

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	376
# contigs ( $\geq 1000$ bp)	361
Total length ( $\geq 0$ bp)	5507886
Total length ( $\geq 1000$ bp)	5497103
# contigs	376
Largest contig	123304
Total length	5507886
Reference length	5478683
GC (%)	50.50
Reference GC (%)	50.51
N50	24569
NG50	25526
N75	13357
NG75	13575
L50	66
LG50	65
L75	141
LG75	139
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.962
Duplication ratio	1.006
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.18
# indels per 100 kbp	0.00
Largest alignment	123304
NA50	24569
NGA50	25526
NA75	13357
NGA75	13575
LA50	66
LGA50	65
LA75	141
LGA75	139

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

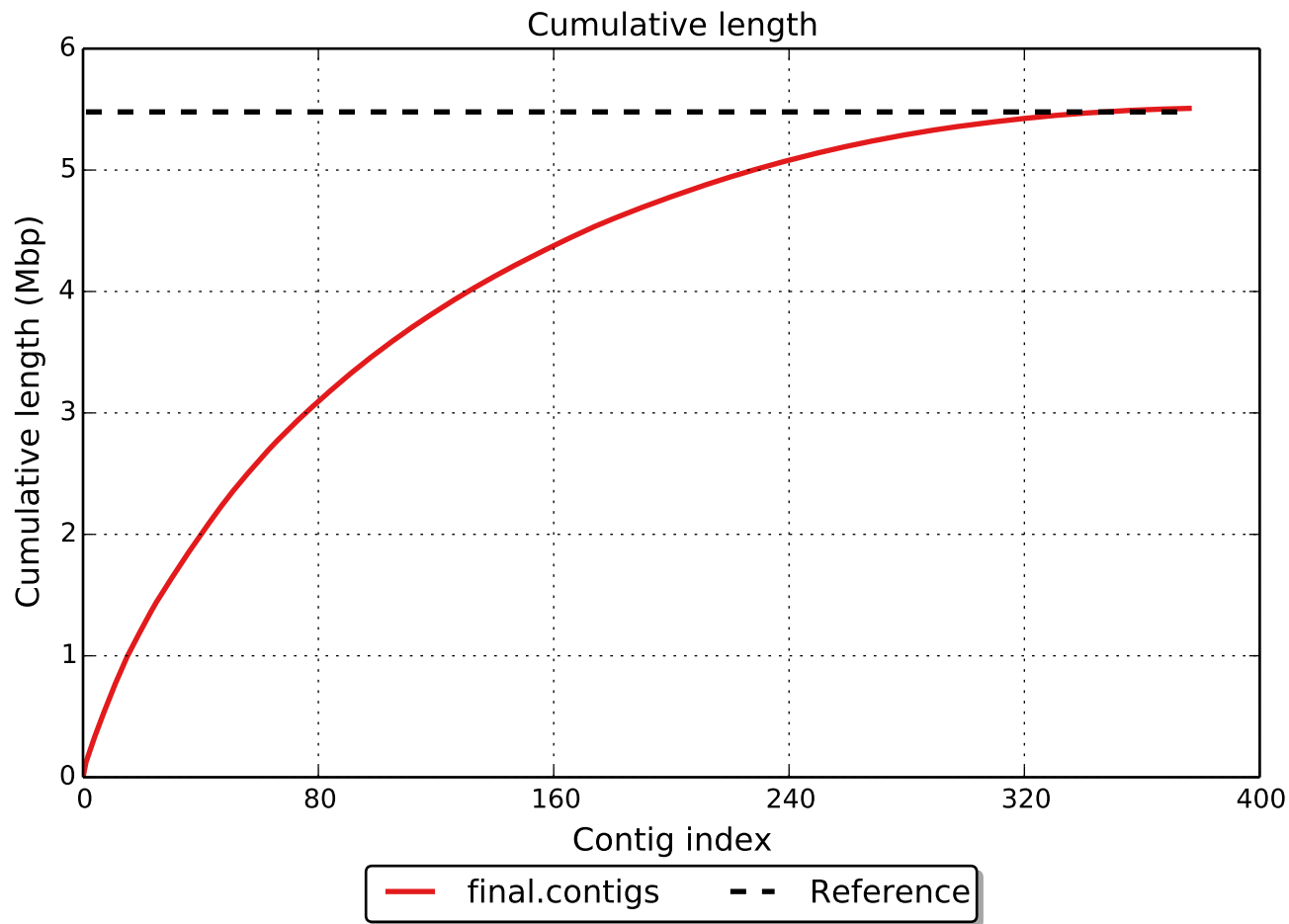
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	10
# indels	0
# short indels	0
# long indels	0
Indels length	0

