

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	13875
# contigs ( $\geq 1000$ bp)	2165
Total length ( $\geq 0$ bp)	9284044
Total length ( $\geq 1000$ bp)	3240078
# contigs	7747
Largest contig	6472
Total length	7114620
Reference length	11094646
GC (%)	50.35
Reference GC (%)	50.48
N50	947
NG50	664
N75	685
L50	2491
LG50	5029
L75	4716
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# unaligned contigs	0 + 1 part
Unaligned length	40
Genome fraction (%)	77.738
Duplication ratio	1.068
# N's per 100 kbp	0.00
# mismatches per 100 kbp	409.57
# indels per 100 kbp	0.14
Largest alignment	6472
NA50	947
NGA50	664
NA75	685
LA50	2491
LGA50	5029
LA75	4716

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

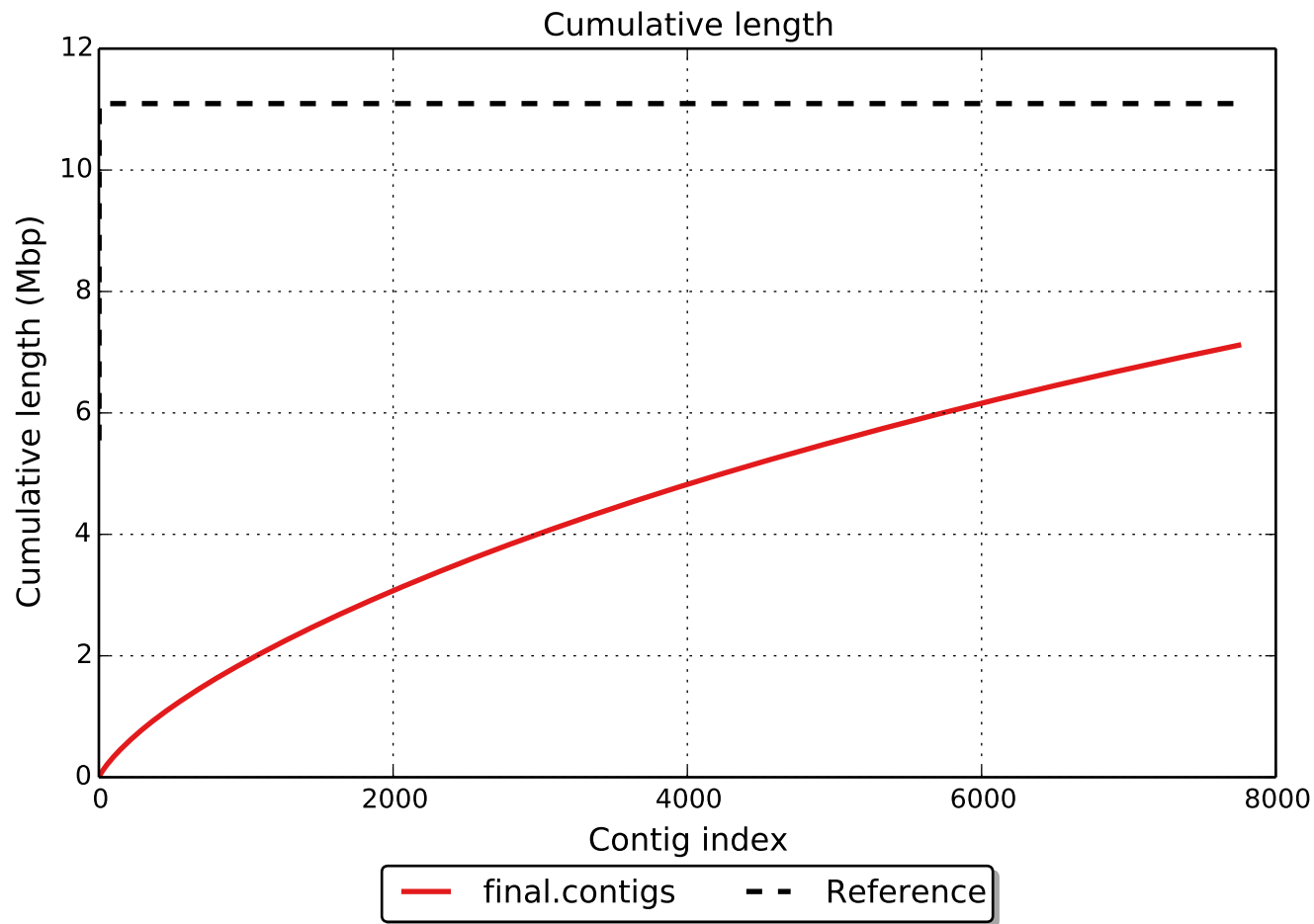
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# mismatches	35325
# indels	12
# short indels	12
# long indels	0
Indels length	13

