Report

	final.contigs
# contigs (>= 1000 bp)	1529
# contigs (>= 5000 bp)	183
# contigs (>= 10000 bp)	16
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4391904
Total length (>= 5000 bp)	1253261
Total length (>= 10000 bp)	196297
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1990
Largest contig	18483
Total length	4731551
Reference length	4641652
GC (%)	50.78
Reference GC (%)	50.78
N50	3221
NG50	3290
N75	1917
NG75	1979
L50	462
LG50	448
L75	936
LG75	901
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 2 part
Unaligned length	140
Genome fraction (%)	98.213
Duplication ratio	1.038
# N's per 100 kbp	0.00
# mismatches per 100 kbp	46.77
# indels per 100 kbp	0.11
Largest alignment	18483
NA50	3221
NGA50	3290
NA75	1917
NGA75	1979
LA50	462
LGA50	448
LA75	936
LGA75	901

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).
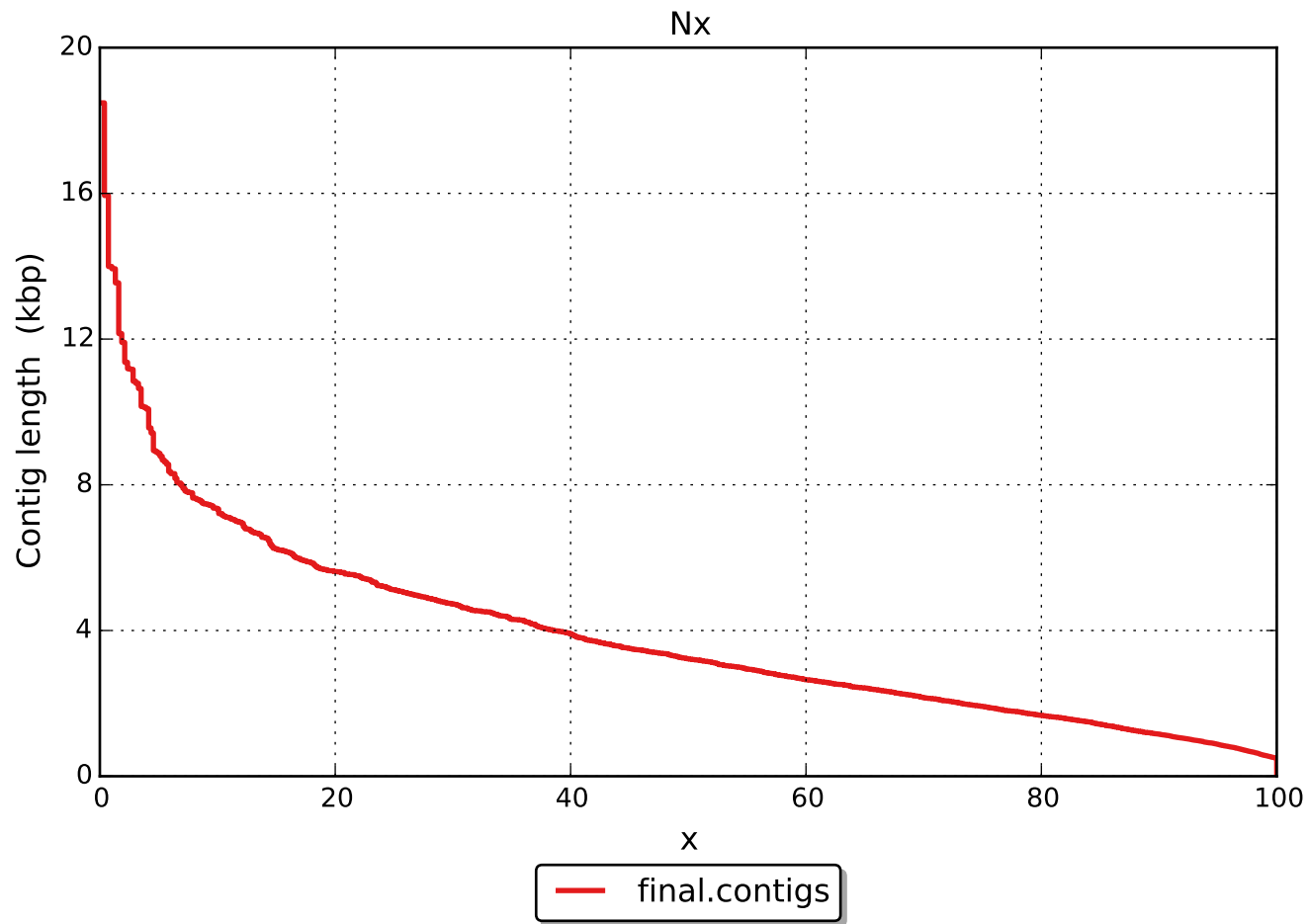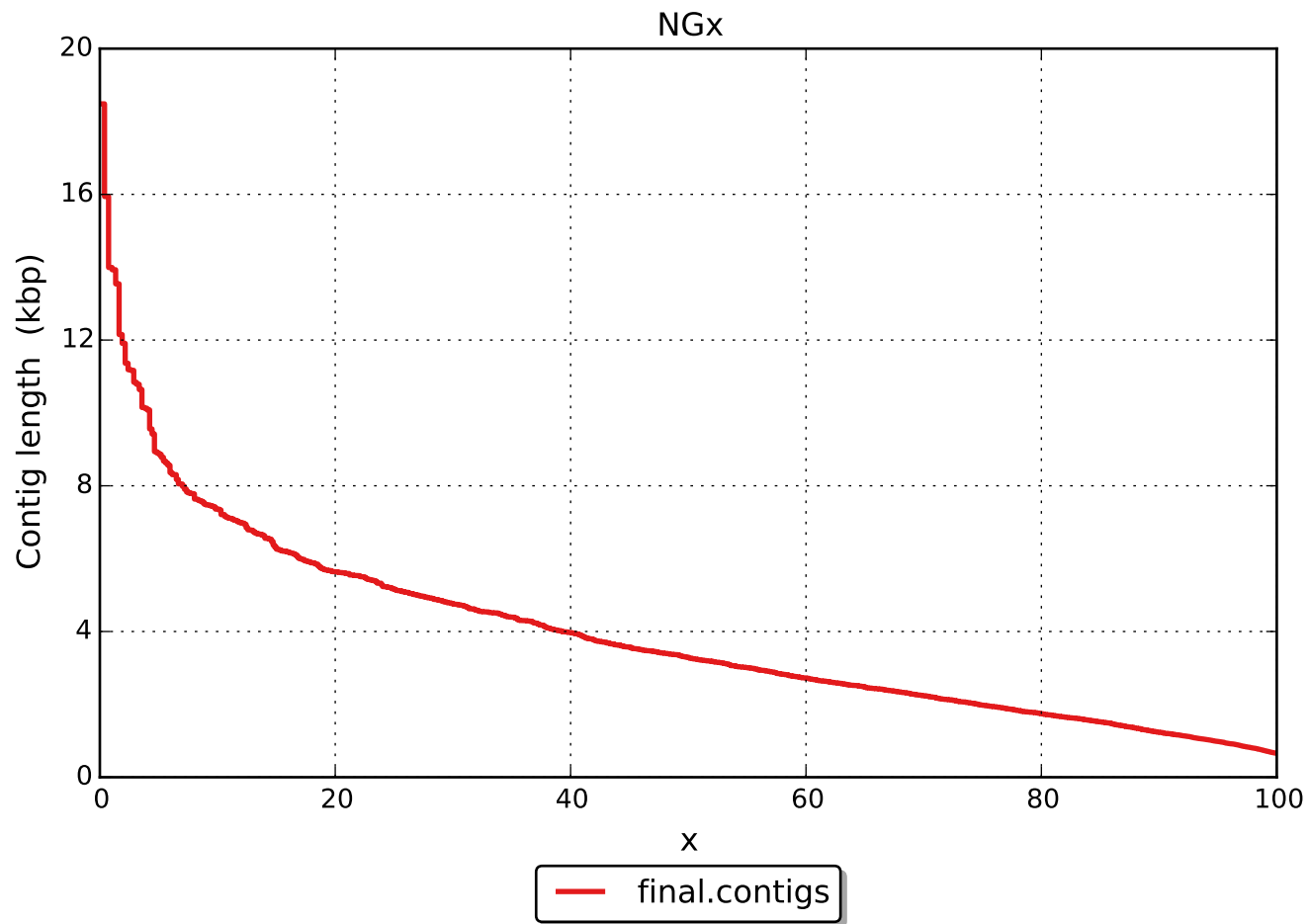
Misassemblies report

