

Report

	final.contigs
# contigs (>= 1000 bp)	219
# contigs (>= 5000 bp)	184
# contigs (>= 10000 bp)	149
# contigs (>= 25000 bp)	73
# contigs (>= 50000 bp)	18
Total length (>= 1000 bp)	4872656
Total length (>= 5000 bp)	4773303
Total length (>= 10000 bp)	4519068
Total length (>= 25000 bp)	3241247
Total length (>= 50000 bp)	1339124
# contigs	224
Largest contig	147879
Total length	4876188
Reference length	4857432
GC (℥)	52.23
Reference GC (℥)	52.23
N50	33291
NG50	33291
N75	20769
NG75	20934
L50	46
LG50	46
L75	92
LG75	91
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (℥)	99.994
Duplication ratio	1.004
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	147879
NA50	33291
NGA50	33291
NA75	20769
NGA75	20934
LA50	46
LGA50	46
LA75	92
LGA75	91

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 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	0
# indels	0
# short indels	0
# long indels	0
Indels length	0

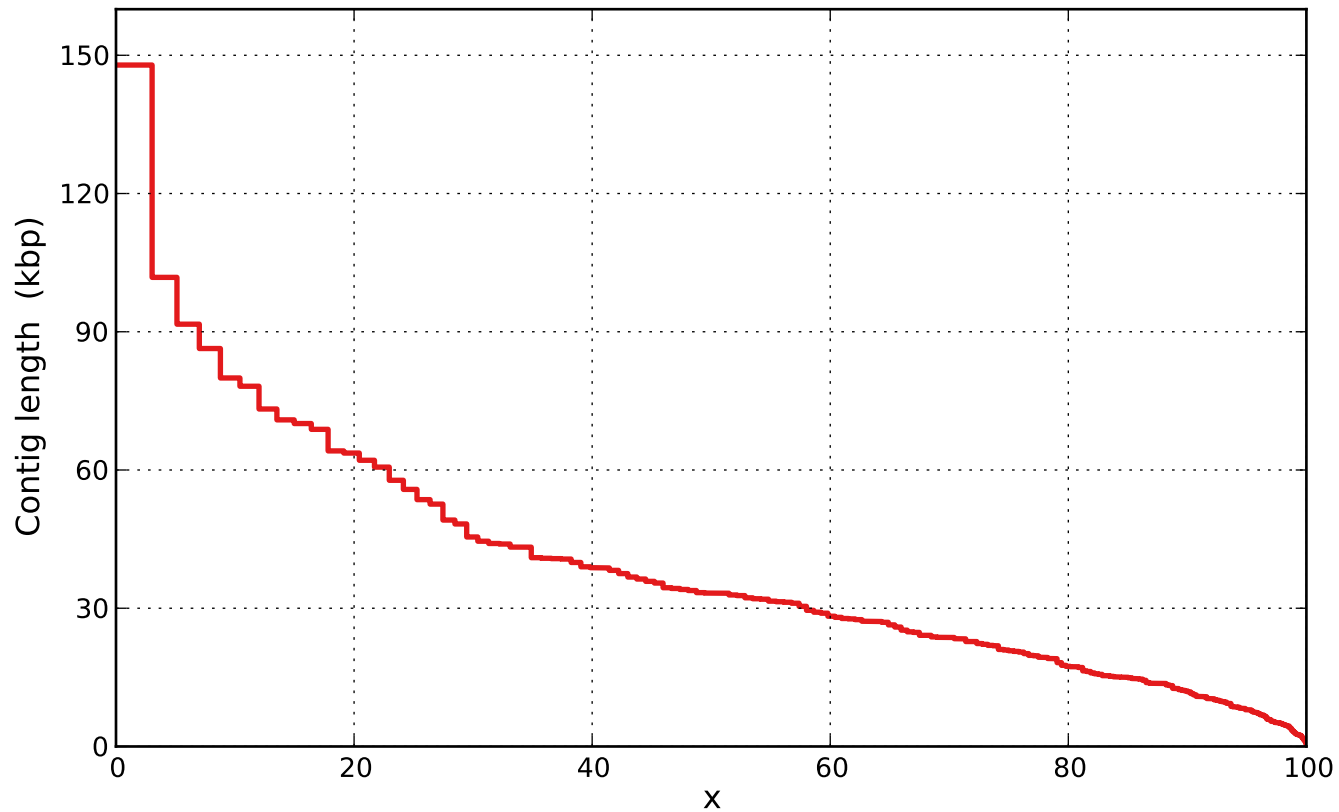
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

