Report

	final.contigs
# contigs (>= 1000 bp)	460
# contigs (>= 5000 bp)	298
# contigs (>= 10000 bp)	171
# contigs (>= 25000 bp)	38
# contigs (>= 50000 bp)	2
Total length (>= 1000 bp)	4887408
Total length (>= 5000 bp)	4397918
Total length (>= 10000 bp)	3461654
Total length (>= 25000 bp)	1337477
Total length (>= 50000 bp)	137285
# contigs	477
Largest contig	78529
Total length	4900340
Reference length	4857432
GC (%)	52.23
Reference GC (%)	52.23
N50	16468
NG50	16525
N75	9056
NG75	9273
L50	92
LG50	91
L75	194
LG75	190
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.917
Duplication ratio	1.010
# N's per 100 kbp	0.00
# mismatches per 100 kbp	11.21
# indels per 100 kbp	0.00
Largest alignment	78529
NA50	16468
NGA50	16525
NA75	9056
NGA75	9273
LA50	92
LGA50	91
LA75	194
LGA75	190

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).
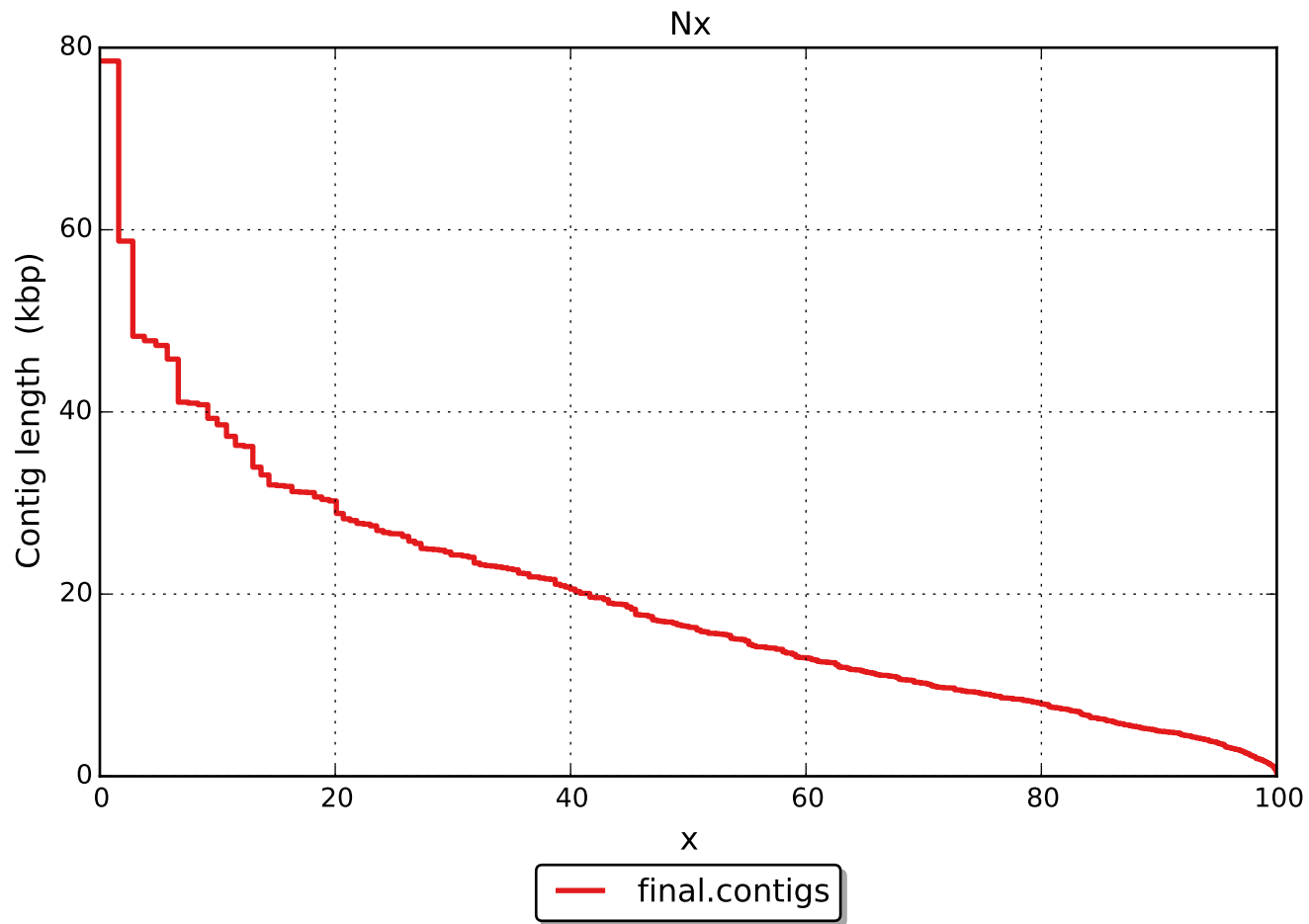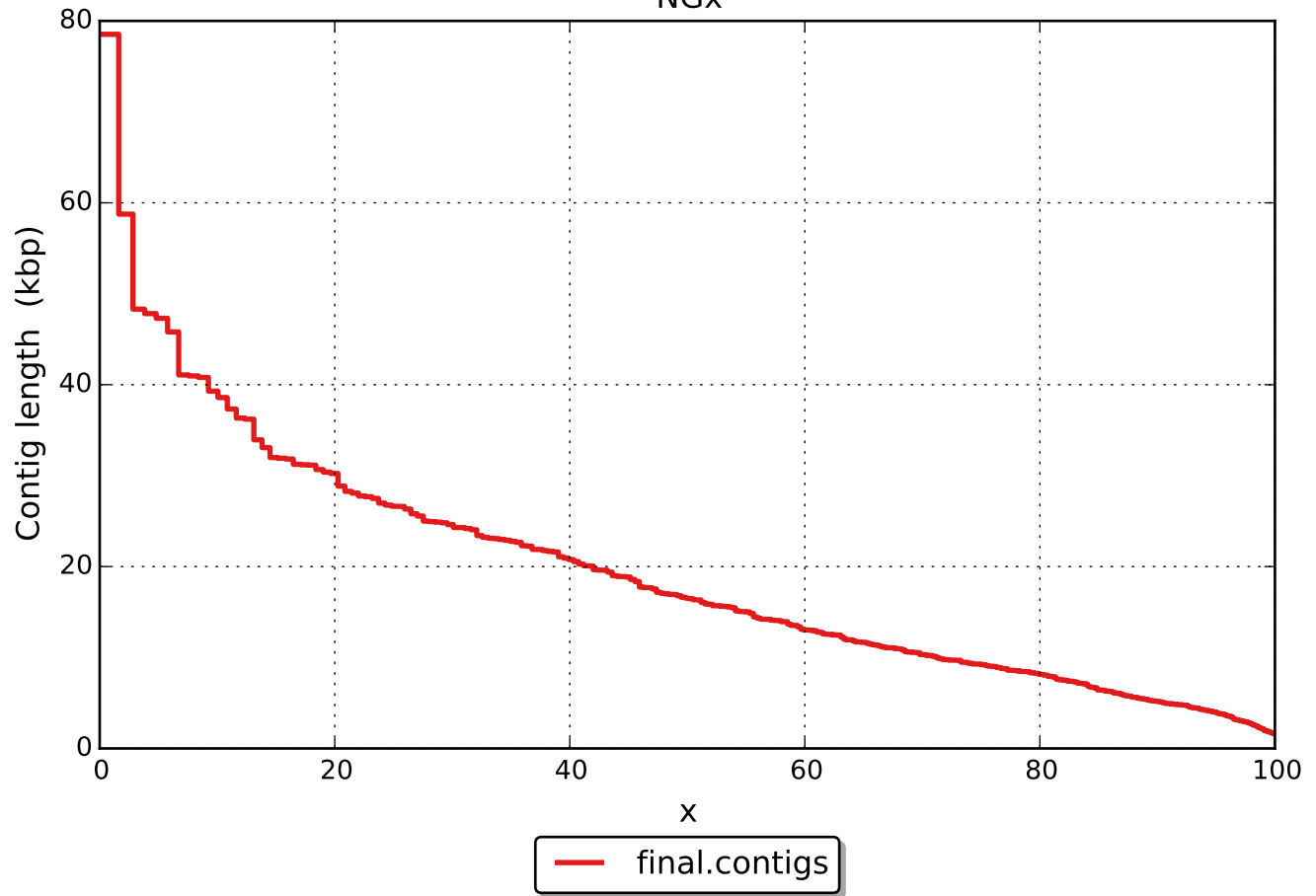
Misassemblies report

