

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	4516
# contigs ( $\geq 1000$ bp)	1494
Total length ( $\geq 0$ bp)	4453398
Total length ( $\geq 1000$ bp)	2339343
# contigs	4516
Largest contig	6472
Total length	4453398
Reference length	5547323
GC (%)	50.30
Reference GC (%)	50.48
N50	1034
NG50	873
N75	726
NG75	554
L50	1384
LG50	1959
L75	2672
LG75	3960
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	75.169
Duplication ratio	1.068
# N's per 100 kbp	0.00
# mismatches per 100 kbp	414.33
# indels per 100 kbp	0.10
Largest alignment	6472
NA50	1034
NGA50	873
NA75	726
NGA75	554
LA50	1384
LGA50	1959
LA75	2672
LGA75	3960

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

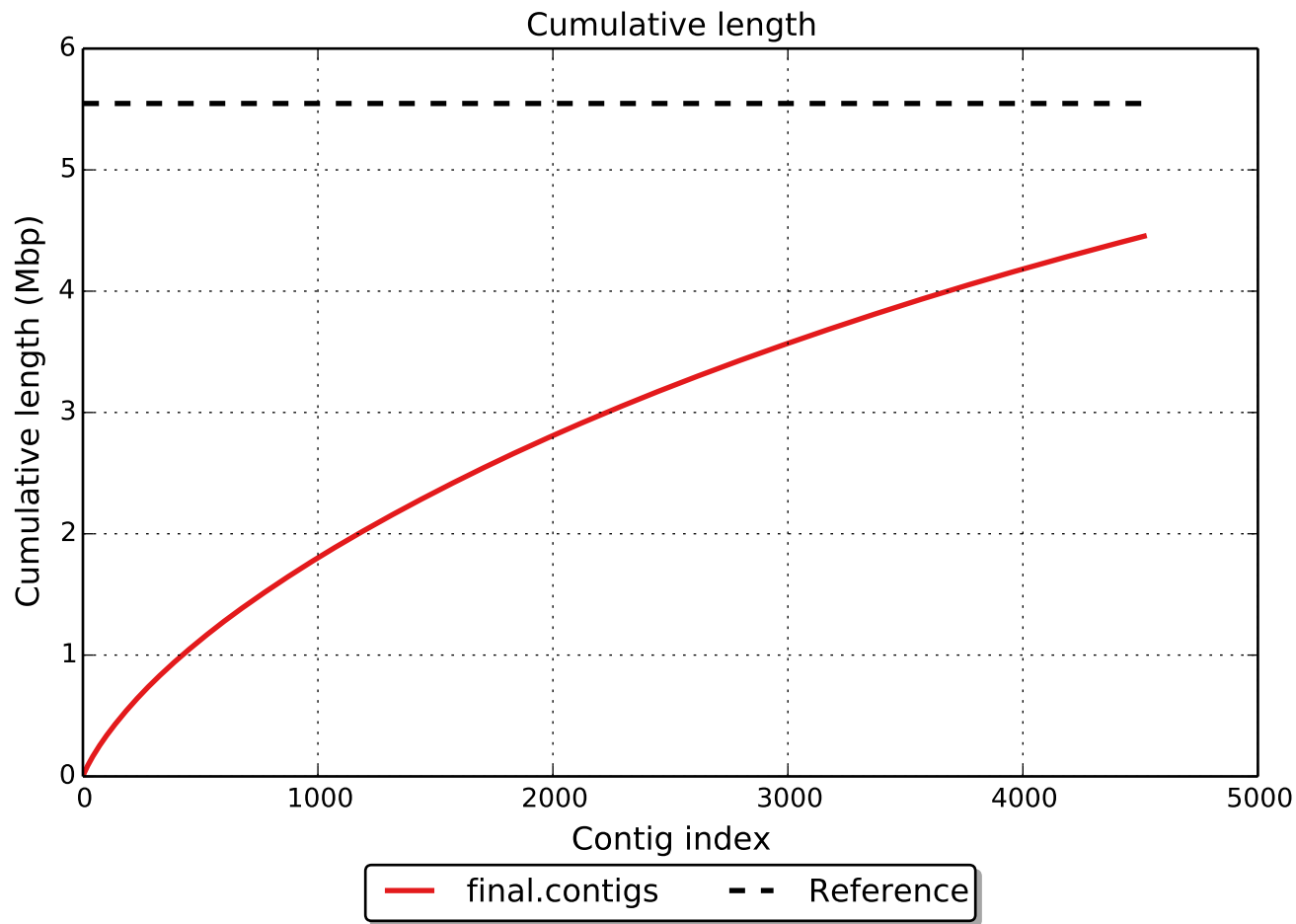
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	17277
# indels	4
# short indels	4
# long indels	0
Indels length	5

