Report

	final.contigs
# contigs (>= 1000 bp)	1292
# contigs (>= 5000 bp)	251
# contigs (>= 10000 bp)	37
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4494726
Total length (>= 5000 bp)	1879477
Total length (>= 10000 bp)	460696
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1612
Largest contig	19708
Total length	4729722
Reference length	4641652
GC (%)	50.78
Reference GC (%)	50.78
N50	4229
NG50	4287
N75	2478
NG75	2548
L50	357
LG50	347
L75	722
LG75	696
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.068
Duplication ratio	1.029
# N's per 100 kbp	0.00
# mismatches per 100 kbp	31.40
# indels per 100 kbp	0.00
Largest alignment	19708
NA50	4229
NGA50	4287
NA75	2478
NGA75	2548
LA50	357
LGA50	347
LA75	722
LGA75	696

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).
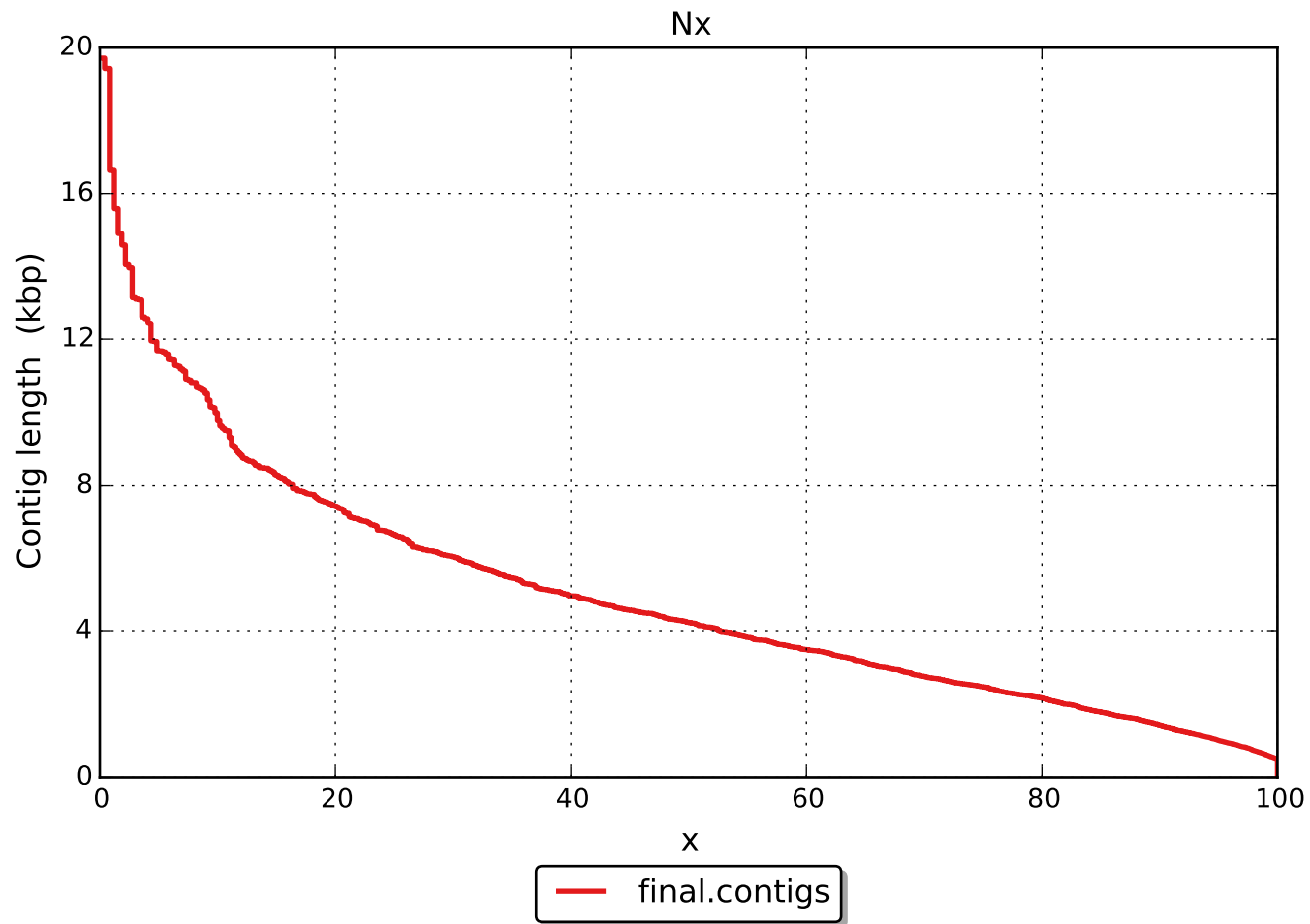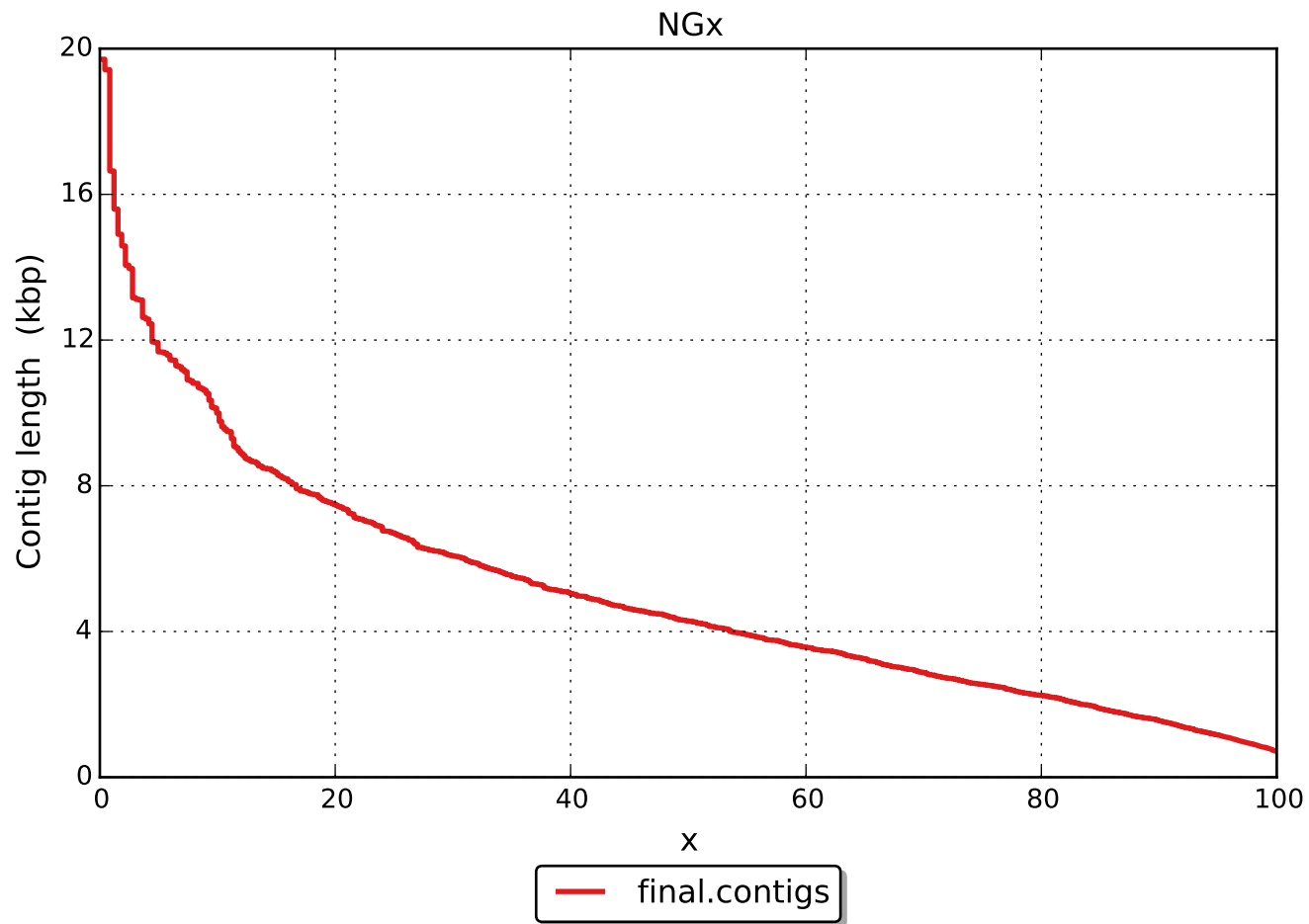
Misassemblies report

