Report

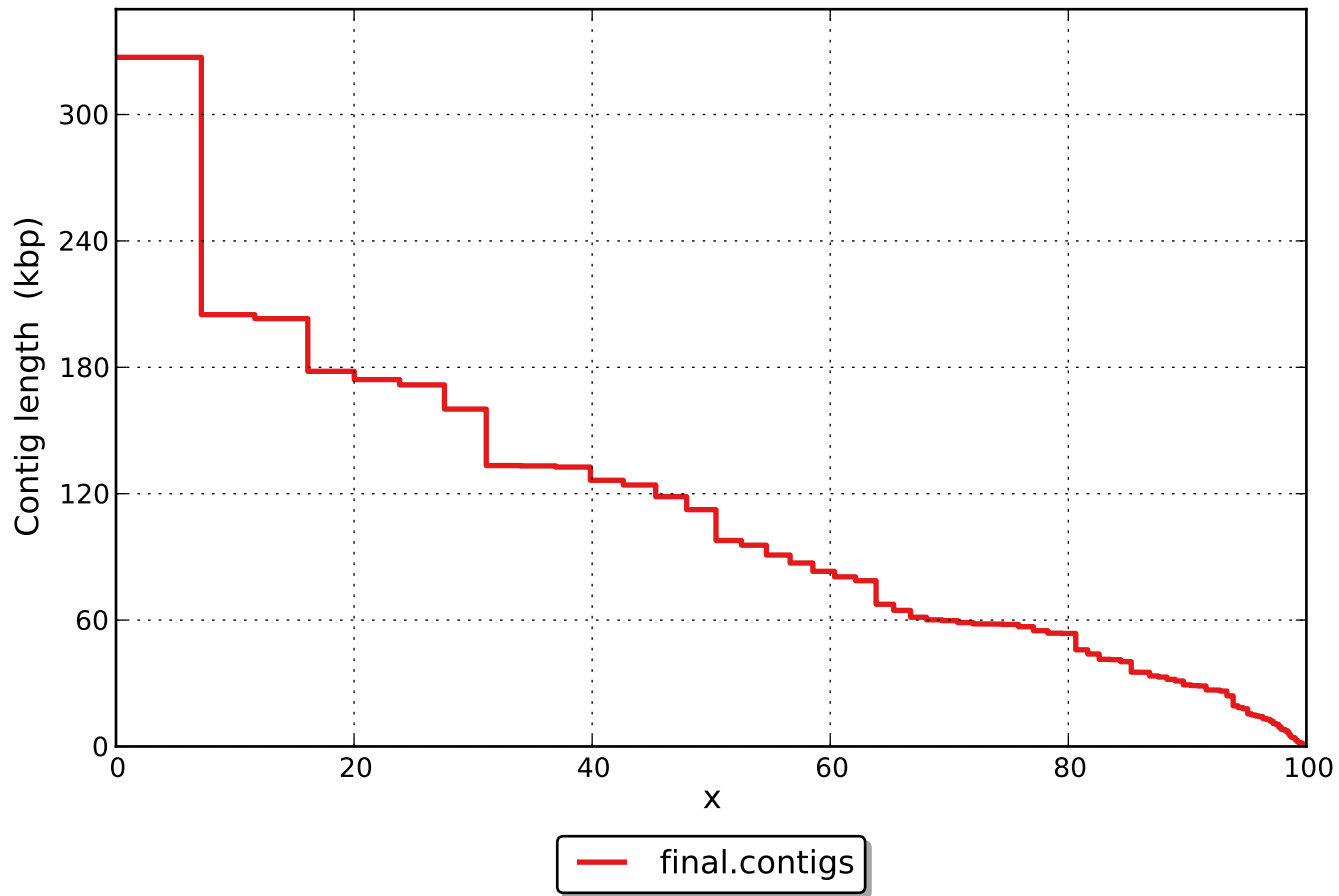|	final.contigs
# contigs (>= 1000 bp)	95
# contigs (>= 5000 bp)	70
# contigs (>= 10000 bp)	64
# contigs (>= 25000 bp)	51
# contigs (>= 50000 bp)	34
Total length (>= 1000 bp)	4555837
Total length (>= 5000 bp)	4502124
Total length (>= 10000 bp)	4456744
Total length (>= 25000 bp)	4258489
Total length (>= 50000 bp)	3679265
# contigs	107
Largest contig	327154
Total length	4563292
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	112427
NG50	97783
N75	57924
NG75	56868
L50	14
LG50	15
L75	30
LG75	31
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	45889
# local misassemblies	11
# unaligned contigs	0 + 1 part
Unaligned length	53
Genome fraction (%)	98.251
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	59.86
# indels per 100 kbp	9.89
Largest alignment	327154
NA50	112427
NGA50	97783
NA75	57924
NGA75	56868
LA50	14
LGA50	15
LA75	30
LGA75	31