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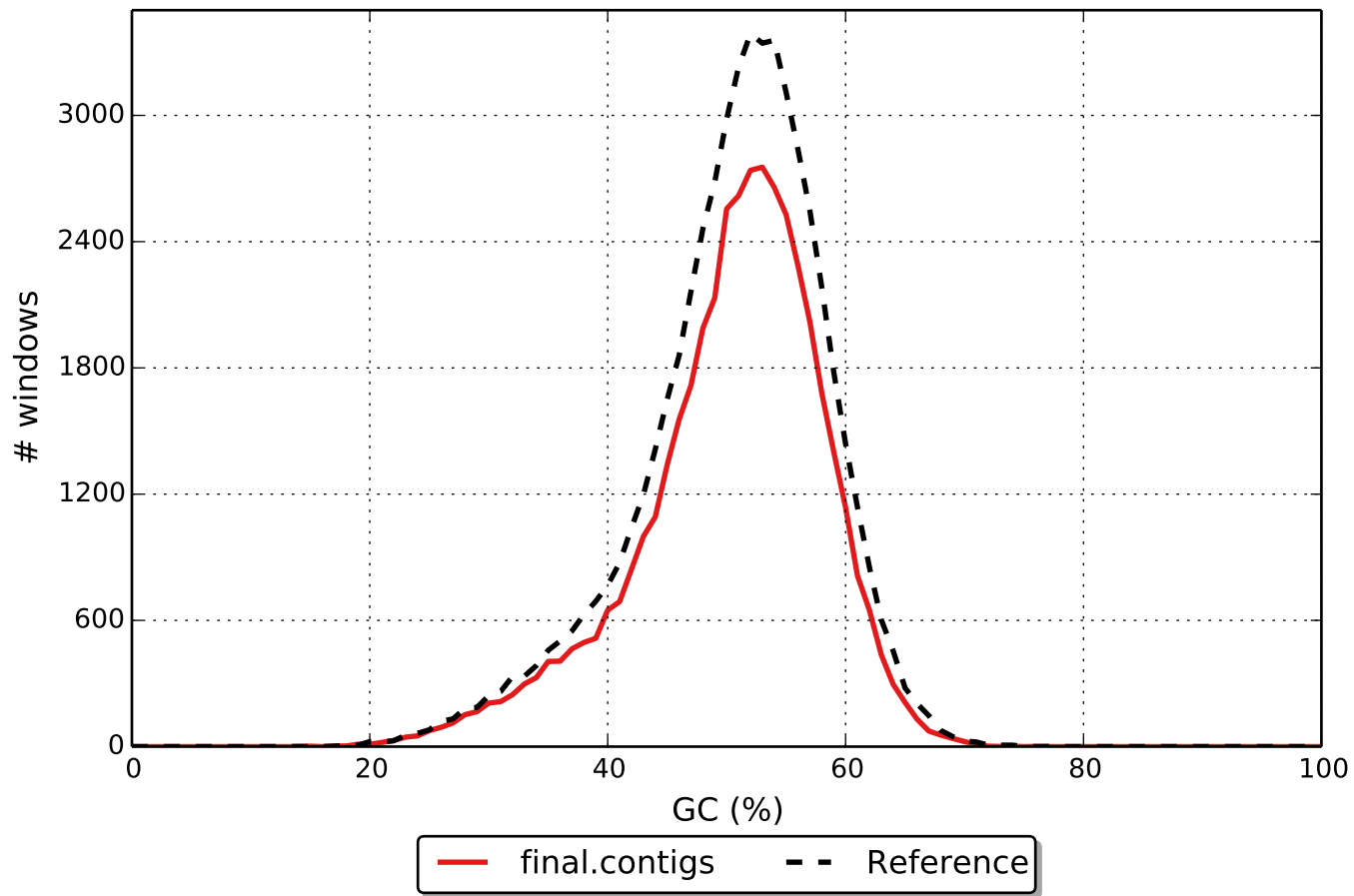
## Unaligned report