	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	1444
# 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).
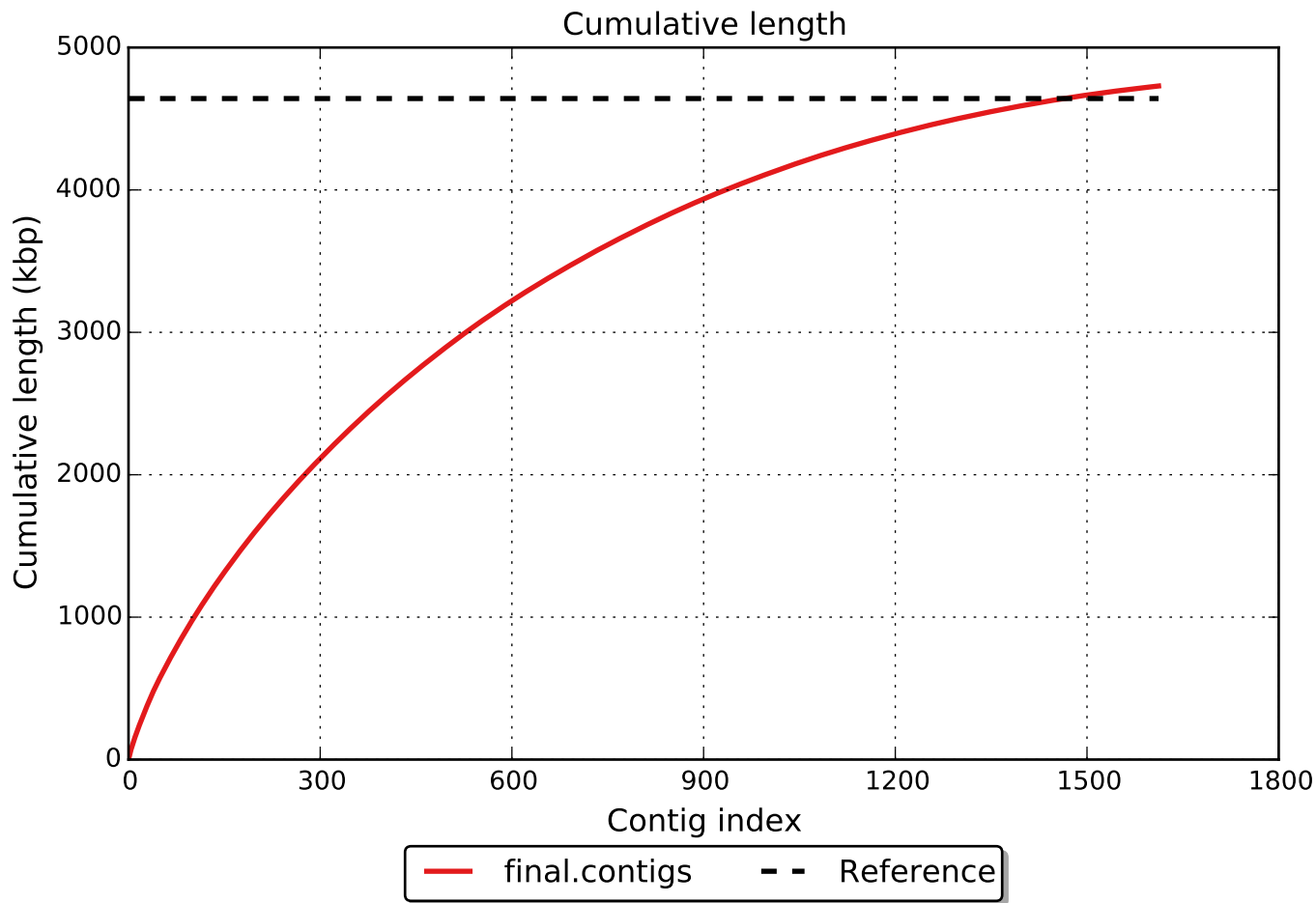
Unaligned report

	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).
