

## Report

	final.contigs
# contigs (>= 1000 bp)	694
# contigs (>= 5000 bp)	345
# contigs (>= 10000 bp)	142
# contigs (>= 25000 bp)	9
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4640565
Total length (>= 5000 bp)	3696014
Total length (>= 10000 bp)	2255158
Total length (>= 25000 bp)	282714
Total length (>= 50000 bp)	0
# contigs	775
Largest contig	44678
Total length	4704277
Reference length	4641652
GC (%)	50.79
Reference GC (%)	50.78
N50	9685
NG50	9764
N75	5624
NG75	5767
L50	152
LG50	149
L75	314
LG75	306
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.782
Duplication ratio	1.016
# N's per 100 kbp	0.00
# mismatches per 100 kbp	15.98
# indels per 100 kbp	0.00
Largest alignment	44678
NA50	9685
NGA50	9764
NA75	5624
NGA75	5767
LA50	152
LGA50	149
LA75	314
LGA75	306

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

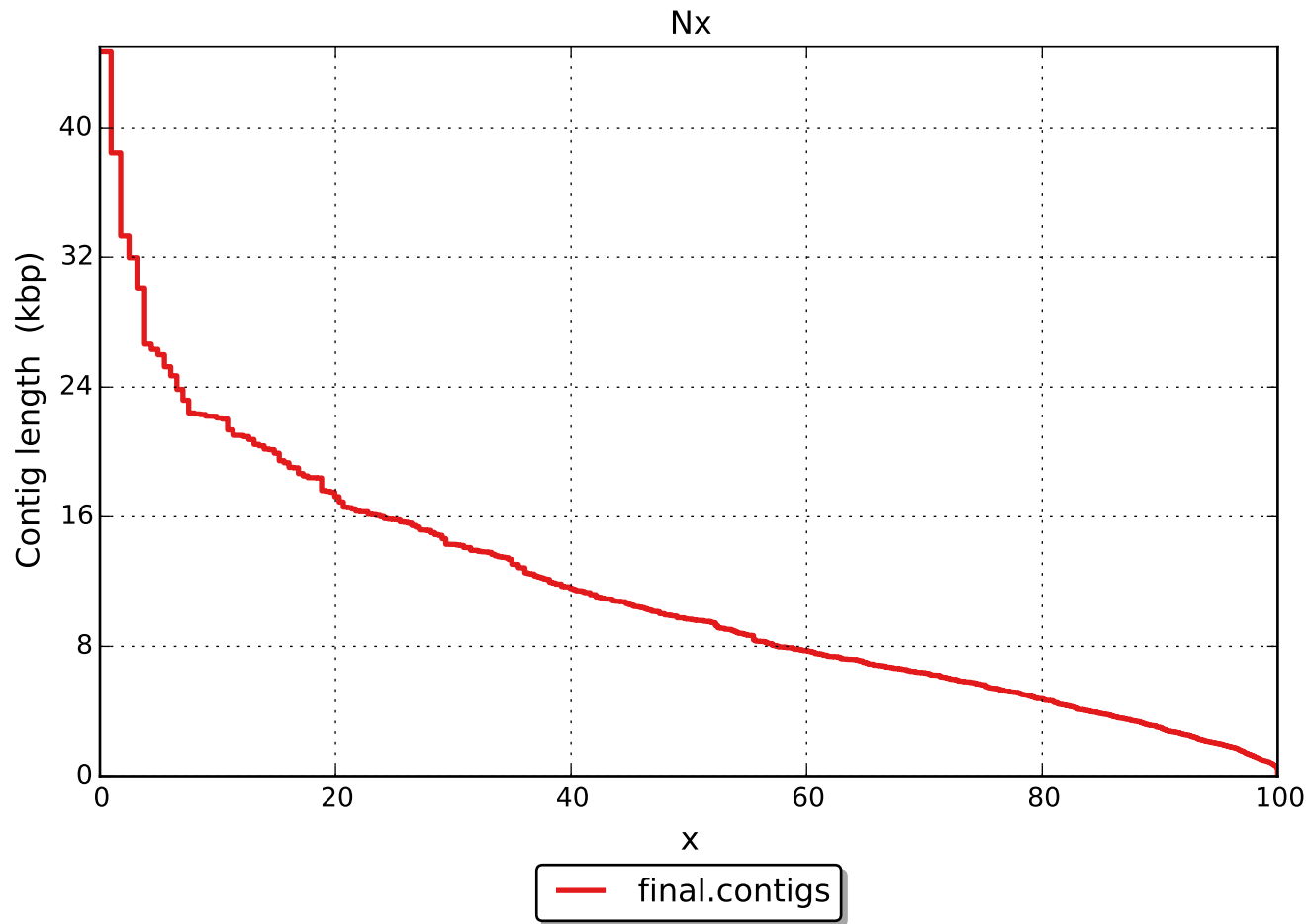
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	740
# indels	0
# short indels	0
# long indels	0
Indels length	0

