

Report

	final.contigs
# contigs (>= 1000 bp)	164
# contigs (>= 5000 bp)	143
# contigs (>= 10000 bp)	118
# contigs (>= 25000 bp)	74
# contigs (>= 50000 bp)	25
Total length (>= 1000 bp)	4653070
Total length (>= 5000 bp)	4581369
Total length (>= 10000 bp)	4390750
Total length (>= 25000 bp)	3601848
Total length (>= 50000 bp)	1841408
# contigs	167
Largest contig	121705
Total length	4655256
Reference length	4641652
GC (℥)	50.79
Reference GC (℥)	50.79
N50	44495
NG50	44495
N75	26893
NG75	26893
L50	36
LG50	36
L75	70
LG75	70
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (℥)	99.989
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	121705
NA50	44495
NGA50	44495
NA75	26893
NGA75	26893
LA50	36
LGA50	36
LA75	70
LGA75	70

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

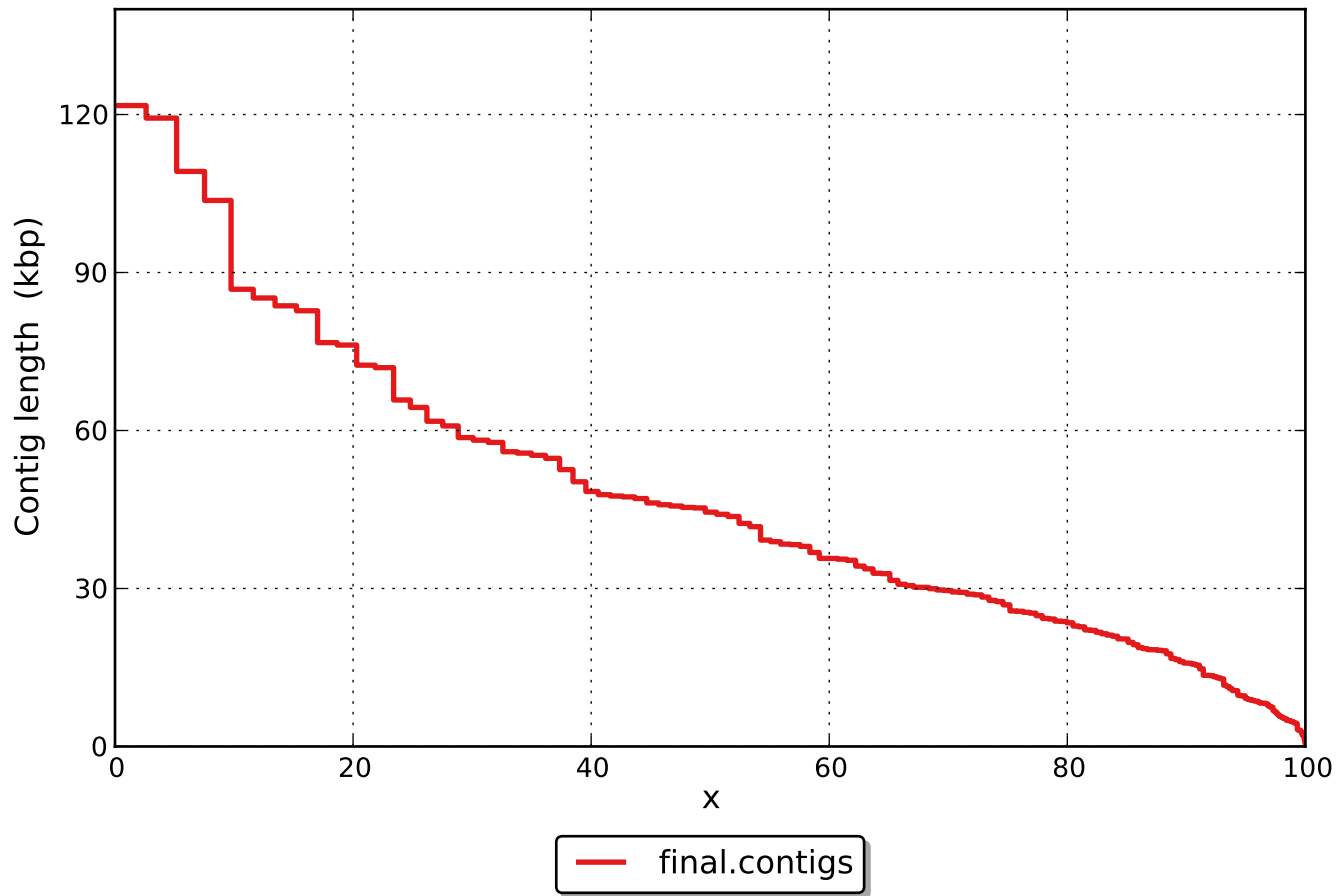
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

