

## Report

	final.contigs
# contigs (>= 1000 bp)	340
# contigs (>= 5000 bp)	234
# contigs (>= 10000 bp)	161
# contigs (>= 25000 bp)	50
# contigs (>= 50000 bp)	6
Total length (>= 1000 bp)	4569721
Total length (>= 5000 bp)	4271145
Total length (>= 10000 bp)	3731263
Total length (>= 25000 bp)	1865981
Total length (>= 50000 bp)	361810
# contigs	367
Largest contig	69147
Total length	4589142
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	22016
NG50	21981
N75	12876
NG75	12232
L50	69
LG50	70
L75	136
LG75	139
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	4
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.152
Duplication ratio	1.007
# N's per 100 kbp	0.00
# mismatches per 100 kbp	13.08
# indels per 100 kbp	0.07
Largest alignment	69147
NA50	22016
NGA50	21981
NA75	12876
NGA75	12232
LA50	69
LGA50	70
LA75	136
LGA75	139

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

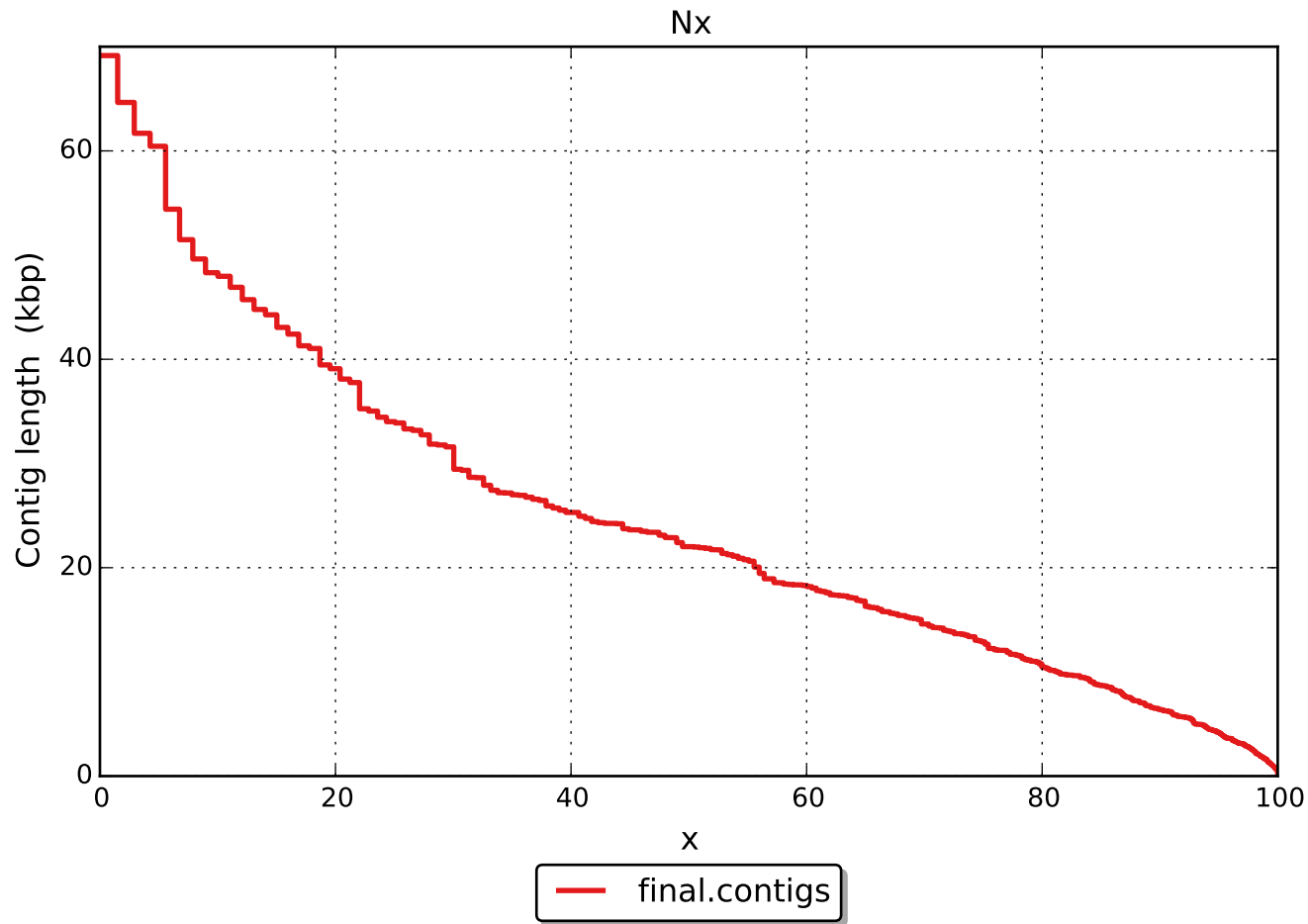
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	4
# mismatches	596
# indels	3
# short indels	3
# long indels	0
Indels length	3

