

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	15392
# contigs ( $\geq 1000$ bp)	2448
Total length ( $\geq 0$ bp)	10336527
Total length ( $\geq 1000$ bp)	3427742
# contigs	9120
Largest contig	4257
Total length	8100357
Reference length	11094646
GC (%)	50.36
Reference GC (%)	50.48
N50	912
NG50	735
N75	683
L50	3099
LG50	4930
L75	5676
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	788
# local misassemblies	0
# unaligned contigs	0 + 2 part
Unaligned length	122
Genome fraction (%)	69.661
Duplication ratio	1.048
# N's per 100 kbp	0.00
# mismatches per 100 kbp	124.96
# indels per 100 kbp	0.10
Largest alignment	4257
NA50	912
NGA50	735
NA75	683
LA50	3099
LGA50	4931
LA75	5676

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

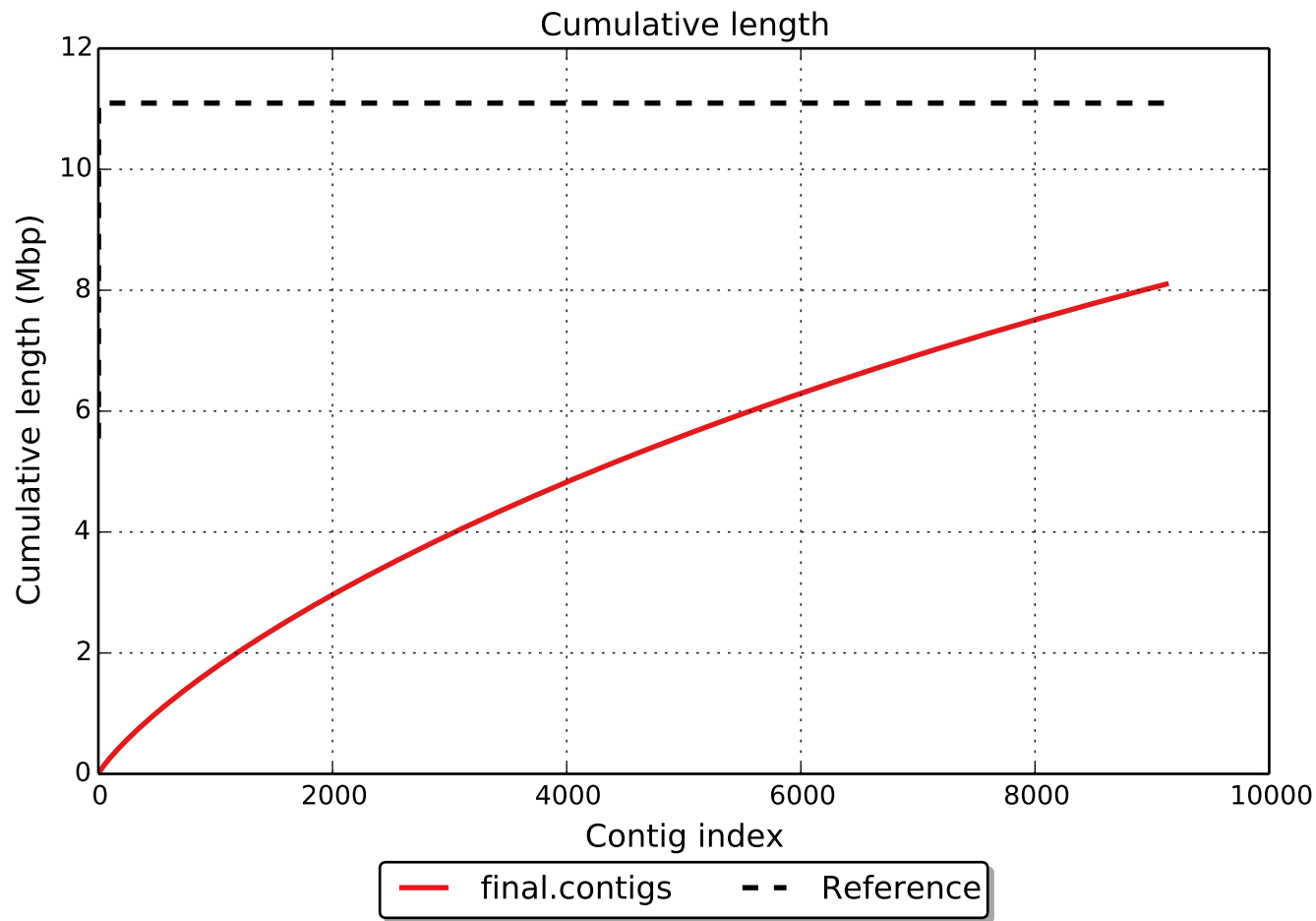
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	788
# local misassemblies	0
# mismatches	9658
# indels	8
# short indels	7
# long indels	1
Indels length	27

