

## Report

	final.contigs
# contigs (>= 0 bp)	189
# contigs (>= 1000 bp)	175
Total length (>= 0 bp)	1297846
Total length (>= 1000 bp)	1289931
# contigs	183
Largest contig	30887
Total length	1295564
Reference length	1283598
GC (%)	26.29
Reference GC (%)	26.30
N50	10988
NG50	11095
N75	6128
NG75	6826
L50	41
LG50	40
L75	78
LG75	77
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.808
Duplication ratio	1.011
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2.97
# indels per 100 kbp	0.00
Largest alignment	30887
NA50	10988
NGA50	11095
NA75	6128
NGA75	6826
LA50	41
LGA50	40
LA75	78
LGA75	77

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	38
# indels	0
# short indels	0
# long indels	0
Indels length	0

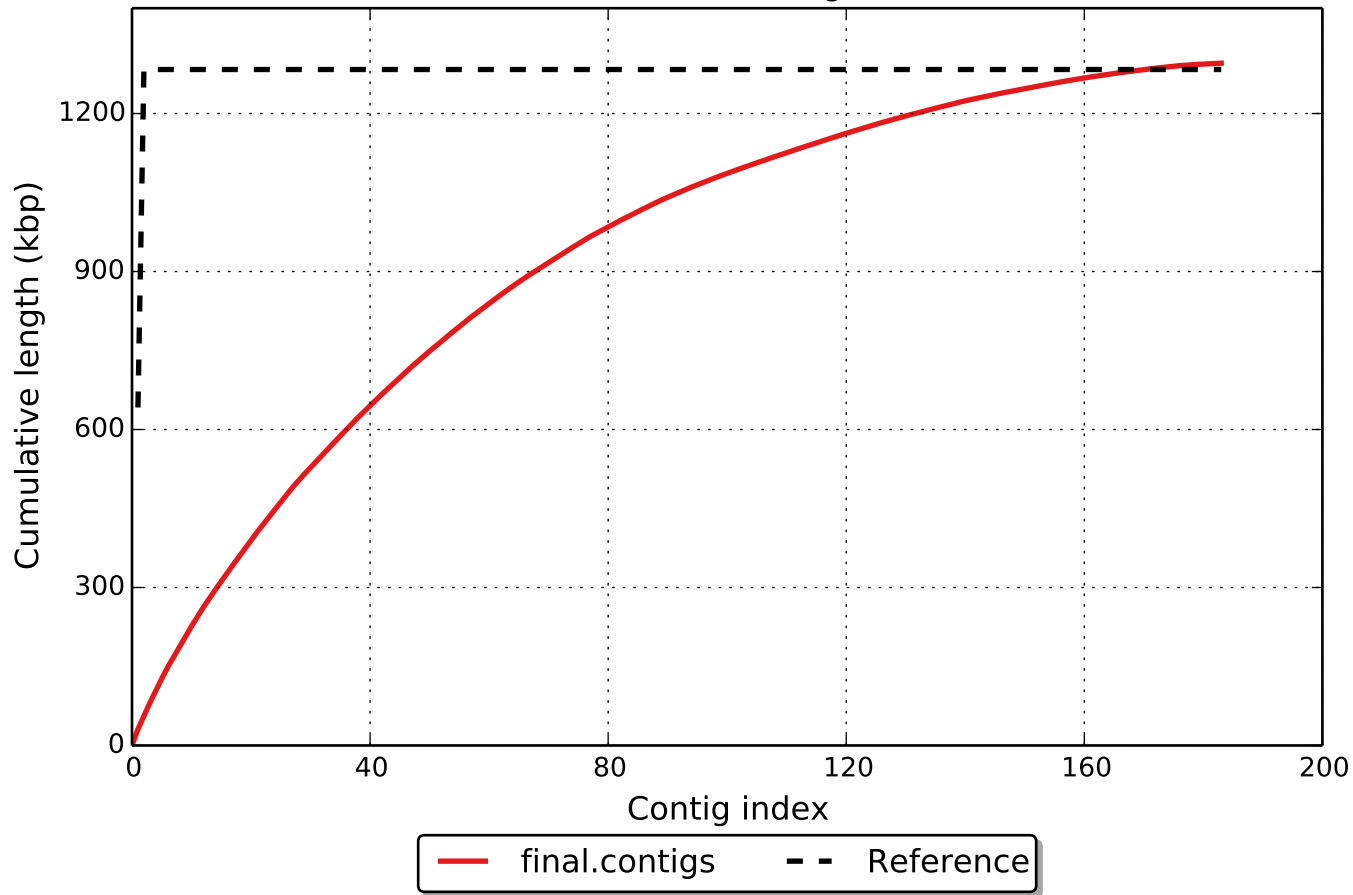
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