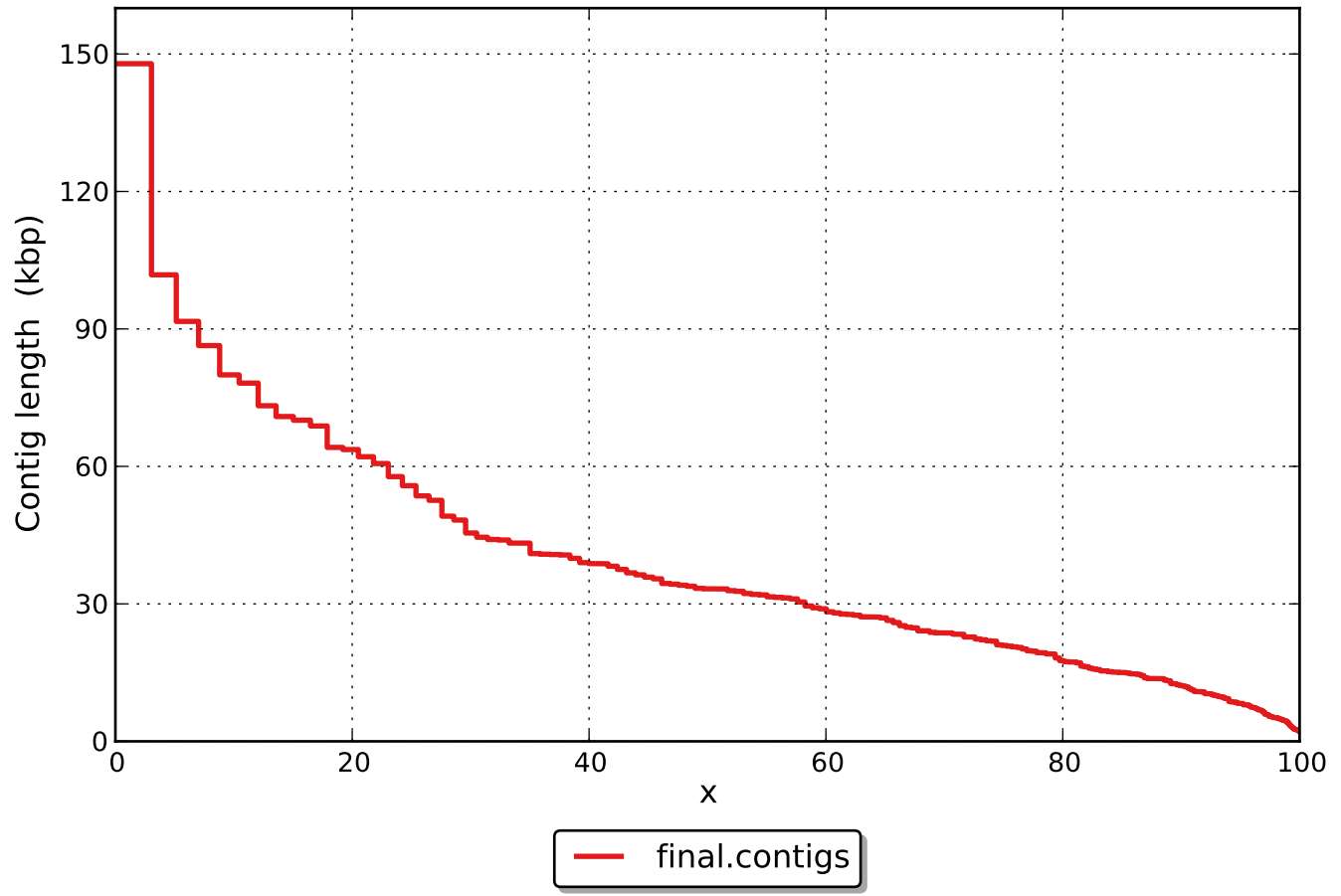
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

