

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	1379
# contigs ( $\geq 1000$ bp)	836
Total length ( $\geq 0$ bp)	10867942
Total length ( $\geq 1000$ bp)	10649819
# contigs	968
Largest contig	123304
Total length	10742664
Reference length	10957366
GC (%)	50.39
Reference GC (%)	50.50
N50	22152
NG50	21650
N75	11826
NG75	11472
L50	141
LG50	146
L75	305
LG75	319
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	25881
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.995
Duplication ratio	1.006
# N's per 100 kbp	0.00
# mismatches per 100 kbp	5.00
# indels per 100 kbp	0.10
Largest alignment	123304
NA50	22140
NGA50	21650
NA75	11826
NGA75	11472
LA50	141
LGA50	146
LA75	305
LGA75	319

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

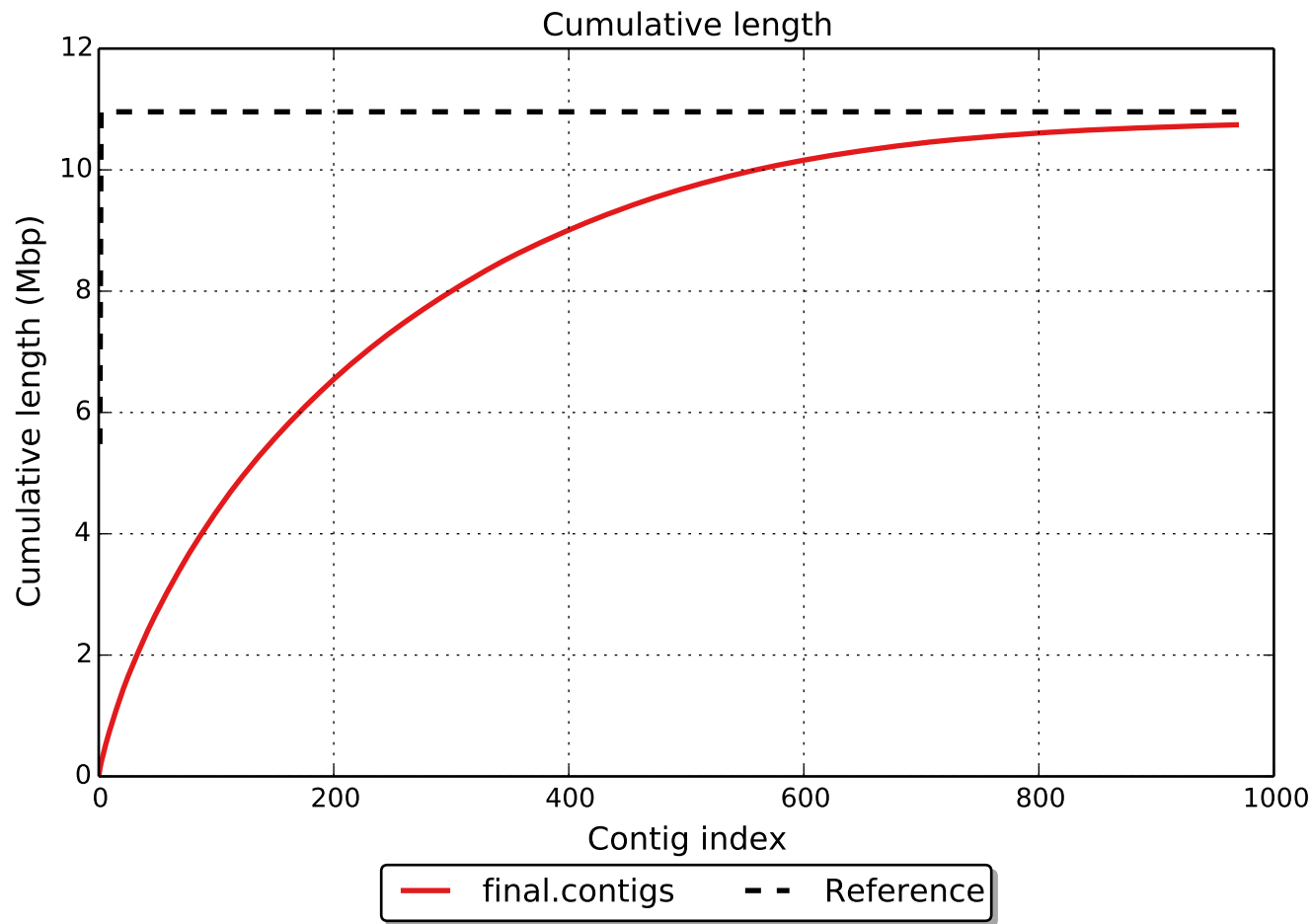
	final.contigs
# misassemblies	2
# relocations	2
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	25881
# local misassemblies	2
# mismatches	537
# indels	11
# short indels	9
# long indels	2
Indels length	38