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	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	45889
# local misassemblies	11
# mismatches	2730
# indels	451
# short indels	450
# long indels	1
Indels length	712

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).
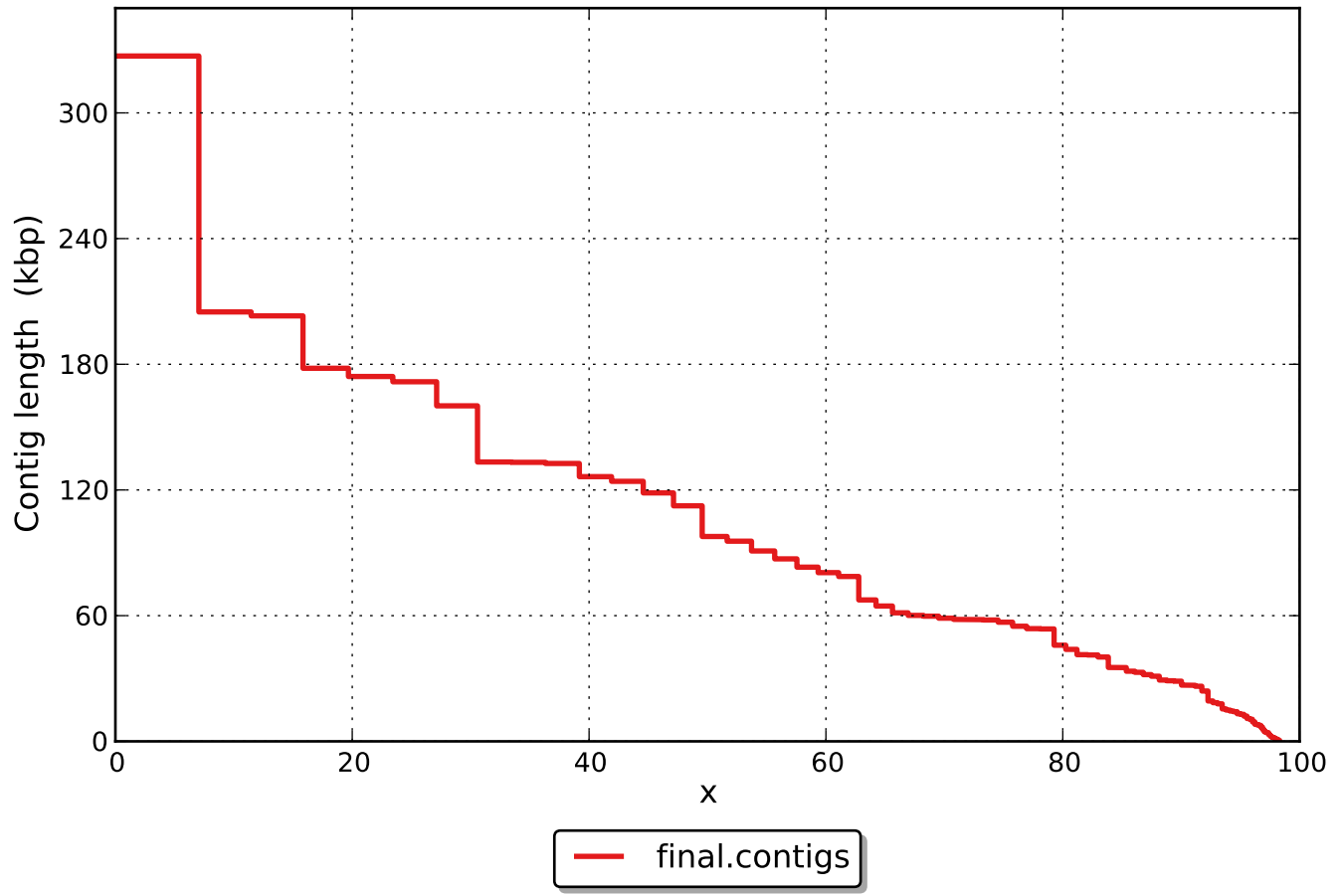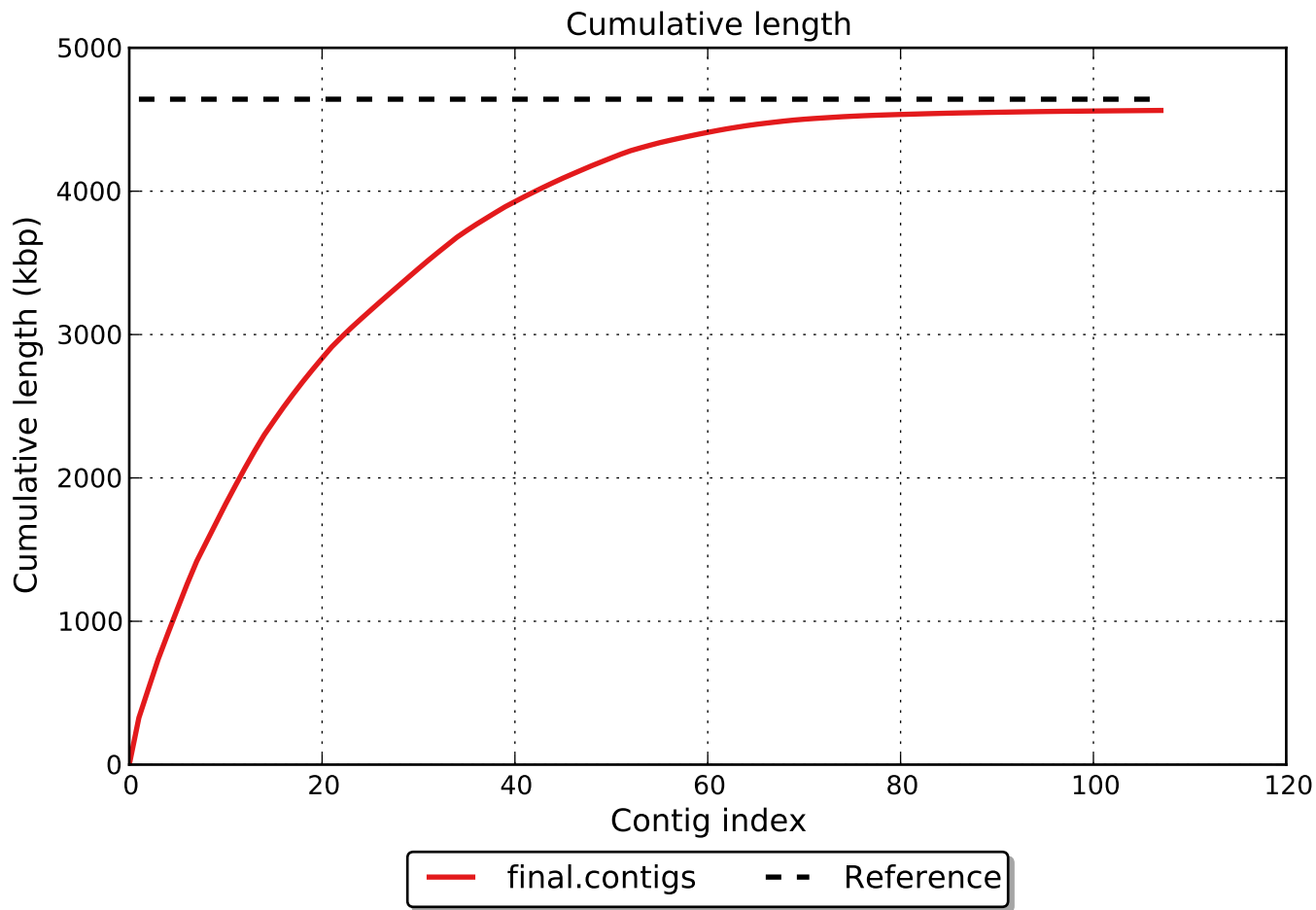
Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	53
# N's	0