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).

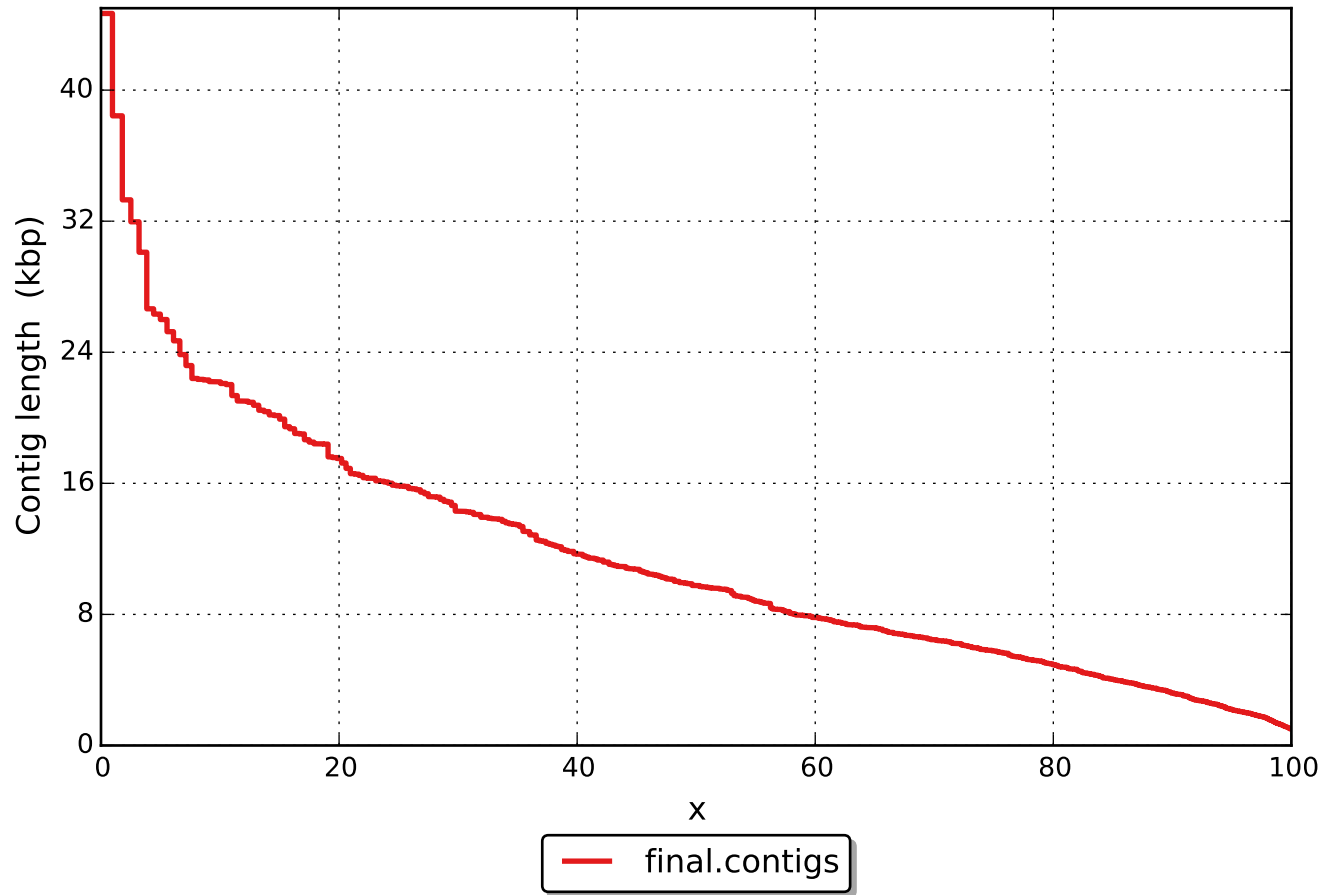
