

## Report

	final.contigs
# contigs (>= 0 bp)	432
# contigs (>= 1000 bp)	84
# contigs (>= 5000 bp)	60
# contigs (>= 10000 bp)	56
# contigs (>= 25000 bp)	45
# contigs (>= 50000 bp)	29
Total length (>= 0 bp)	4708519
Total length (>= 1000 bp)	4568777
Total length (>= 5000 bp)	4512347
Total length (>= 10000 bp)	4481962
Total length (>= 25000 bp)	4320765
Total length (>= 50000 bp)	3749929
# contigs	134
Largest contig	327235
Total length	4599731
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	132823
NG50	125703
N75	64856
NG75	64066
L50	12
LG50	13
L75	24
LG75	25
# misassemblies	4
# misassembled contigs	4
Misassembled contigs length	4800
# local misassemblies	10
# unaligned contigs	1 + 4 part
Unaligned length	985
Genome fraction (%)	98.616
Duplication ratio	1.005
# N's per 100 kbp	0.00
# mismatches per 100 kbp	12.08
# indels per 100 kbp	0.13
Largest alignment	327235
NA50	132823
NGA50	125703
NA75	64856
NGA75	64066
LA50	12
LGA50	13
LA75	24
LGA75	25

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	4
# relocations	3
# translocations	0
# inversions	1
# misassembled contigs	4
Misassembled contigs length	4800
# local misassemblies	10
# mismatches	553
# indels	6
# short indels	6
# long indels	0
Indels length	6

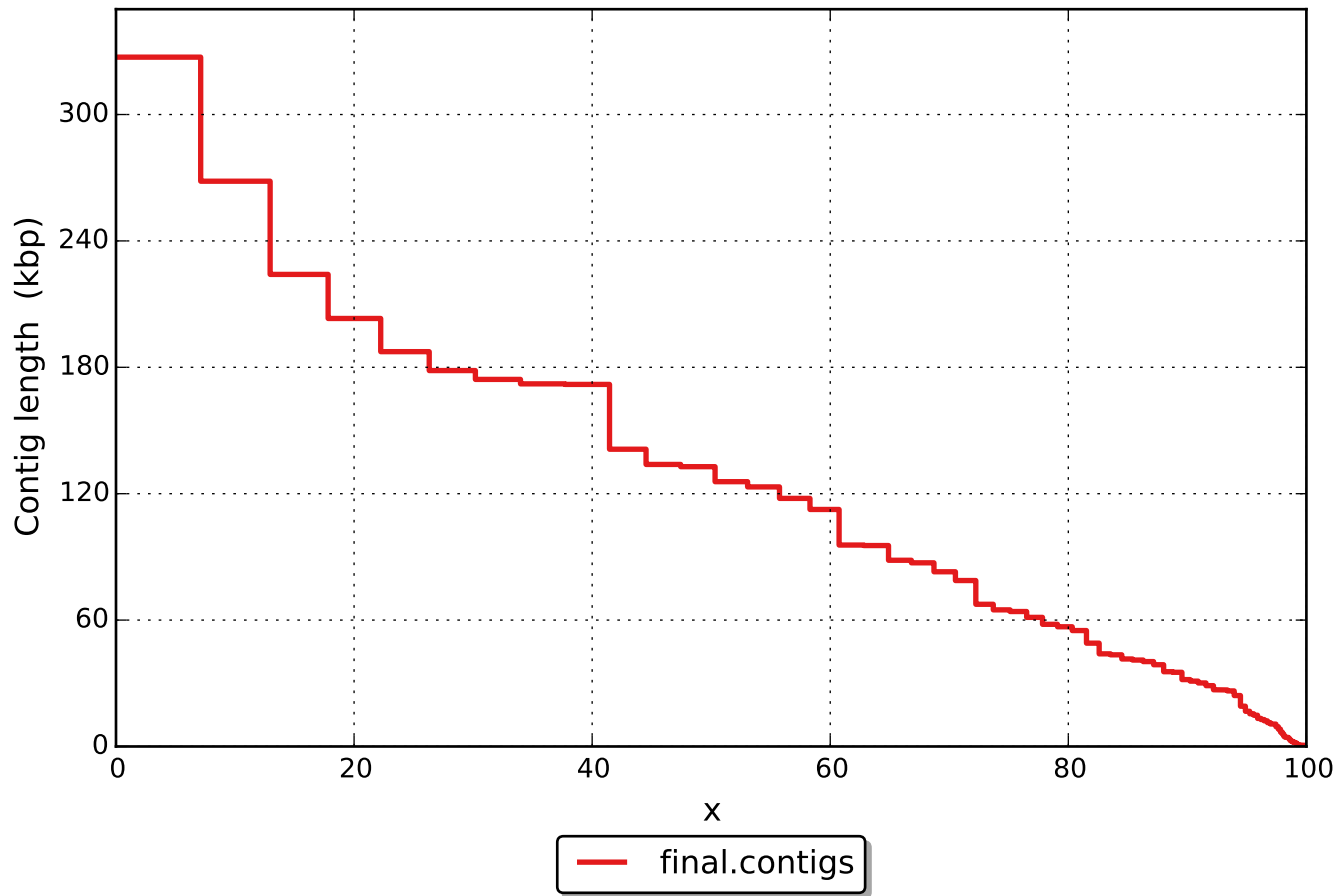
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