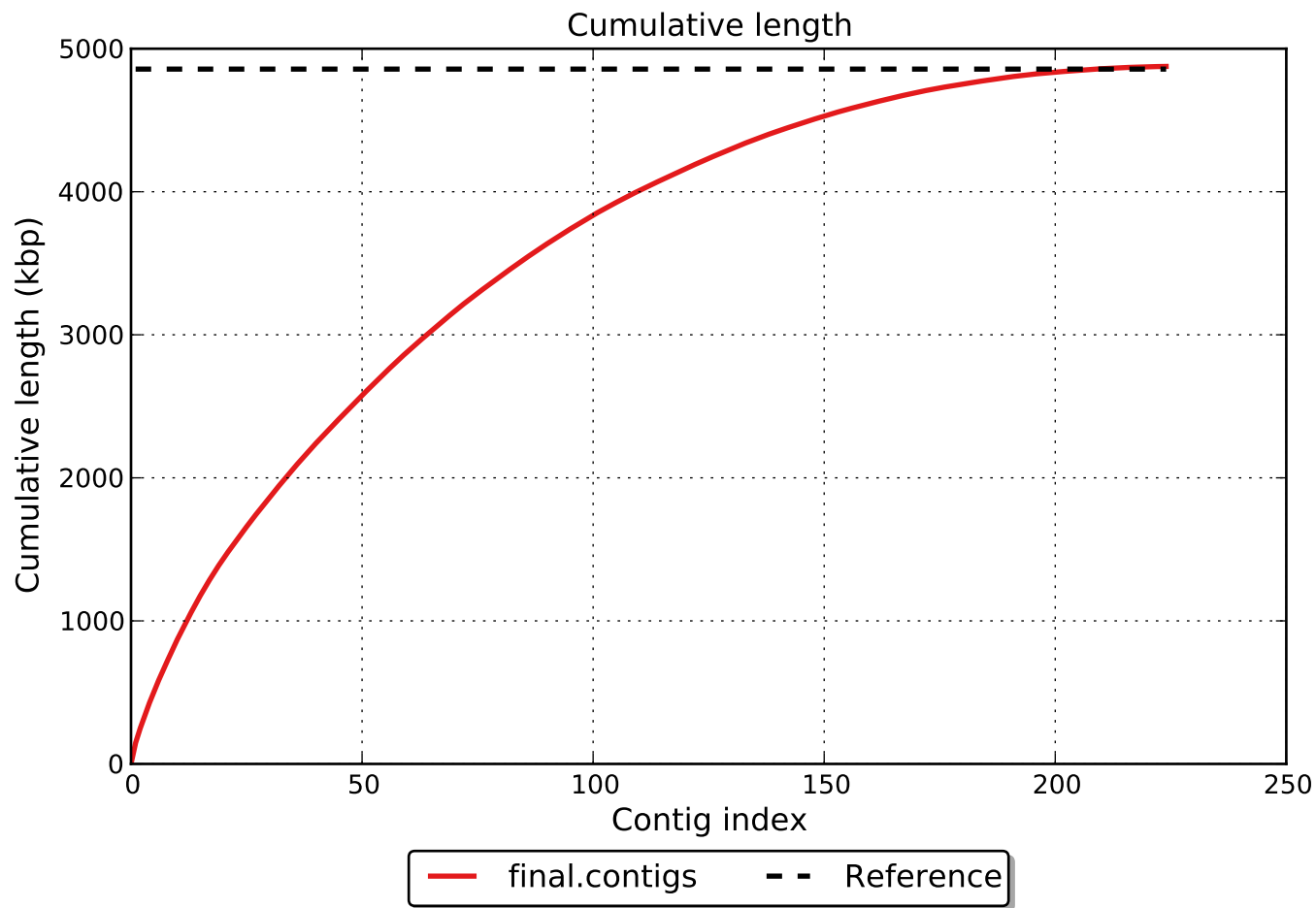
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

