Report

	final.contigs
# contigs (>= 1000 bp)	1109
# contigs (>= 5000 bp)	352
# contigs (>= 10000 bp)	73
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4807338
Total length (>= 5000 bp)	2829453
Total length (>= 10000 bp)	951641
Total length (>= 25000 bp)	26127
Total length (>= 50000 bp)	0
# contigs	1276
Largest contig	26127
Total length	4933596
Reference length	4857432
GC (%)	52.24
Reference GC (%)	52.23
N50	5552
NG50	5675
N75	3301
NG75	3388
L50	284
LG50	277
L75	565
LG75	547
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	131
Genome fraction (%)	99.319
Duplication ratio	1.023
# N's per 100 kbp	0.00
# mismatches per 100 kbp	20.48
# indels per 100 kbp	0.00
Largest alignment	26127
NA50	5552
NGA50	5675
NA75	3301
NGA75	3386
LA50	284
LGA50	277
LA75	565
LGA75	548

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).
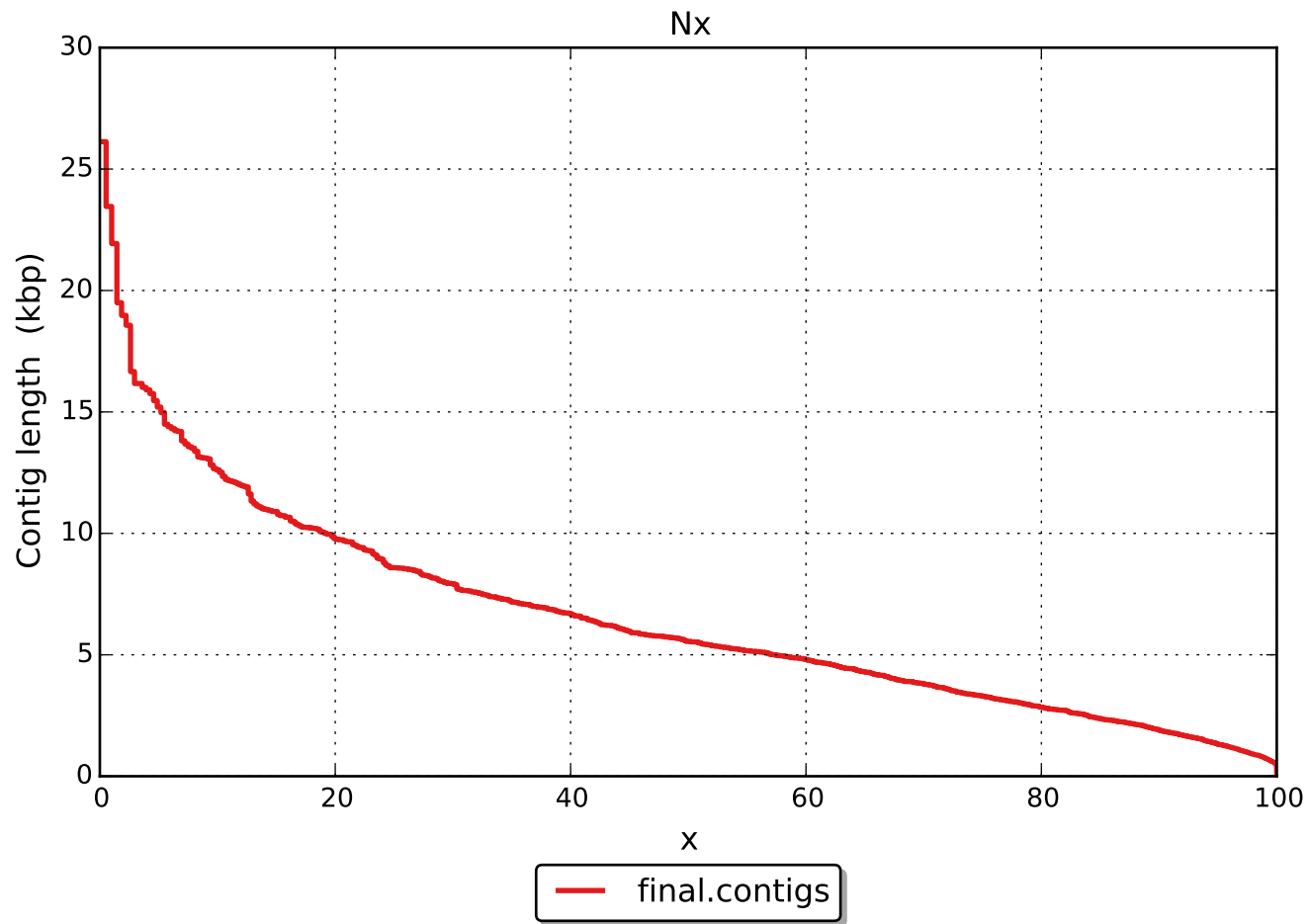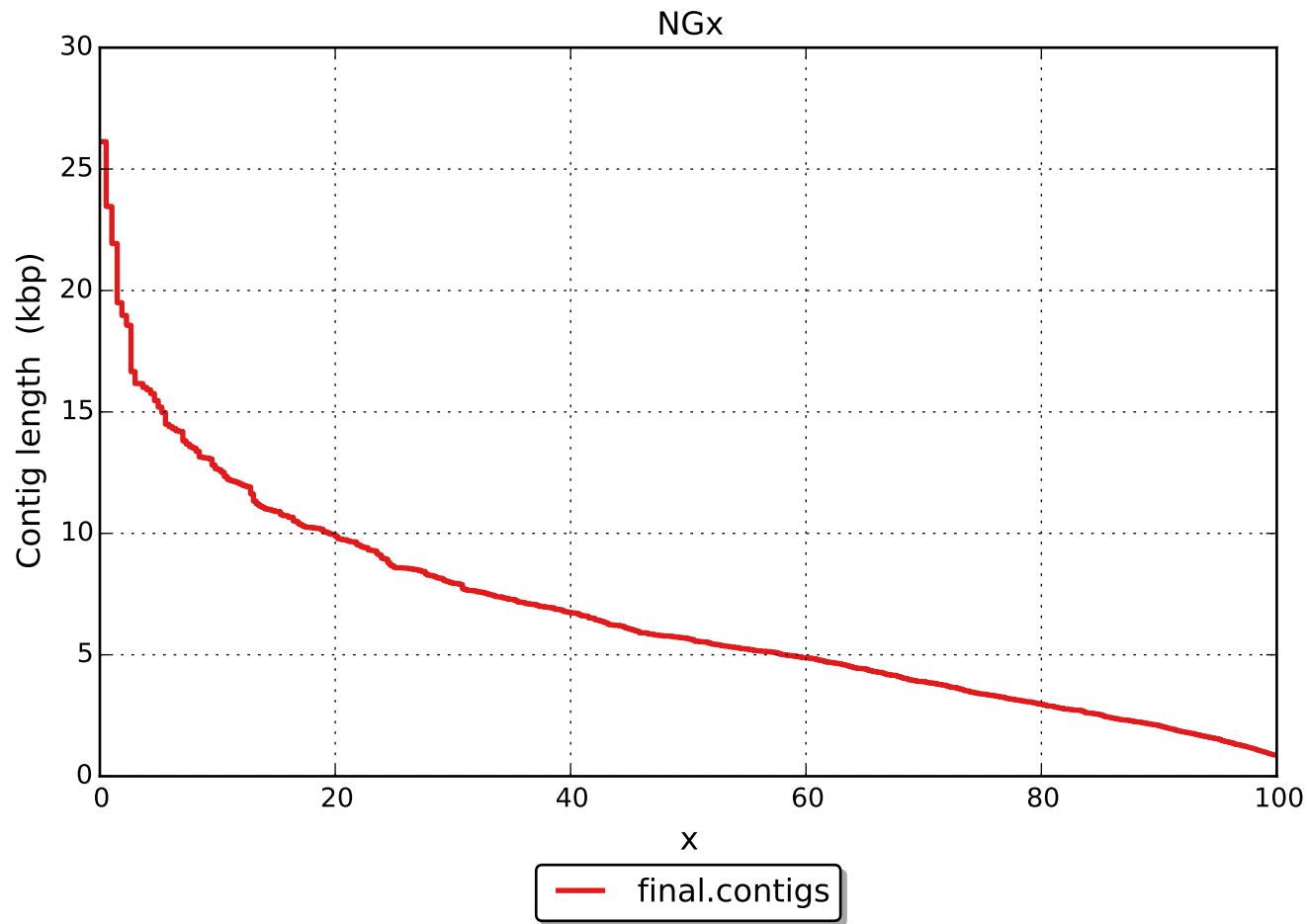
Misassemblies report

