

## Report

	final.contigs
# contigs (>= 1000 bp)	1896
# contigs (>= 5000 bp)	15
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	3433112
Total length (>= 5000 bp)	85502
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3527
Largest contig	6560
Total length	4613265
Reference length	4857432
GC (%)	52.21
Reference GC (%)	52.22
N50	1516
NG50	1467
N75	988
NG75	914
L50	986
LG50	1068
L75	1924
LG75	2116
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	90.698
Duplication ratio	1.047
# N's per 100 kbp	0.00
# mismatches per 100 kbp	69.96
# indels per 100 kbp	0.11
Largest alignment	6560
NA50	1516
NGA50	1467
NA75	988
NGA75	914
LA50	986
LGA50	1068
LA75	1924
LGA75	2116

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

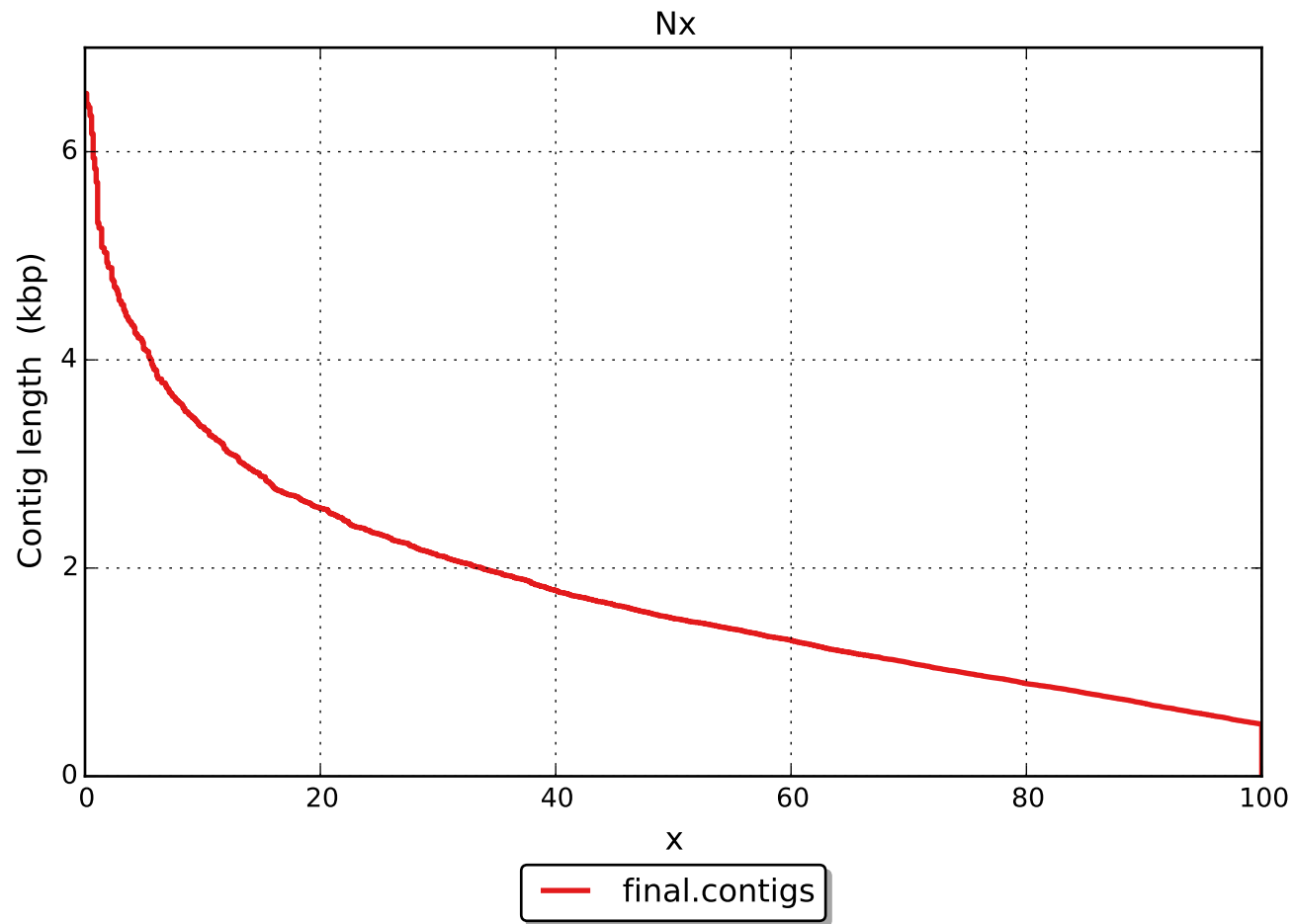
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	3082
# indels	5
# short indels	5
# long indels	0
Indels length	8