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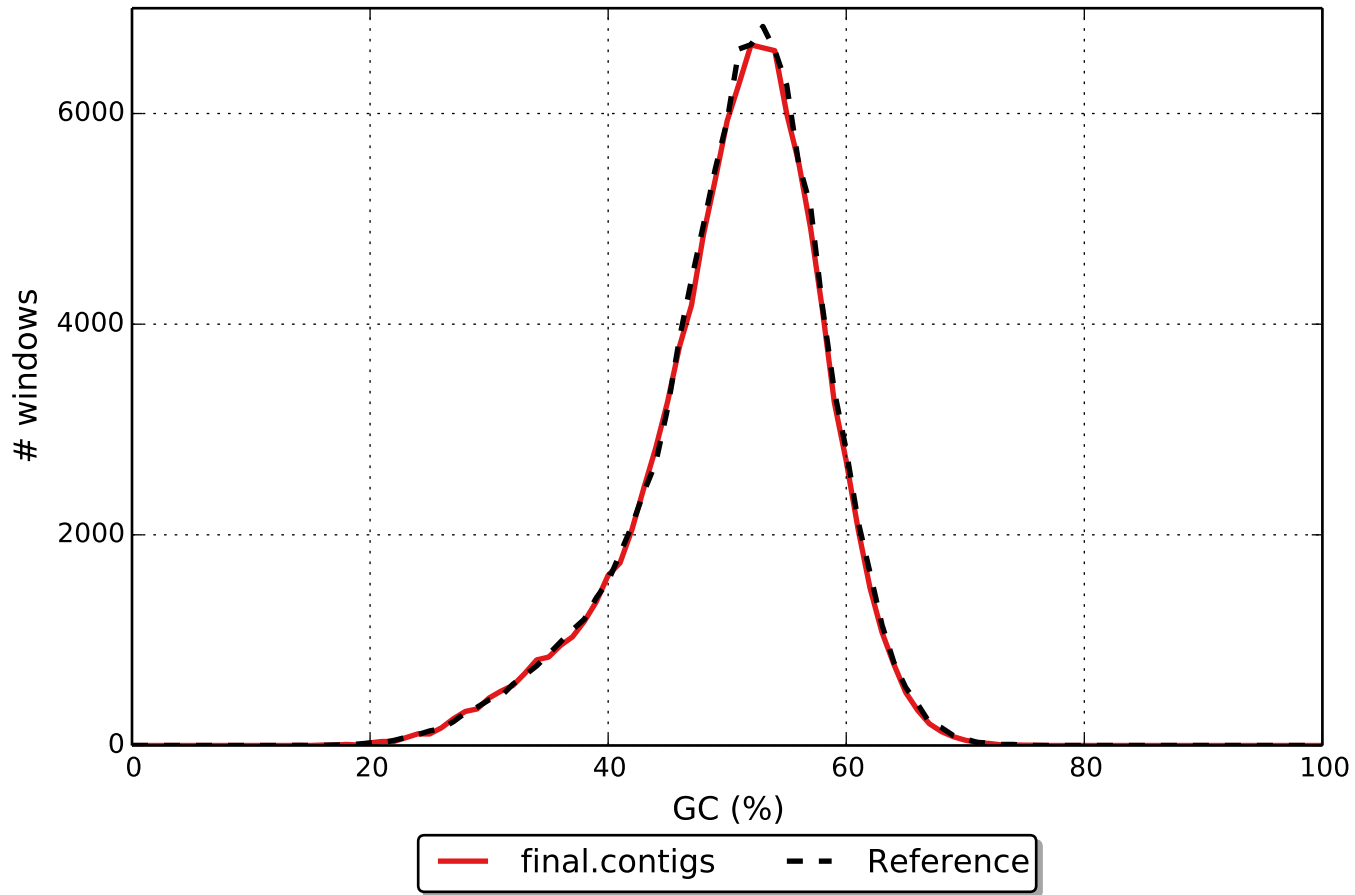
## Unaligned report

