

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	1551
# contigs ( $\geq 1000$ bp)	401
Total length ( $\geq 0$ bp)	1257889
Total length ( $\geq 1000$ bp)	598099
# contigs	1082
Largest contig	4336
Total length	1083010
Reference length	1231960
GC (%)	25.43
Reference GC (%)	25.35
N50	1053
NG50	983
N75	760
NG75	650
L50	346
LG50	420
L75	645
LG75	804
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	83.802
Duplication ratio	1.049
# N's per 100 kbp	0.00
# mismatches per 100 kbp	56.57
# indels per 100 kbp	0.00
Largest alignment	4336
NA50	1052
NGA50	983
NA75	760
NGA75	650
LA50	346
LGA50	420
LA75	645
LGA75	804

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	584
# indels	0
# short indels	0
# long indels	0
Indels length	0

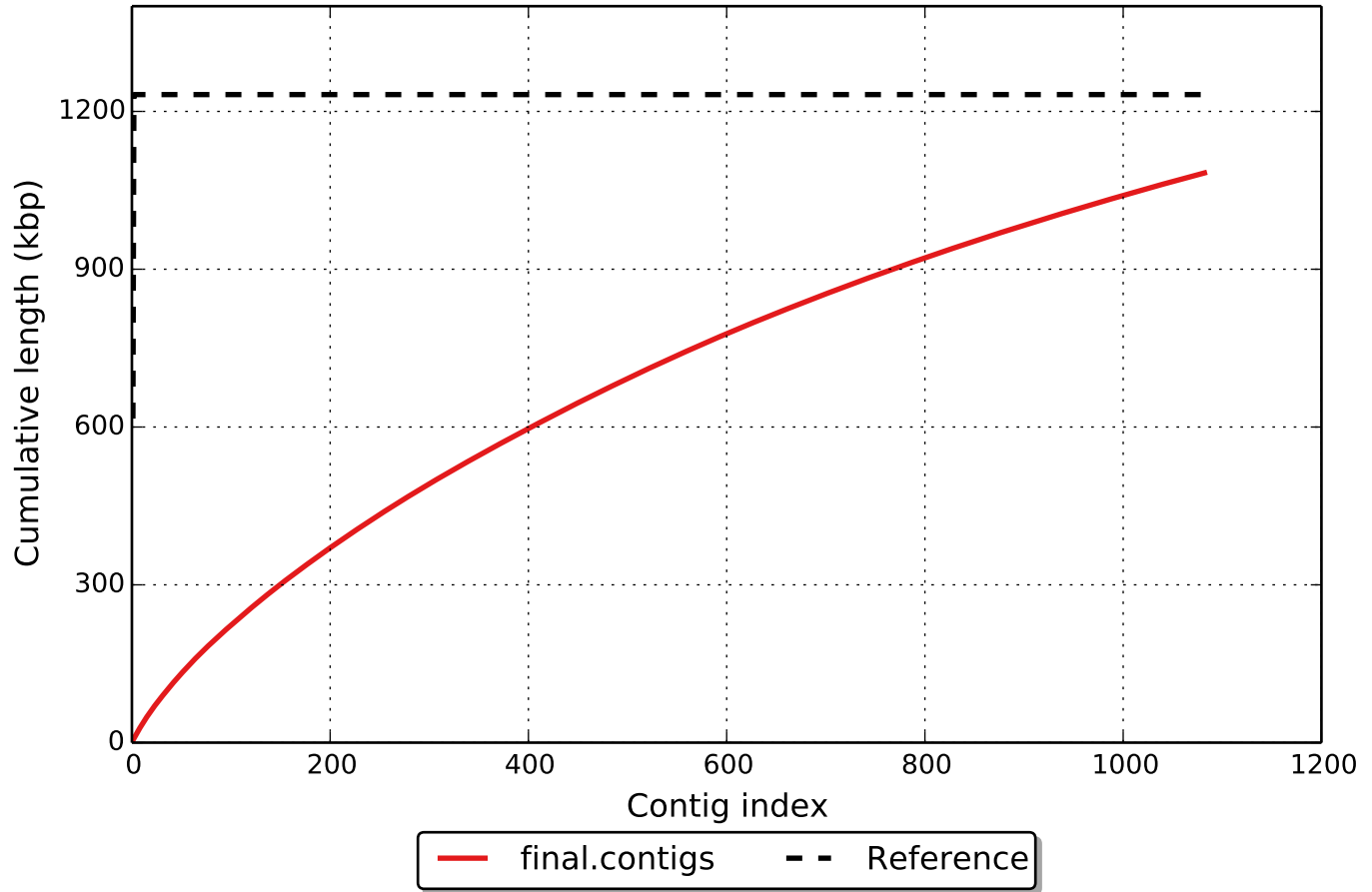
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

