

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	69
# contigs ( $\geq 1000$ bp)	69
Total length ( $\geq 0$ bp)	1237426
Total length ( $\geq 1000$ bp)	1237426
# contigs	69
Largest contig	108160
Total length	1237426
Reference length	615980
GC (%)	25.35
Reference GC (%)	25.35
N50	30198
NG50	43825
N75	15327
NG75	38435
L50	13
LG50	5
L75	28
LG75	8
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	31 + 3 part
Unaligned length	617663
Genome fraction (%)	99.994
Duplication ratio	1.006
# N's per 100 kbp	0.00
# mismatches per 100 kbp	5.36
# indels per 100 kbp	0.00
Largest alignment	108160
NA50	723
NGA50	35200
NGA75	16354
LA50	36
LGA50	6
LGA75	13

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	33
# indels	0
# short indels	0
# long indels	0
Indels length	0

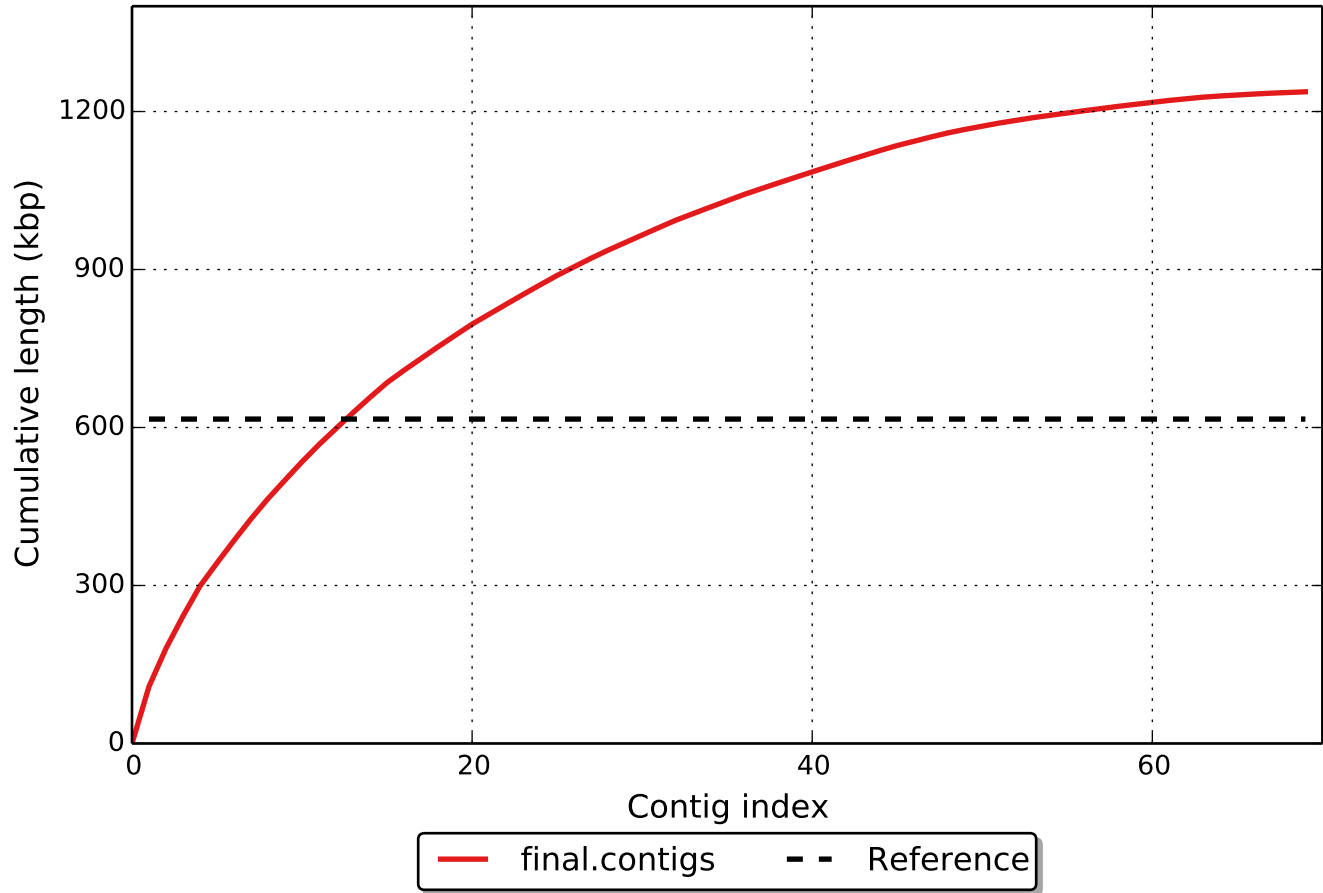
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

