Report

	final.contigs
# contigs (>= 1000 bp)	1526
# contigs (>= 5000 bp)	183
# contigs (>= 10000 bp)	16
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4384437
Total length (>= 5000 bp)	1253261
Total length (>= 10000 bp)	196297
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1985
Largest contig	18483
Total length	4722706
Reference length	4641652
GC (%)	50.79
Reference GC (%)	50.78
N50	3221
NG50	3268
N75	1917
NG75	1976
L50	461
LG50	449
L75	934
LG75	903
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 2 part
Unaligned length	140
Genome fraction (%)	98.129
Duplication ratio	1.037
# N's per 100 kbp	0.00
# mismatches per 100 kbp	43.89
# indels per 100 kbp	0.11
Largest alignment	18483
NA50	3221
NGA50	3268
NA75	1917
NGA75	1976
LA50	461
LGA50	449
LA75	934
LGA75	903

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).
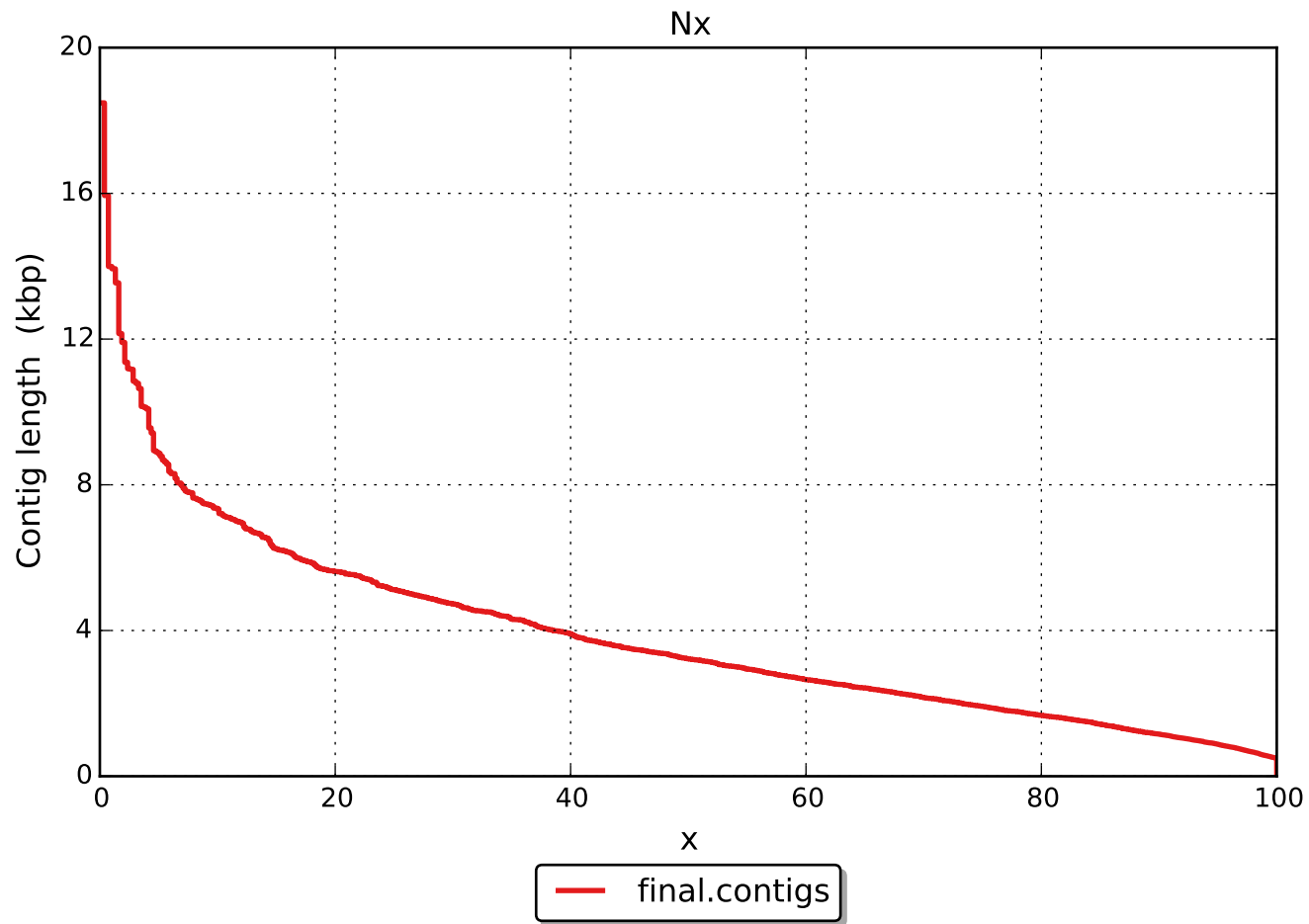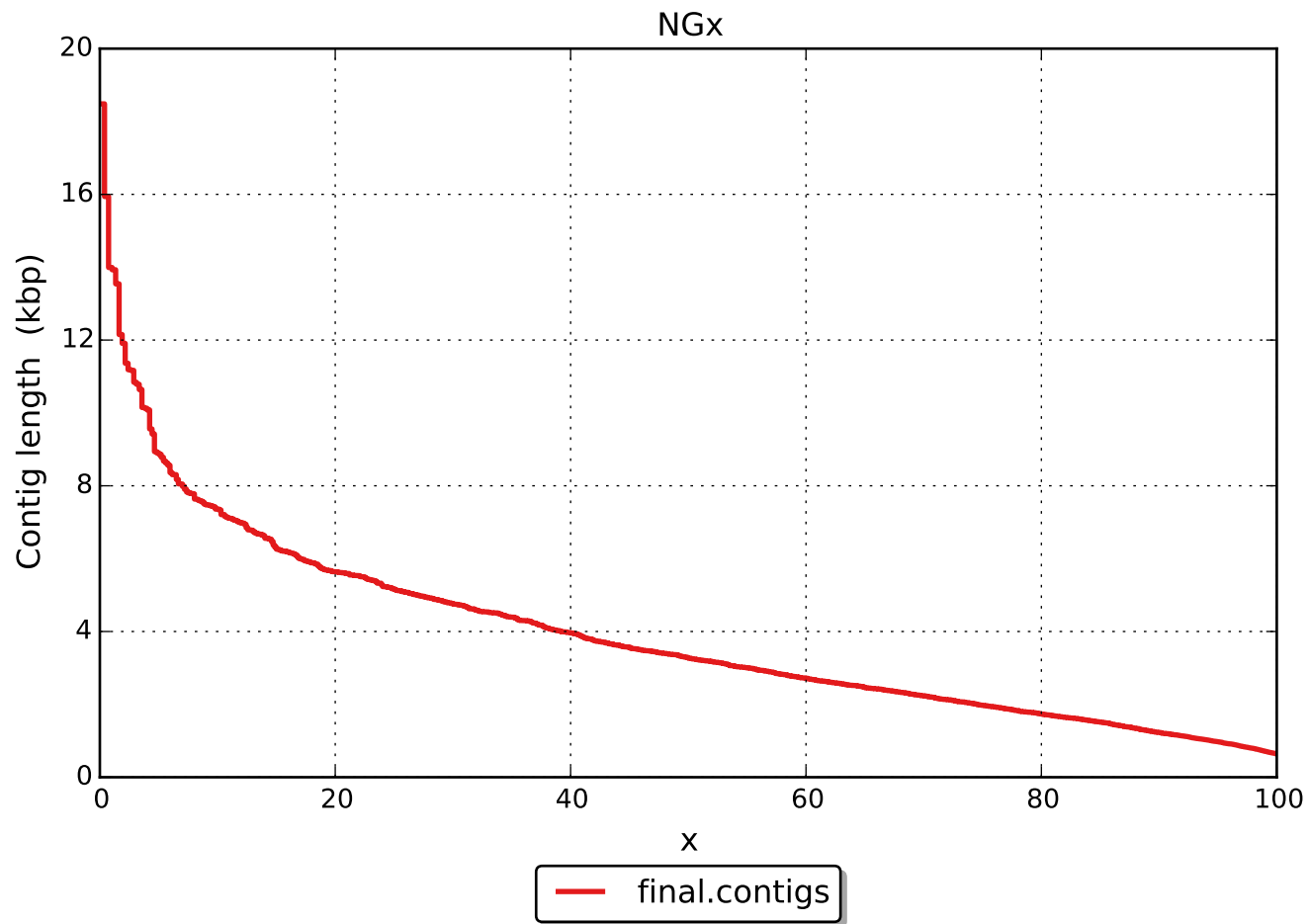
Misassemblies report

	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	1999
# indels	5
# short indels	5
# long indels	0
Indels length	5

