Report

	contigs
# contigs (>= 1000 bp)	893
# contigs (>= 5000 bp)	280
# contigs (>= 10000 bp)	65
# contigs (>= 25000 bp)	4
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4042635
Total length (>= 5000 bp)	2429453
Total length (>= 10000 bp)	922494
Total length (>= 25000 bp)	125579
Total length (>= 50000 bp)	0
# contigs	1059
Largest contig	36999
Total length	4156991
Reference length	4641652
GC (%)	50.71
Reference GC (%)	50.79
N50	6057
NG50	5387
N75	3445
NG75	2617
L50	217
LG50	260
L75	445
LG75	567
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	88.711
Duplication ratio	1.010
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1004.82
# indels per 100 kbp	0.73
Largest alignment	36999
NA50	6057
NGA50	5387
NA75	3445
NGA75	2617
LA50	217
LGA50	260
LA75	445
LGA75	567

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).
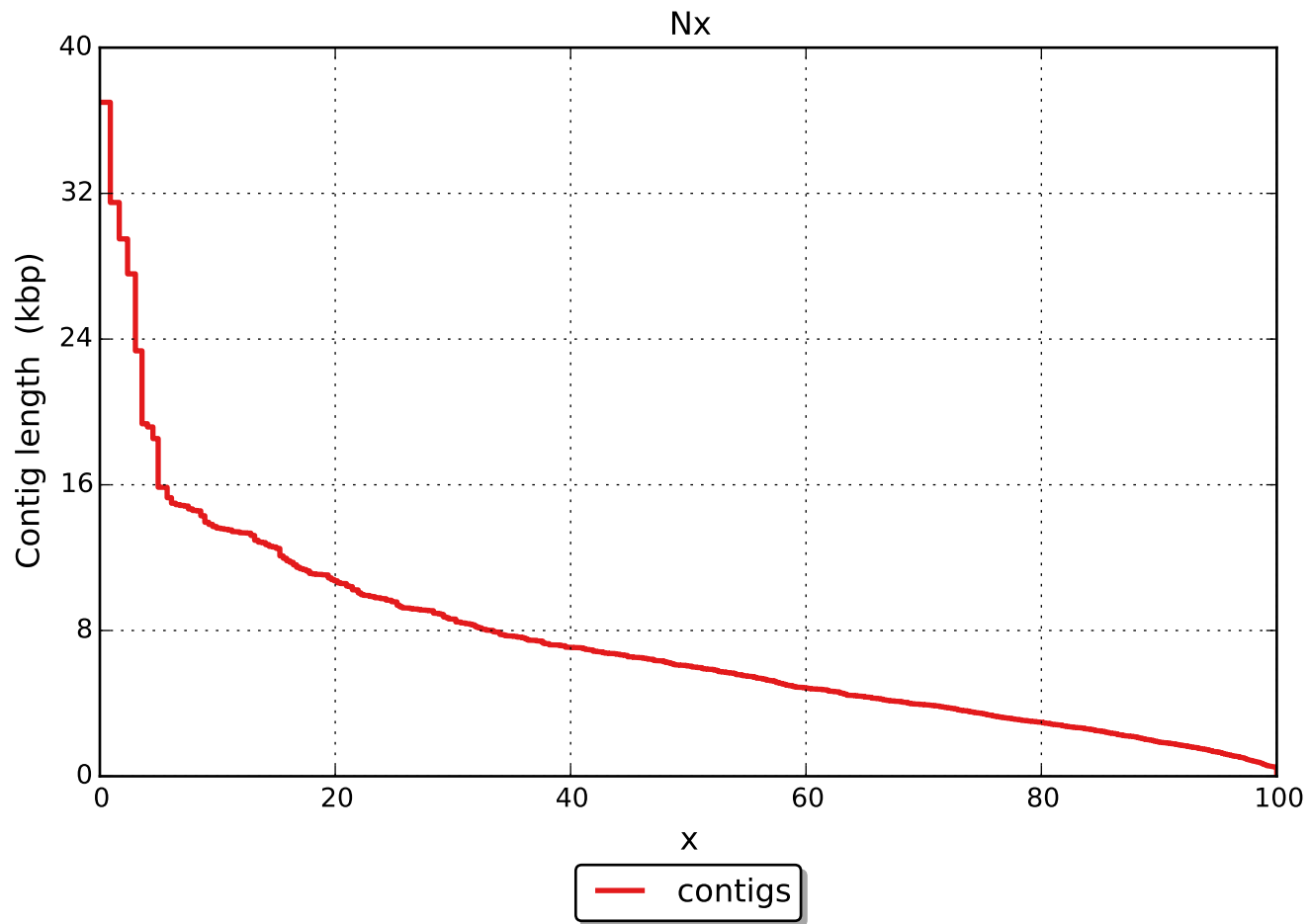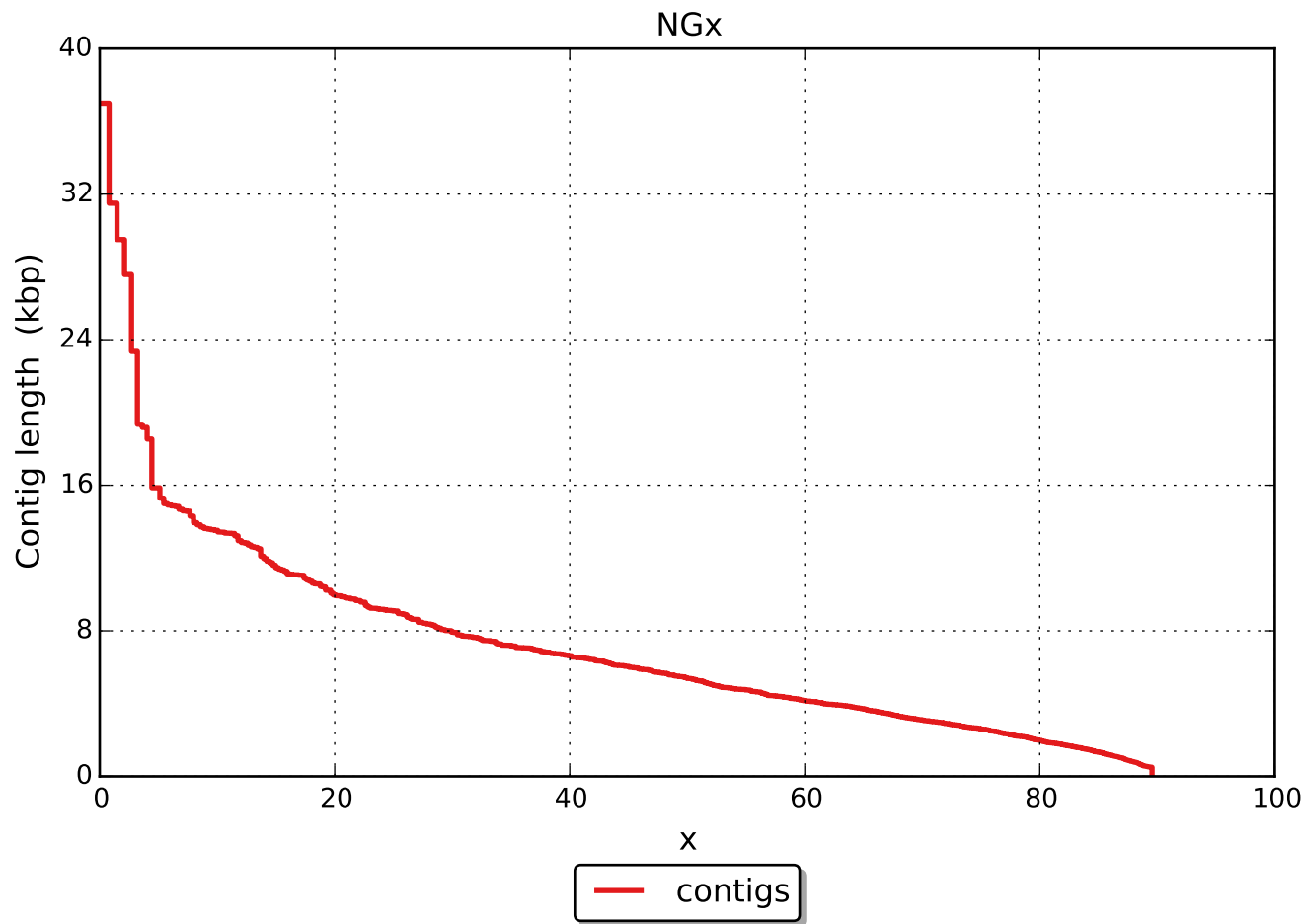
Misassemblies report

	contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# mismatches	41375
# indels	30
# short indels	30
# long indels	0
Indels length	37

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

	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).
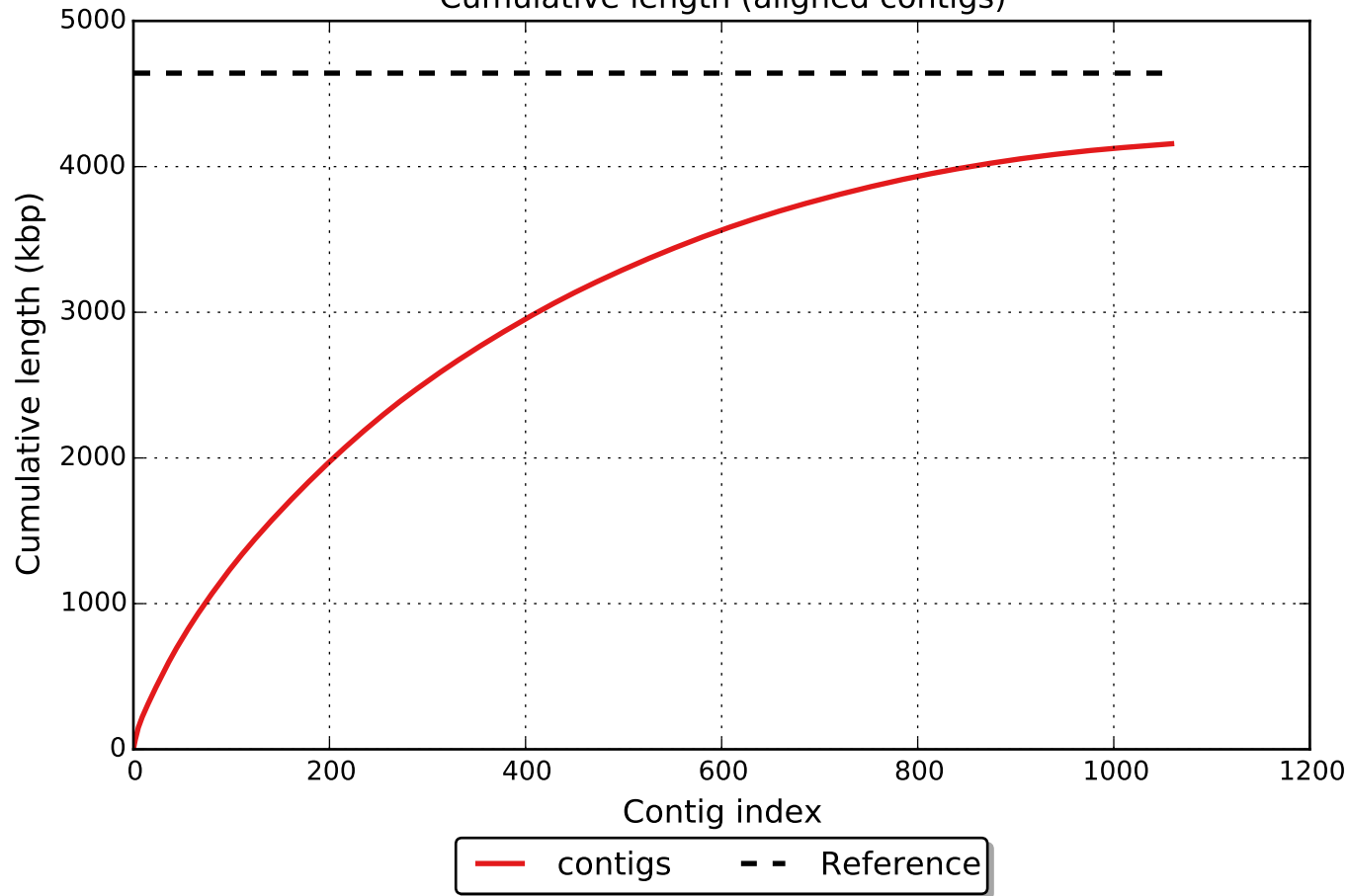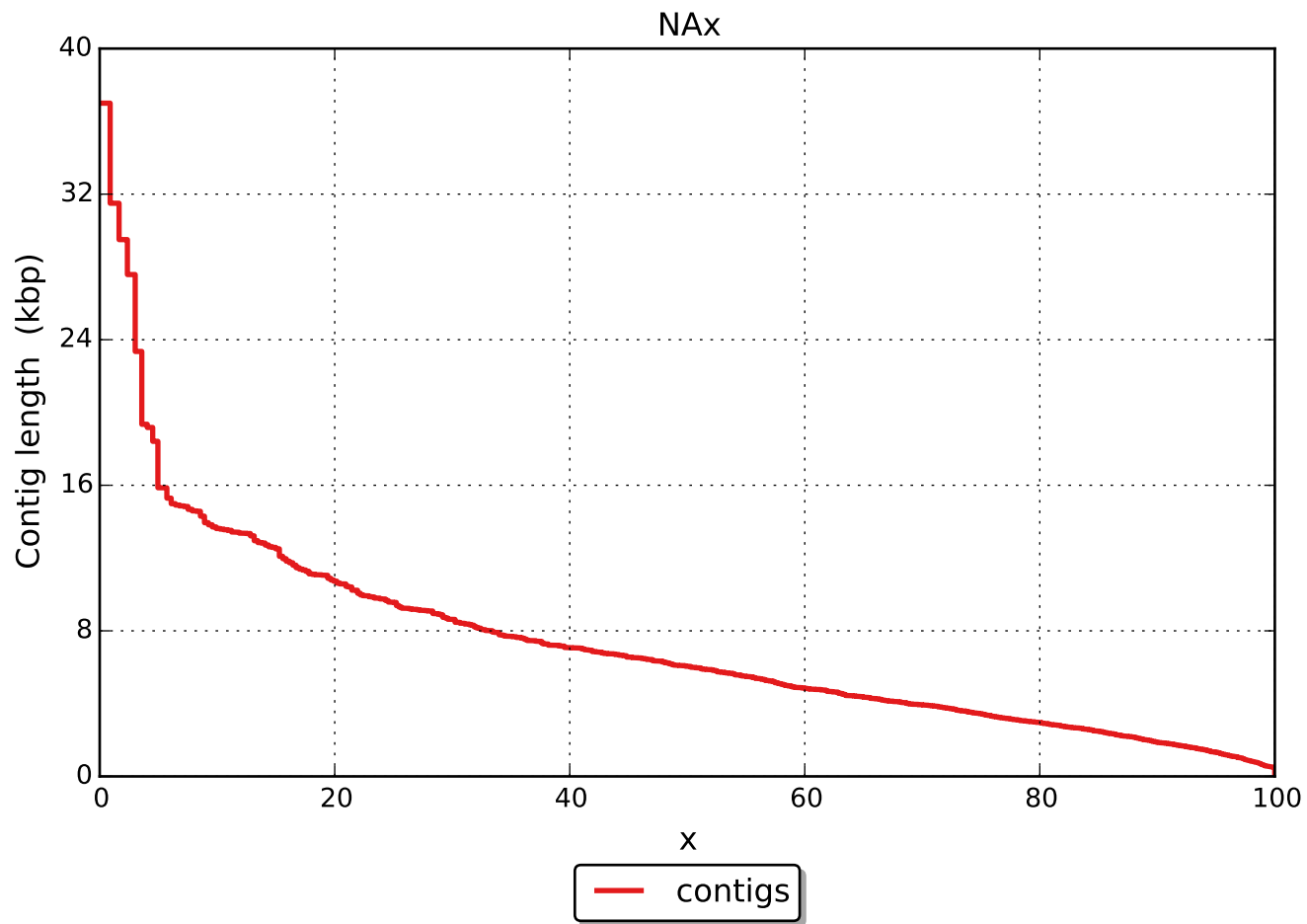
Cumulative length