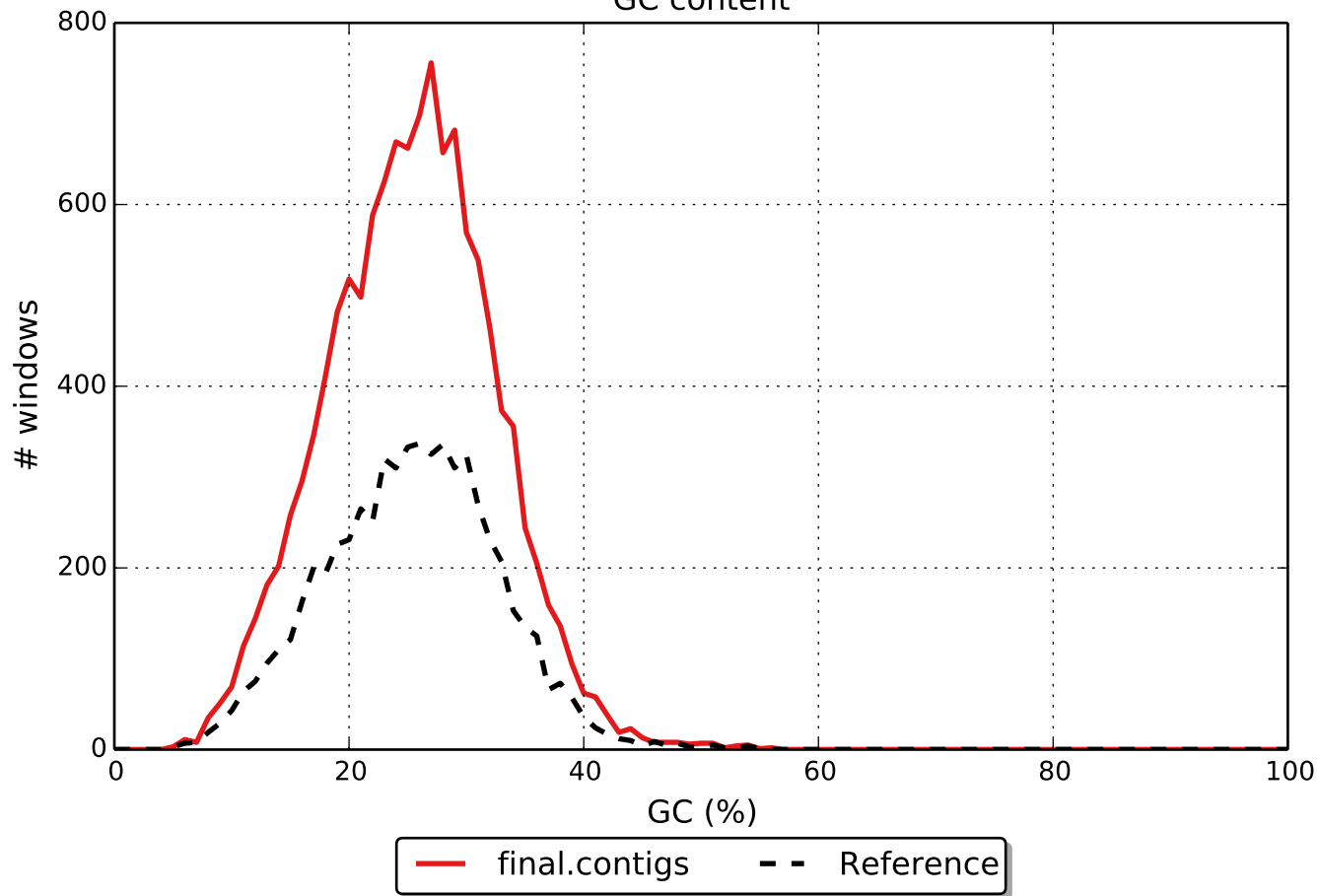
	final.contigs
# fully unaligned contigs	31
Fully unaligned length	571709
# partially unaligned contigs	3
# with misassembly	0
# both parts are significant	1
Partially unaligned length	45954
# N's	0