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).

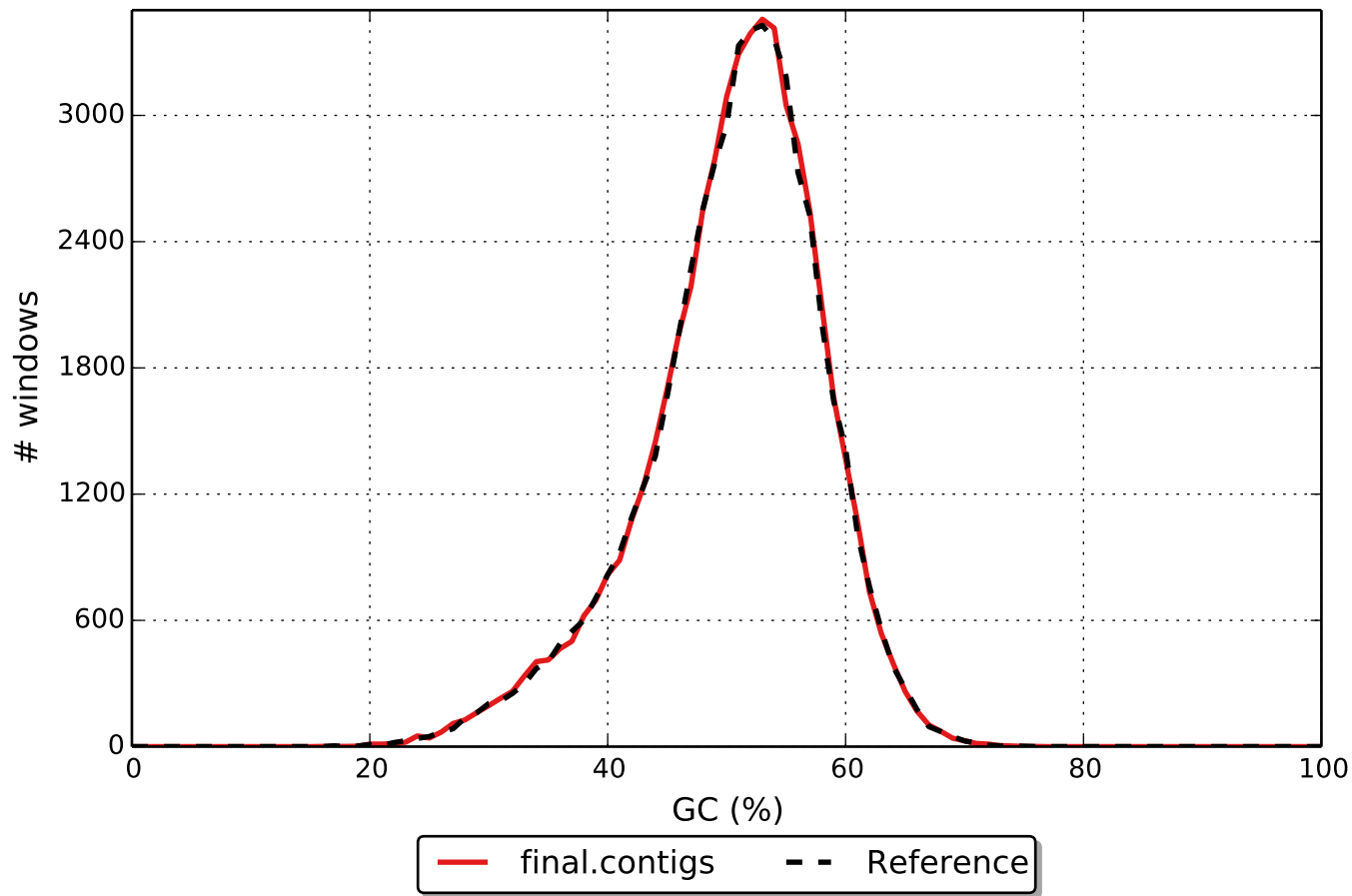
## Unaligned report

