

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	2600
# contigs ( $\geq 1000$ bp)	1773
Total length ( $\geq 0$ bp)	11009440
Total length ( $\geq 1000$ bp)	10638239
# contigs	2046
Largest contig	41898
Total length	10836142
Reference length	11094646
GC (%)	50.39
Reference GC (%)	50.48
N50	8692
NG50	8452
N75	4699
NG75	4451
L50	388
LG50	404
L75	808
LG75	850
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	2233
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	96.175
Duplication ratio	1.016
# N's per 100 kbp	0.00
# mismatches per 100 kbp	31.70
# indels per 100 kbp	0.18
Largest alignment	41898
NA50	8692
NGA50	8452
NA75	4699
NGA75	4451
LA50	388
LGA50	404
LA75	808
LGA75	850

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

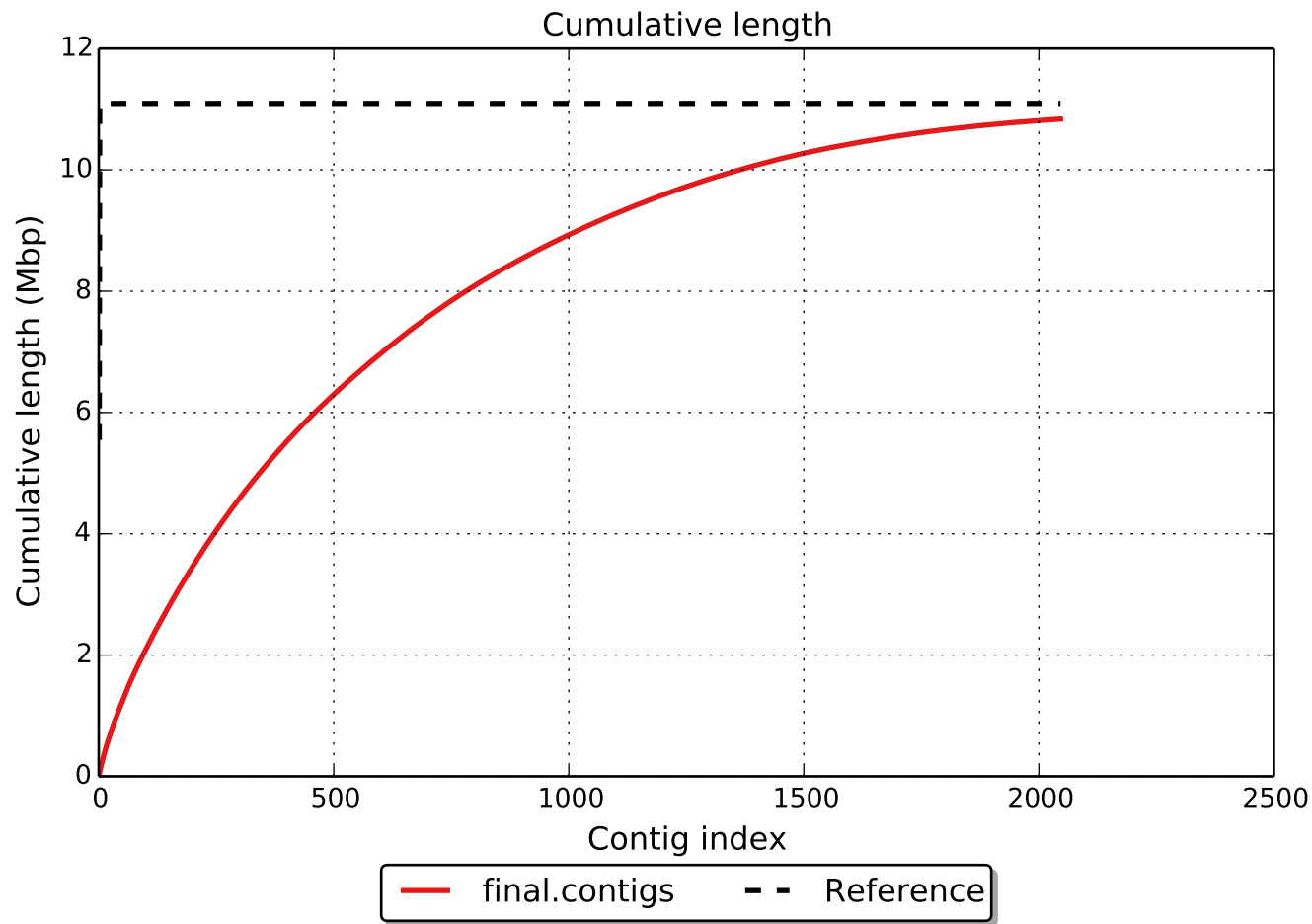
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	2233
# local misassemblies	3
# mismatches	3383
# indels	19
# short indels	18
# long indels	1
Indels length	24