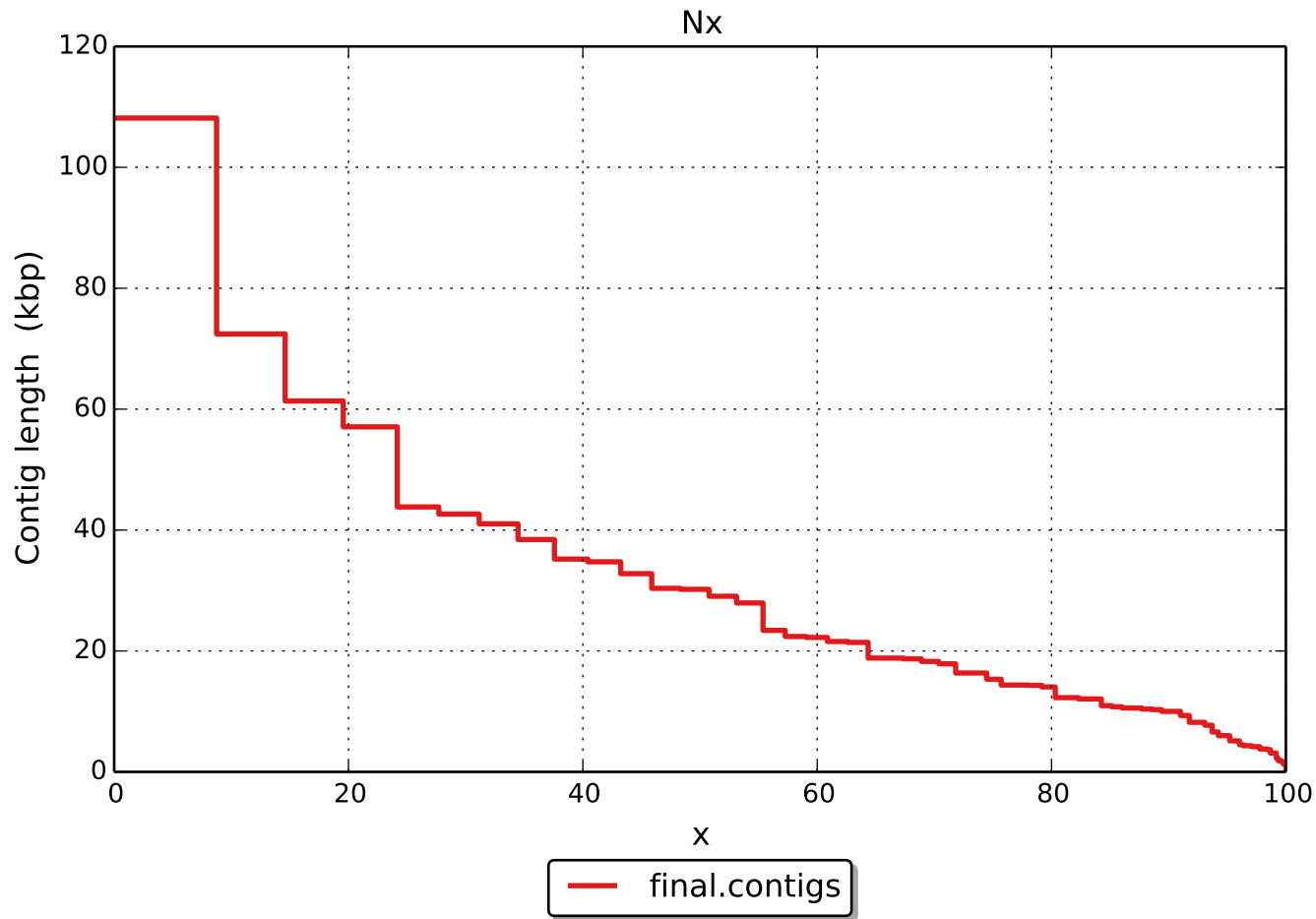
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Cumulative length

