

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	894
# contigs ( $\geq 1000$ bp)	224
Total length ( $\geq 0$ bp)	840803
Total length ( $\geq 1000$ bp)	506273
# contigs	524
Largest contig	13980
Total length	710395
Reference length	1231960
GC (%)	25.24
Reference GC (%)	25.35
N50	1718
NG50	668
N75	900
L50	110
LG50	361
L75	252
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	55.660
Duplication ratio	1.036
# N's per 100 kbp	0.00
# mismatches per 100 kbp	385.30
# indels per 100 kbp	0.00
Largest alignment	13980
NA50	1718
NGA50	668
NA75	900
LA50	110
LGA50	361
LA75	252

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	2642
# indels	0
# short indels	0
# long indels	0
Indels length	0

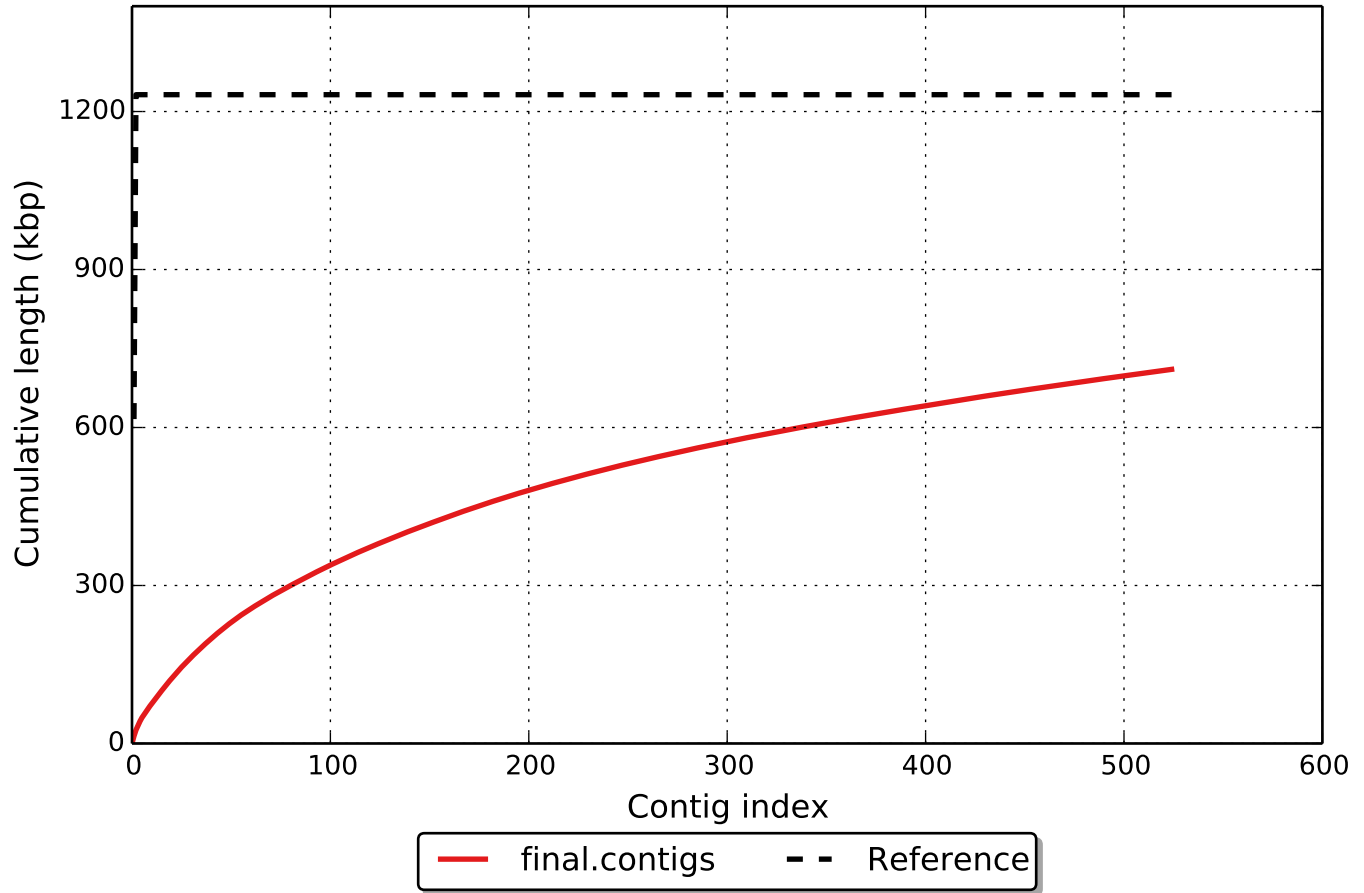
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

