

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	3711
# contigs ( $\geq 1000$ bp)	1065
Total length ( $\geq 0$ bp)	3439182
Total length ( $\geq 1000$ bp)	1599025
# contigs	3711
Largest contig	6472
Total length	3439182
Reference length	5547323
GC (%)	50.24
Reference GC (%)	50.48
N50	956
NG50	649
N75	692
L50	1189
LG50	2544
L75	2254
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	59.333
Duplication ratio	1.045
# N's per 100 kbp	0.00
# mismatches per 100 kbp	217.45
# indels per 100 kbp	0.12
Largest alignment	6472
NA50	956
NGA50	649
NA75	692
LA50	1189
LGA50	2544
LA75	2254

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

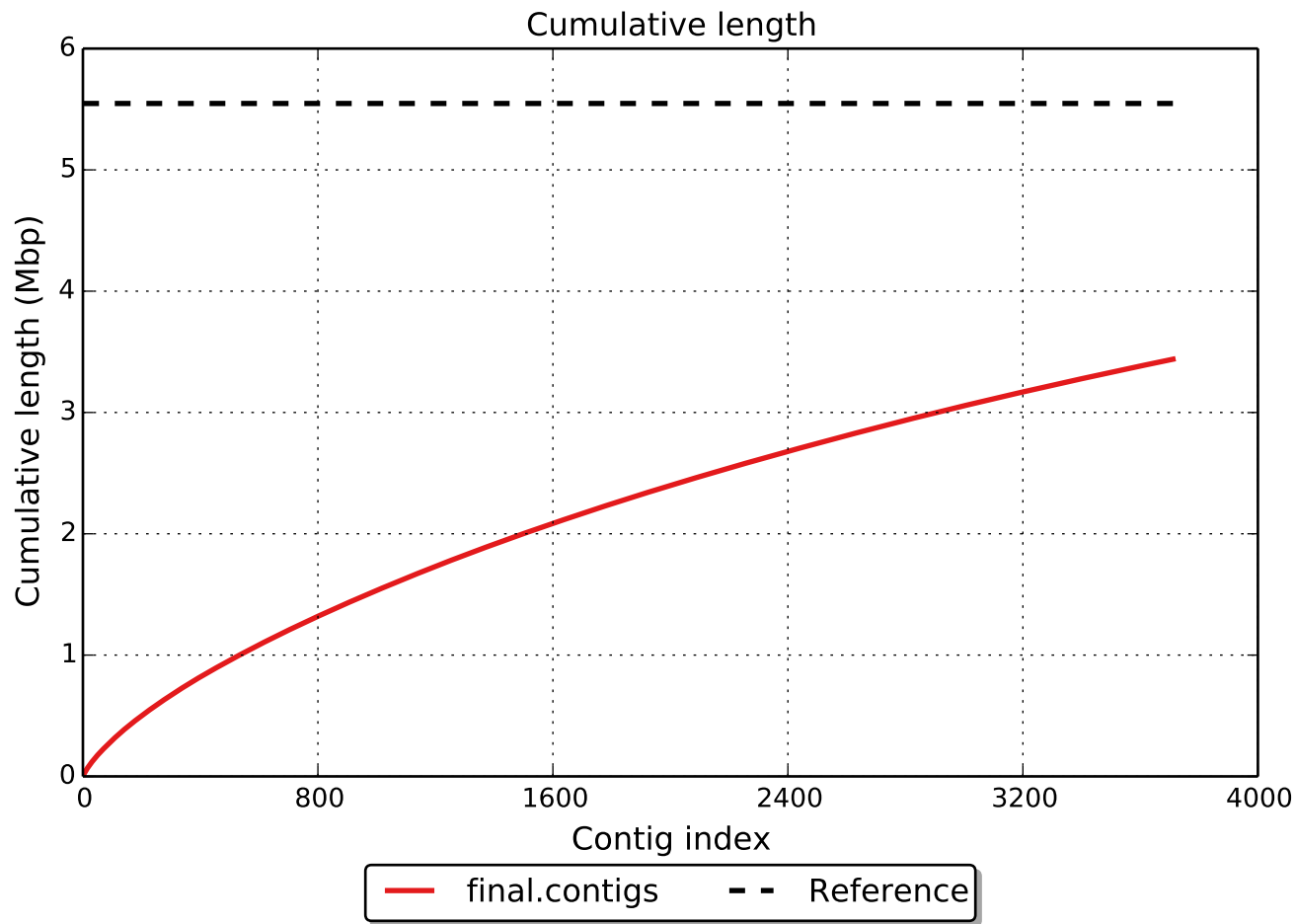
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	7157
# indels	4
# short indels	4
# long indels	0
Indels length	5