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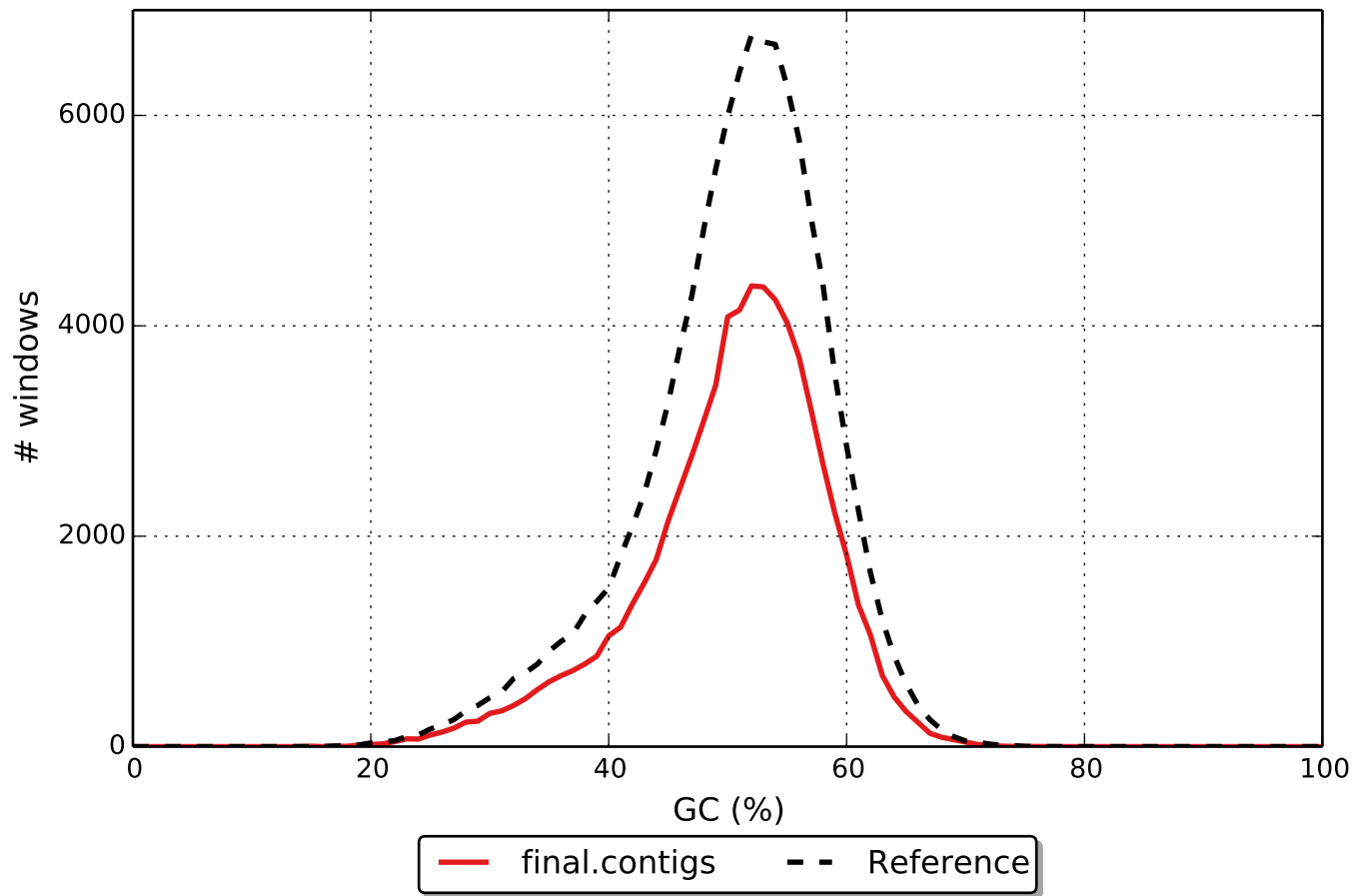
## Unaligned report

