Report

|	scaffolds
# contigs (>= 1000 bp)	79
# contigs (>= 5000 bp)	49
# contigs (>= 10000 bp)	47
# contigs (>= 25000 bp)	41
# contigs (>= 50000 bp)	28
Total length (>= 1000 bp)	4434342
Total length (>= 5000 bp)	4368531
Total length (>= 10000 bp)	4354332
Total length (>= 25000 bp)	4245246
Total length (>= 50000 bp)	3796503
# contigs	122
Largest contig	330825
Total length	4462275
Reference length	4641652
GC (%)	50.77
Reference GC (%)	50.79
N50	149239
NG50	132163
N75	79547
NG75	75686
L50	11
LG50	12
L75	22
LG75	24
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	95.792
Duplication ratio	1.004
# N's per 100 kbp	0.00
# mismatches per 100 kbp	816.61
# indels per 100 kbp	0.94
Largest alignment	330825
NA50	149239
NGA50	132163
NA75	79547
NGA75	75686
LA50	11
LGA50	12
LA75	22
LGA75	24

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

	scaffolds
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	36309
# indels	42
# short indels	42
# long indels	0
Indels length	48

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

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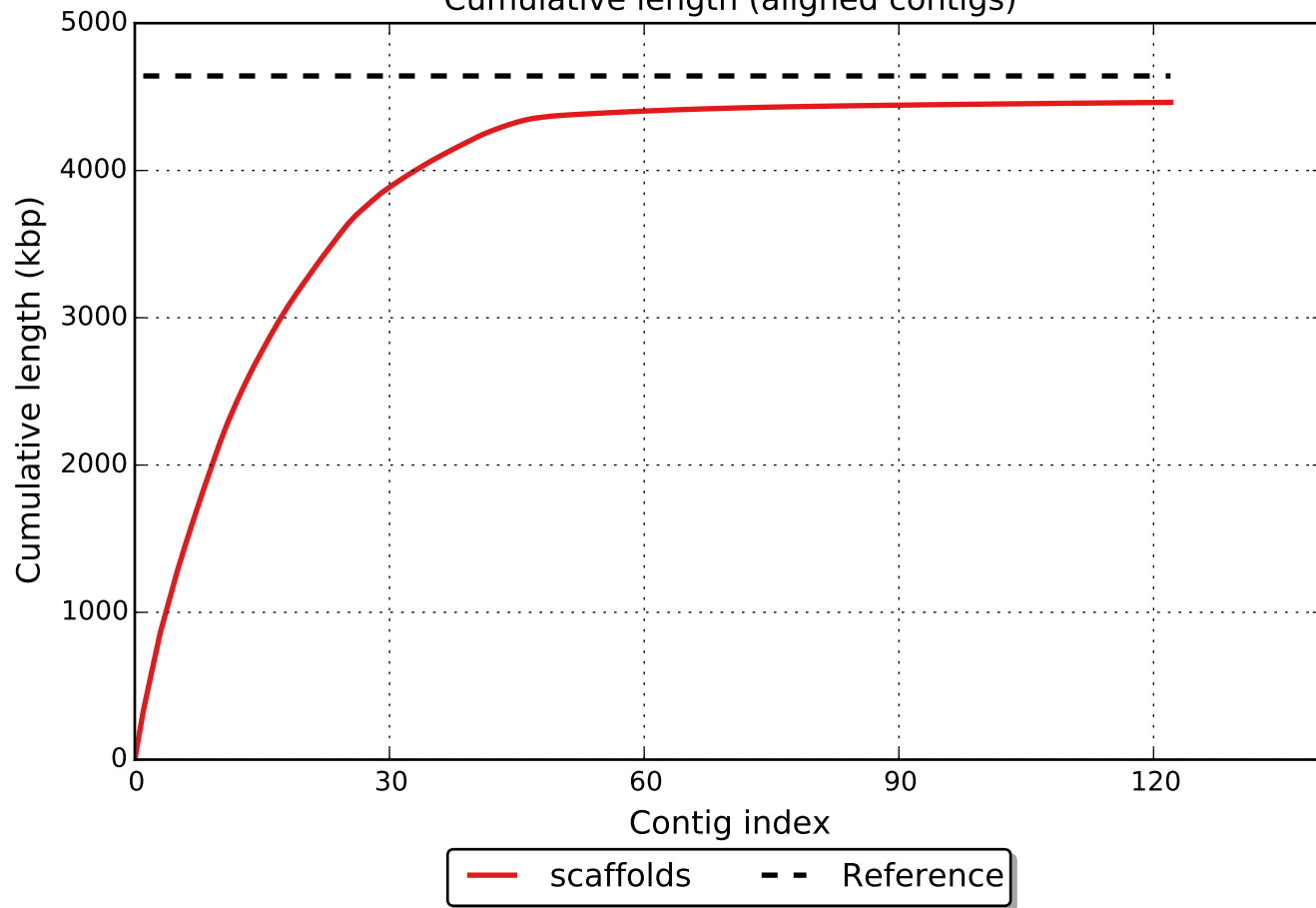(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Cumulative length
