

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	4599
# contigs ( $\geq 1000$ bp)	1324
Total length ( $\geq 0$ bp)	4168390
Total length ( $\geq 1000$ bp)	1851386
# contigs	4599
Largest contig	4380
Total length	4168390
Reference length	5478683
GC (%)	50.46
Reference GC (%)	50.50
N50	940
NG50	786
N75	704
NG75	512
L50	1565
LG50	2327
L75	2847
LG75	4482
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	72.742
Duplication ratio	1.046
# N's per 100 kbp	0.00
# mismatches per 100 kbp	121.70
# indels per 100 kbp	0.08
Largest alignment	4380
NA50	940
NGA50	786
NA75	704
NGA75	512
LA50	1565
LGA50	2327
LA75	2847
LGA75	4482

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

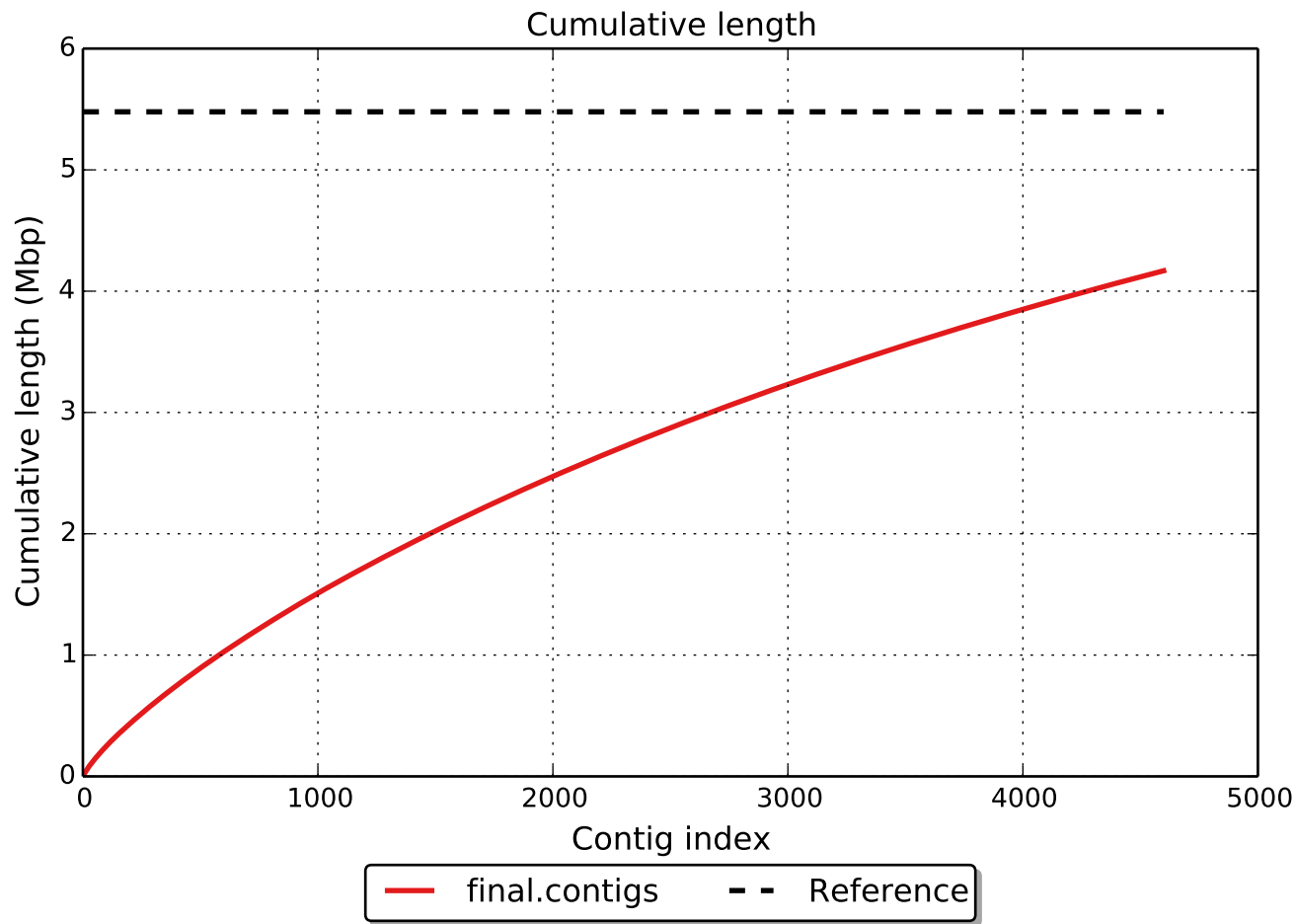
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	4850
# indels	3
# short indels	2
# long indels	1
Indels length	8