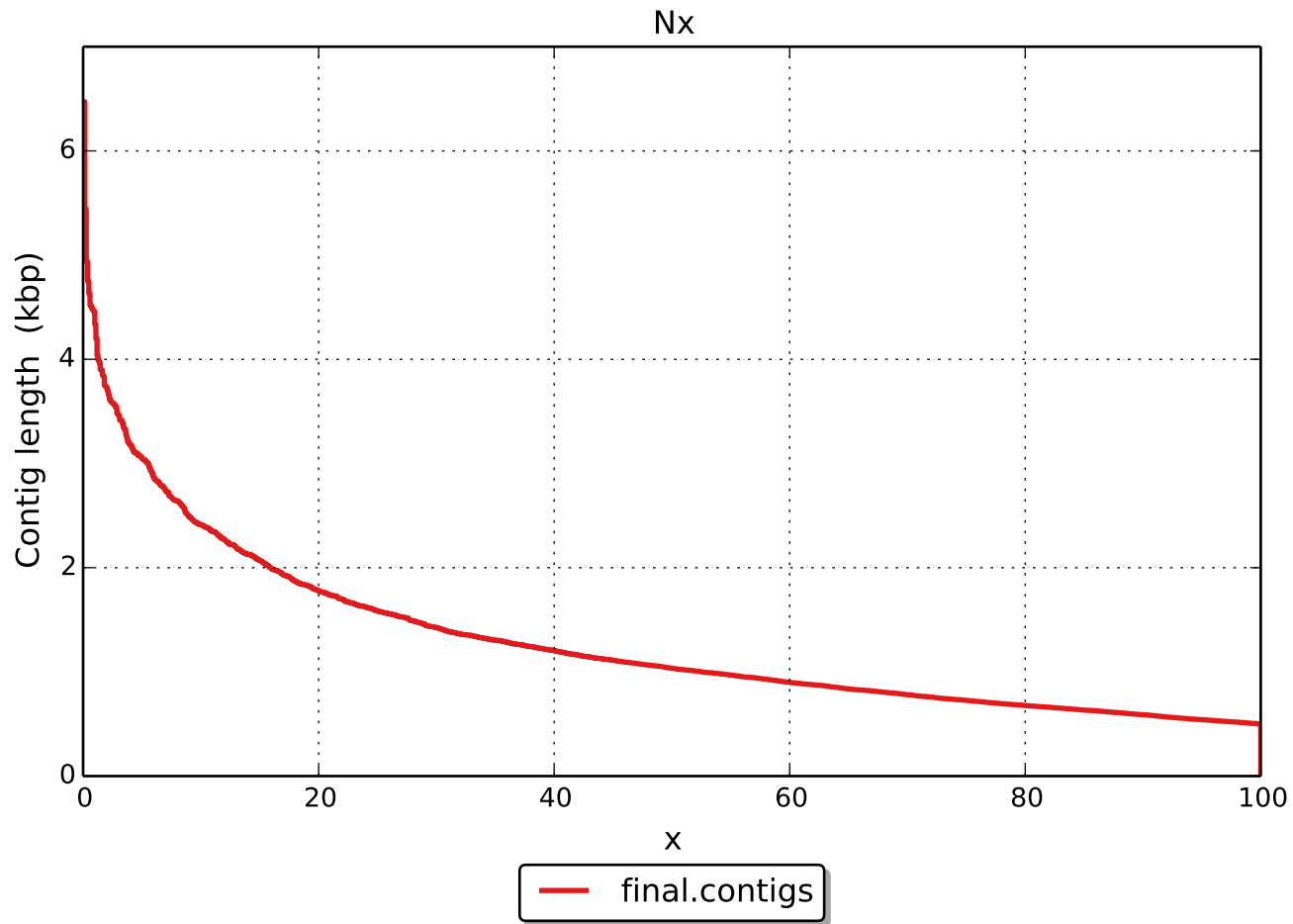
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

