Report

|	final.contigs
# contigs (>= 0 bp)	238
# contigs (>= 1000 bp)	127
# contigs (>= 5000 bp)	100
# contigs (>= 10000 bp)	87
# contigs (>= 25000 bp)	63
# contigs (>= 50000 bp)	32
Total length (>= 0 bp)	4597283
Total length (>= 1000 bp)	4556951
Total length (>= 5000 bp)	4495313
Total length (>= 10000 bp)	4396217
Total length (>= 25000 bp)	3992149
Total length (>= 50000 bp)	2877275
# contigs	147
Largest contig	309478
Total length	4569580
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	71793
NG50	71793
N75	38366
NG75	35546
L50	23
LG50	23
L75	45
LG75	47
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.239
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	7.52
# indels per 100 kbp	0.02
Largest alignment	309478
NA50	71793
NGA50	71793
NA75	38366
NGA75	35546
LA50	23
LGA50	23
LA75	45
LGA75	47

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).
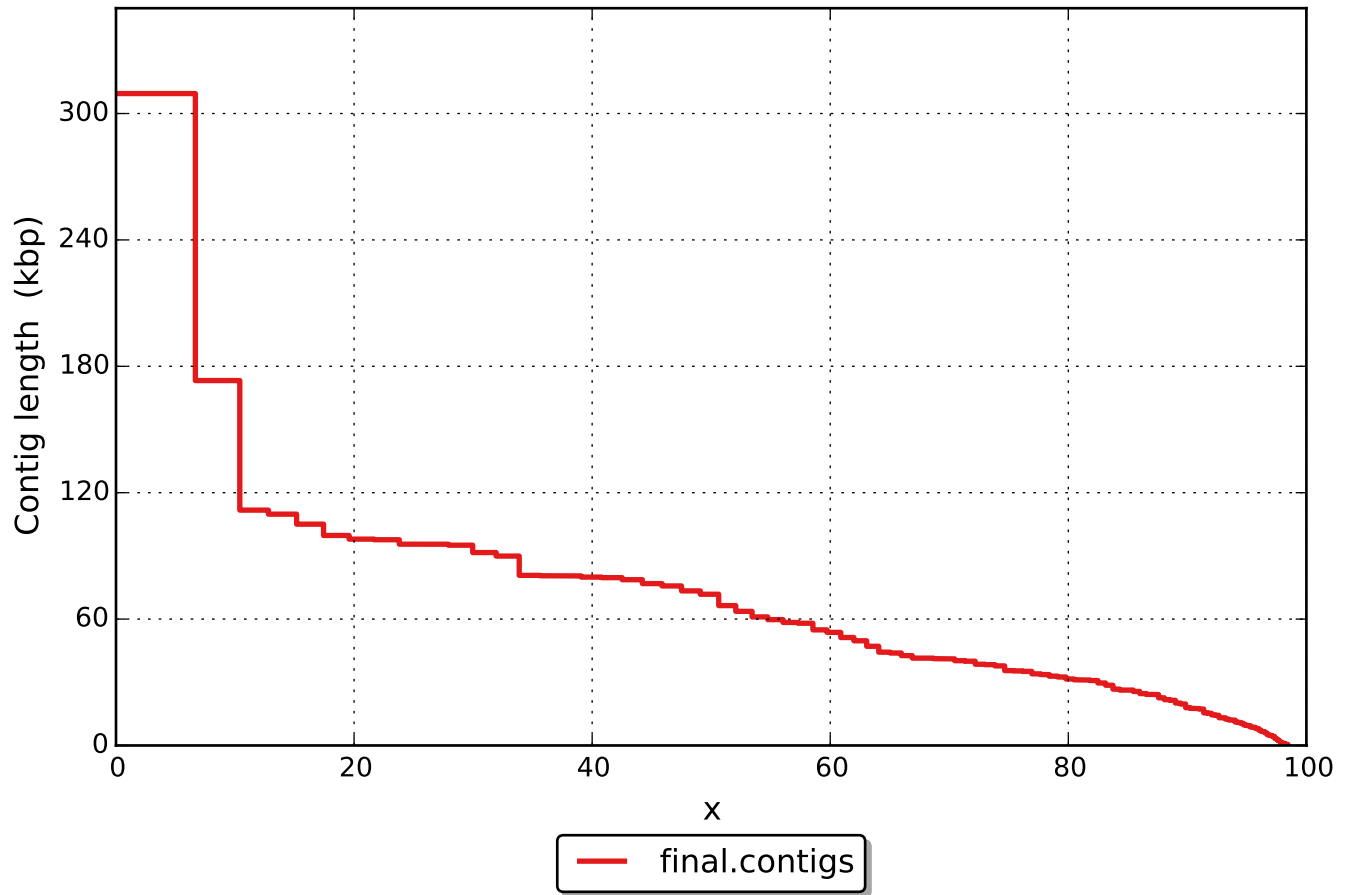