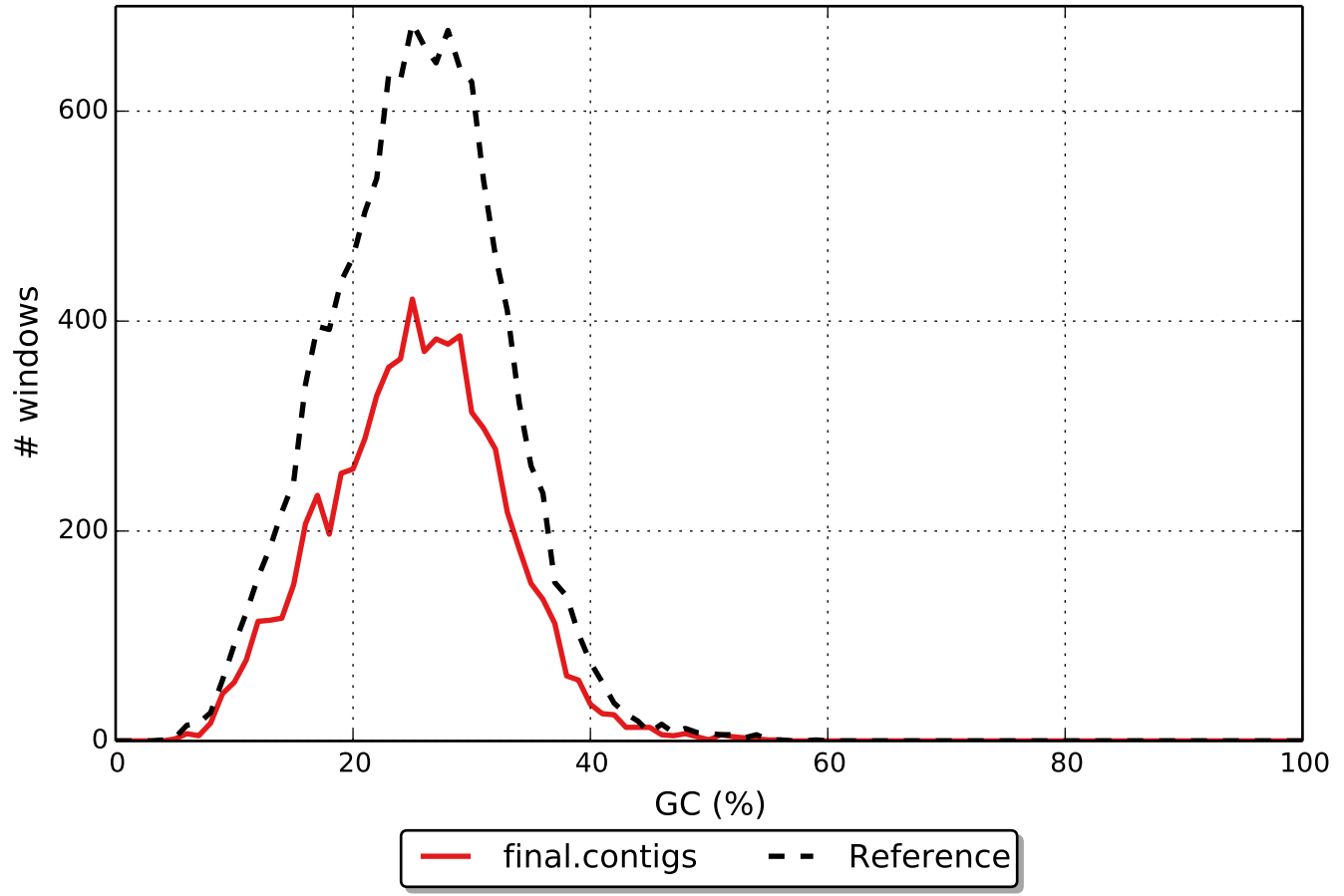
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