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).

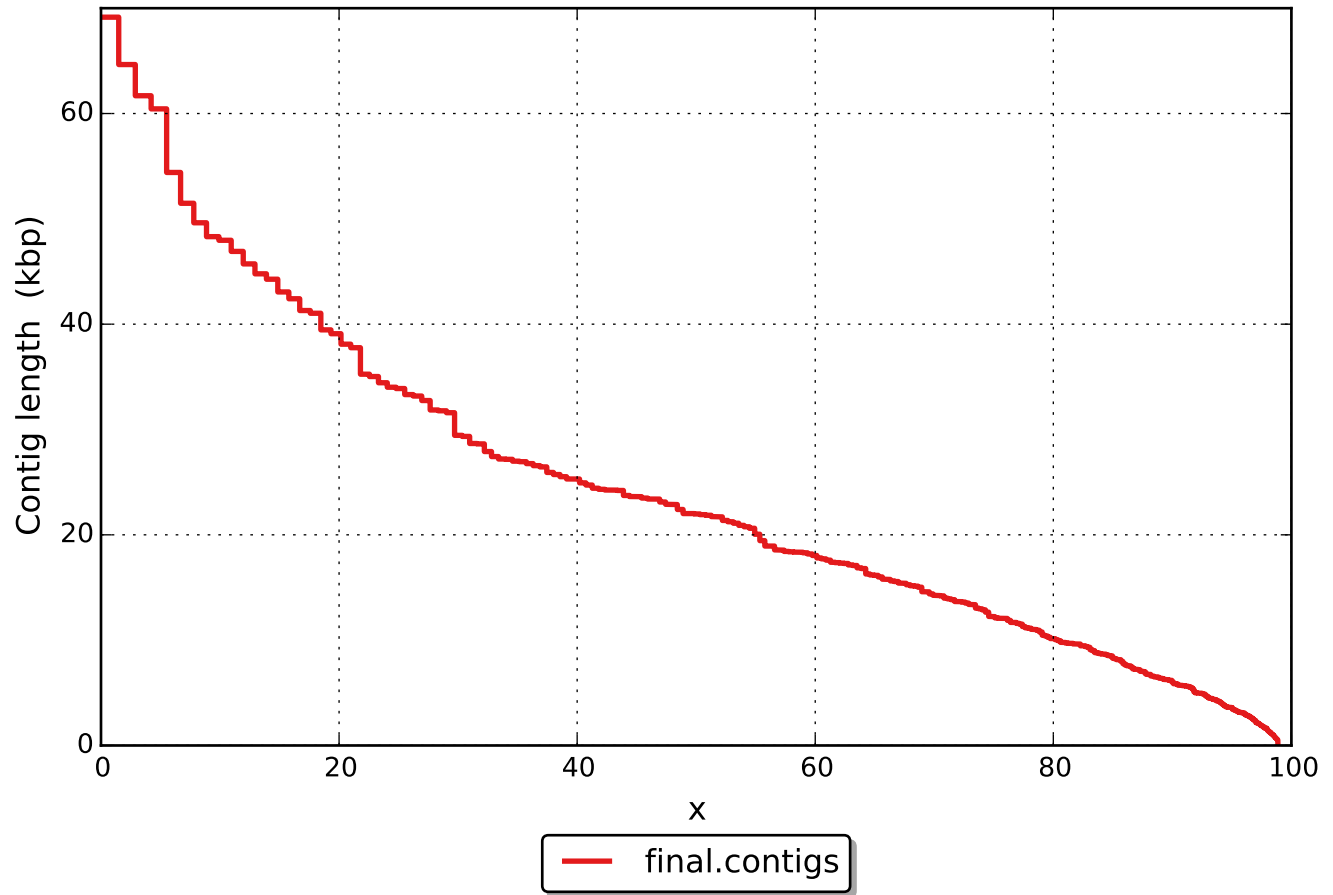