	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	544
# 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).
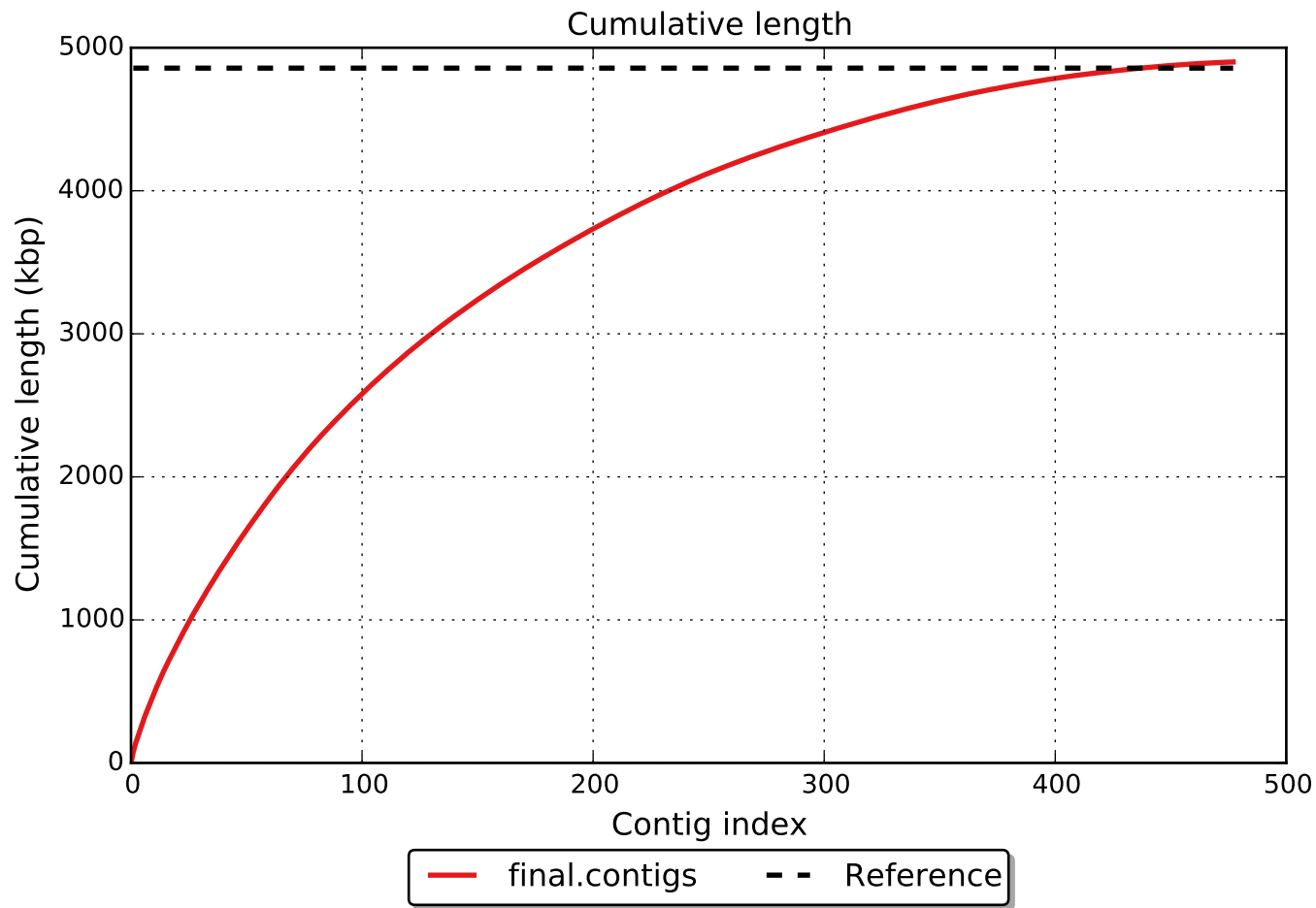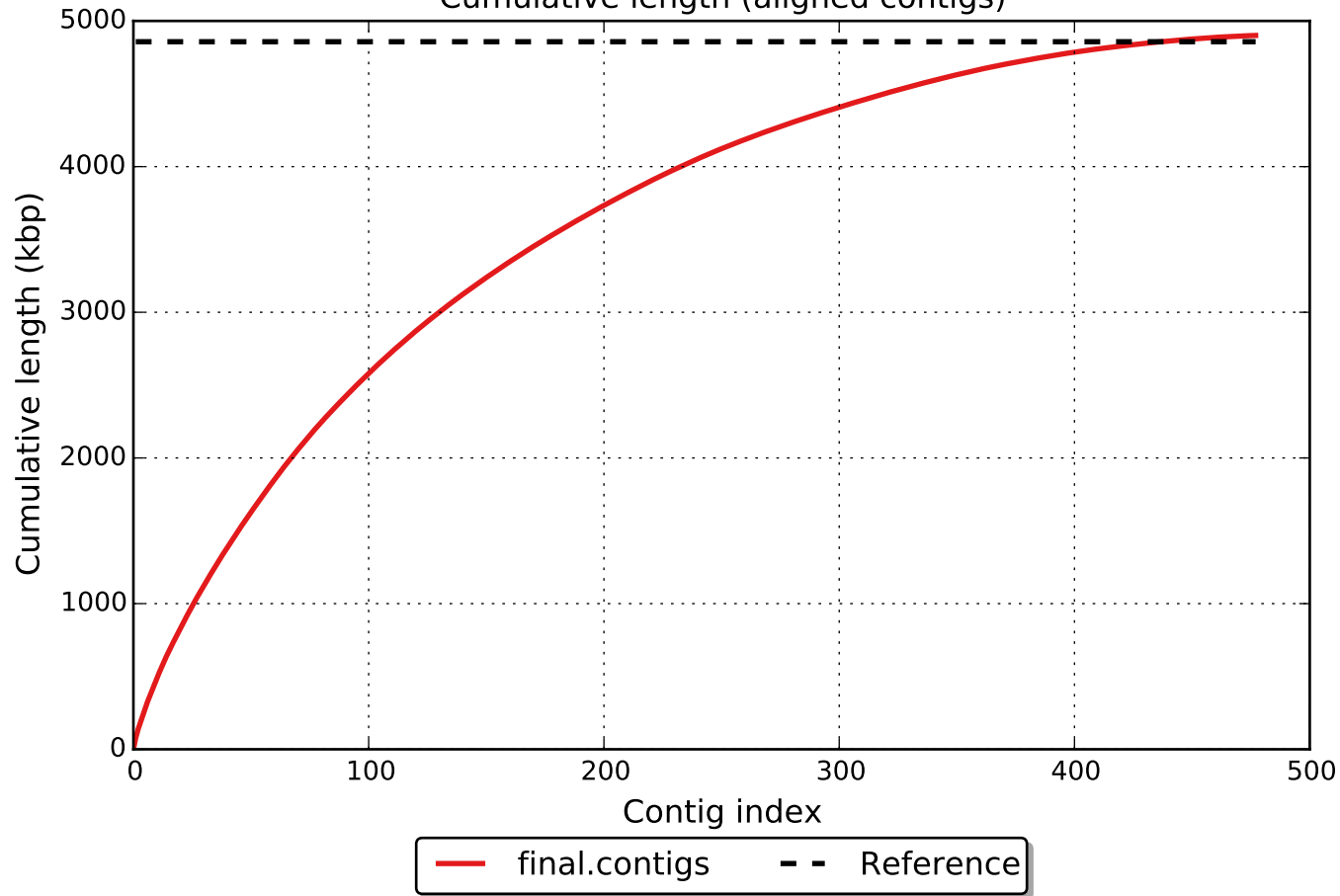
