

Report

	final.contigs
# contigs (>= 1000 bp)	371
# contigs (>= 5000 bp)	264
# contigs (>= 10000 bp)	170
# contigs (>= 25000 bp)	59
# contigs (>= 50000 bp)	9
Total length (>= 1000 bp)	4873808
Total length (>= 5000 bp)	4580198
Total length (>= 10000 bp)	3901740
Total length (>= 25000 bp)	2156397
Total length (>= 50000 bp)	515994
# contigs	390
Largest contig	66131
Total length	4888401
Reference length	4857432
GC (℥)	52.23
Reference GC (℥)	52.23
N50	21732
NG50	22022
N75	12104
NG75	12138
L50	72
LG50	71
L75	149
LG75	147
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (℥)	99.971
Duplication ratio	1.007
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	66131
NA50	21732
NGA50	22022
NA75	12104
NGA75	12138
LA50	72
LGA50	71
LA75	149
LGA75	147

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

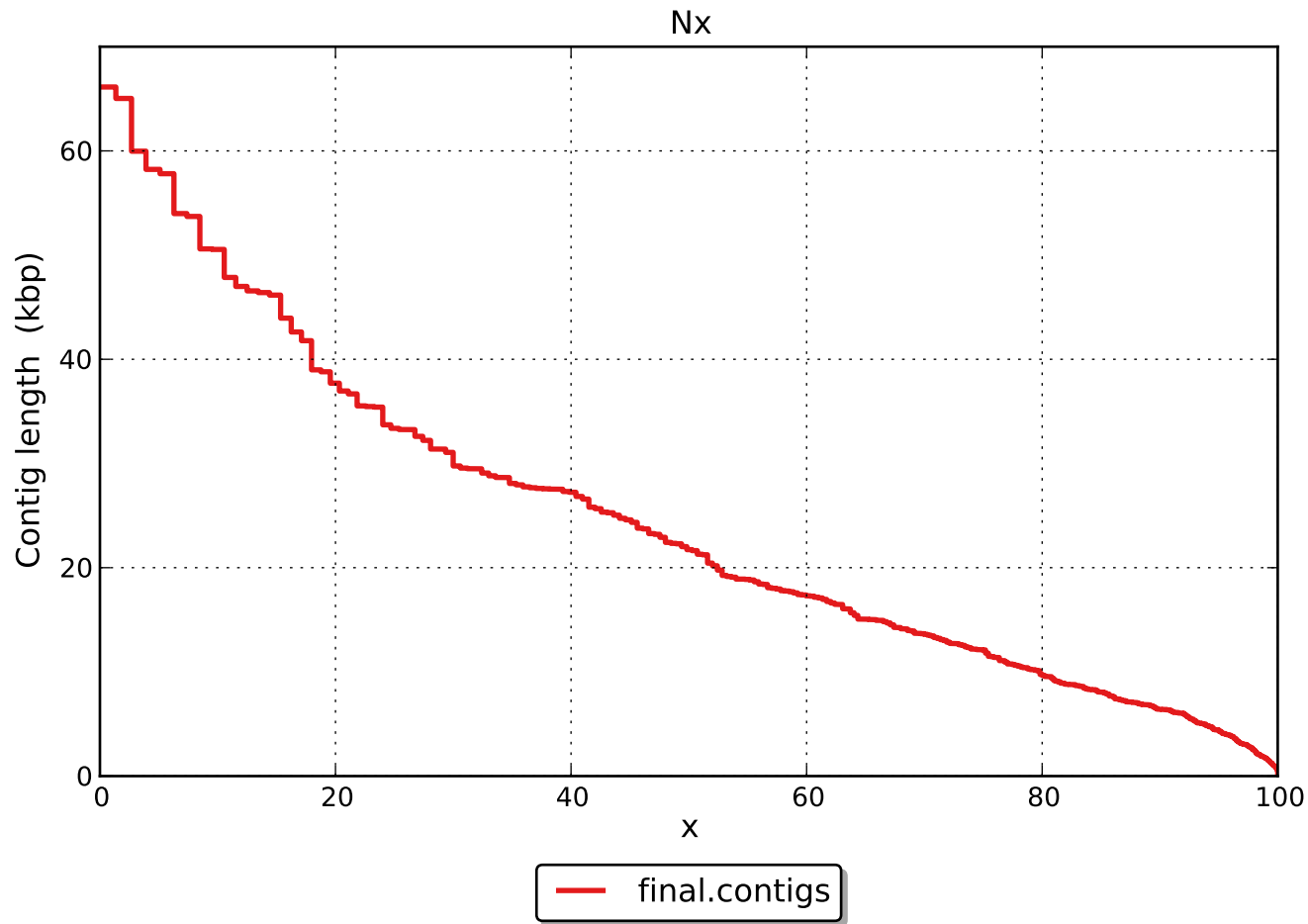
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	0
# indels	0
# short indels	0
# long indels	0
Indels length	0