## Unaligned report

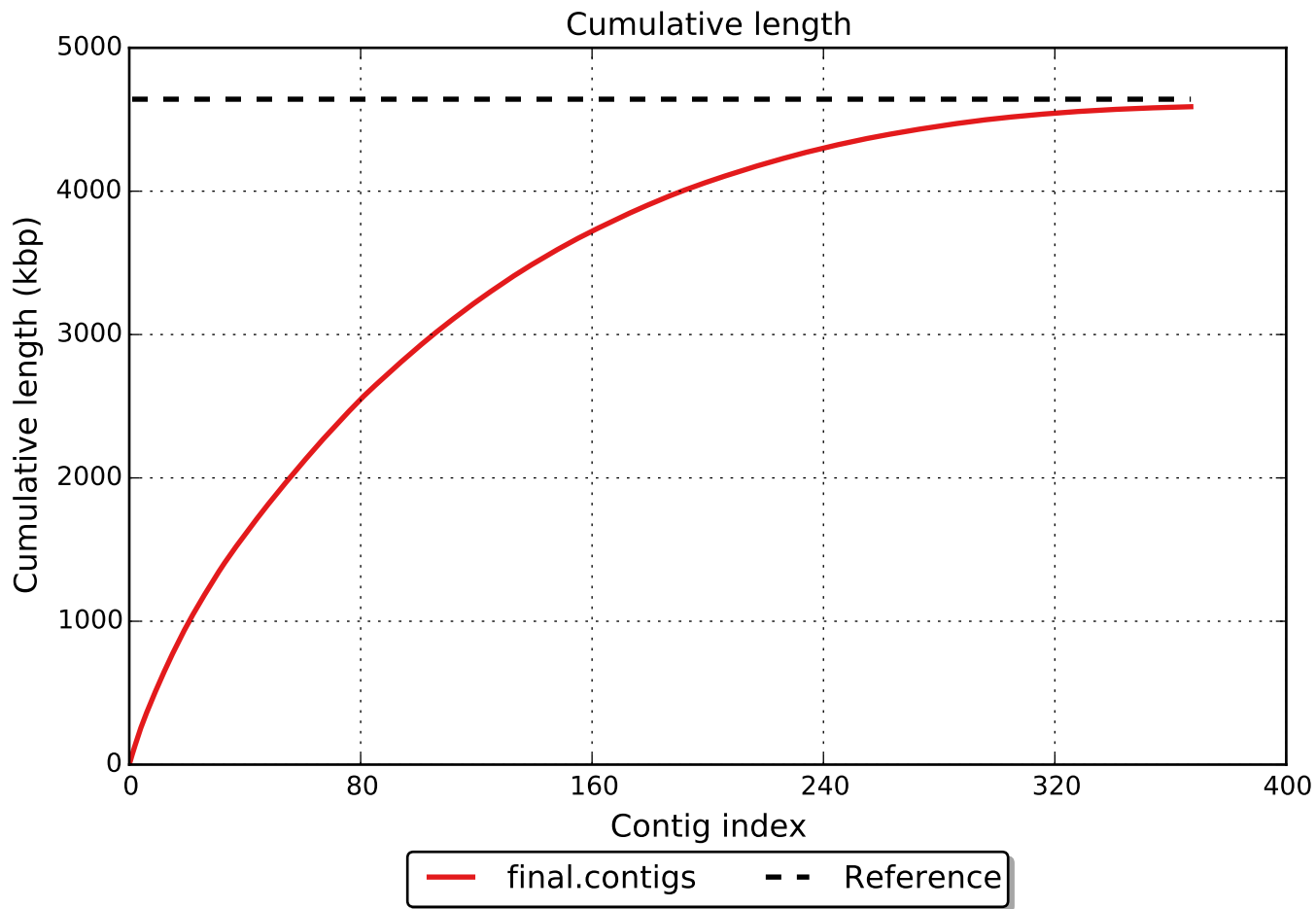
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