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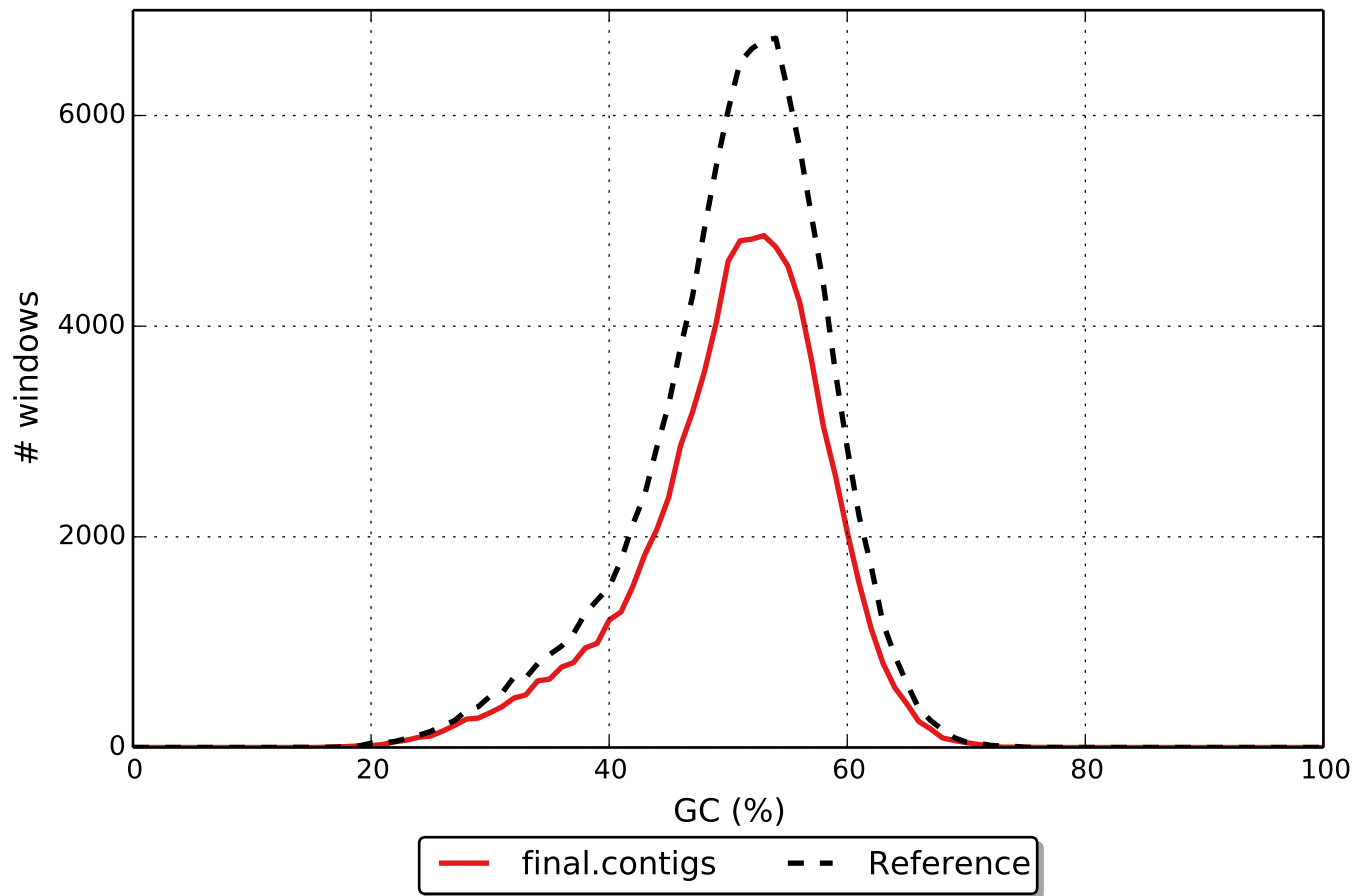
## Unaligned report

