

# Report

	final.contigs
# contigs ( $\geq 0$ bp)	183
# contigs ( $\geq 1000$ bp)	175
Total length ( $\geq 0$ bp)	1295564
Total length ( $\geq 1000$ bp)	1289931
# contigs	183
Largest contig	30887
Total length	1295564
Reference length	641799
GC (%)	26.29
Reference GC (%)	26.30
N50	10988
NG50	15937
N75	6128
NG75	14184
L50	41
LG50	16
L75	78
LG75	27
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	73 + 13 part
Unaligned length	628251
Genome fraction (%)	99.870
Duplication ratio	1.041
# N's per 100 kbp	0.00
# mismatches per 100 kbp	61.16
# indels per 100 kbp	0.00
Largest alignment	30887
NA50	1545
NGA50	11959
NGA75	6104
LA50	86
LGA50	19
LGA75	38

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	8
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	392
# indels	0
# short indels	0
# long indels	0
Indels length	0

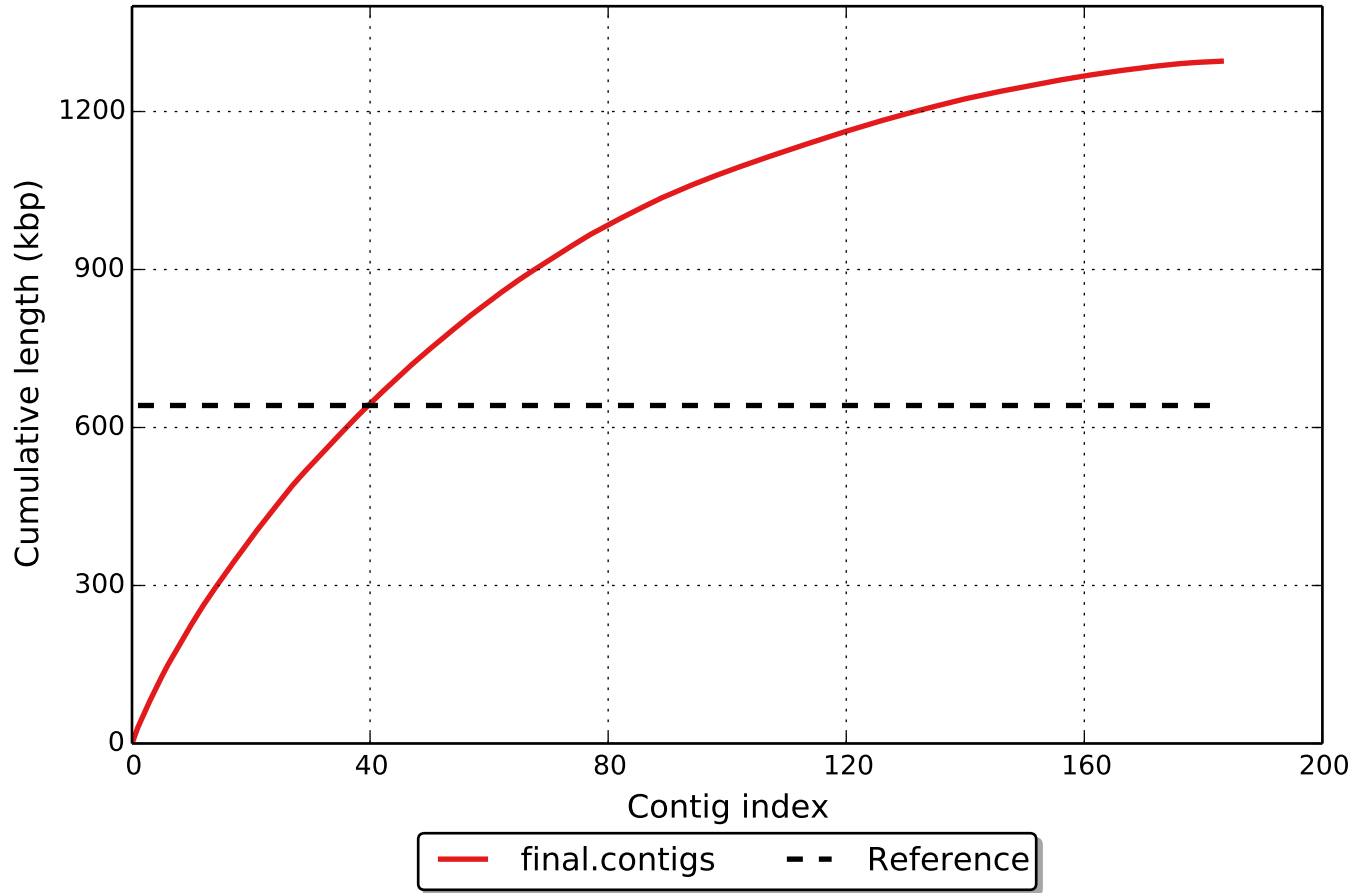
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