	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

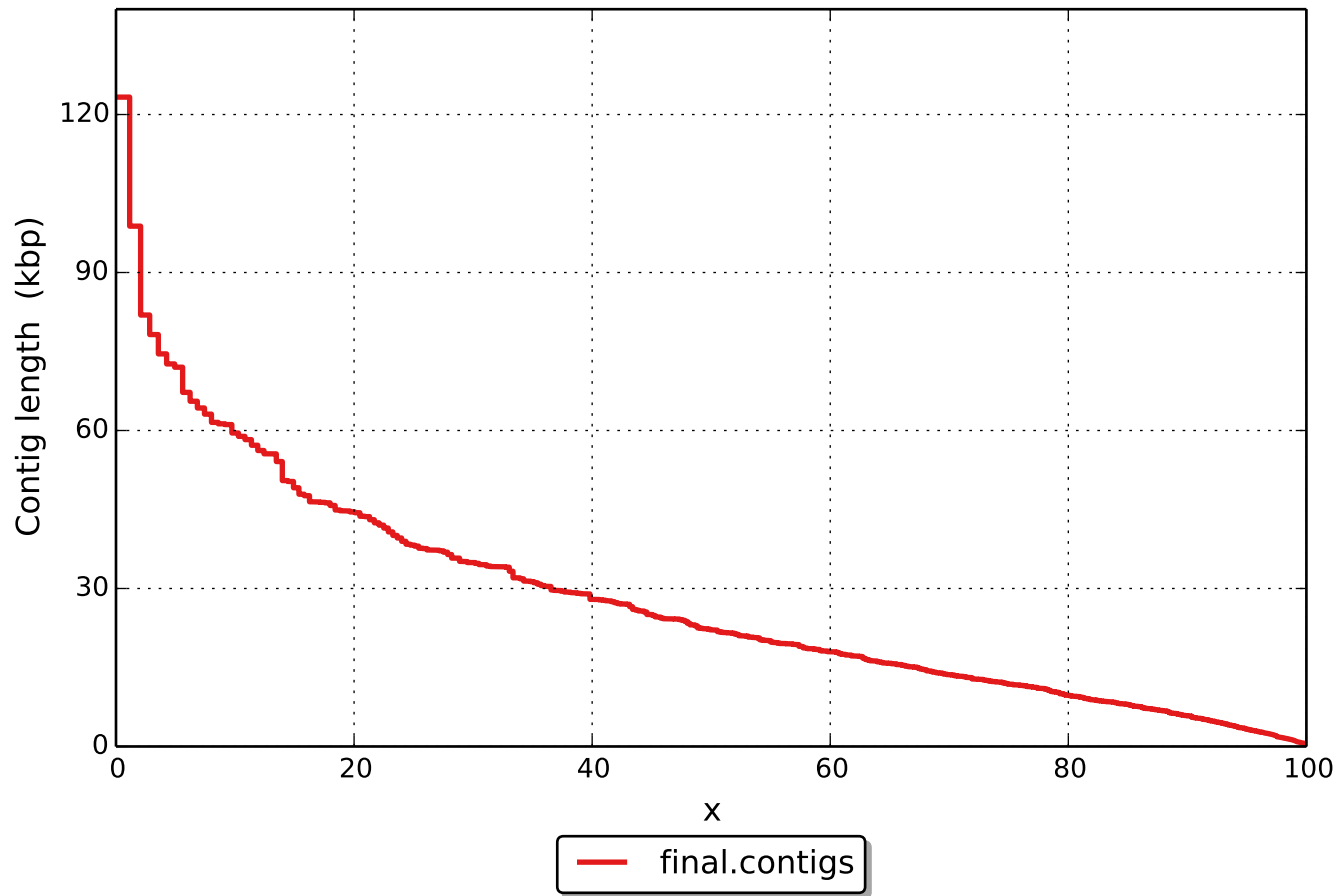
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