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).

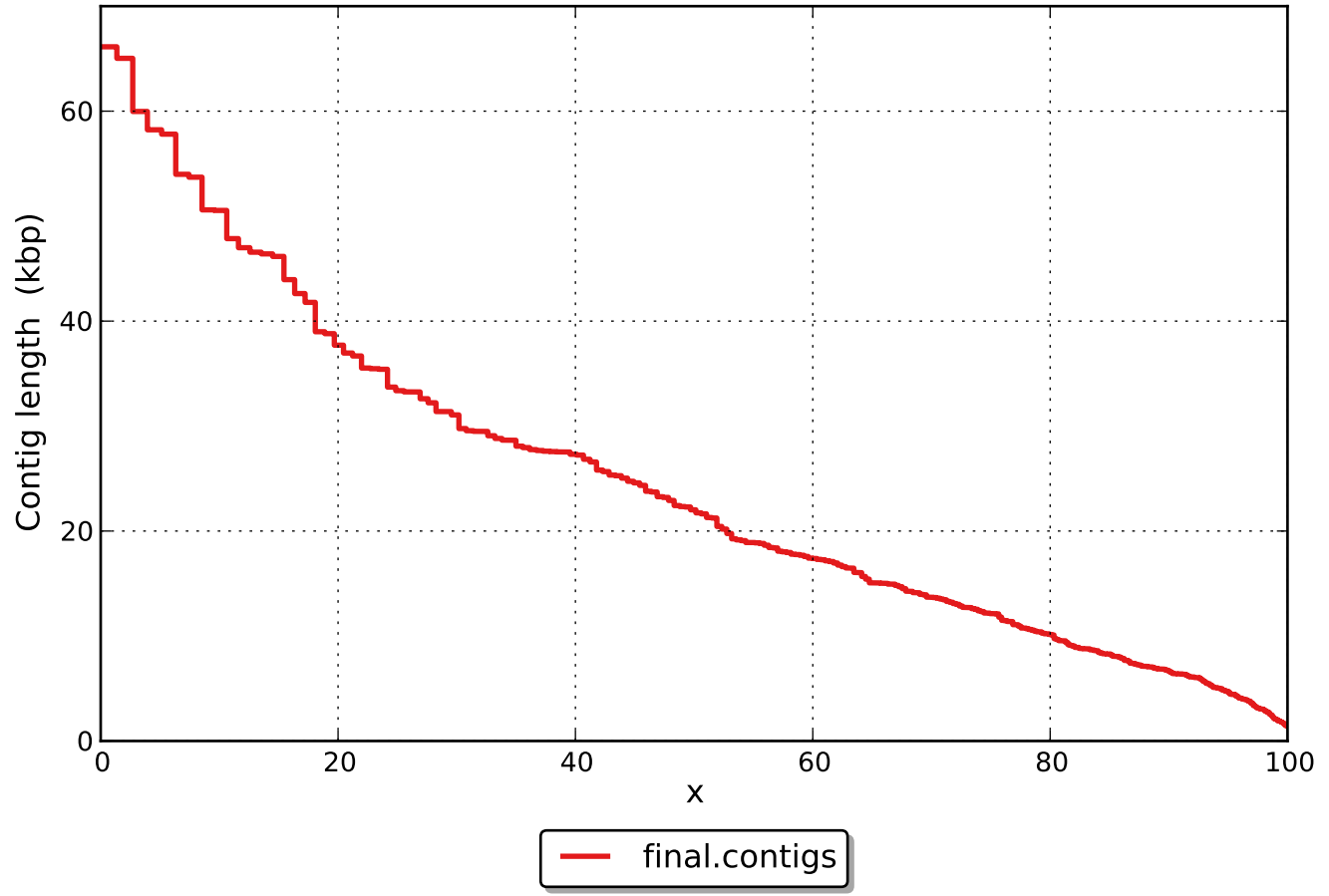