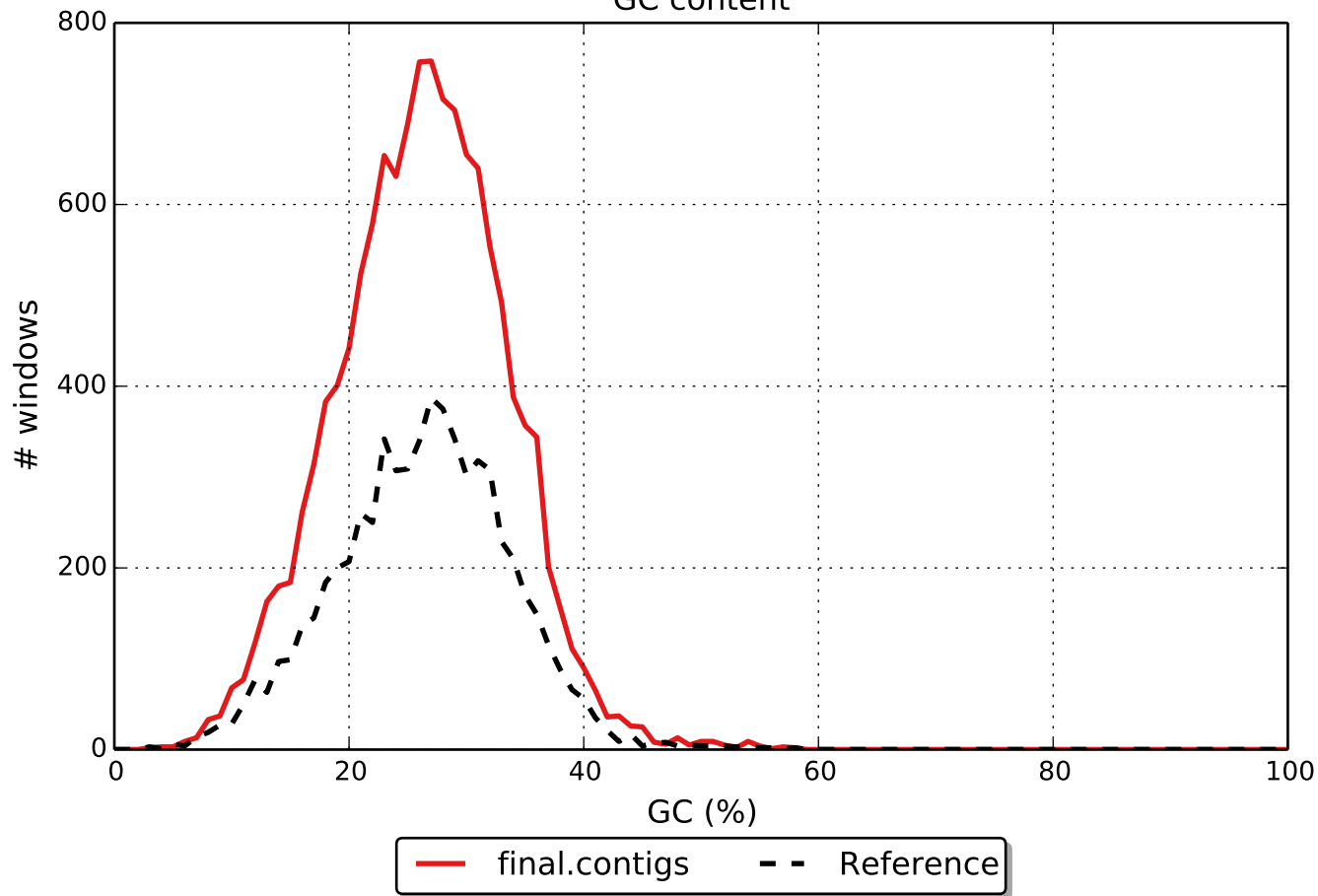
	final.contigs
# fully unaligned contigs	73
Fully unaligned length	515624
# partially unaligned contigs	13
# with misassembly	0
# both parts are significant	8
Partially unaligned length	112627
# N's	0

