

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	1568
# contigs ( $\geq 1000$ bp)	302
Total length ( $\geq 0$ bp)	1148514
Total length ( $\geq 1000$ bp)	432774
# contigs	1025
Largest contig	4169
Total length	945995
Reference length	1283598
GC (%)	26.40
Reference GC (%)	26.31
N50	935
NG50	774
N75	714
L50	344
LG50	542
L75	633
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	82.913
Duplication ratio	1.068
# N's per 100 kbp	0.00
# mismatches per 100 kbp	318.71
# indels per 100 kbp	0.38
Largest alignment	4169
NA50	935
NGA50	774
NA75	714
LA50	344
LGA50	542
LA75	633

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).

## Misassemblies report

	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	3392
# indels	4
# short indels	4
# long indels	0
Indels length	4

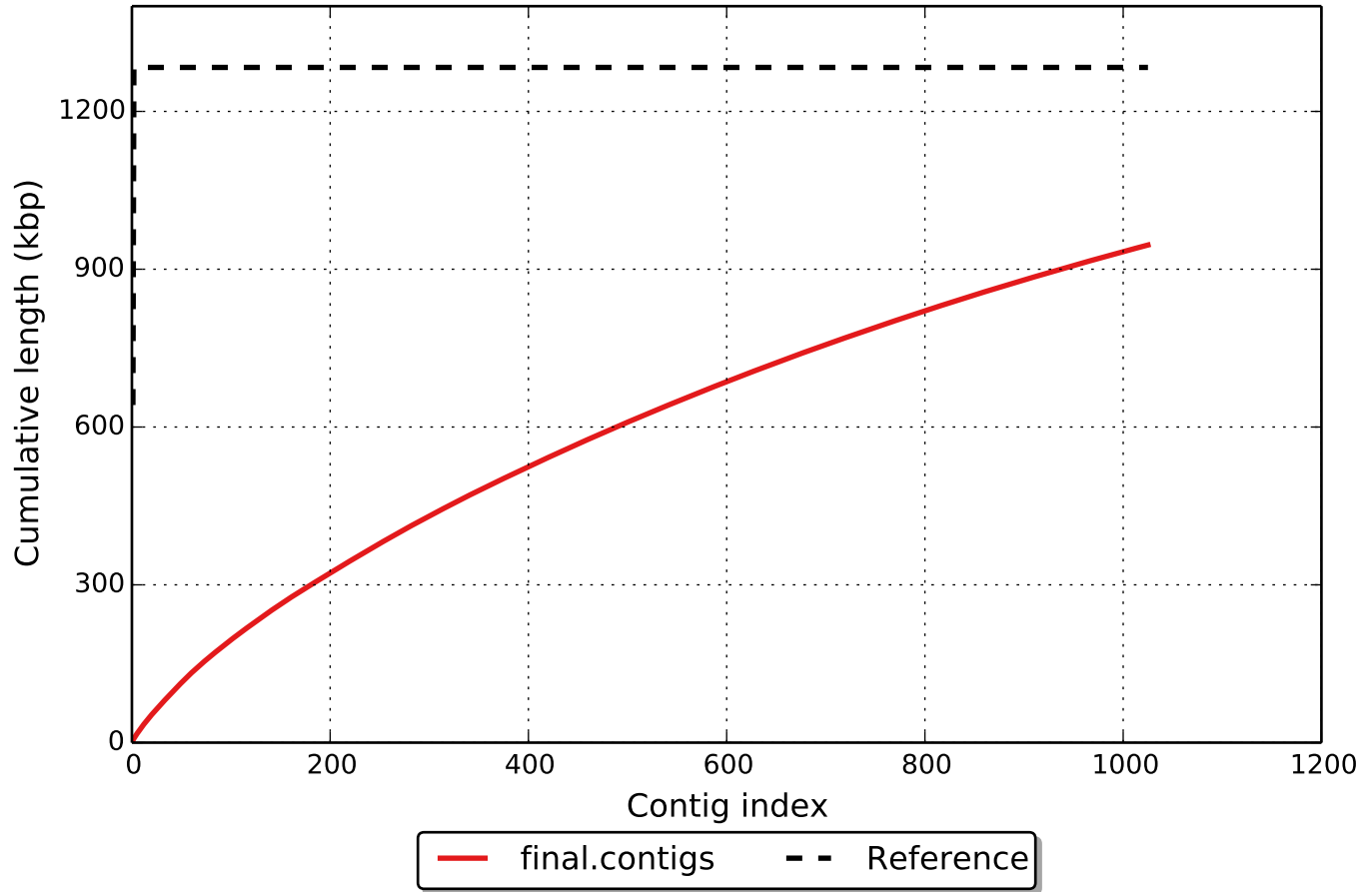
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

