Report

	final.contigs
# contigs (>= 1000 bp)	1241
# contigs (>= 5000 bp)	212
# contigs (>= 10000 bp)	21
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	3977737
Total length (>= 5000 bp)	1522120
Total length (>= 10000 bp)	254666
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1919
Largest contig	21375
Total length	4437463
Reference length	4641652
GC (%)	50.77
Reference GC (%)	50.79
N50	3596
NG50	3412
N75	1993
NG75	1766
L50	378
LG50	407
L75	792
LG75	873
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	91.854
Duplication ratio	1.041
# N's per 100 kbp	0.00
# mismatches per 100 kbp	617.16
# indels per 100 kbp	0.09
Largest alignment	21375
NA50	3596
NGA50	3412
NA75	1993
NGA75	1766
LA50	378
LGA50	407
LA75	792
LGA75	873

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).
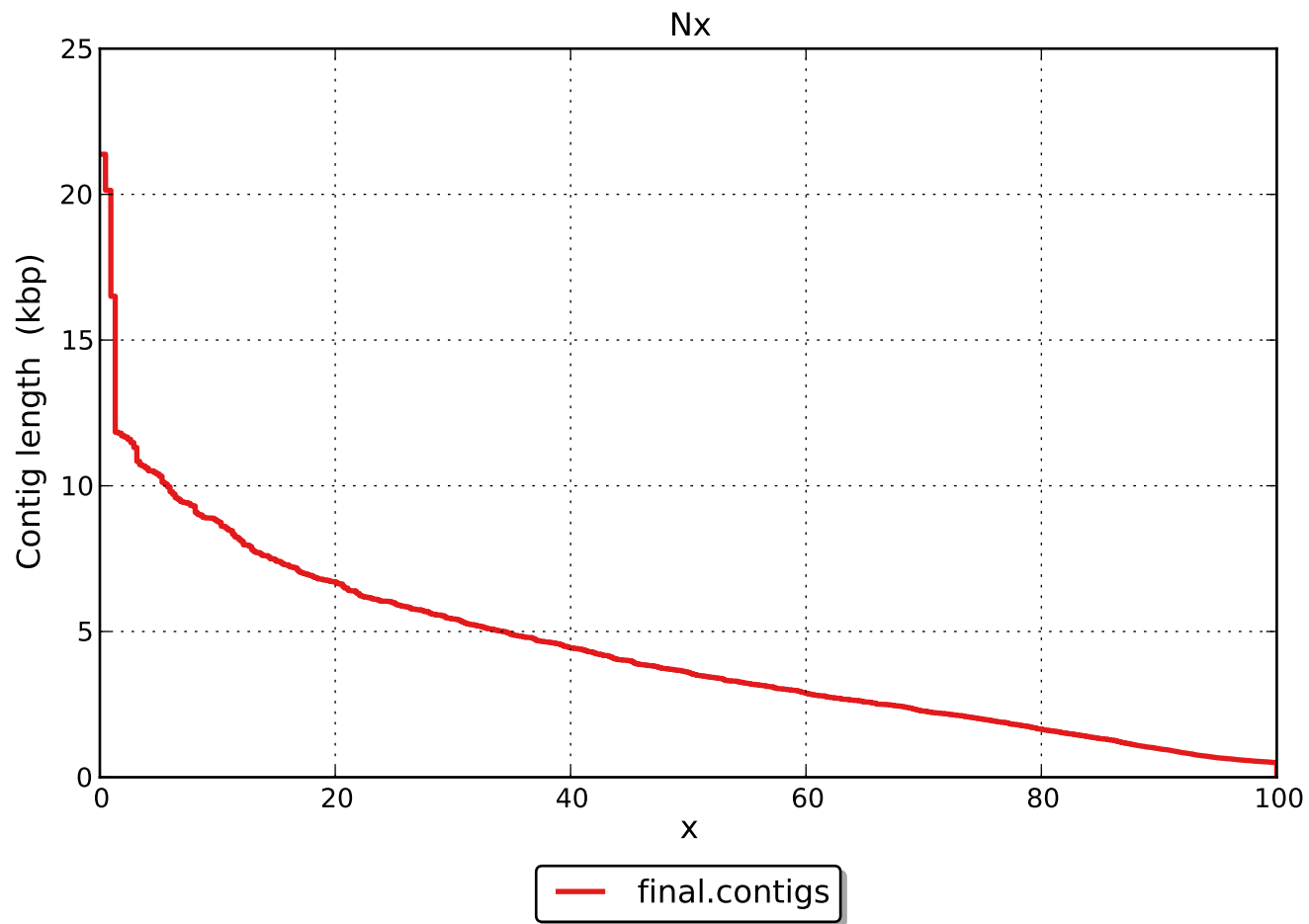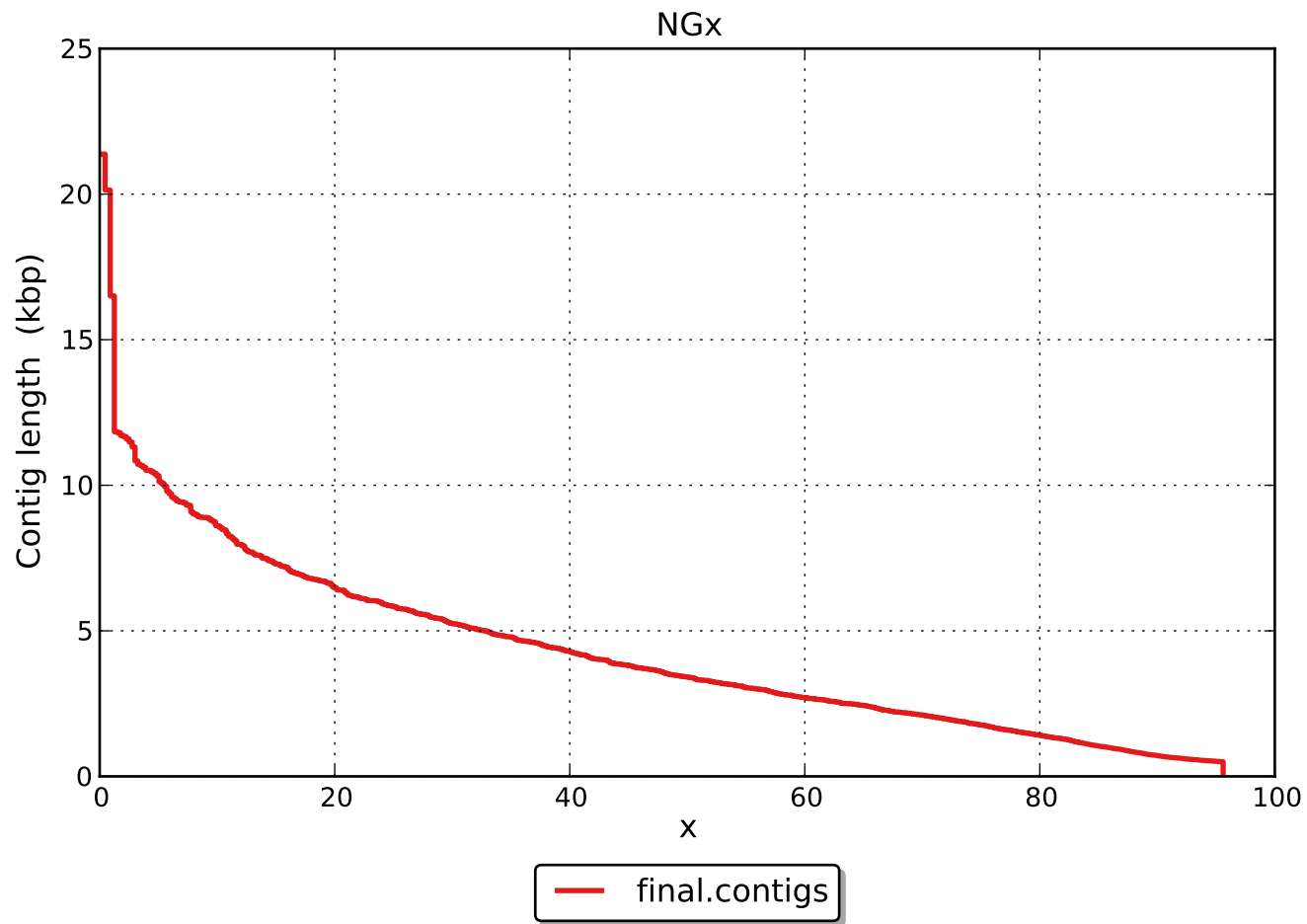
Misassemblies report

	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	26313
