

## Report

	final.contigs
# contigs (>= 0 bp)	106
# contigs (>= 1000 bp)	98
Total length (>= 0 bp)	1240089
Total length (>= 1000 bp)	1233969
# contigs	105
Largest contig	42035
Total length	1239635
Reference length	1231960
GC (%)	25.35
Reference GC (%)	25.35
N50	17928
NG50	17928
N75	10565
NG75	10765
L50	22
LG50	22
L75	44
LG75	43
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.409
Duplication ratio	1.022
# N's per 100 kbp	0.00
# mismatches per 100 kbp	75.89
# indels per 100 kbp	0.00
Largest alignment	42035
NA50	17928
NGA50	17928
NA75	10565
NGA75	10765
LA50	22
LGA50	22
LA75	44
LGA75	43

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
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	920
# indels	0
# short indels	0
# long indels	0
Indels length	0

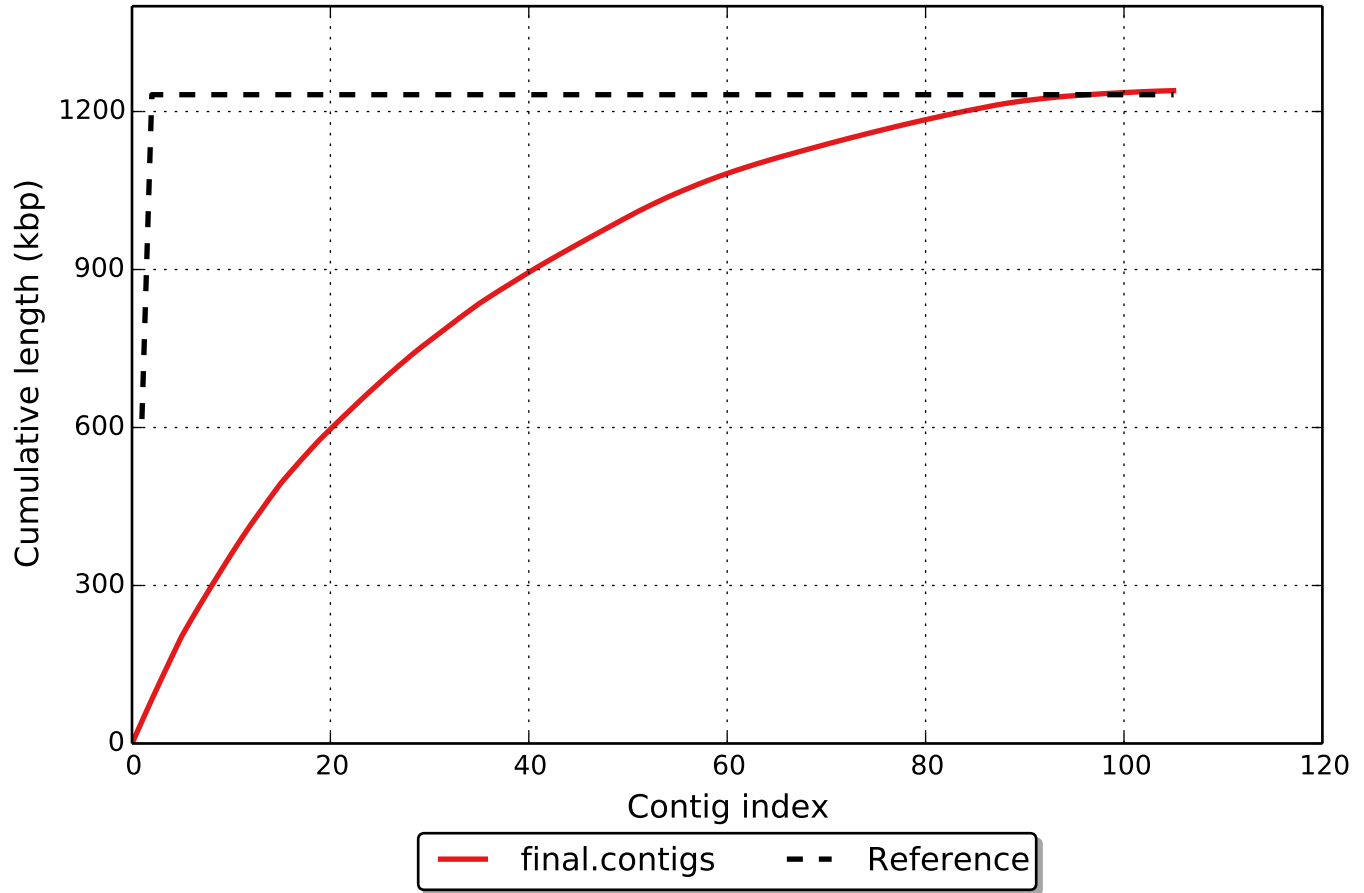
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