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

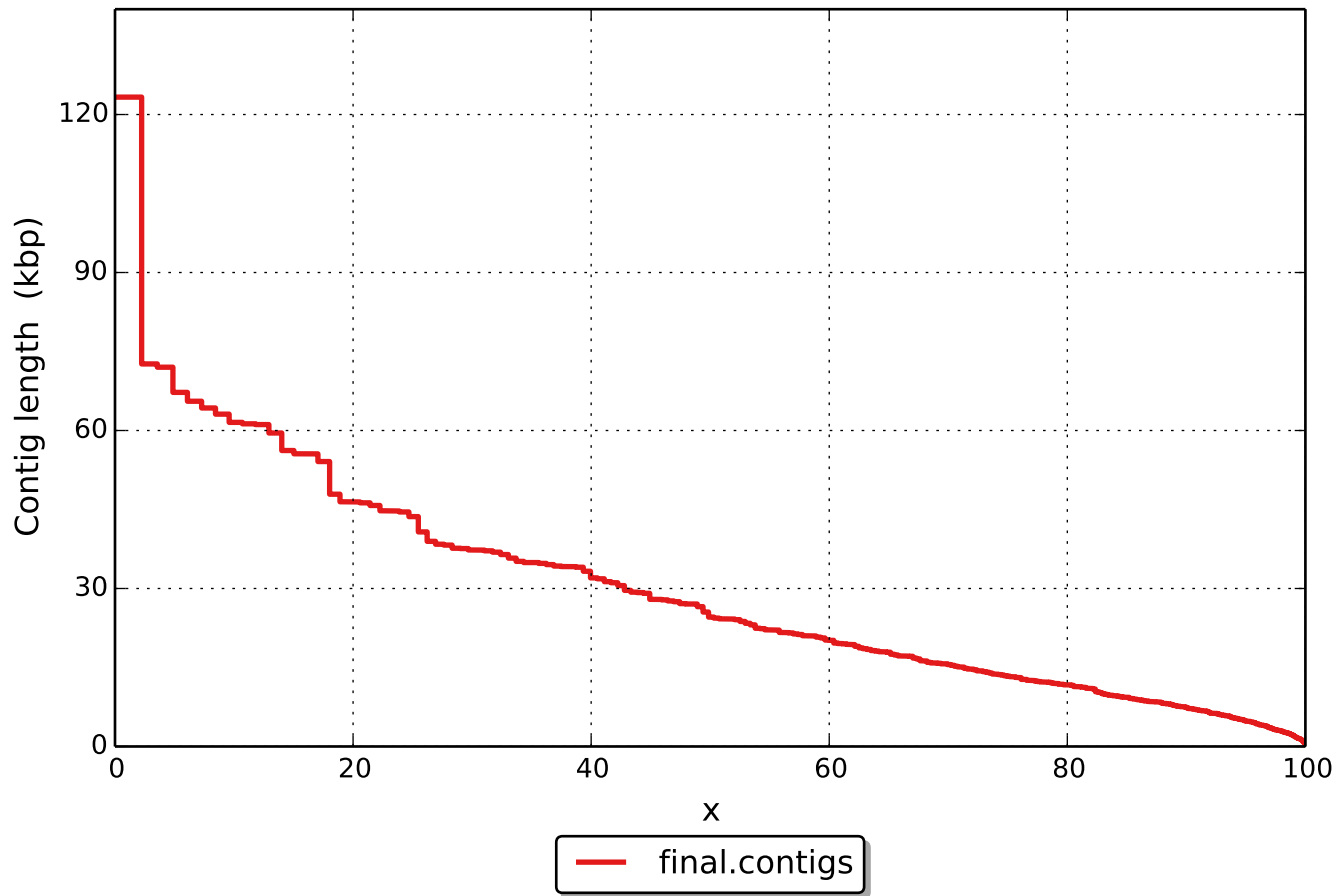
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