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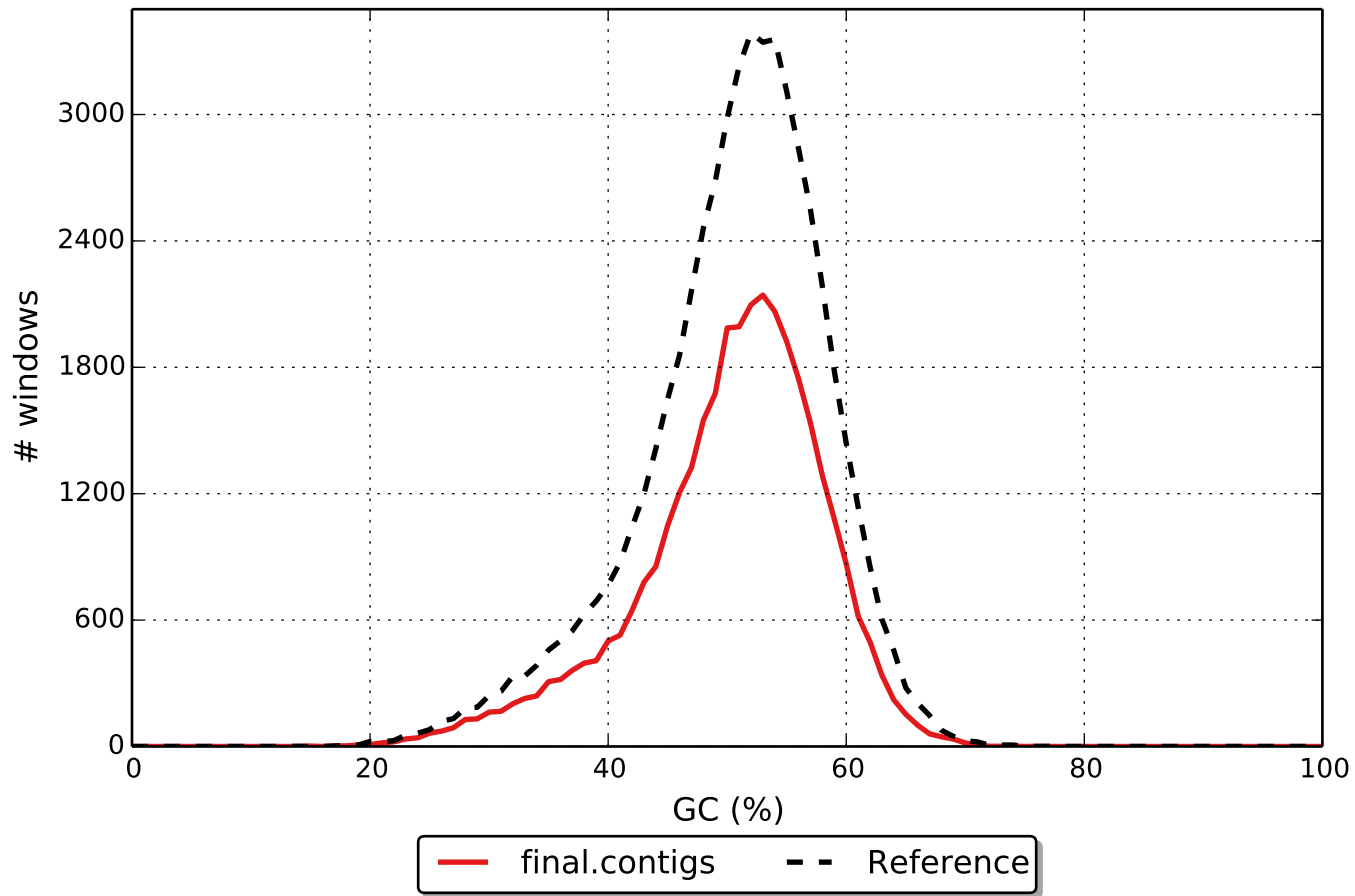
## Unaligned report