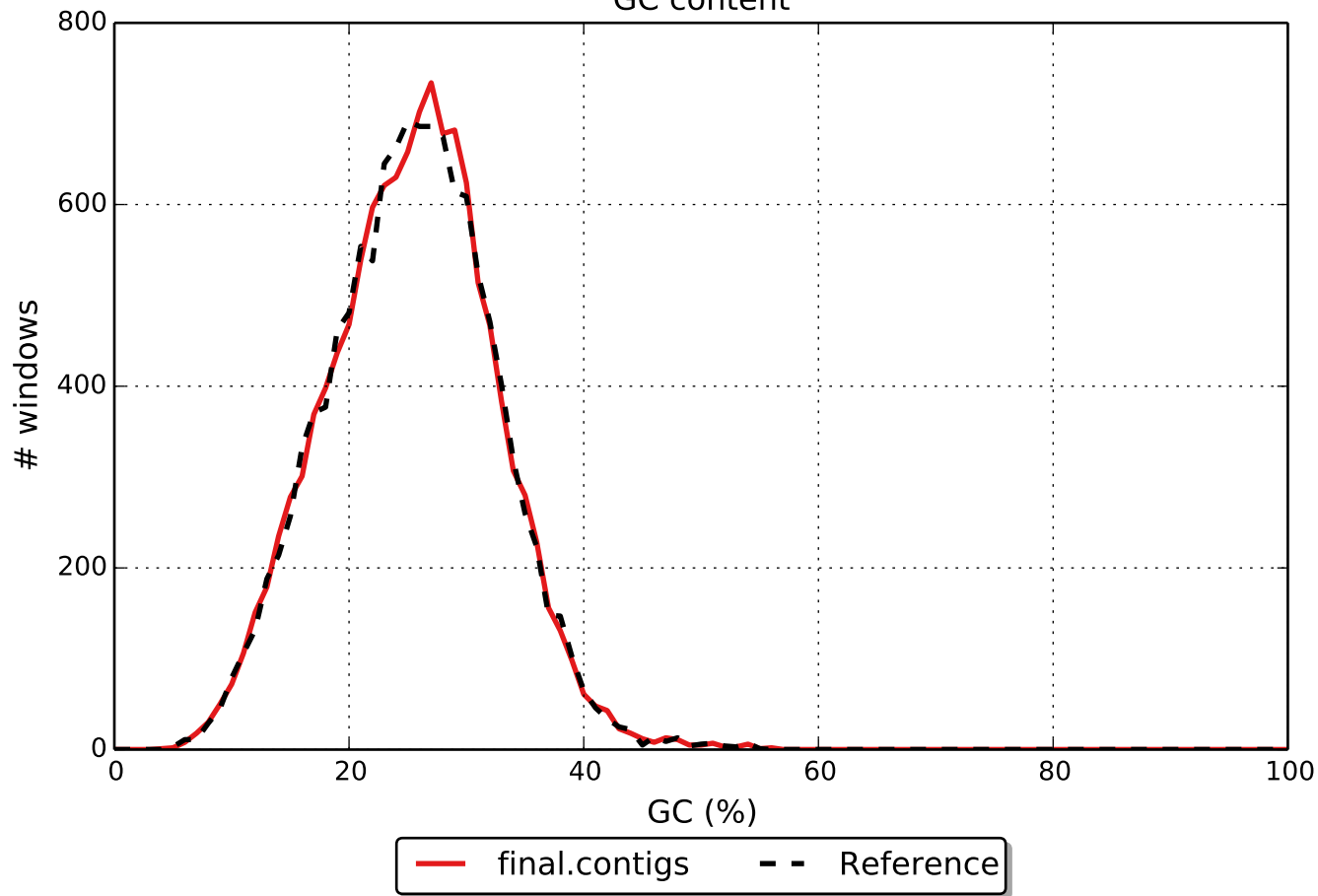
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