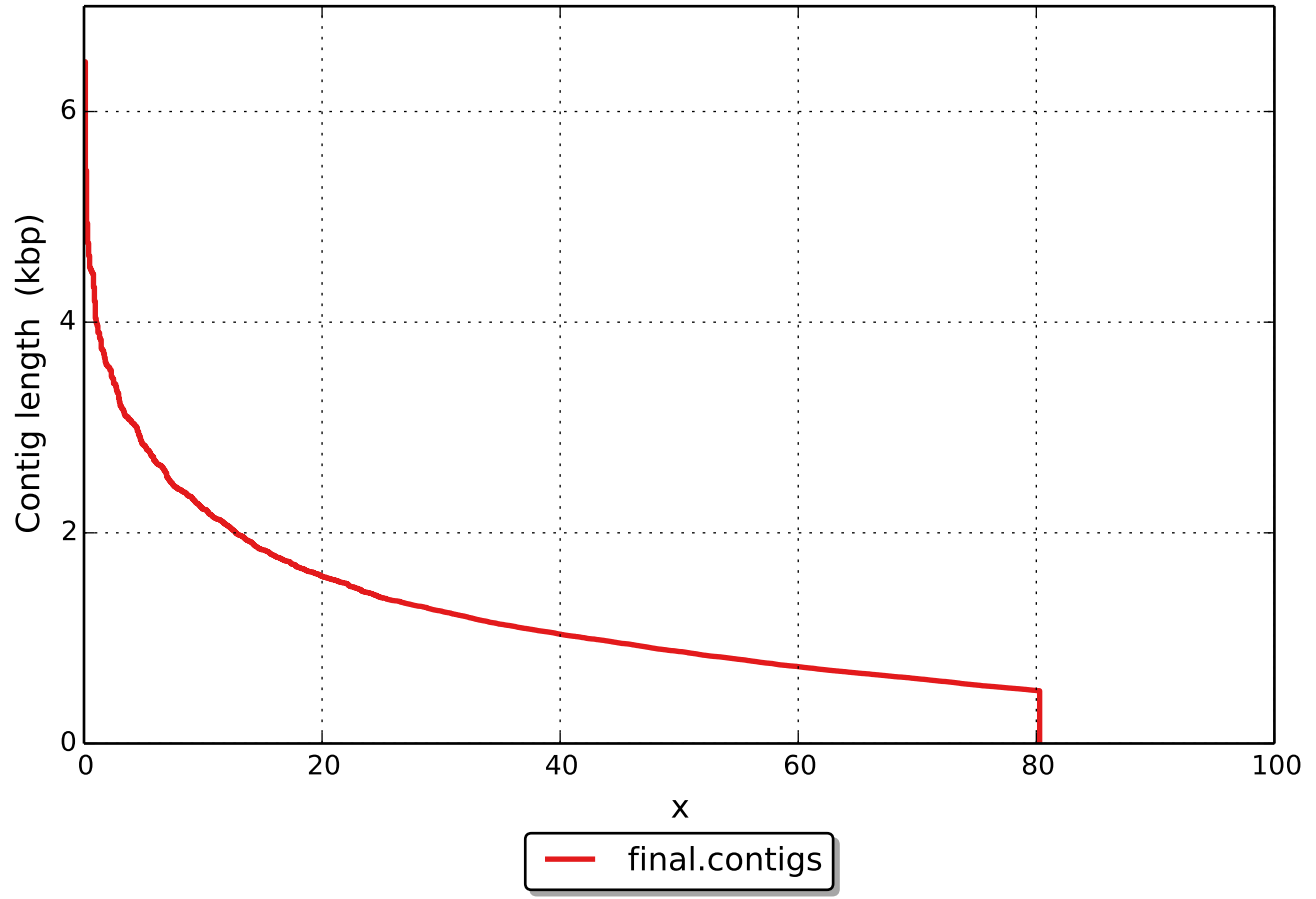


GC content





