Report

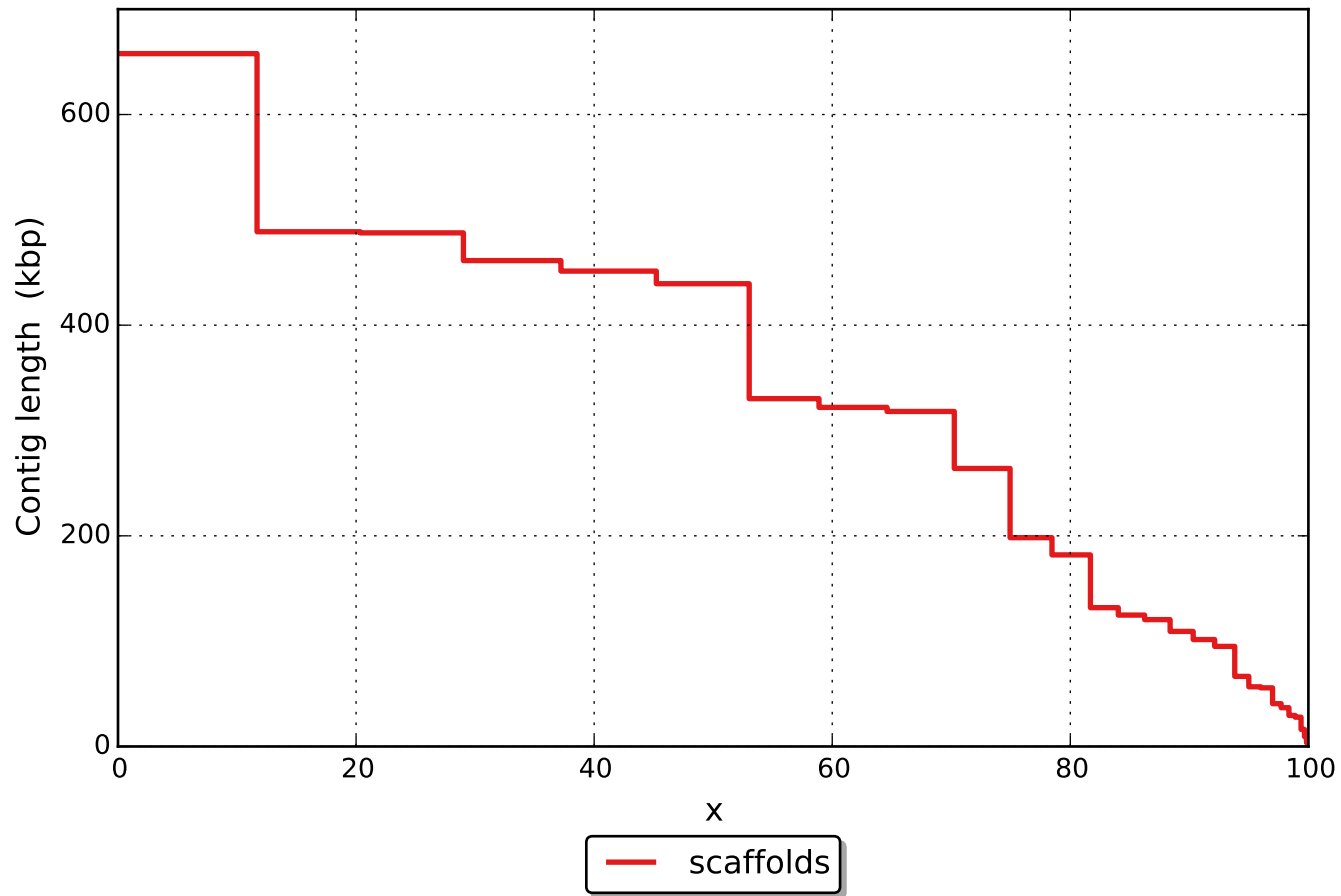|	scaffolds
# contigs (>= 1000 bp)	29
# contigs (>= 5000 bp)	27
# contigs (>= 10000 bp)	26
# contigs (>= 25000 bp)	25
# contigs (>= 50000 bp)	21
Total length (>= 1000 bp)	5628273
Total length (>= 5000 bp)	5622557
Total length (>= 10000 bp)	5613119
Total length (>= 25000 bp)	5596905
Total length (>= 50000 bp)	5462161
# contigs	33
Largest contig	657825
Total length	5631708
Reference length	4641652
GC (%)	50.76
Reference GC (%)	50.79
N50	439363
NG50	451329
N75	198255
NG75	321933
L50	6
LG50	5
L75	11
LG75	8
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 11 part
Unaligned length	1008530
Genome fraction (%)	99.506
Duplication ratio	1.001
# N's per 100 kbp	1.37
# mismatches per 100 kbp	235.97
# indels per 100 kbp	1.02
Largest alignment	657825
NA50	439363
NGA50	451329
NA75	124745
NGA75	321933
LA50	6
LGA50	5
LA75	11
LGA75	8