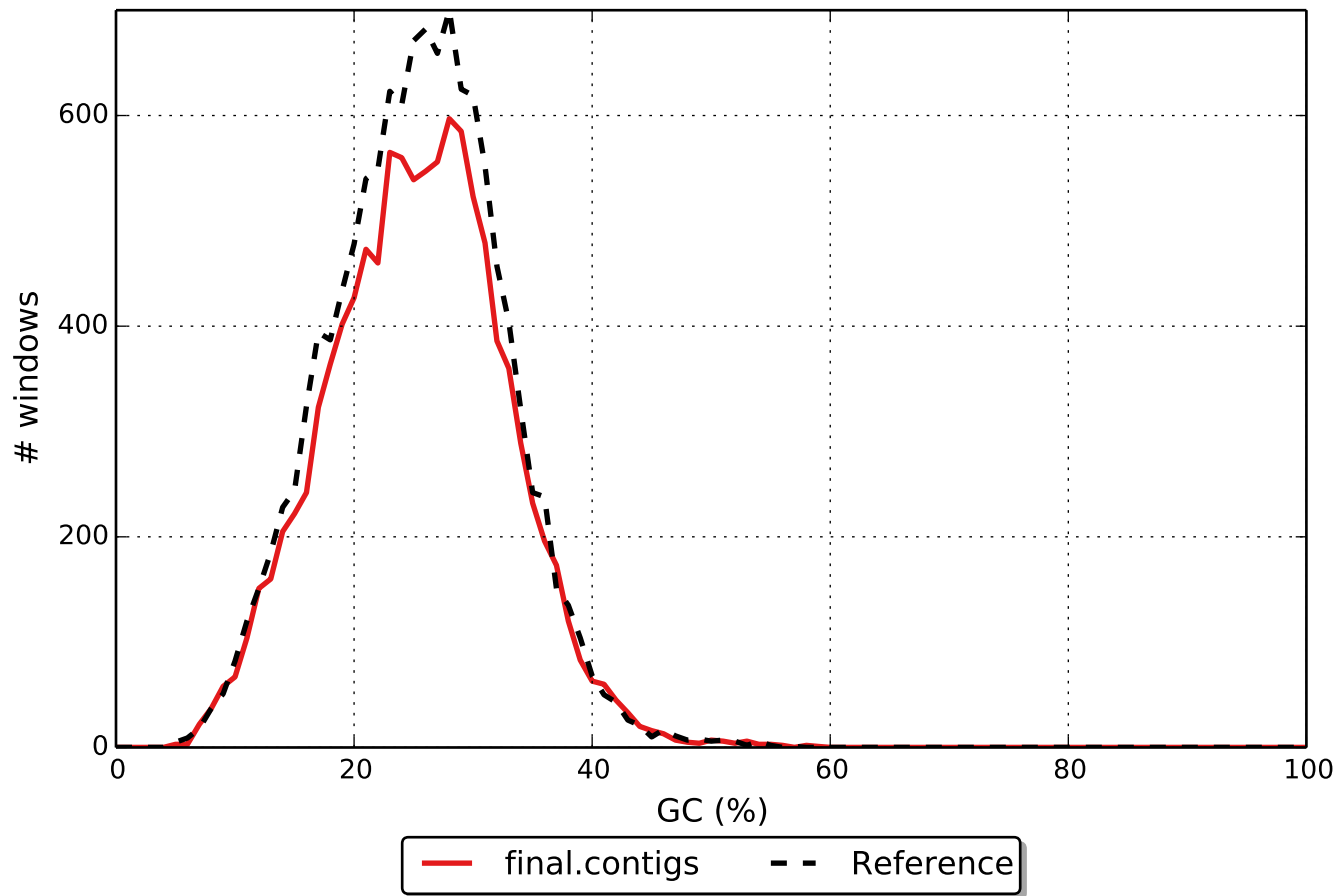
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