Misassemblies report

|	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# mismatches	343
# indels	1
# short indels	1
# long indels	0
Indels length	2

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	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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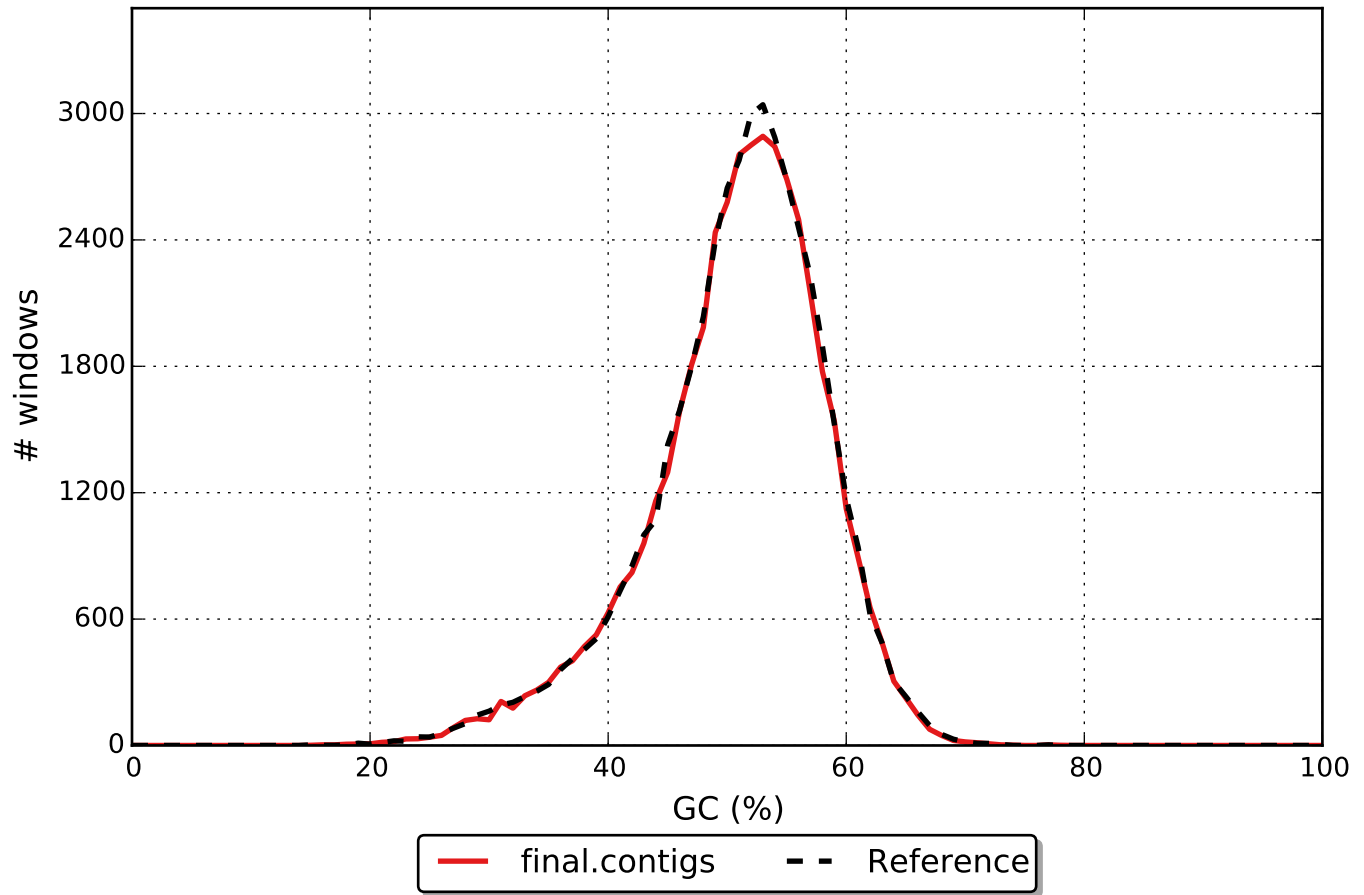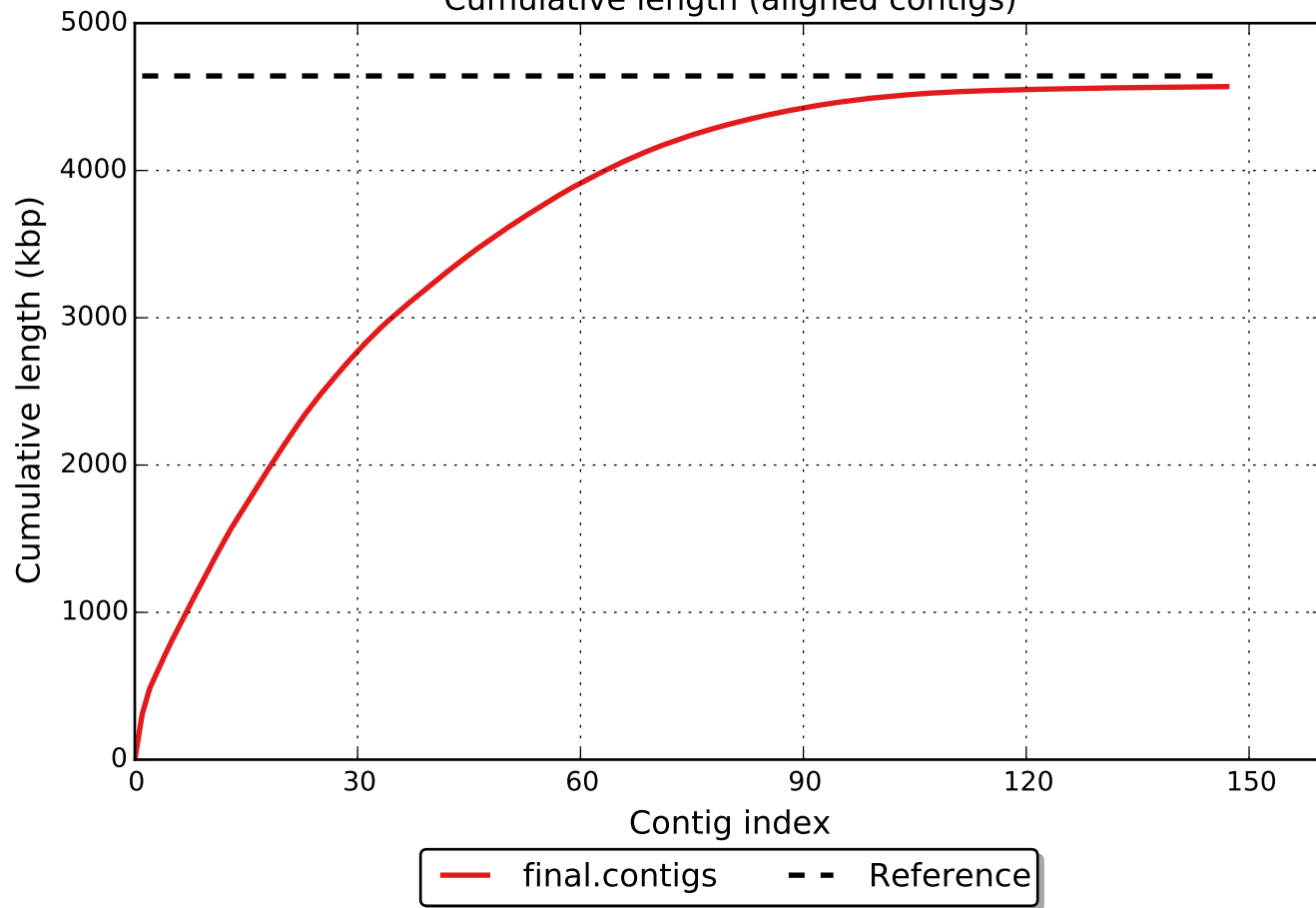(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).