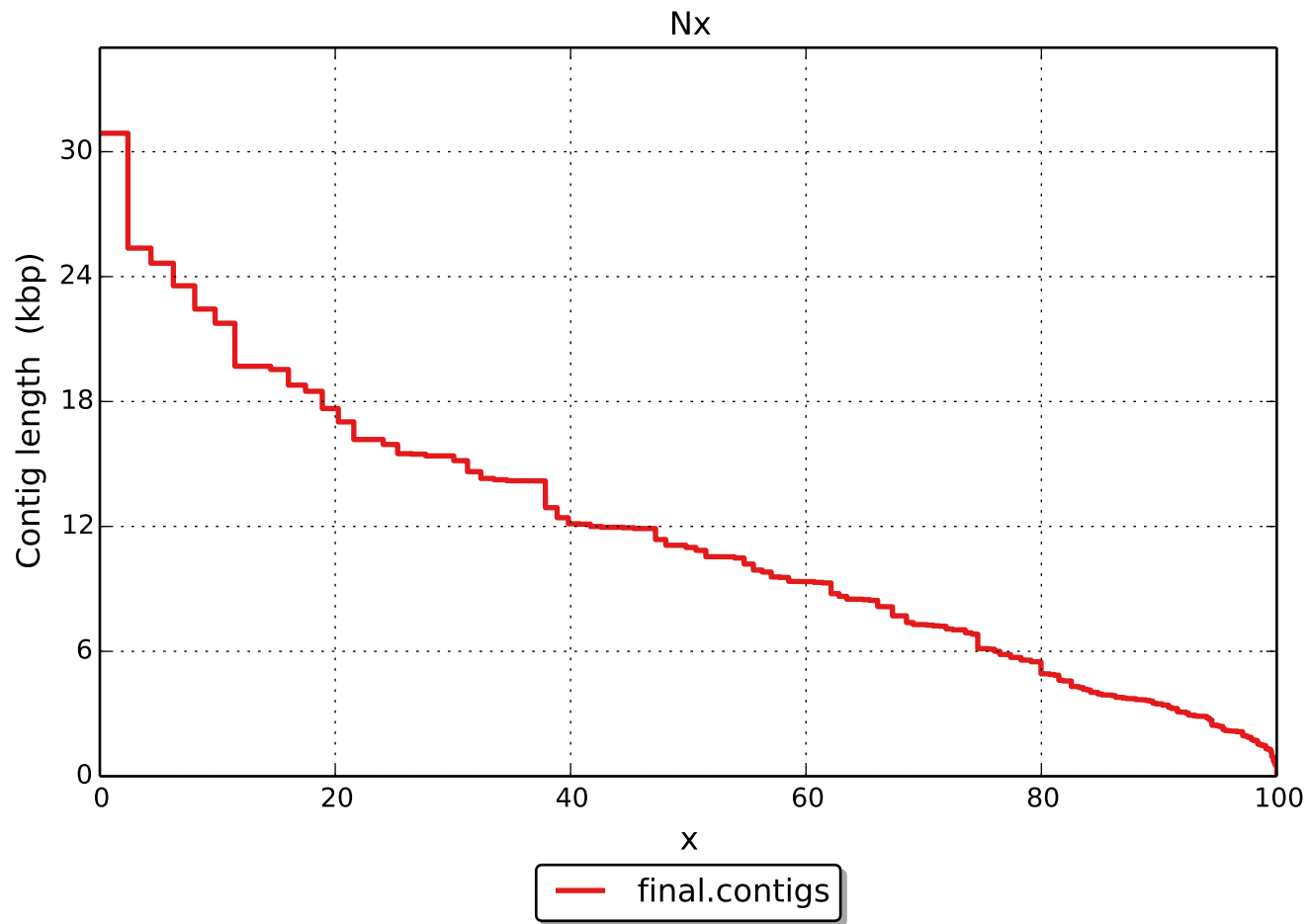
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Cumulative length