## Unaligned report

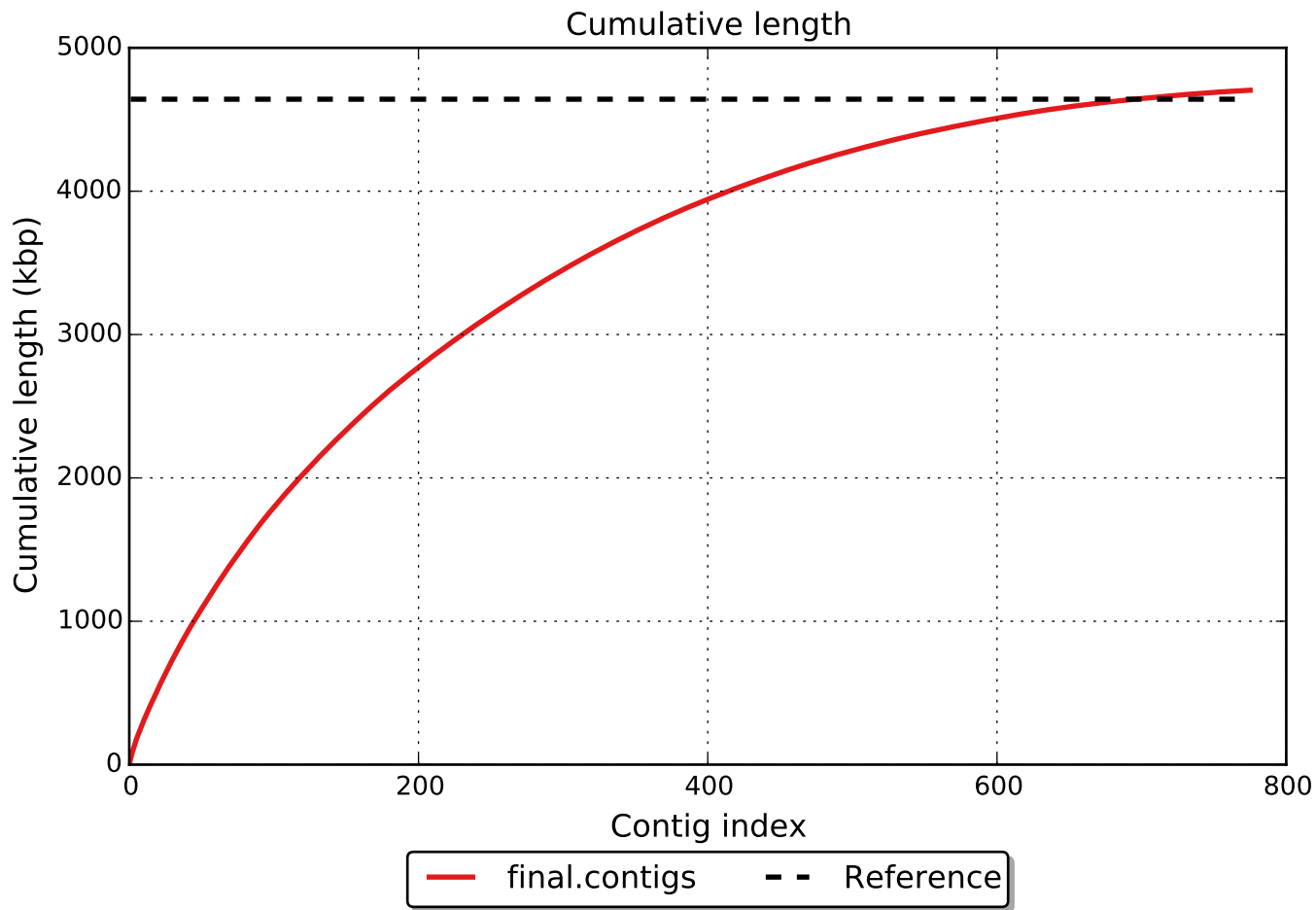
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