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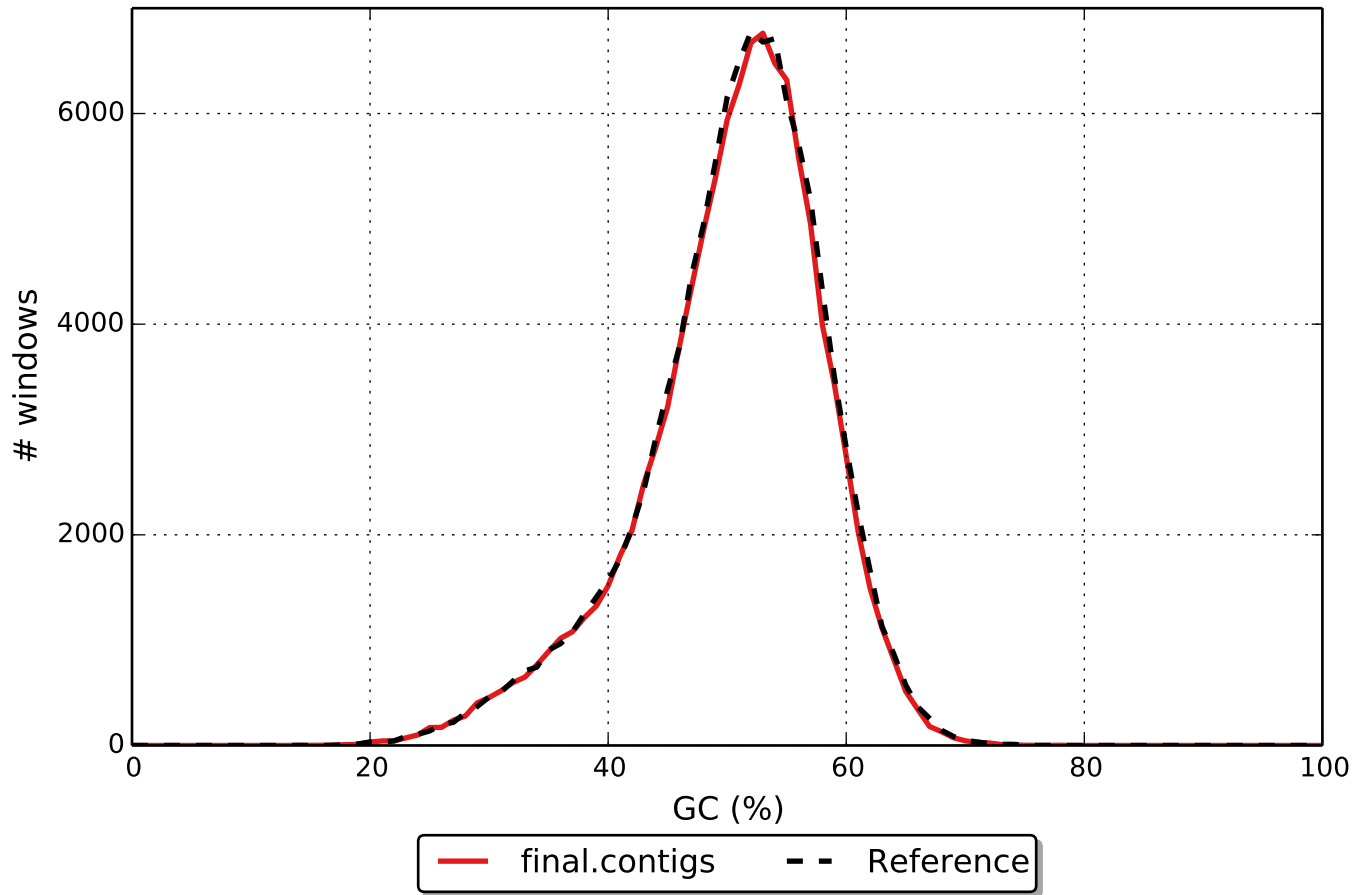
## Unaligned report

