Report

	final.contigs
# contigs (>= 1000 bp)	441
# contigs (>= 5000 bp)	281
# contigs (>= 10000 bp)	166
# contigs (>= 25000 bp)	33
# contigs (>= 50000 bp)	3
Total length (>= 1000 bp)	4552077
Total length (>= 5000 bp)	4107471
Total length (>= 10000 bp)	3252868
Total length (>= 25000 bp)	1125695
Total length (>= 50000 bp)	160935
# contigs	488
Largest contig	55140
Total length	4588866
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	15916
NG50	15879
N75	8869
NG75	8688
L50	92
LG50	94
L75	186
LG75	191
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	7679
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.132
Duplication ratio	1.007
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.35
# indels per 100 kbp	0.00
Largest alignment	55140
NA50	15916
NGA50	15879
NA75	8869
NGA75	8688
LA50	92
LGA50	94
LA75	186
LGA75	191

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	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	7679
# local misassemblies	0
# mismatches	16
# indels	0
# short indels	0
# long indels	0
Indels length	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).

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).

Cumulative length
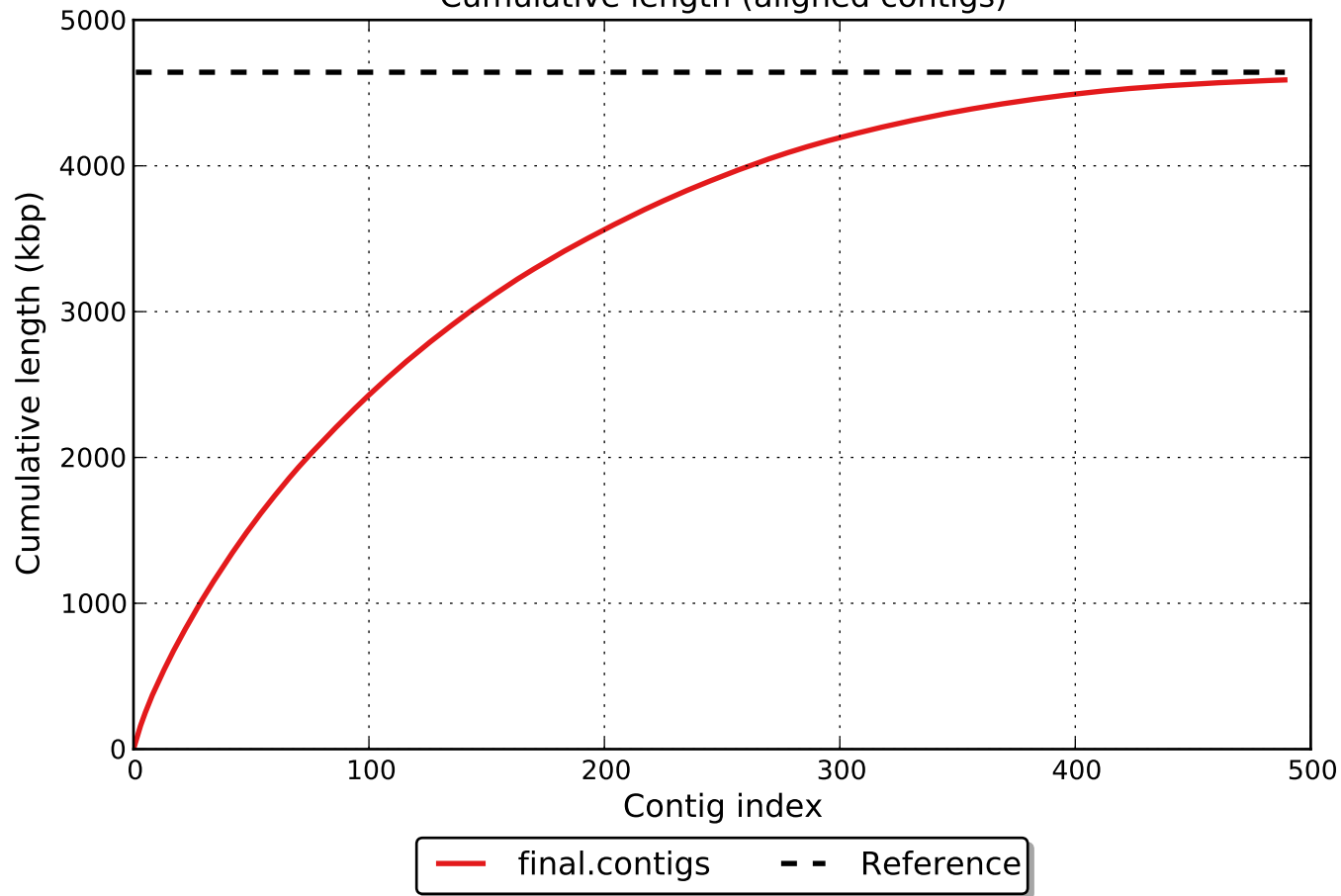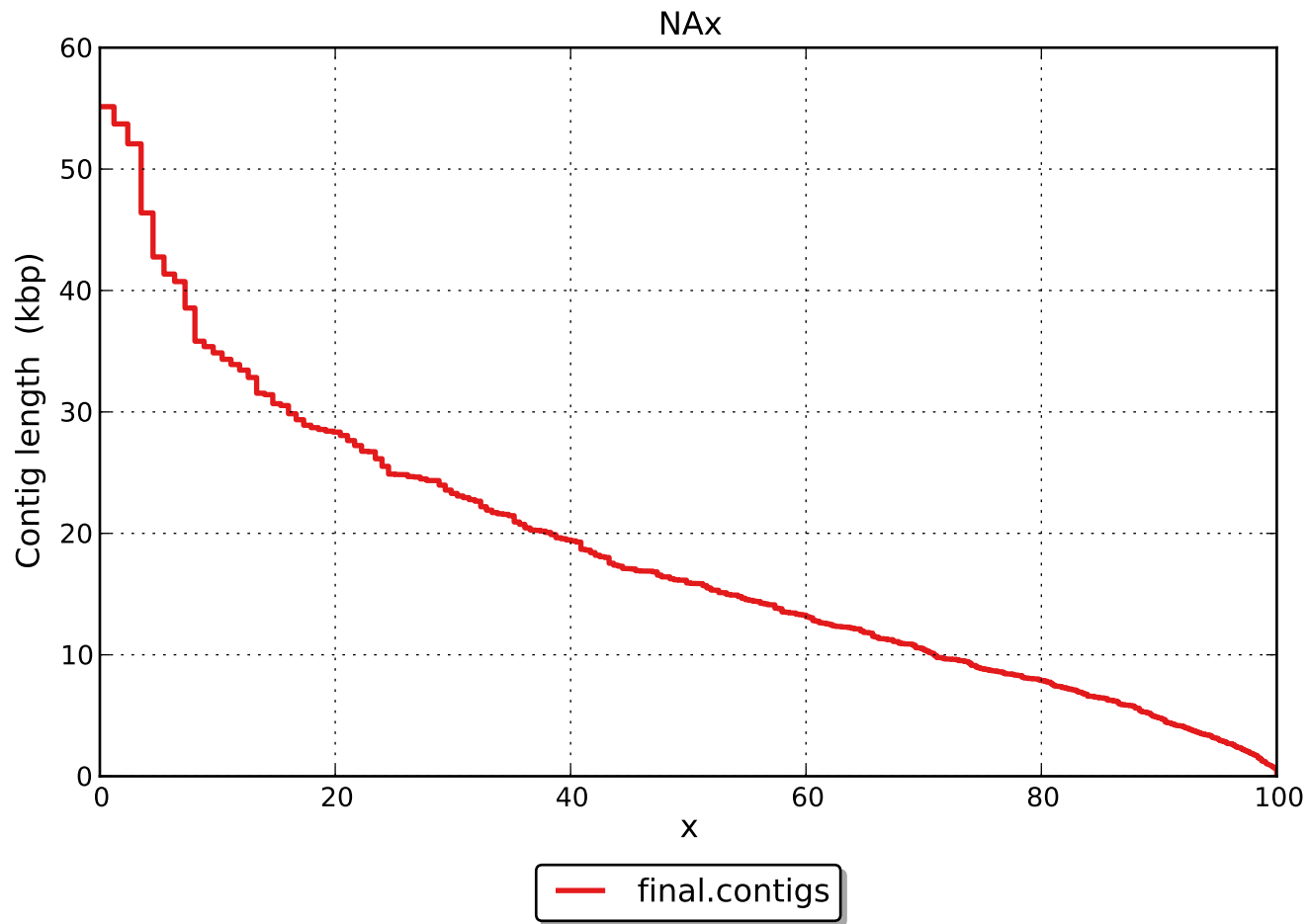