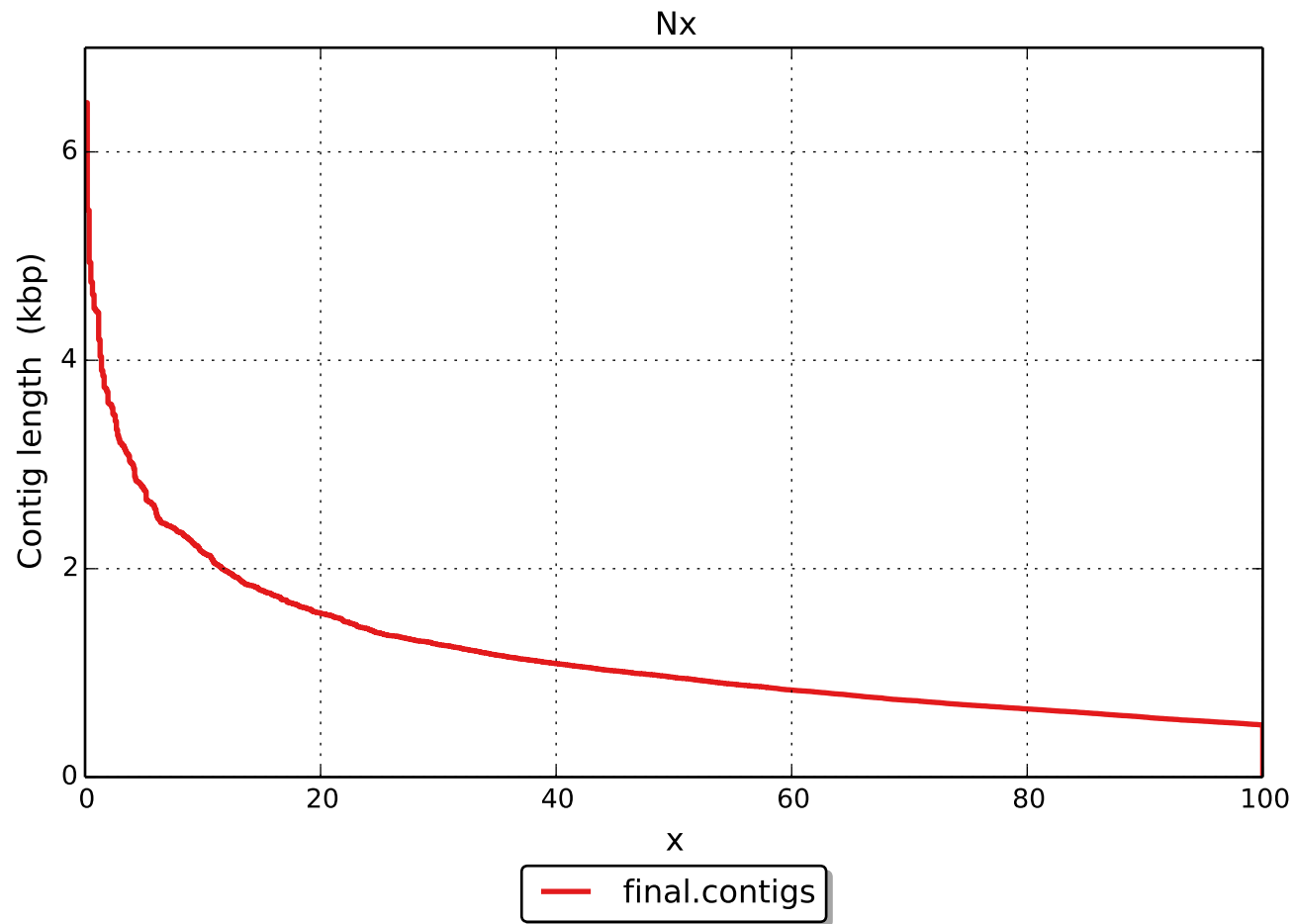
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

