

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	105
# contigs ( $\geq 1000$ bp)	98
Total length ( $\geq 0$ bp)	1239635
Total length ( $\geq 1000$ bp)	1233969
# contigs	105
Largest contig	42035
Total length	1239635
Reference length	615980
GC (%)	25.35
Reference GC (%)	25.36
N50	17928
NG50	30431
N75	10565
NG75	26266
L50	22
LG50	9
L75	44
LG75	14
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	48 + 3 part
Unaligned length	599251
Genome fraction (%)	99.999
Duplication ratio	1.040
# N's per 100 kbp	0.00
# mismatches per 100 kbp	157.96
# indels per 100 kbp	0.00
Largest alignment	42035
NA50	3683
NGA50	20171
NGA75	12075
LA50	43
LGA50	10
LGA75	20

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
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	973
# indels	0
# short indels	0
# long indels	0
Indels length	0

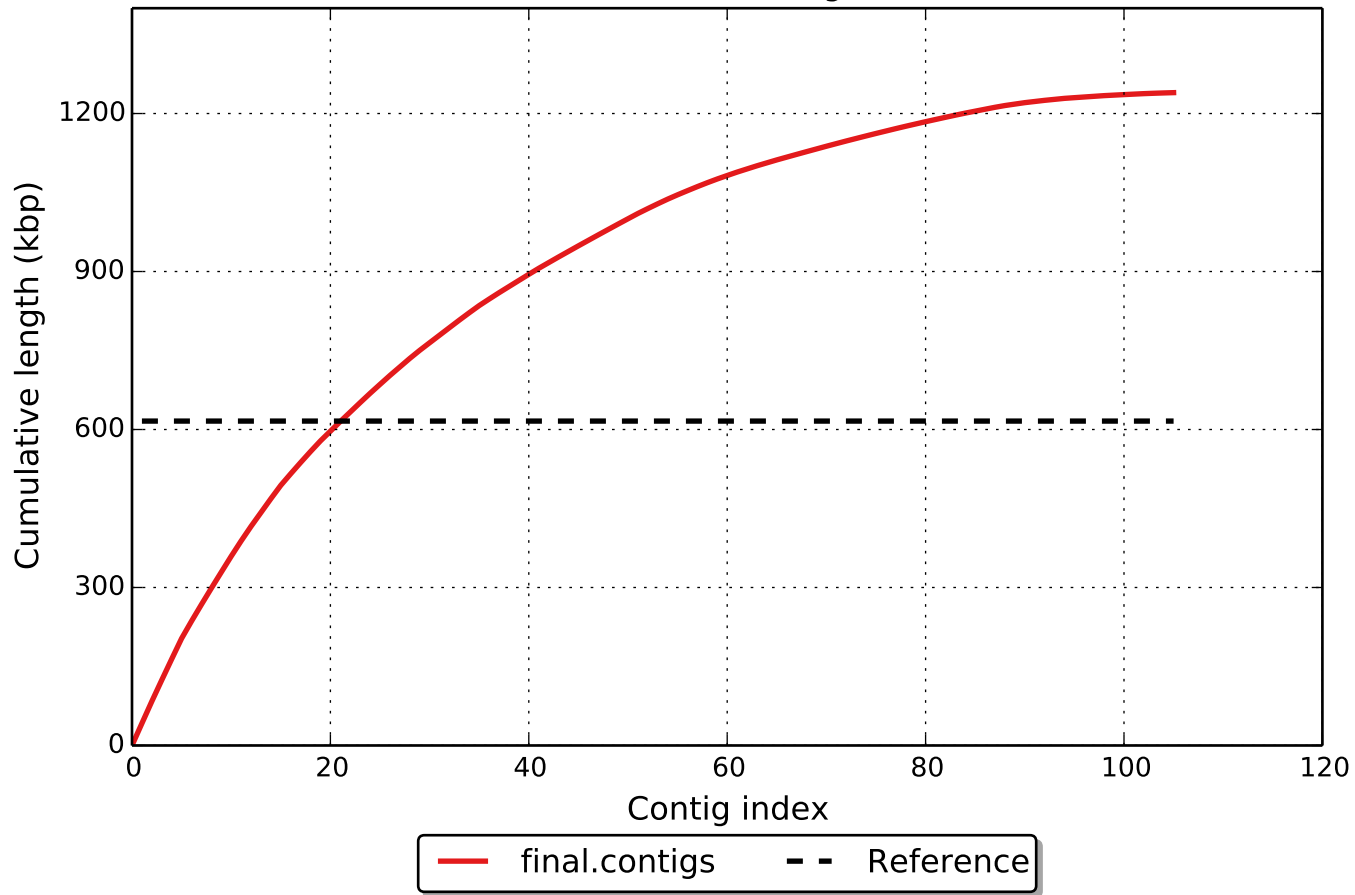
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