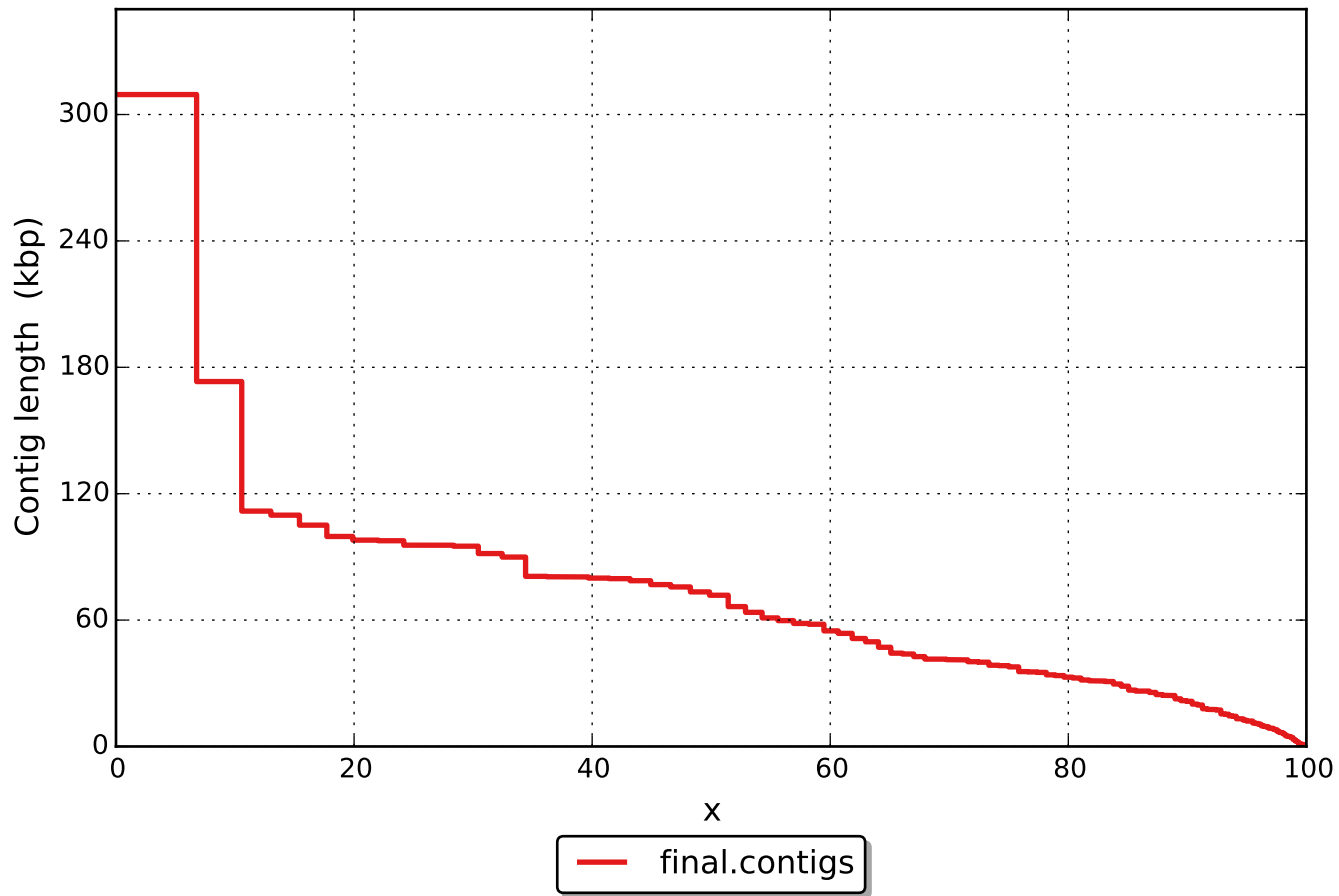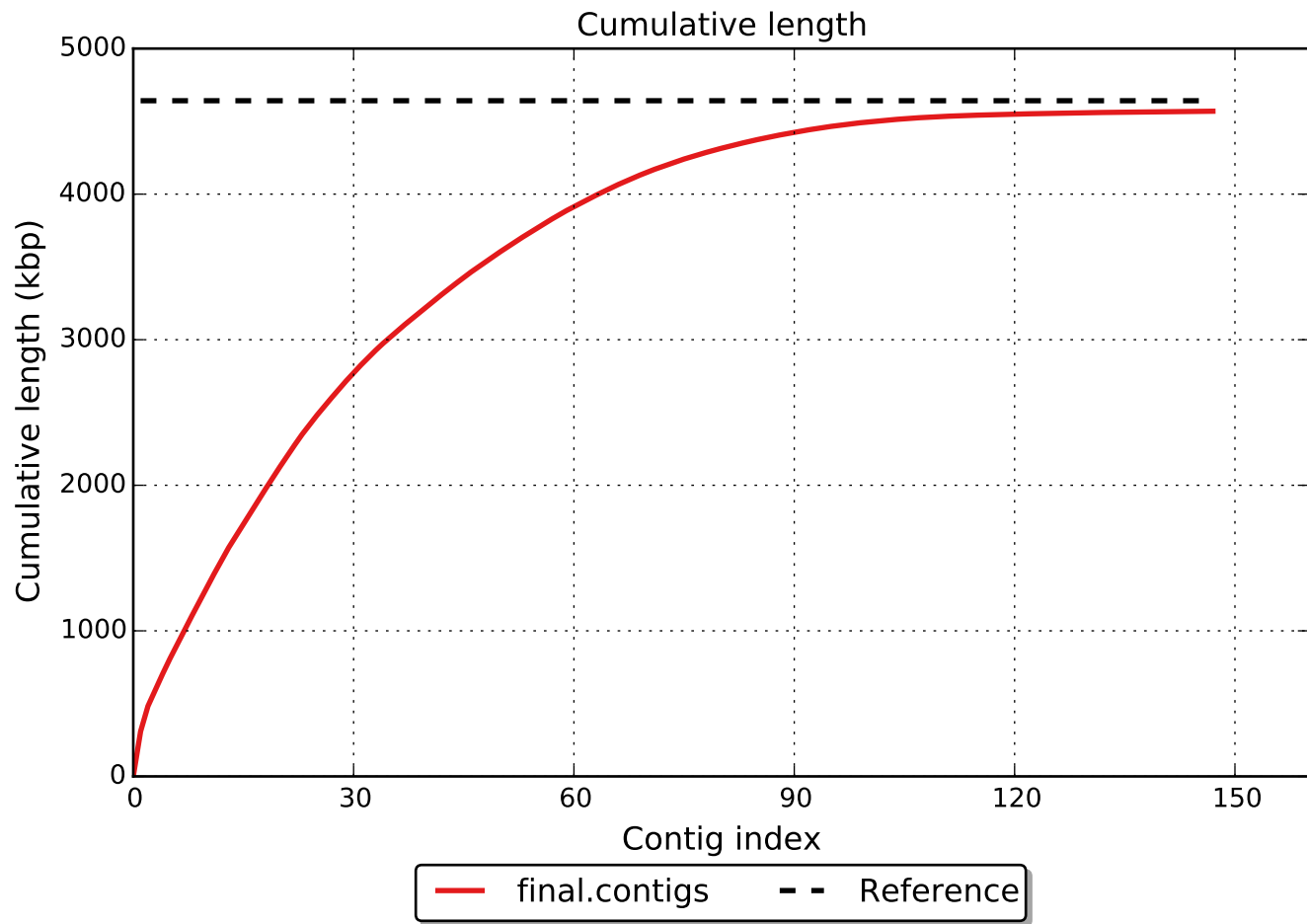