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	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	140
# N's	0

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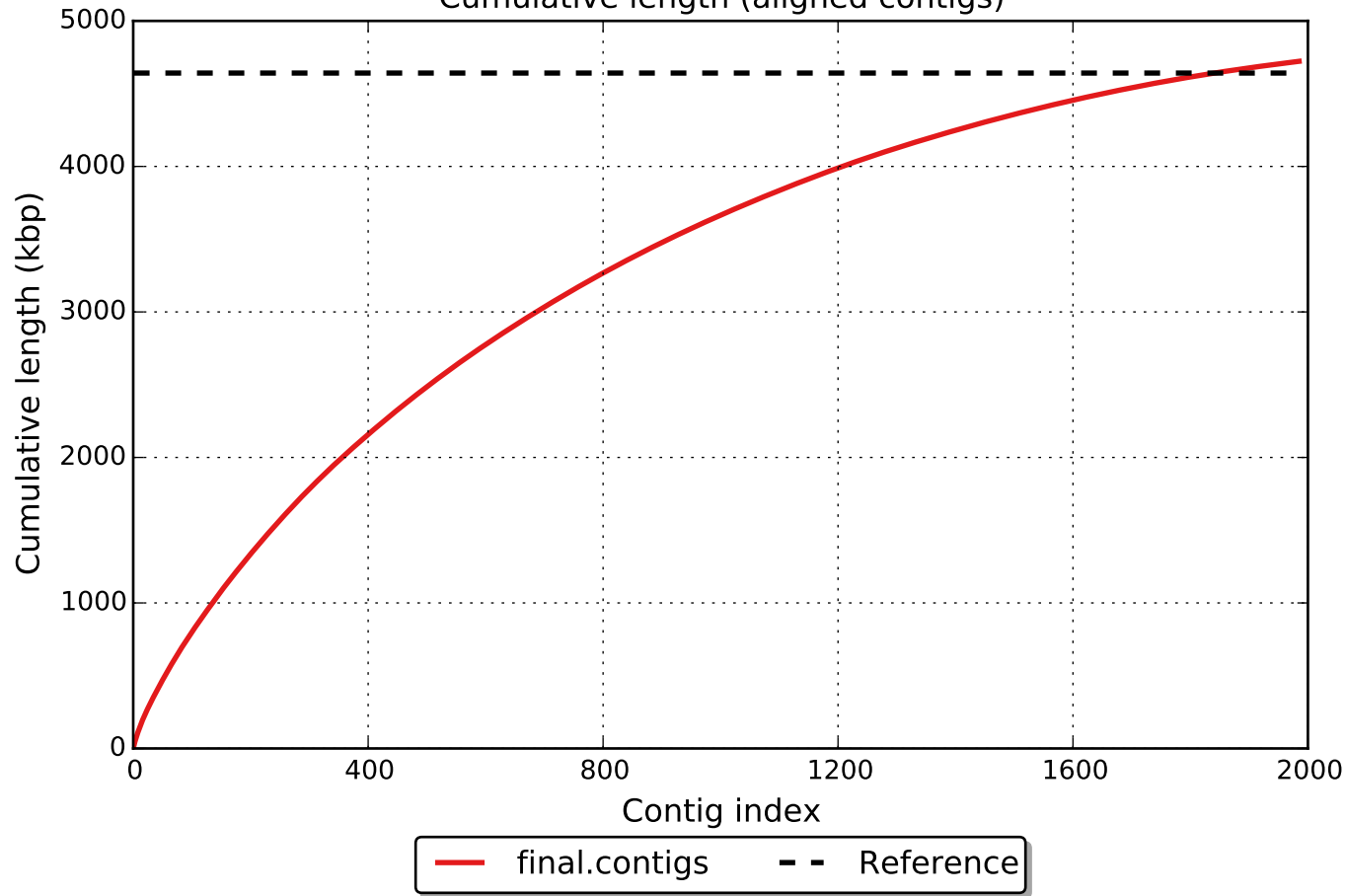