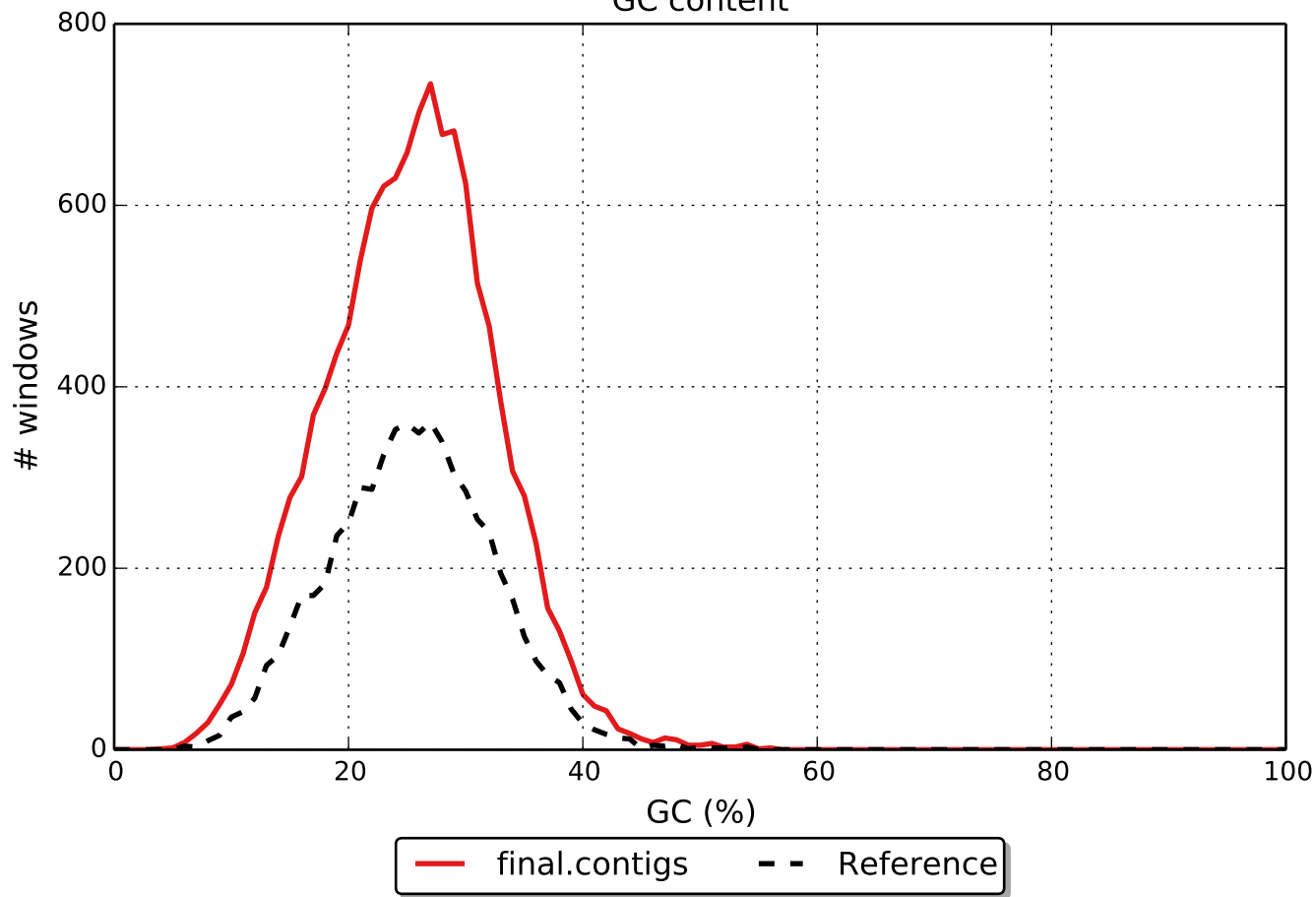
	final.contigs
# fully unaligned contigs	48
Fully unaligned length	550714
# partially unaligned contigs	3
# with misassembly	0
# both parts are significant	0
Partially unaligned length	48537
# N's	0