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).

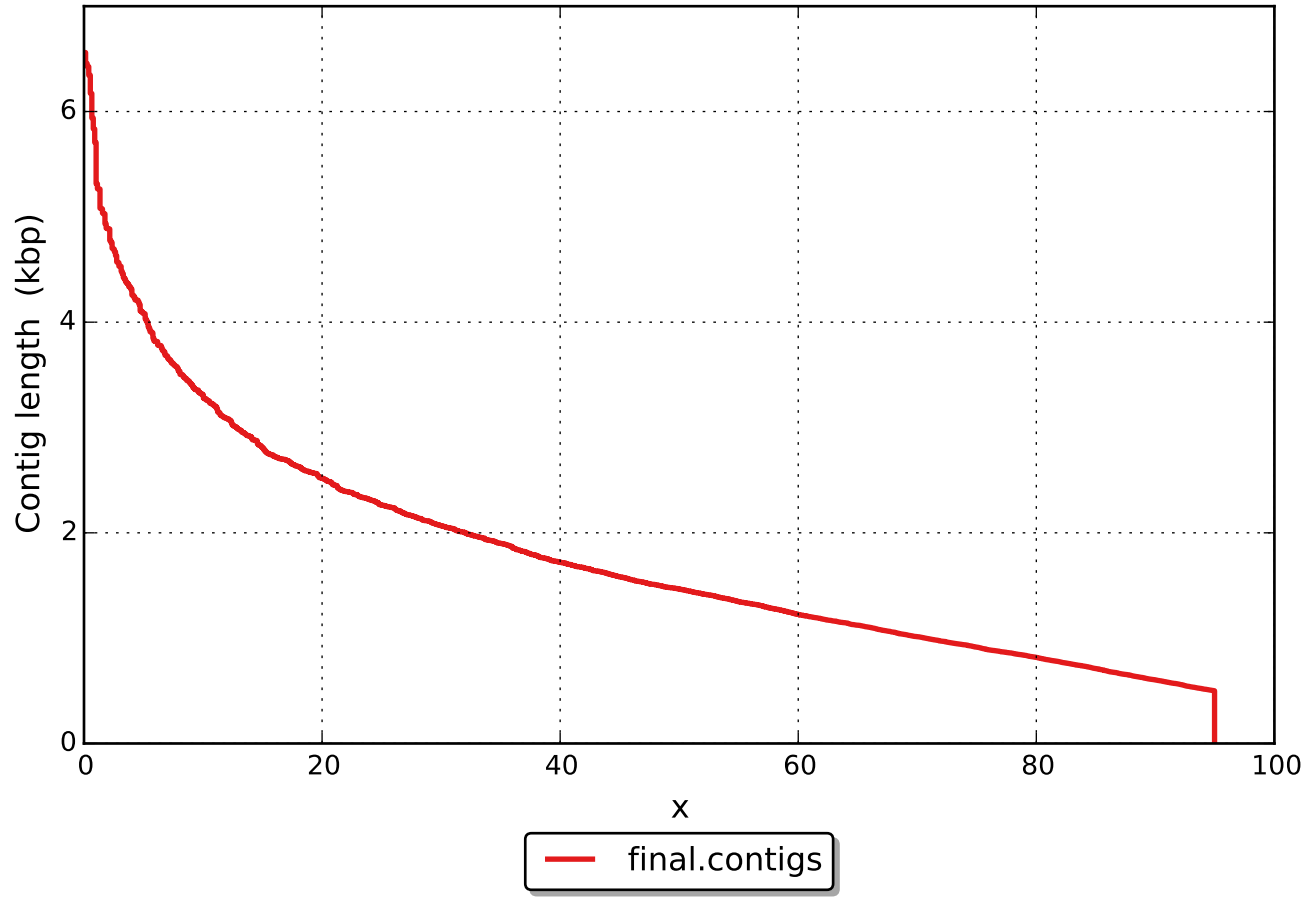