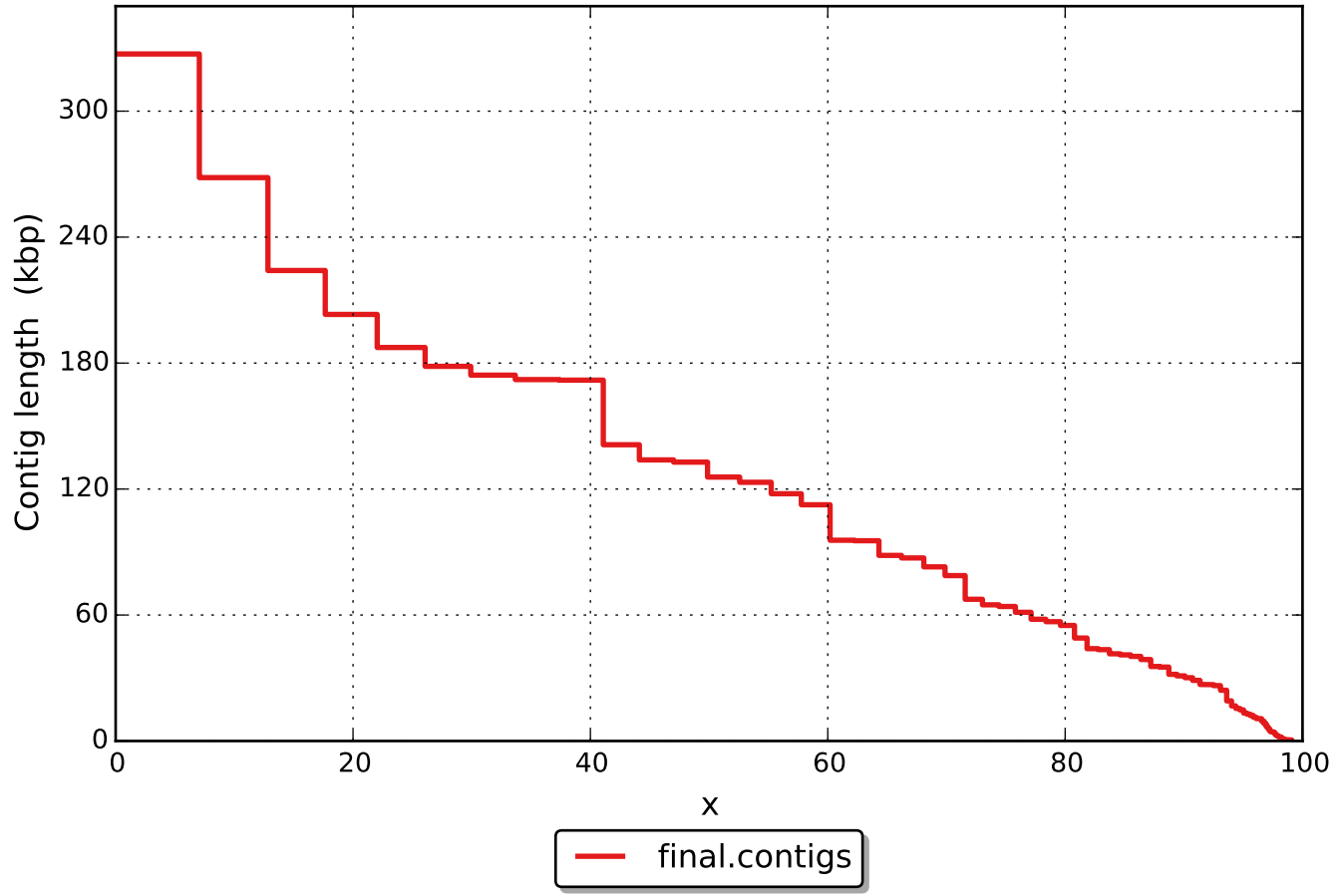
	final.contigs
# fully unaligned contigs	1
Fully unaligned length	501
# partially unaligned contigs	4
# with misassembly	0
# both parts are significant	0
Partially unaligned length	484
# N's	0