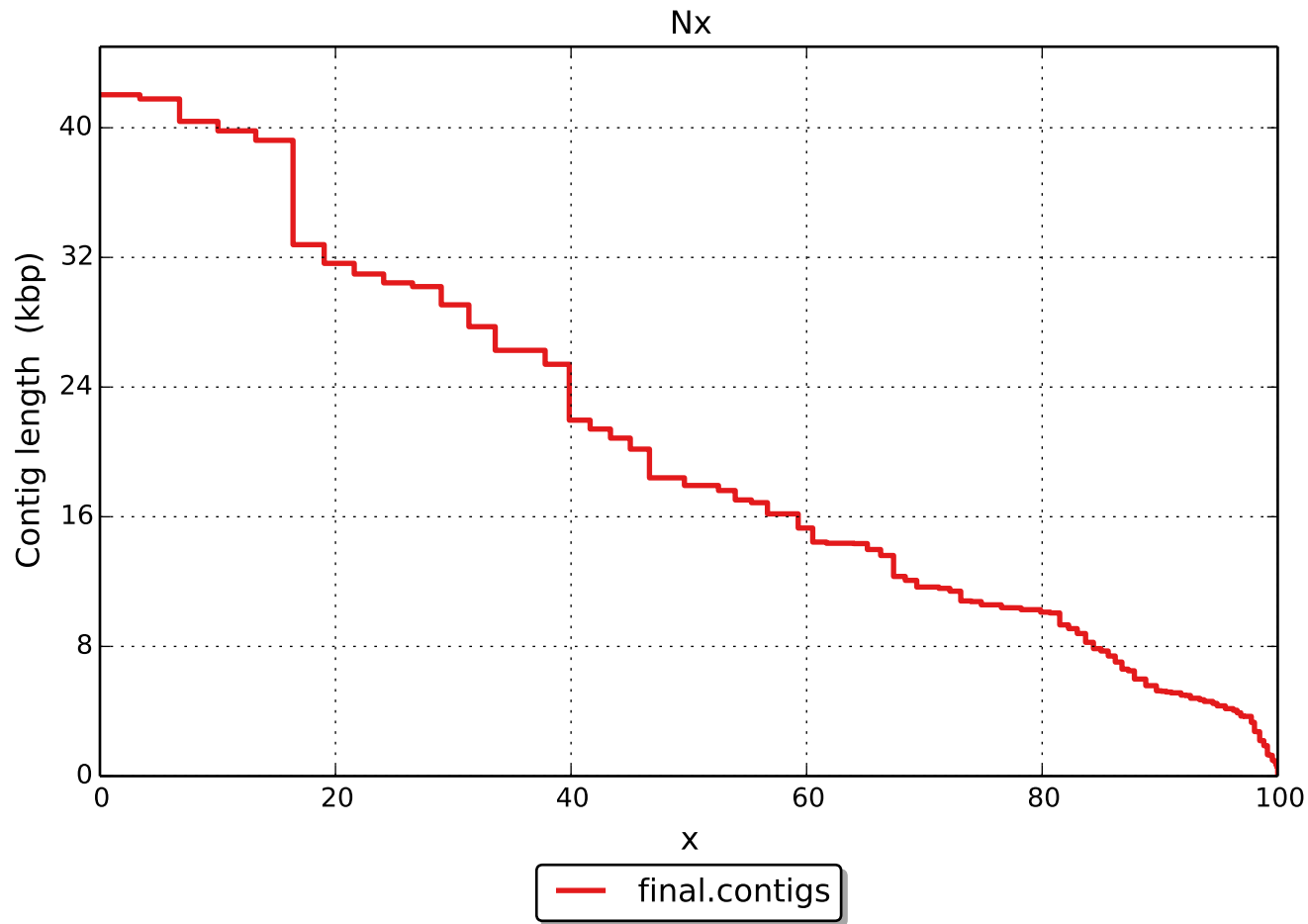
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Cumulative length