## Unaligned report

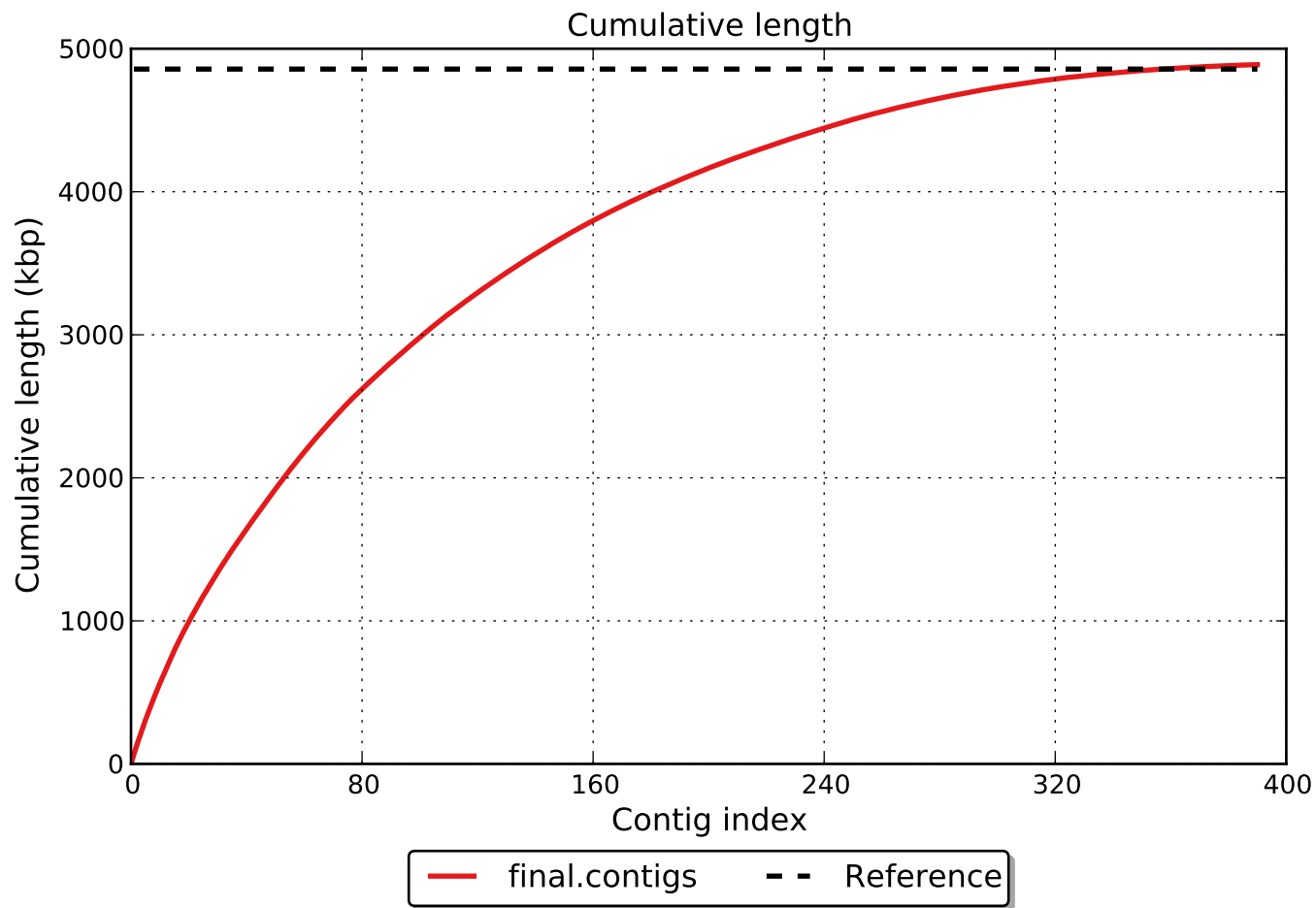
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

