Report

|	final.contigs
# contigs (>= 0 bp)	178
# contigs (>= 1000 bp)	93
# contigs (>= 5000 bp)	69
# contigs (>= 10000 bp)	63
# contigs (>= 25000 bp)	49
# contigs (>= 50000 bp)	30
Total length (>= 0 bp)	4581476
Total length (>= 1000 bp)	4551138
Total length (>= 5000 bp)	4498615
Total length (>= 10000 bp)	4453002
Total length (>= 25000 bp)	4228113
Total length (>= 50000 bp)	3587812
# contigs	110
Largest contig	327151
Total length	4562888
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	124047
NG50	112430
N75	58008
NG75	54946
L50	13
LG50	14
L75	28
LG75	29
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	163
Genome fraction (%)	98.247
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.44
# indels per 100 kbp	0.00
Largest alignment	327151
NA50	124047
NGA50	112430
NA75	58008
NGA75	54946
LA50	13
LGA50	14
LA75	28
LGA75	29

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).
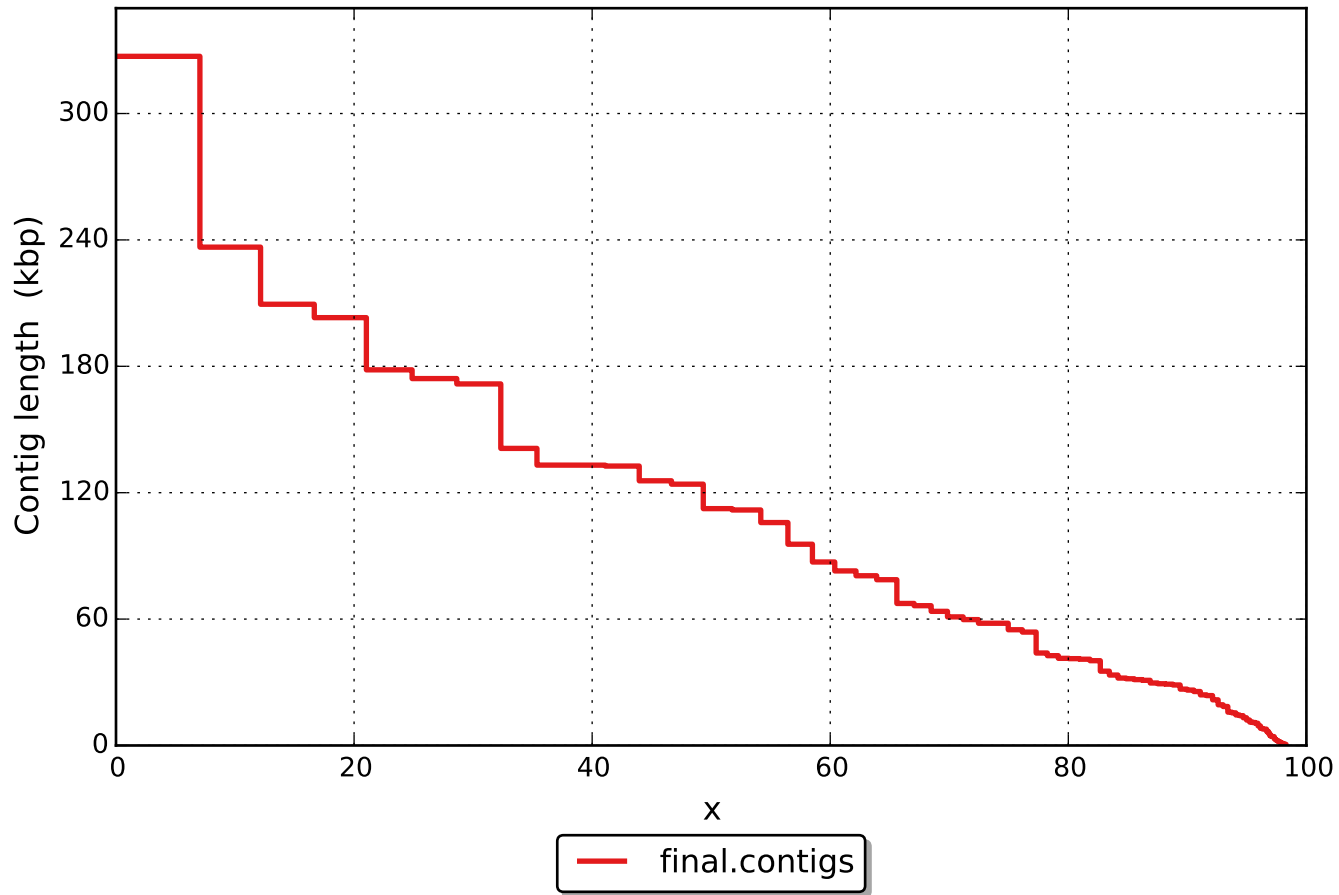
Misassemblies report

|	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	20
# indels	0
# short indels	0
# long indels	0
Indels length	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).