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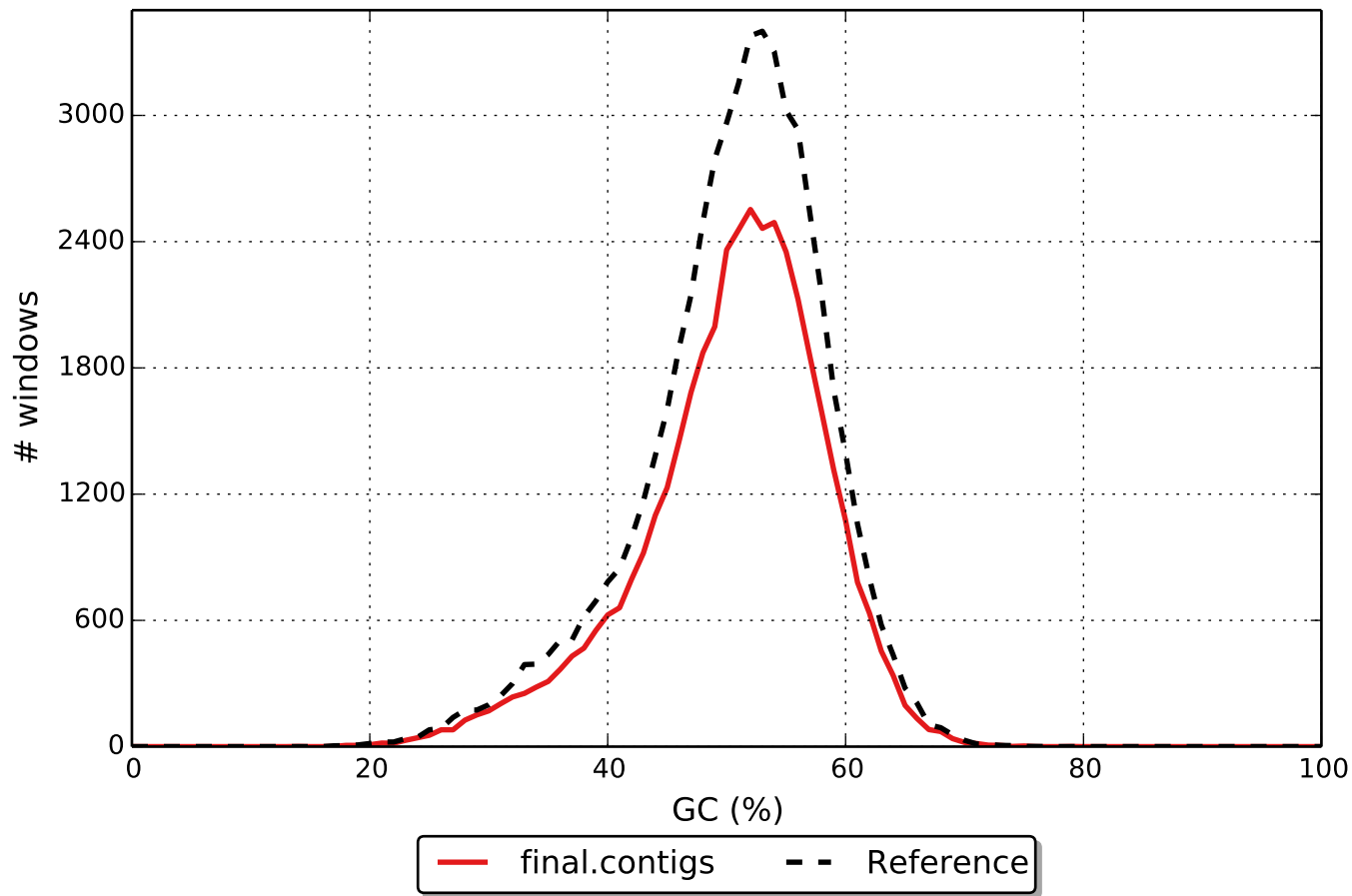
## Unaligned report

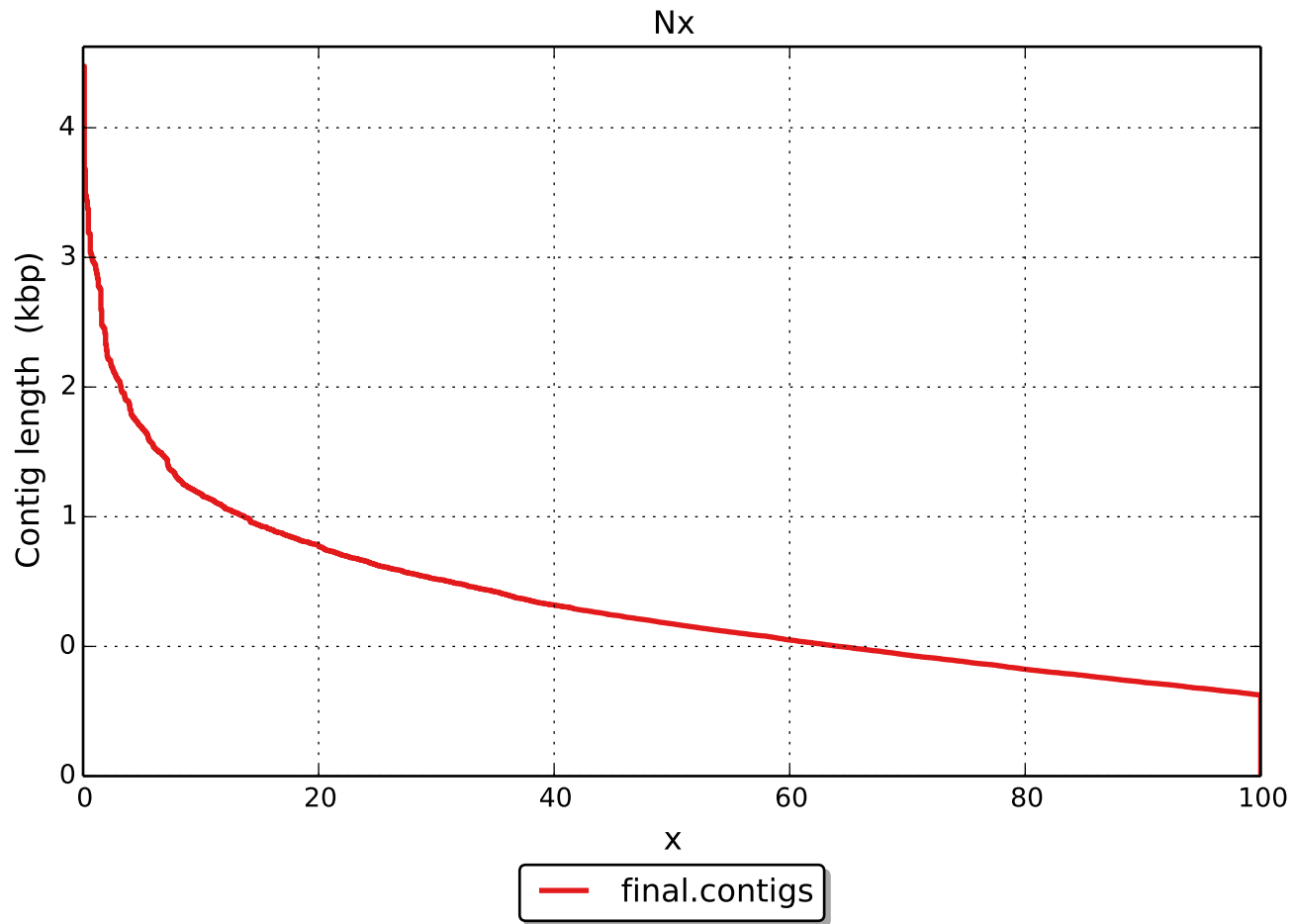
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