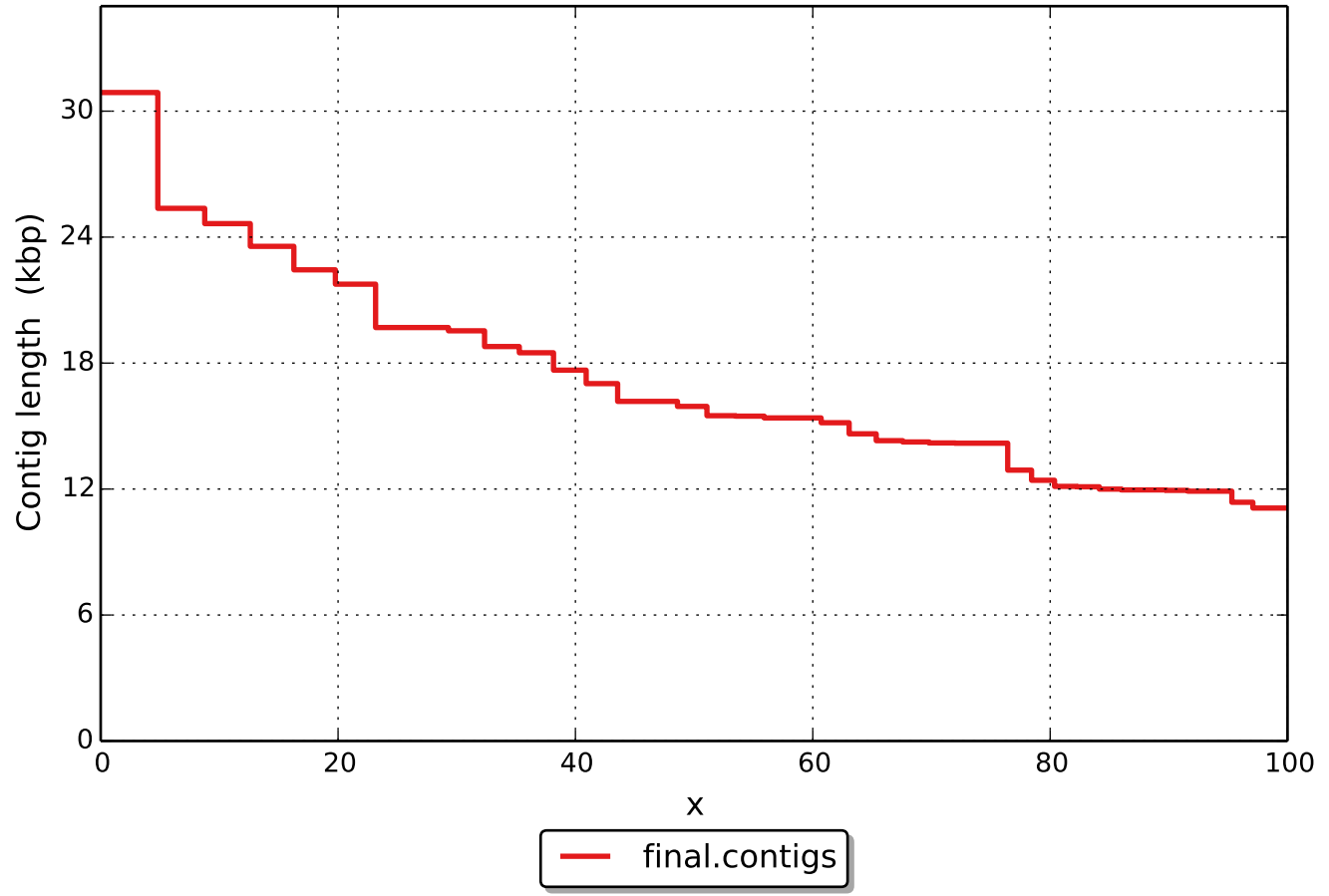


GC content