	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	2132
# 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).
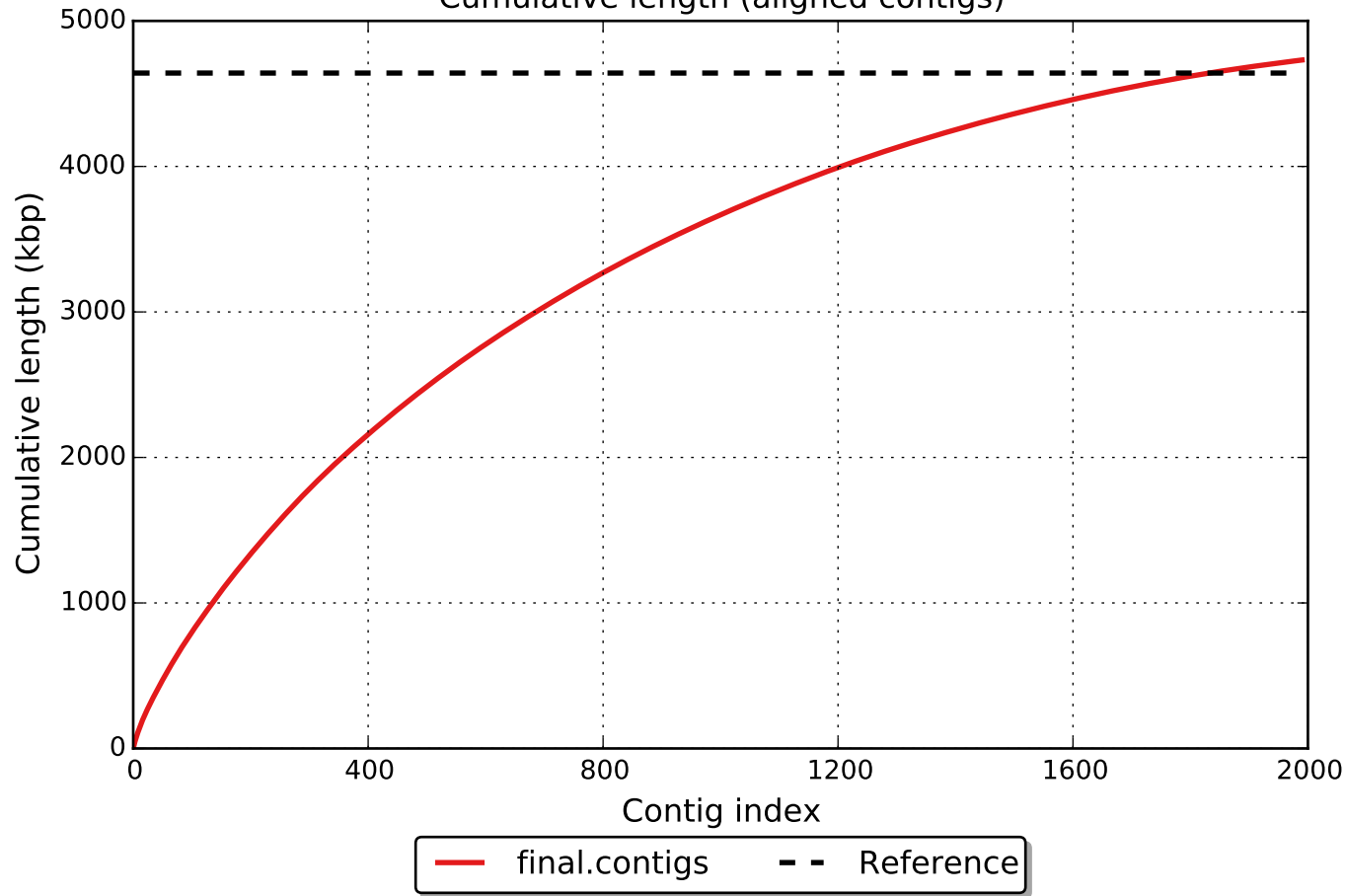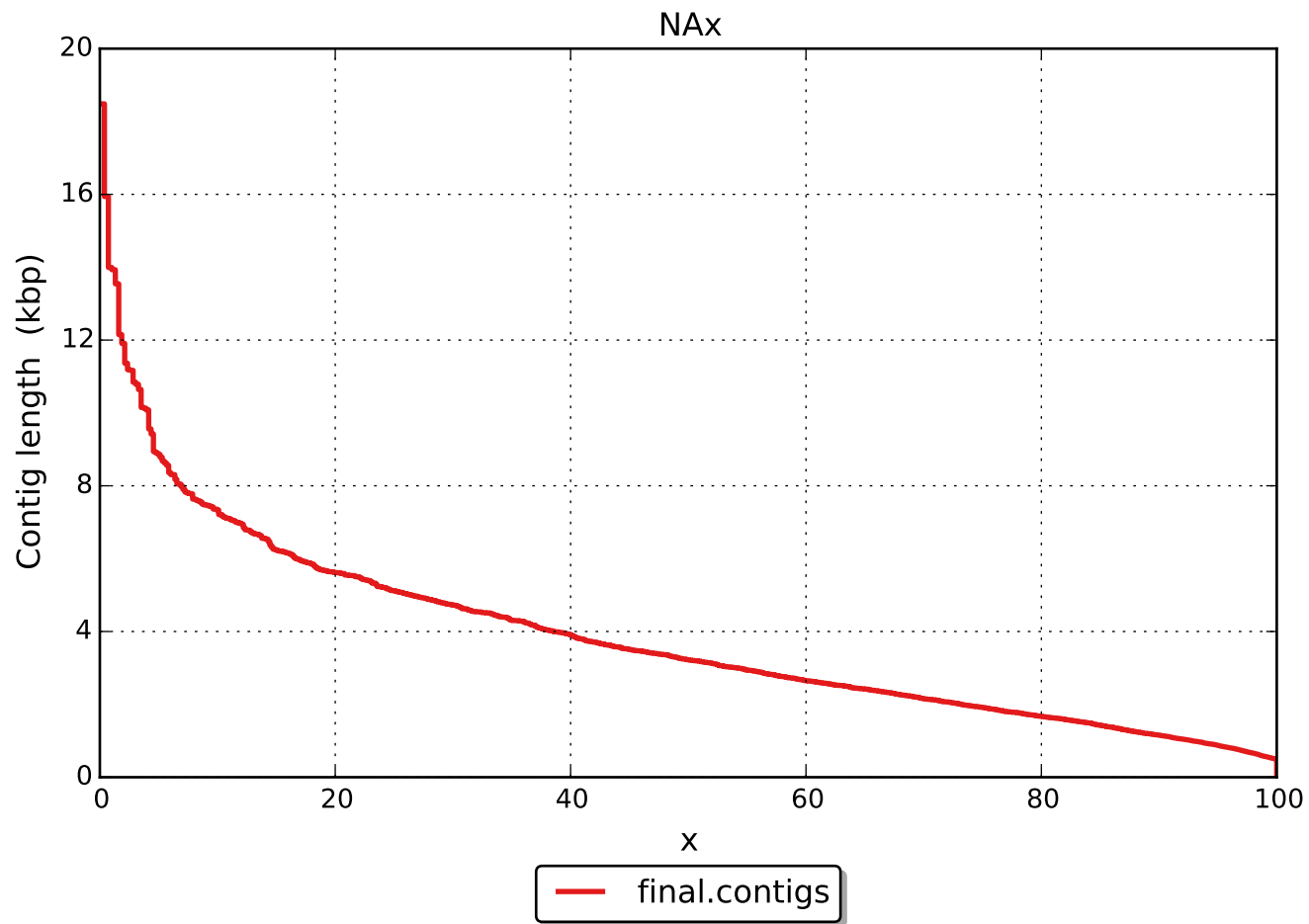