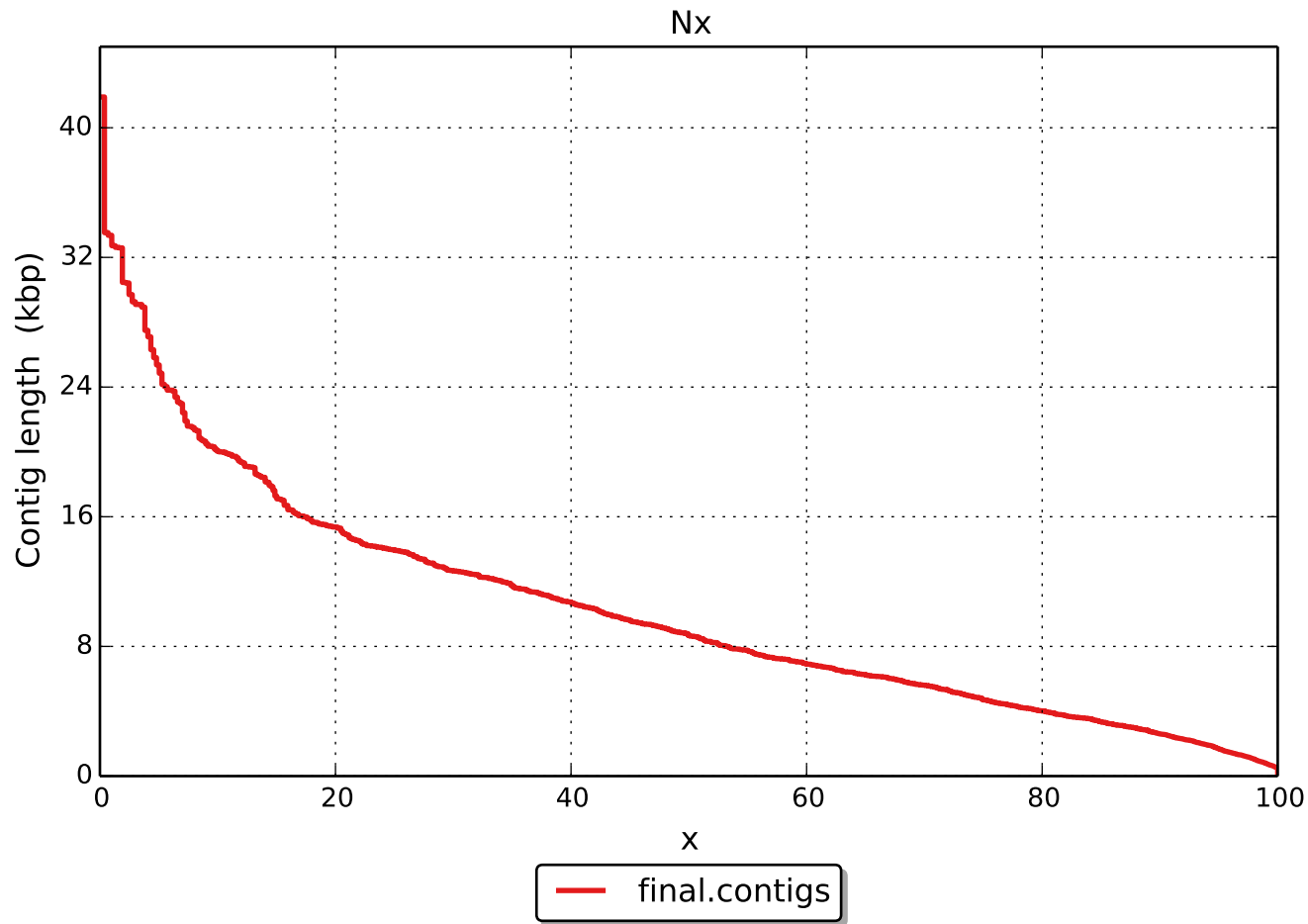
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