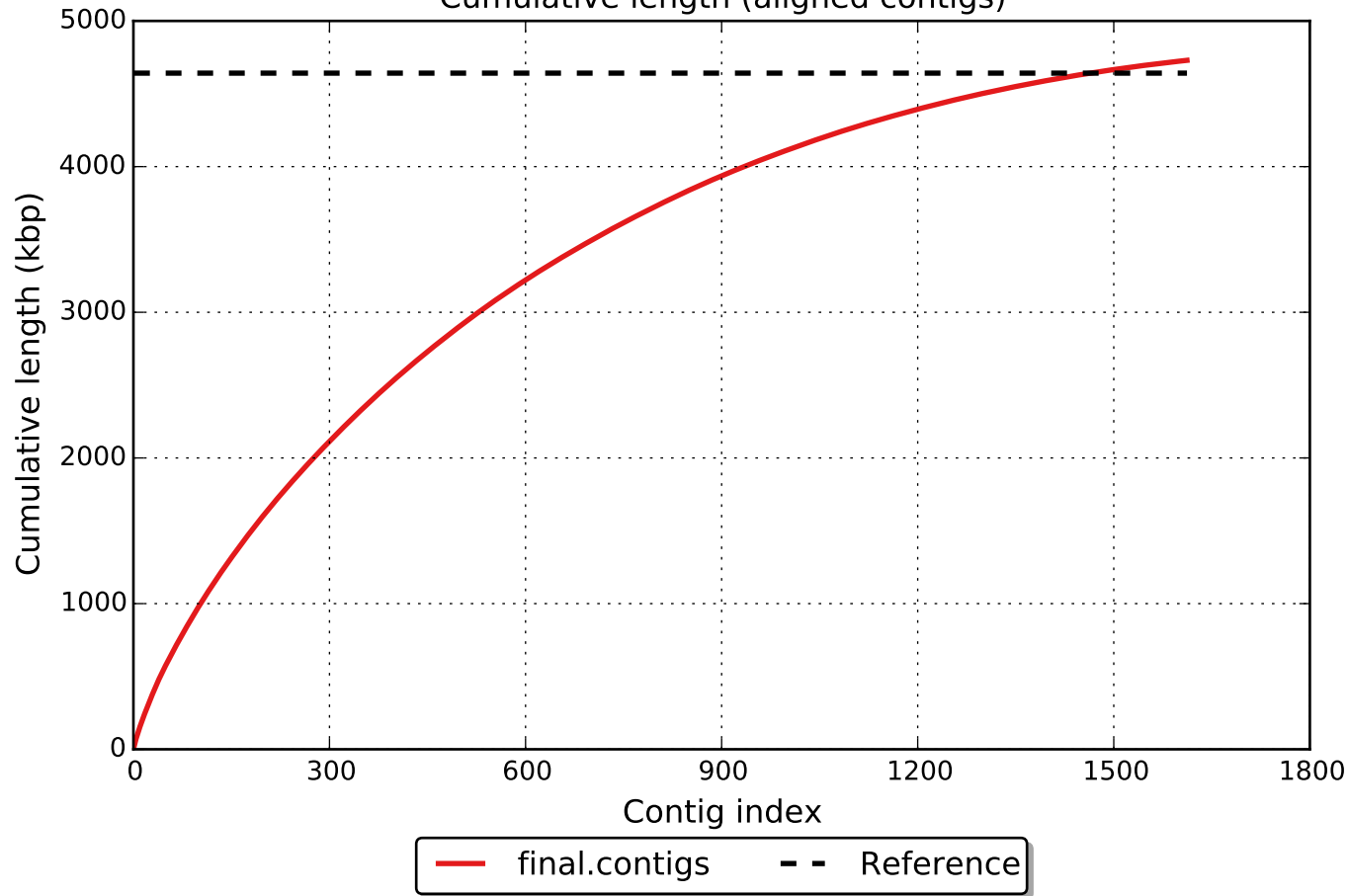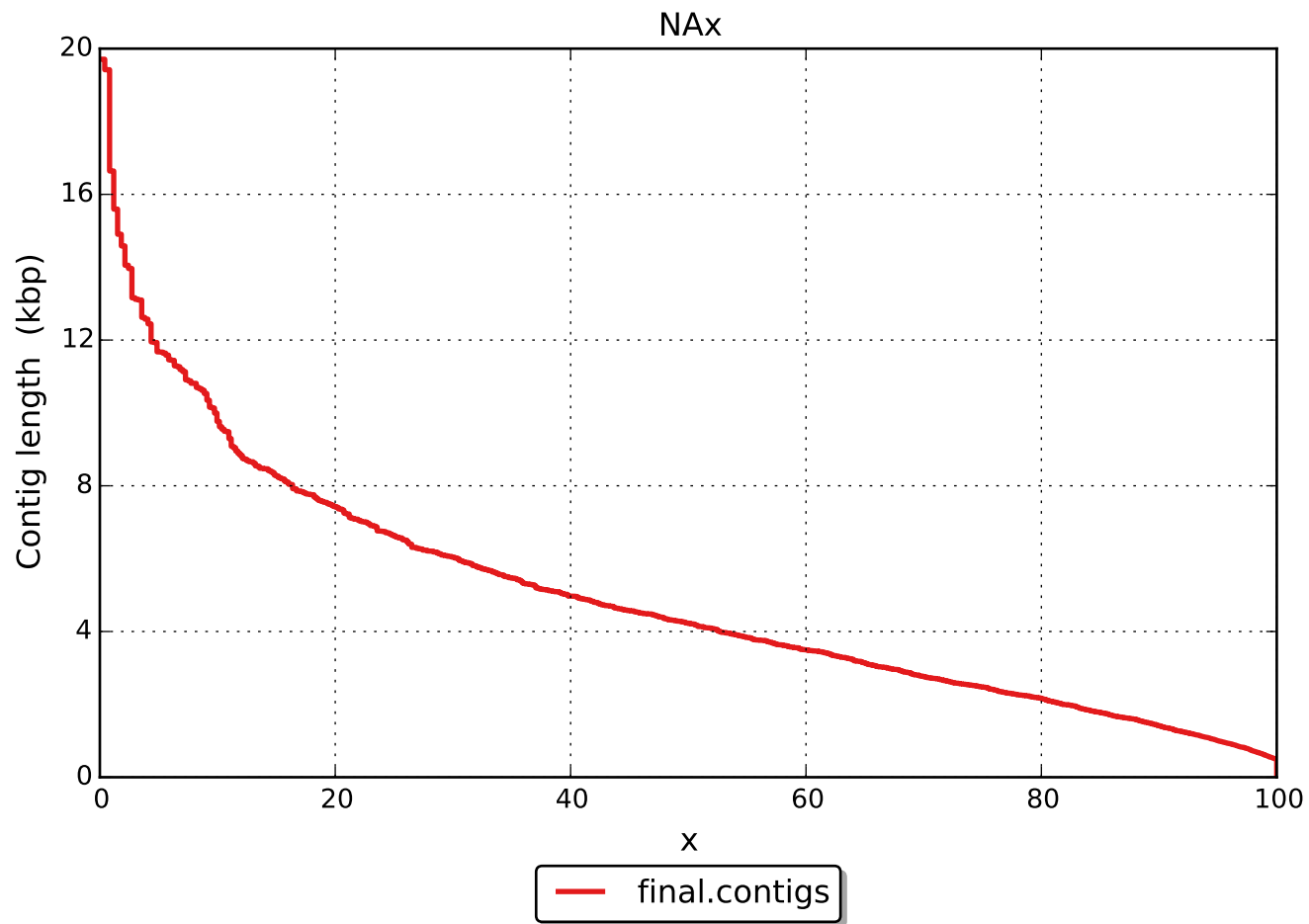