## Unaligned report

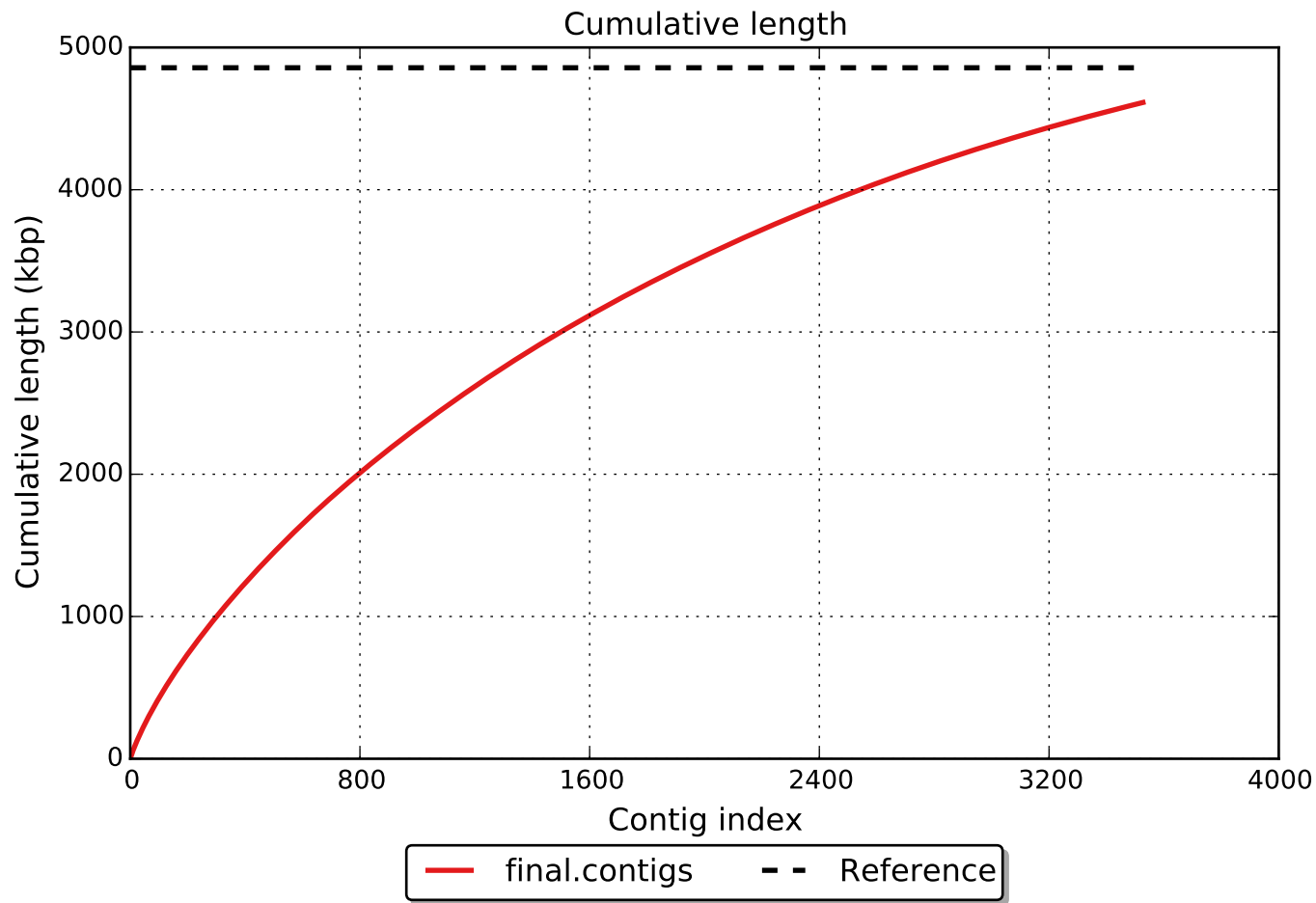
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