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	163
# 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).
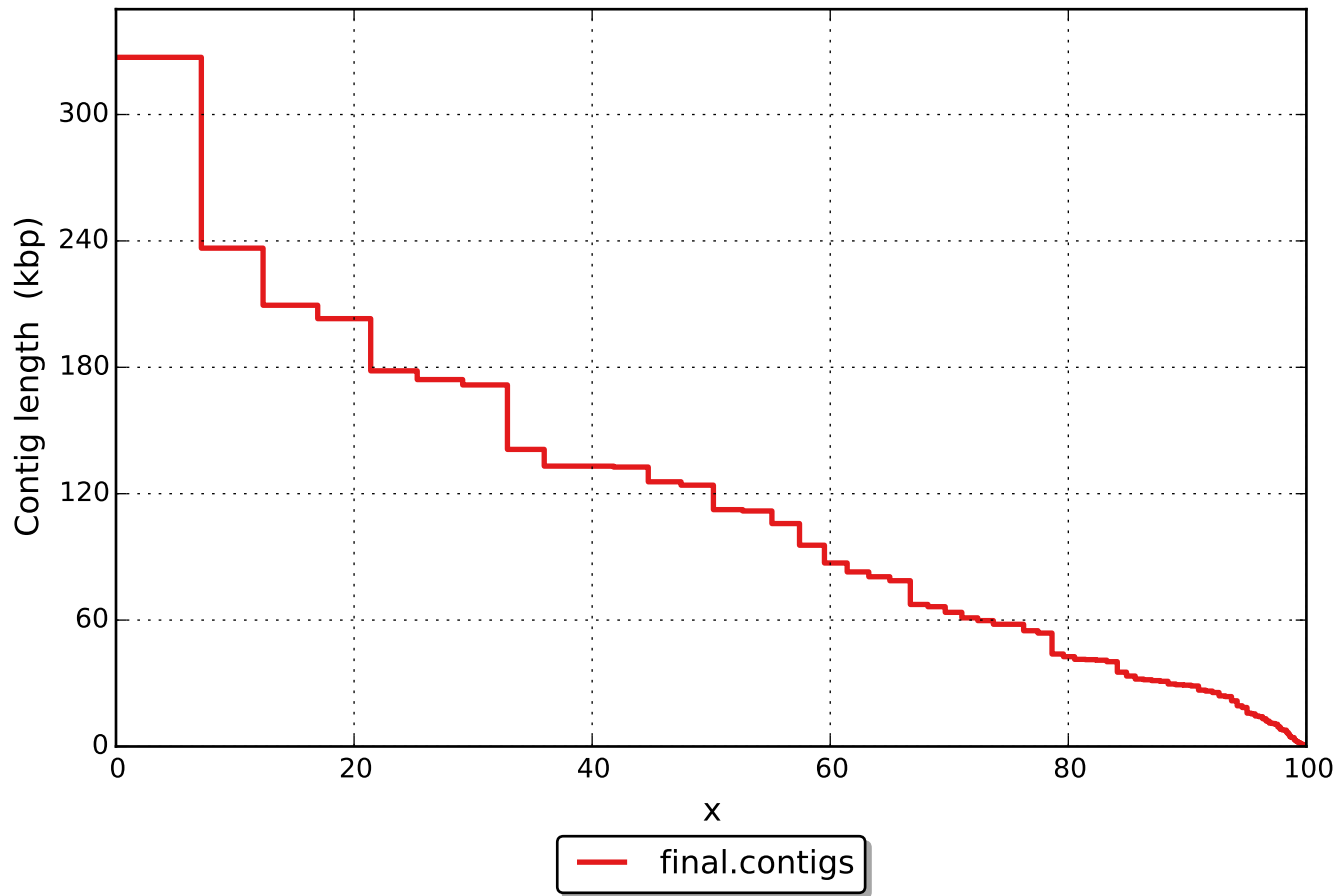