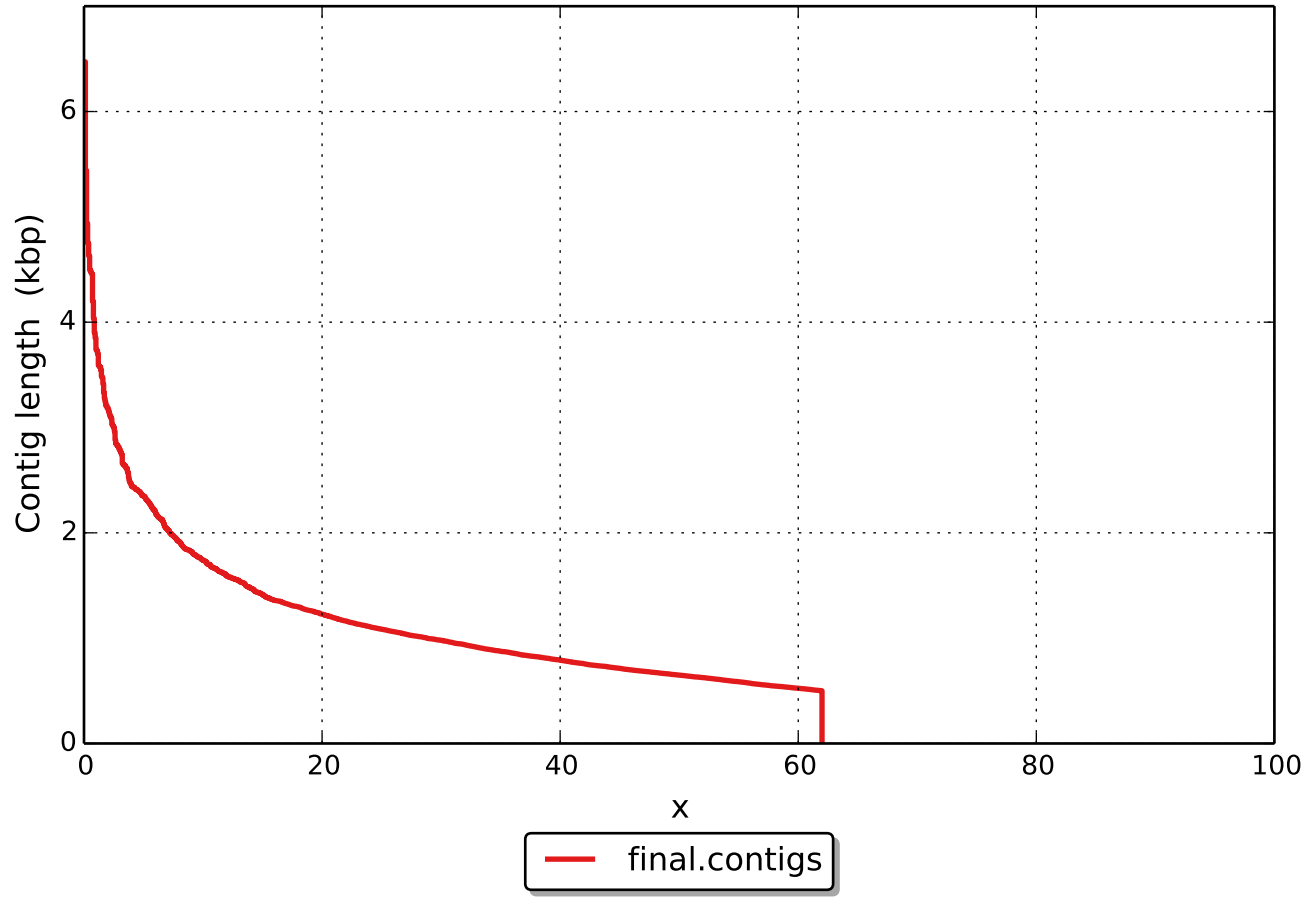


GC content