Nx
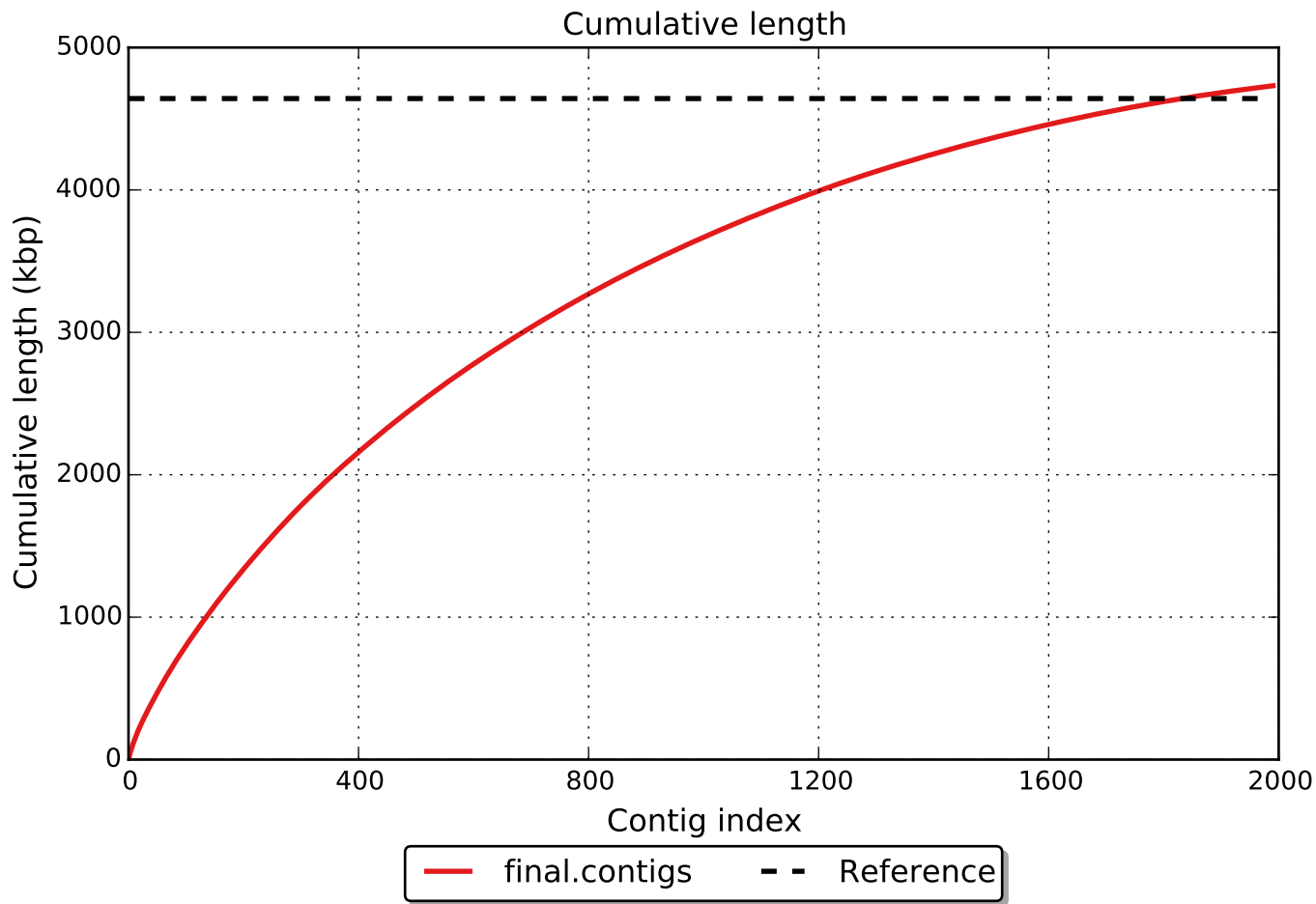
Cumulative length

GC content