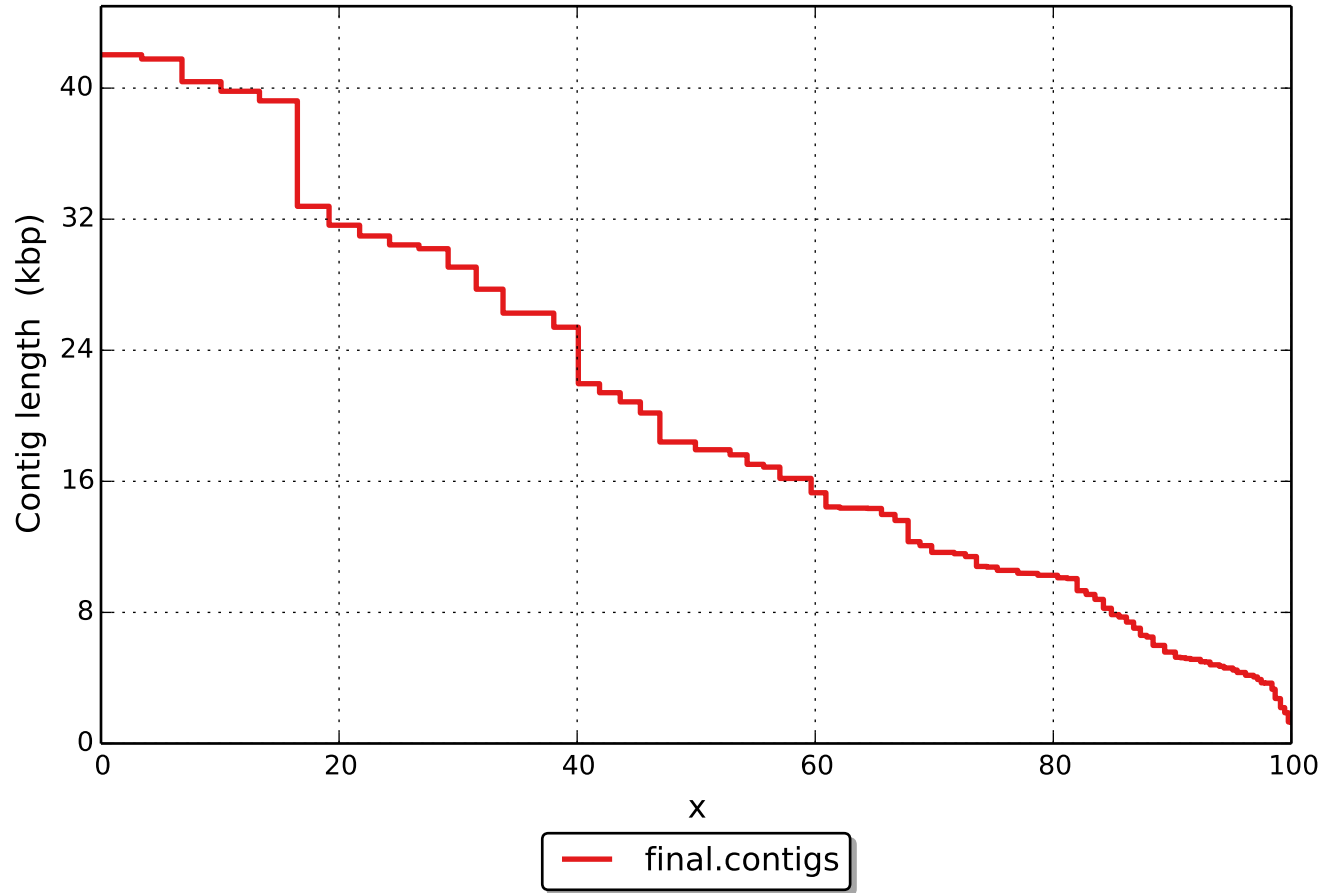


GC content





NGx