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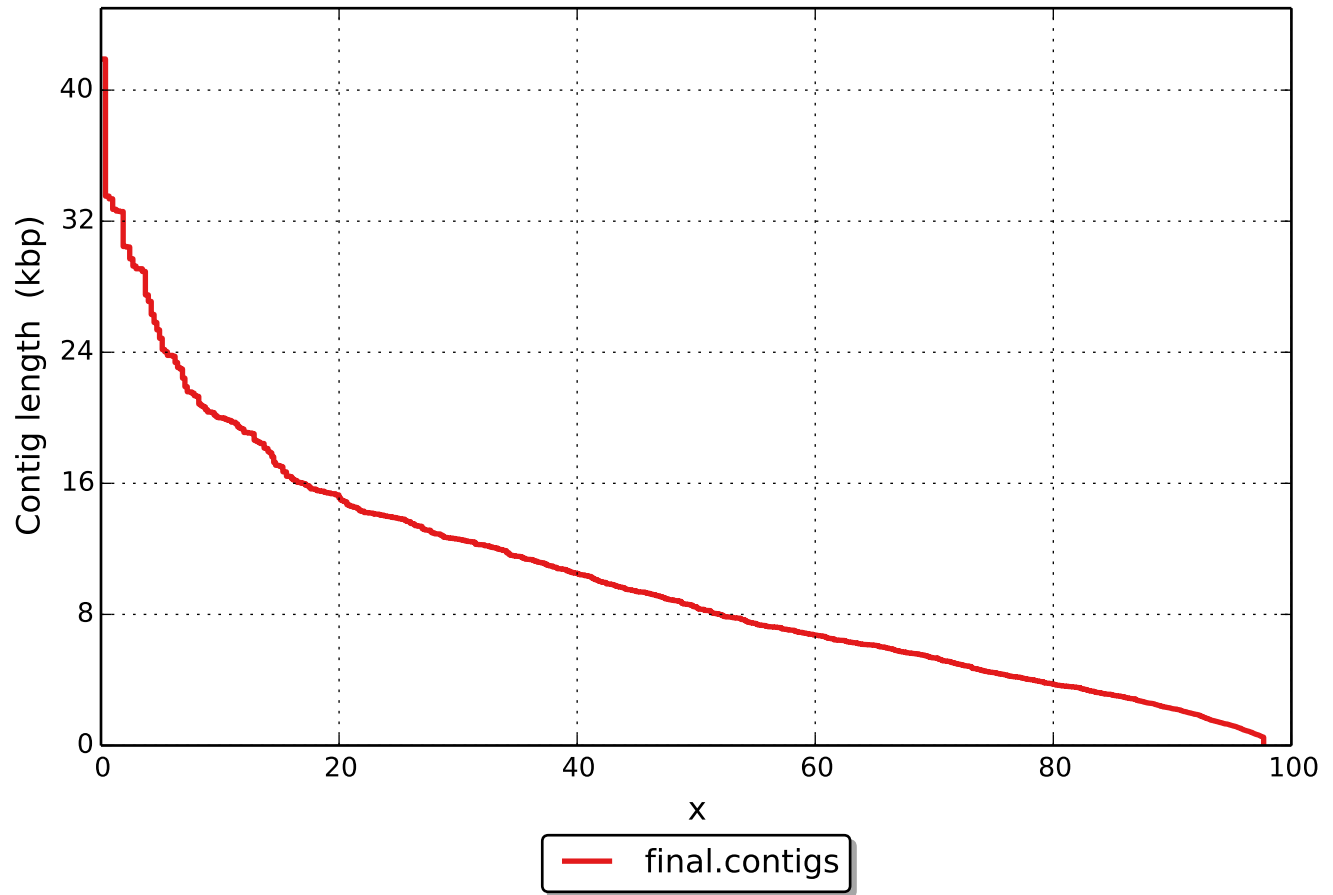