# indels	4
# short indels	4
# long indels	0
Indels length	4

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
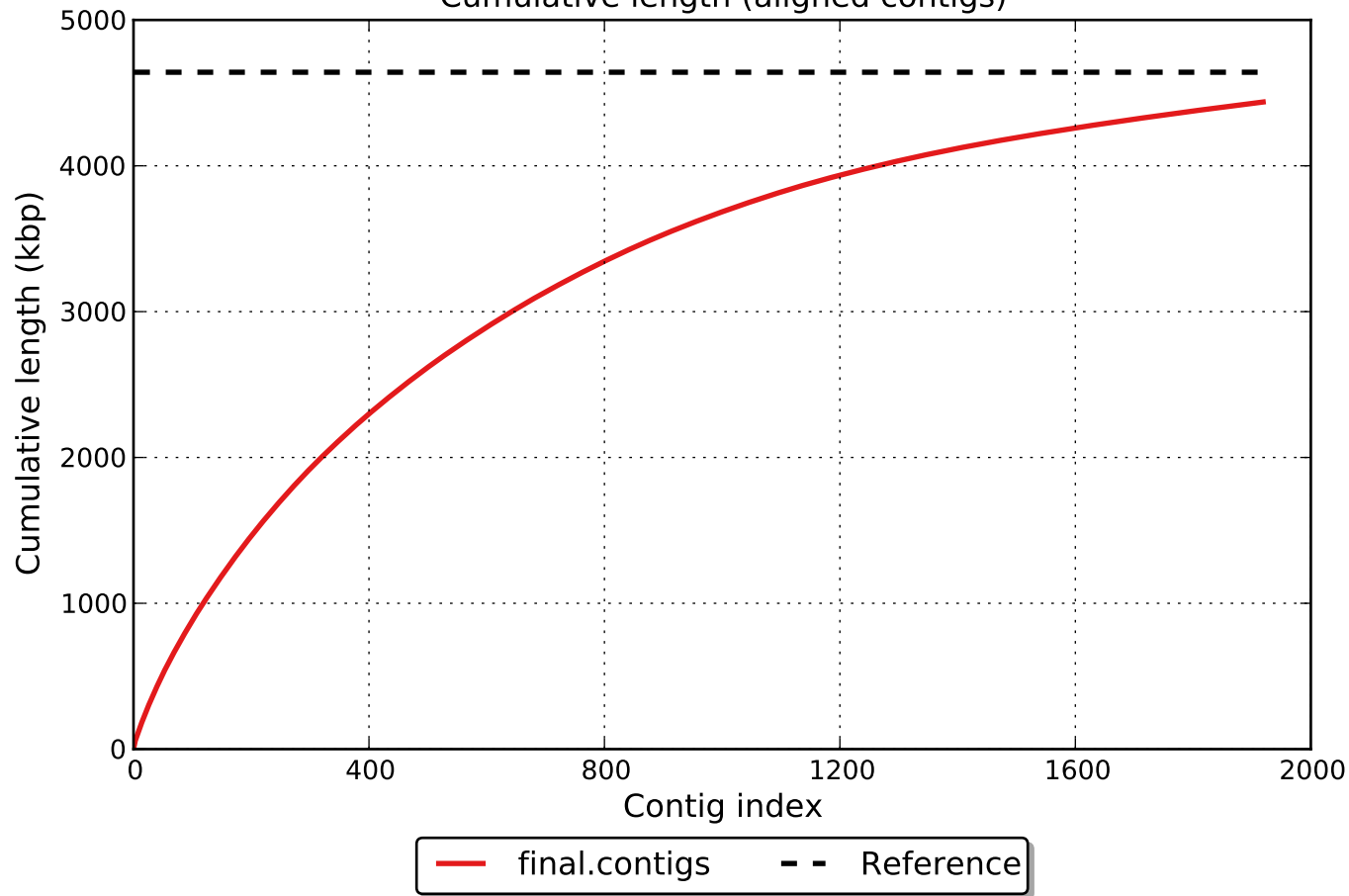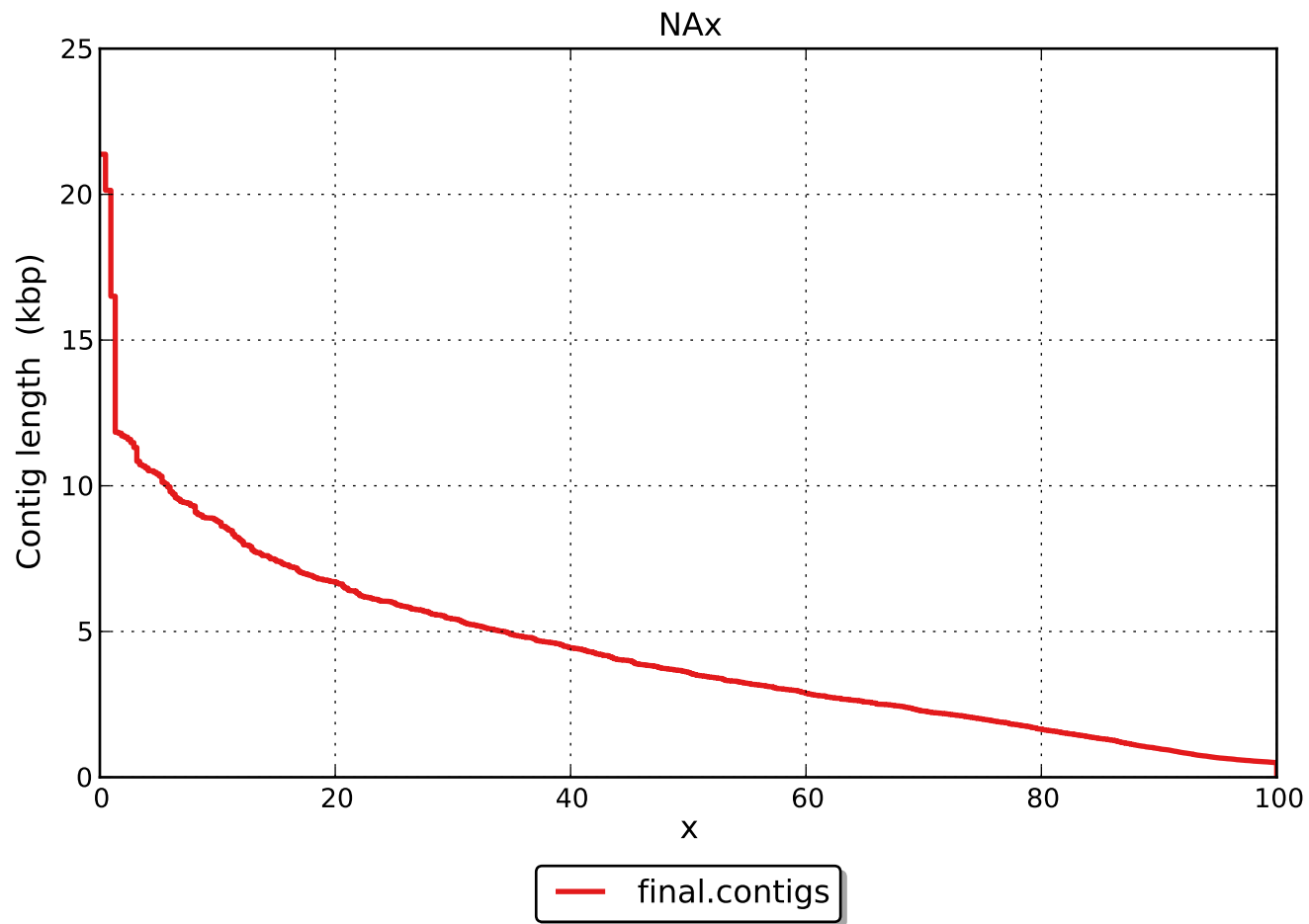(