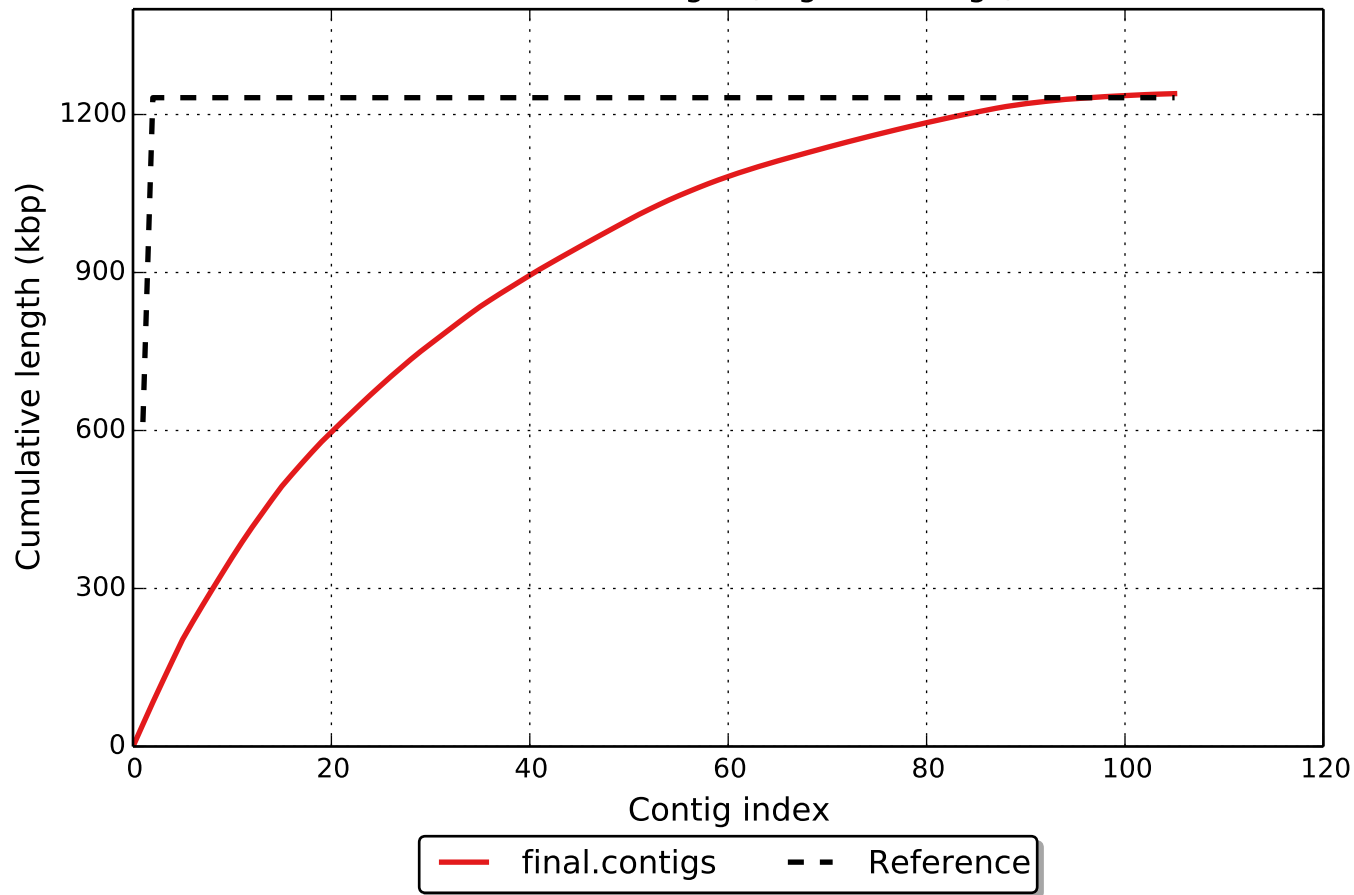


# Misassemblies

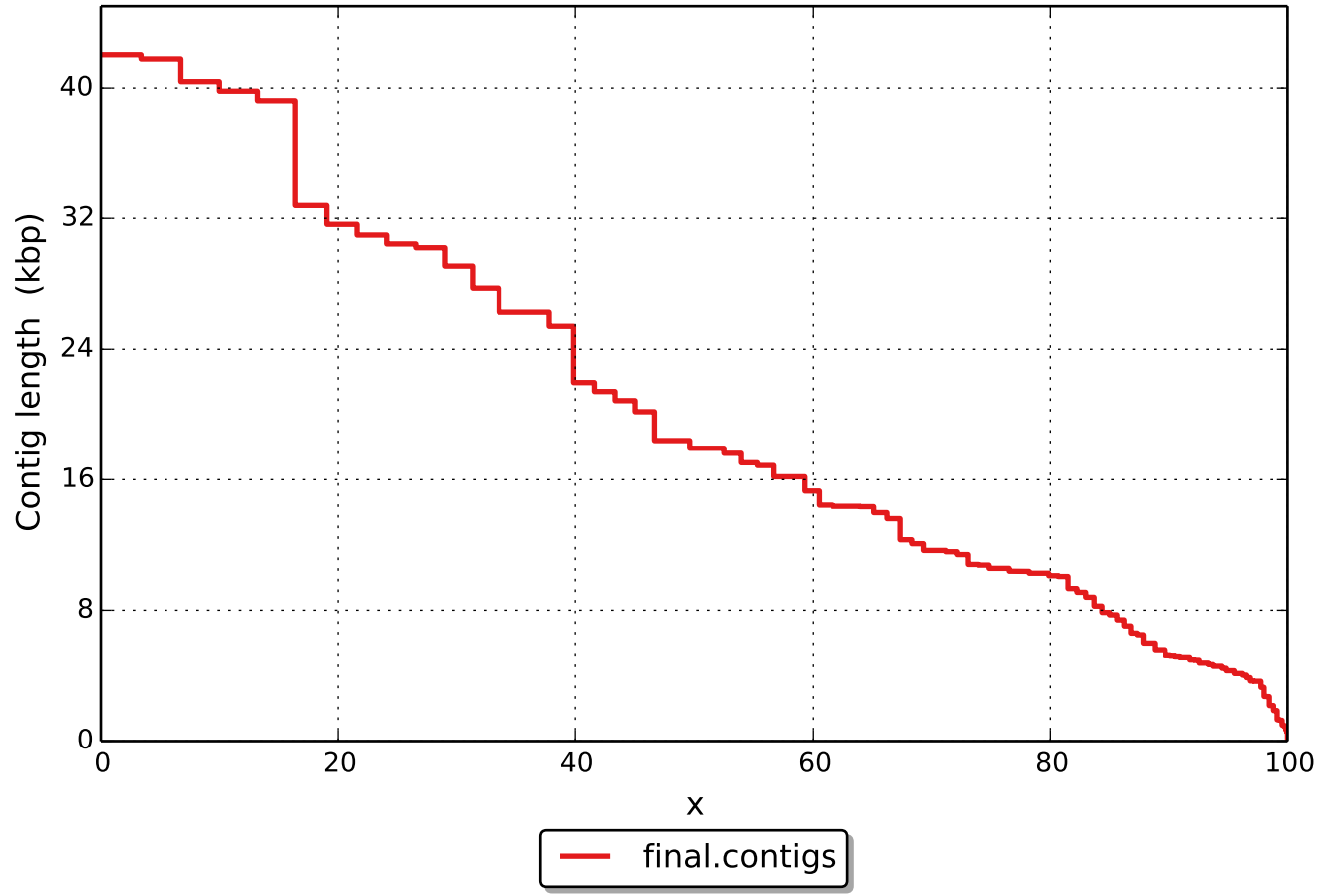




Cumulative length (aligned contigs)



NAx



# NGAx