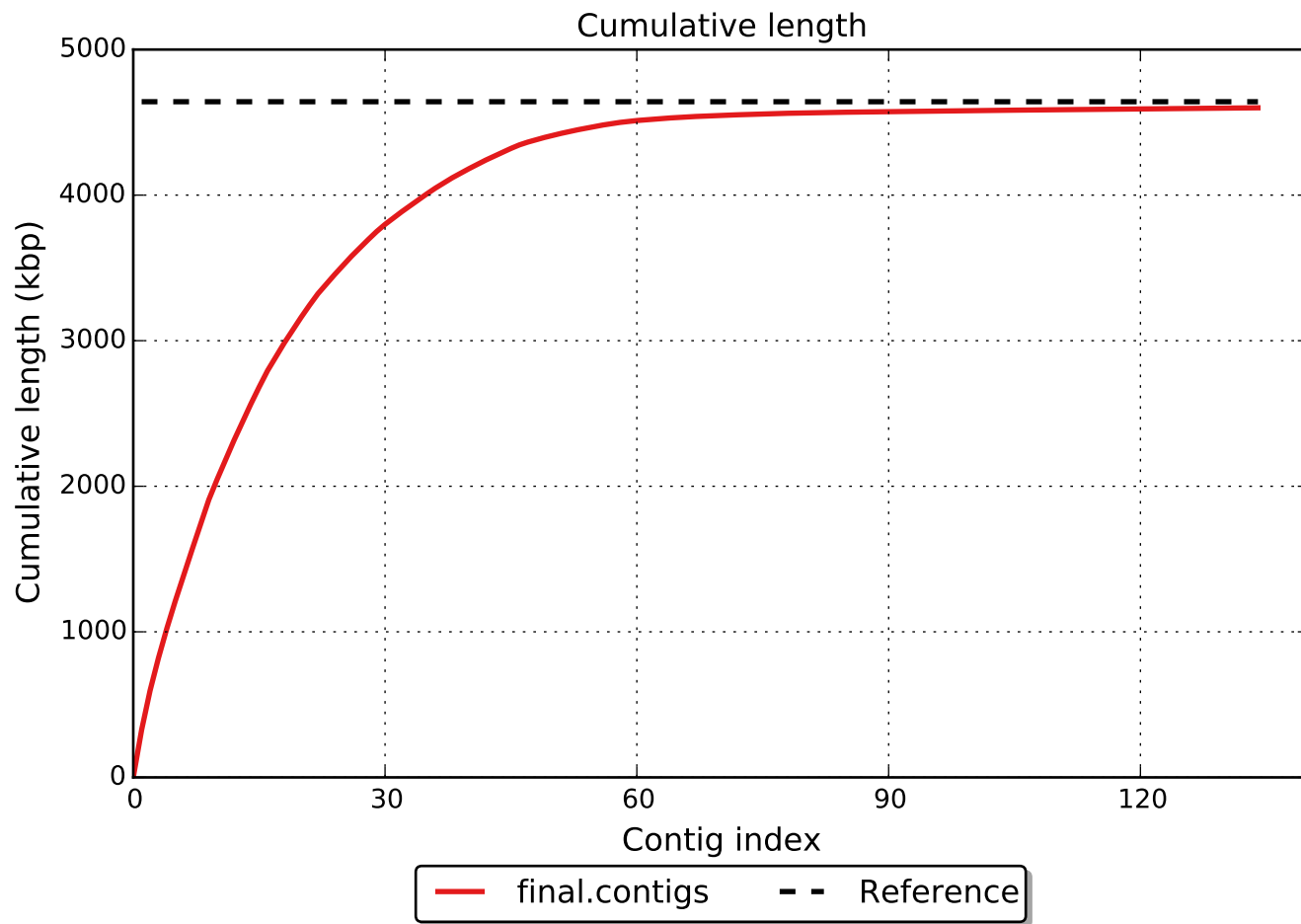
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