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Nx

Cumulative length

GC content

windows vs GC (%)
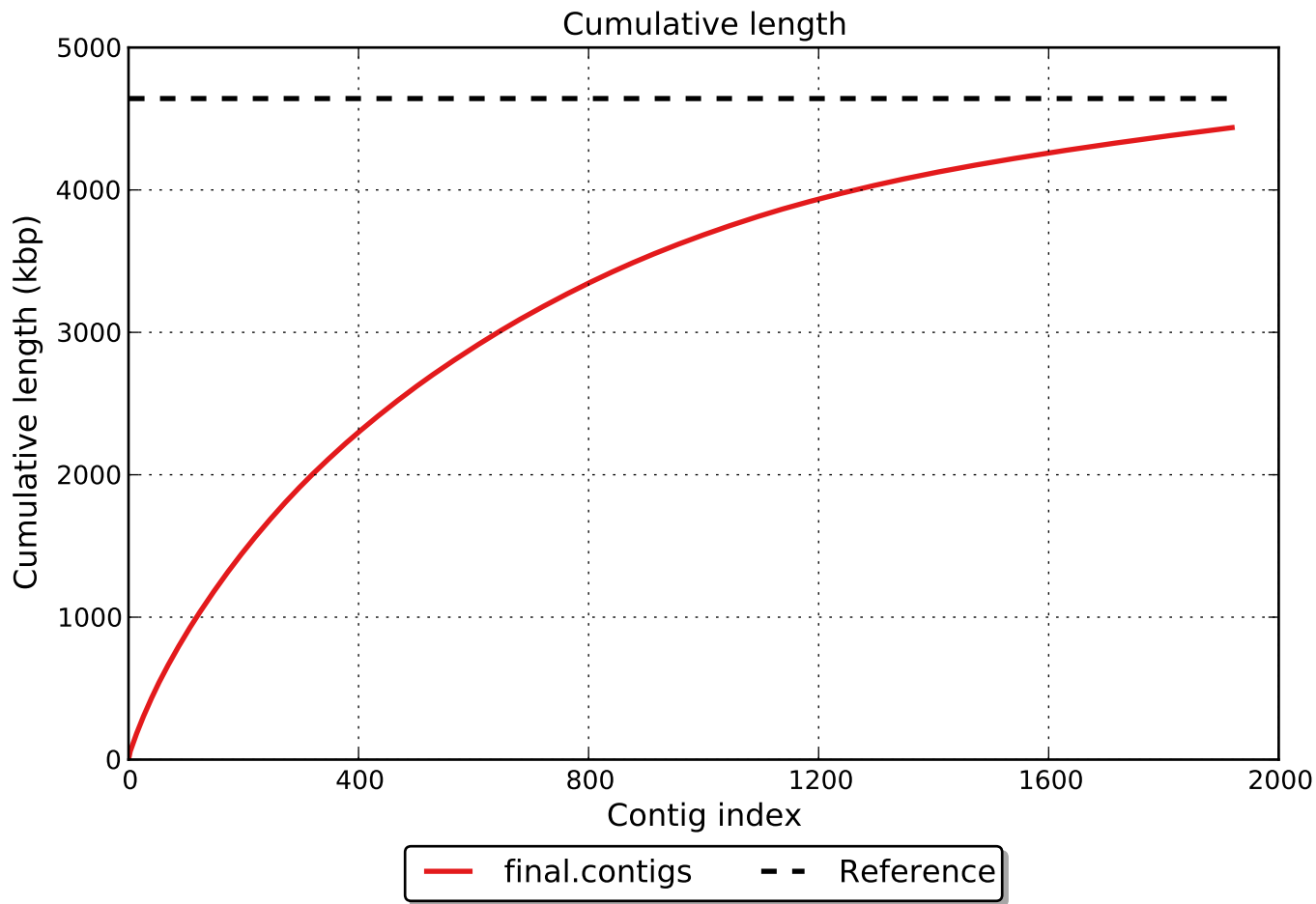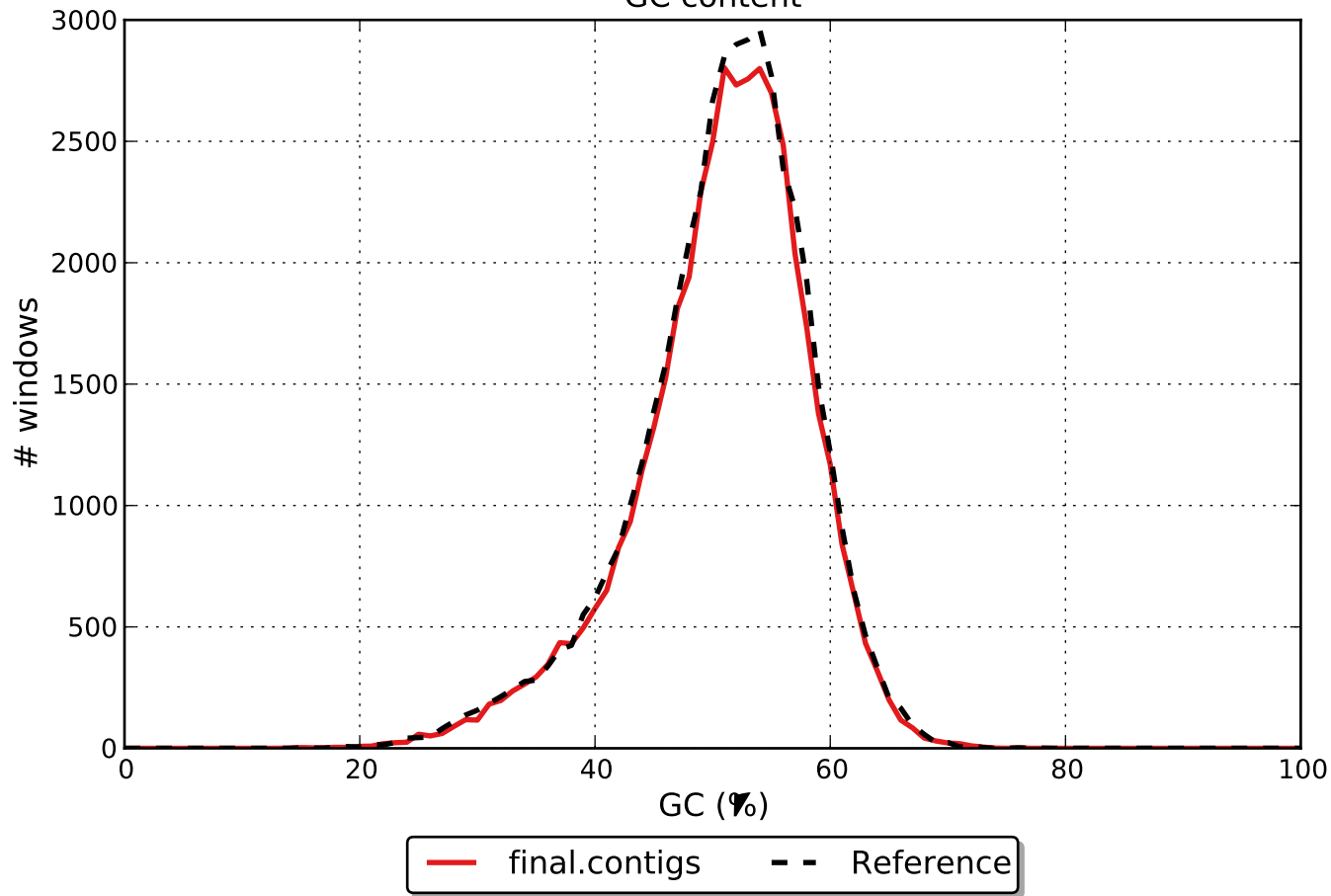
Misassemblies

final.contigs

Cumulative length (aligned contigs)