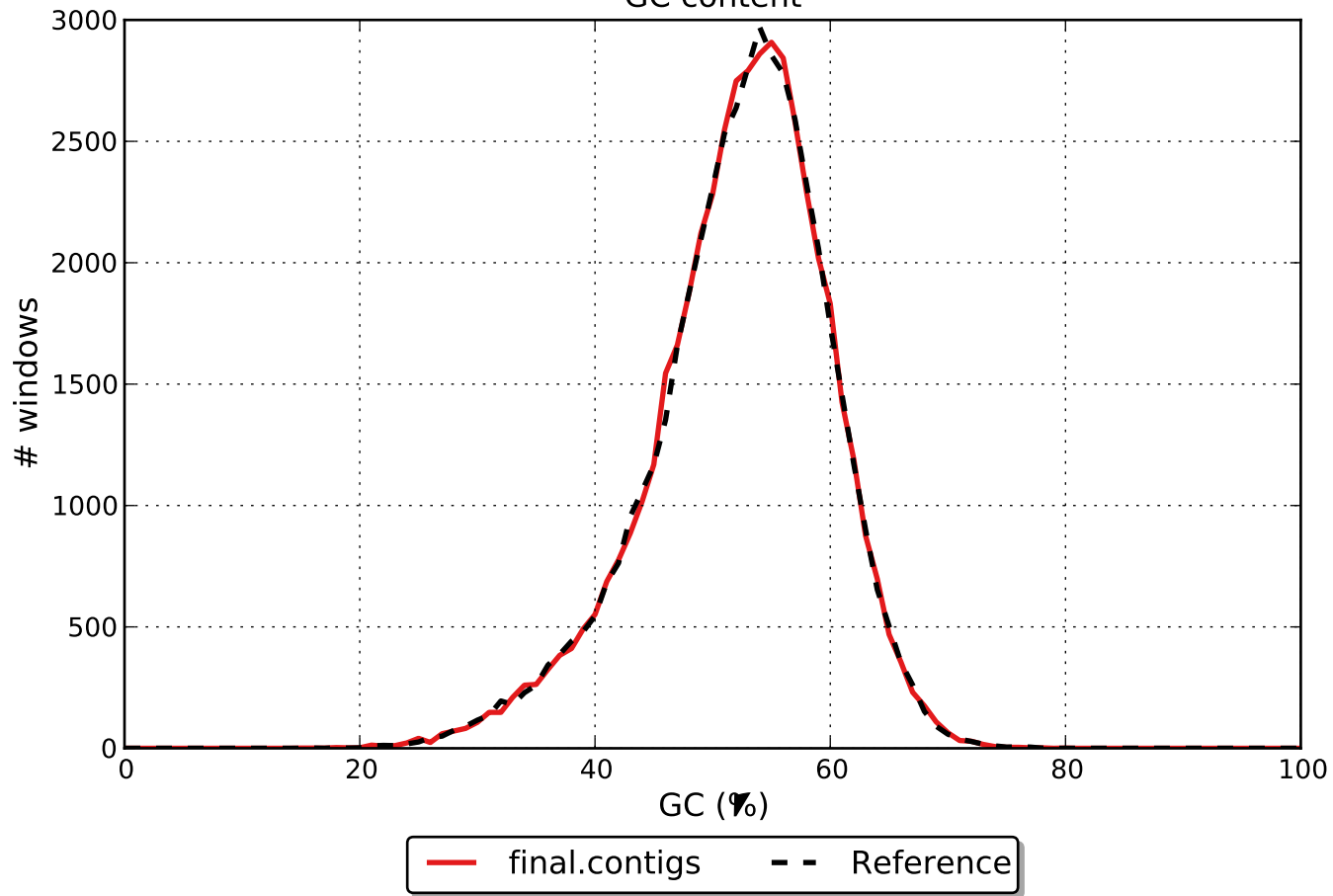


NGx