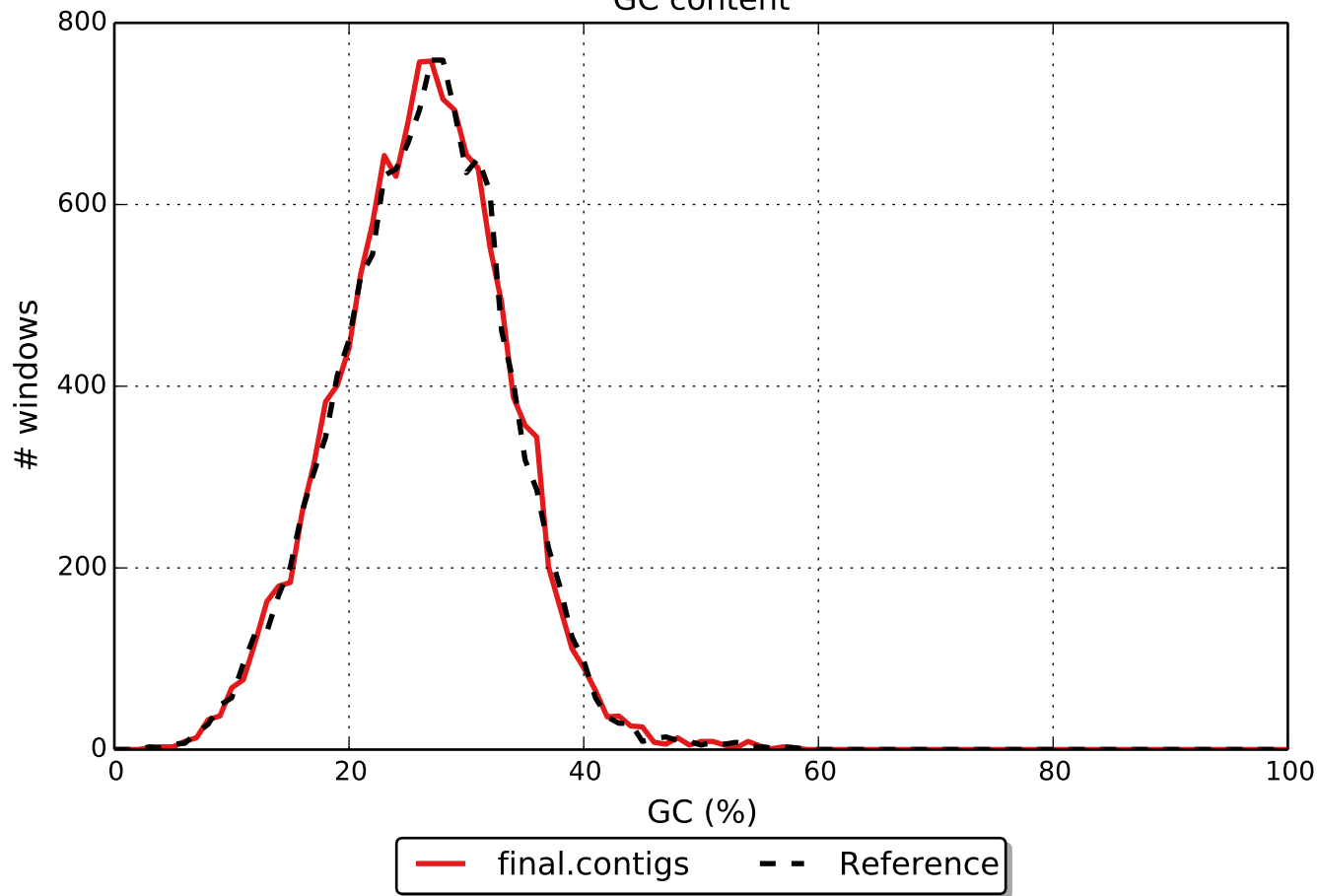
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

