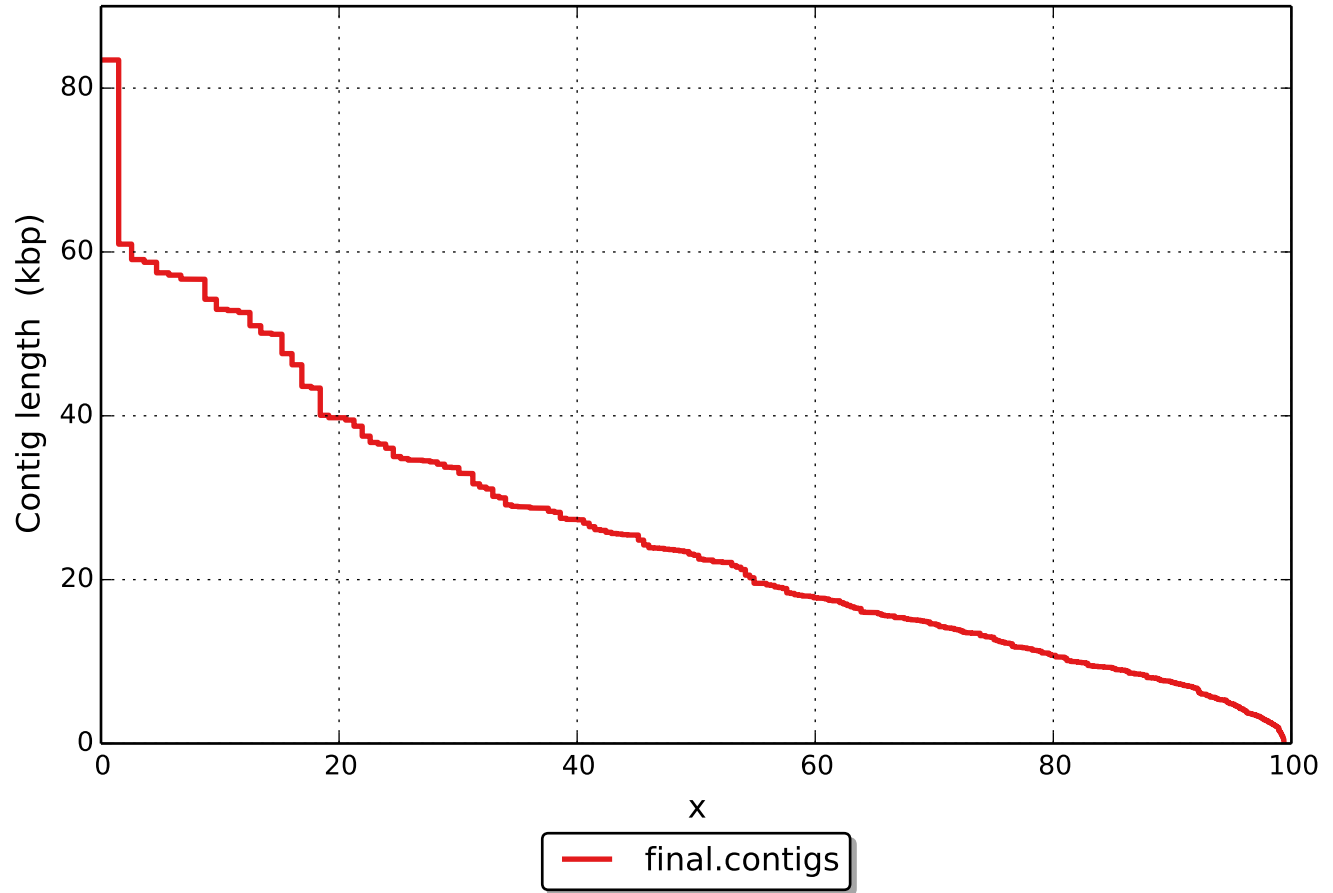
# Misassemblies







NAx



# NGAx