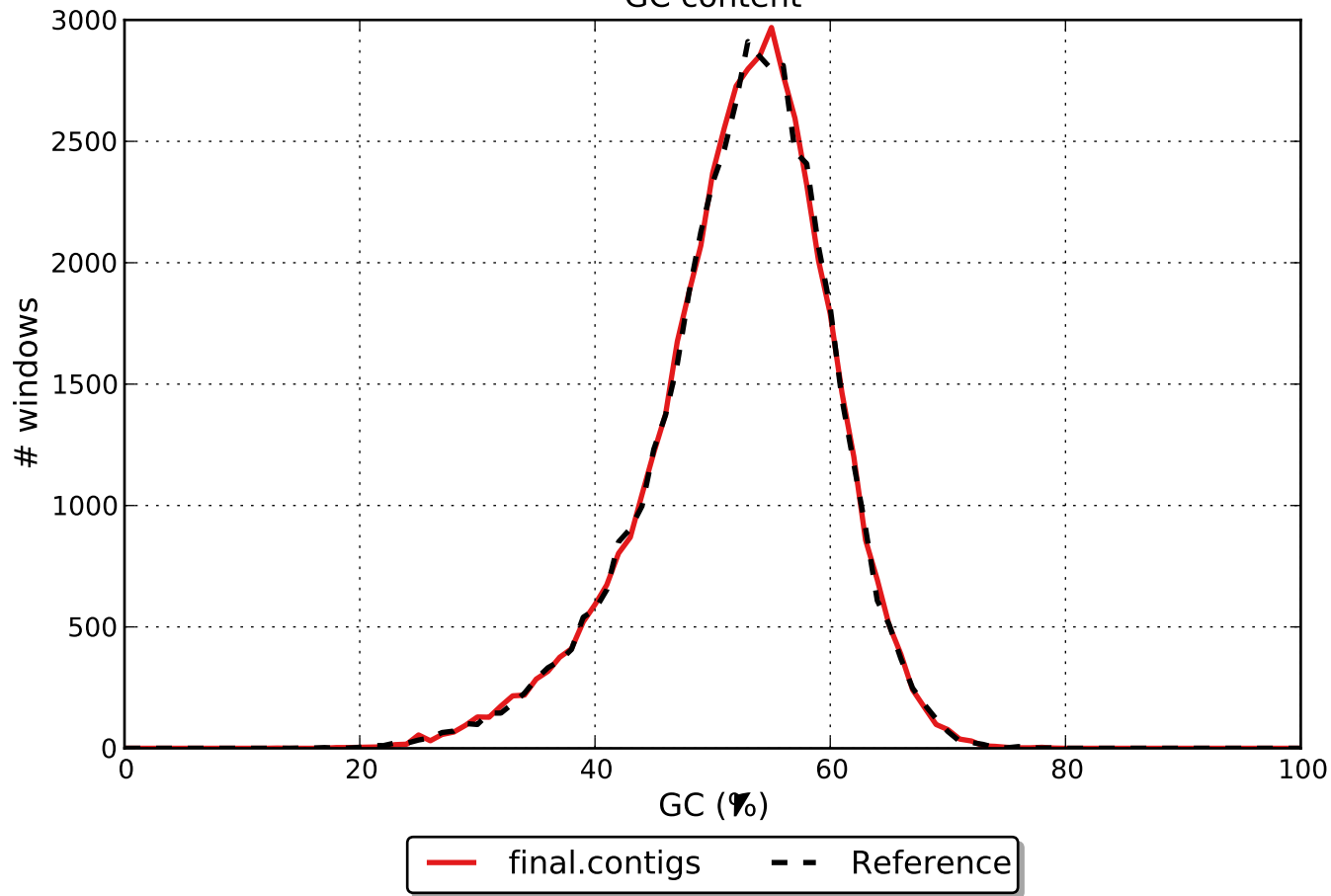


NGx





GC content