GC content

windows

GC (%)

contigs — — Reference
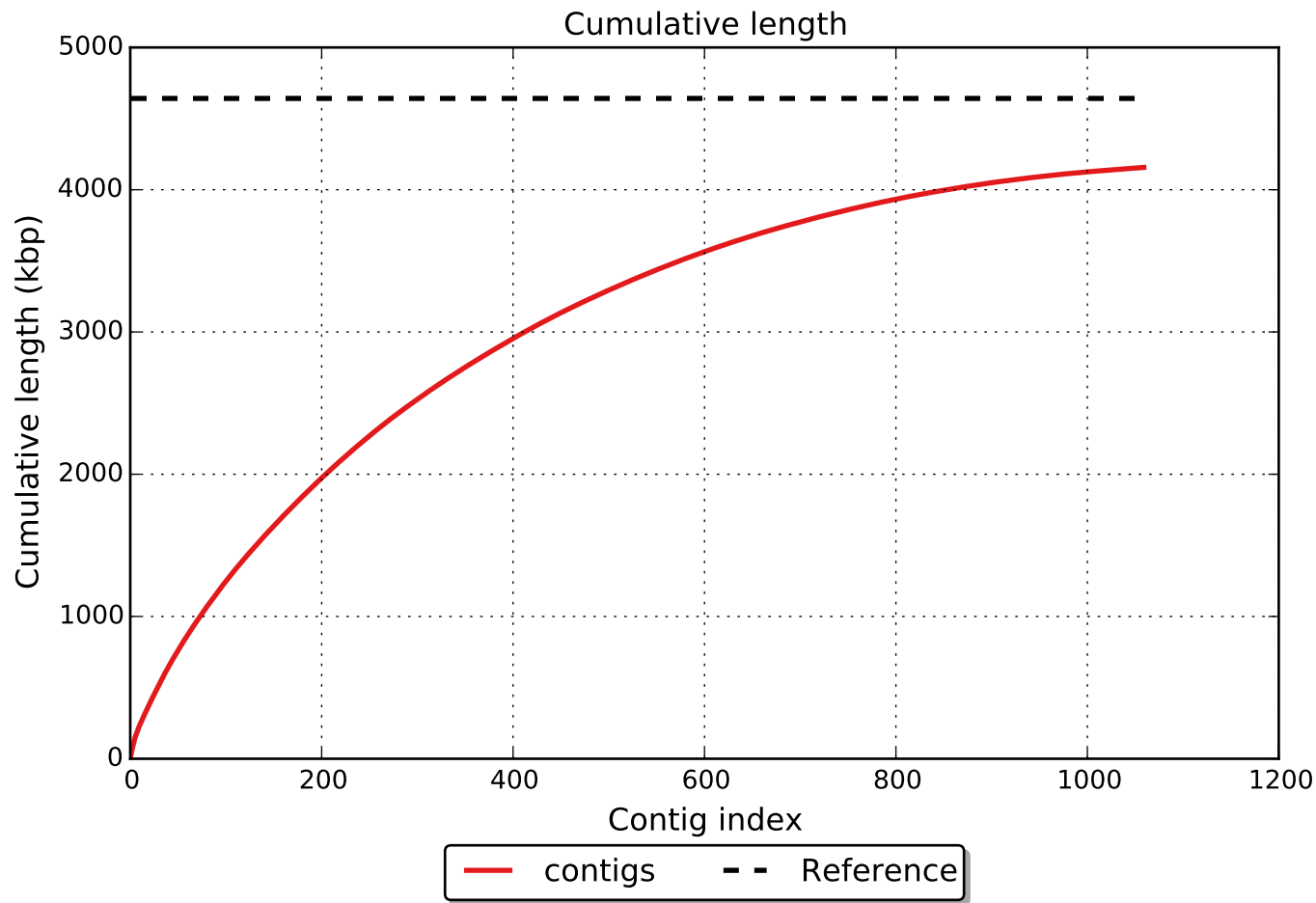