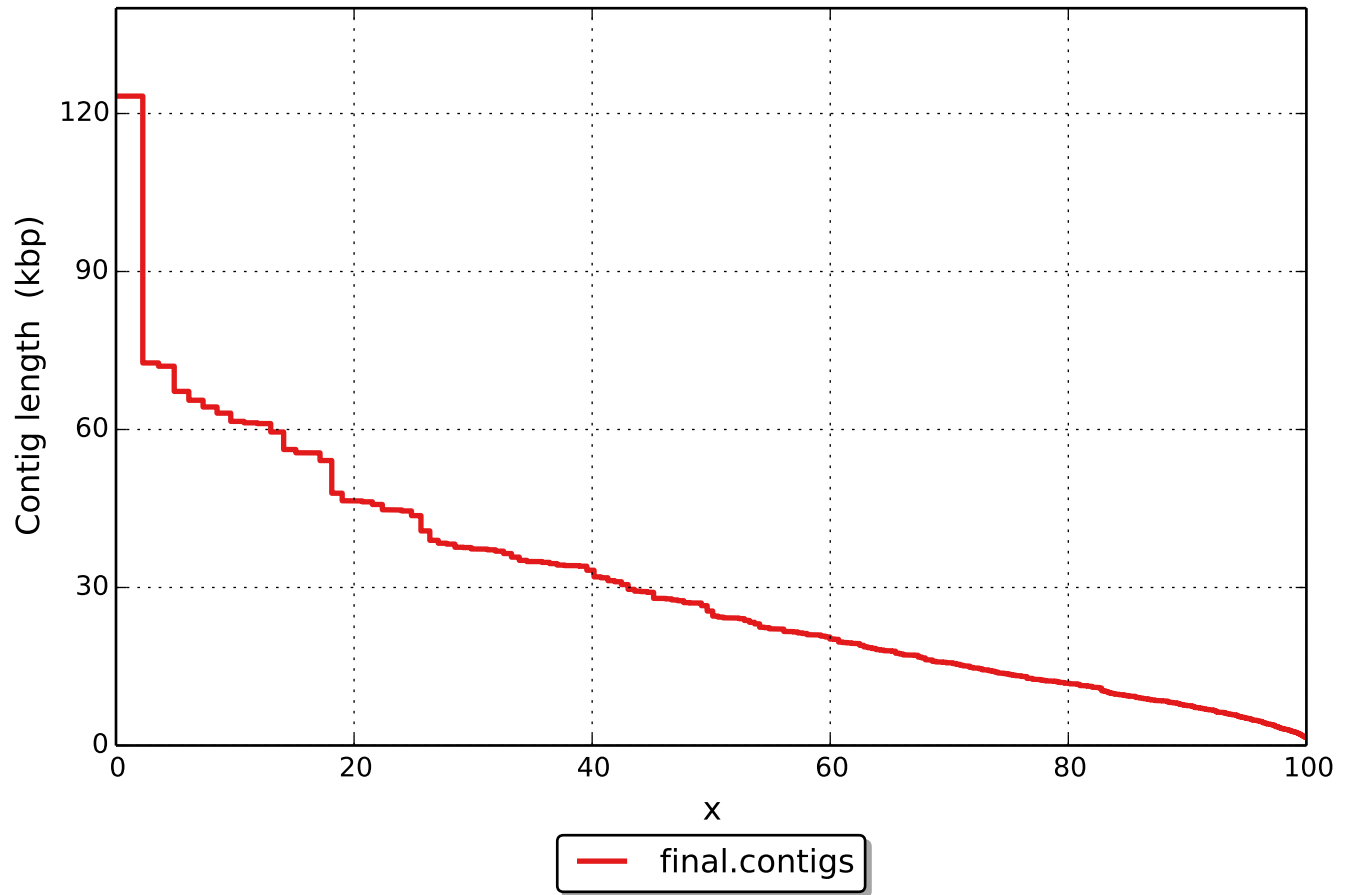
# GC content



Nx