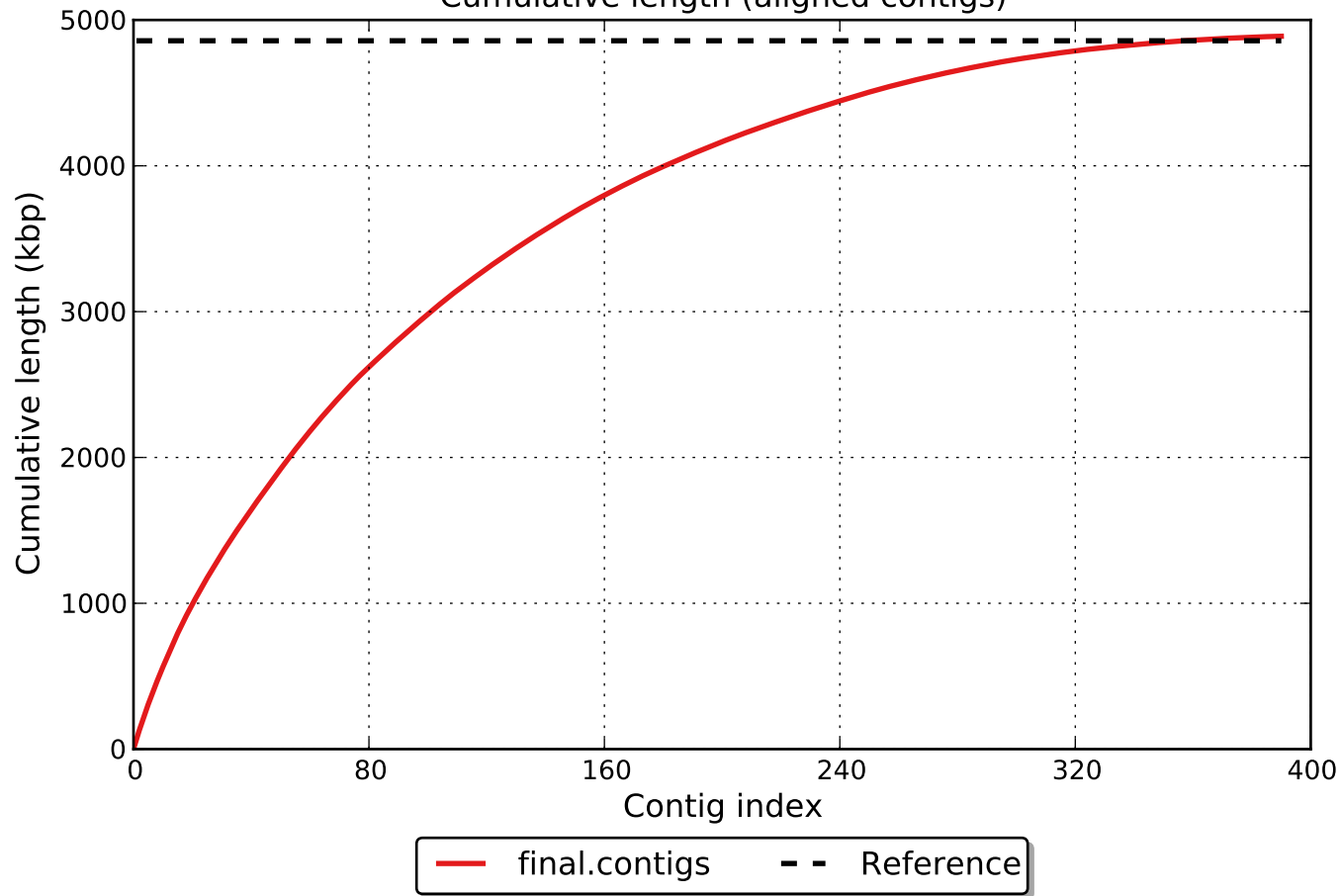


# Misassemblies

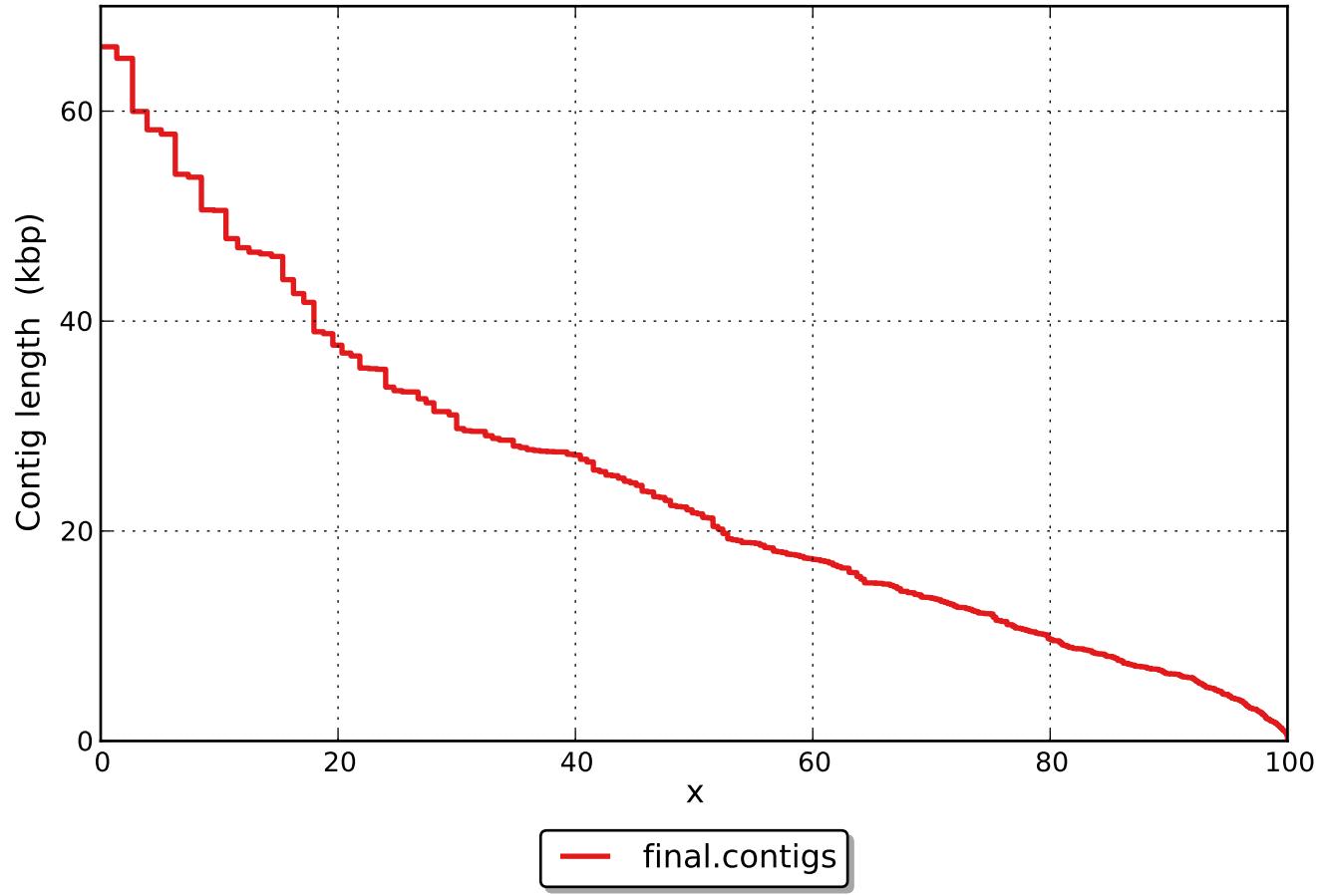




Cumulative length (aligned contigs)



NAx



# NGAx