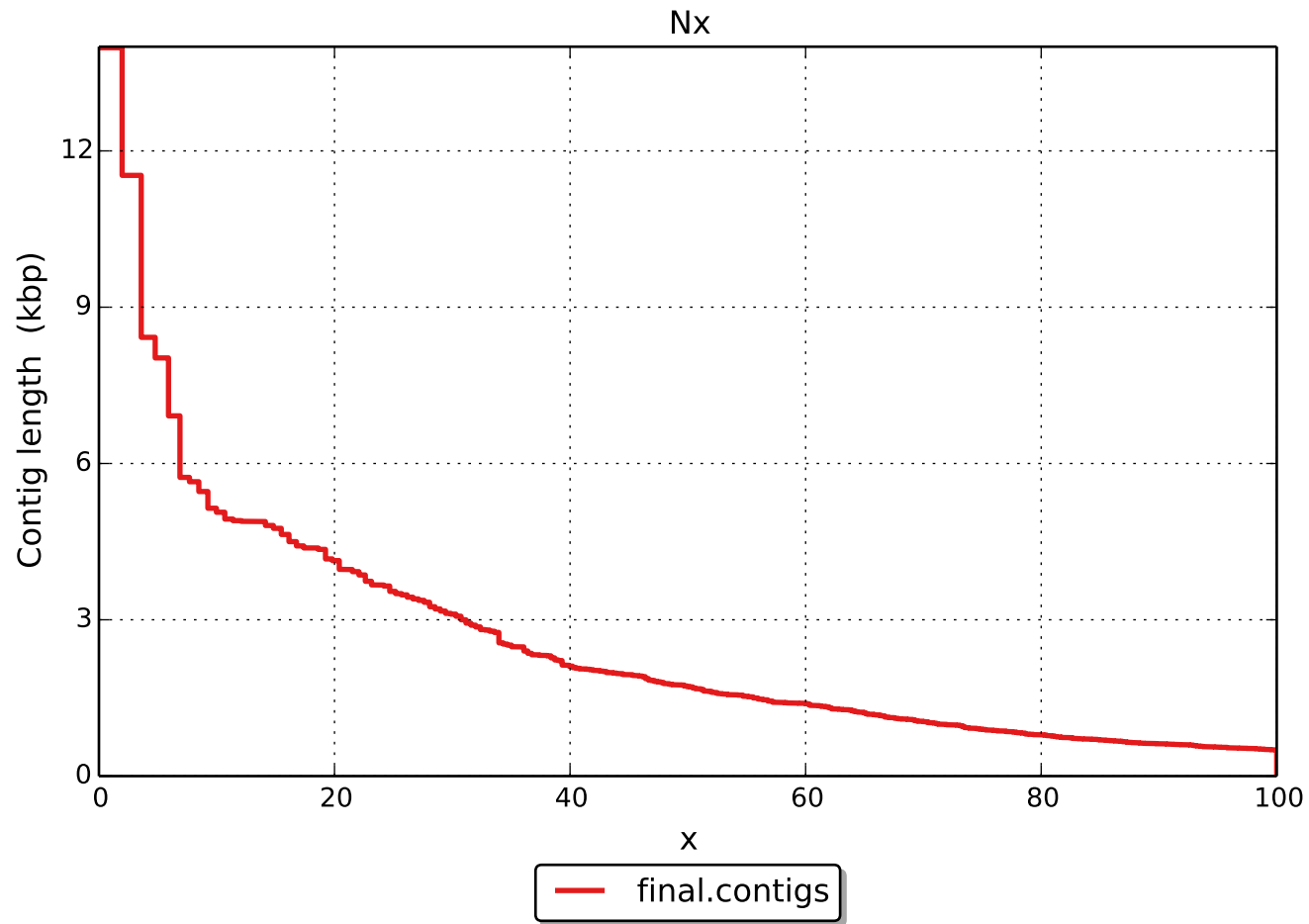
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Cumulative length