GC content

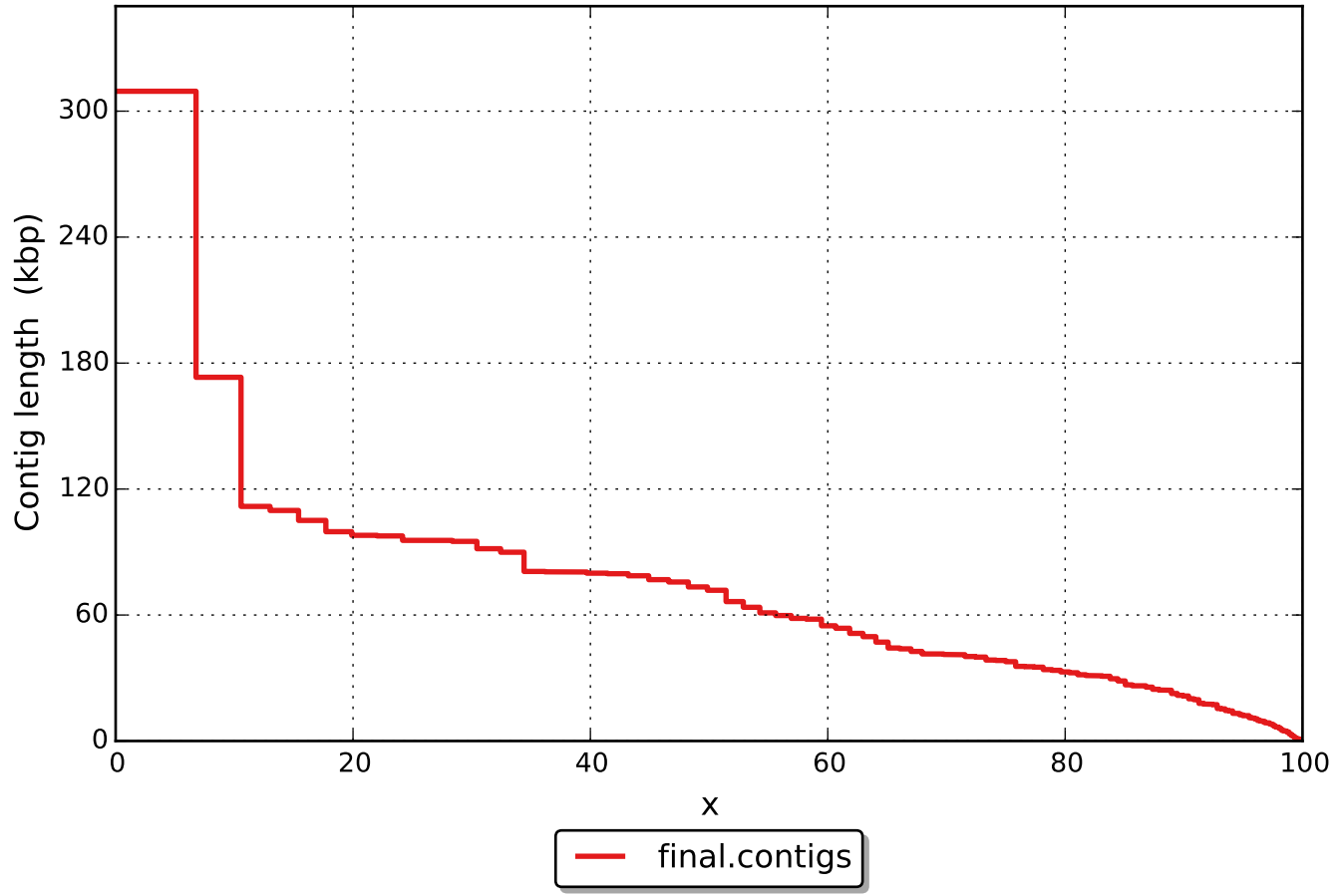# Misassemblies

final.contigs

Cumulative length (aligned contigs)

NGAx