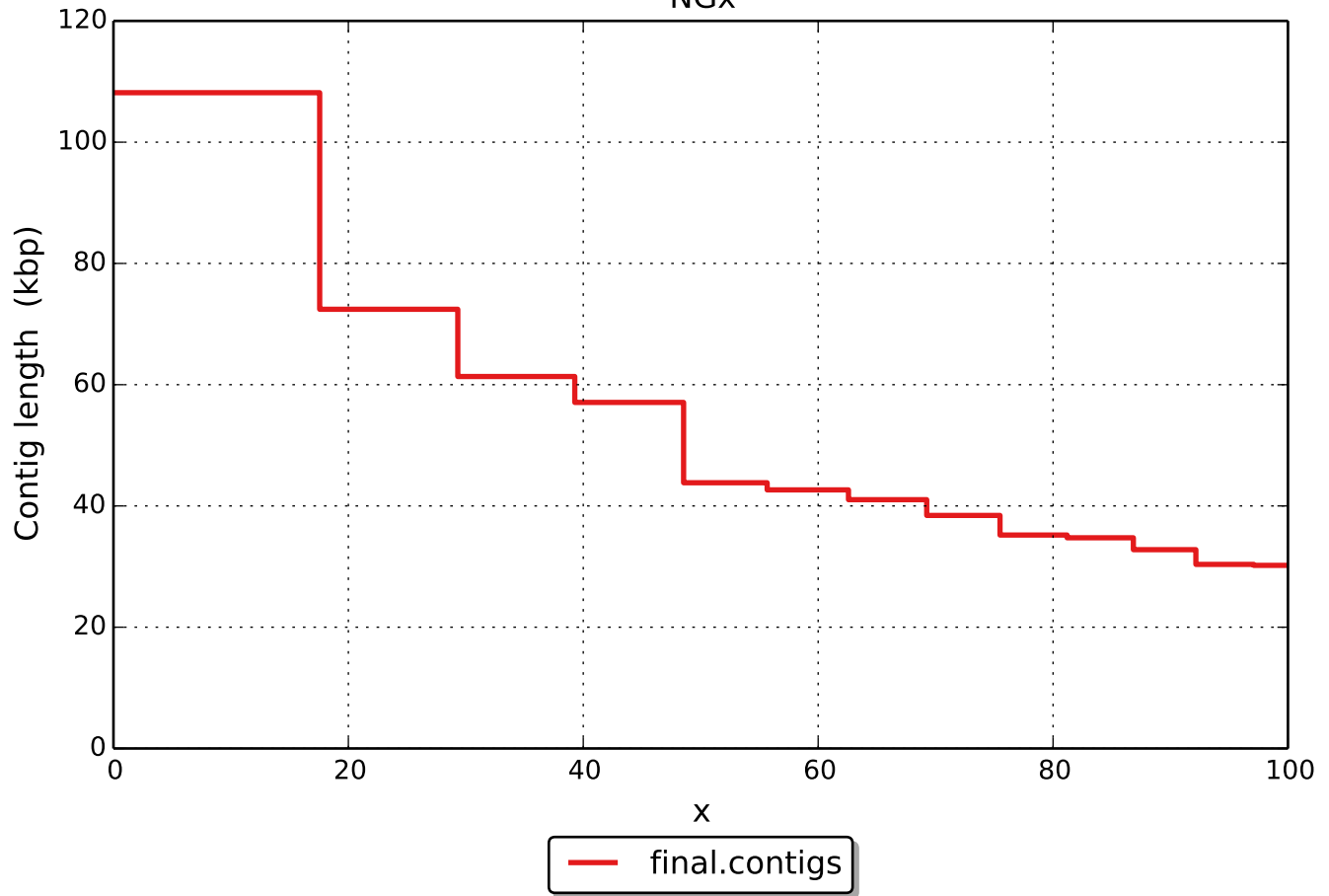


GC content