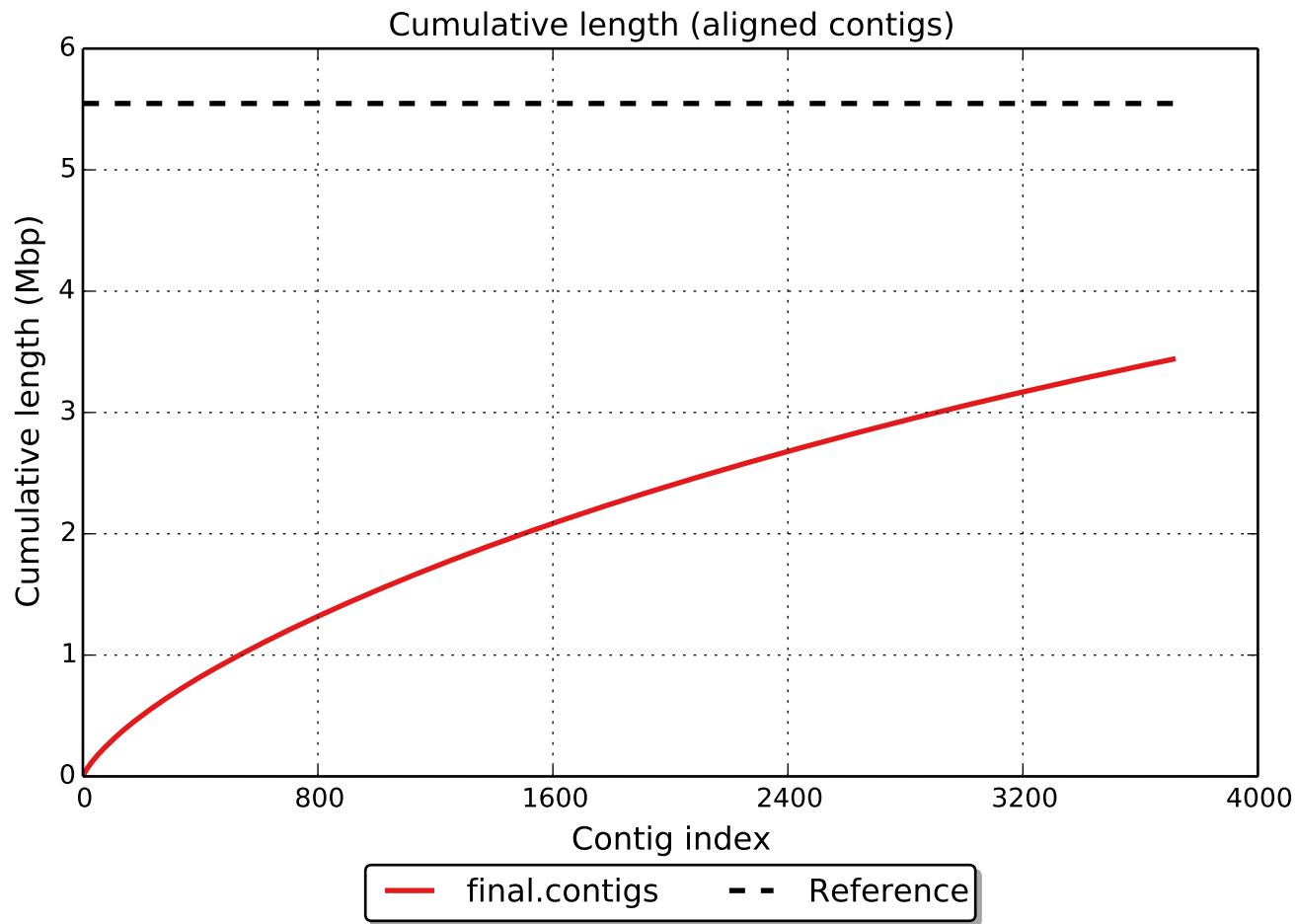
NGx