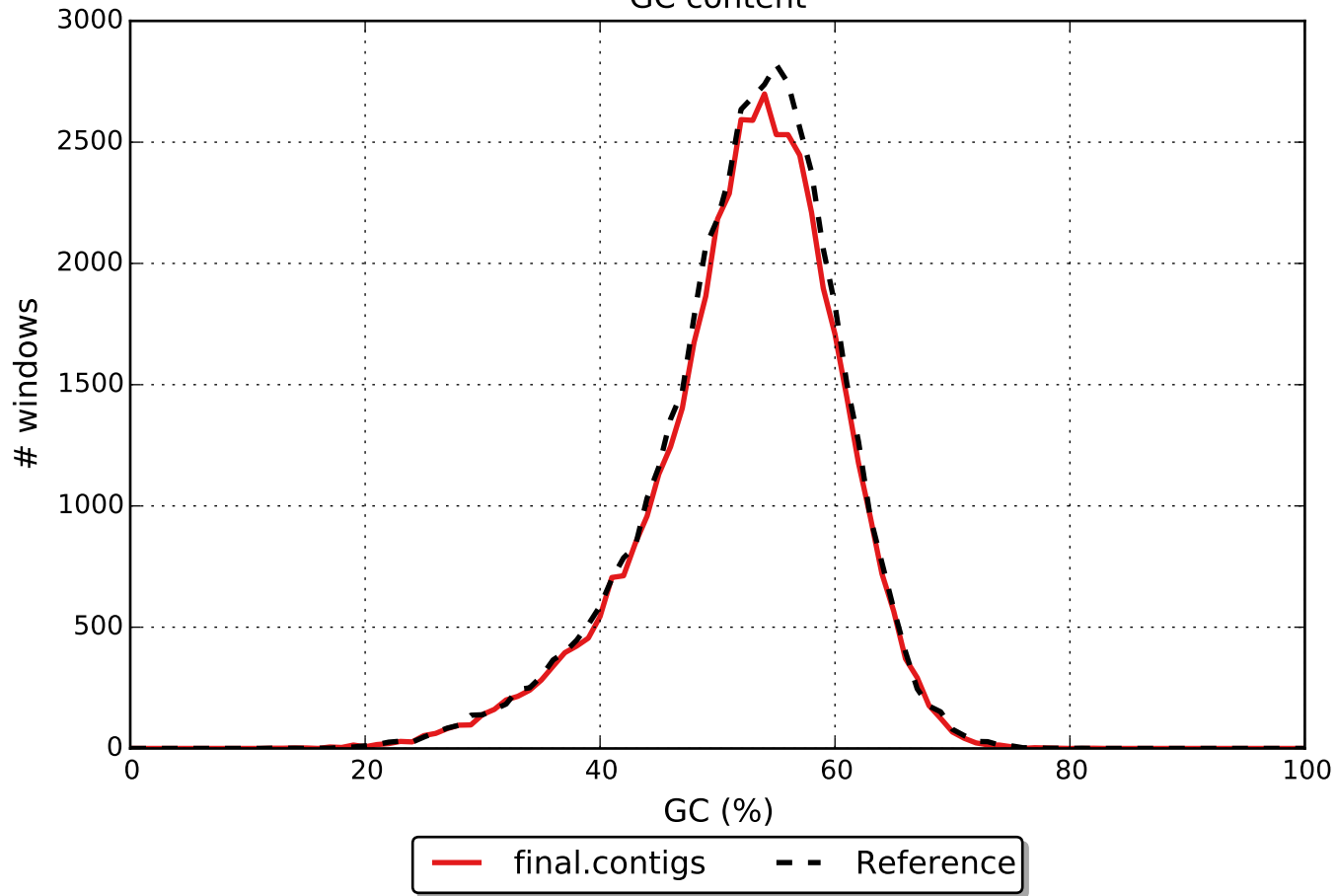


NGx





GC content

