

## Report

	final.contigs
# contigs (>= 0 bp)	219
# contigs (>= 1000 bp)	80
# contigs (>= 5000 bp)	62
# contigs (>= 10000 bp)	55
# contigs (>= 25000 bp)	49
# contigs (>= 50000 bp)	29
Total length (>= 0 bp)	4625815
Total length (>= 1000 bp)	4565513
Total length (>= 5000 bp)	4521873
Total length (>= 10000 bp)	4469704
Total length (>= 25000 bp)	4365334
Total length (>= 50000 bp)	3654957
# contigs	112
Largest contig	327235
Total length	4587121
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	125735
NG50	125735
N75	64128
NG75	64128
L50	13
LG50	13
L75	26
LG75	26
# misassemblies	3
# misassembled contigs	3
Misassembled contigs length	143701
# local misassemblies	4
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.565
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	7.10
# indels per 100 kbp	0.26
Largest alignment	327235
NA50	125735
NGA50	125735
NA75	63984
NGA75	58140
LA50	13
LGA50	13
LA75	26
LGA75	27

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	3
# relocations	3
# translocations	0
# inversions	0
# misassembled contigs	3
Misassembled contigs length	143701
# local misassemblies	4
# mismatches	325
# indels	12
# short indels	7
# long indels	5
Indels length	88

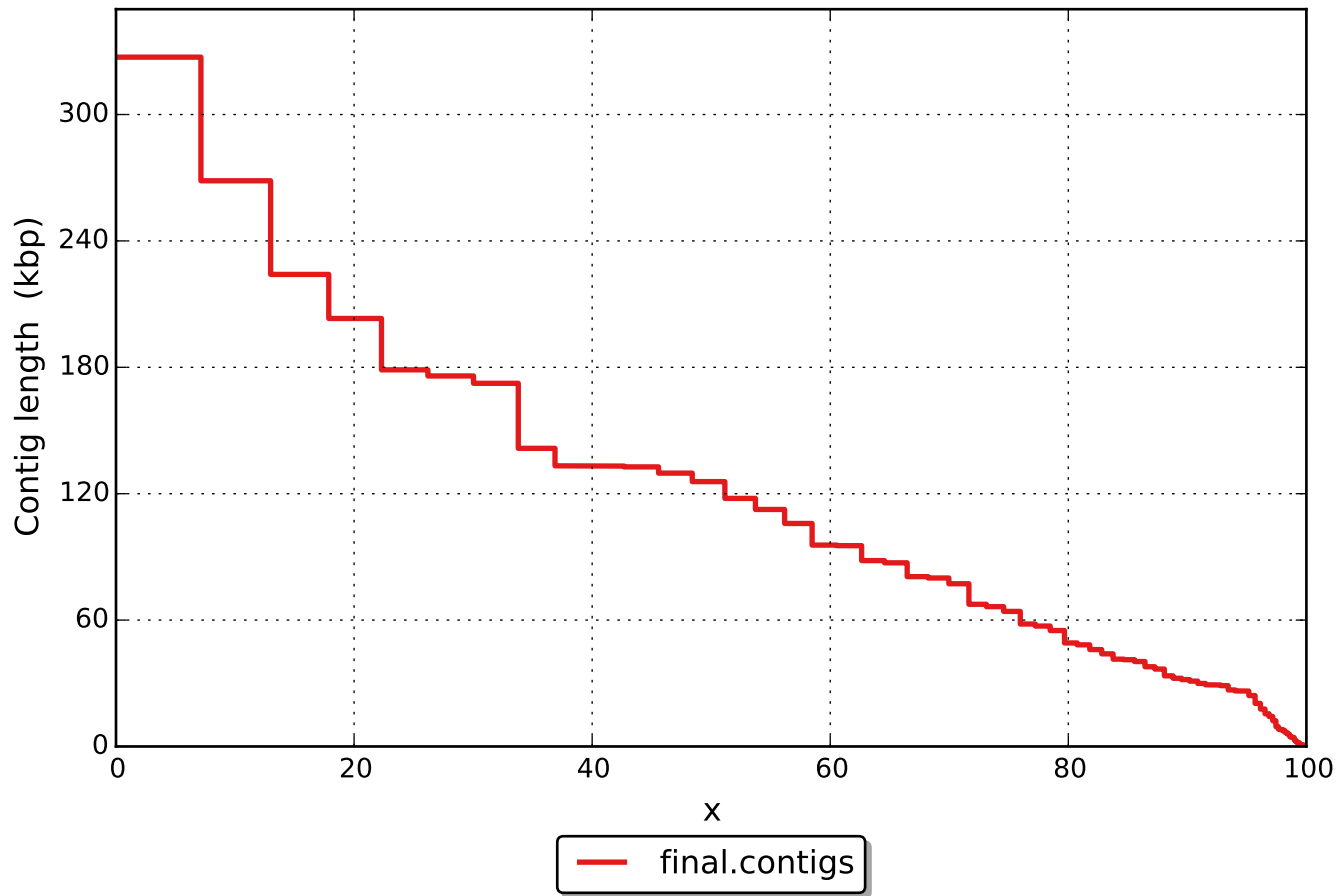
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