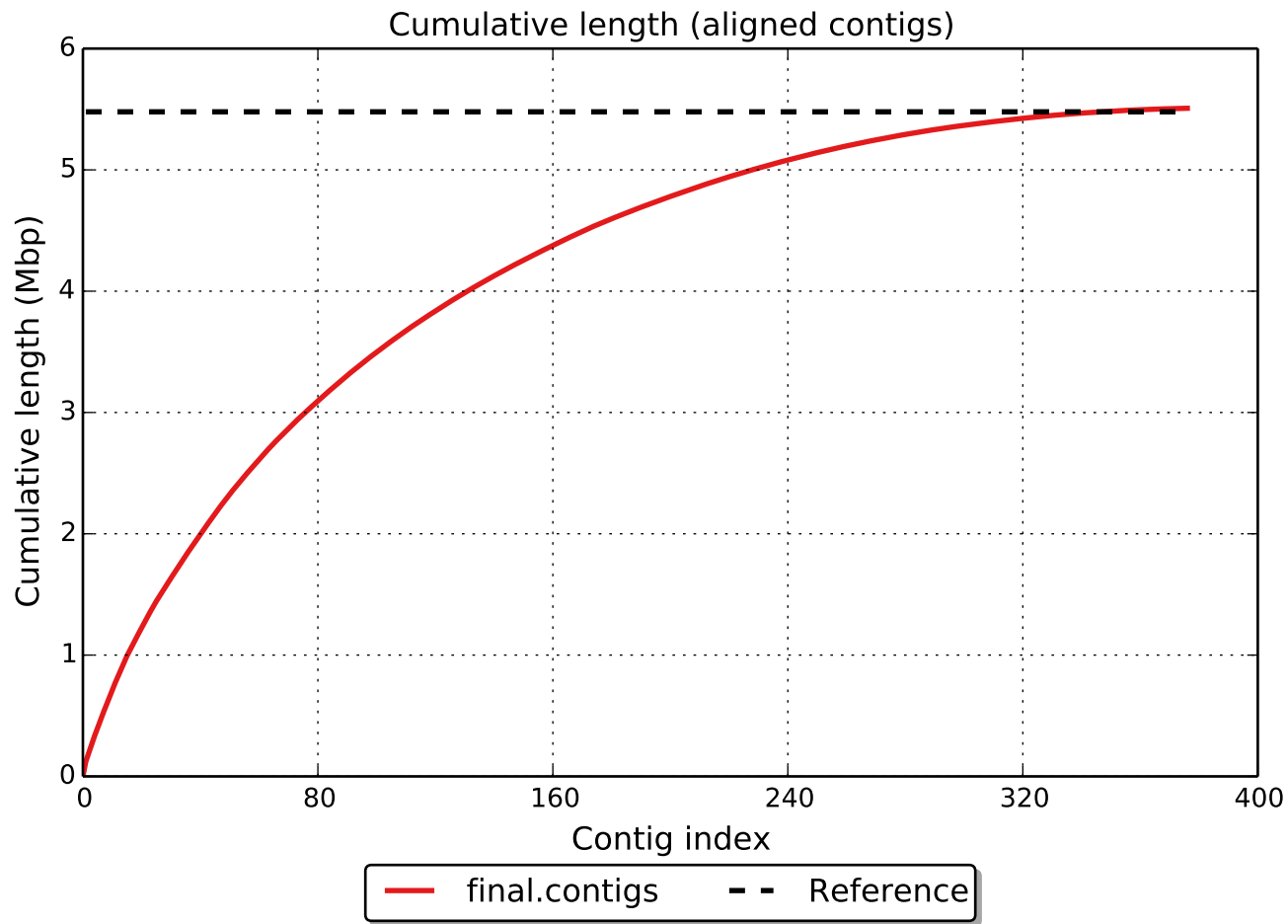
NGx