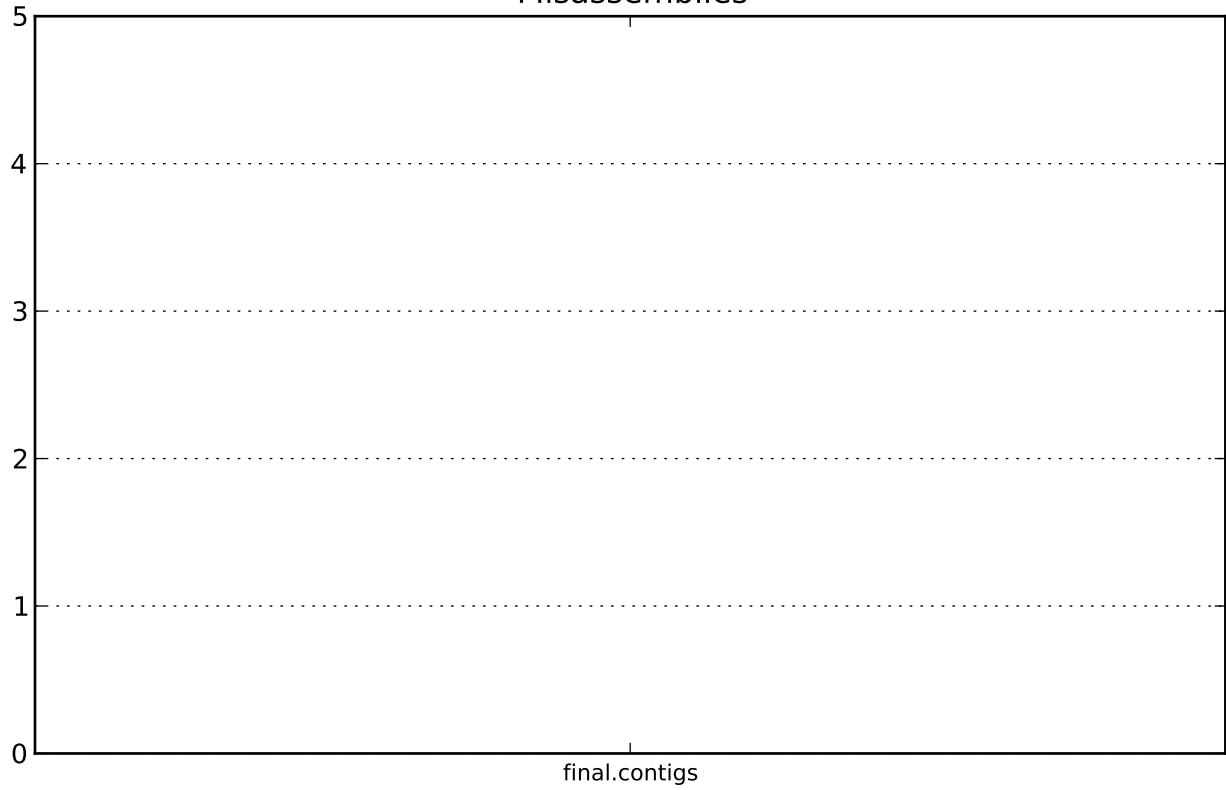




GC content

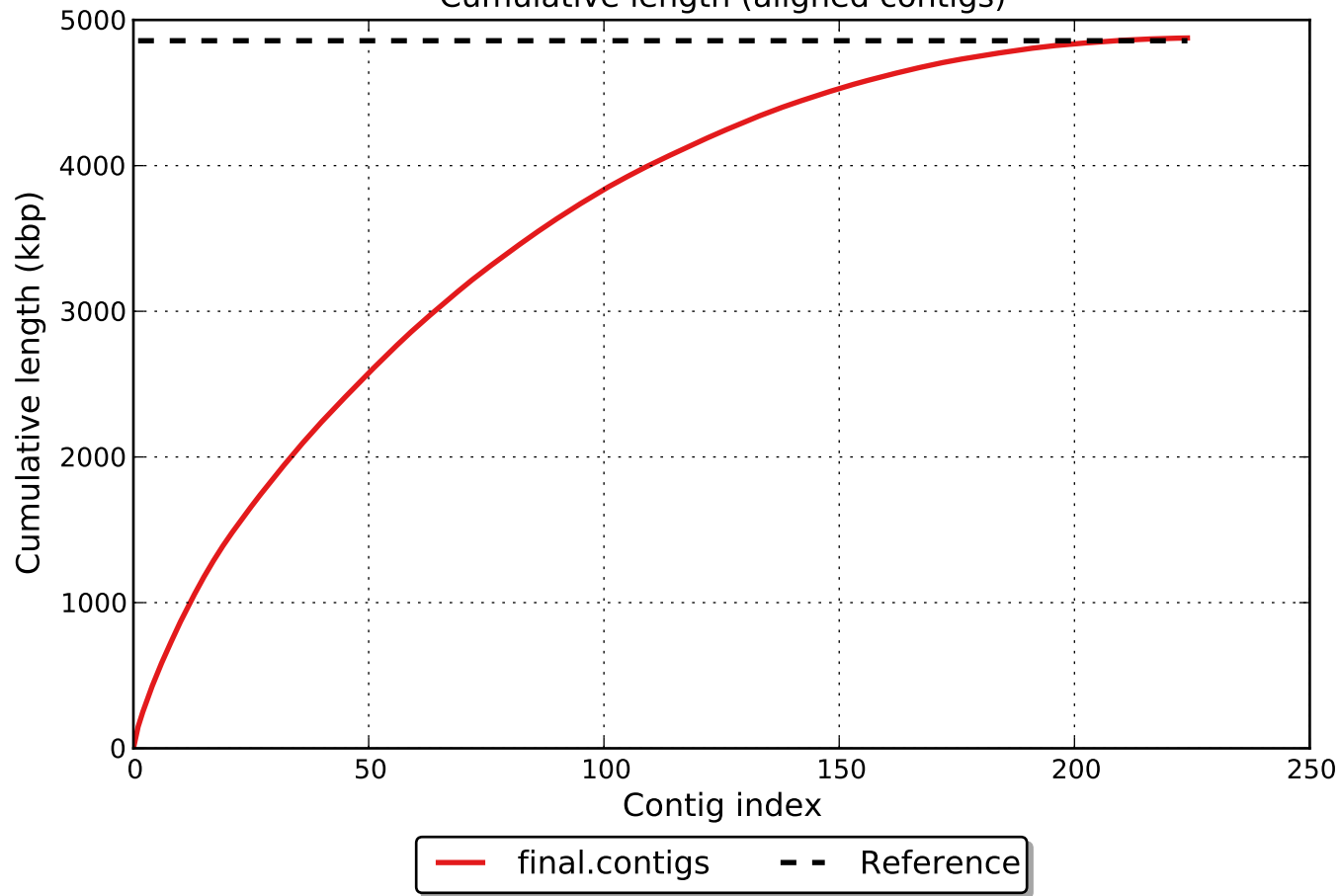