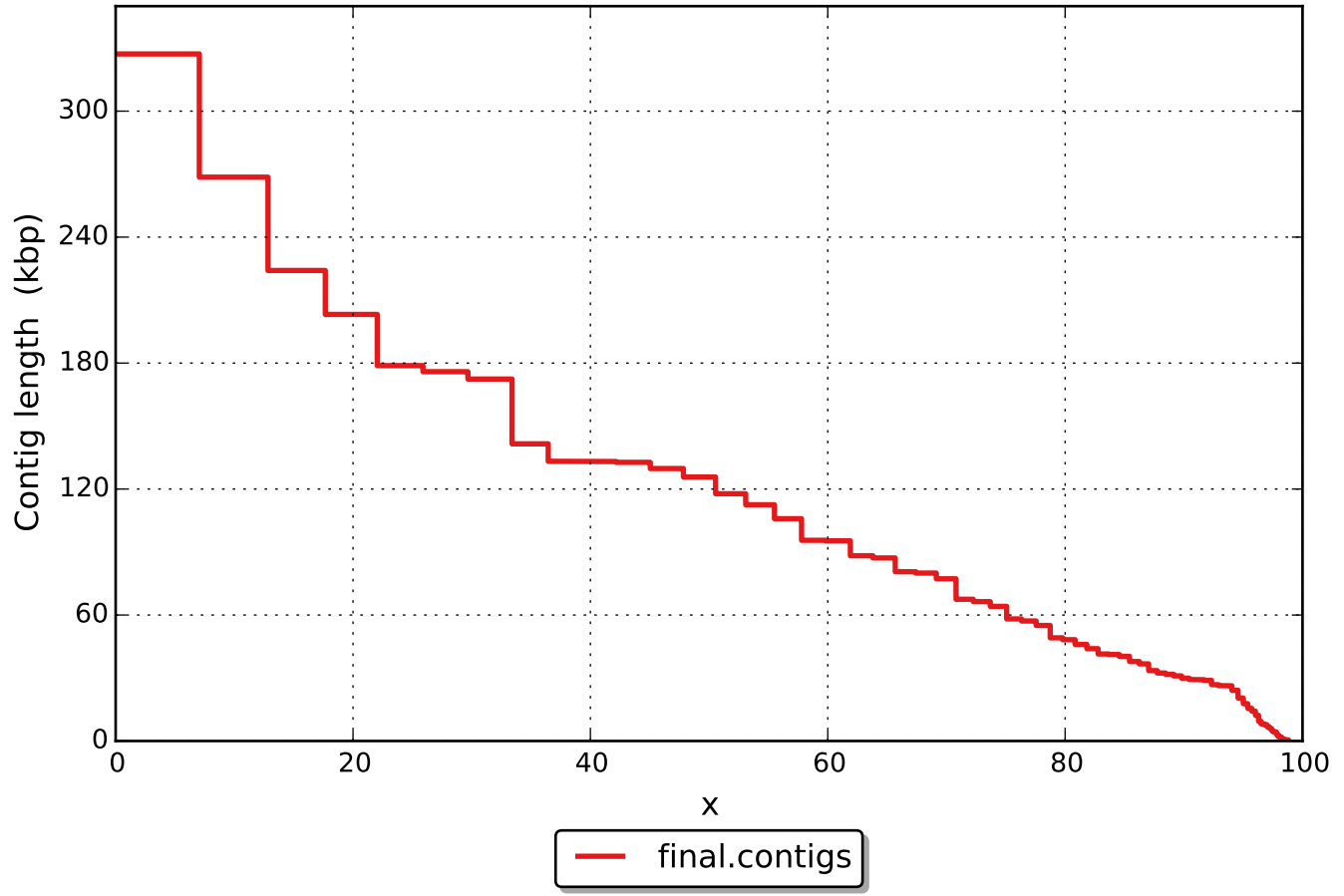
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