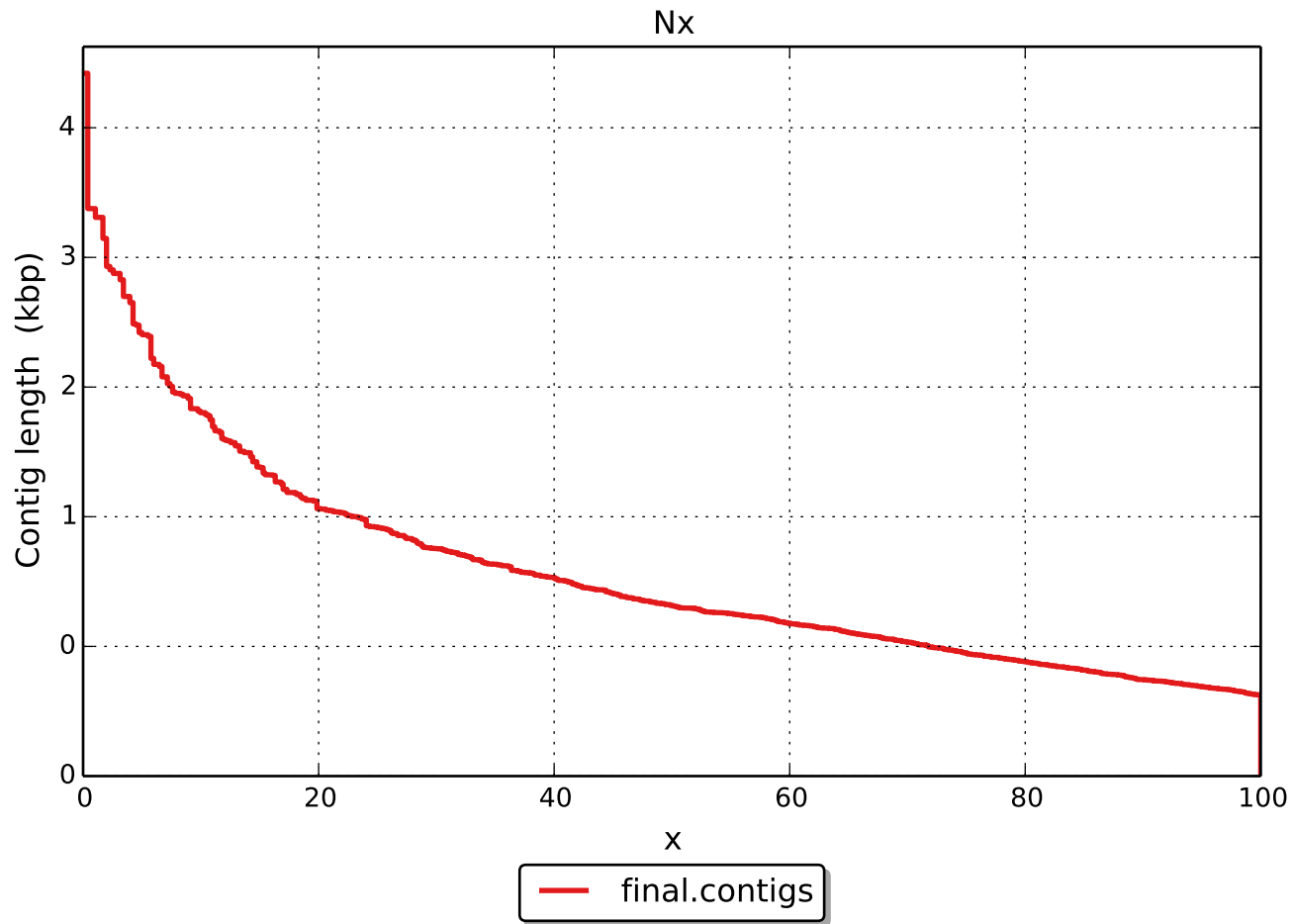
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Cumulative length