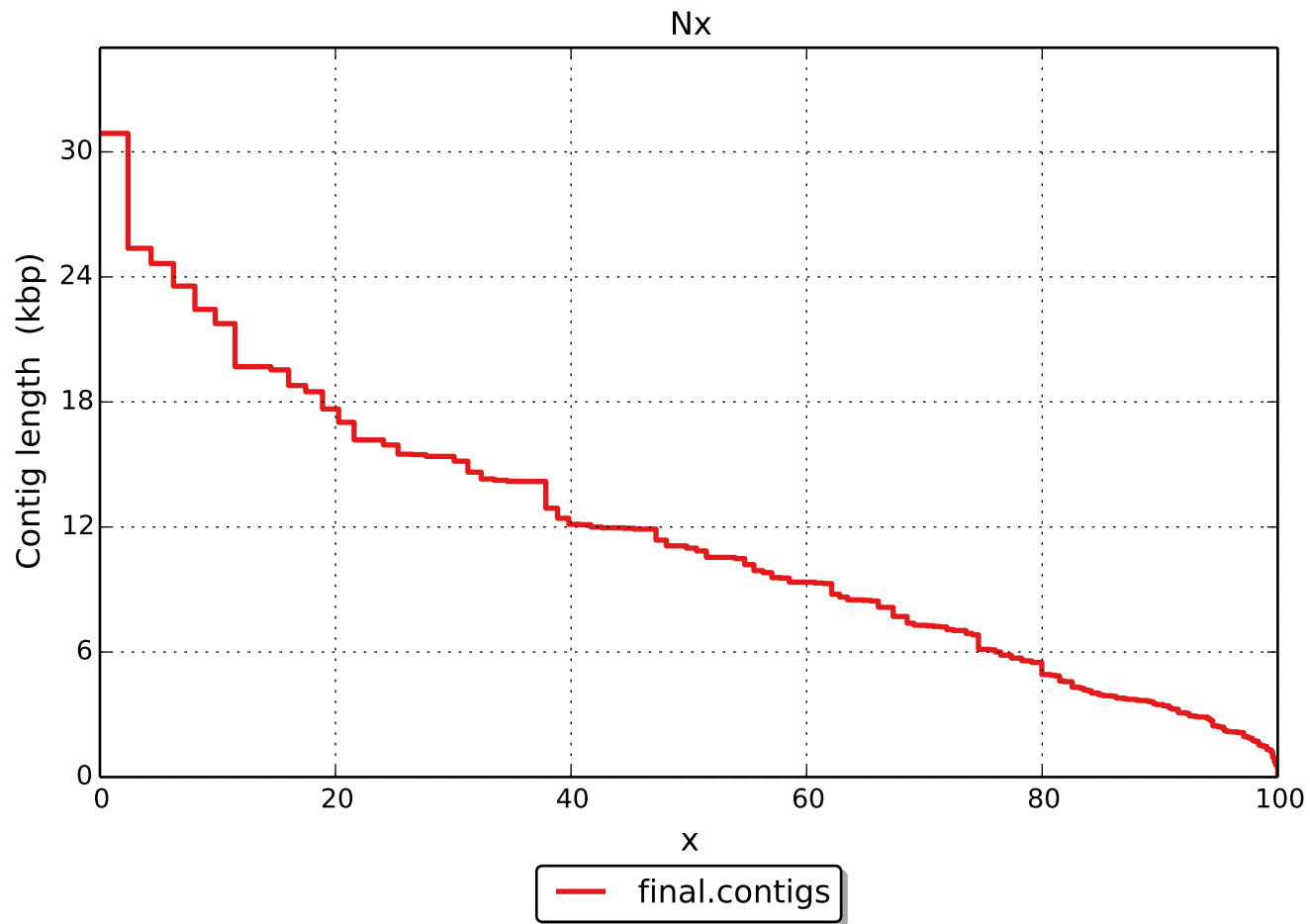
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Cumulative length