Cumulative length

GC content

Misassemblies

final.contigs
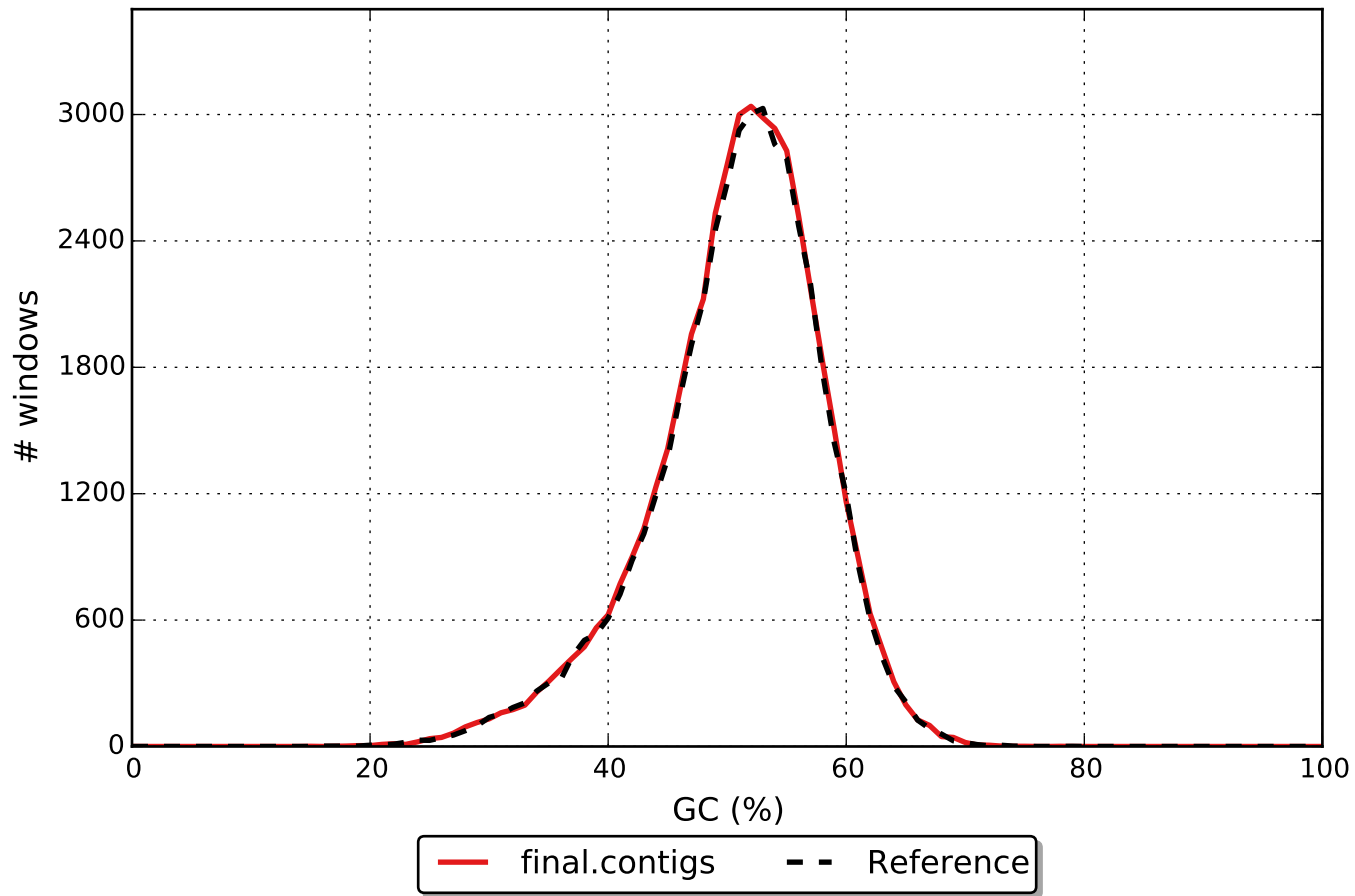
Cumulative length (aligned contigs)