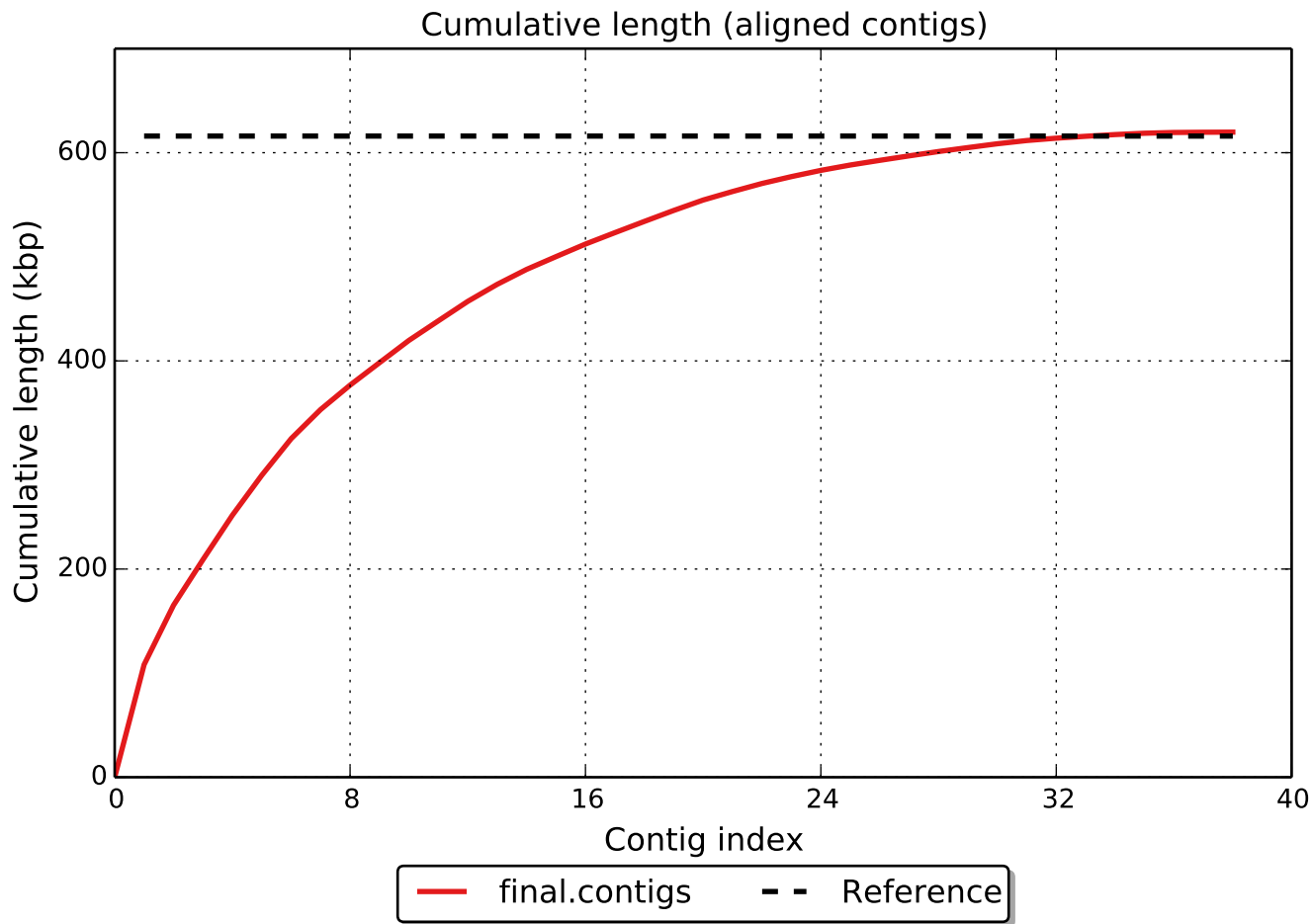
NGx