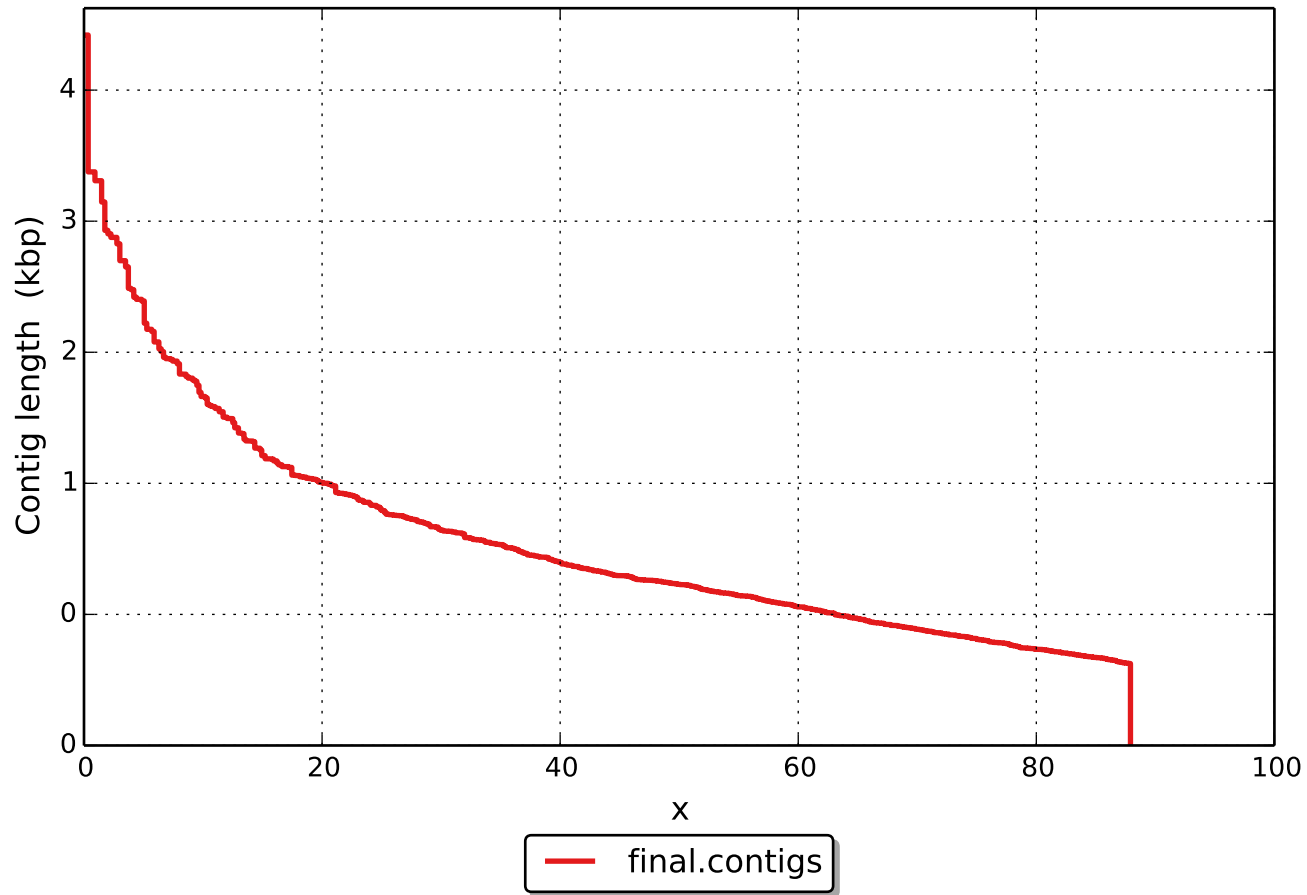


GC content





NGx