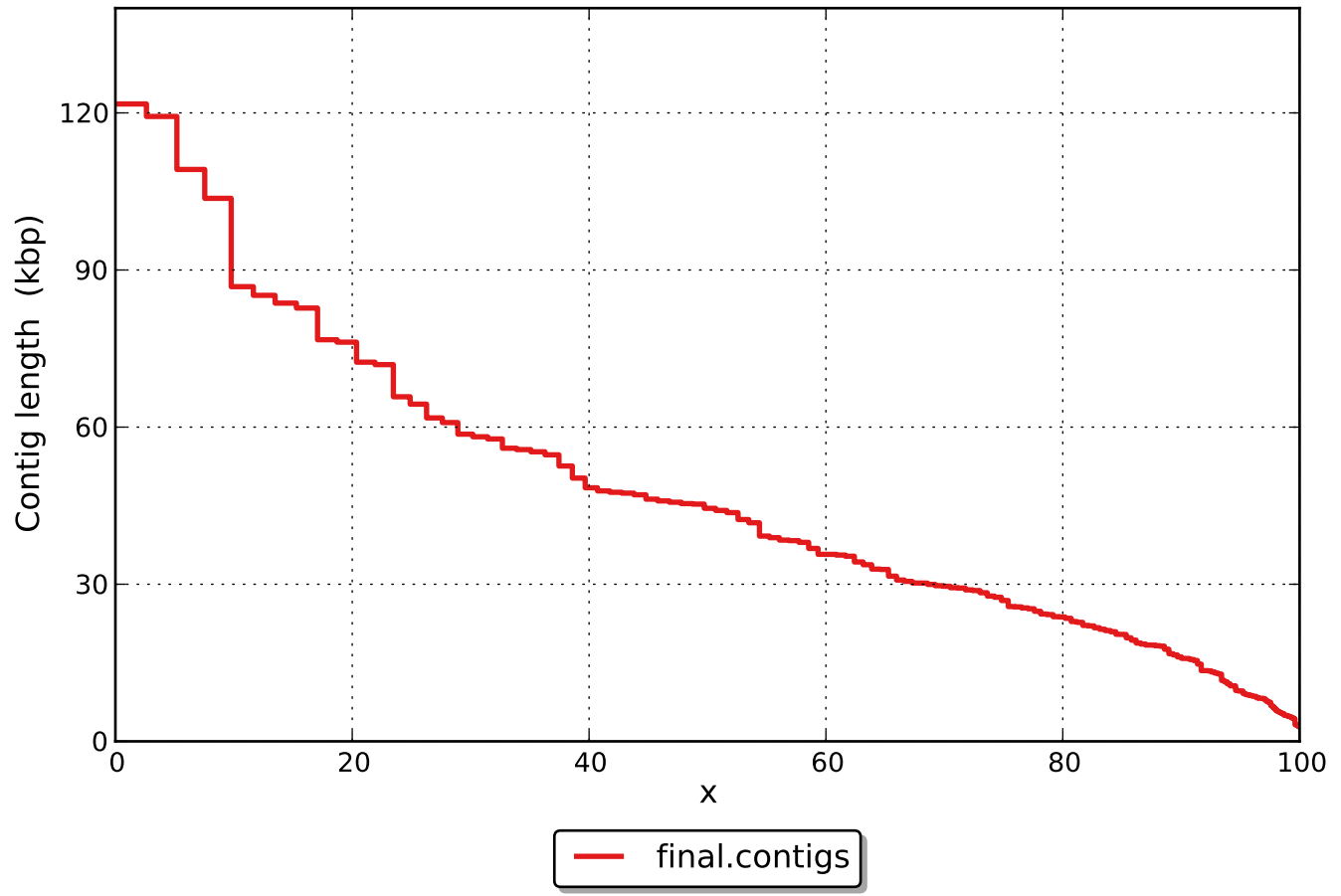
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