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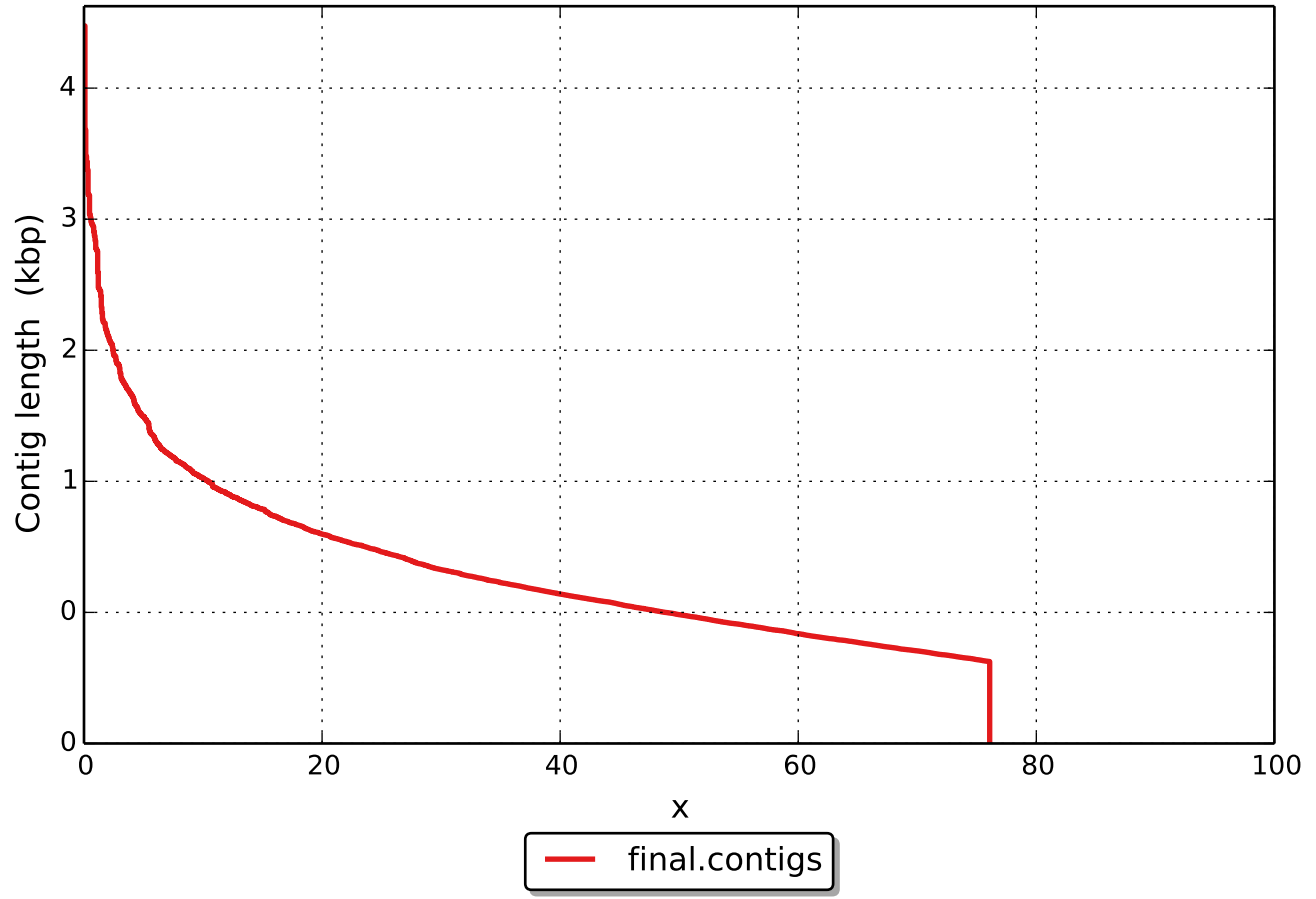


GC content





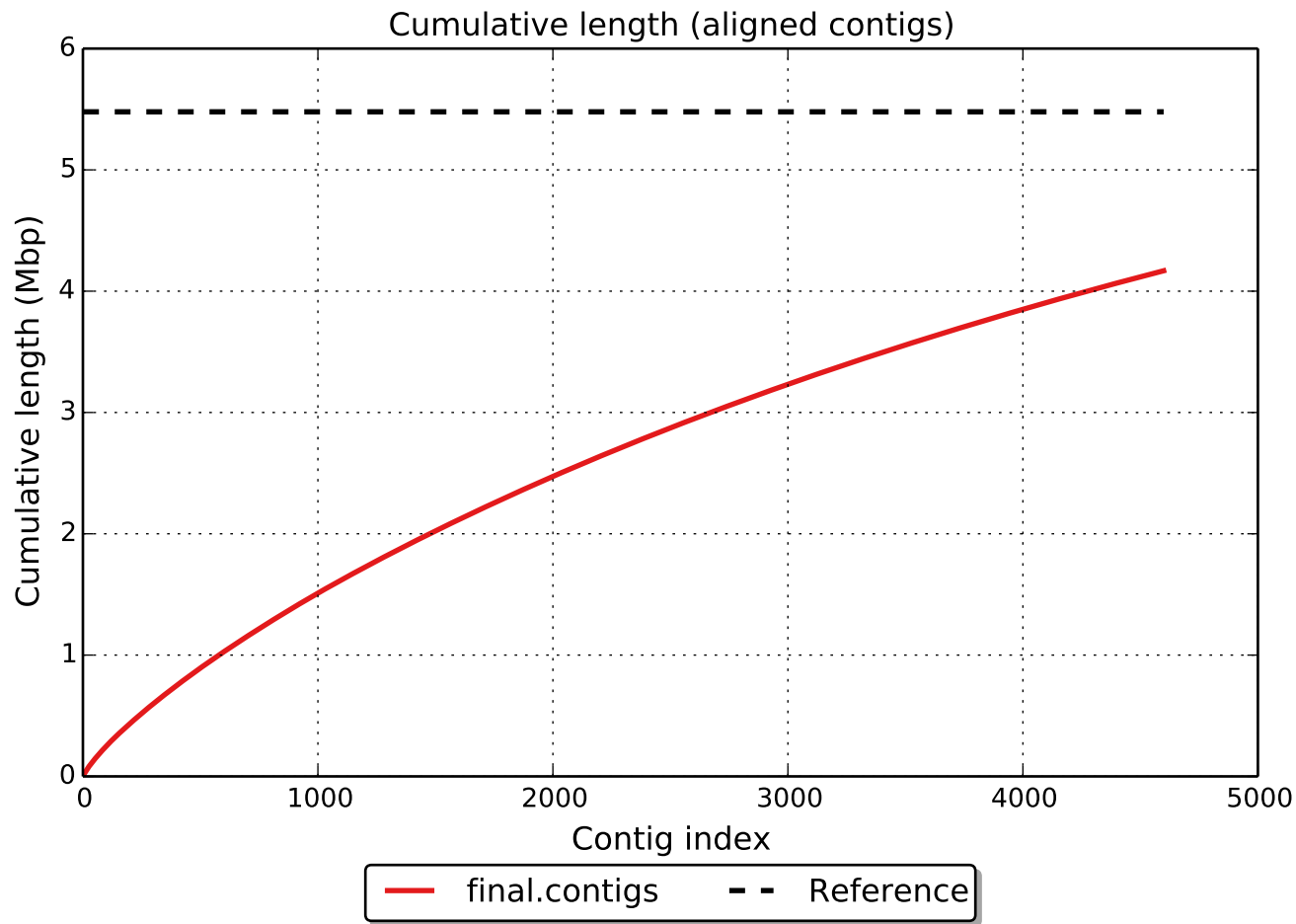
NGx



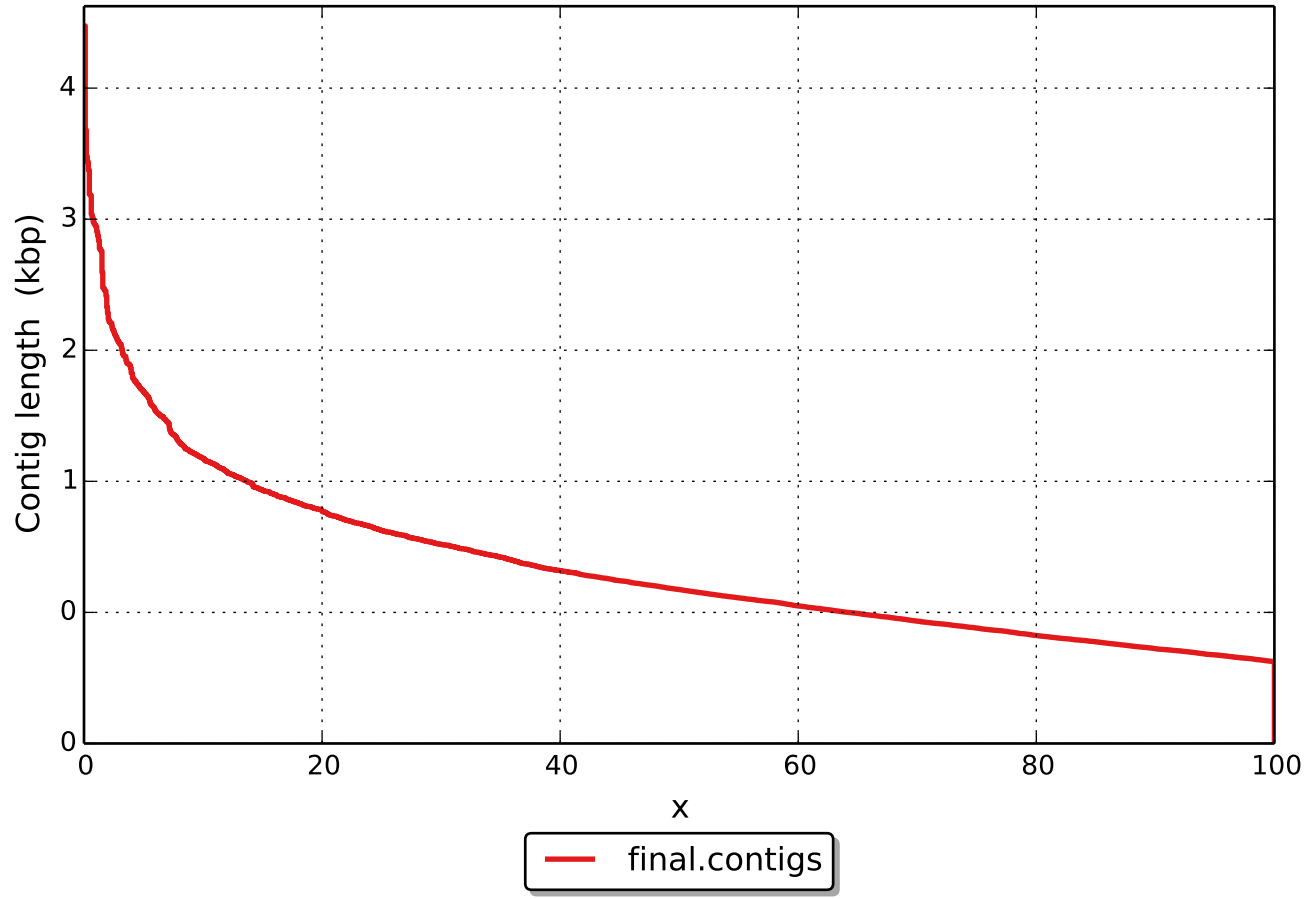
# Misassemblies







NAx



NGAx