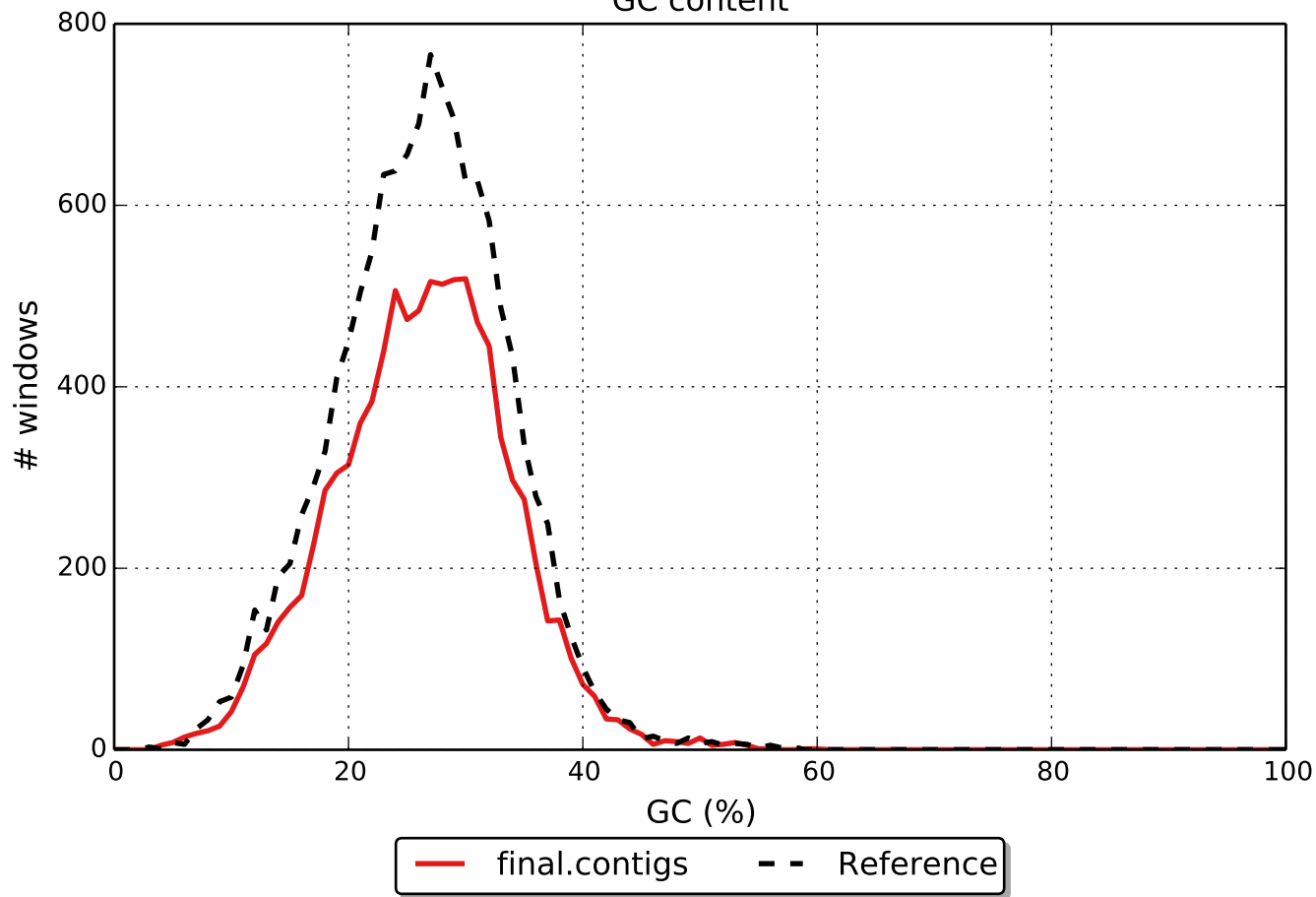
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