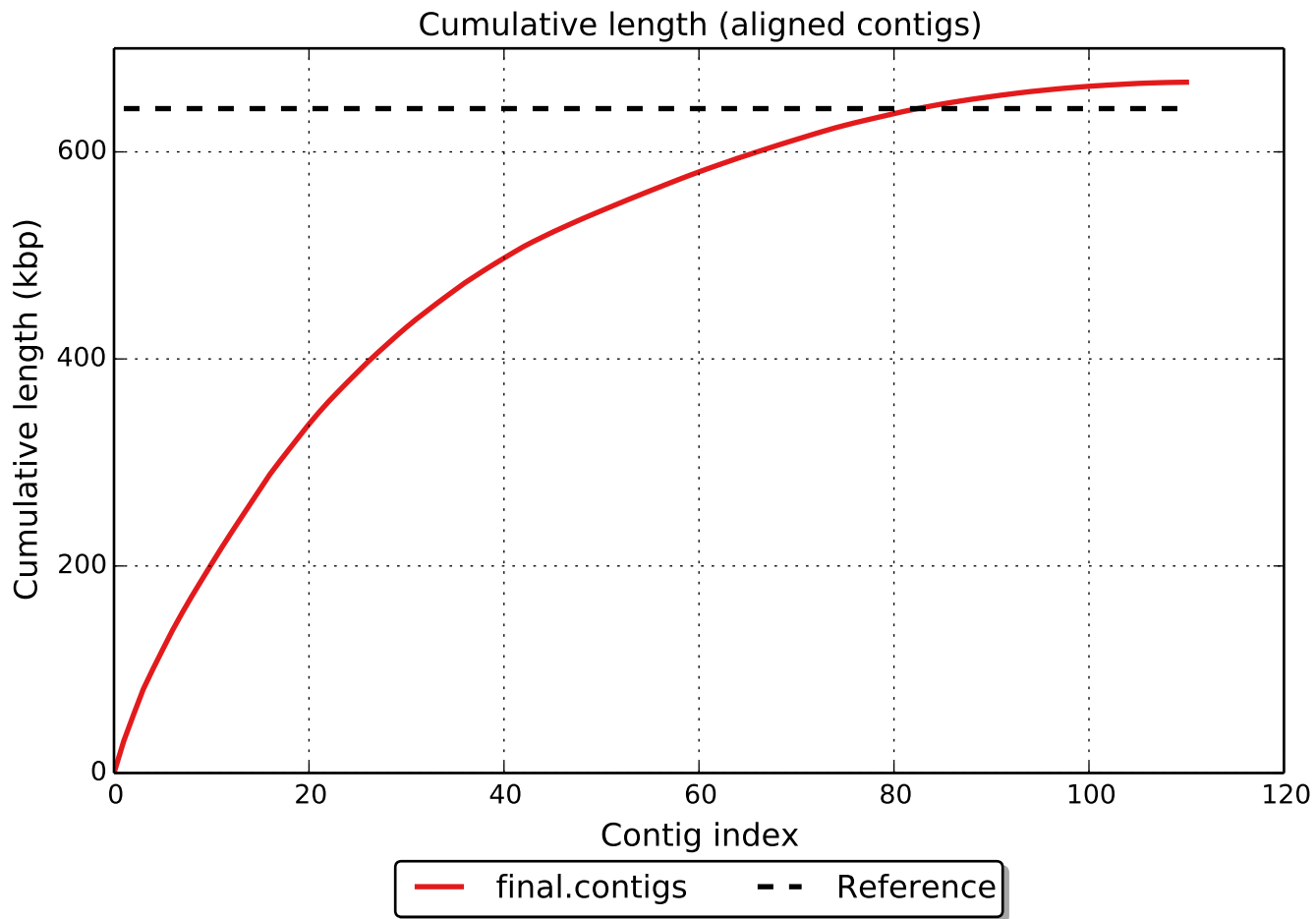
NGx



