Report

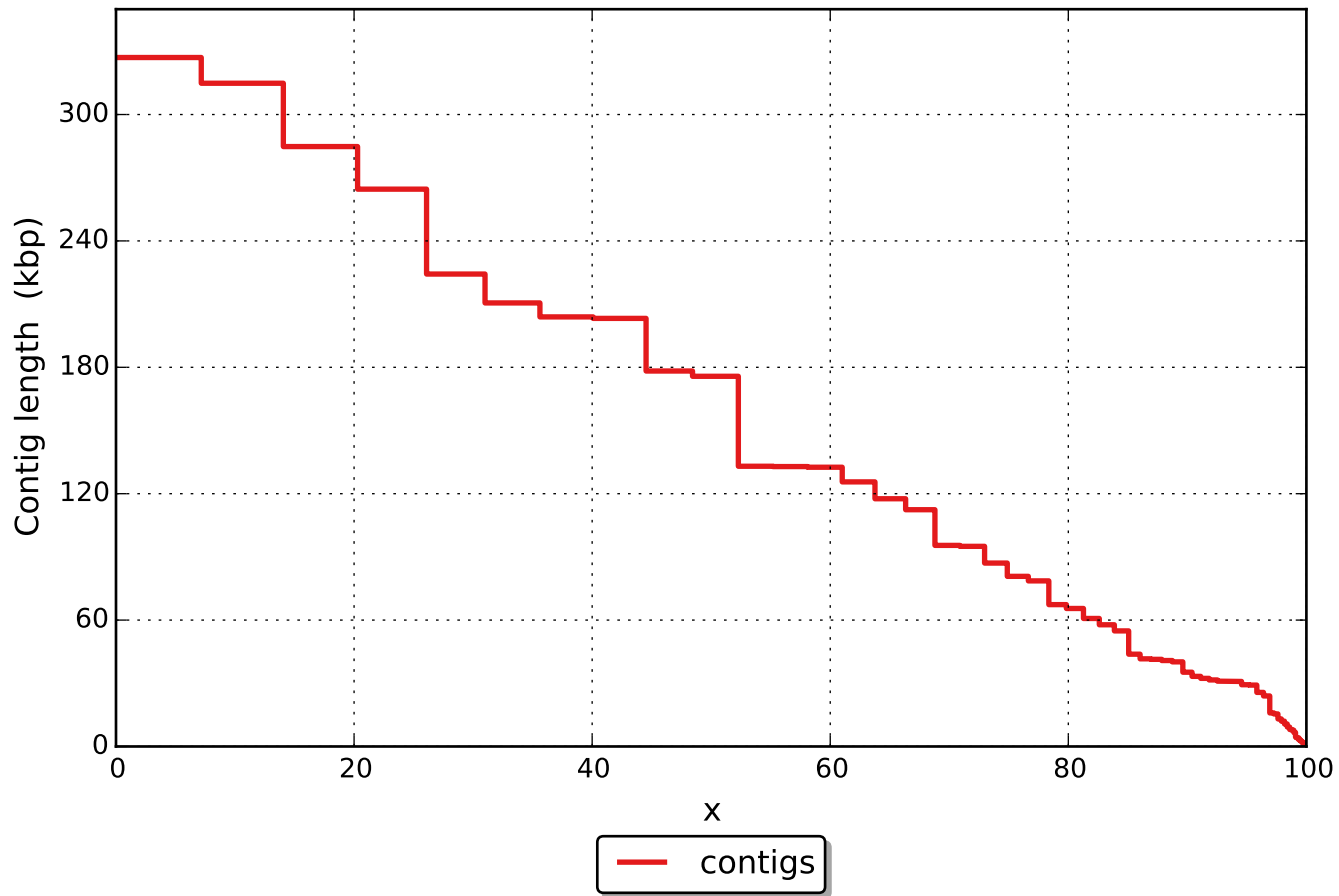|	contigs
# contigs (>= 0 bp)	85
# contigs (>= 1000 bp)	68
# contigs (>= 5000 bp)	51
# contigs (>= 10000 bp)	47
# contigs (>= 25000 bp)	41
# contigs (>= 50000 bp)	26
Total length (>= 0 bp)	4568325
Total length (>= 1000 bp)	4562588
Total length (>= 5000 bp)	4524483
Total length (>= 10000 bp)	4492791
Total length (>= 25000 bp)	4401655
Total length (>= 50000 bp)	3884456