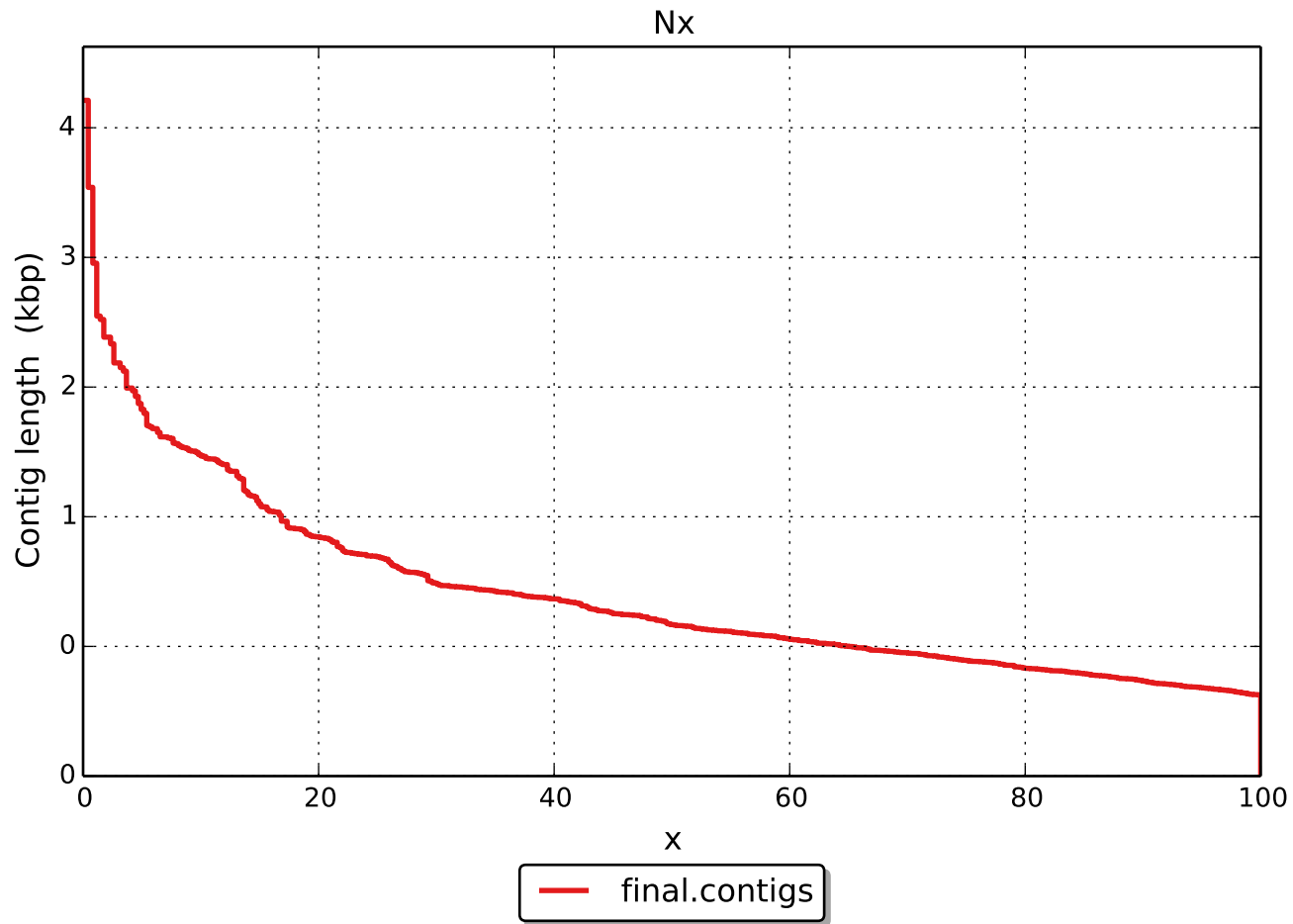
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Cumulative length