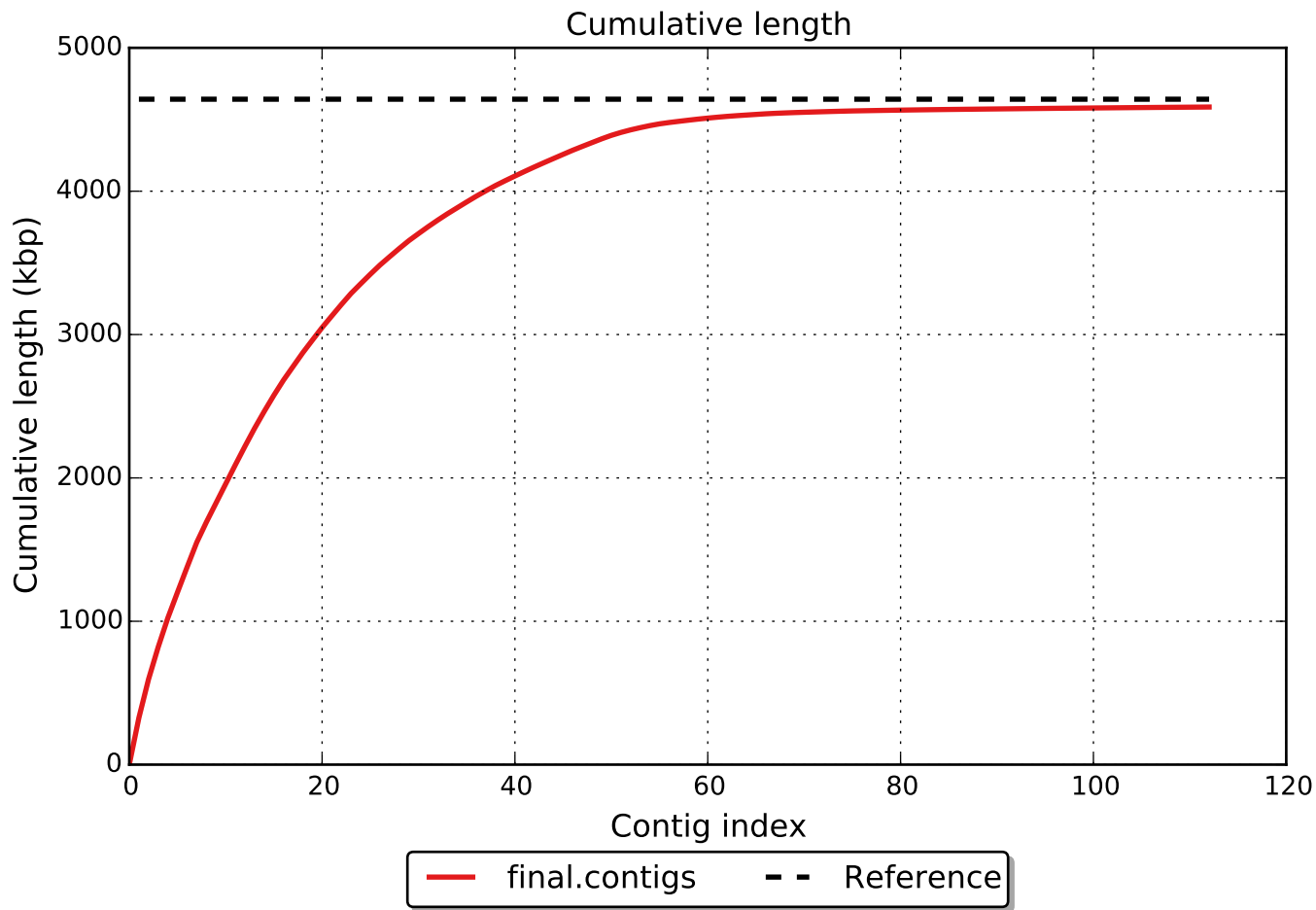
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