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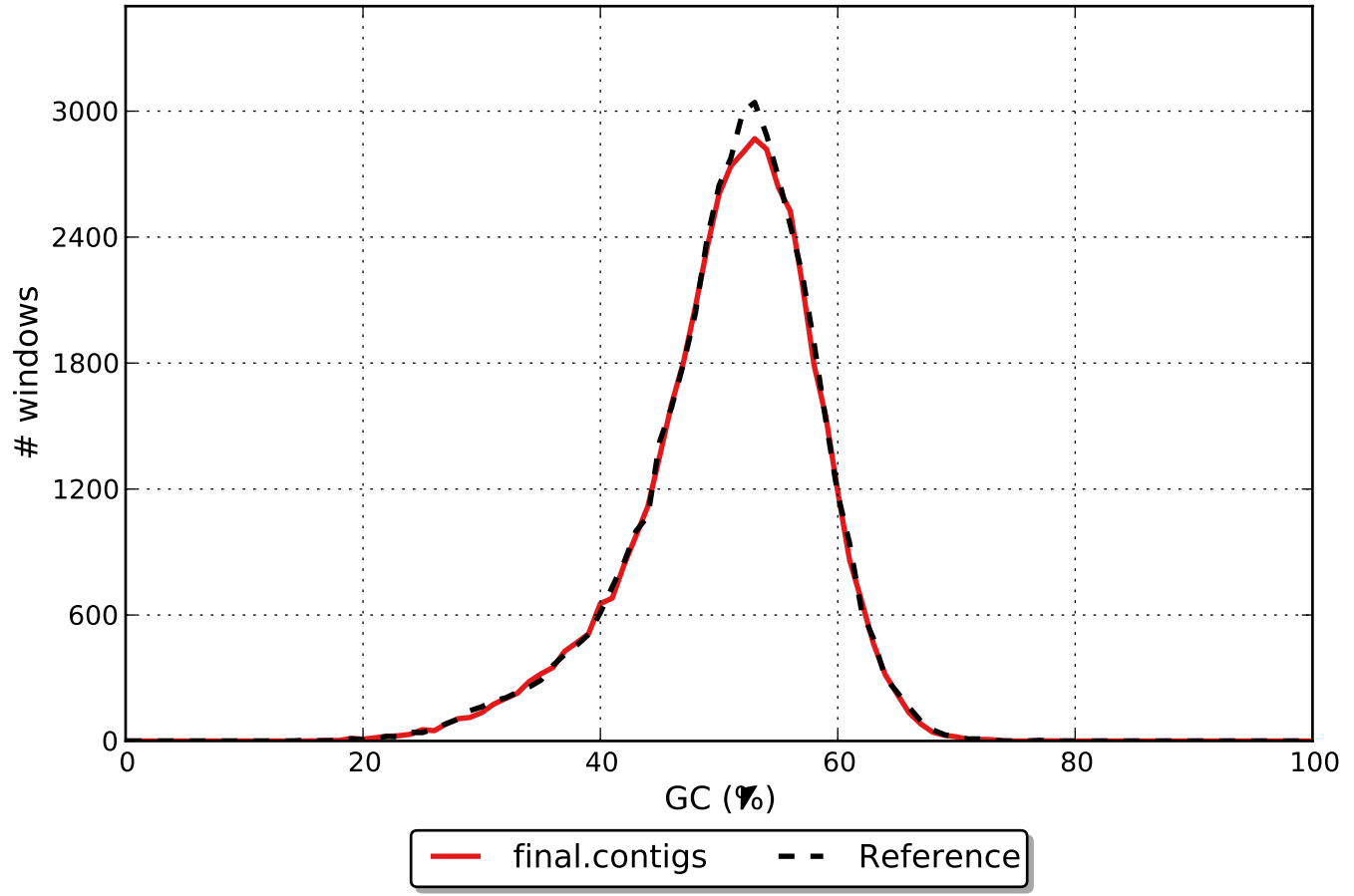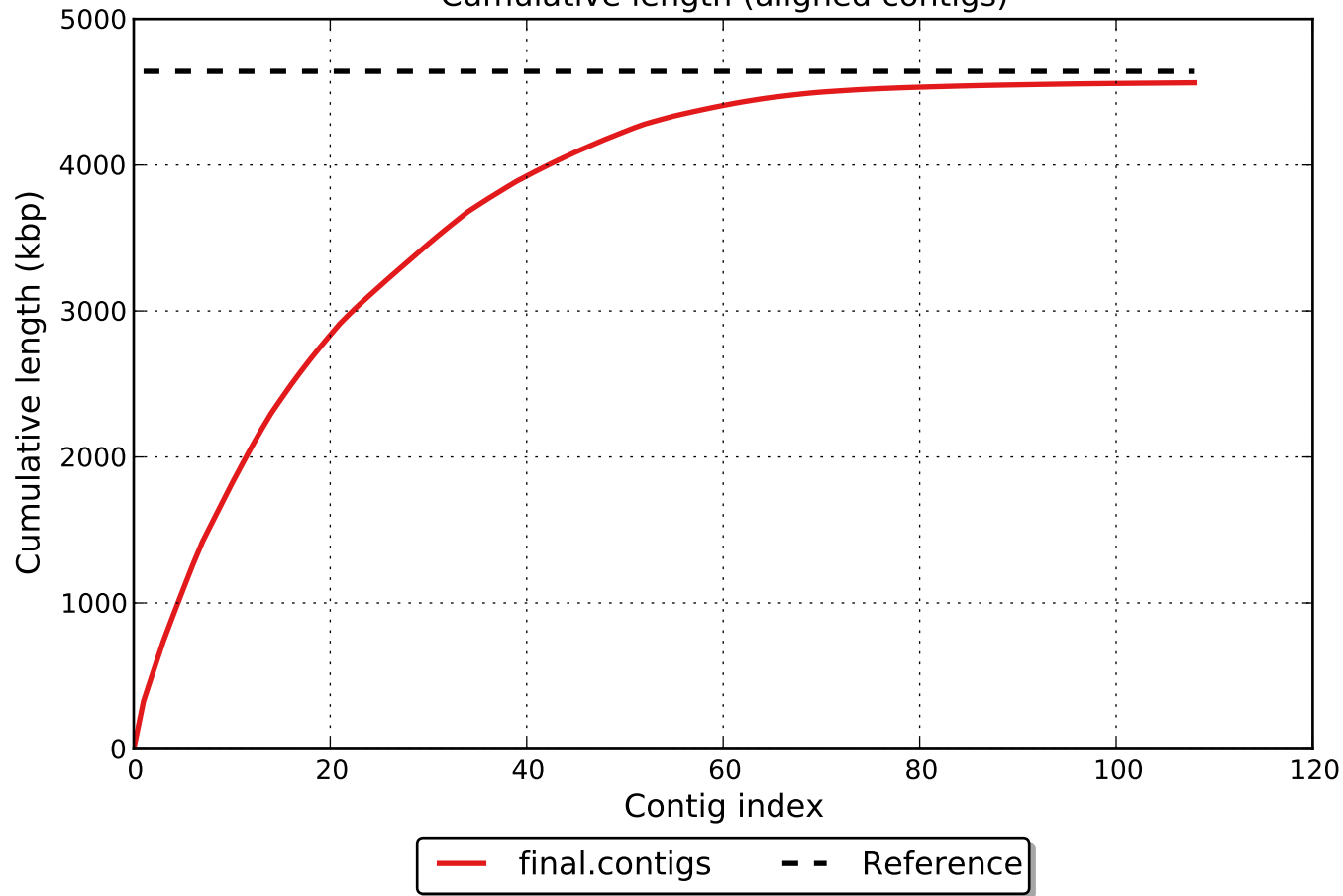