# contigs	73
Largest contig	327064
Total length	4566161
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	175735
NG50	175735
N75	80764
NG75	80764
L50	10
LG50	10
L75	20
LG75	20
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.311
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4.82
# indels per 100 kbp	0.33
Largest alignment	327064
NA50	175735
NGA50	175735
NA75	80764
NGA75	80764
LA50	10
LGA50	10
LA75	20
LGA75	20

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
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# mismatches	220
# indels	15
# short indels	15
# long indels	0
Indels length	21

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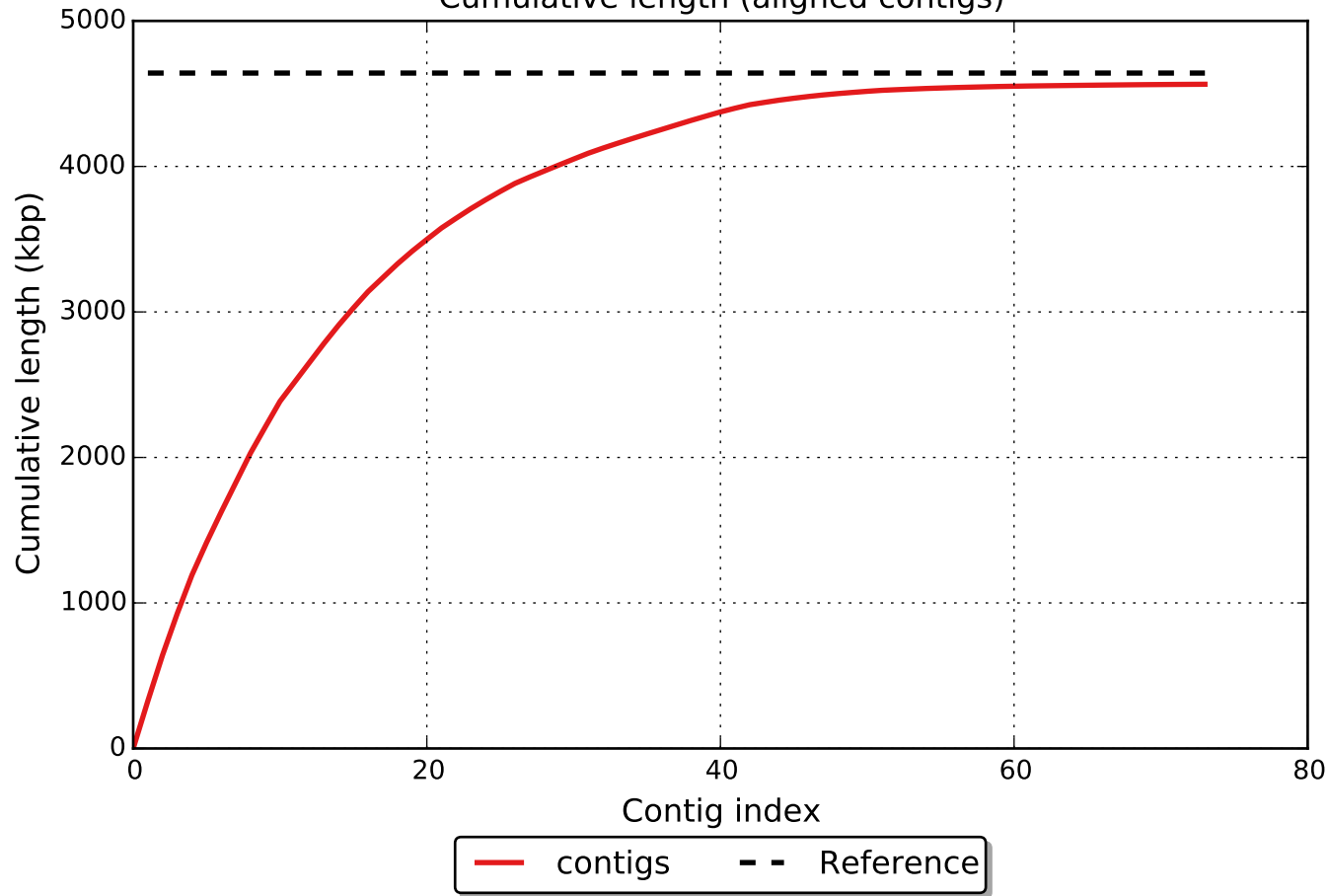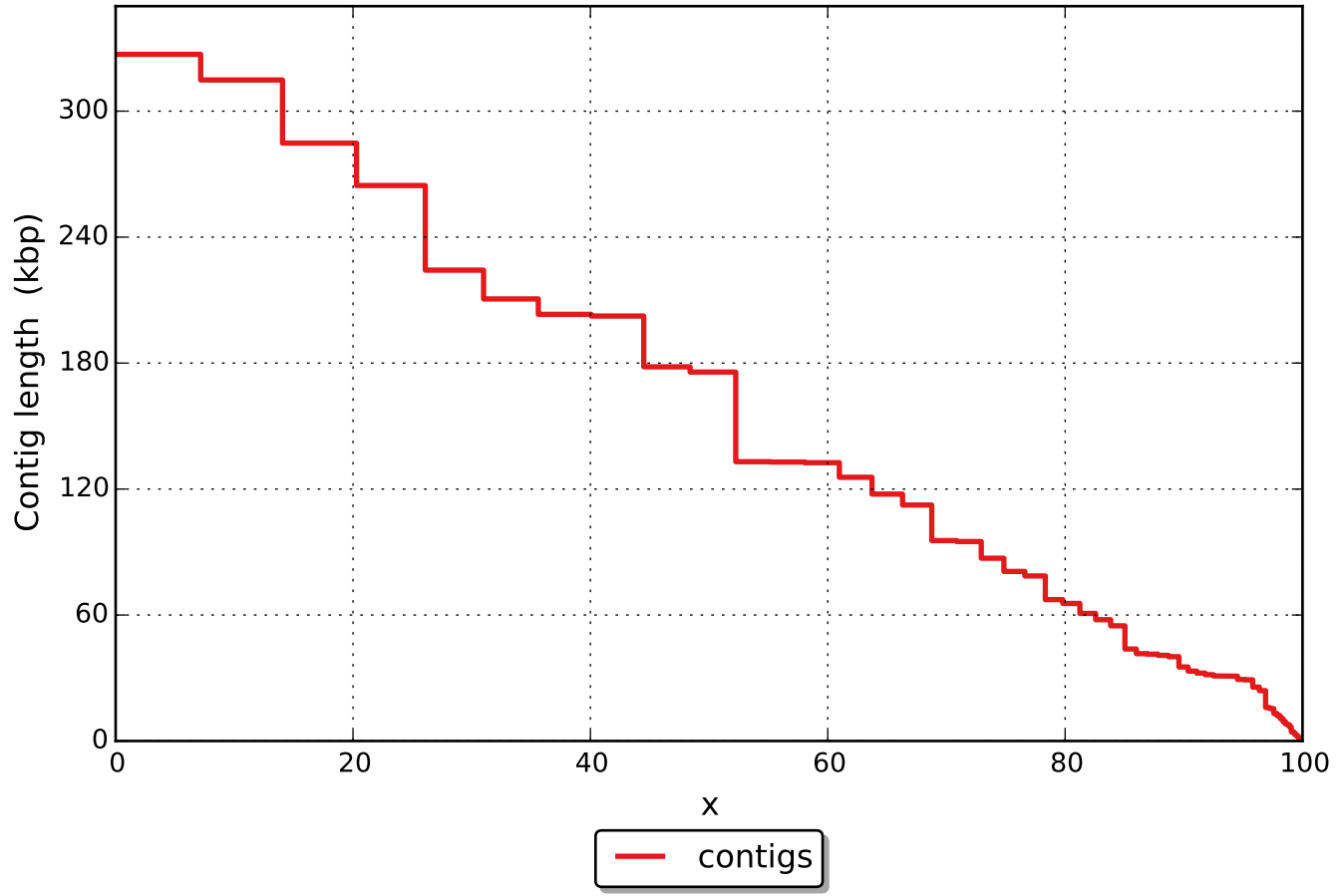(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).