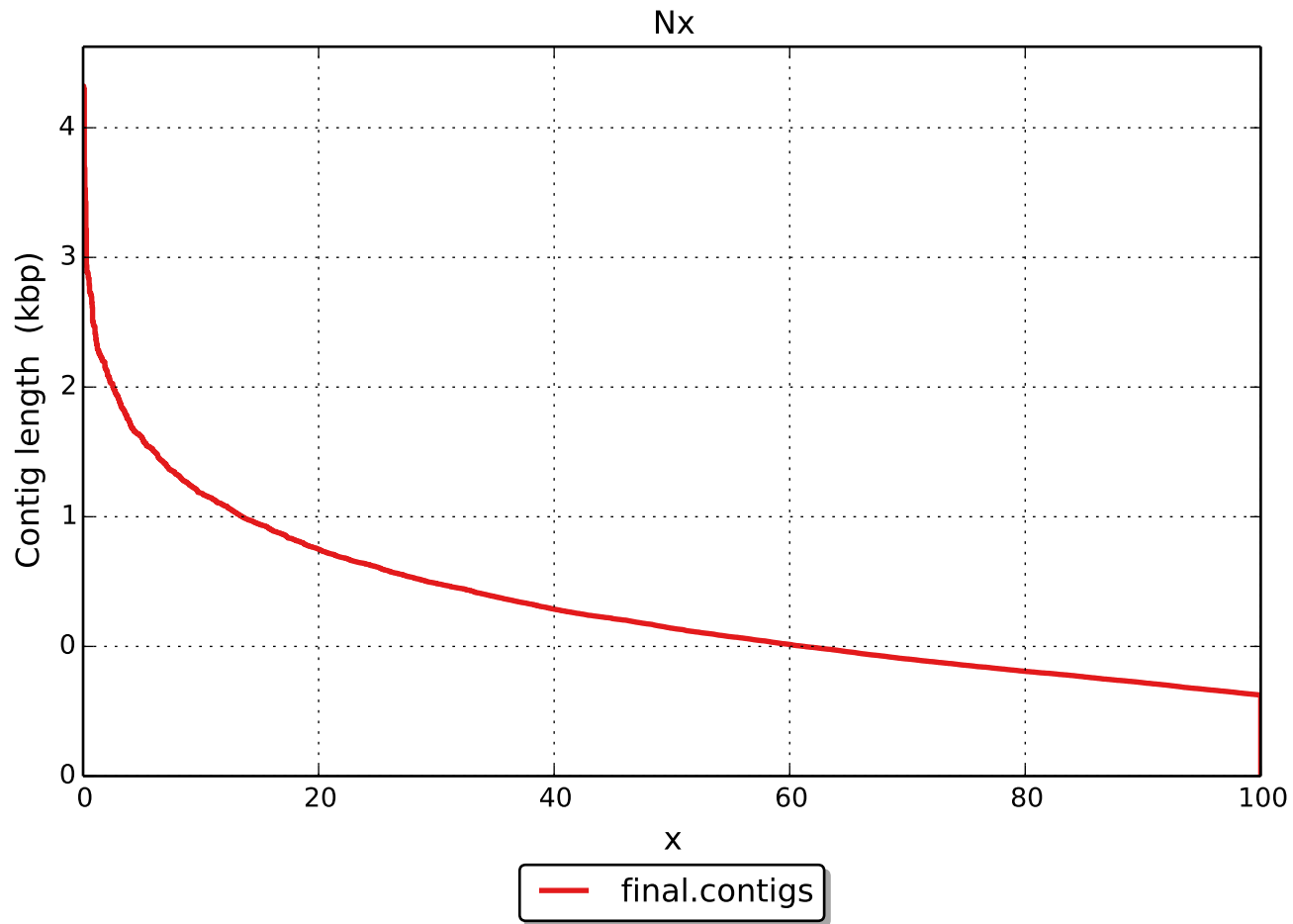
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	122
# N's	0