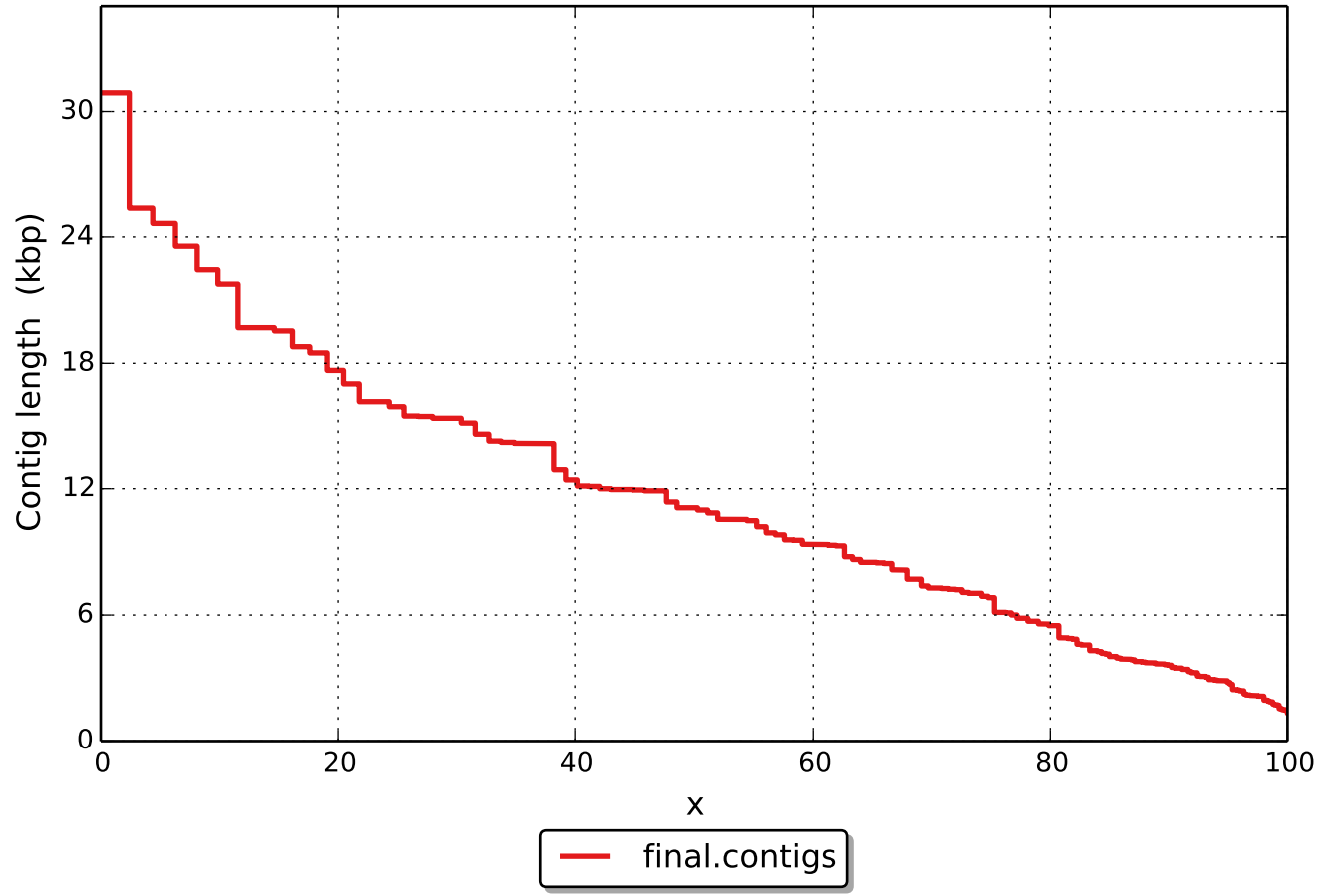


GC content





NGx