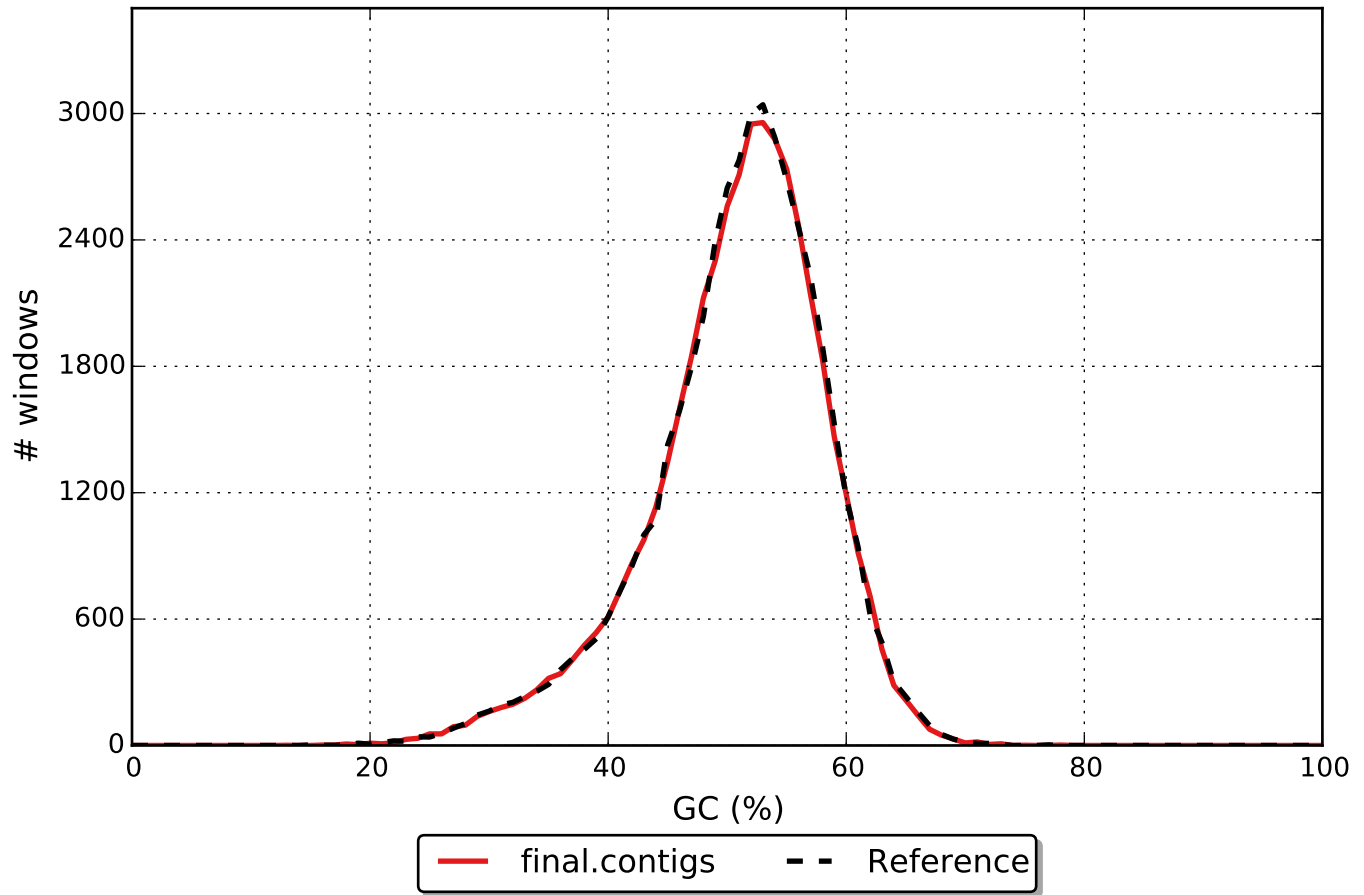


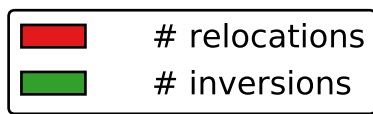