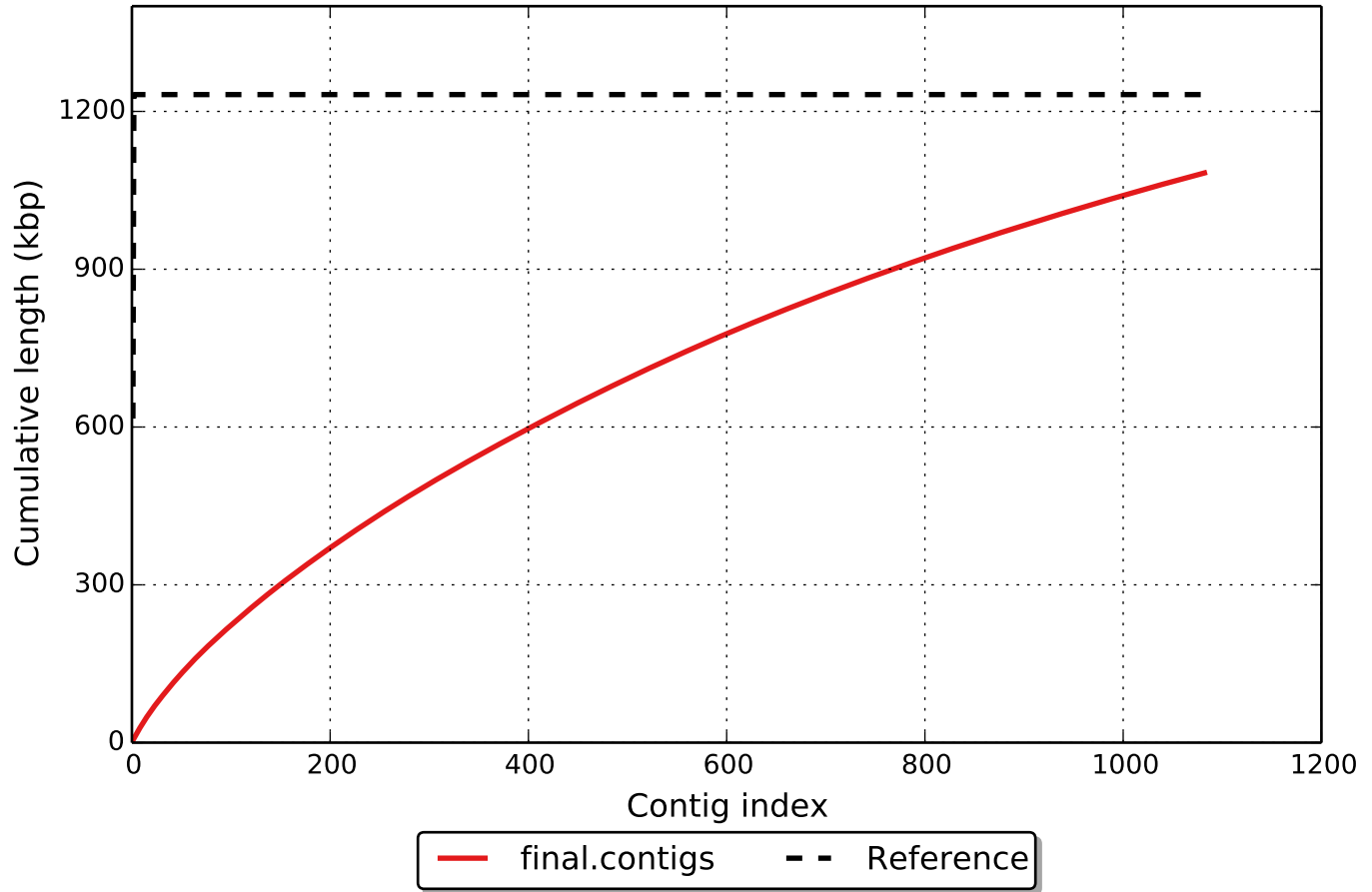


# Misassemblies

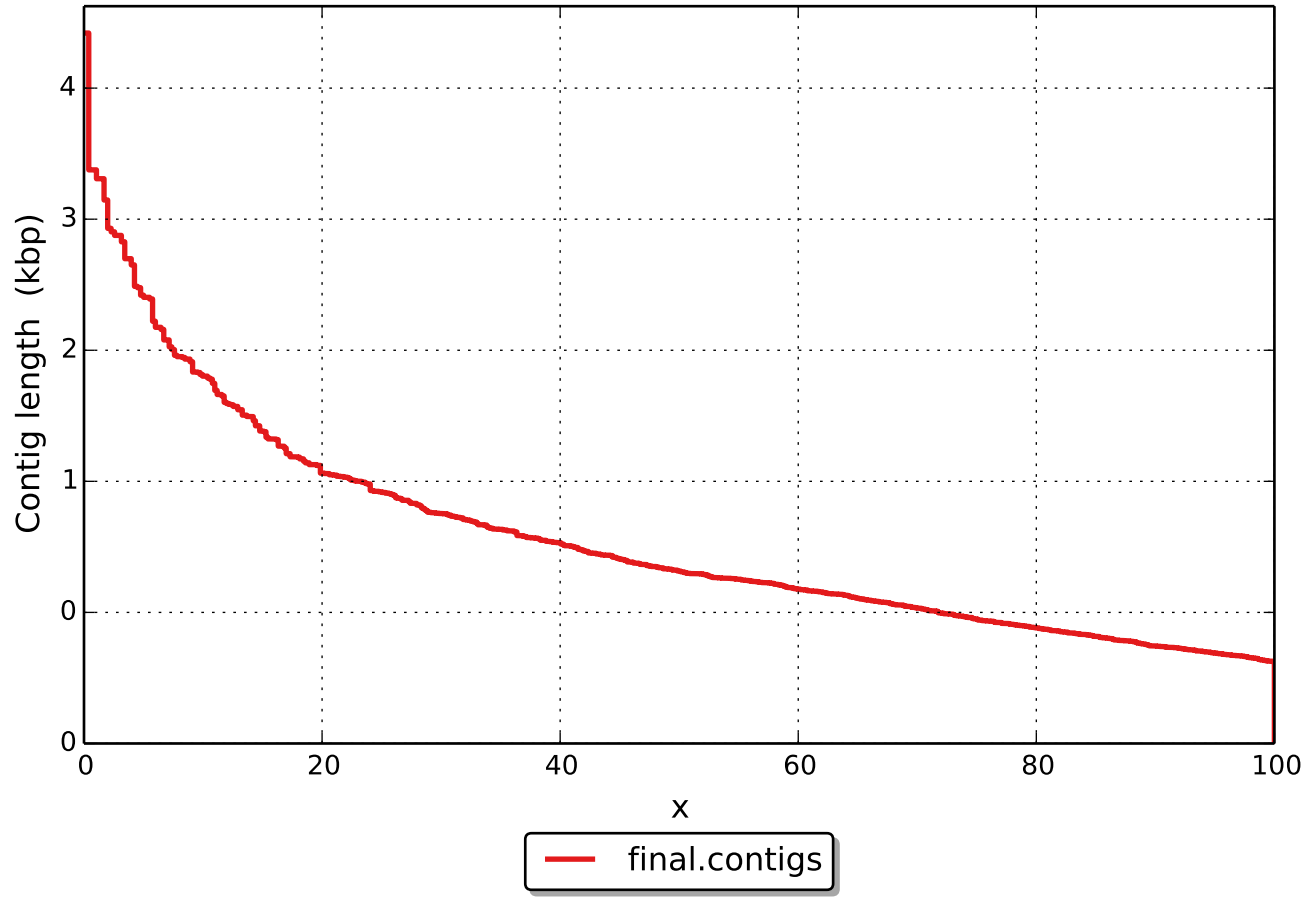




Cumulative length (aligned contigs)



NAx



# NGAx