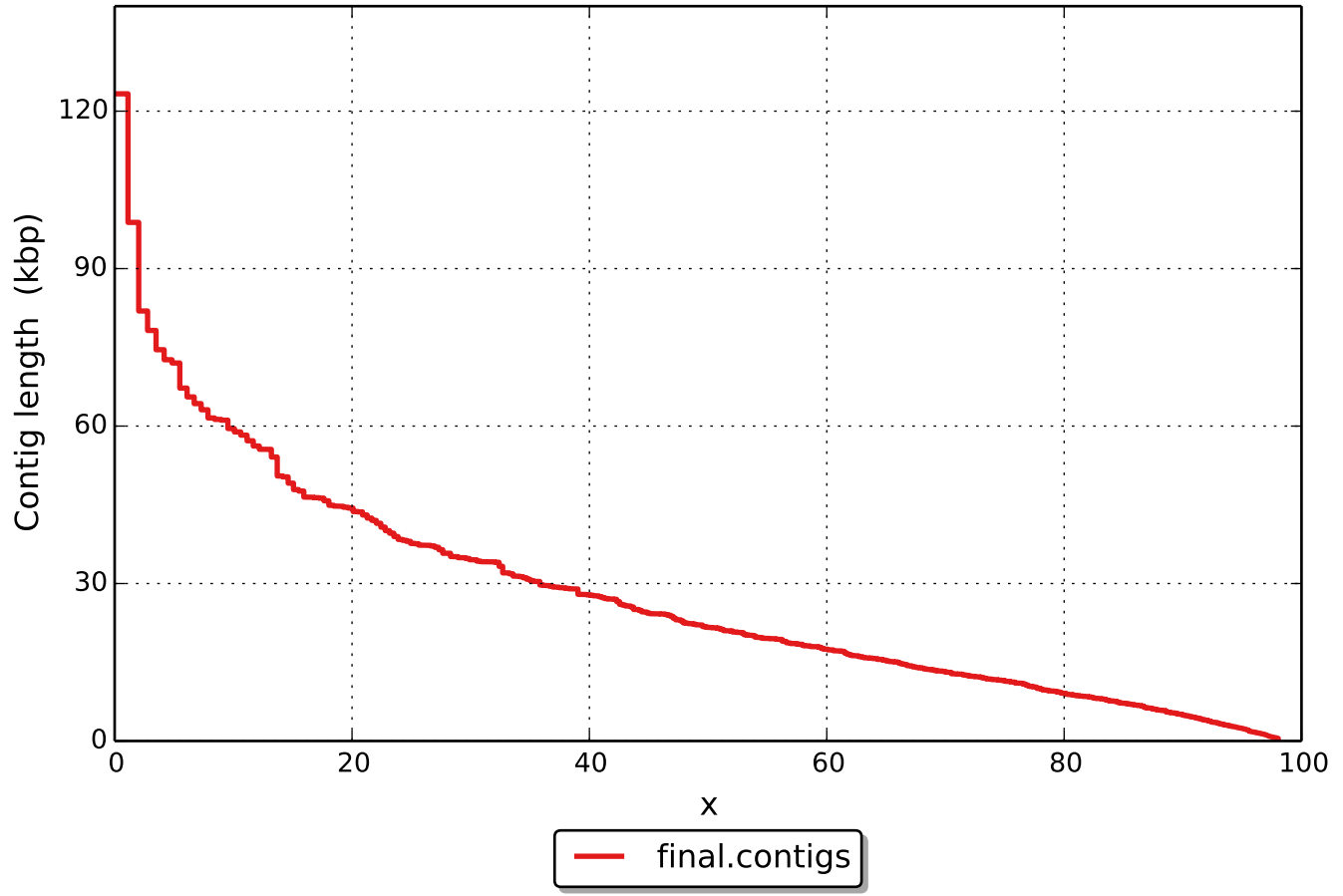
GC content