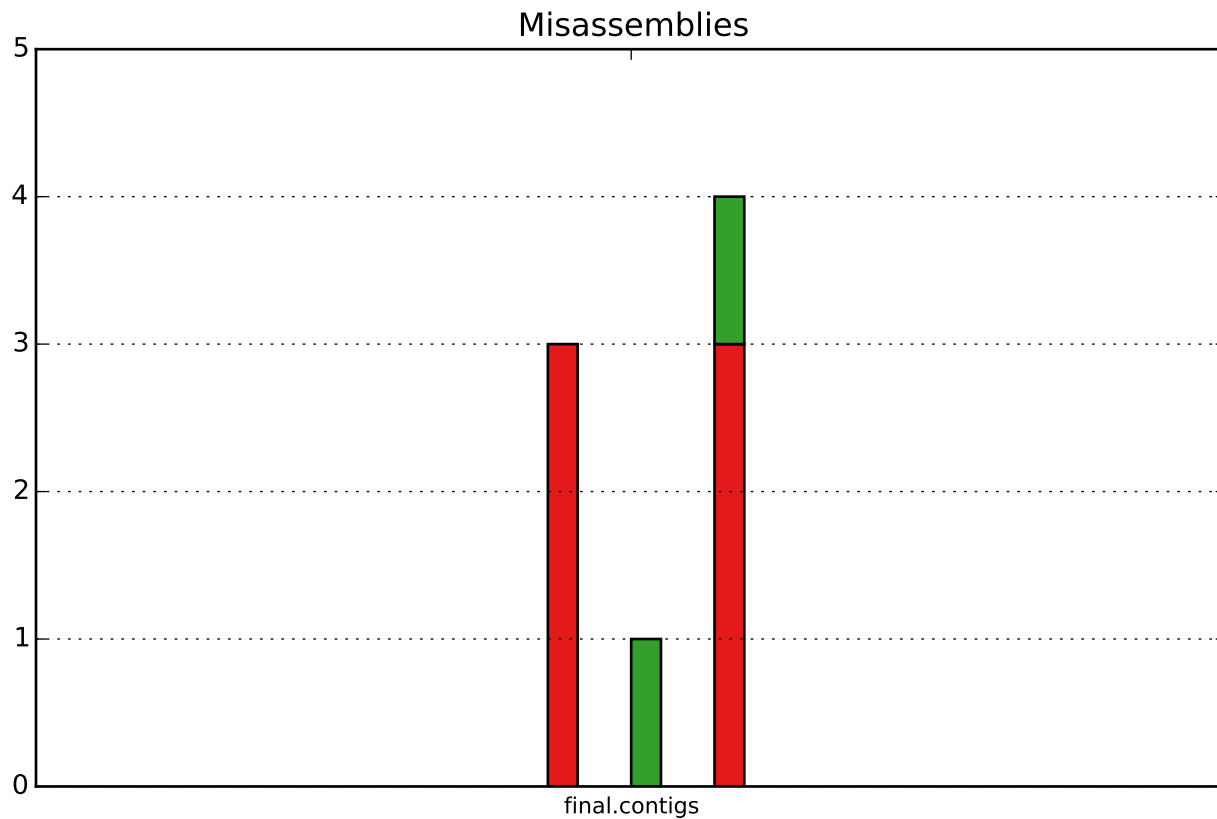
NGx