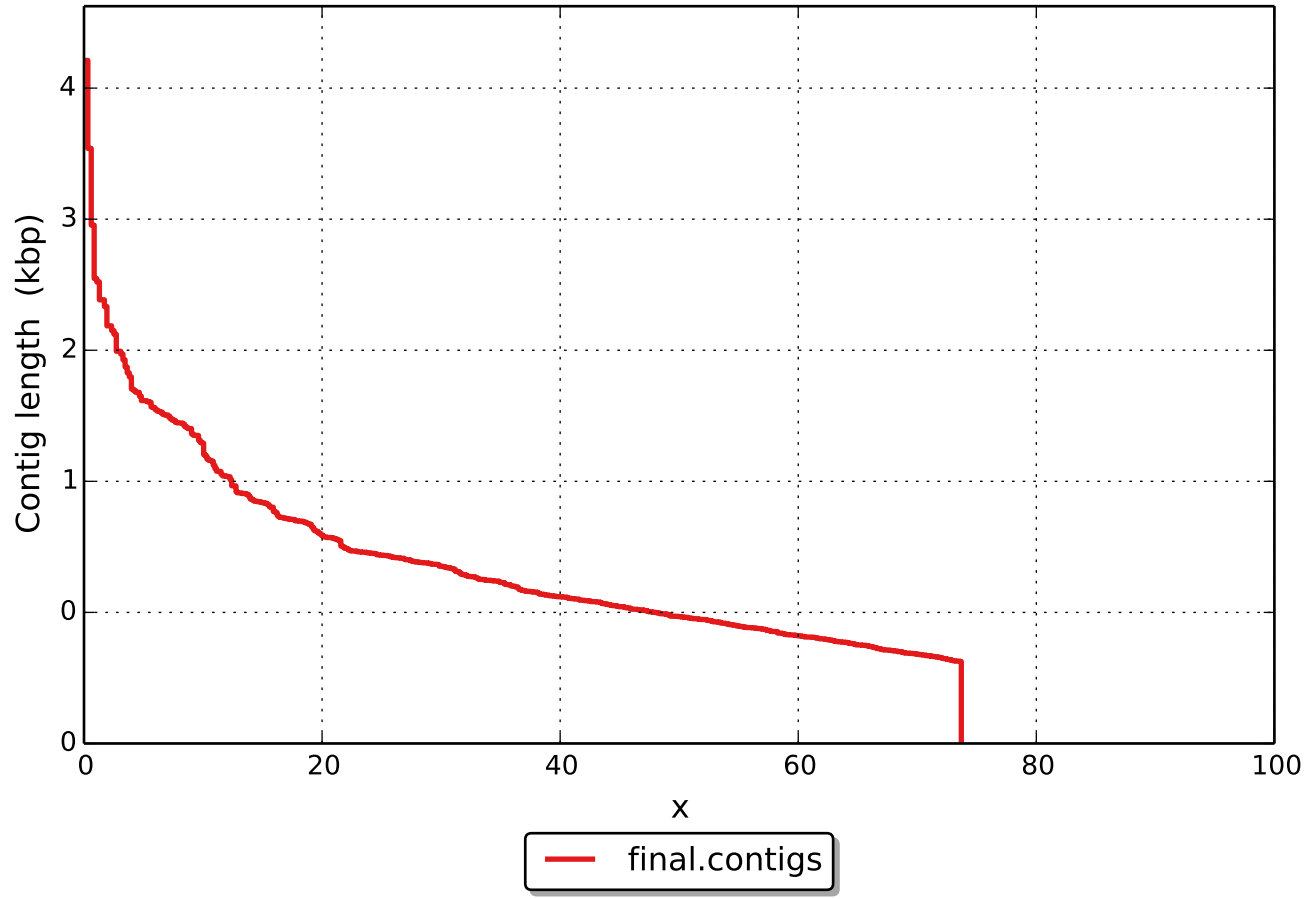


# GC content





NGx