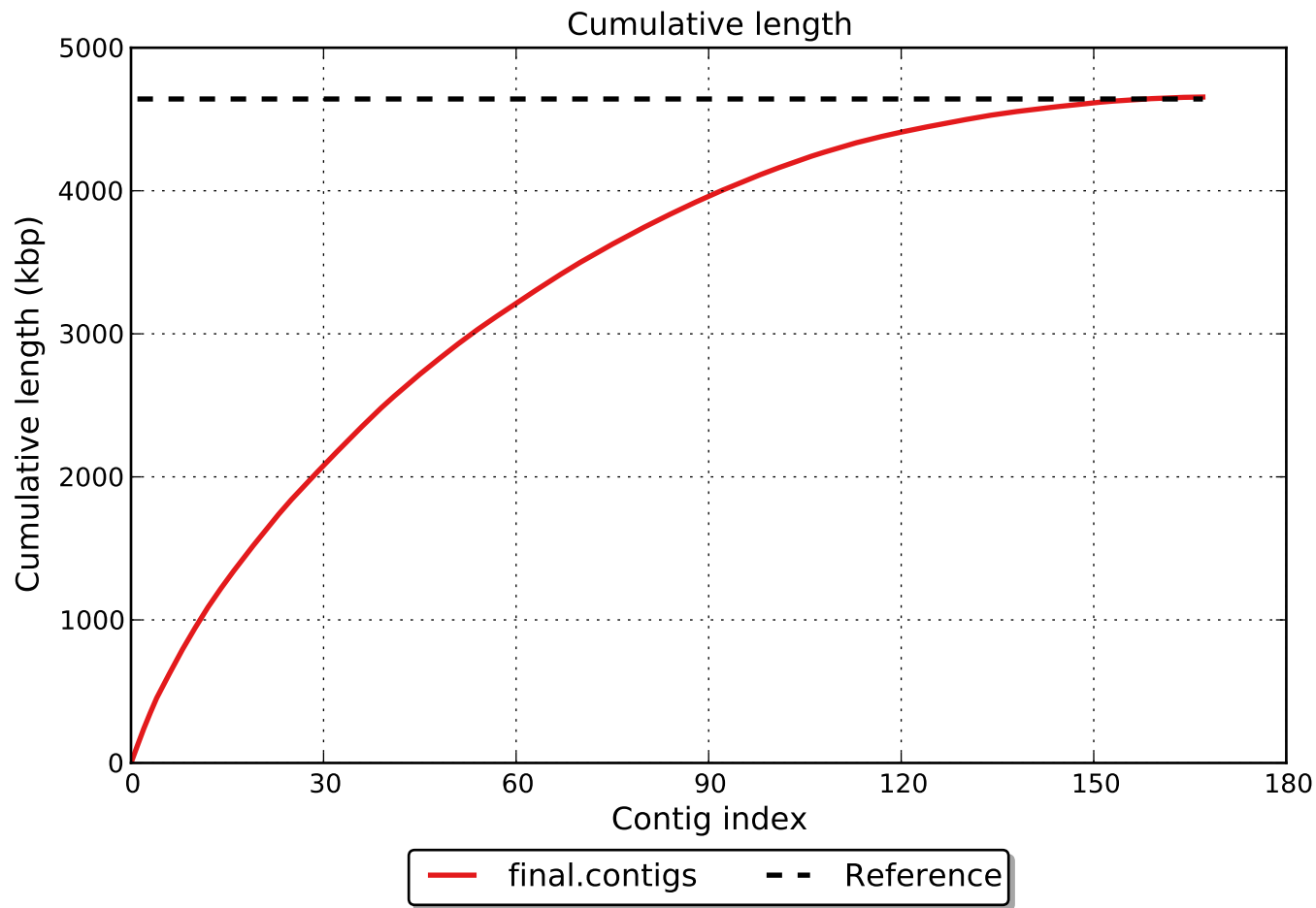
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