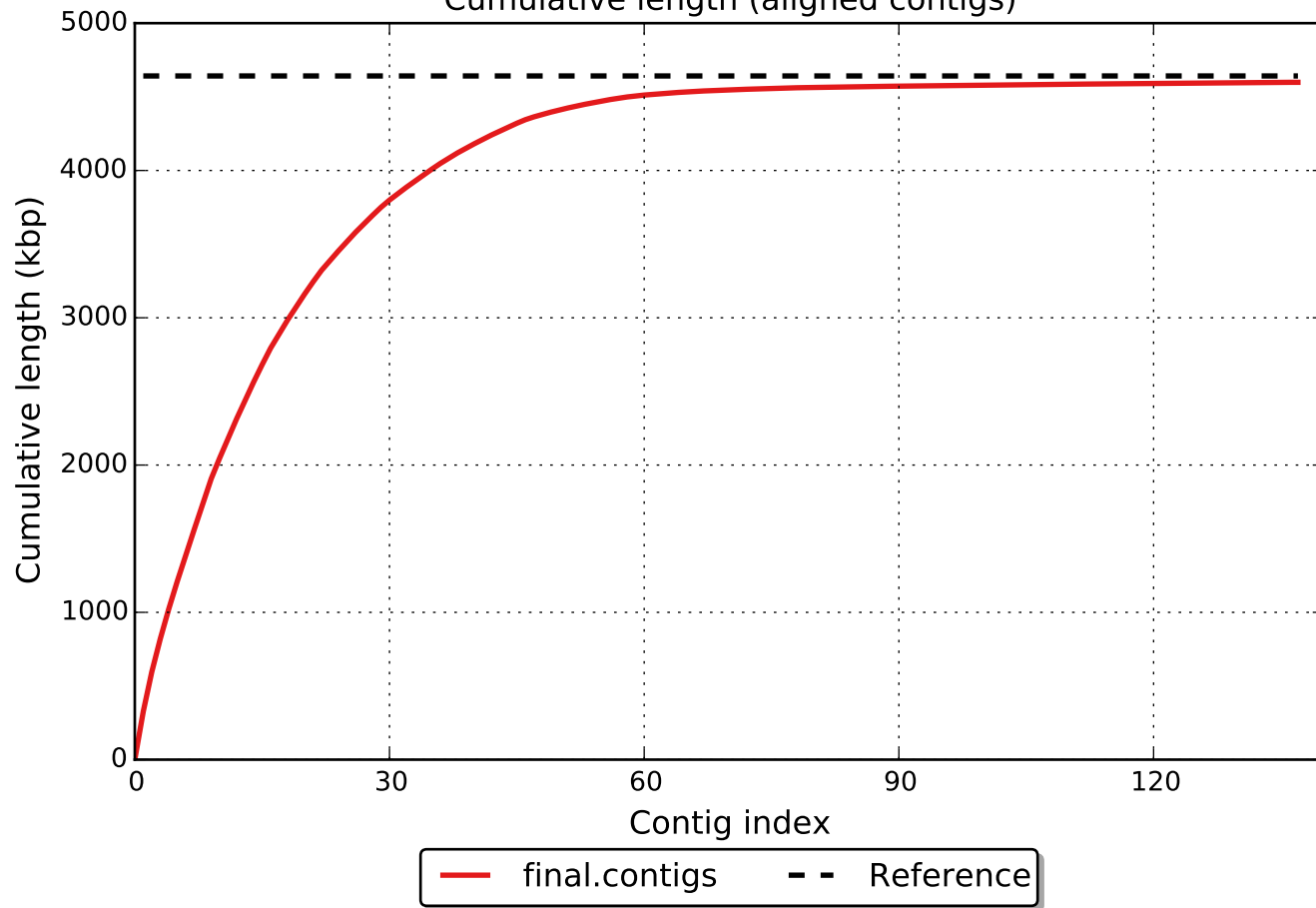
GC content



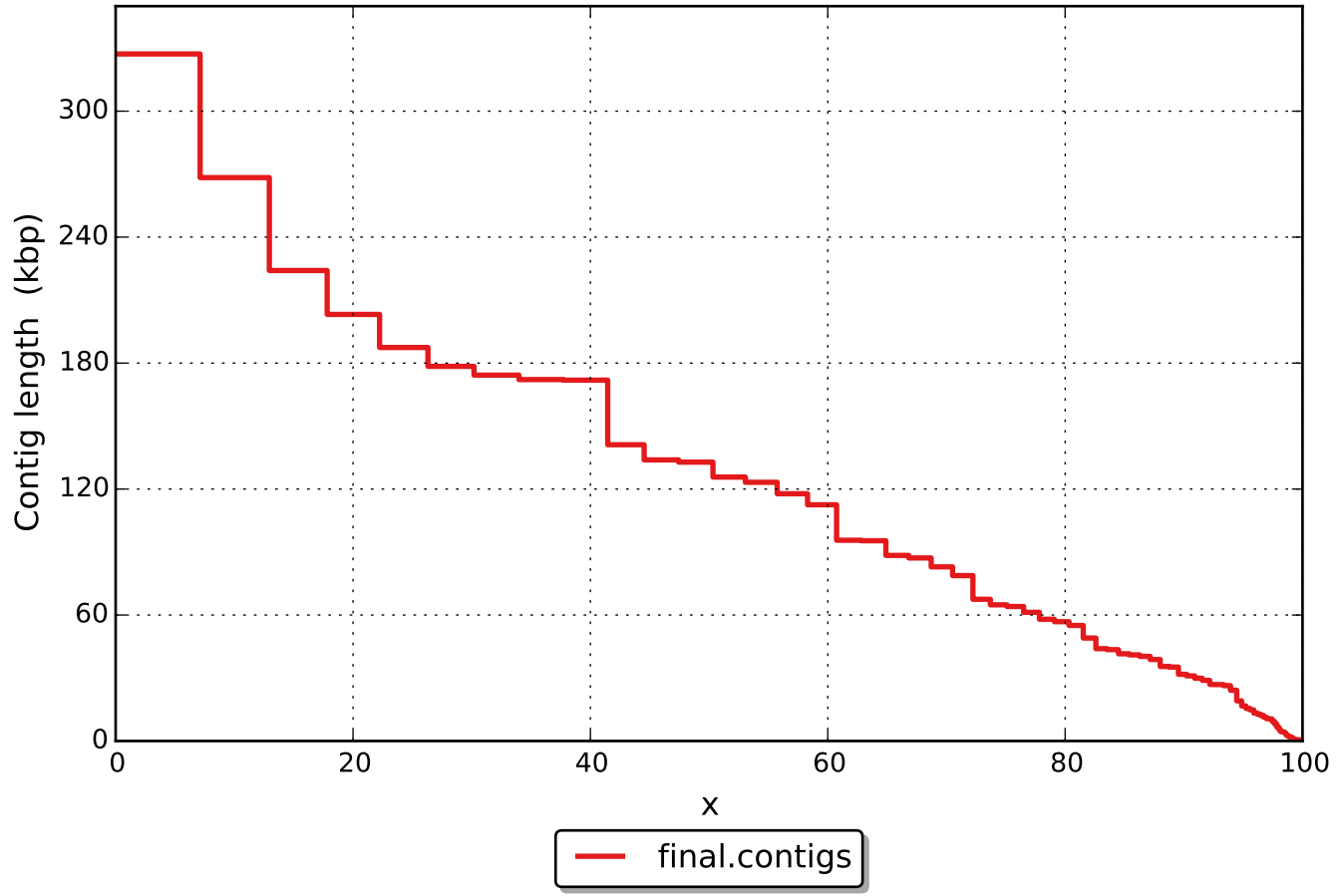




Cumulative length (aligned contigs)



NAx



# NGAx