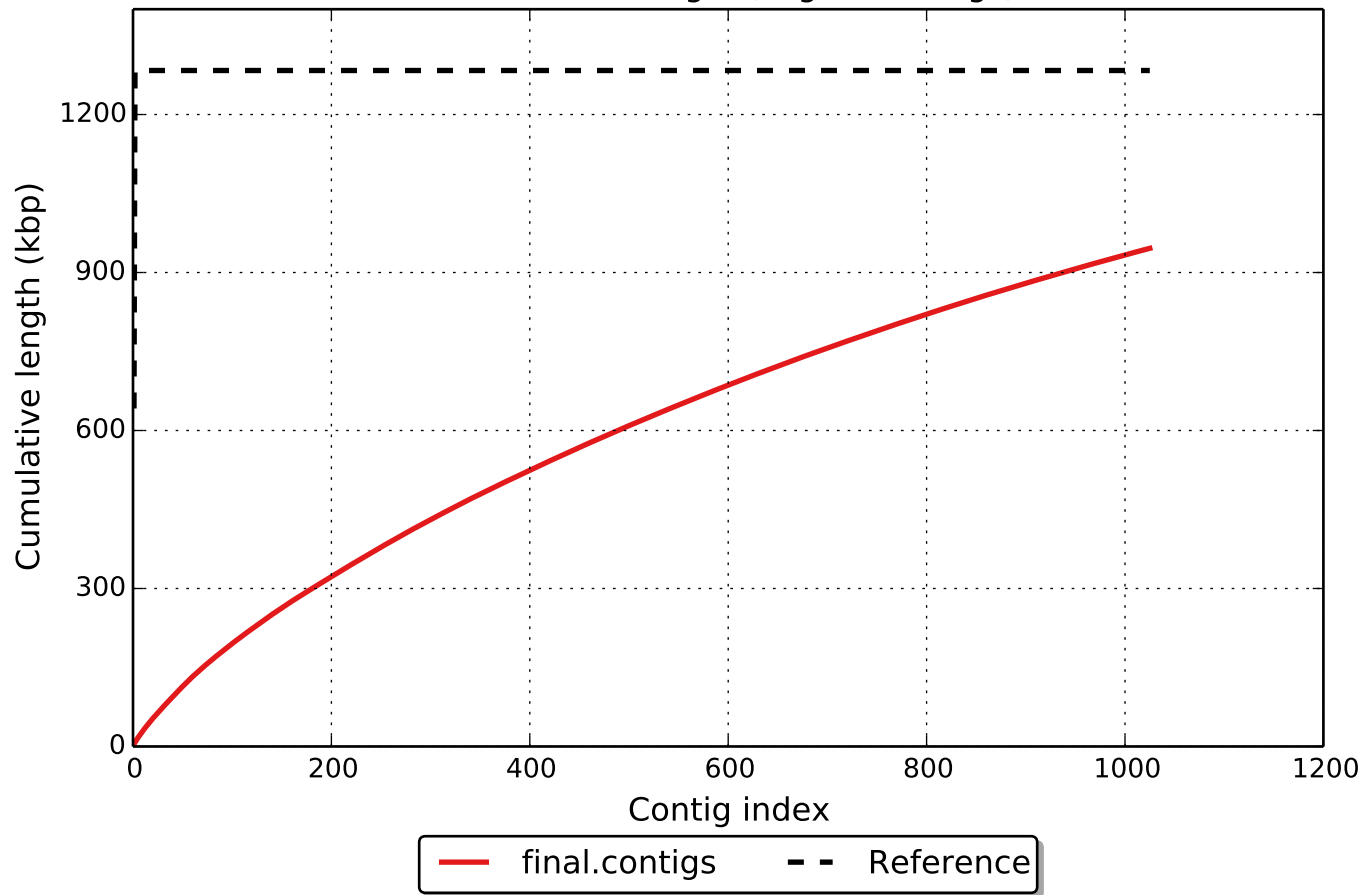


# Misassemblies

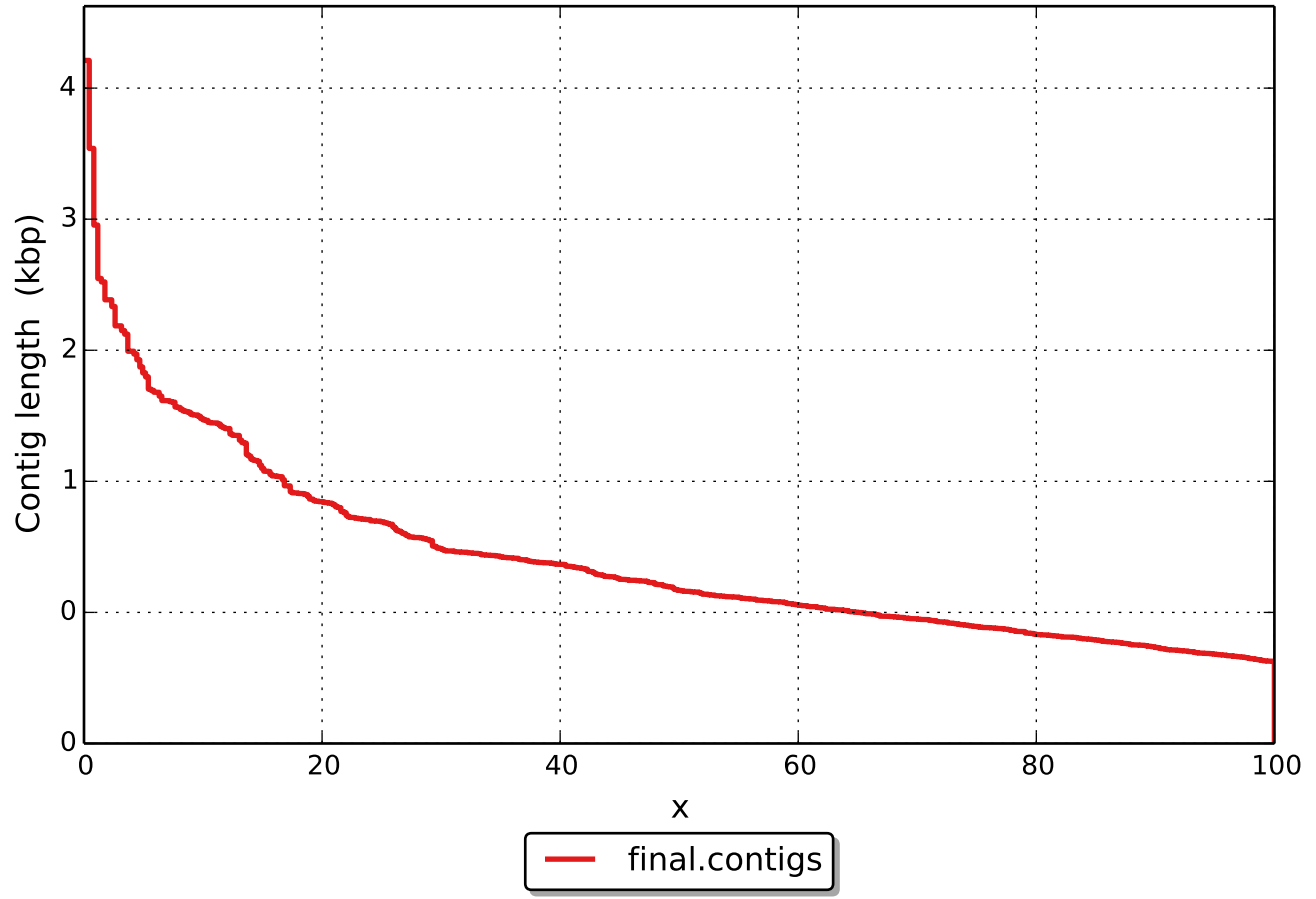




Cumulative length (aligned contigs)



NAx



# NGAx