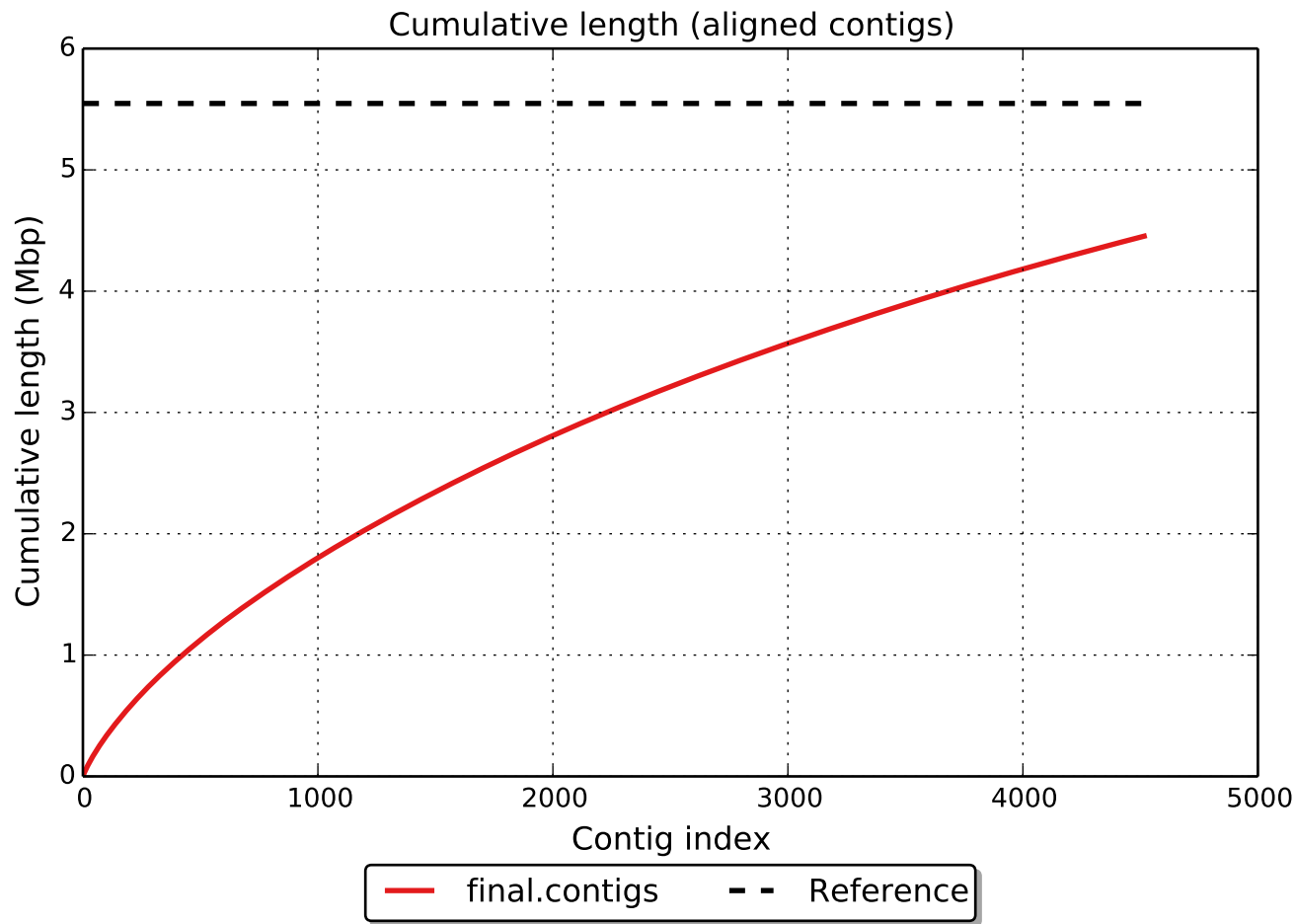
NGx