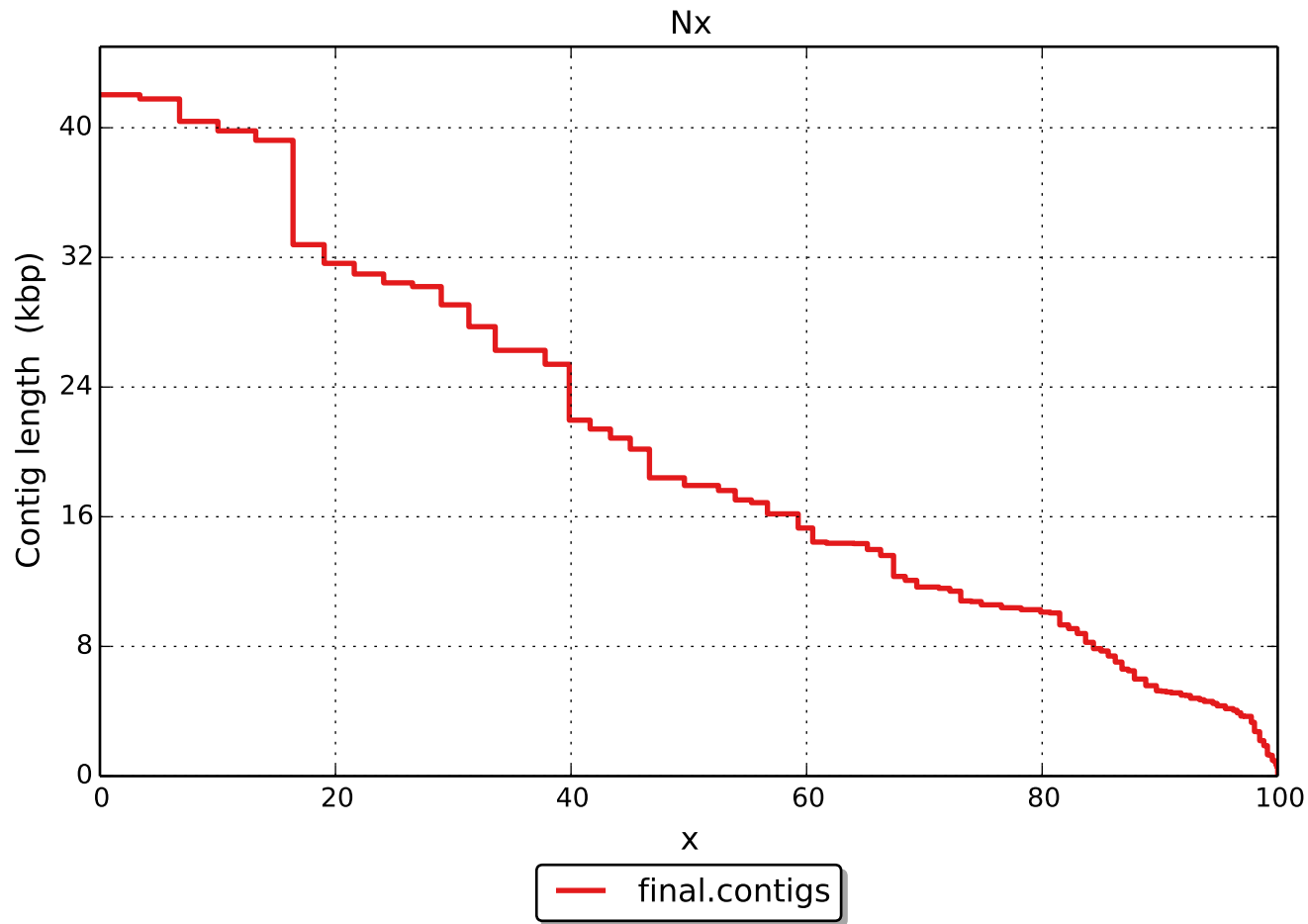
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Cumulative length