Cumulative length
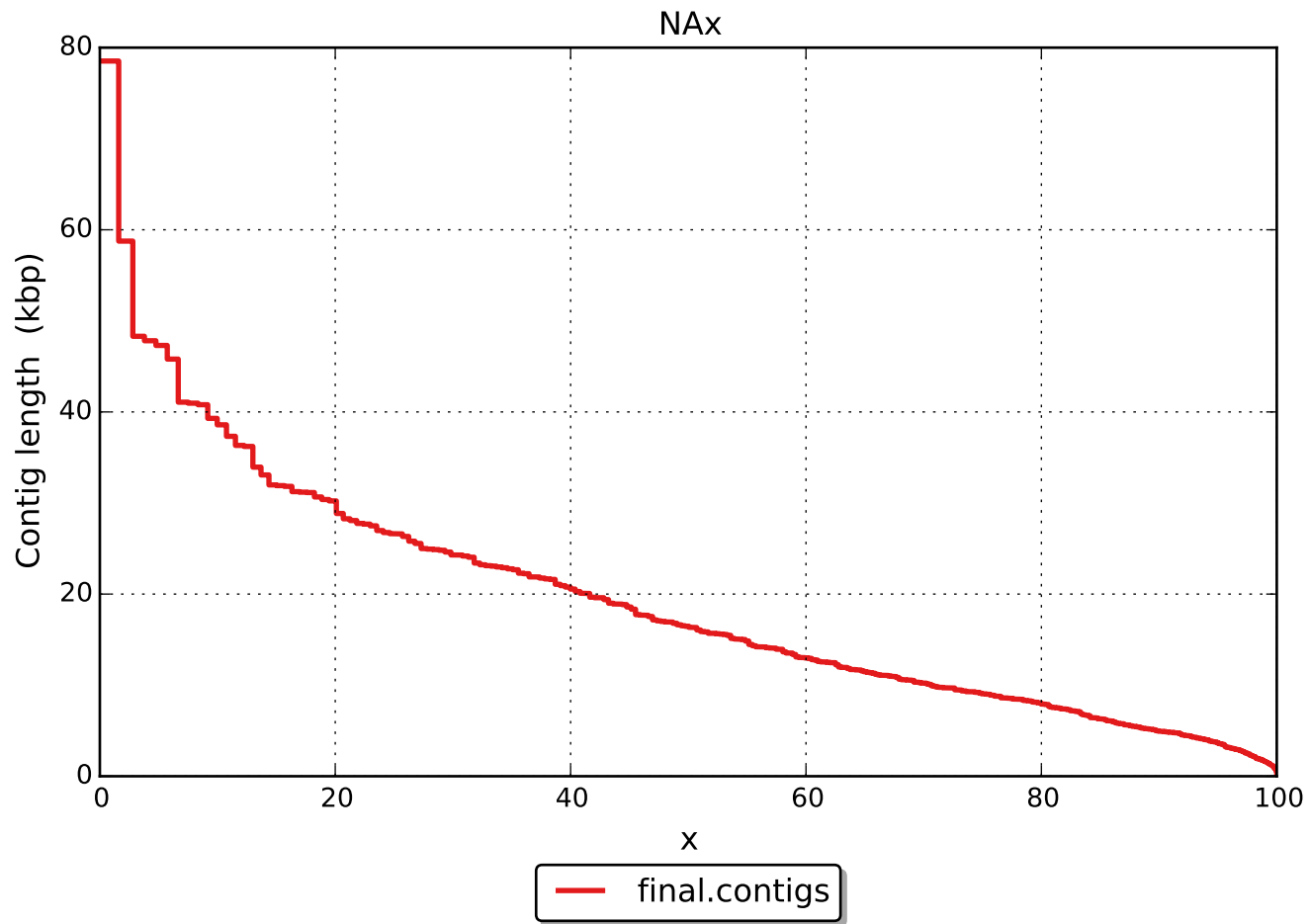
GC content

Misassemblies