Nx

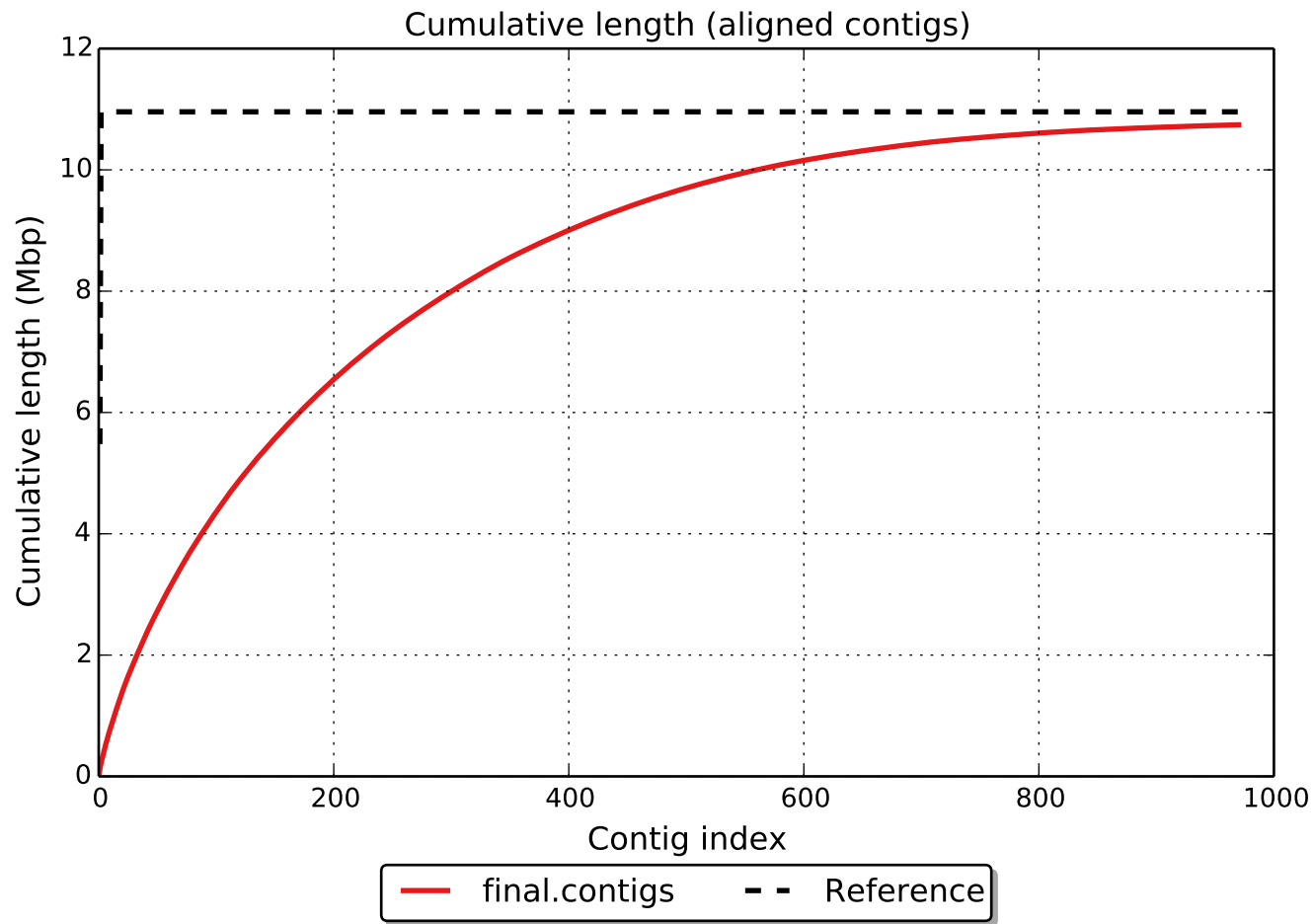


NGx