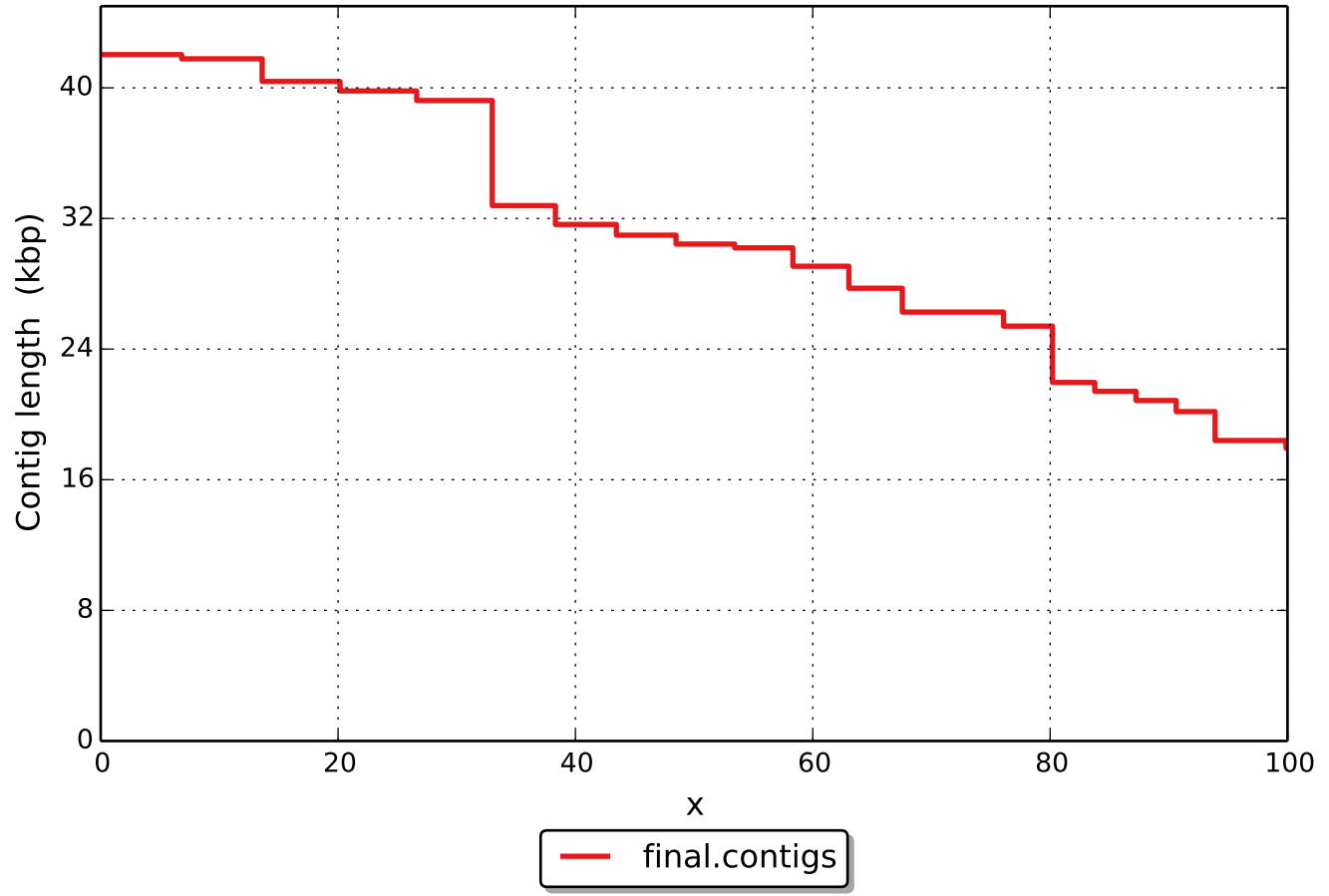


# GC content





NGx