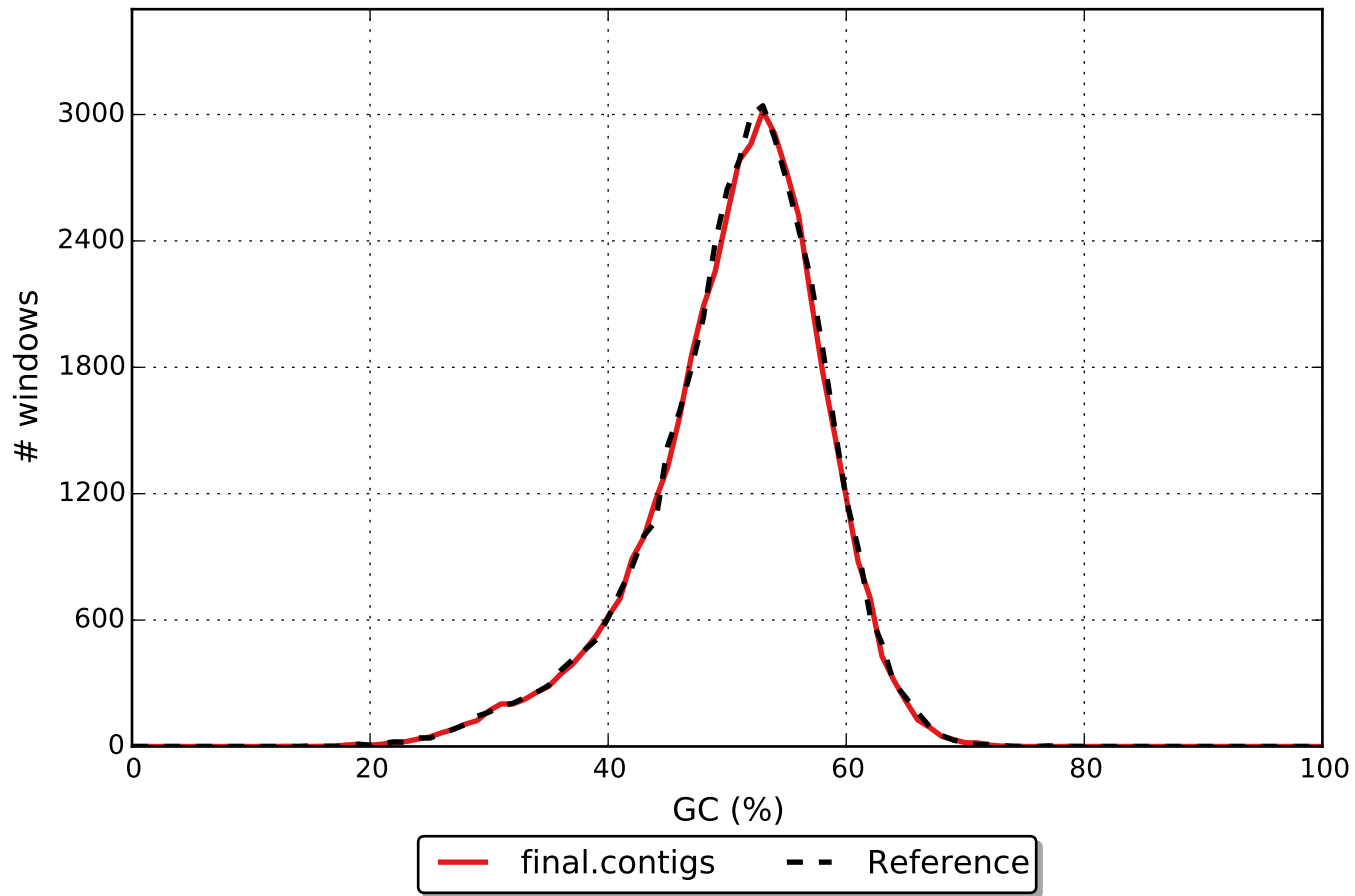


NGx