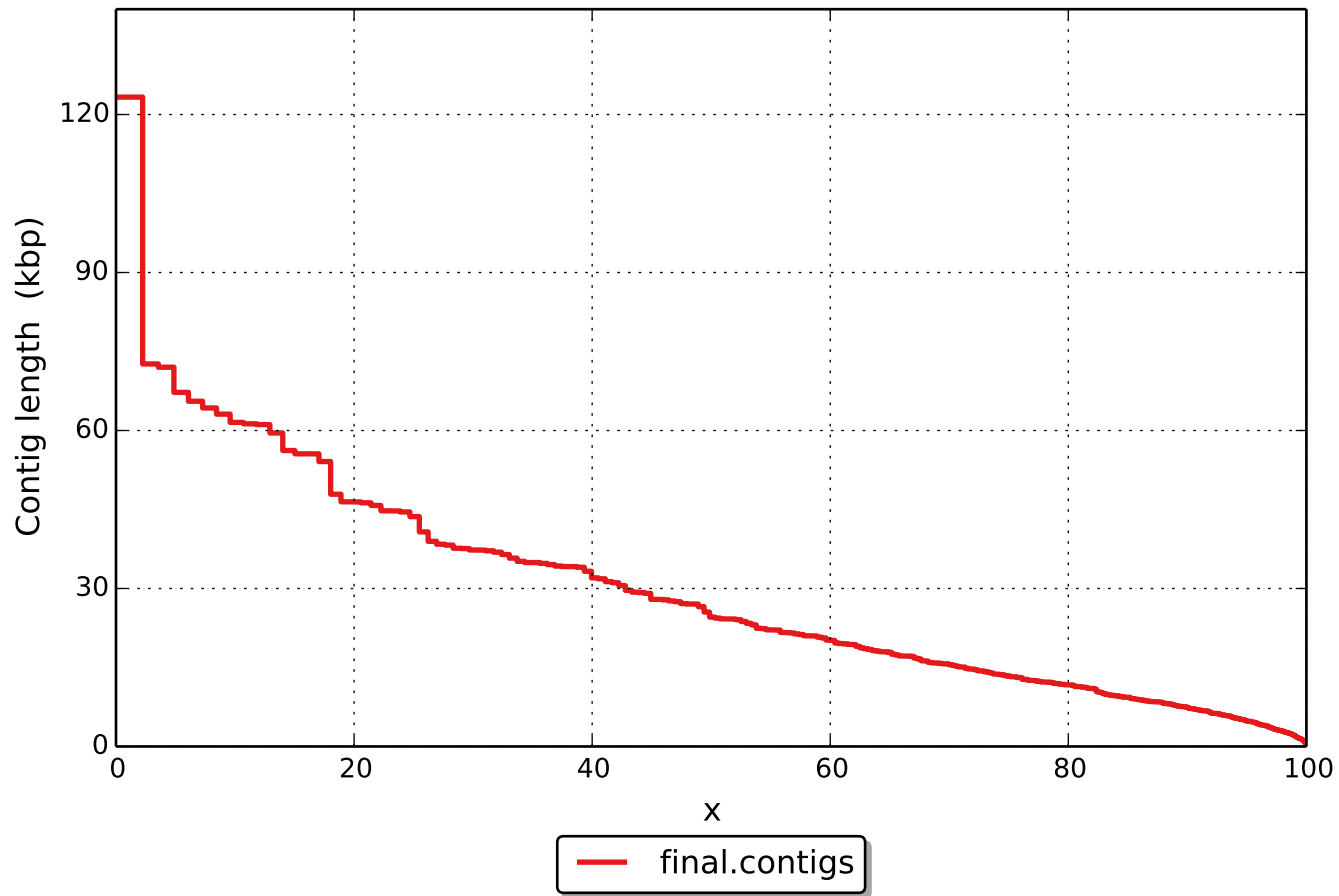
# Misassemblies







NAx



# NGAx