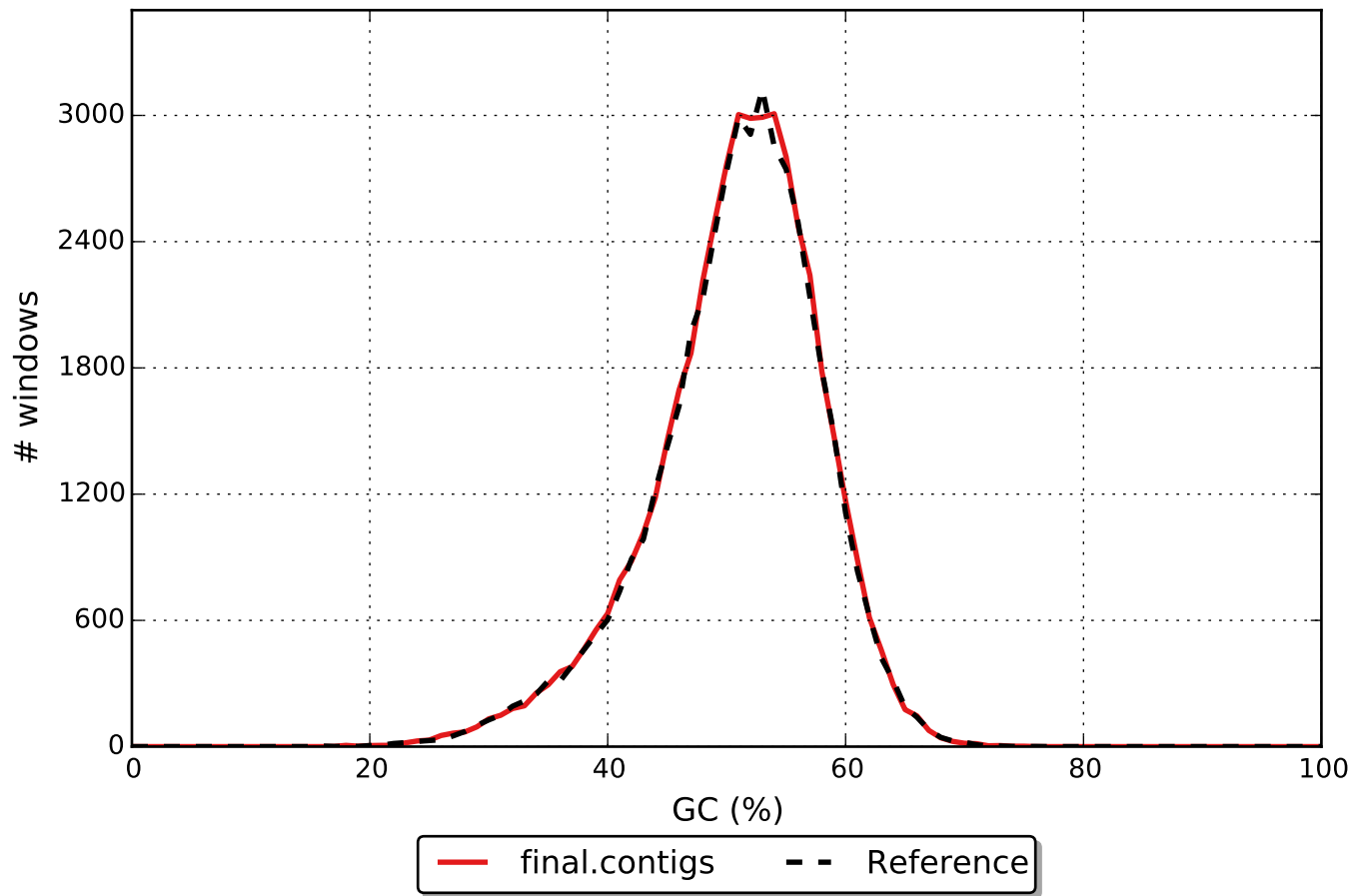


NGx





# GC content