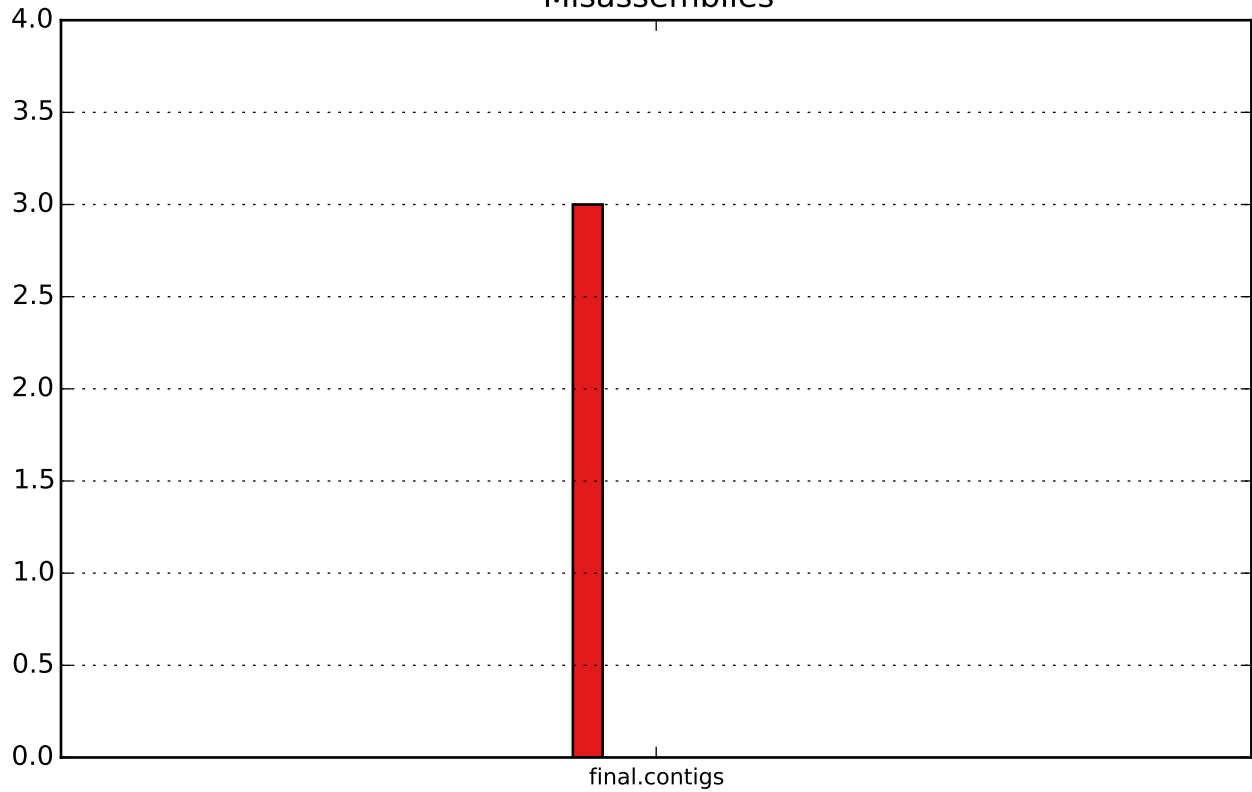




GC content

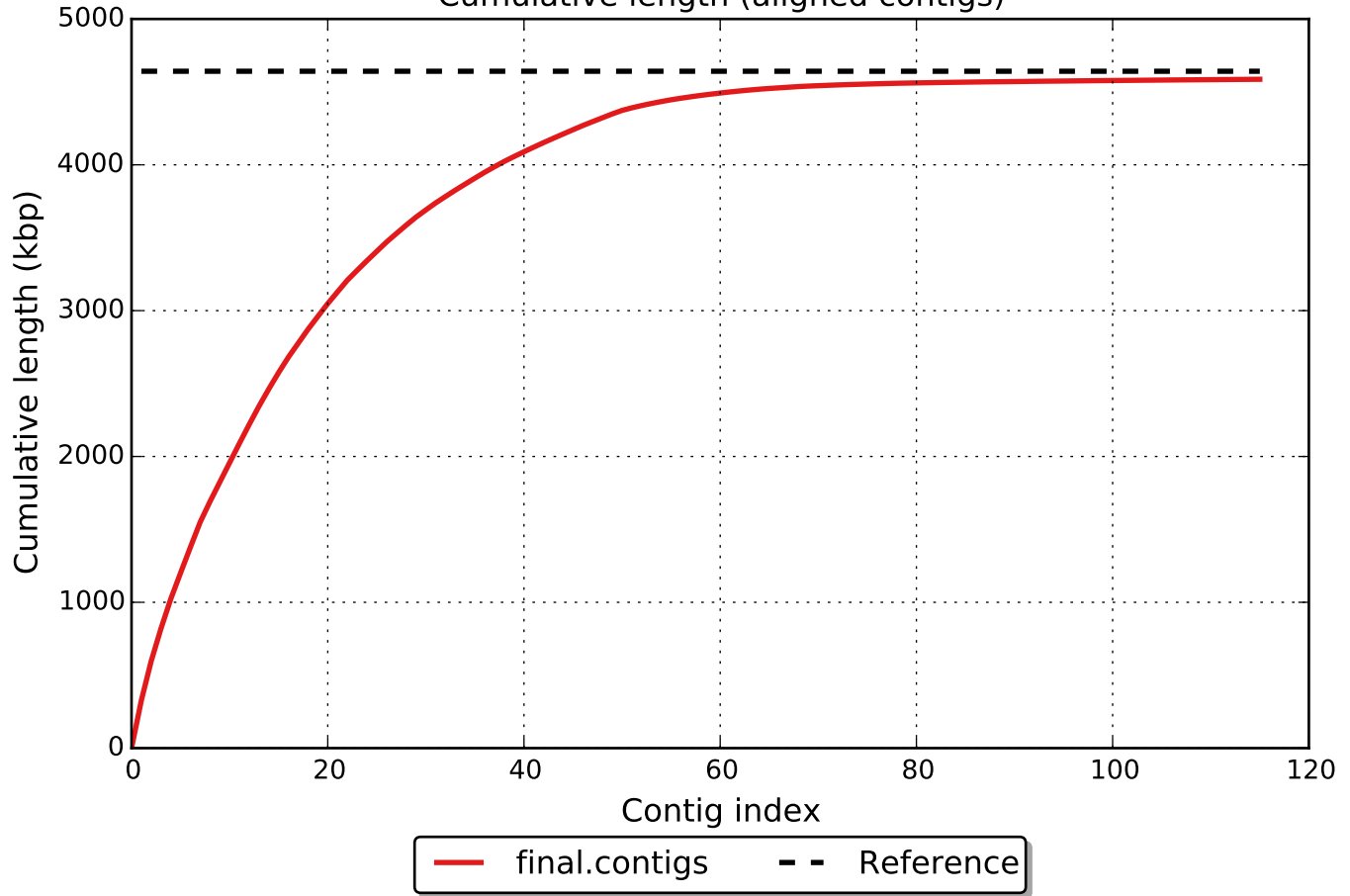