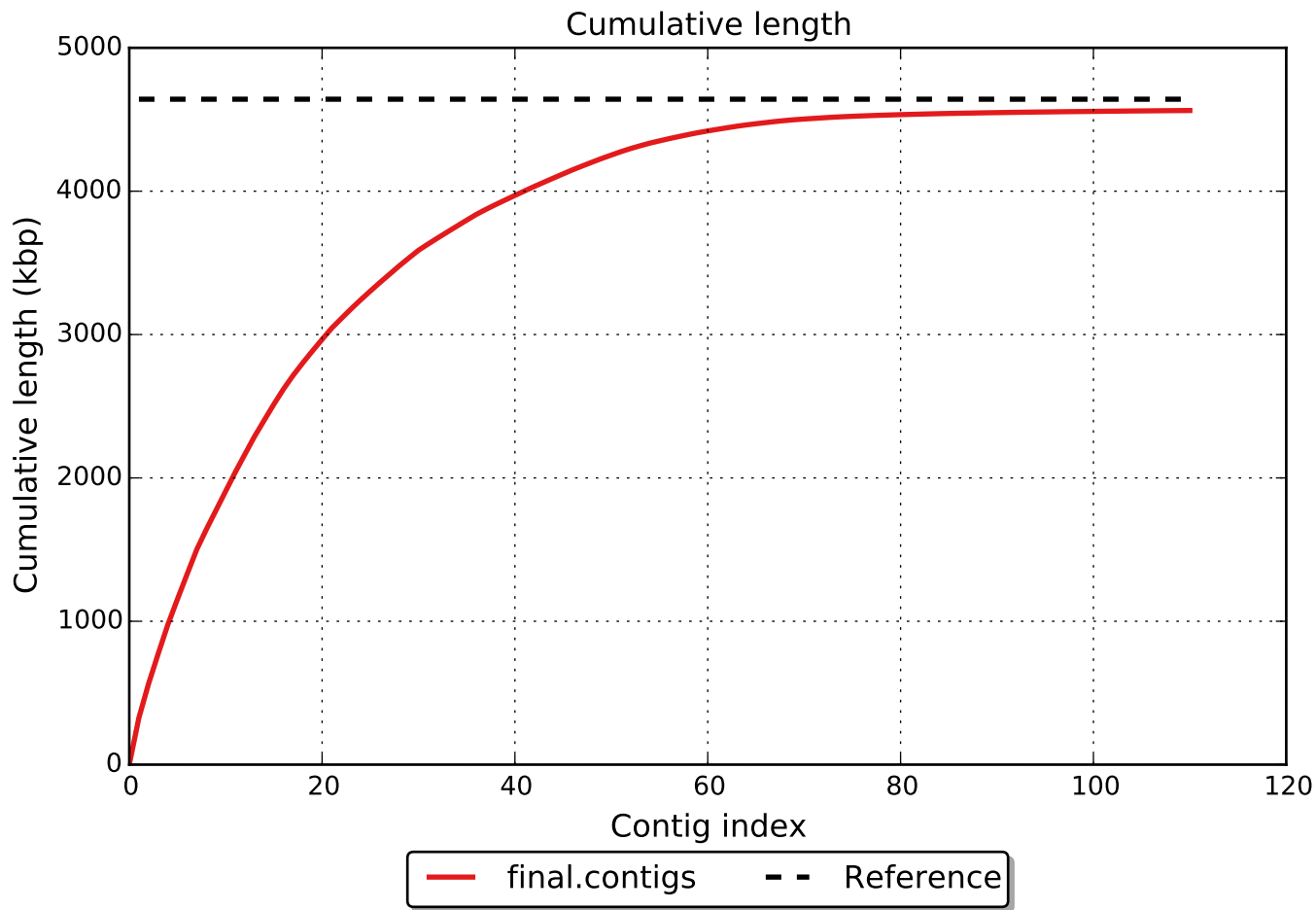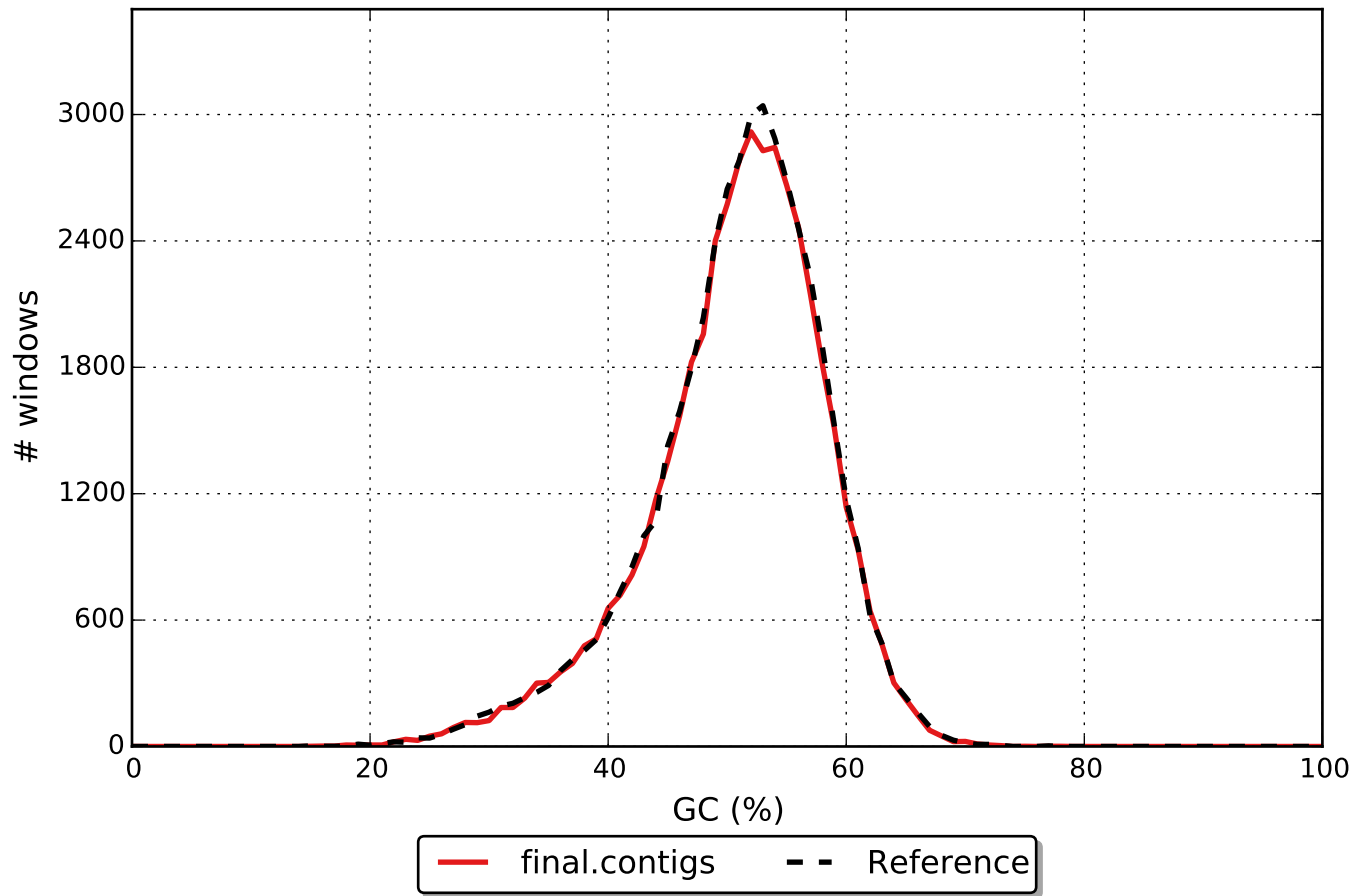