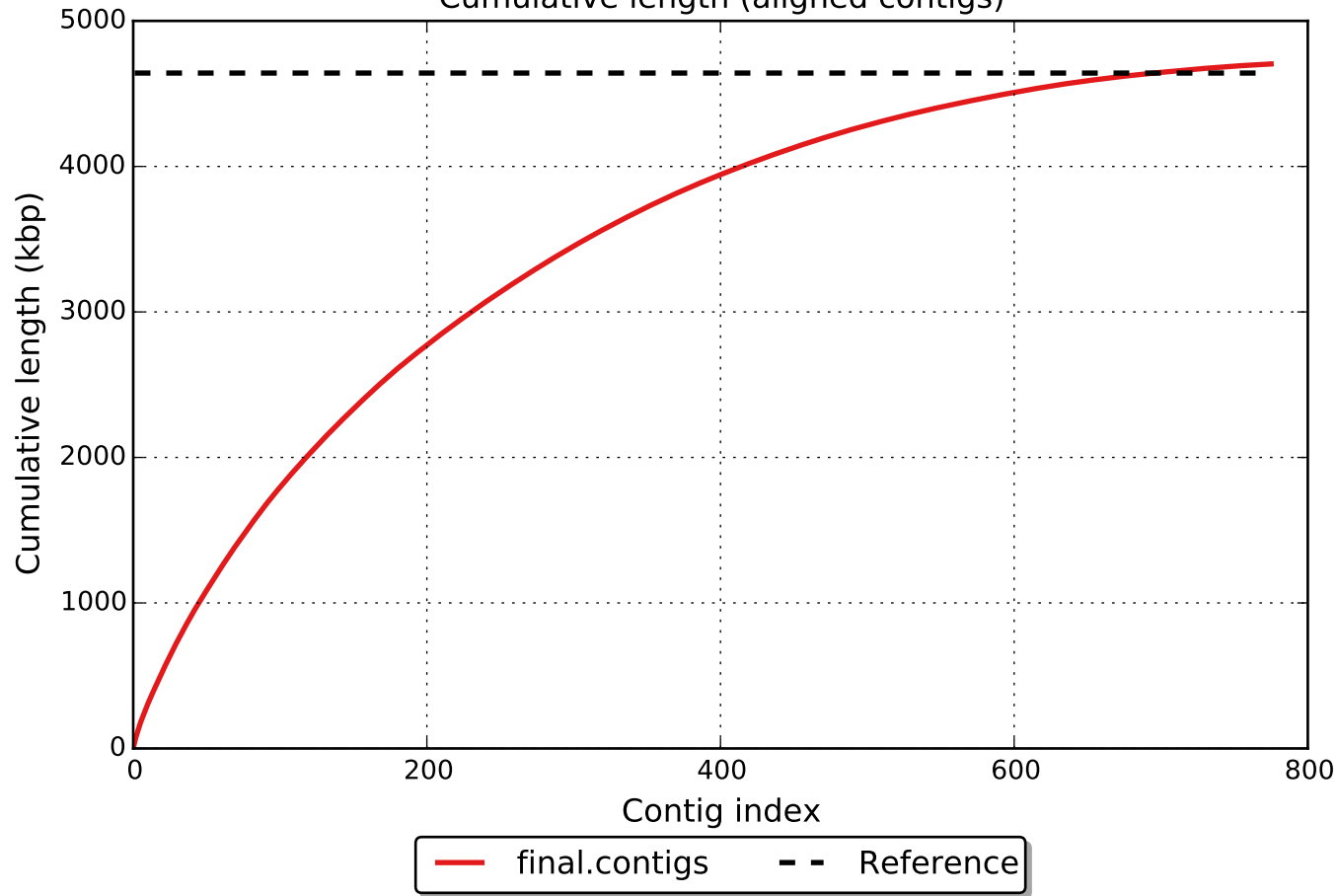


# Misassemblies

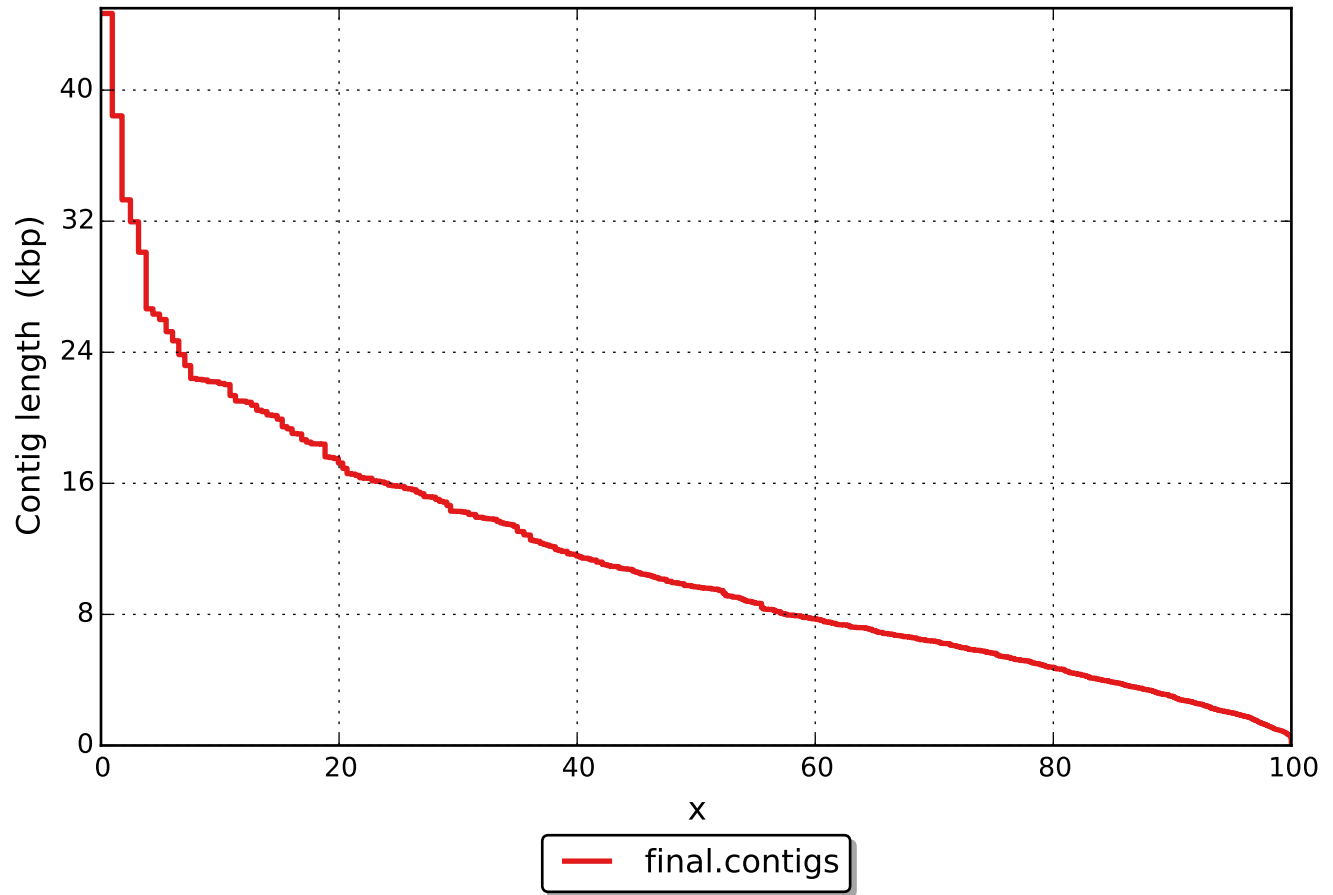




Cumulative length (aligned contigs)



NAx



# NGAx