	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	988
# 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	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	131
# 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).
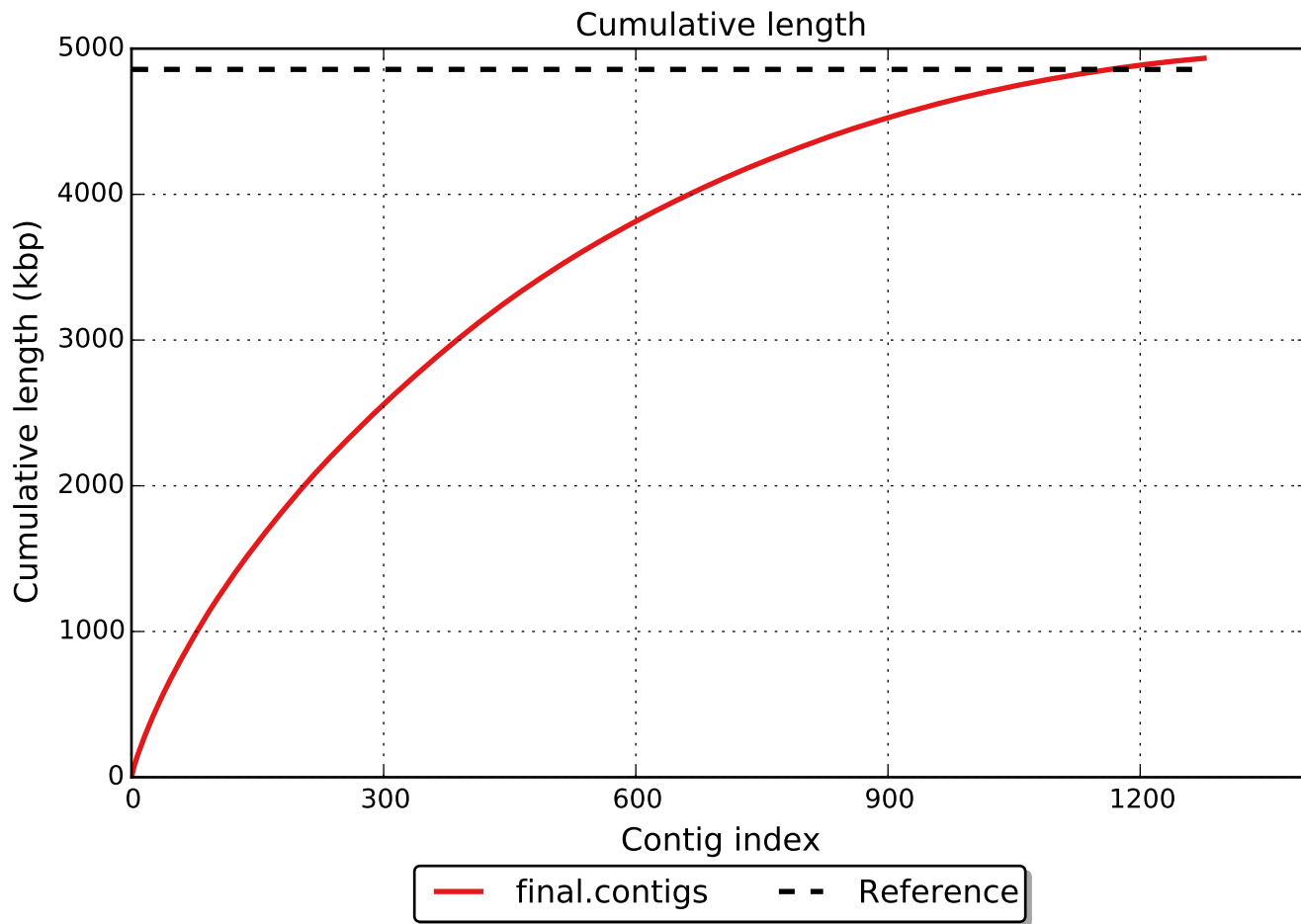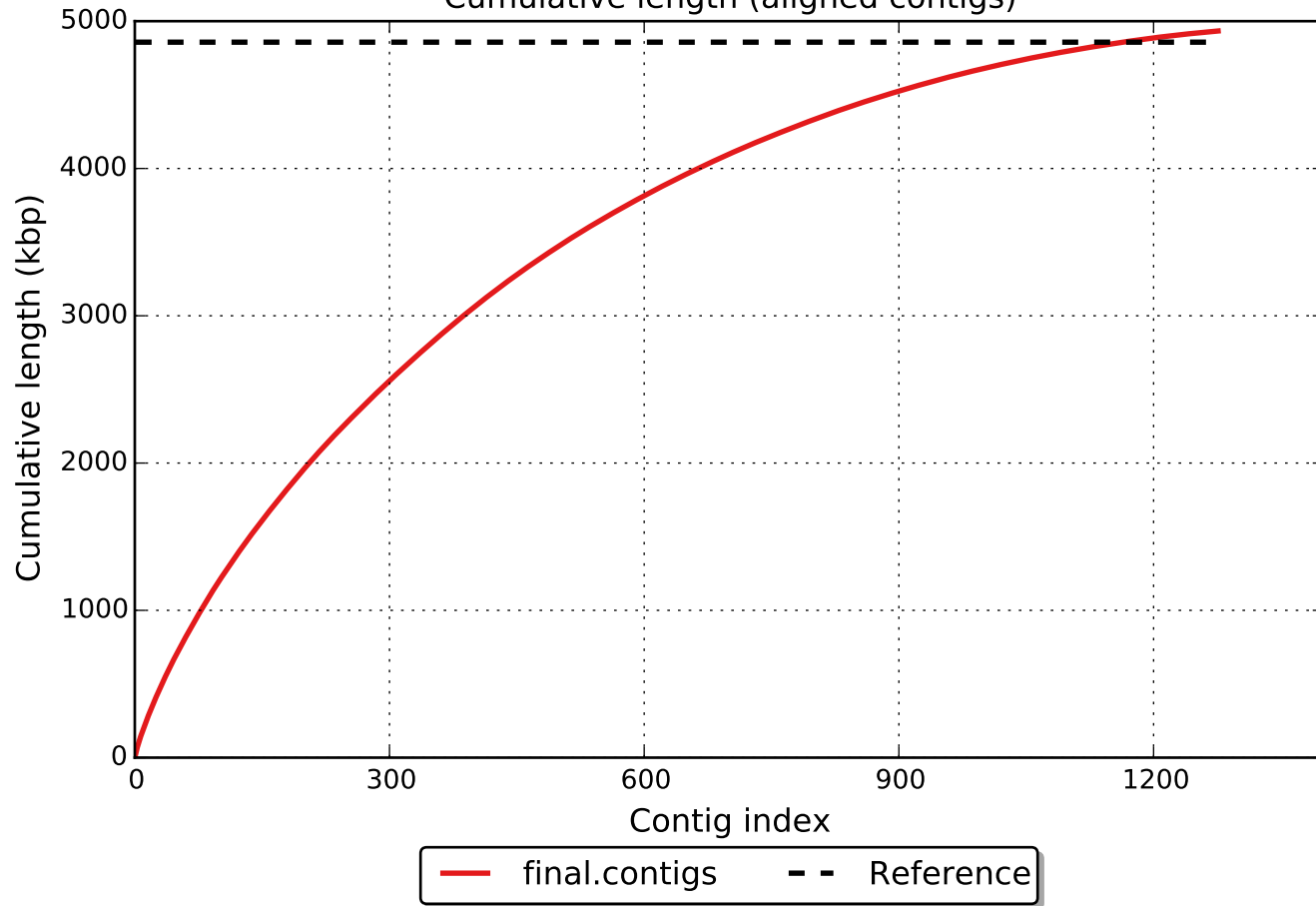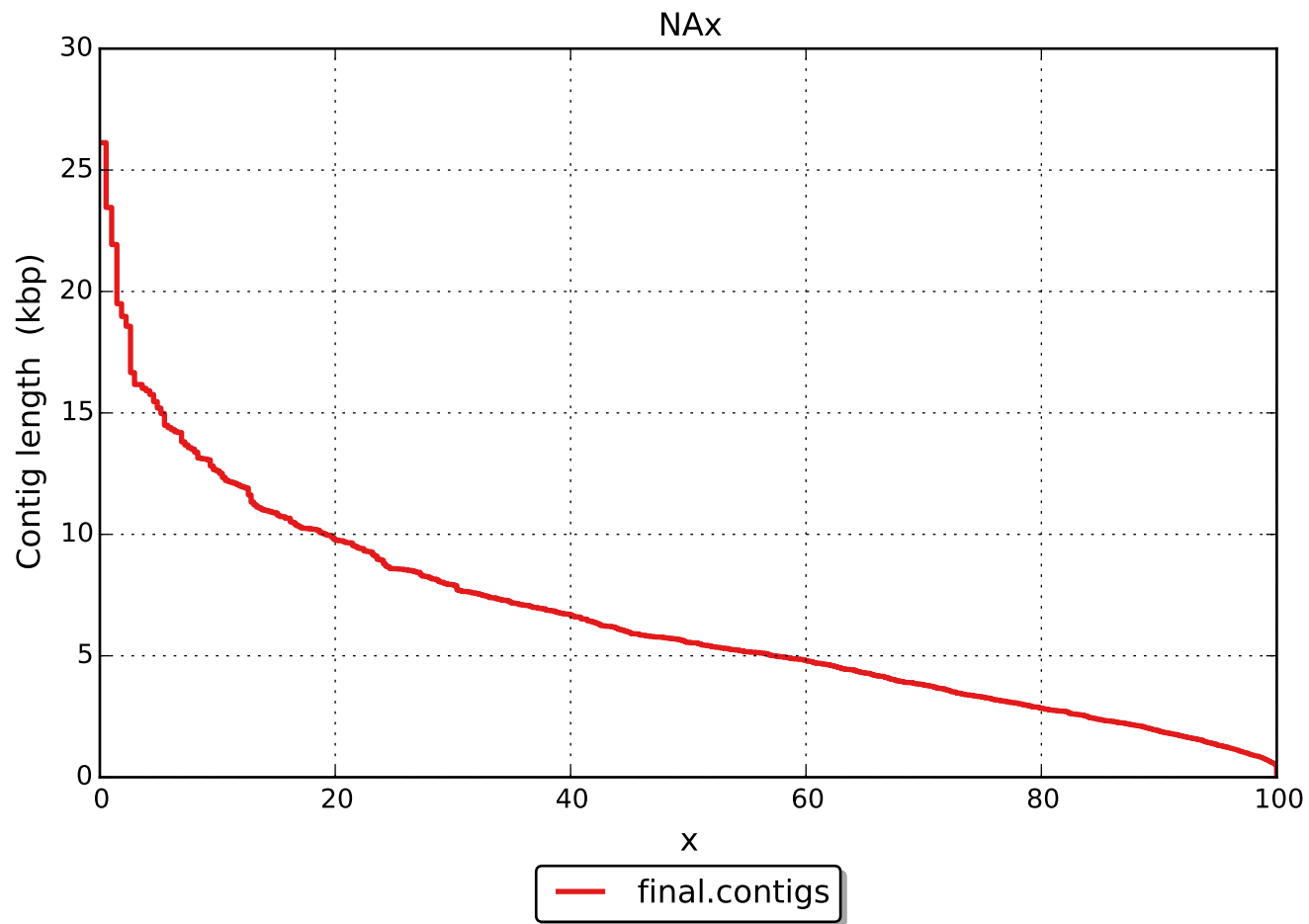
Cumulative length