GC content



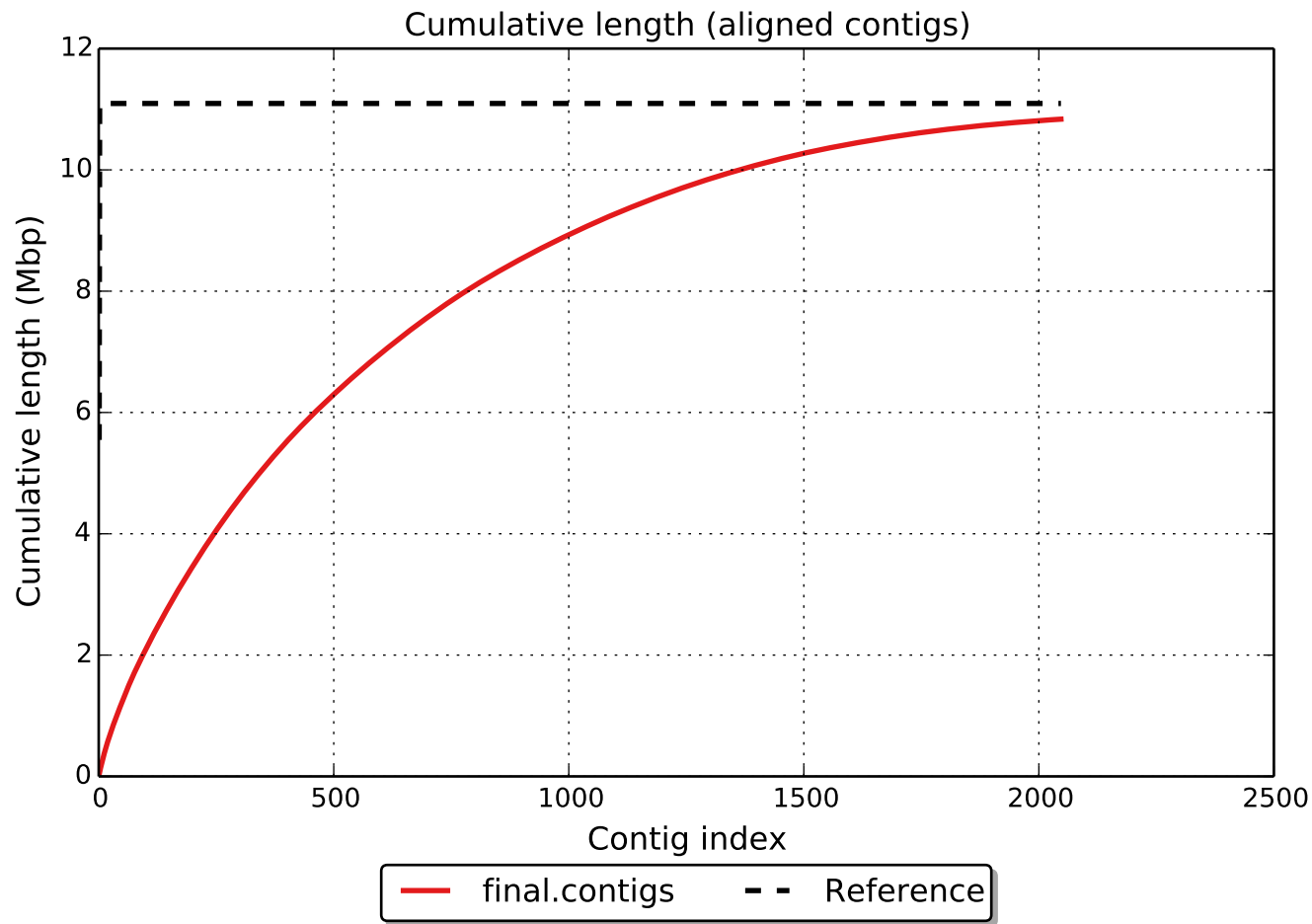


NGx