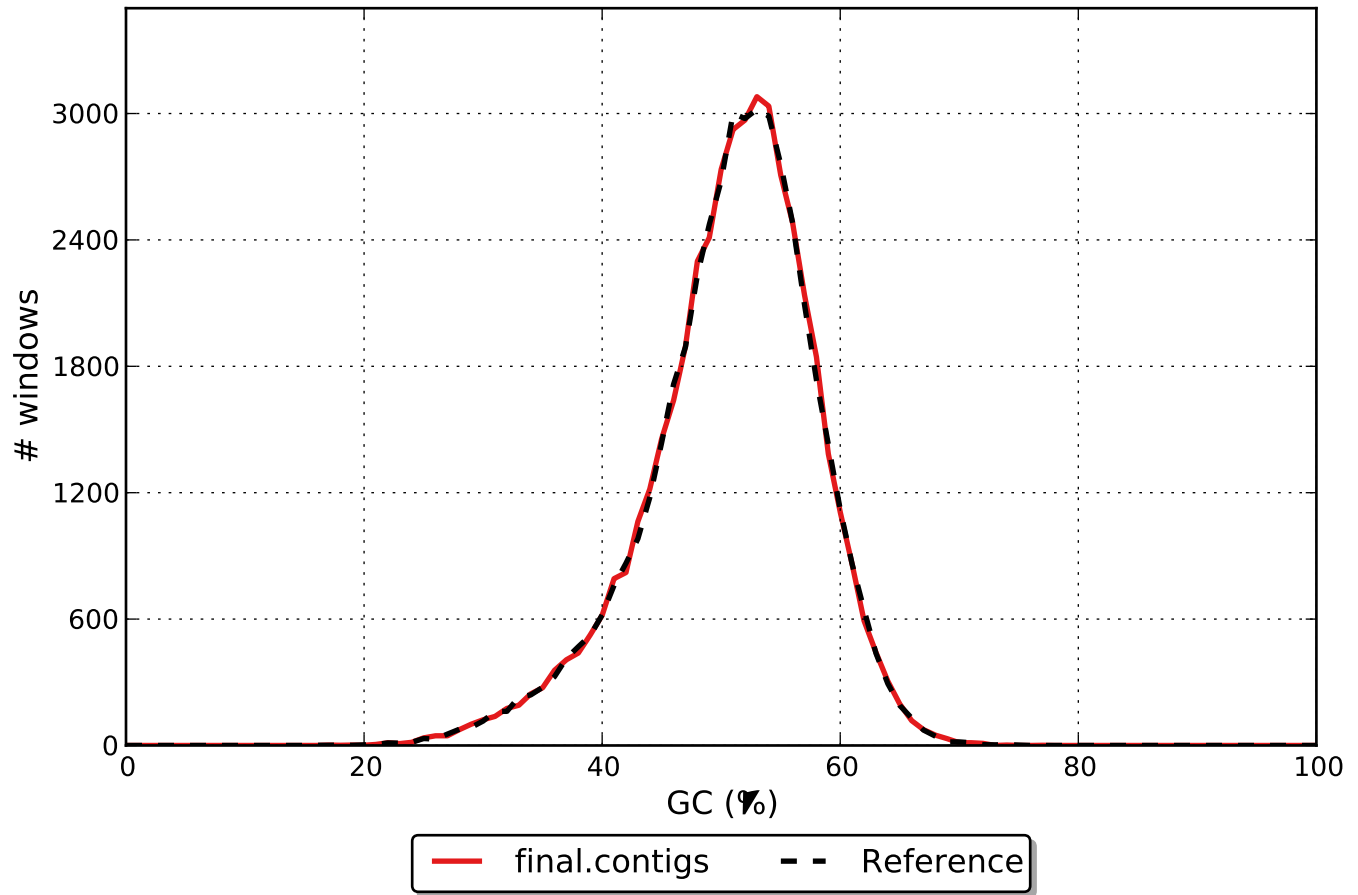


NGx





GC content

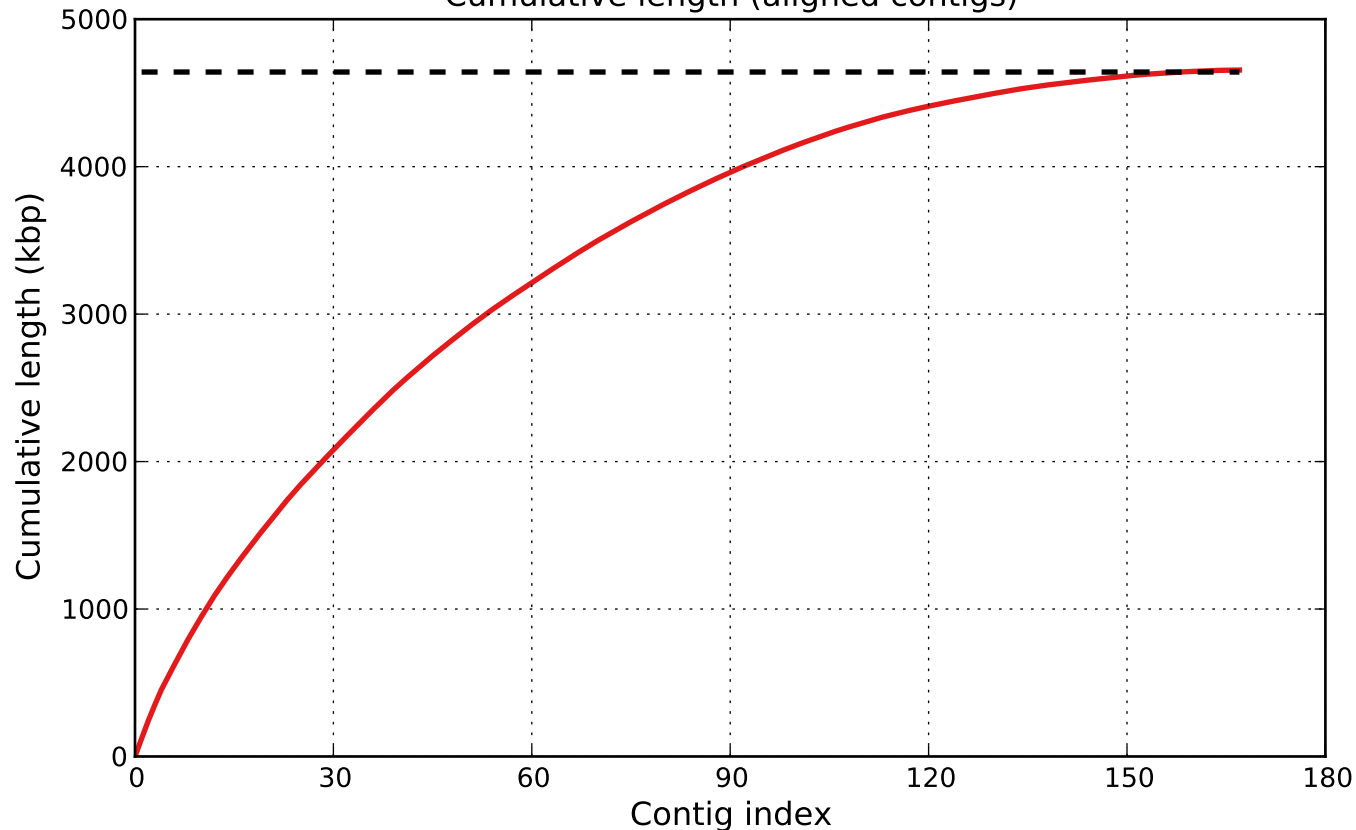