final.contigs
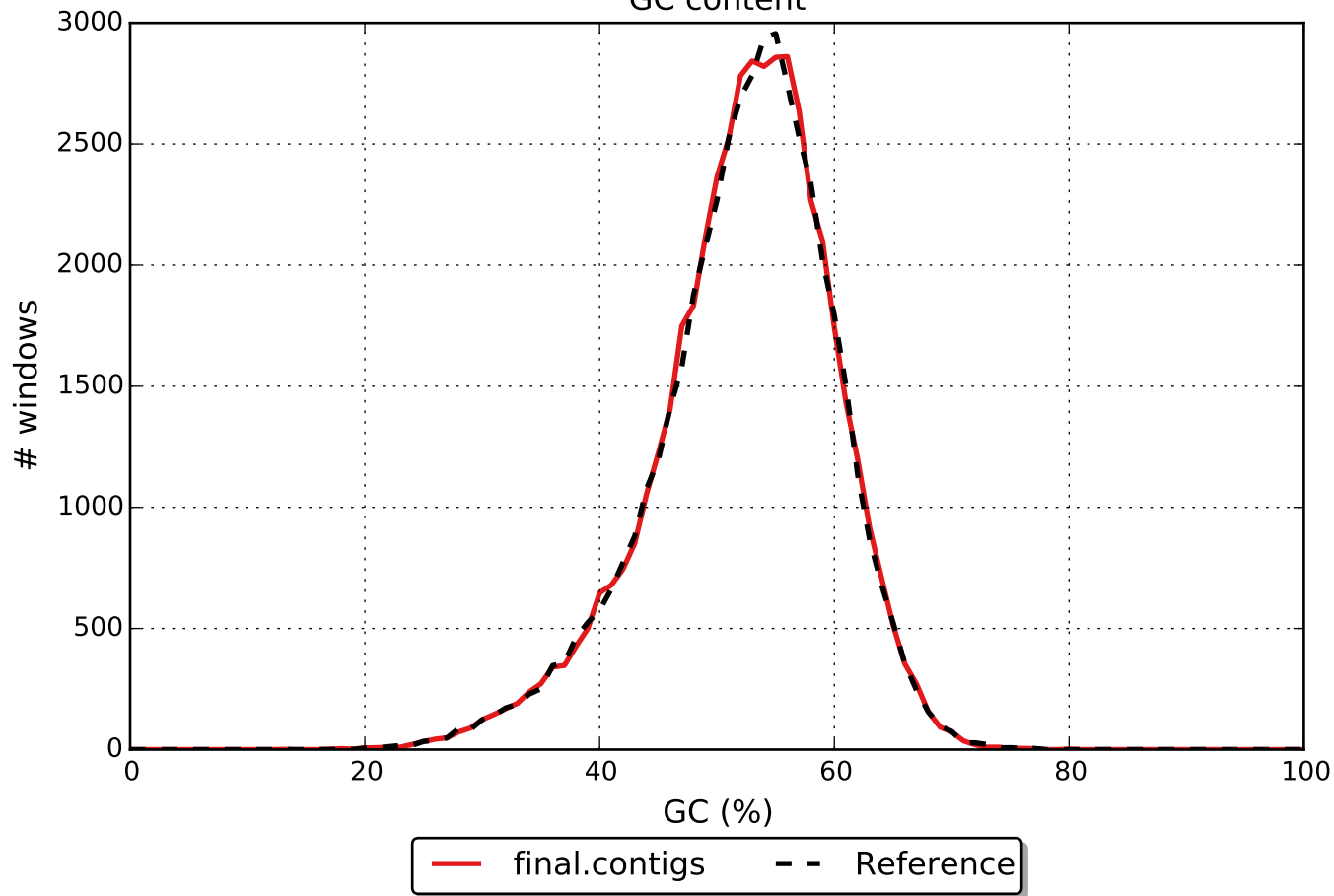
Cumulative length (aligned contigs)