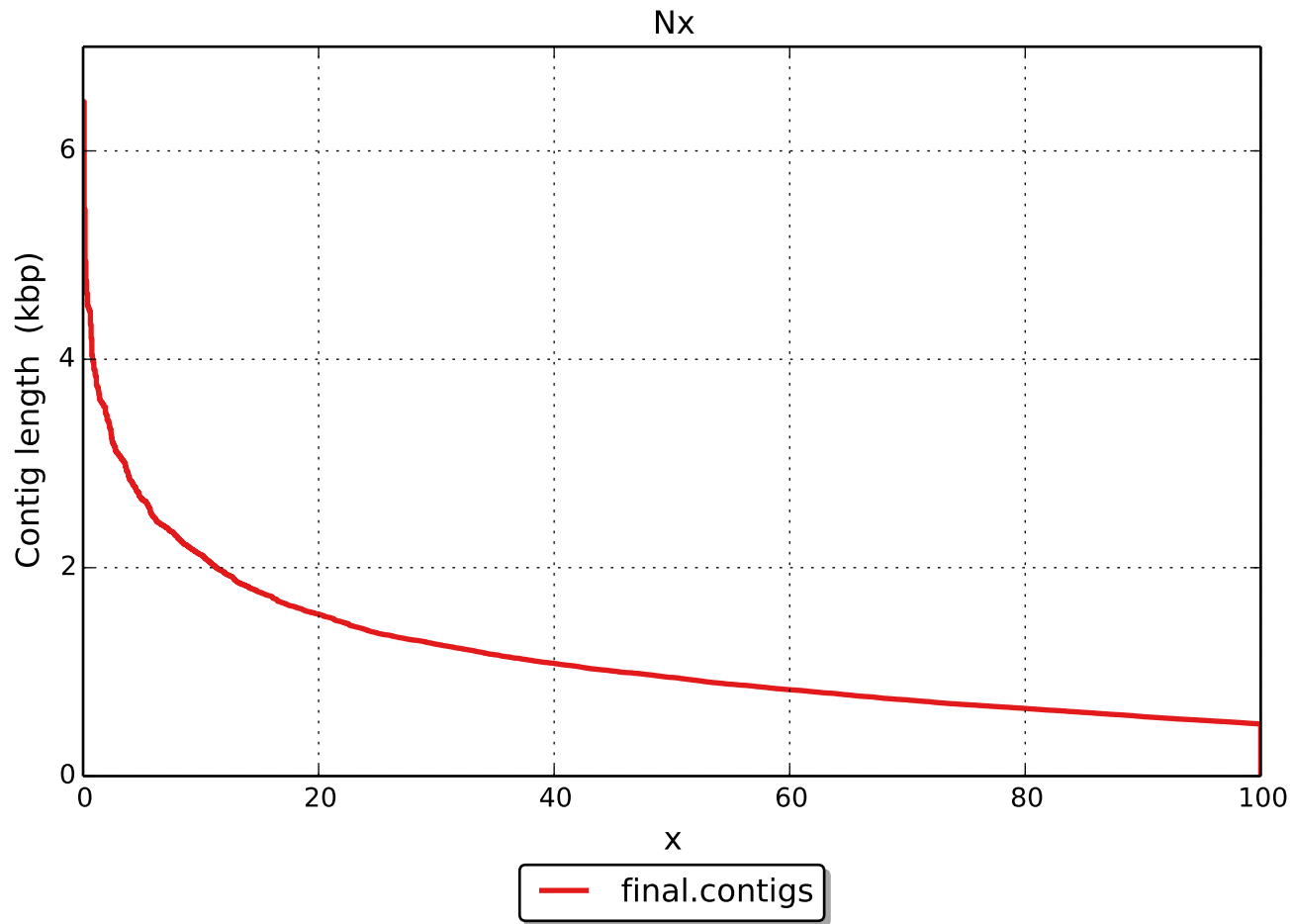
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	40
# N's	0