# Misassemblies



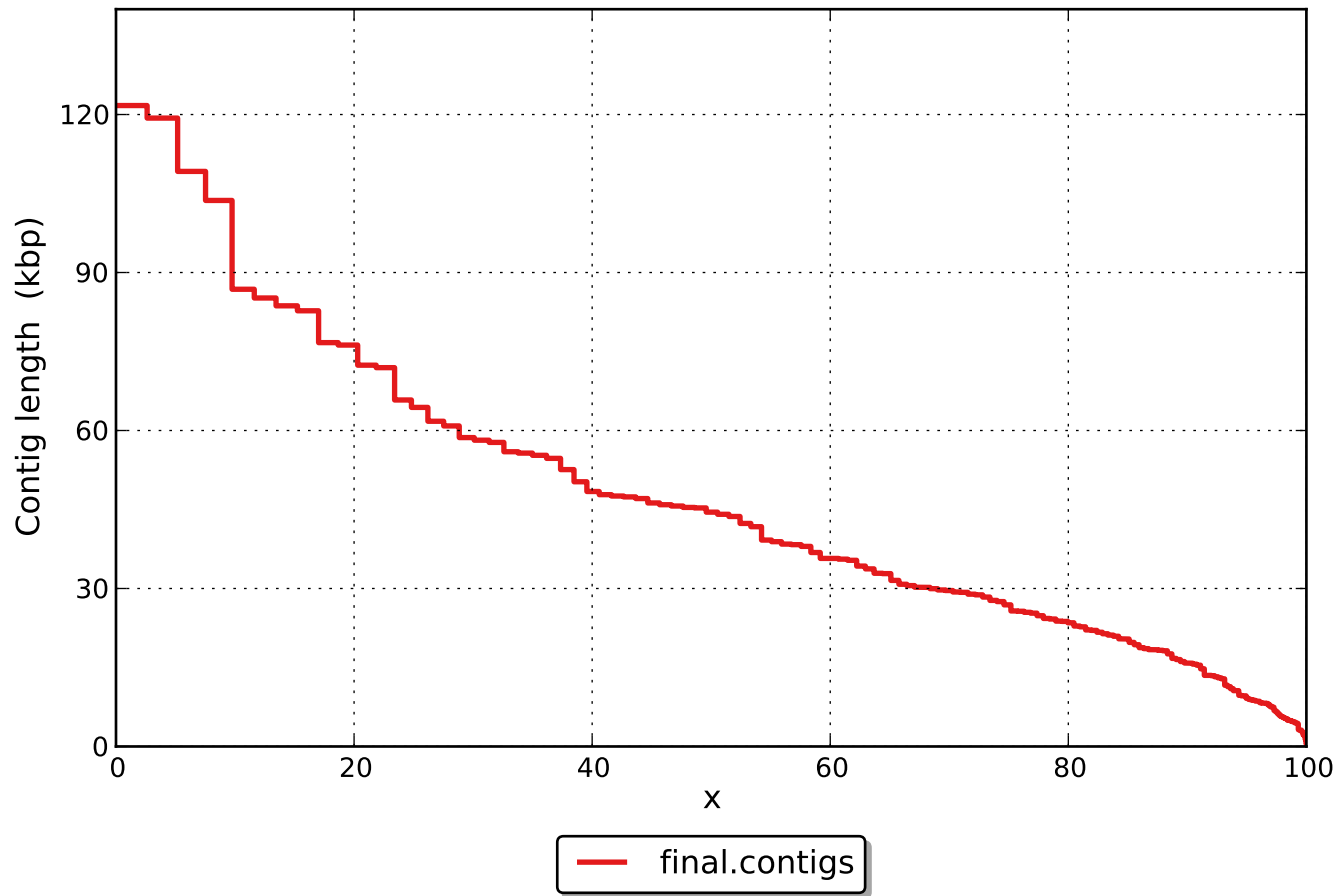


Cumulative length (aligned contigs)



— final.contigs    - - Reference

NAx



# NGAx