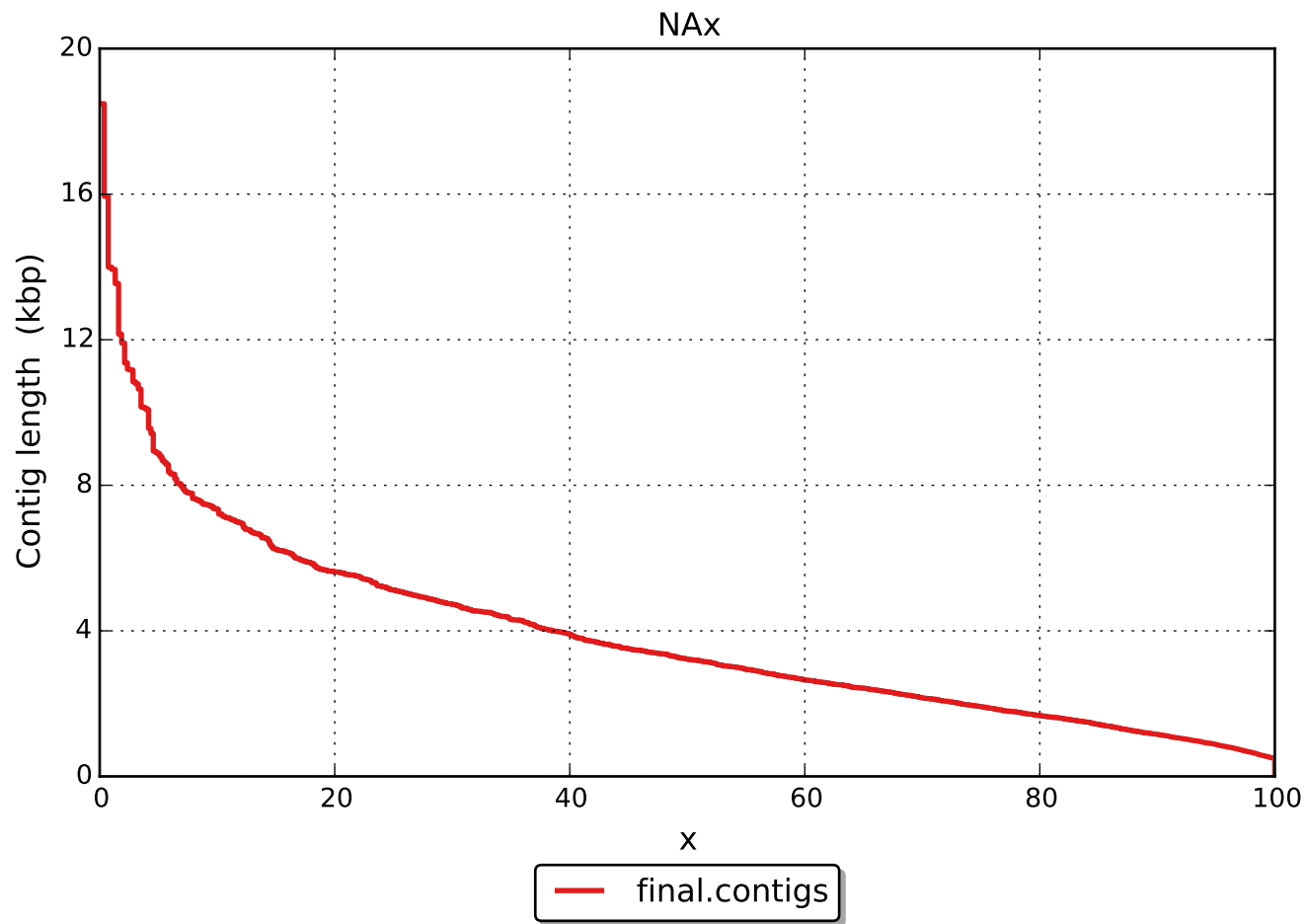(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Nx
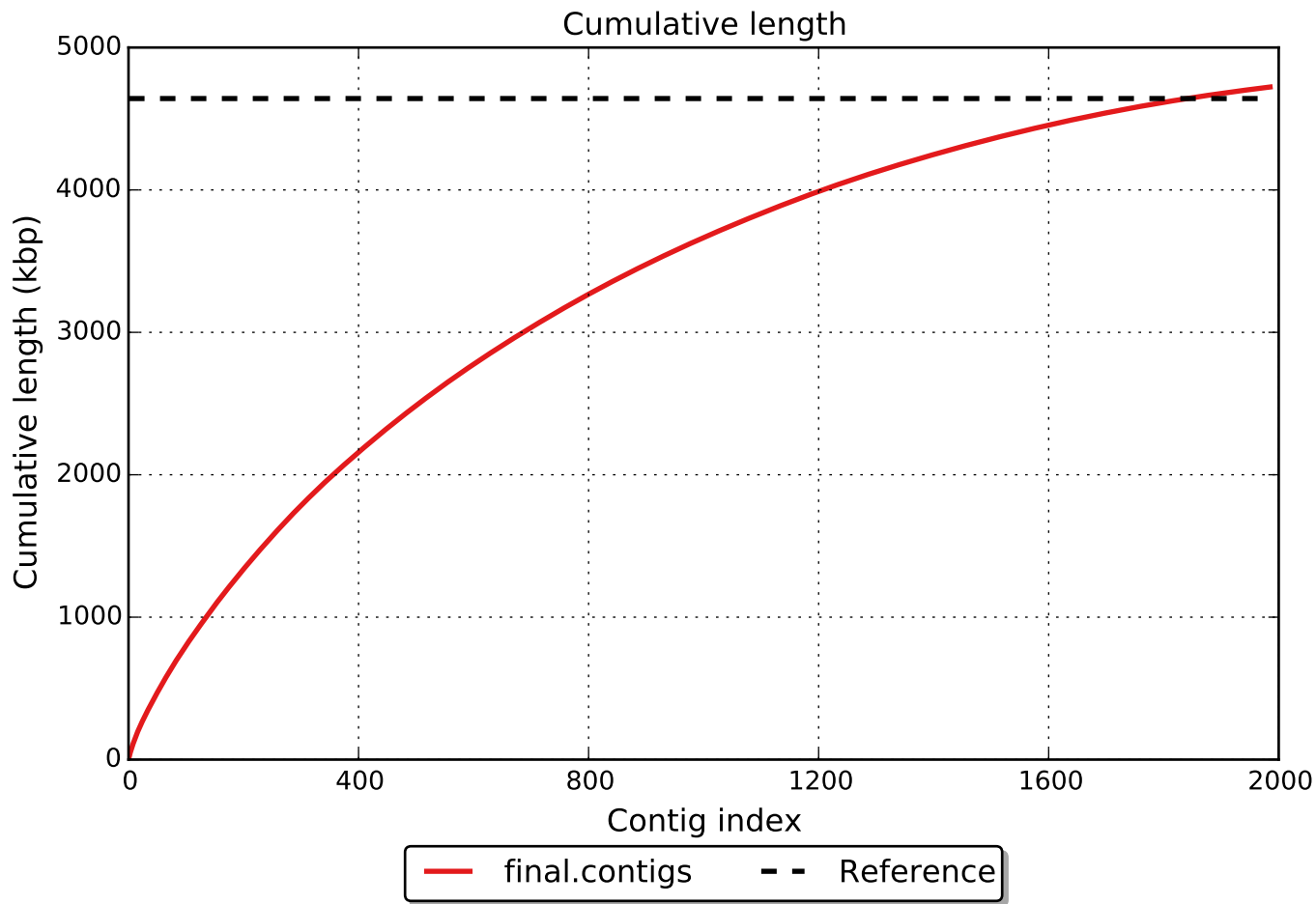
Cumulative length

GC content
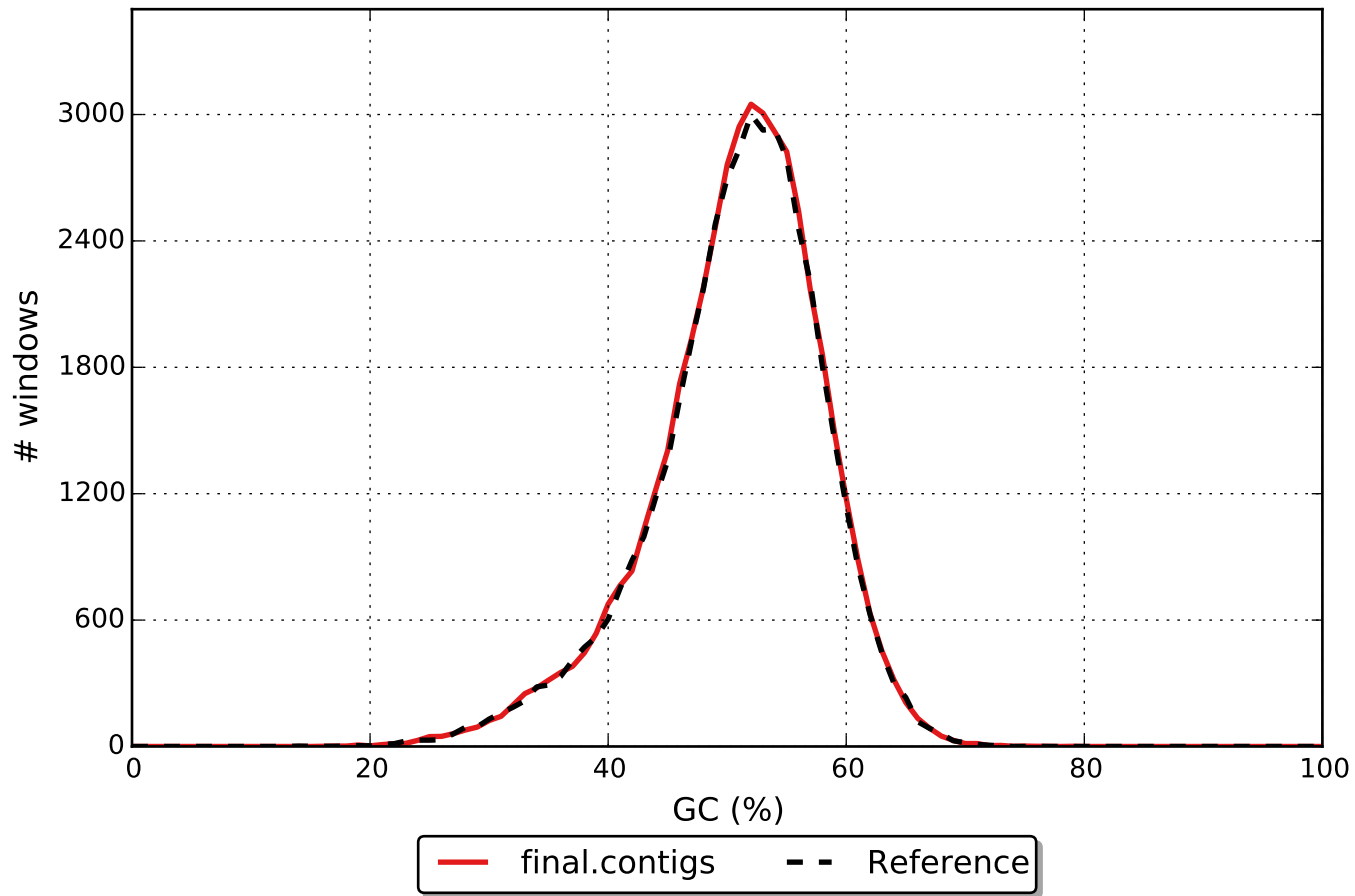
Misassemblies

final.contigs

Cumulative length (aligned contigs)