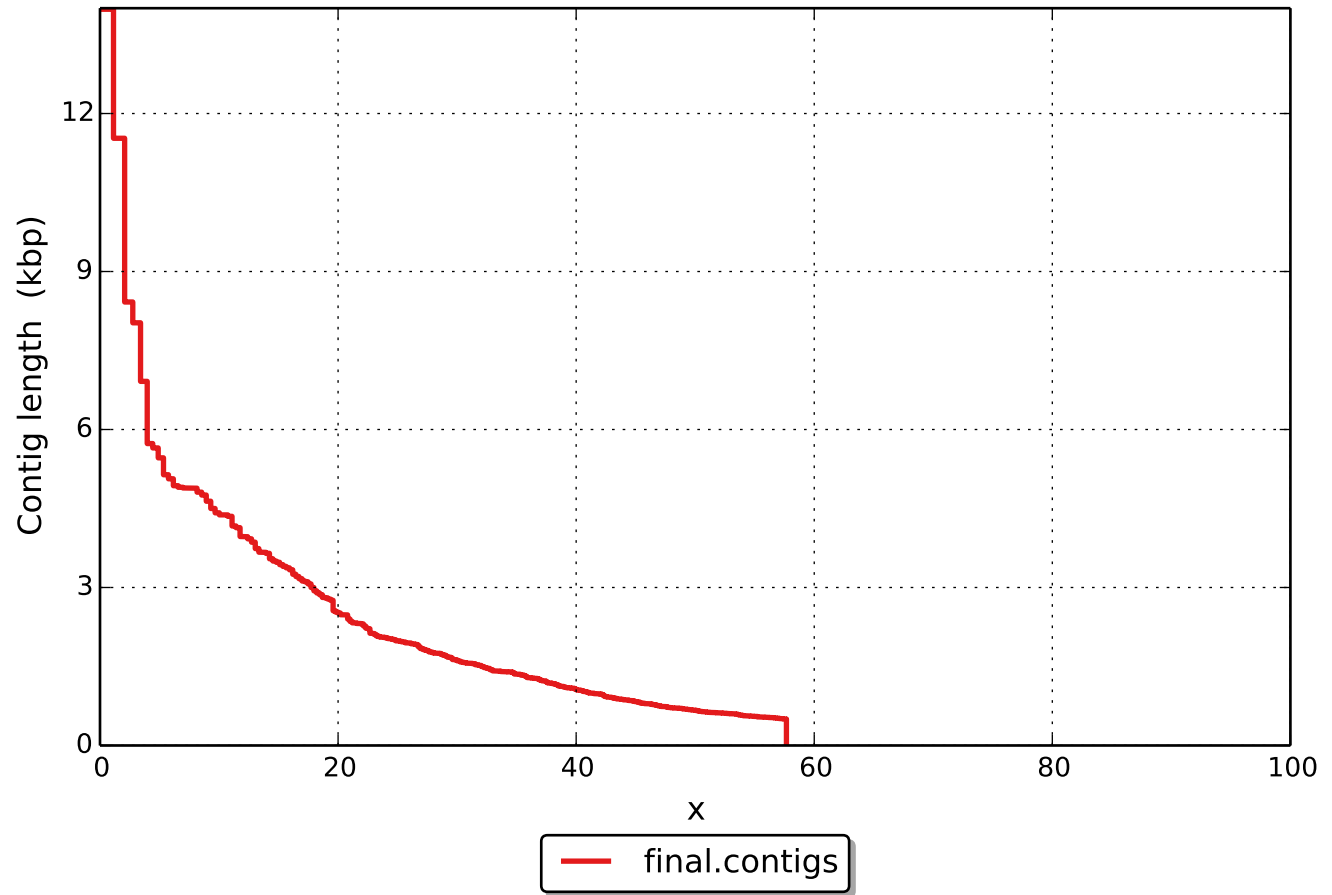


# GC content





NGx