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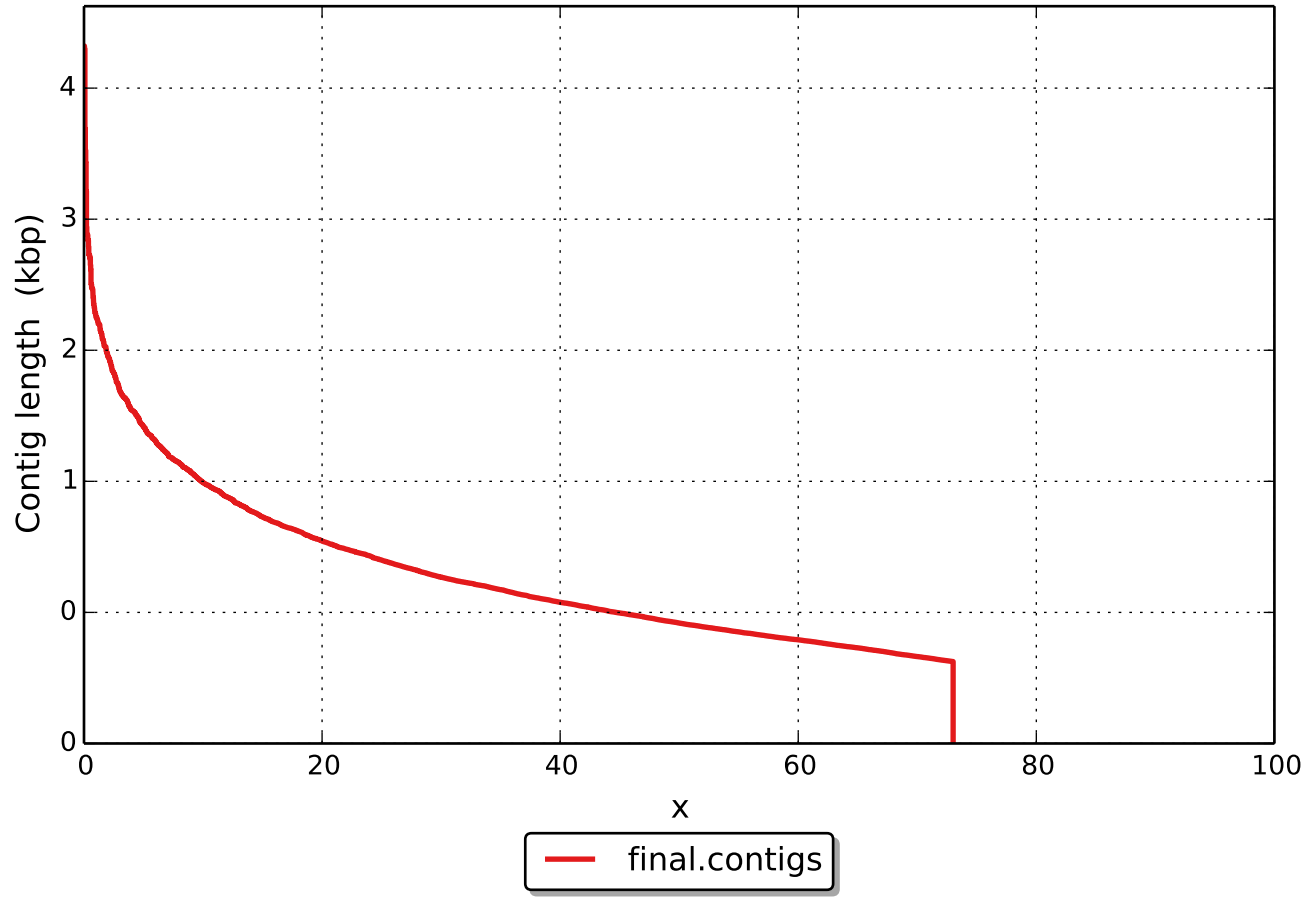