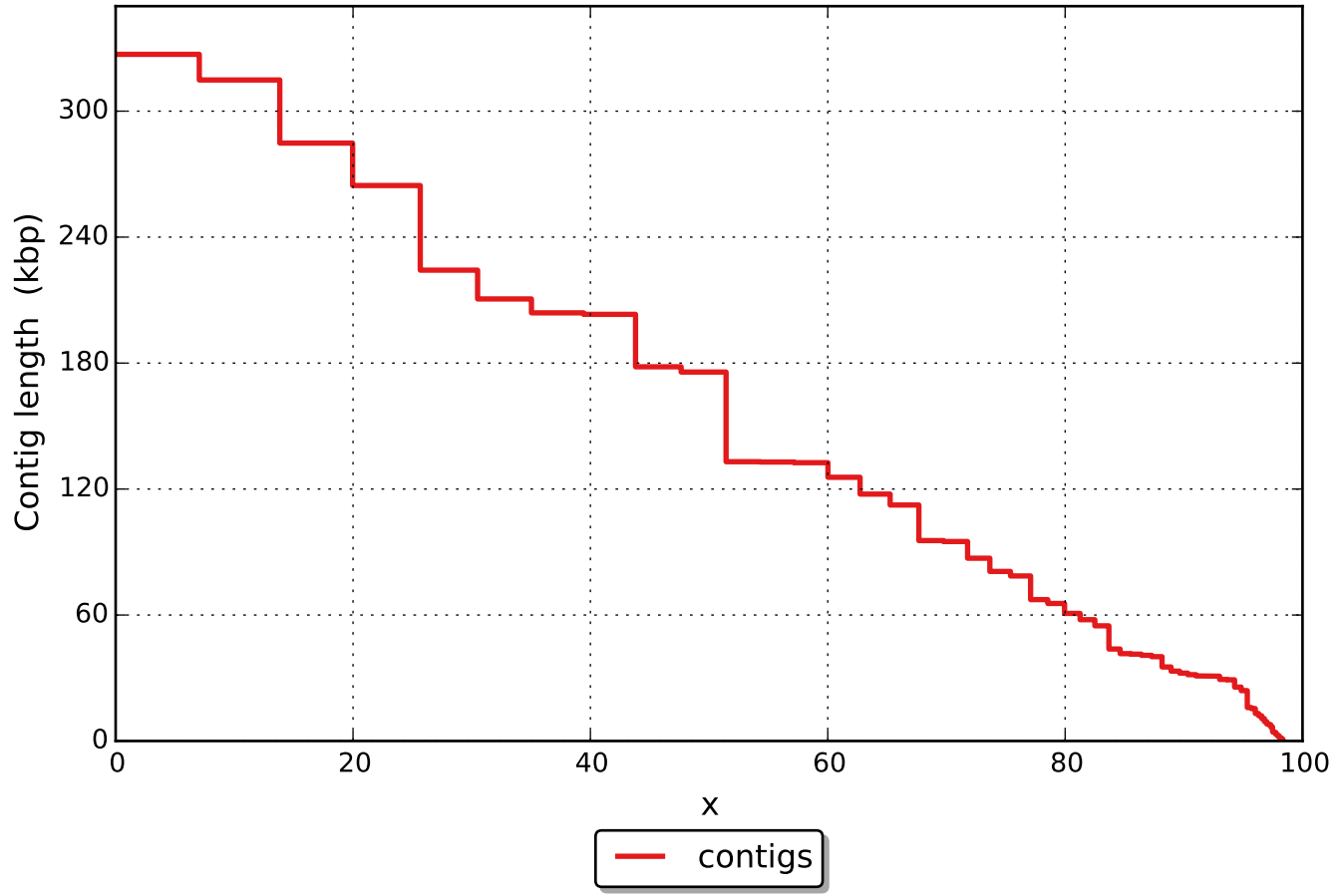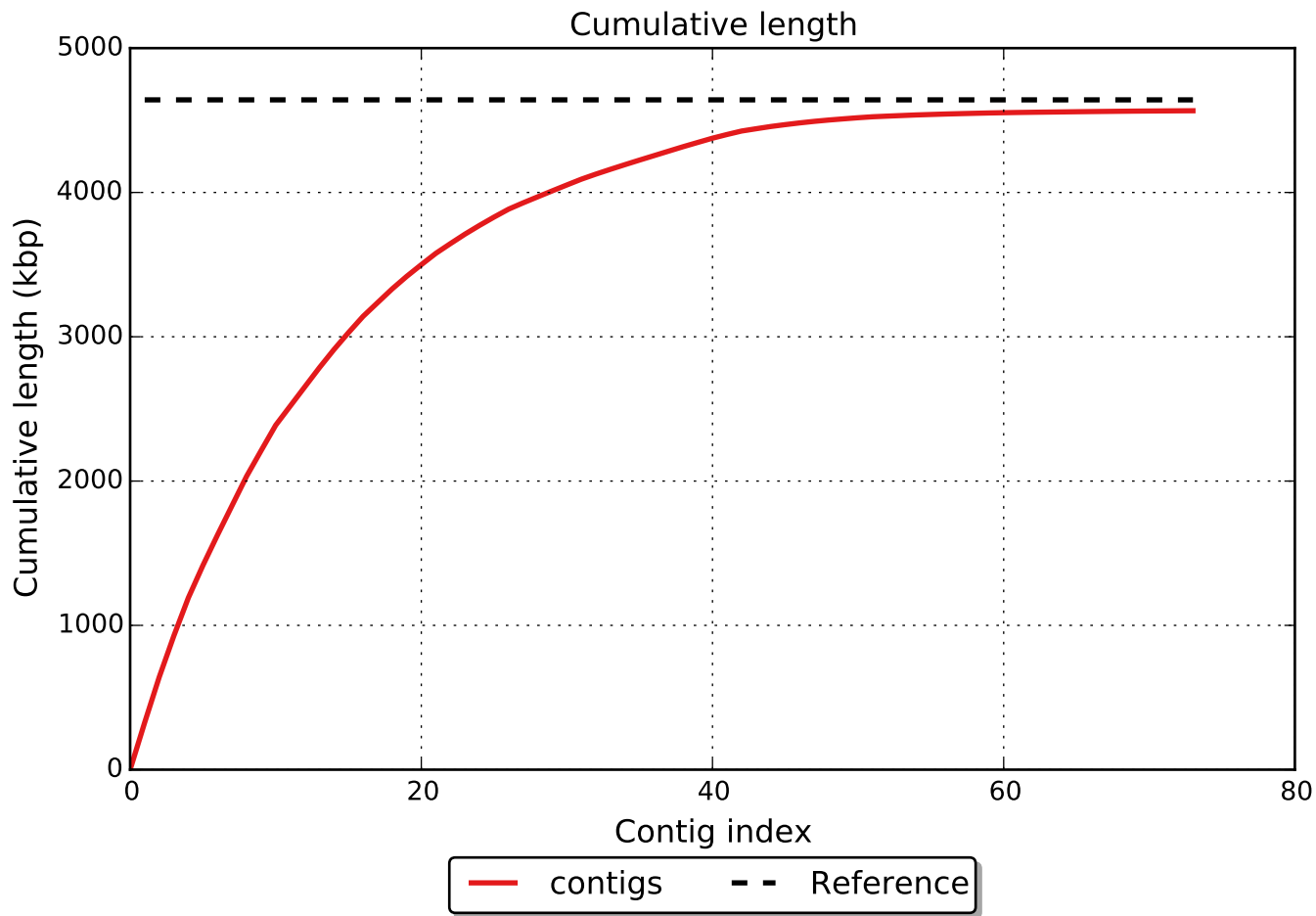