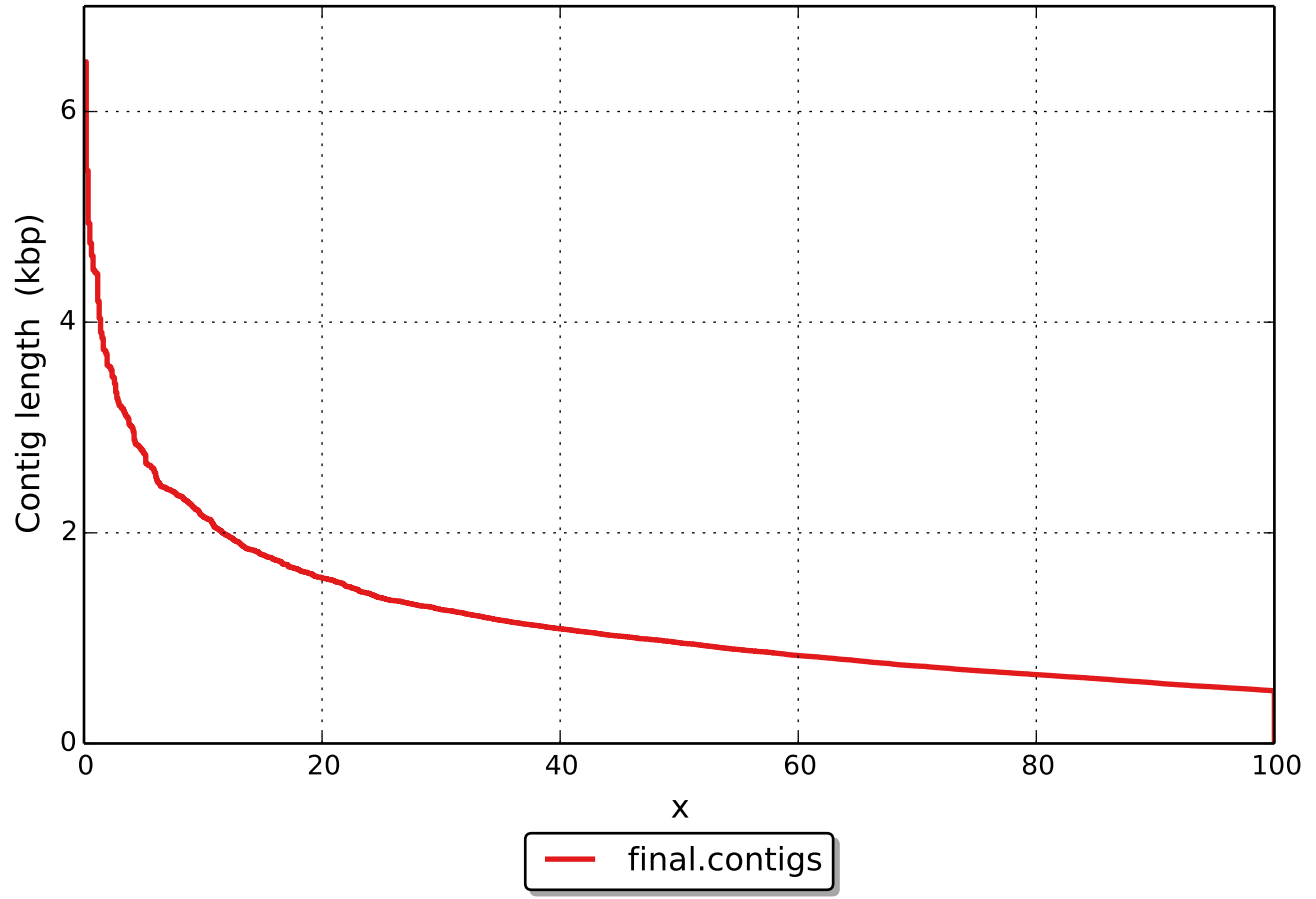
# Misassemblies







NAx



NGAx