GC content



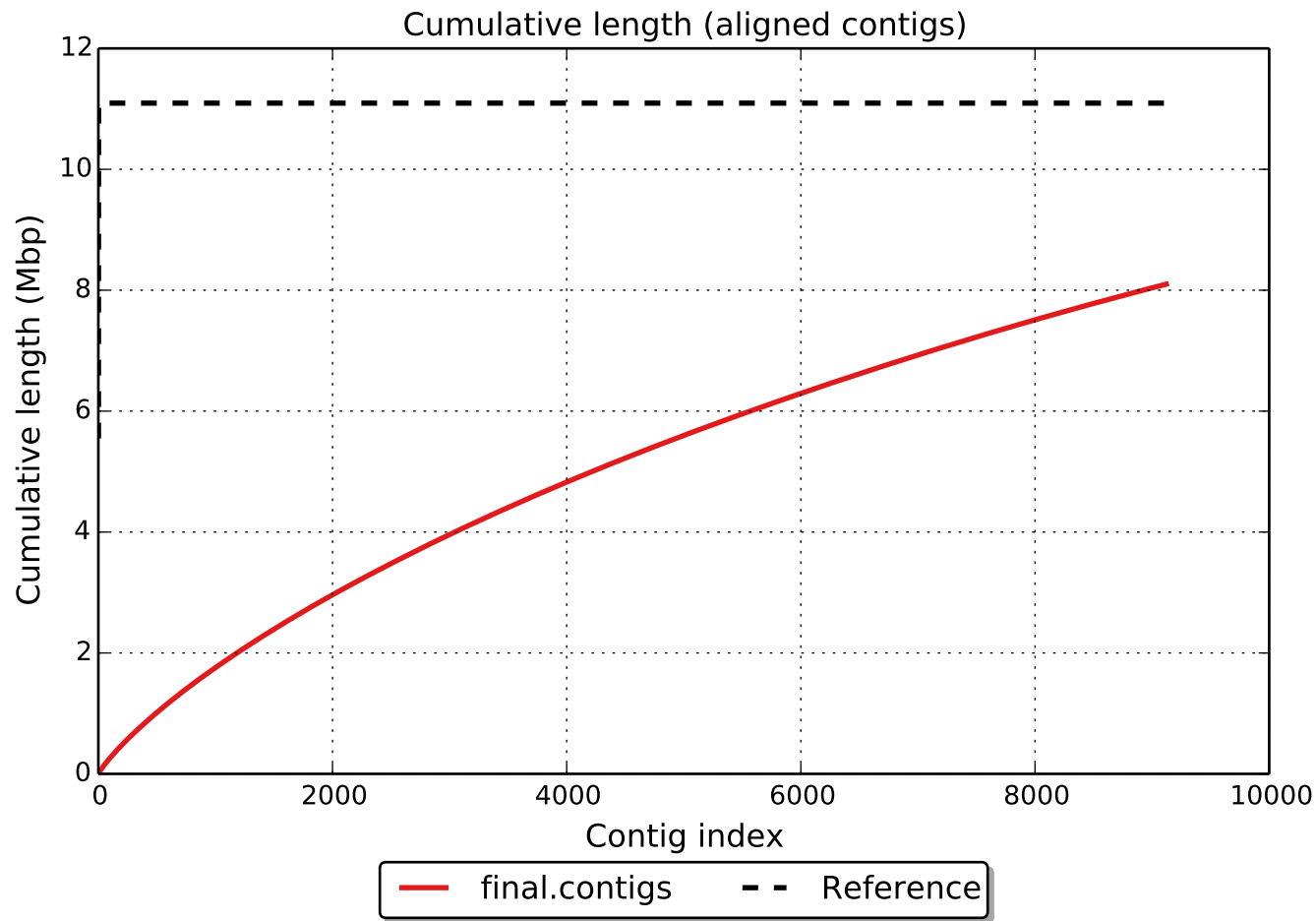


NGx