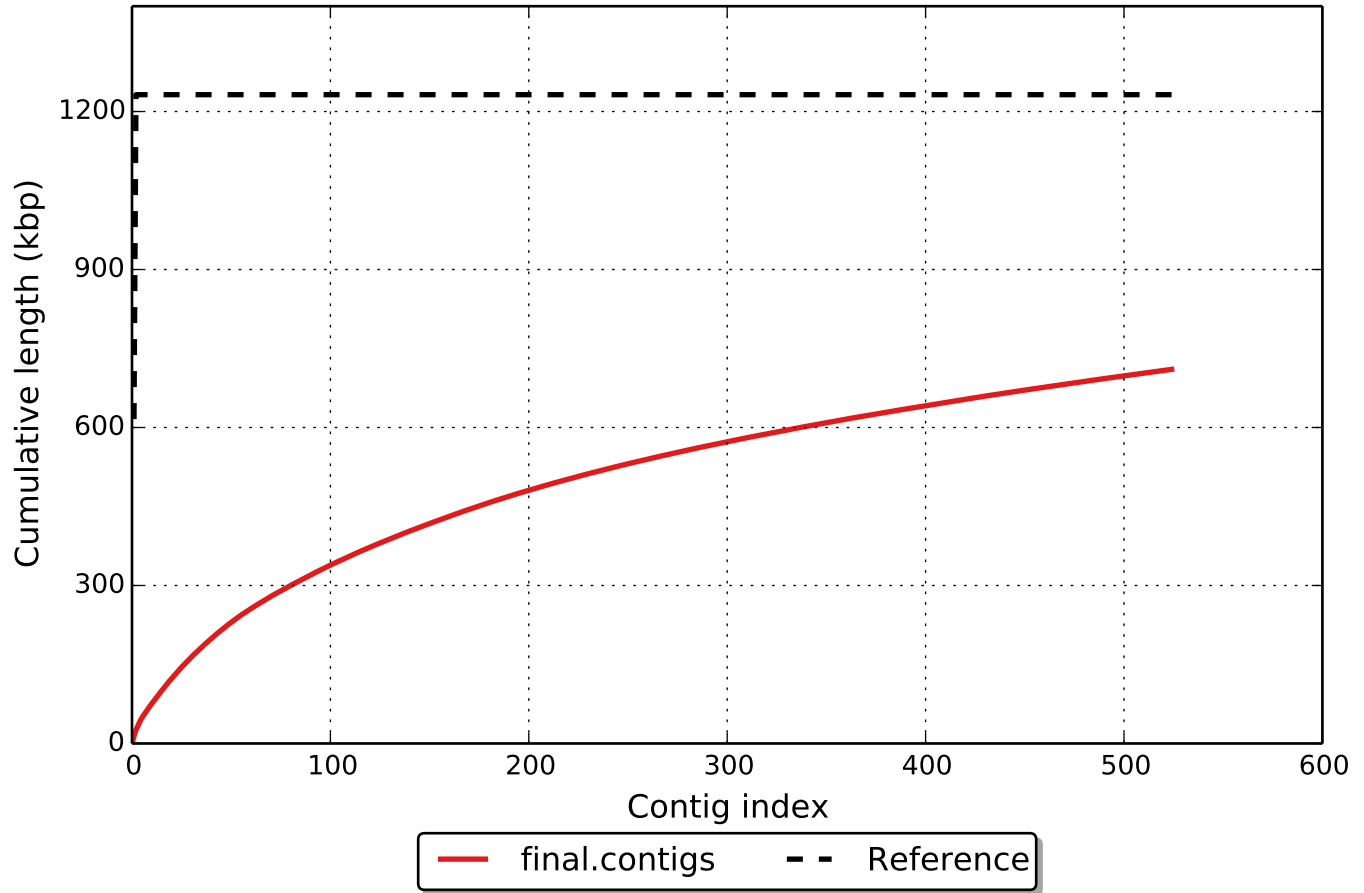


# Misassemblies

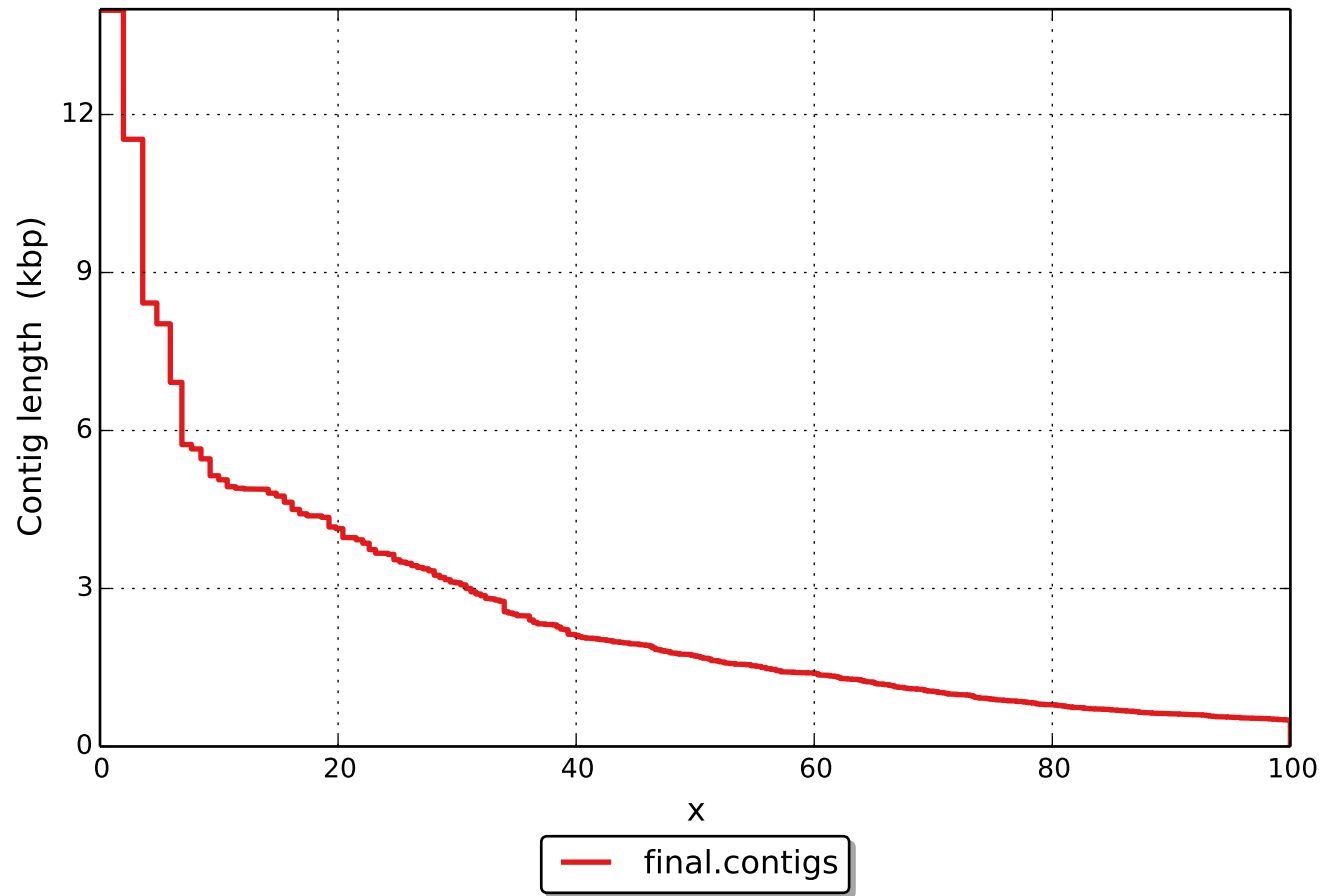




Cumulative length (aligned contigs)



NAx



NGAx