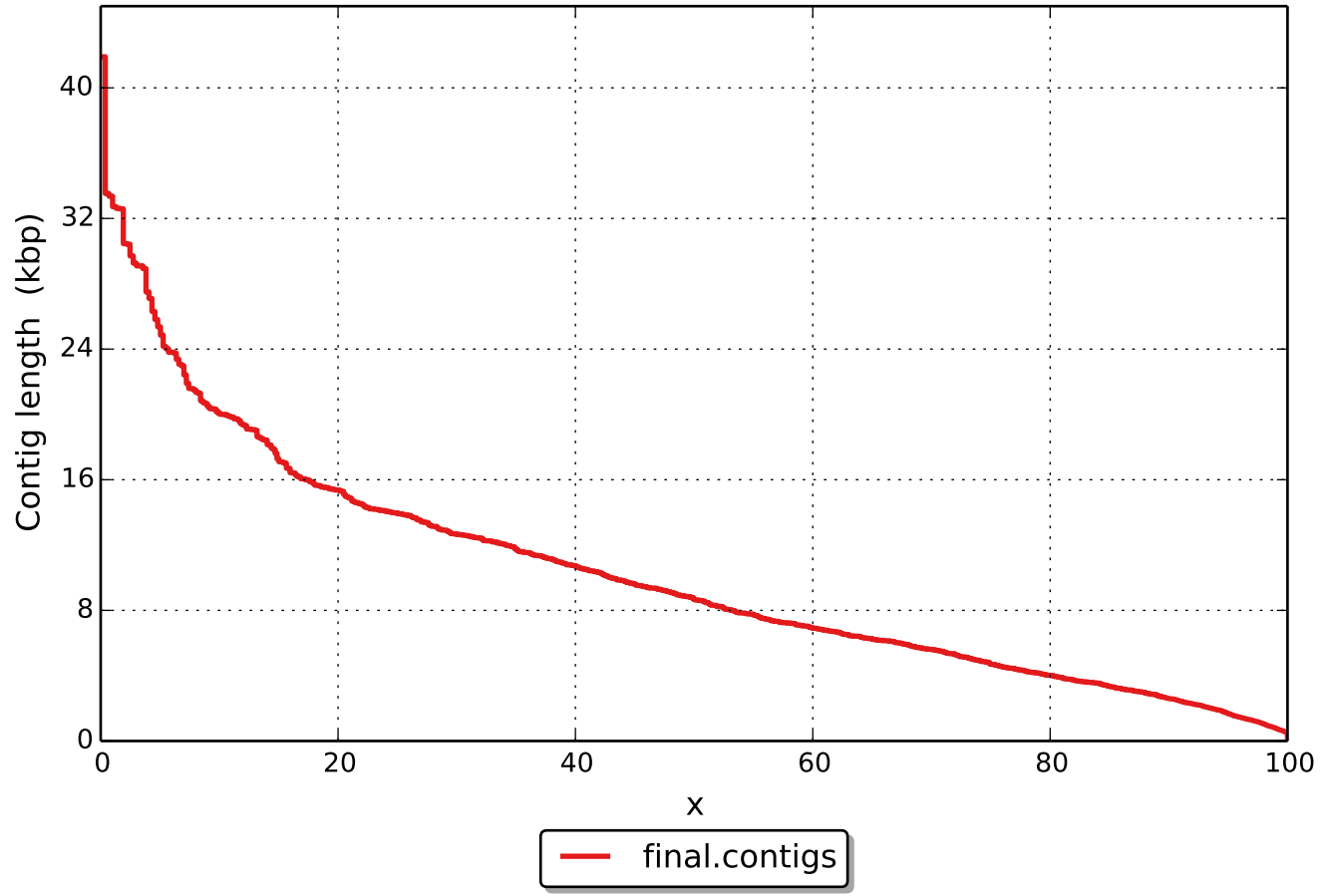








NAx



# NGAx