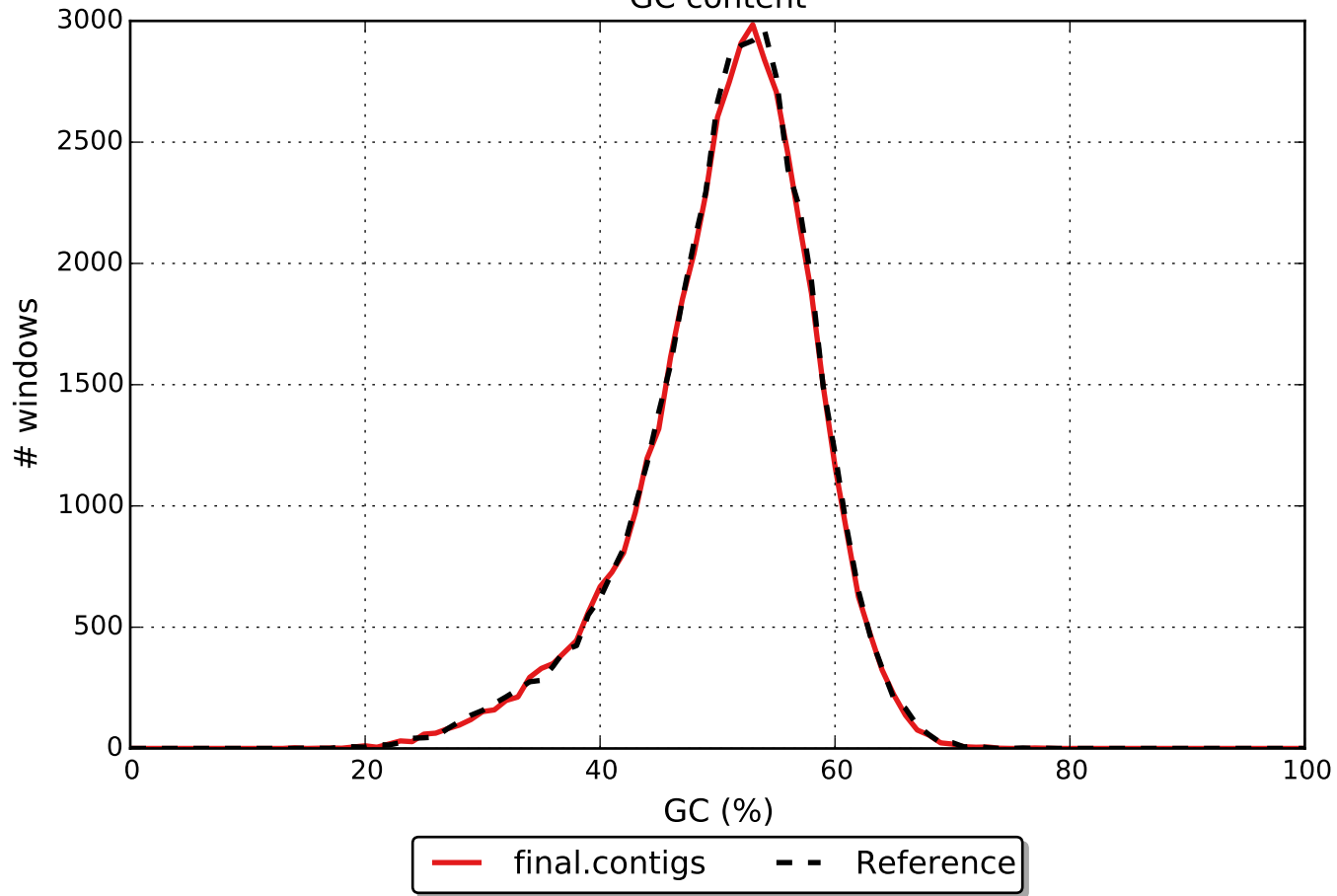


NGx





GC content