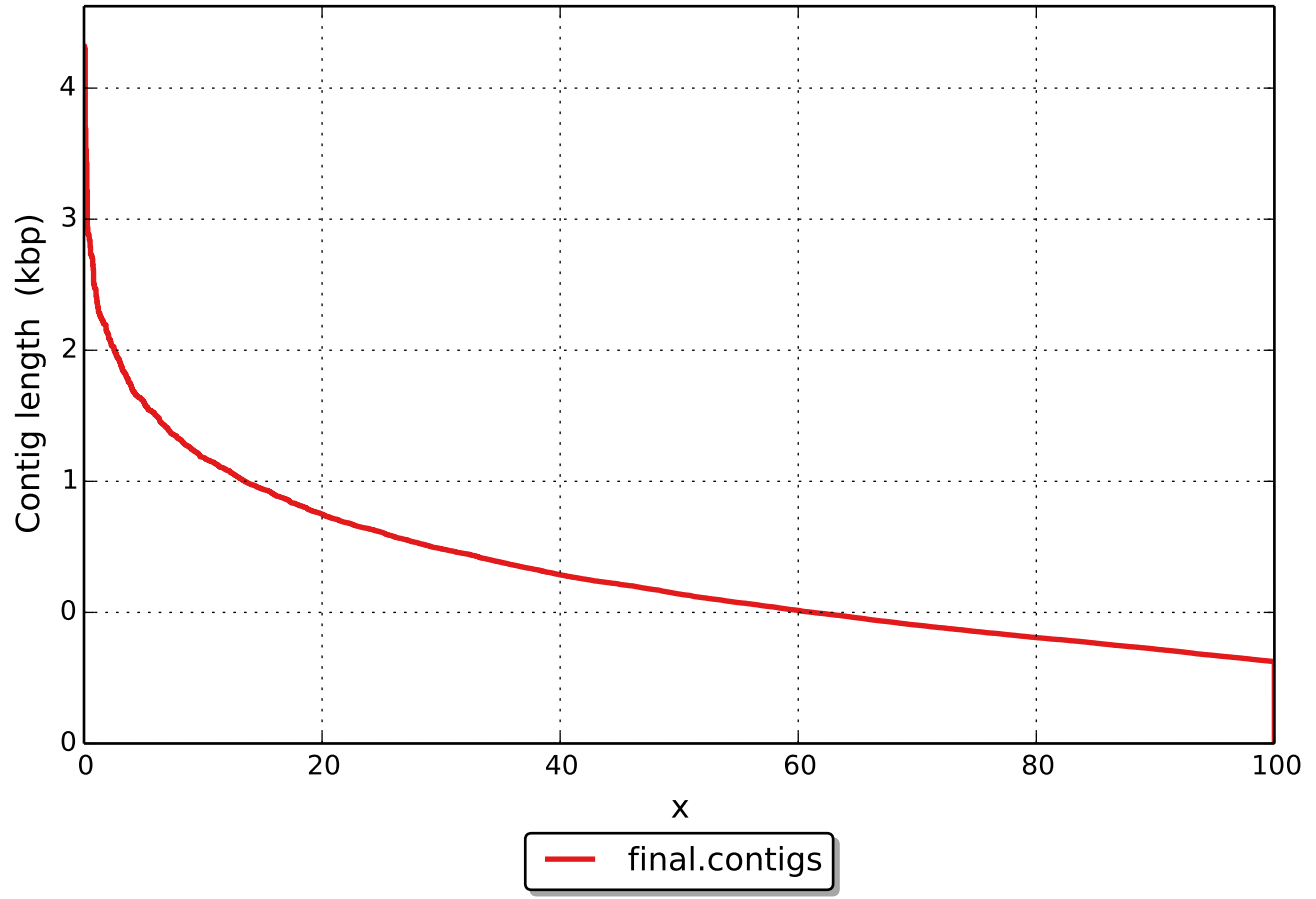








NAx



NGAx