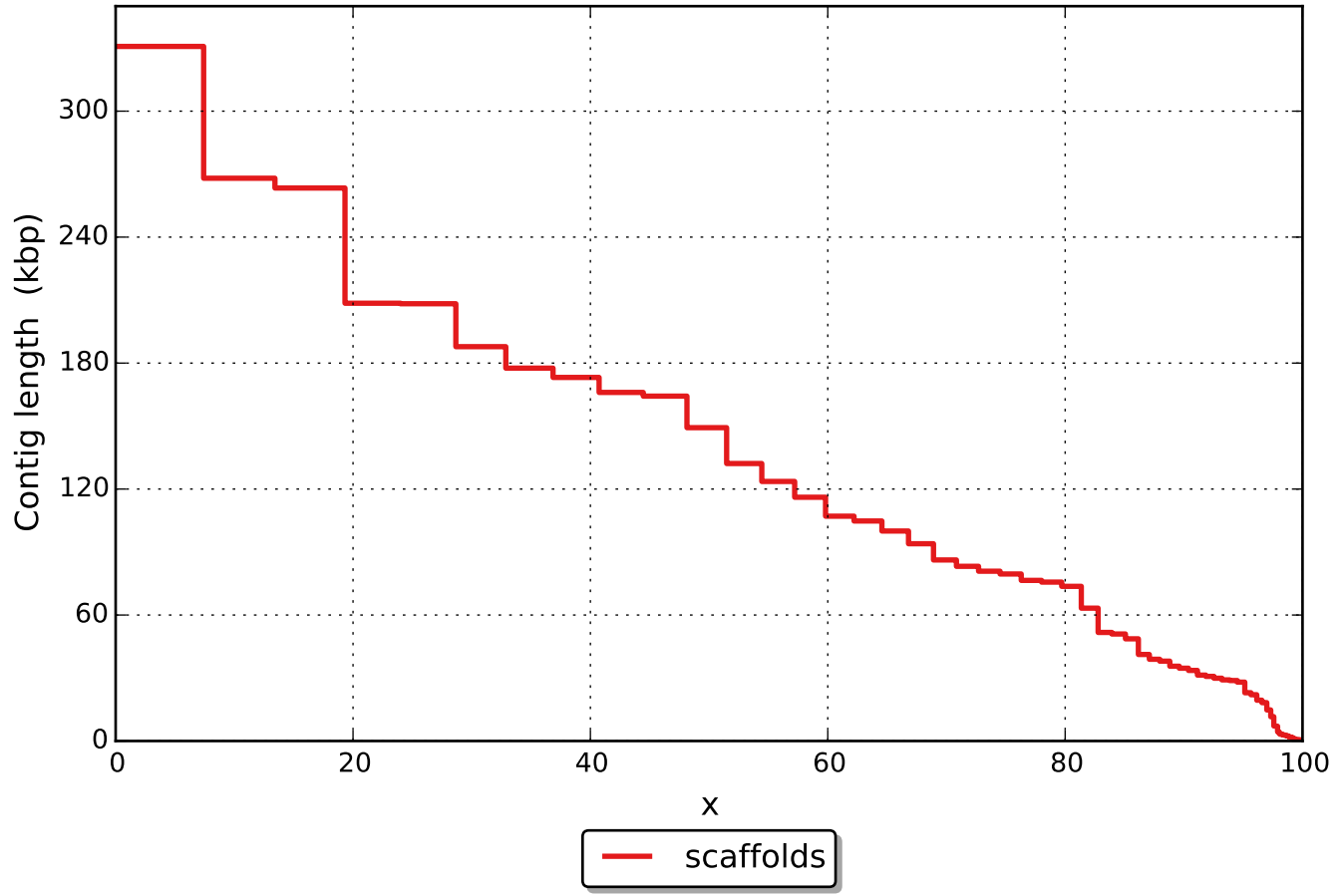
Misassemblies

scaffolds
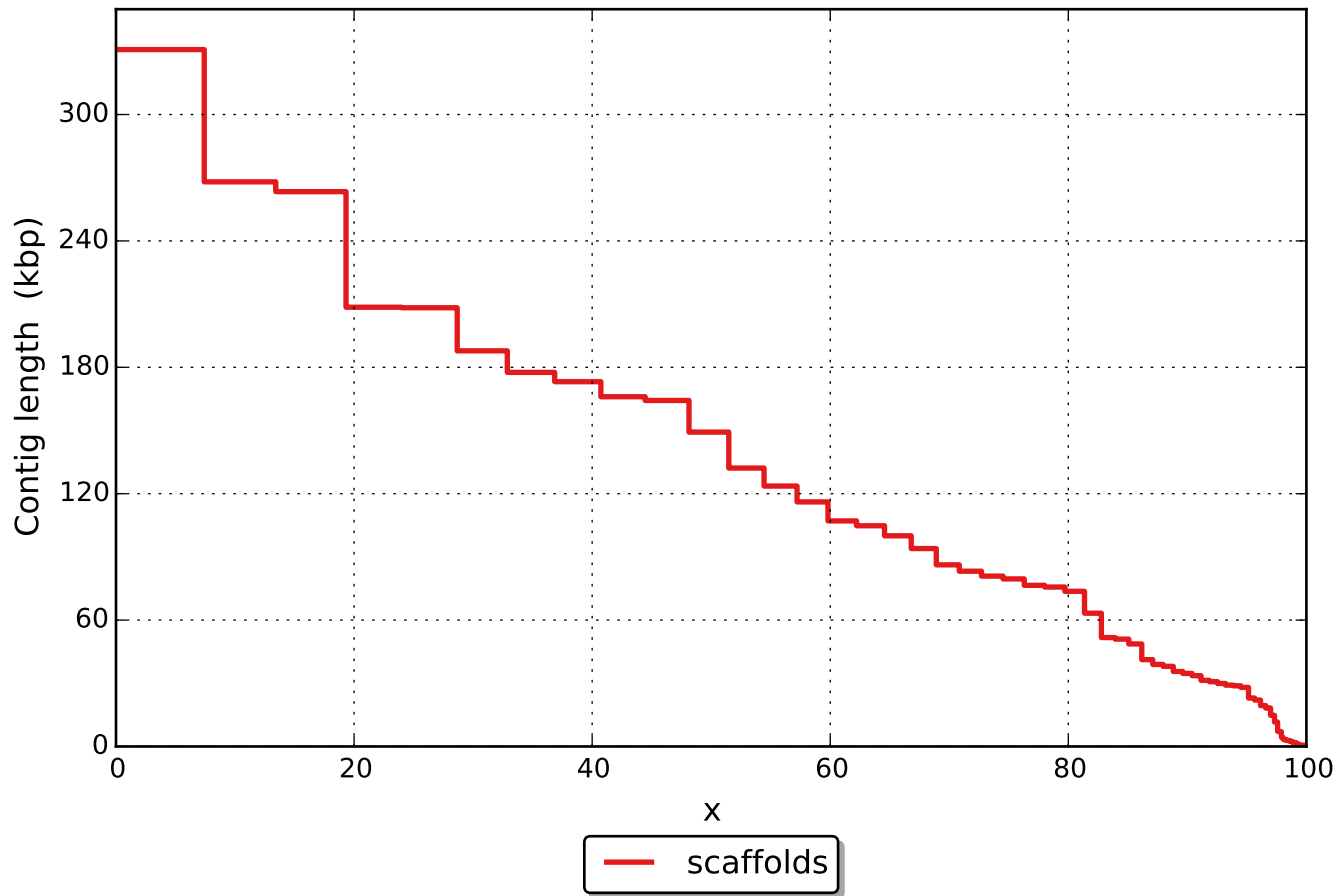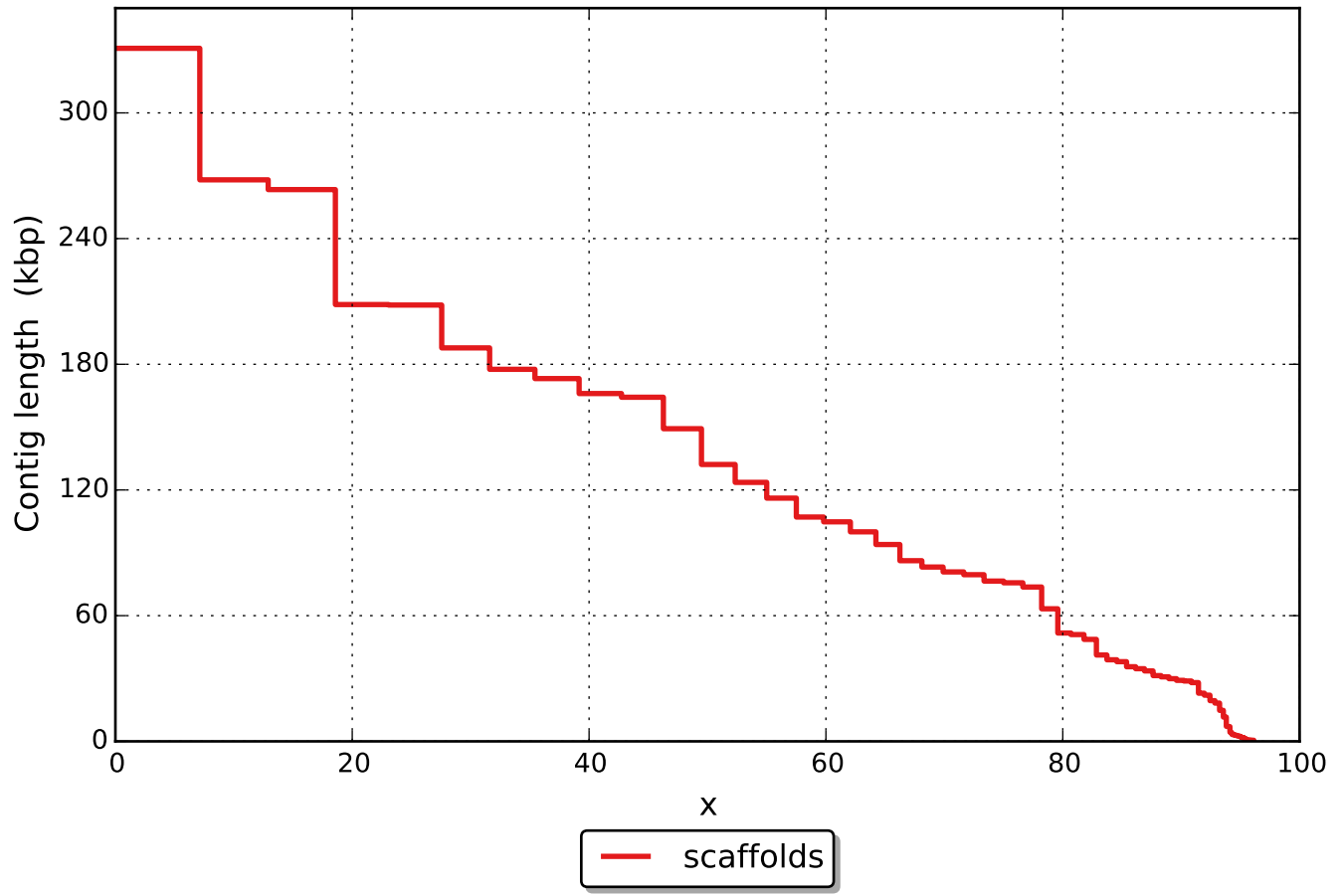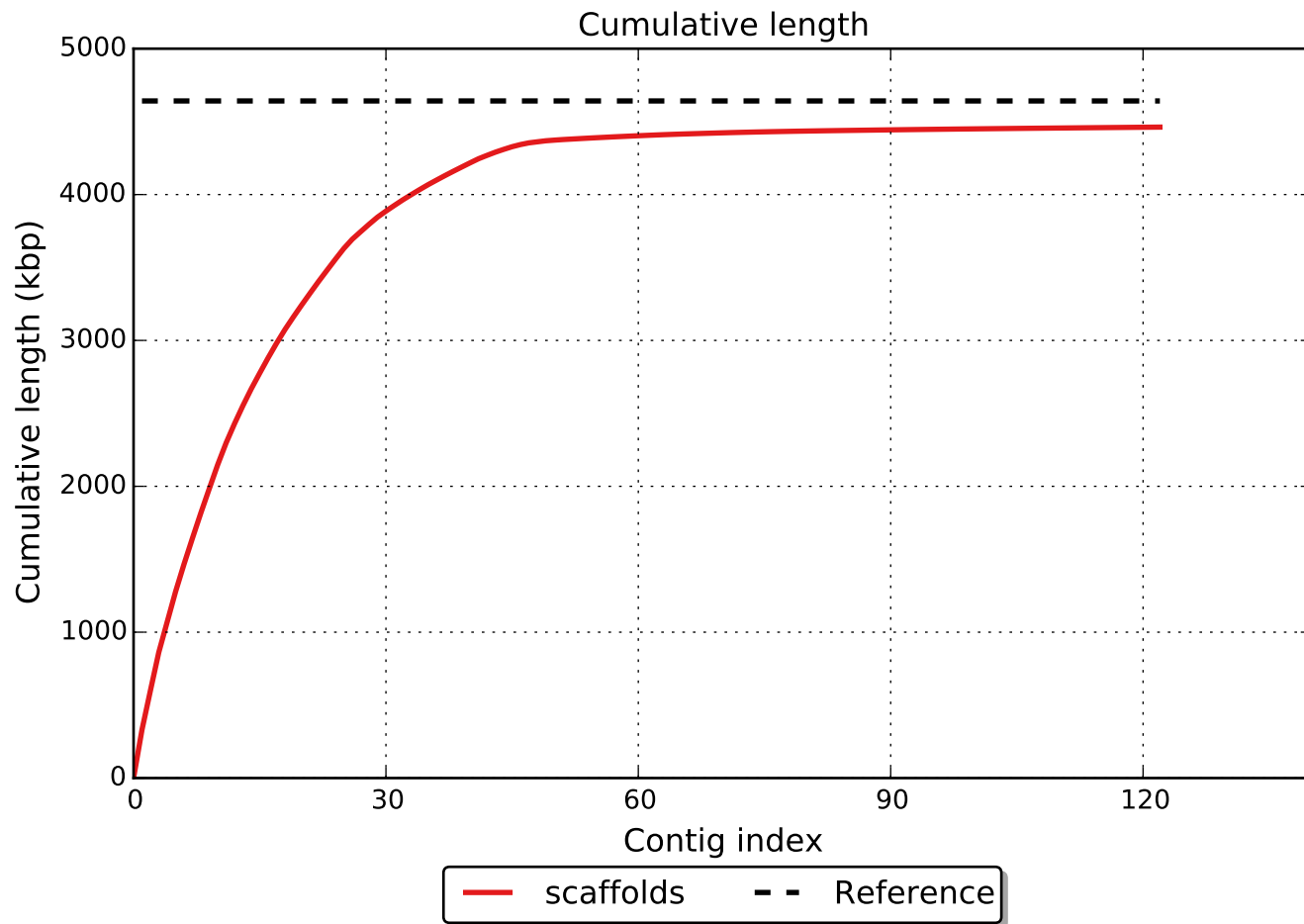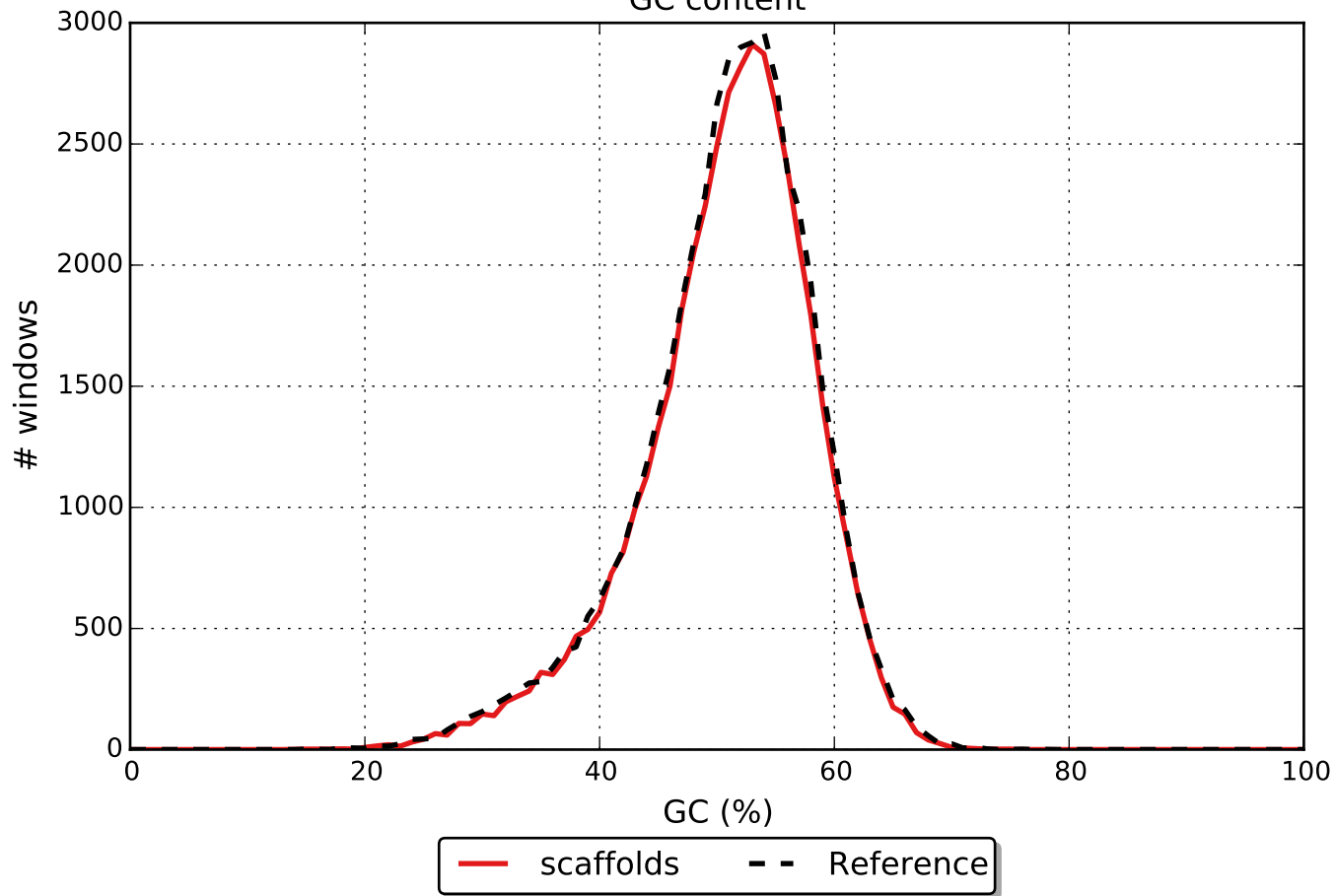
Cumulative length (aligned contigs)