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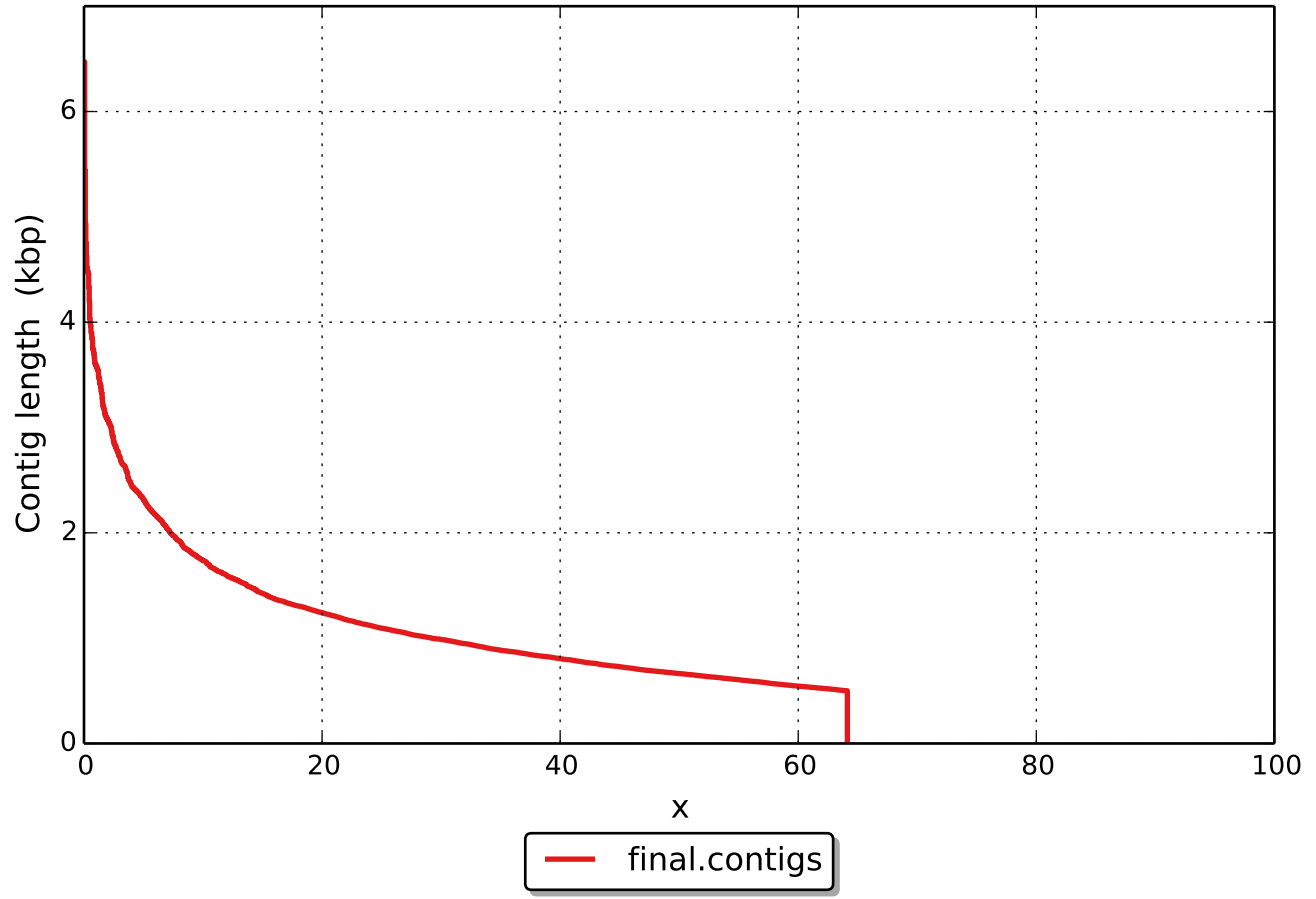