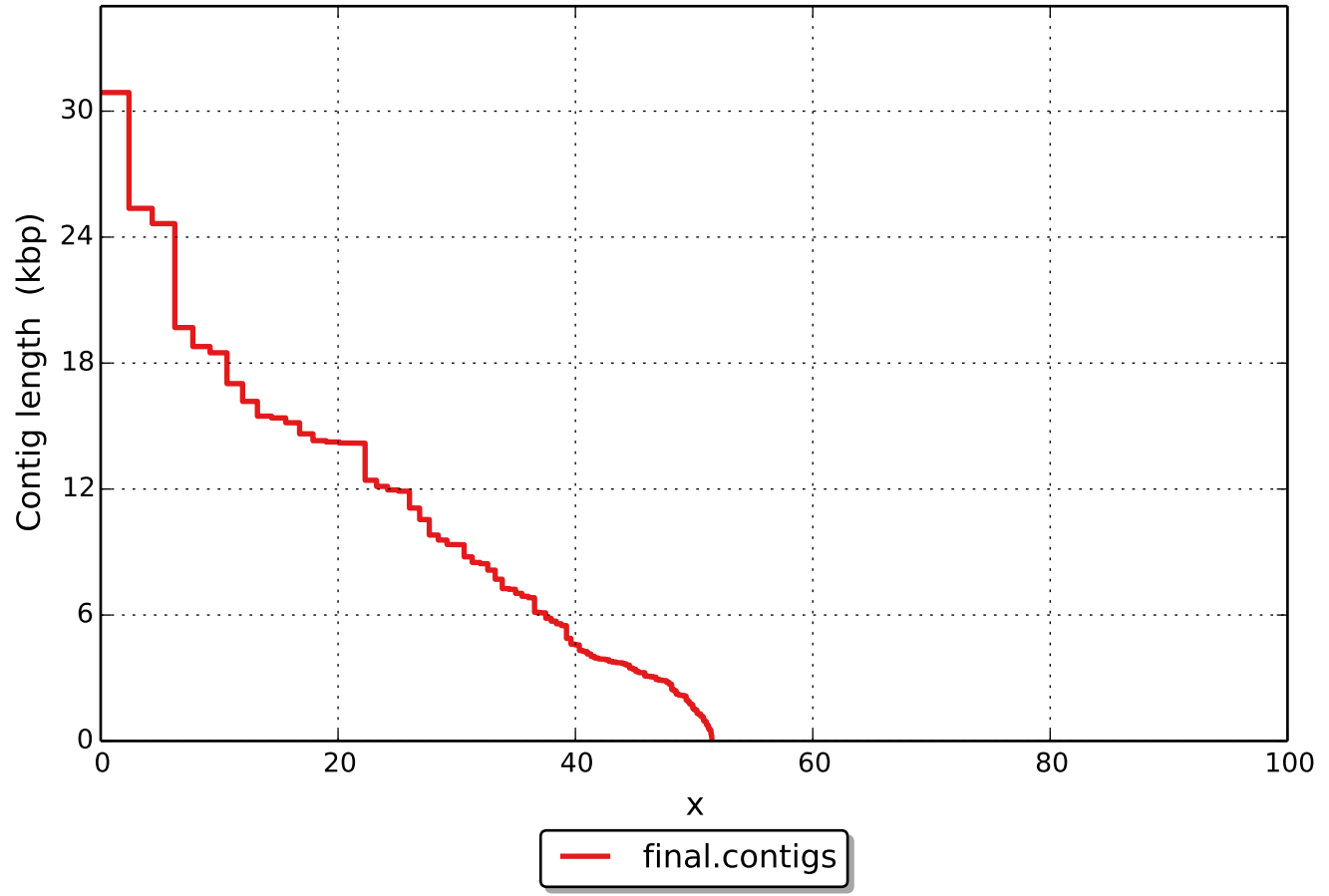
# Misassemblies







NAx



# NGAx