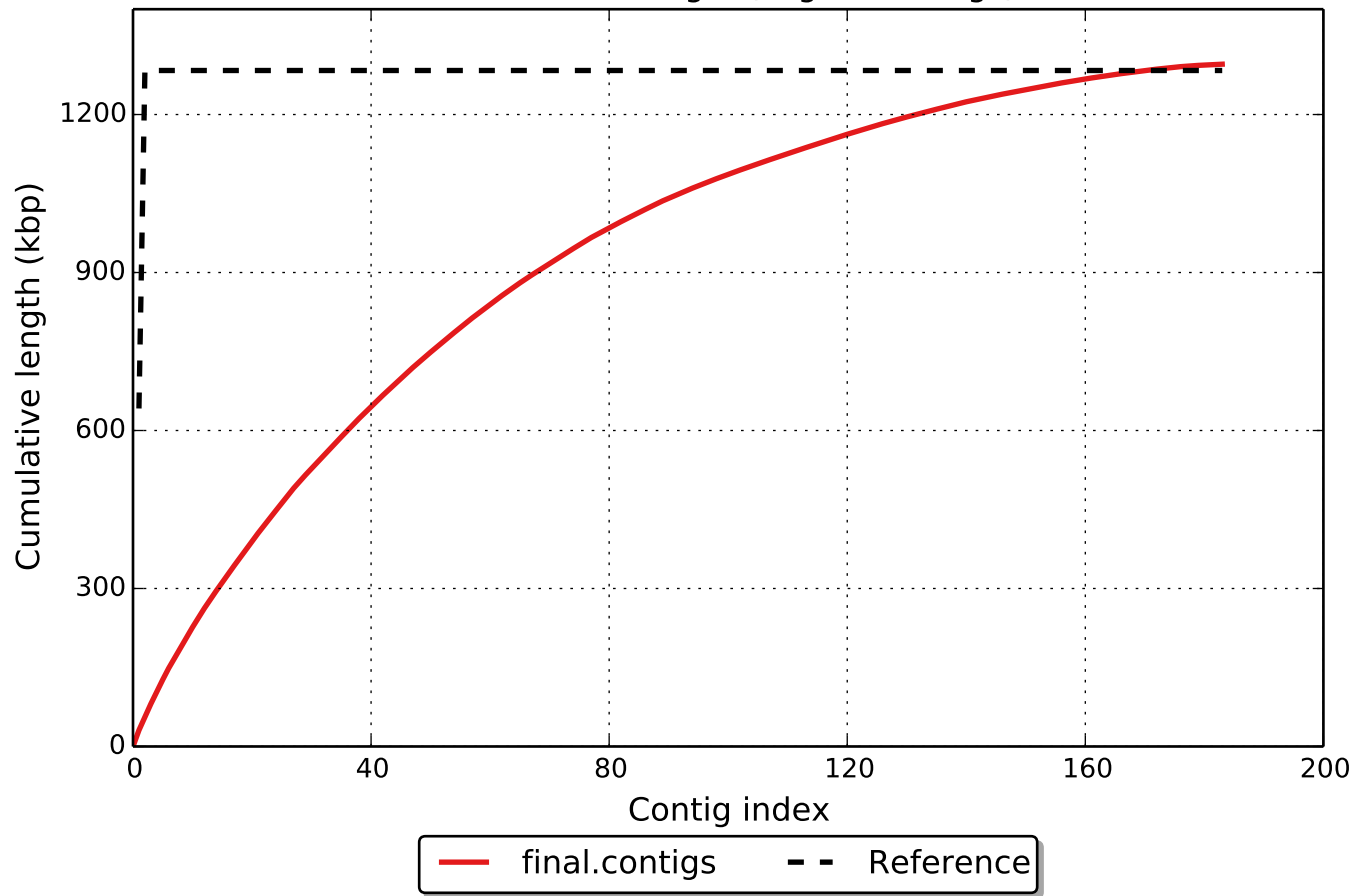


# Misassemblies

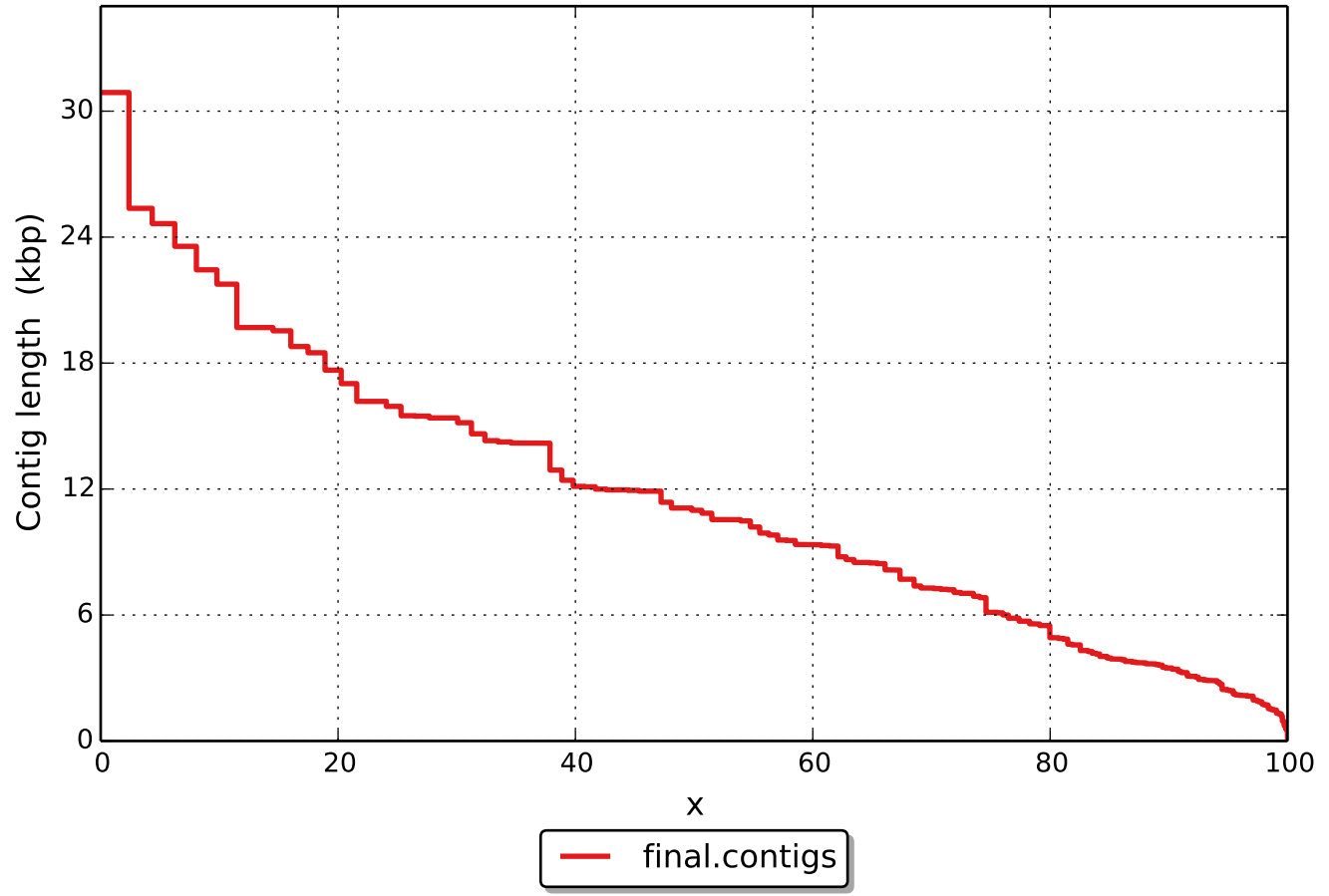




Cumulative length (aligned contigs)



NAx



# NGAx