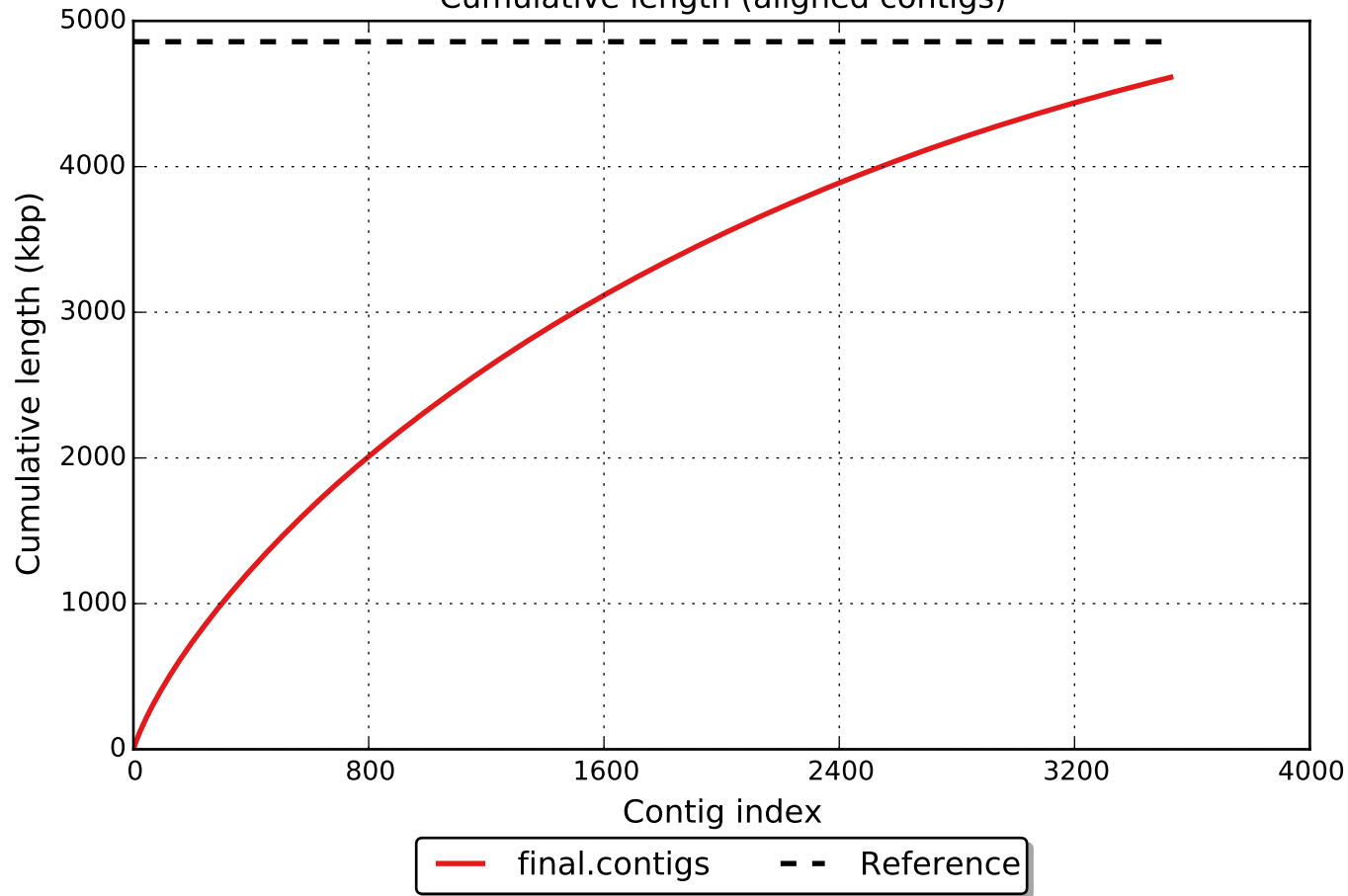


# Misassemblies

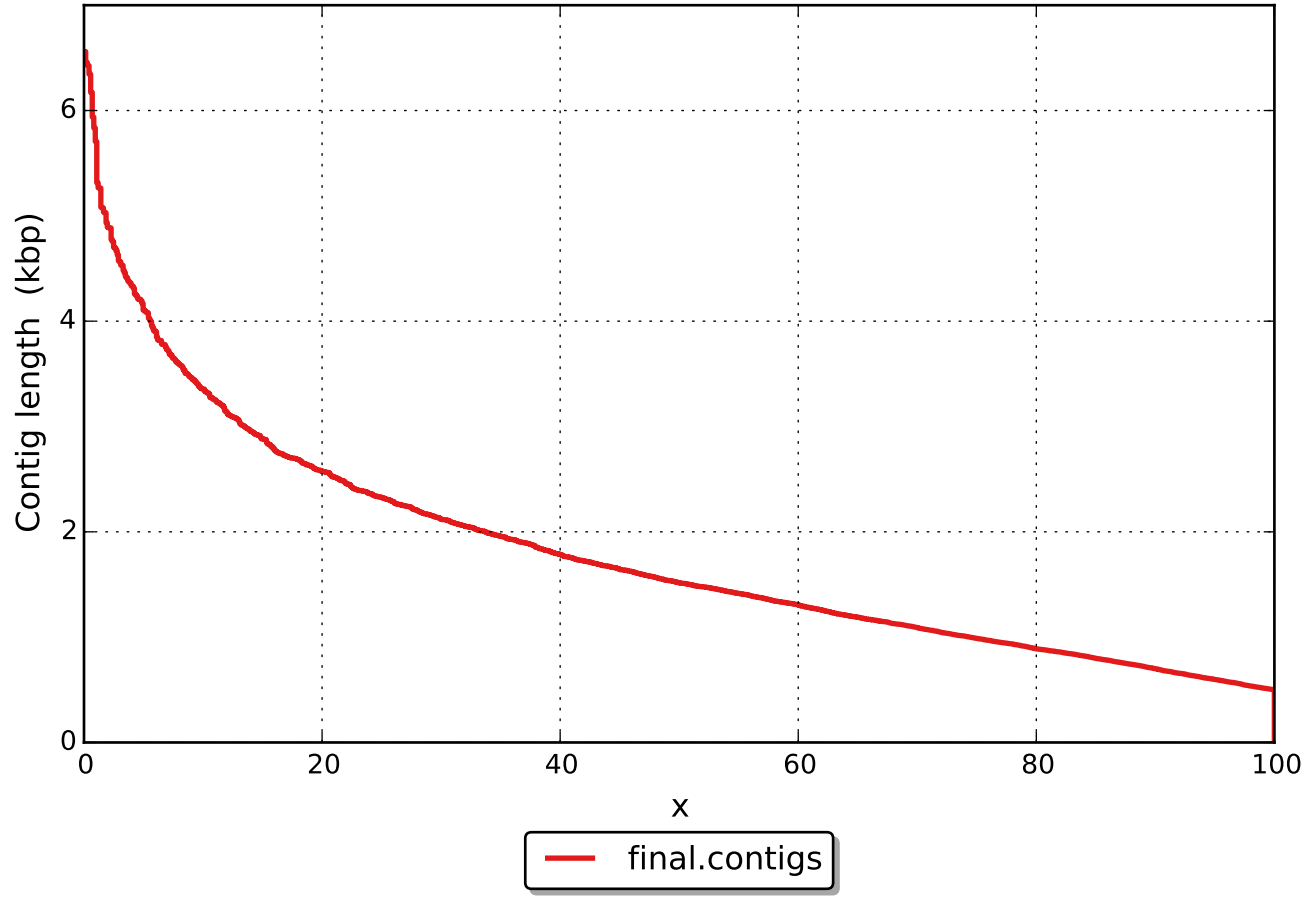




Cumulative length (aligned contigs)



NAx



NGAx