GC content

Misassemblies

final.contigs
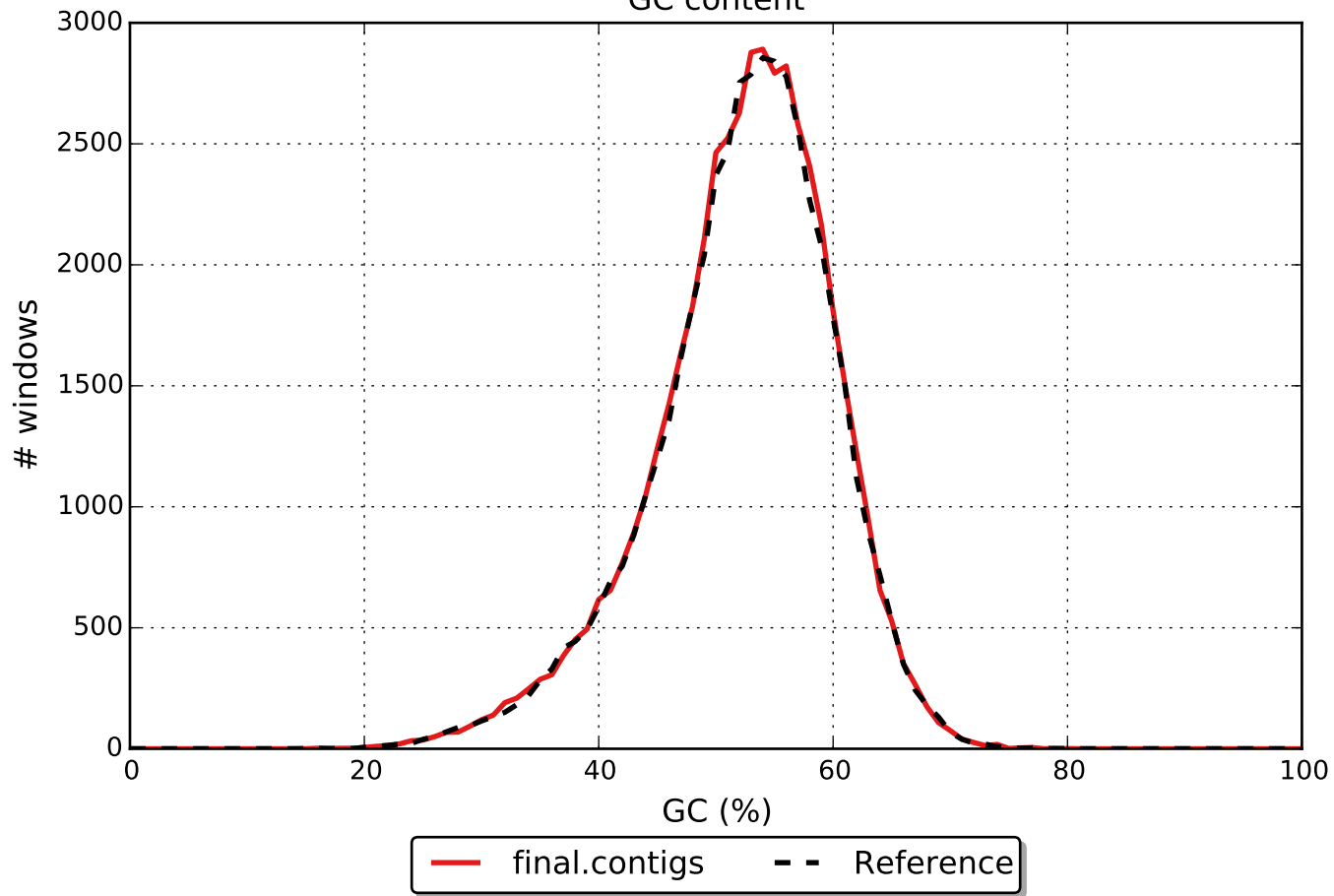
Cumulative length (aligned contigs)