# Misassemblies

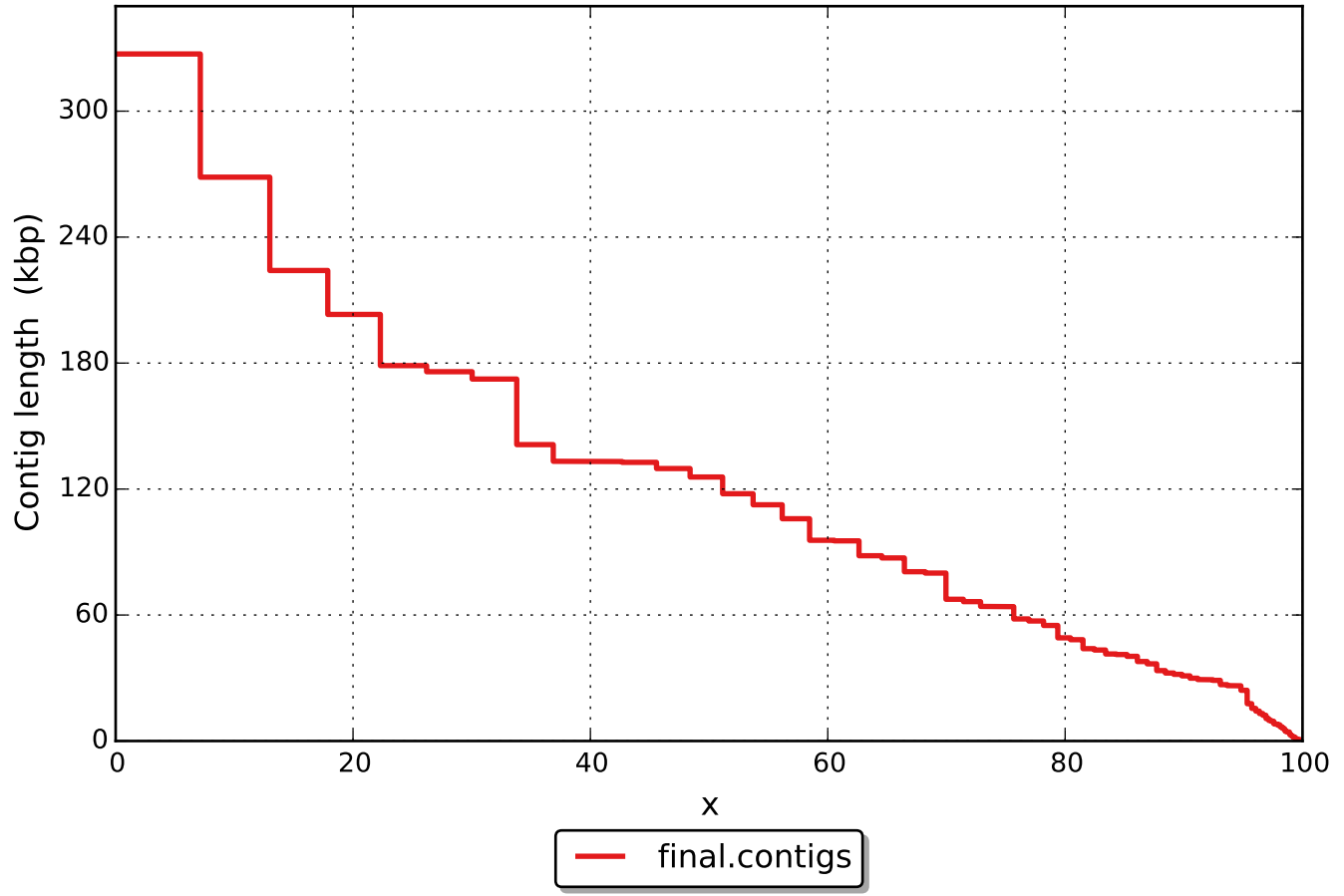




Cumulative length (aligned contigs)



NAx



# NGAx