# Misassemblies

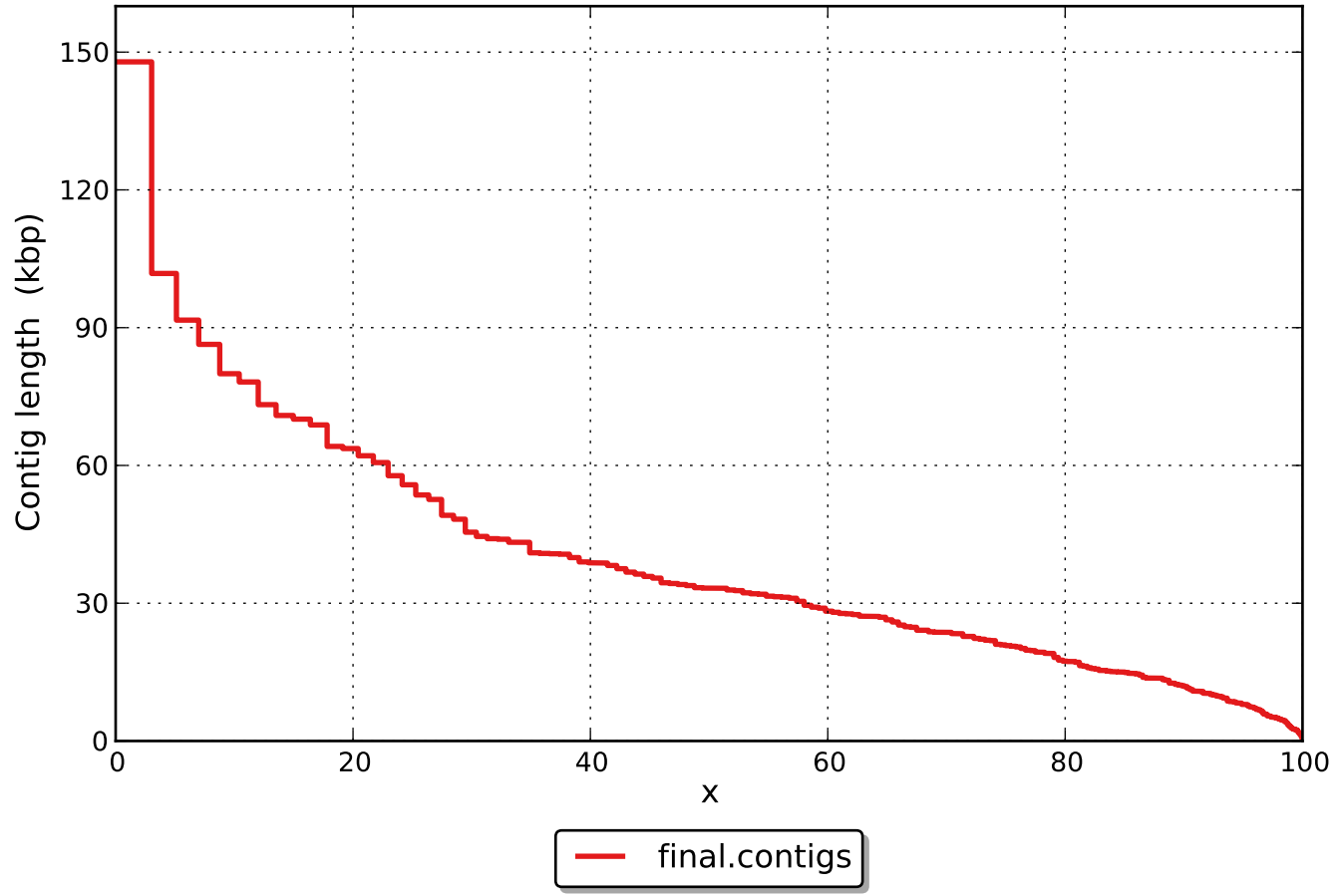




Cumulative length (aligned contigs)



NAx



# NGAx