GC content





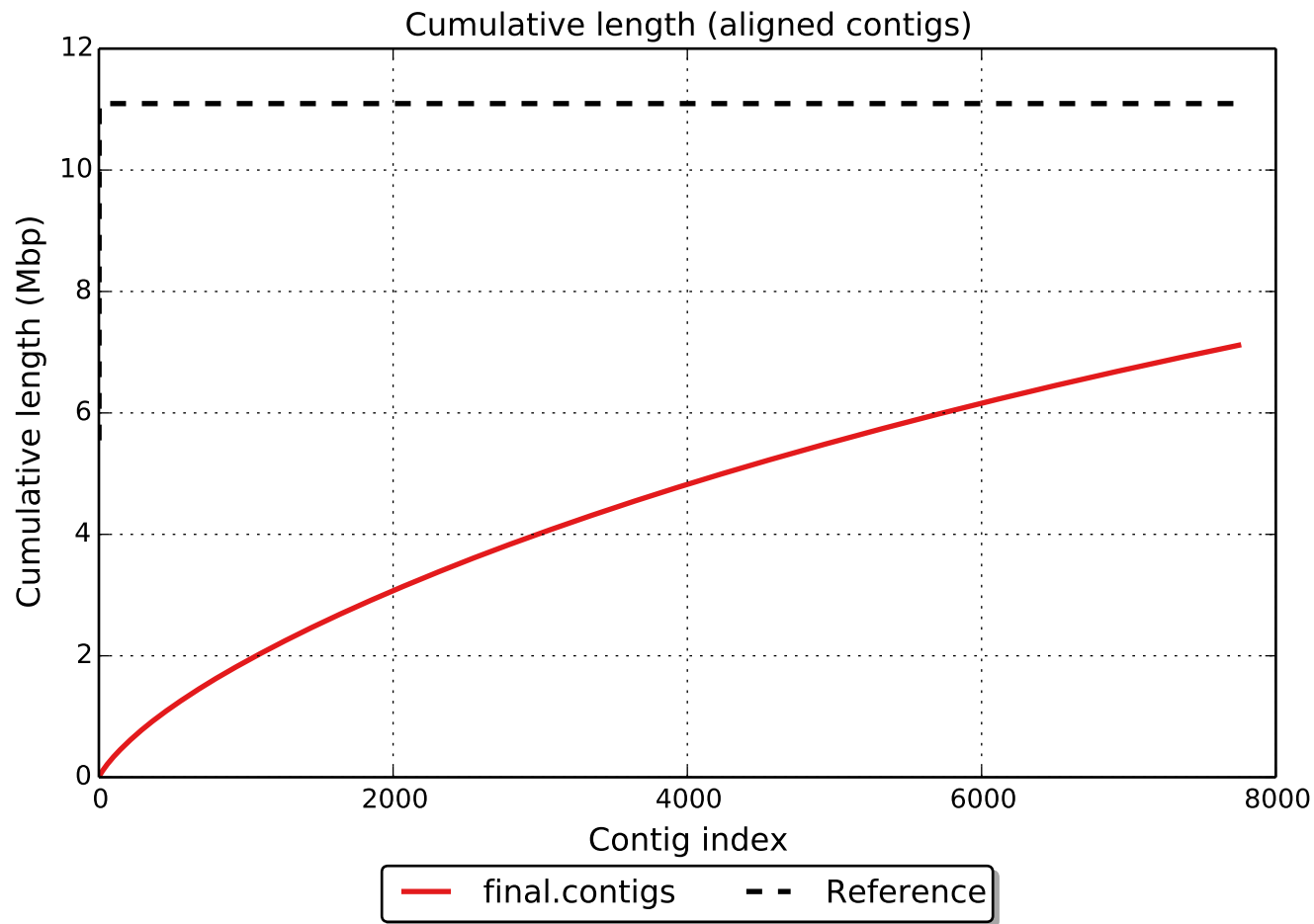
NGx