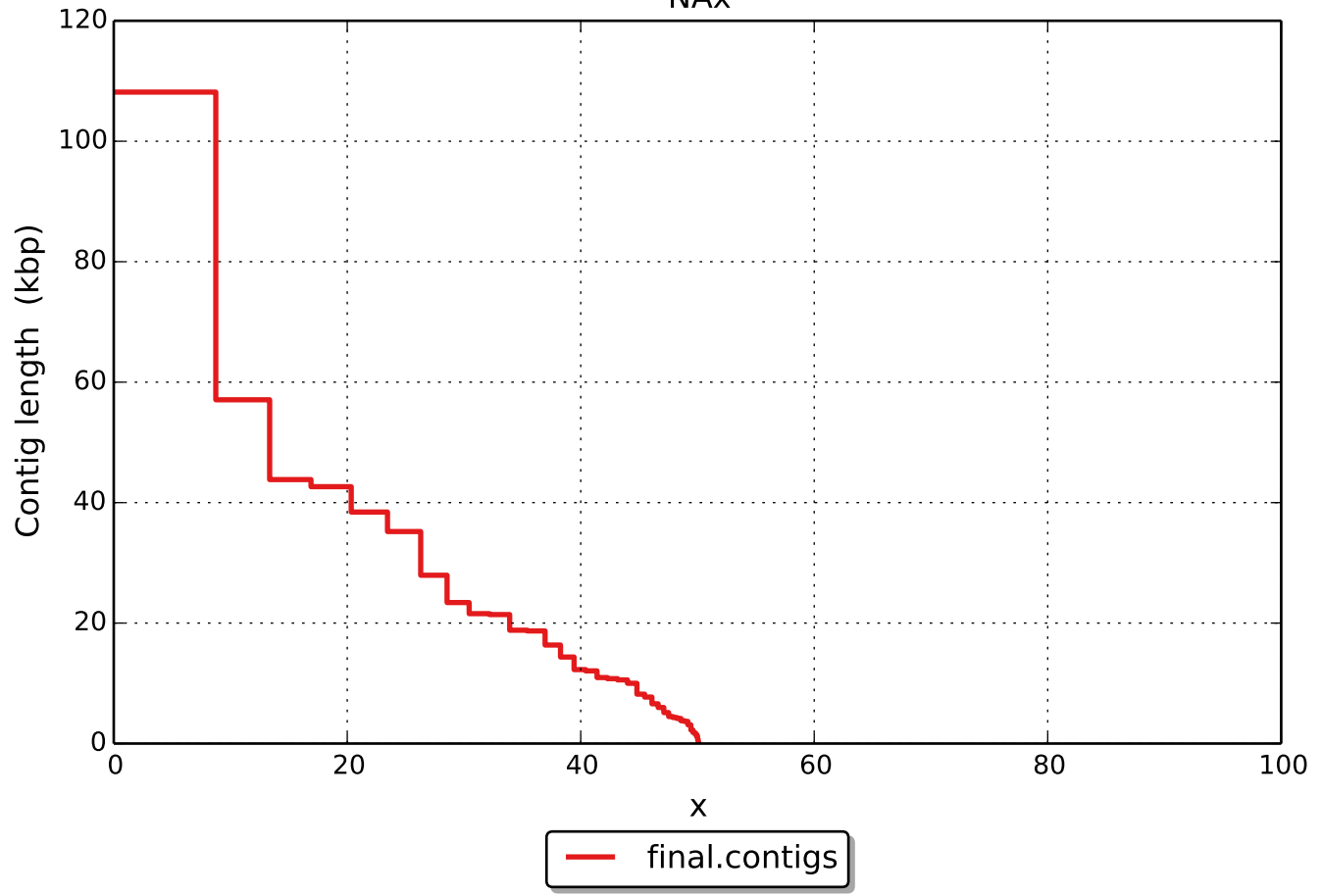
# Misassemblies







NAx



# NGAx