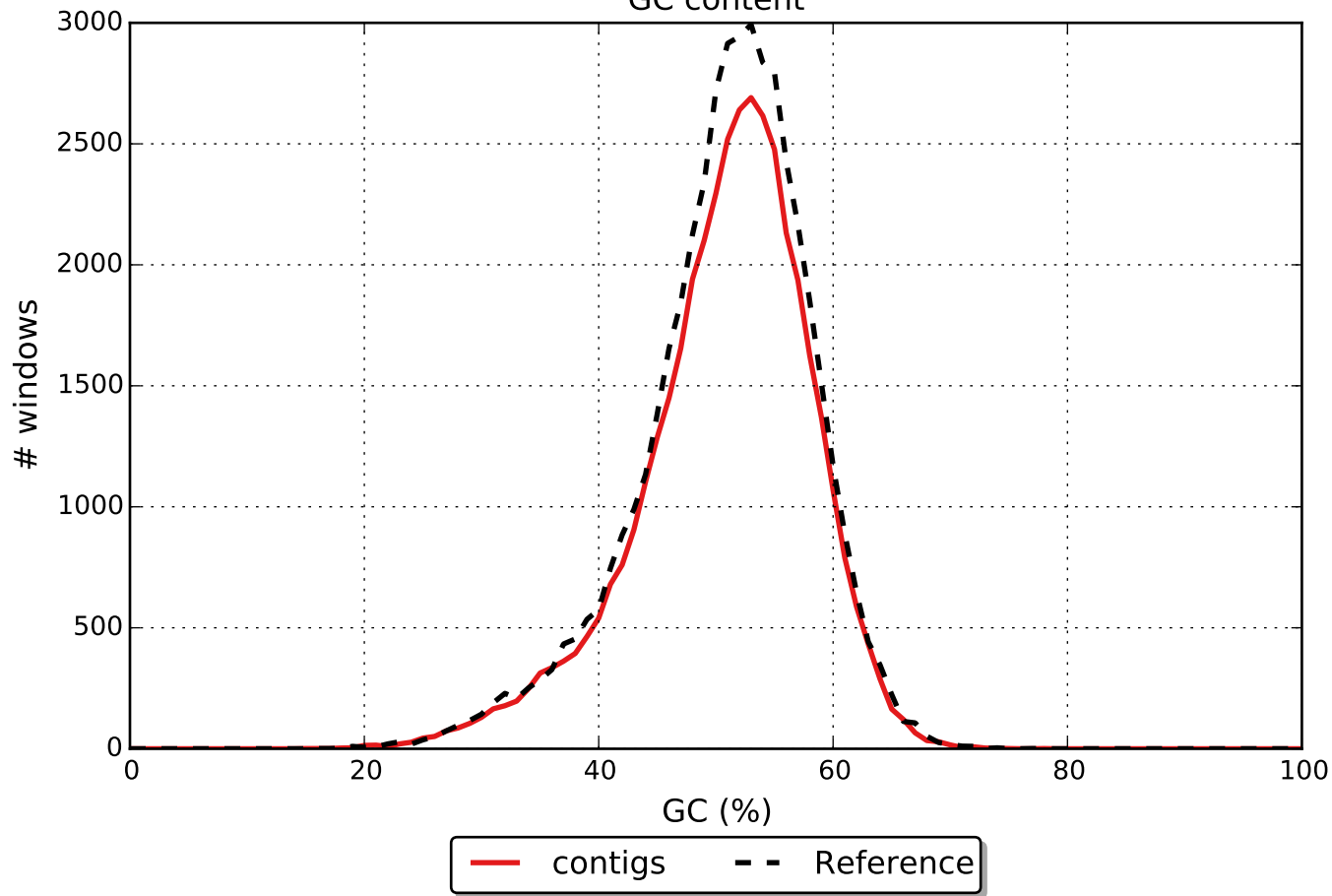
Misassemblies

contigs

Cumulative length (aligned contigs)