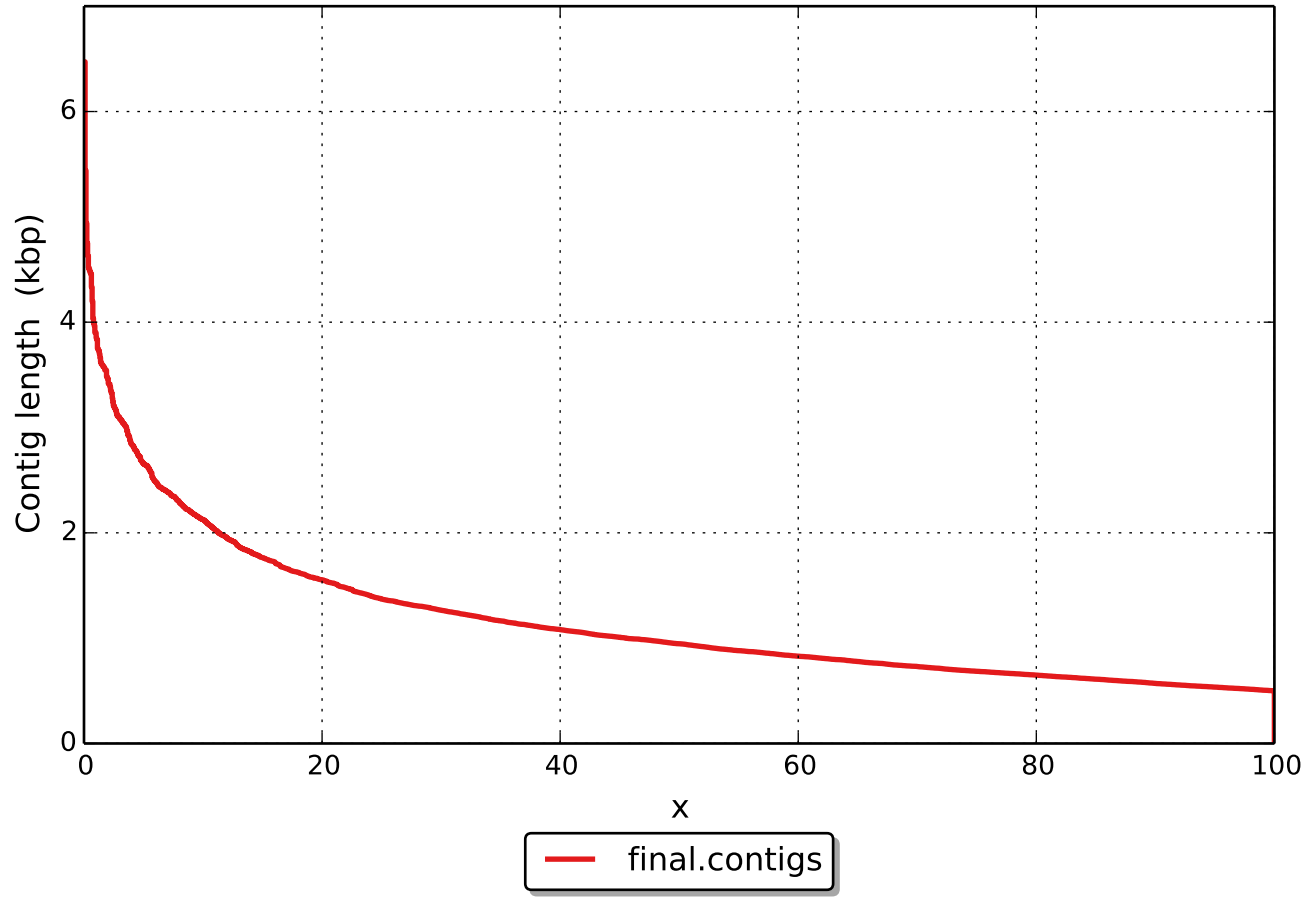
# Misassemblies







NAx



NGAx