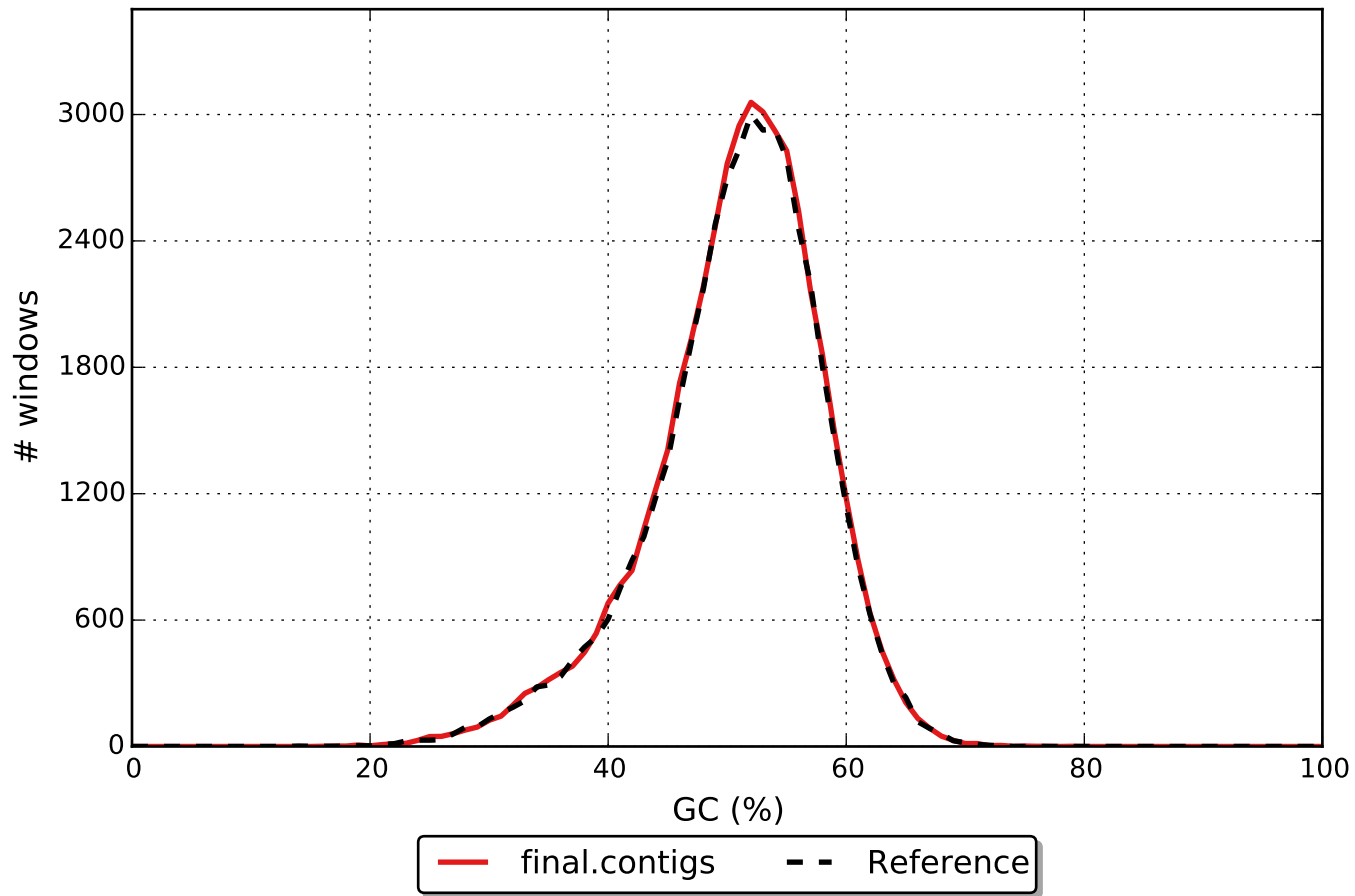
Misassemblies

final.contigs

Cumulative length (aligned contigs)

NGAx