GC content

Misassemblies

final.contigs

relocations
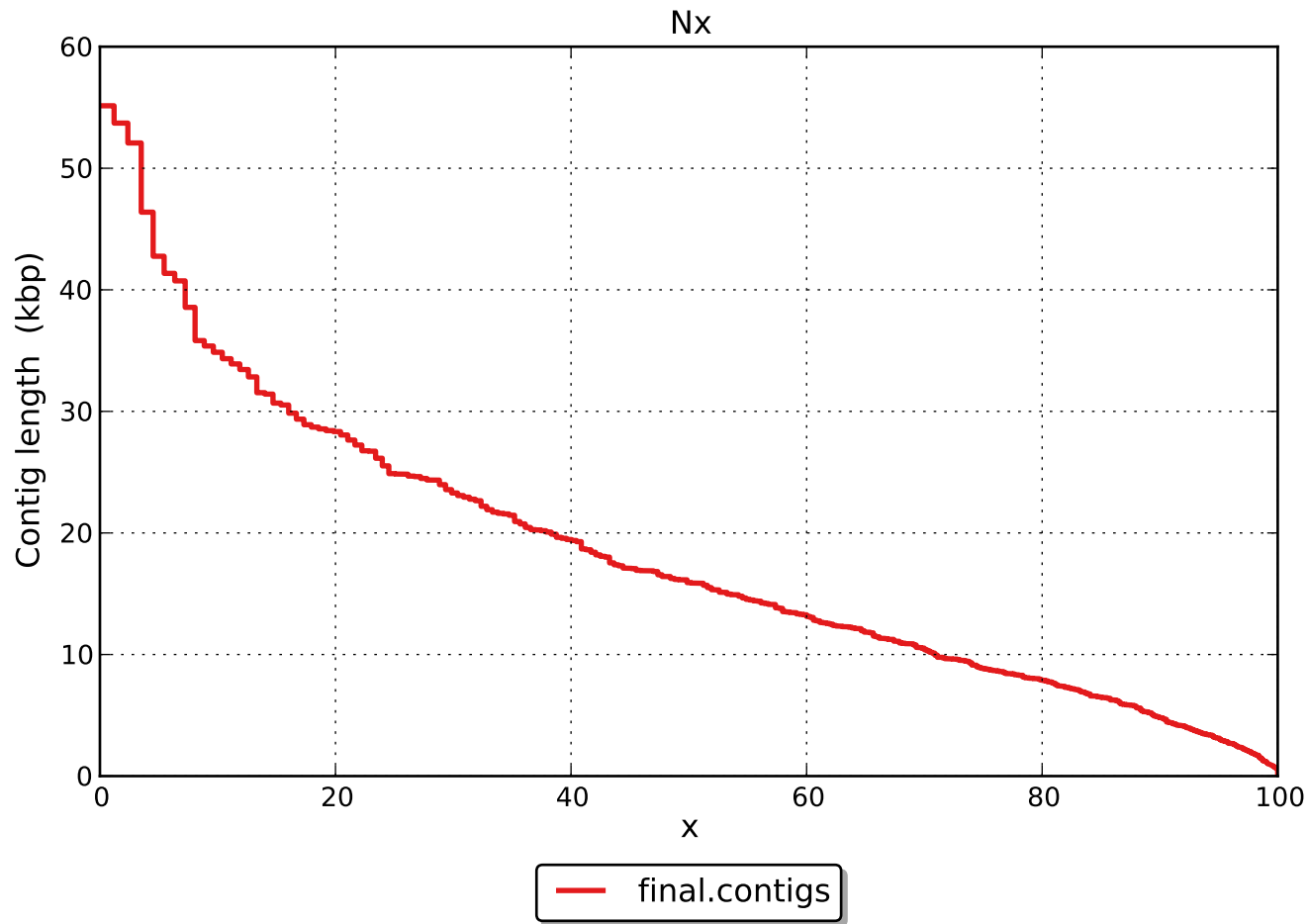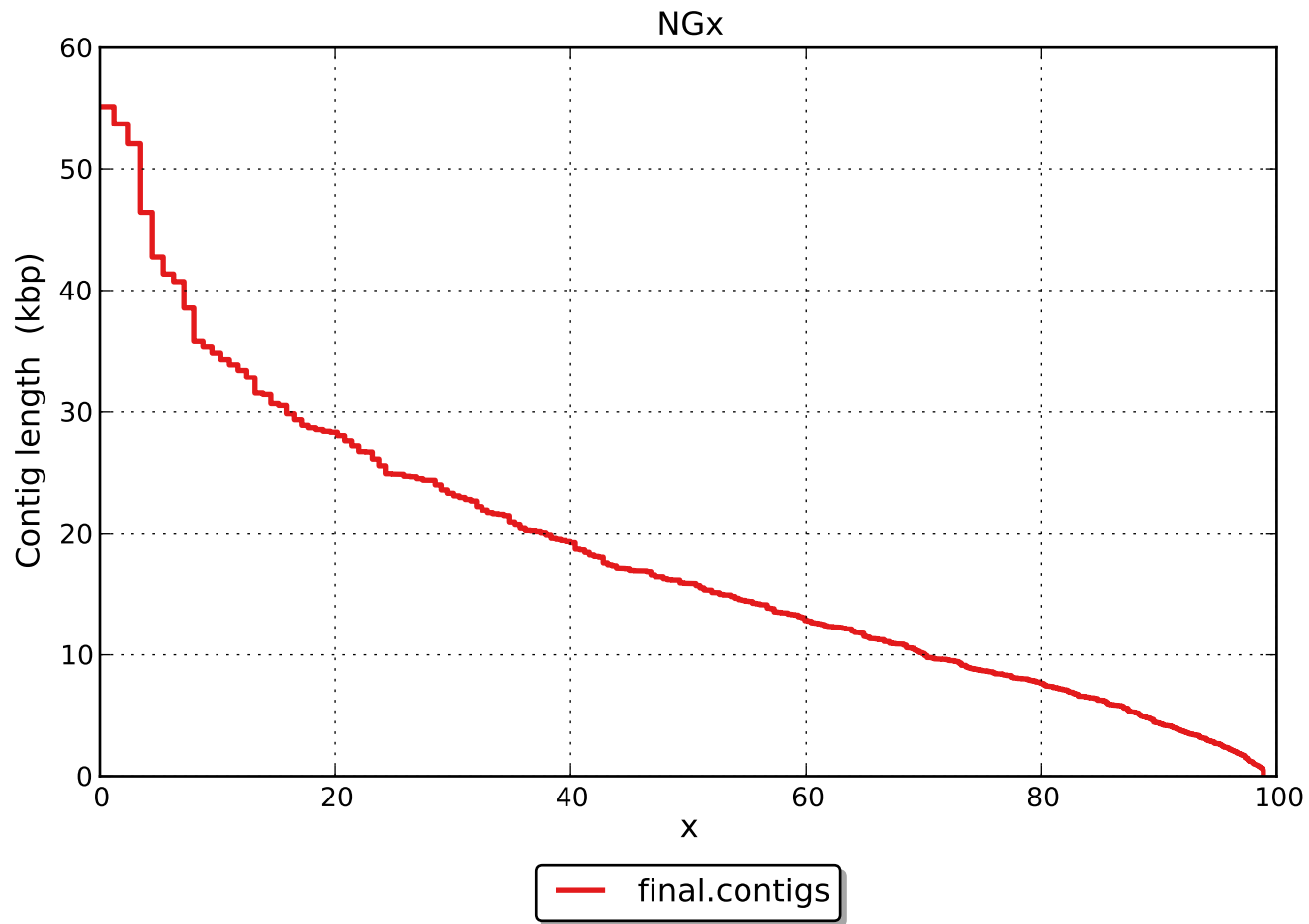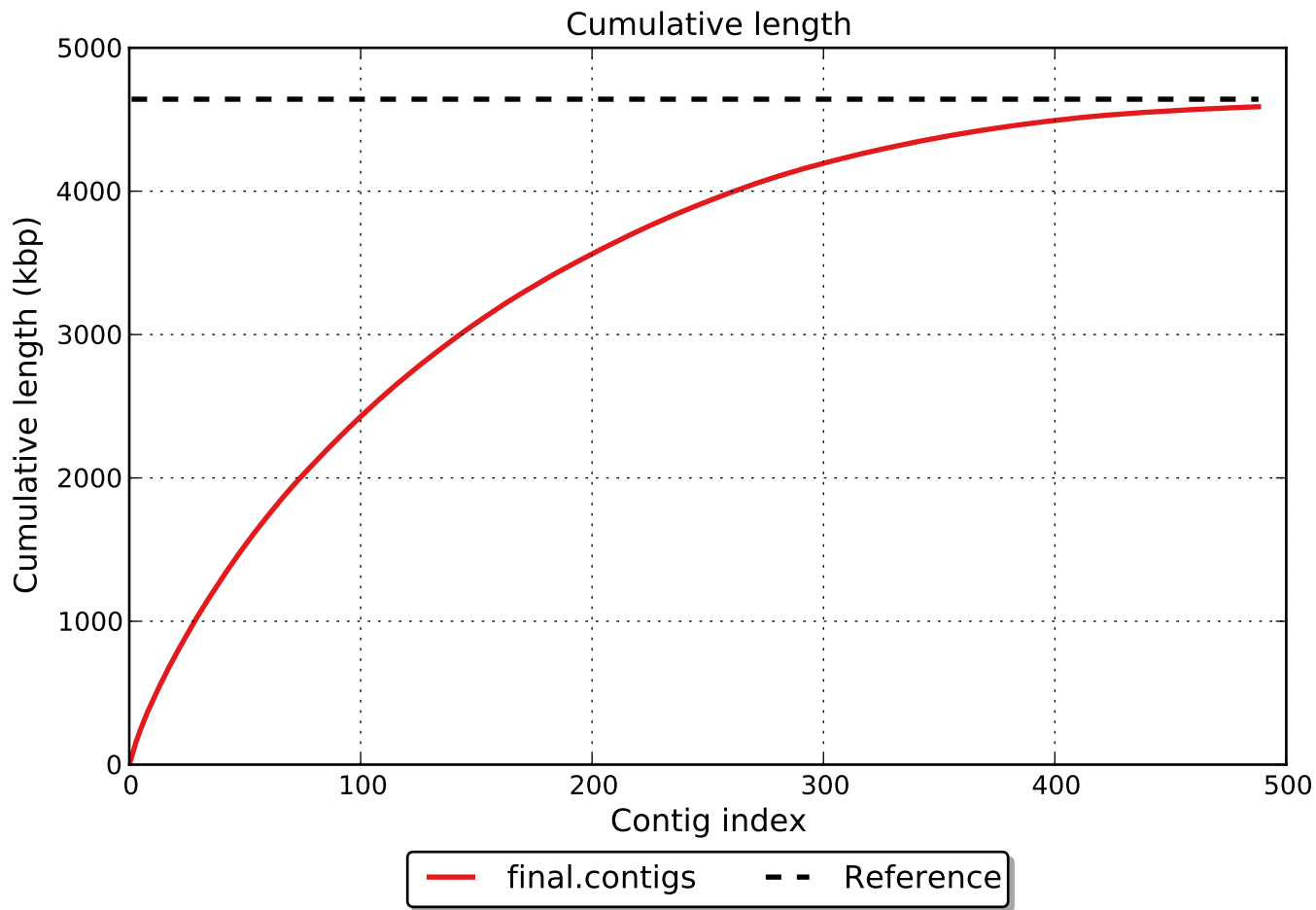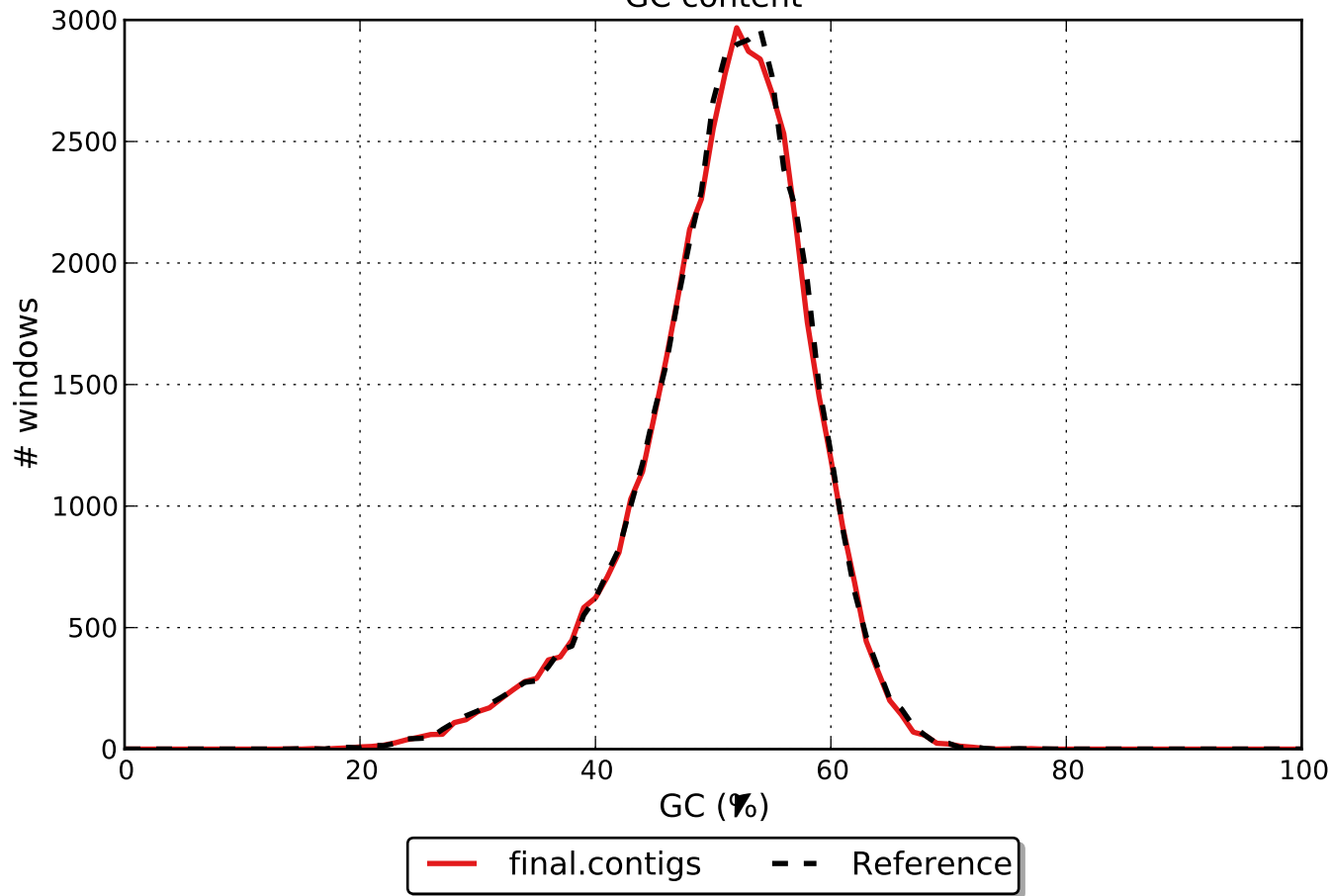
Cumulative length (aligned contigs)