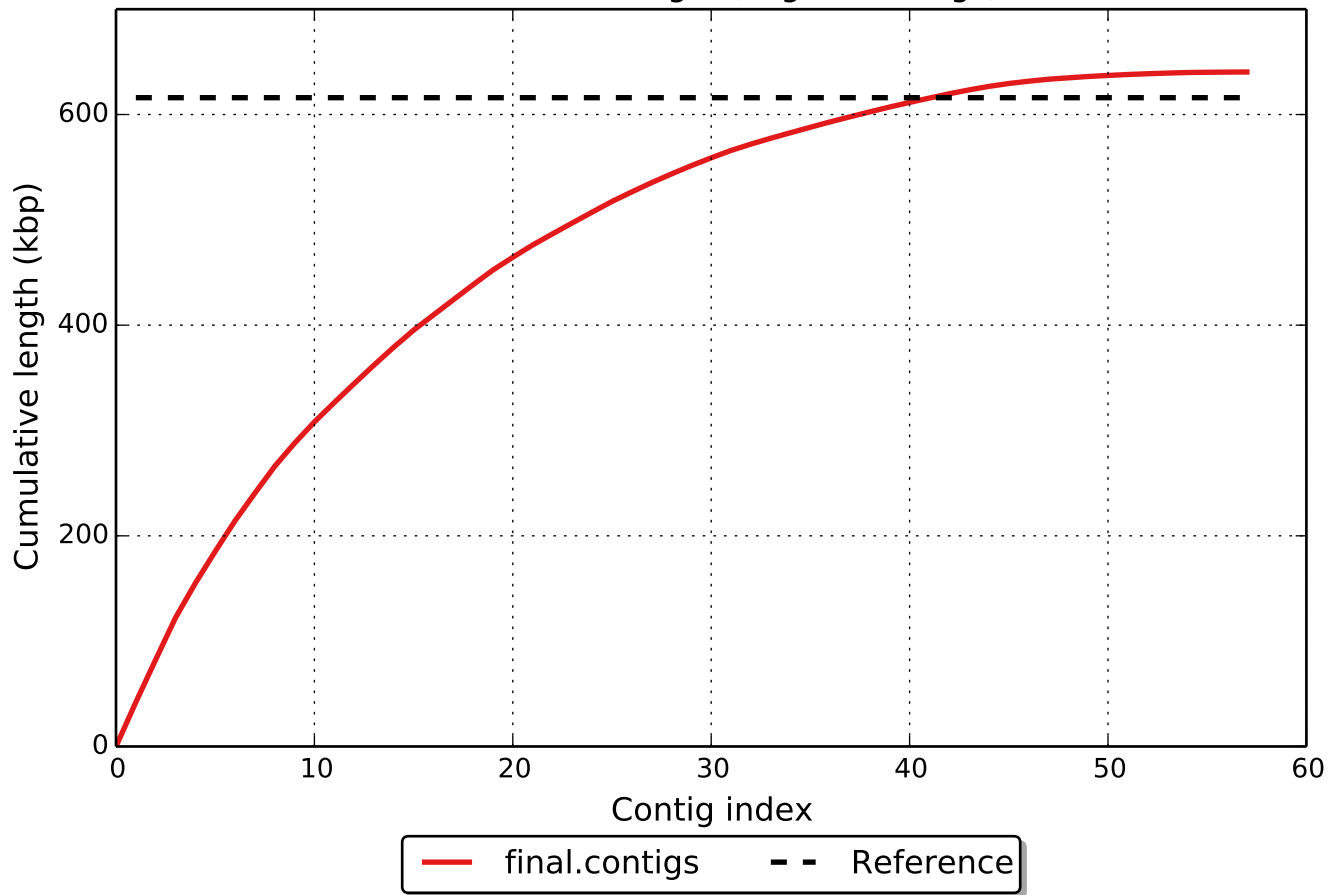


# Misassemblies

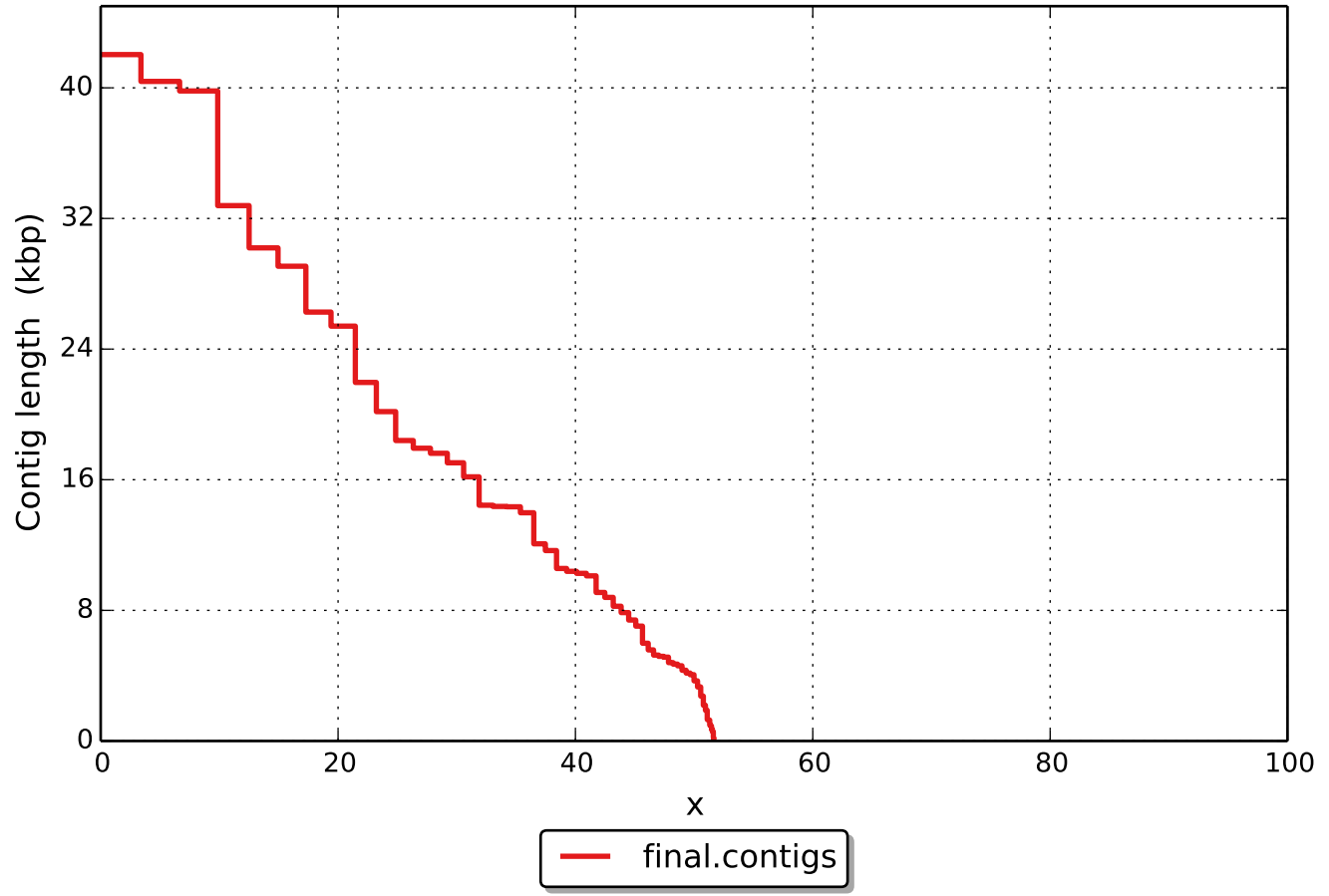




Cumulative length (aligned contigs)



NAx



# NGAx