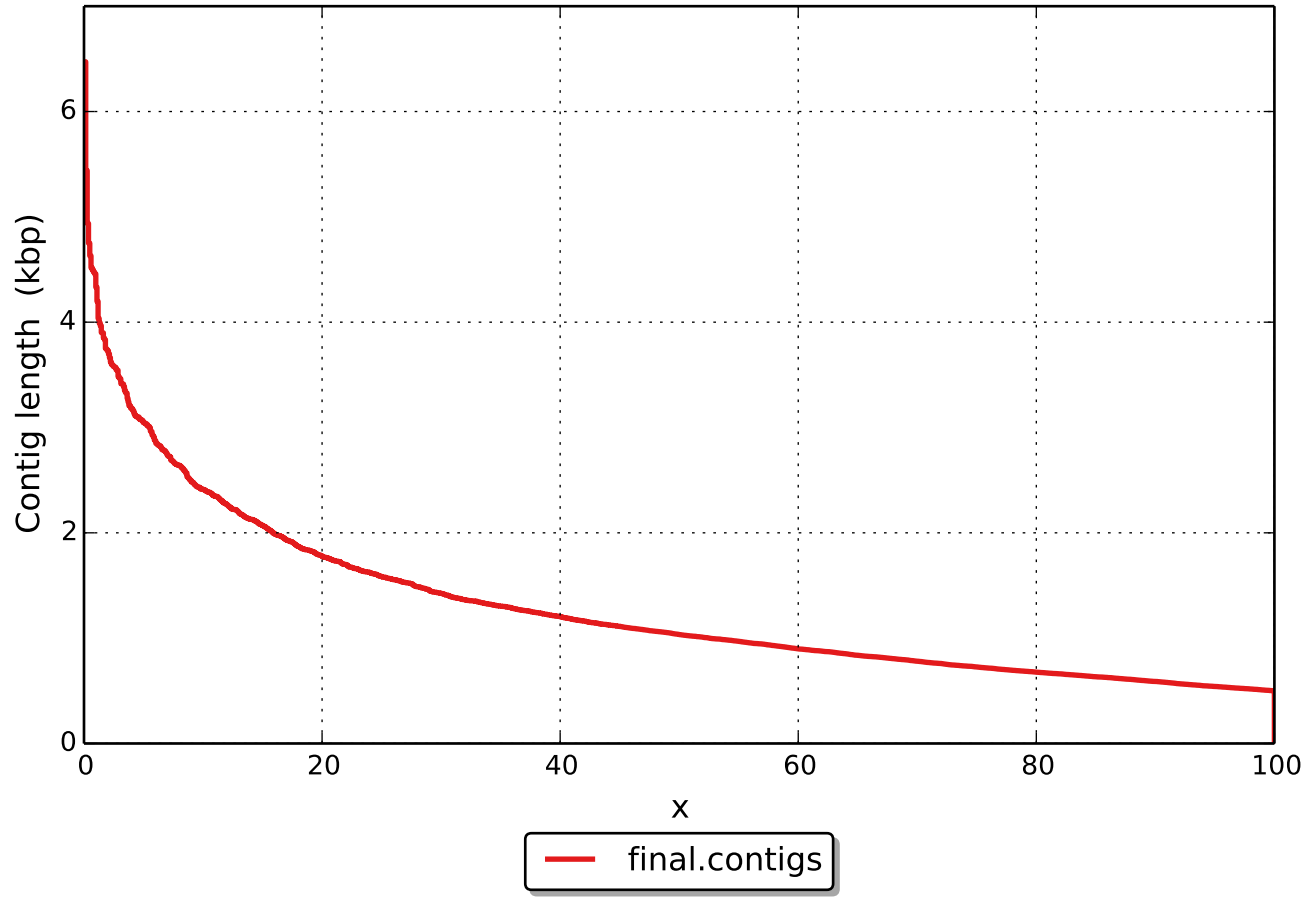
# Misassemblies







NAx



NGAx