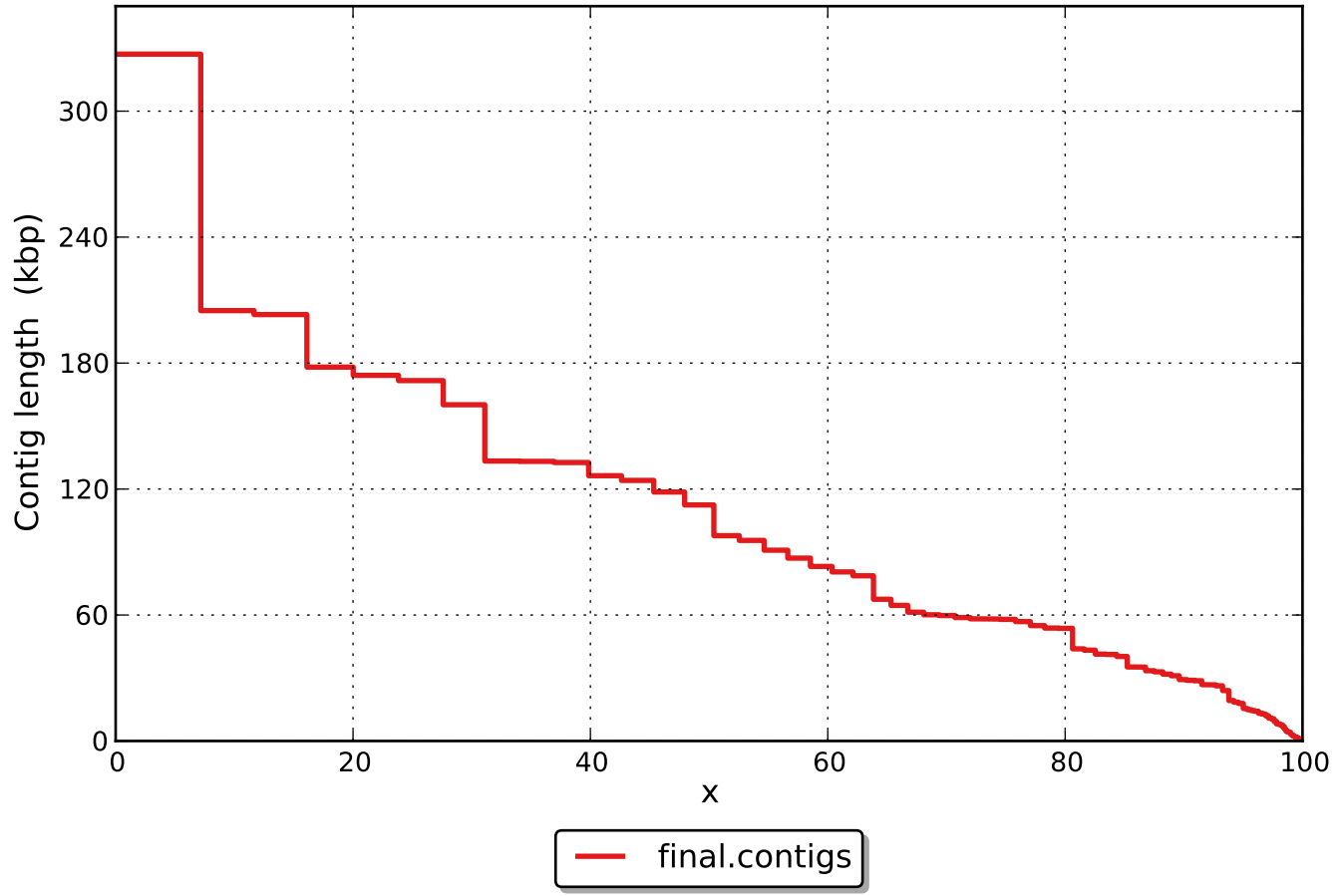(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Nx

NGx

Contig length (kbp)

x

final.contigs

Cumulative length

GC content

windows vs GC (%)

Legend: final.contigs, Reference

Misassemblies

final.contigs

relocations

Cumulative length (aligned contigs)