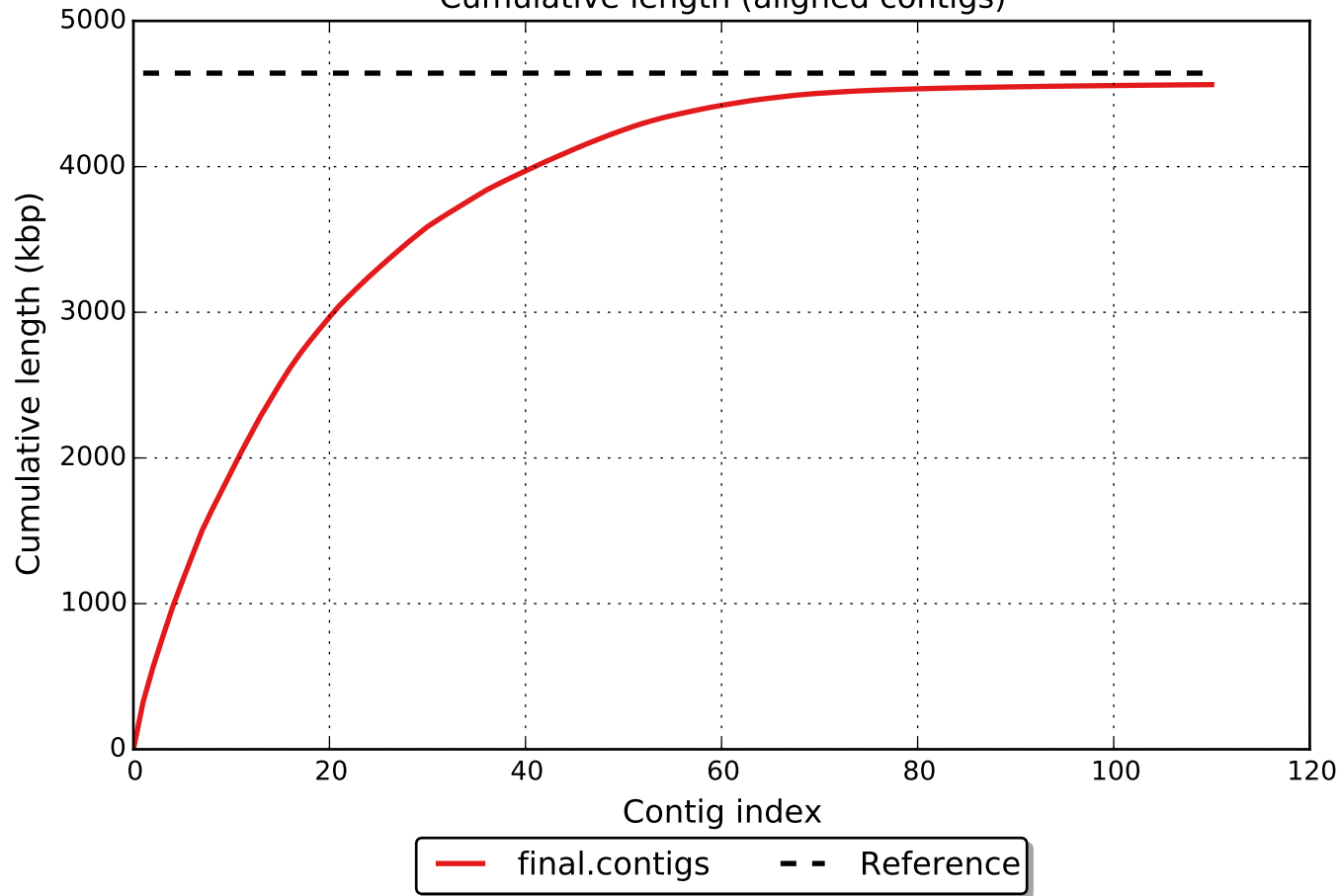
Cumulative length
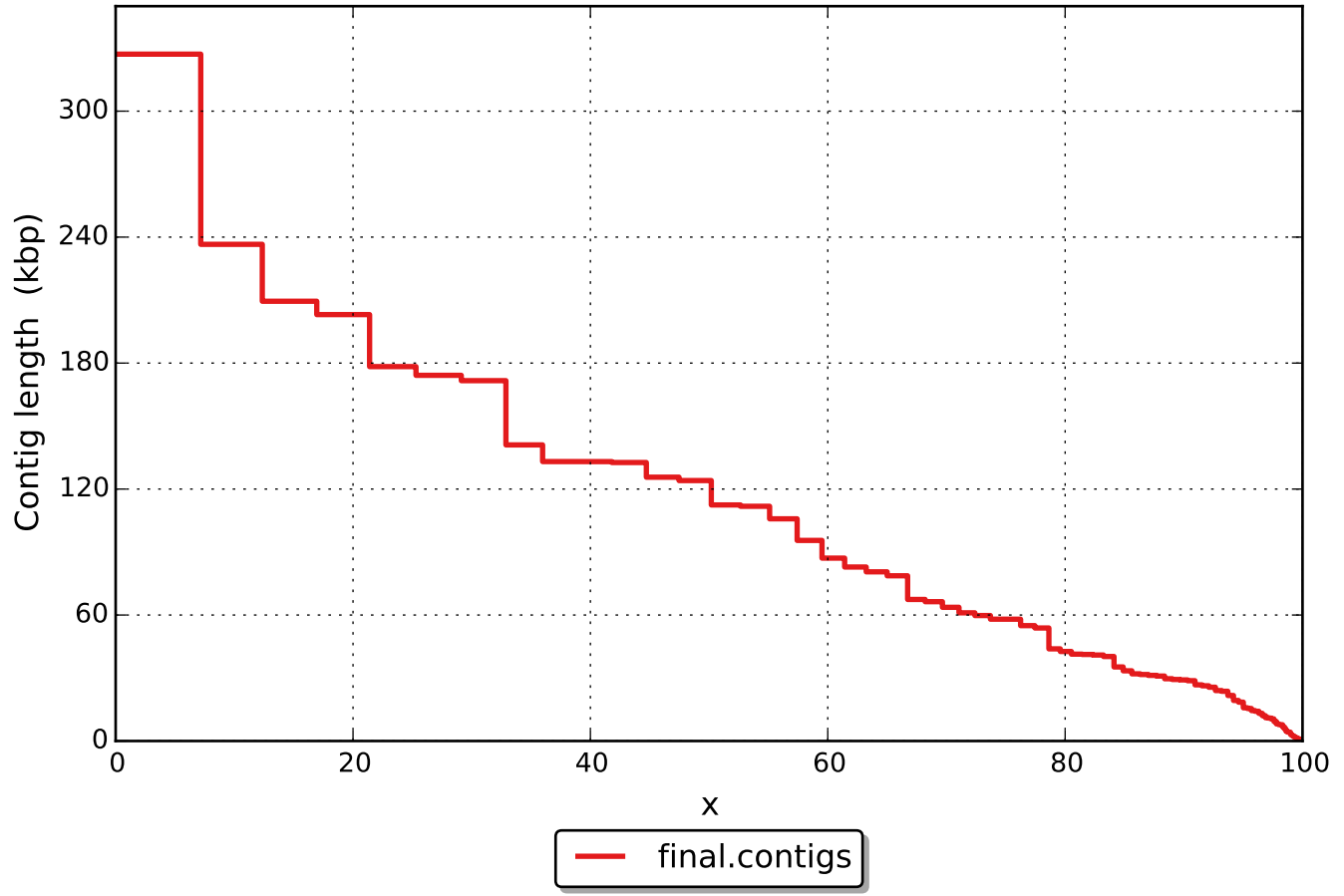
GC content

Misassemblies

final.contigs

Cumulative length (aligned contigs)