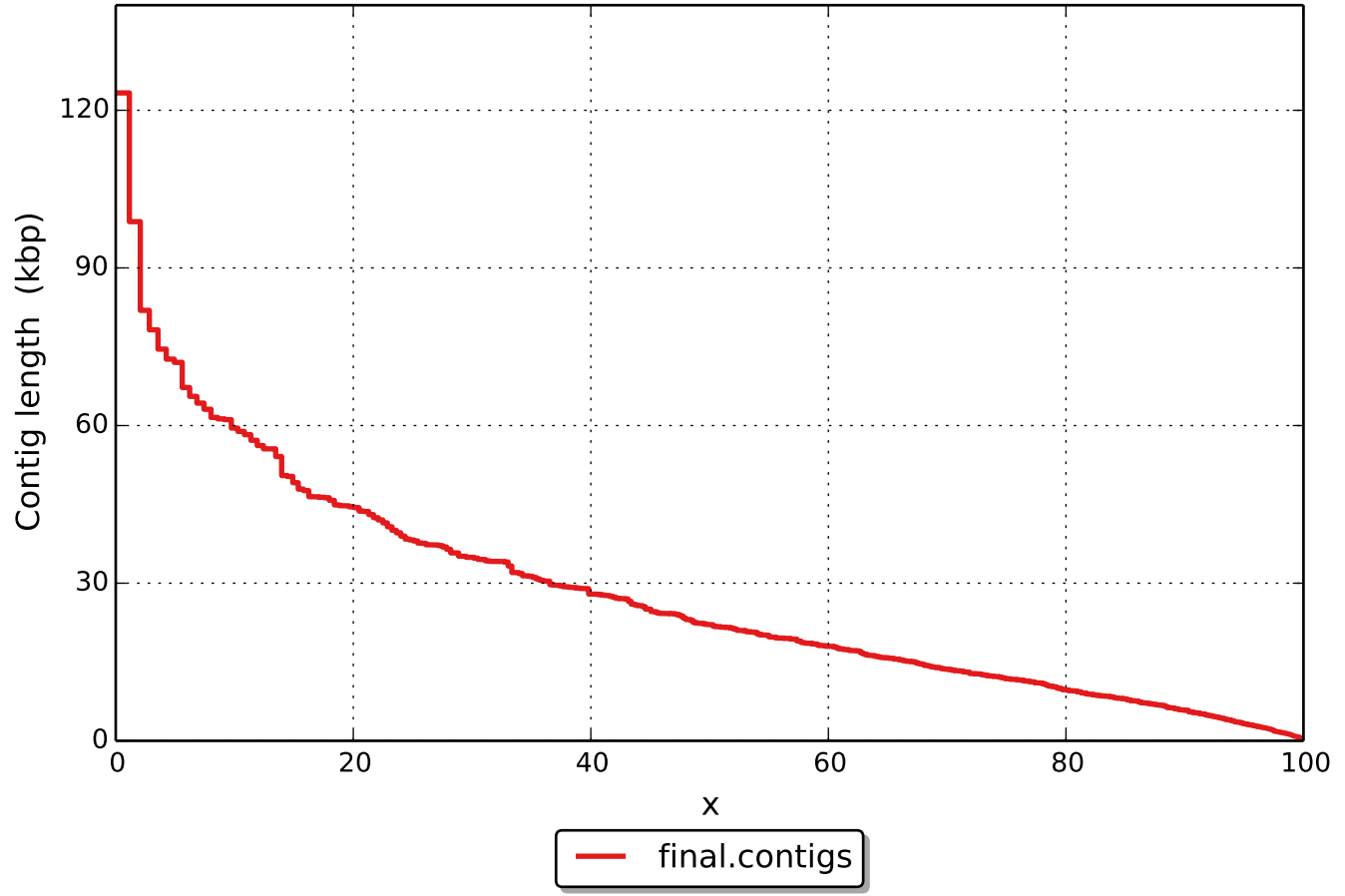








NAx



# NGAx