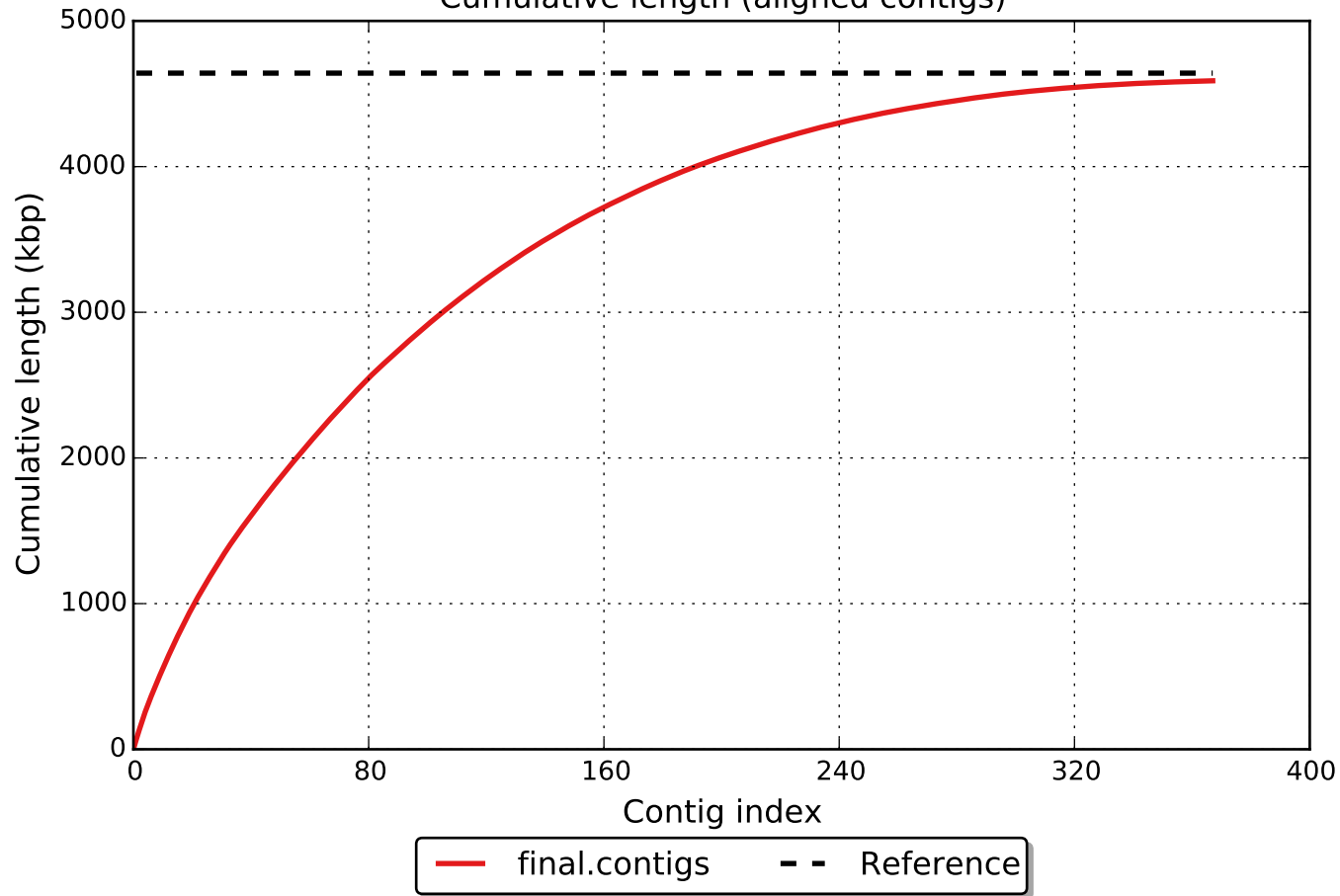


# Misassemblies

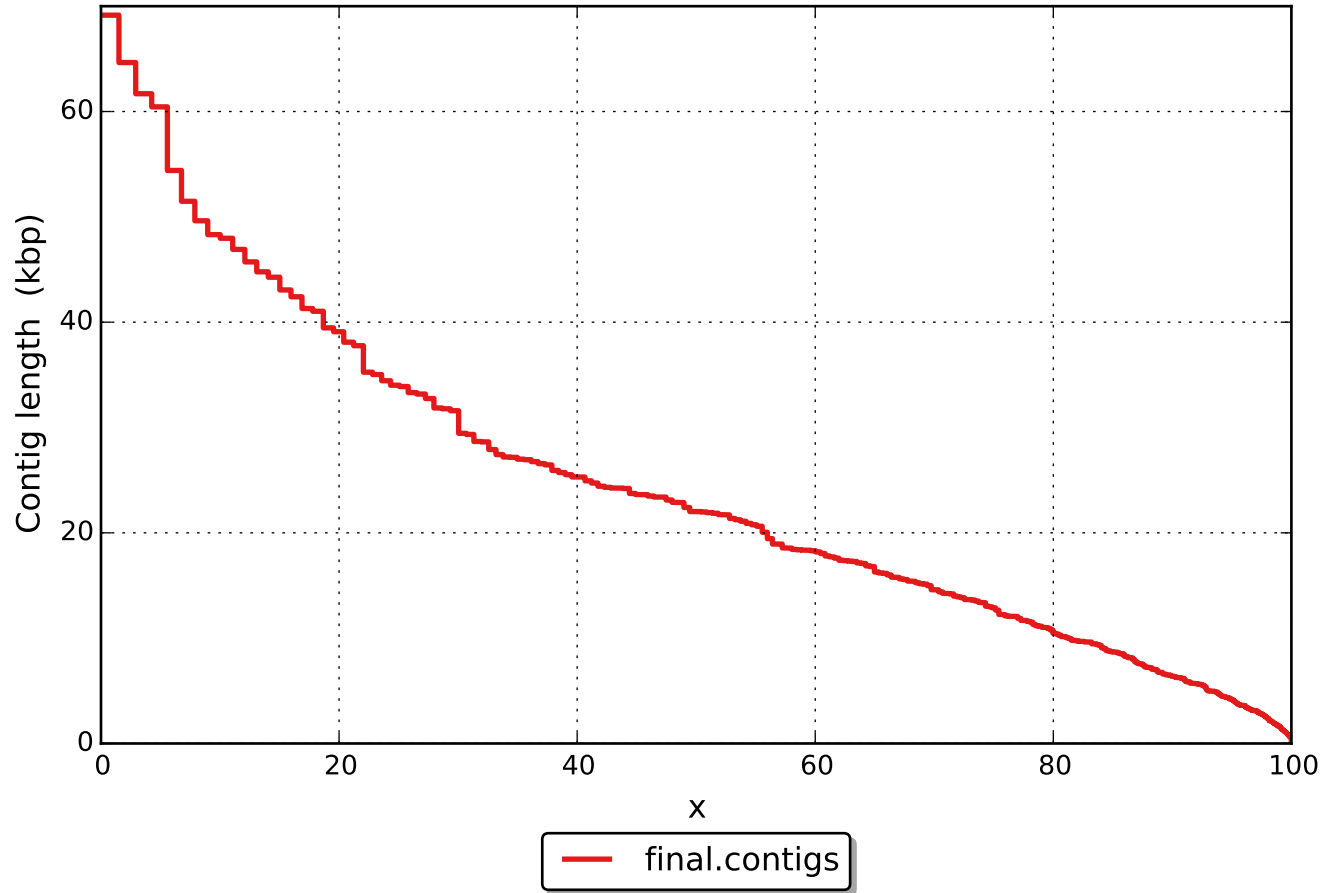




Cumulative length (aligned contigs)



NAx



NGAx