Cumulative length

GC content
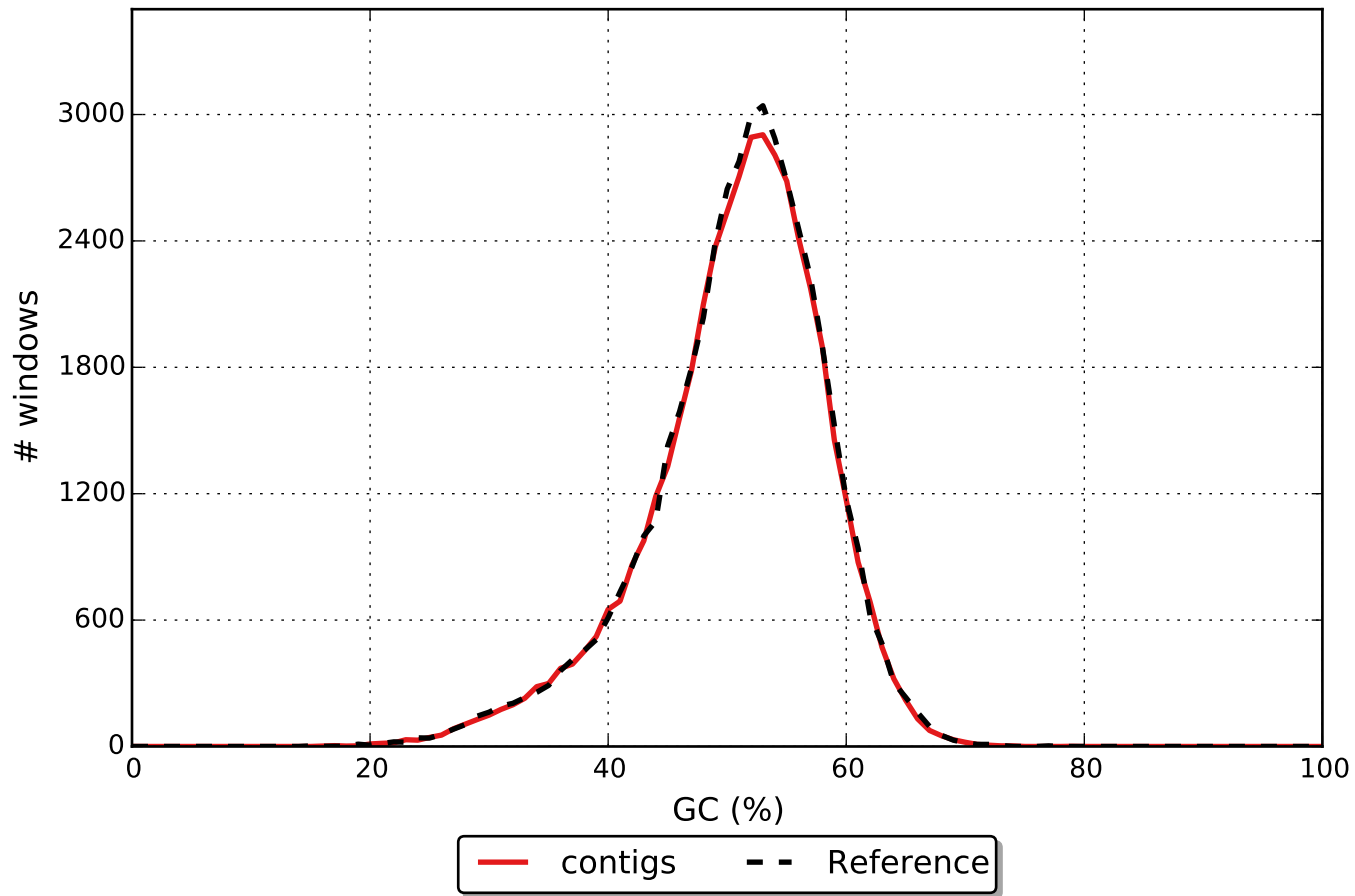
Misassemblies

contigs

Cumulative length (aligned contigs)

NAx