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	3
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	10899
# indels	47
# short indels	46
# long indels	1
Indels length	116

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).
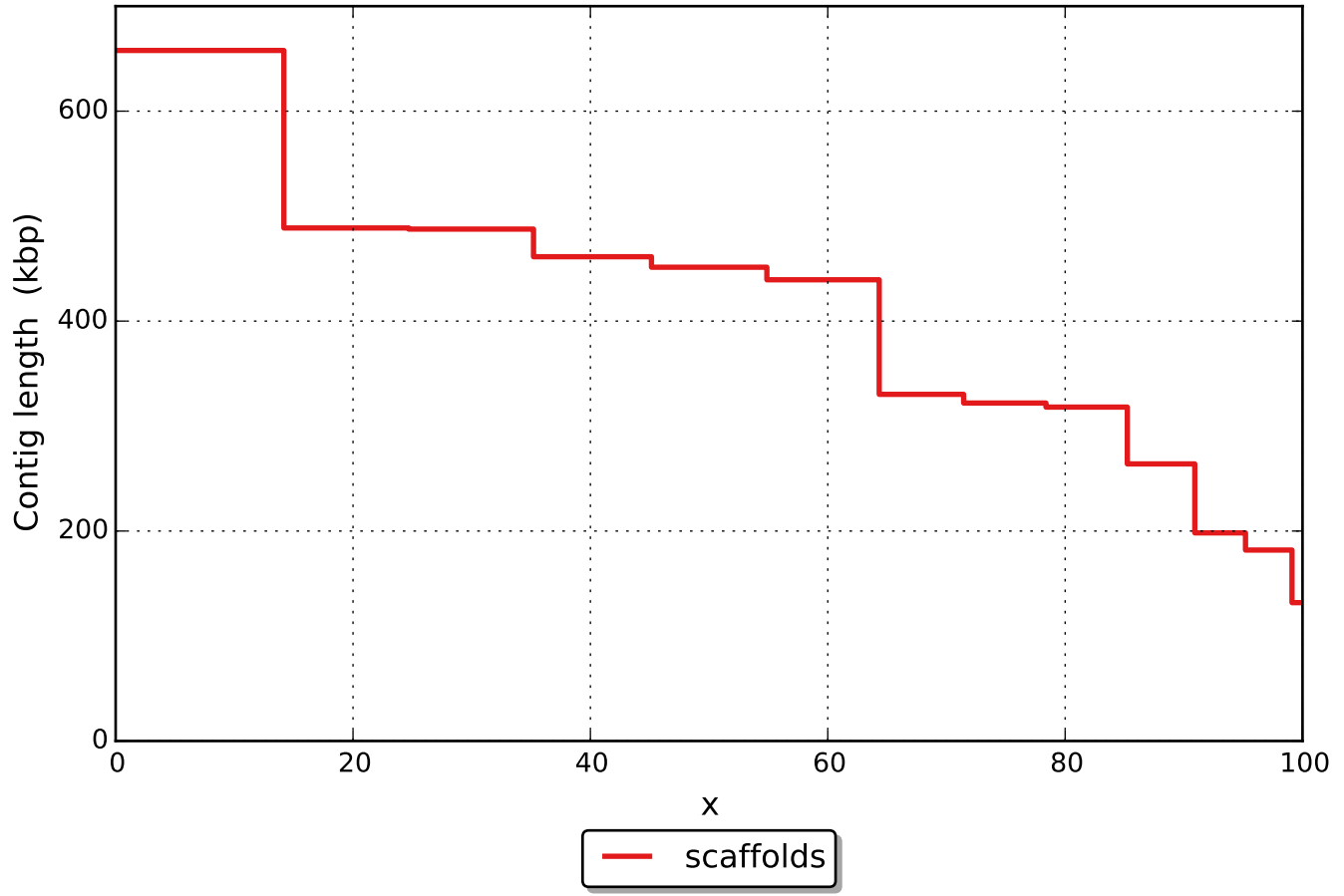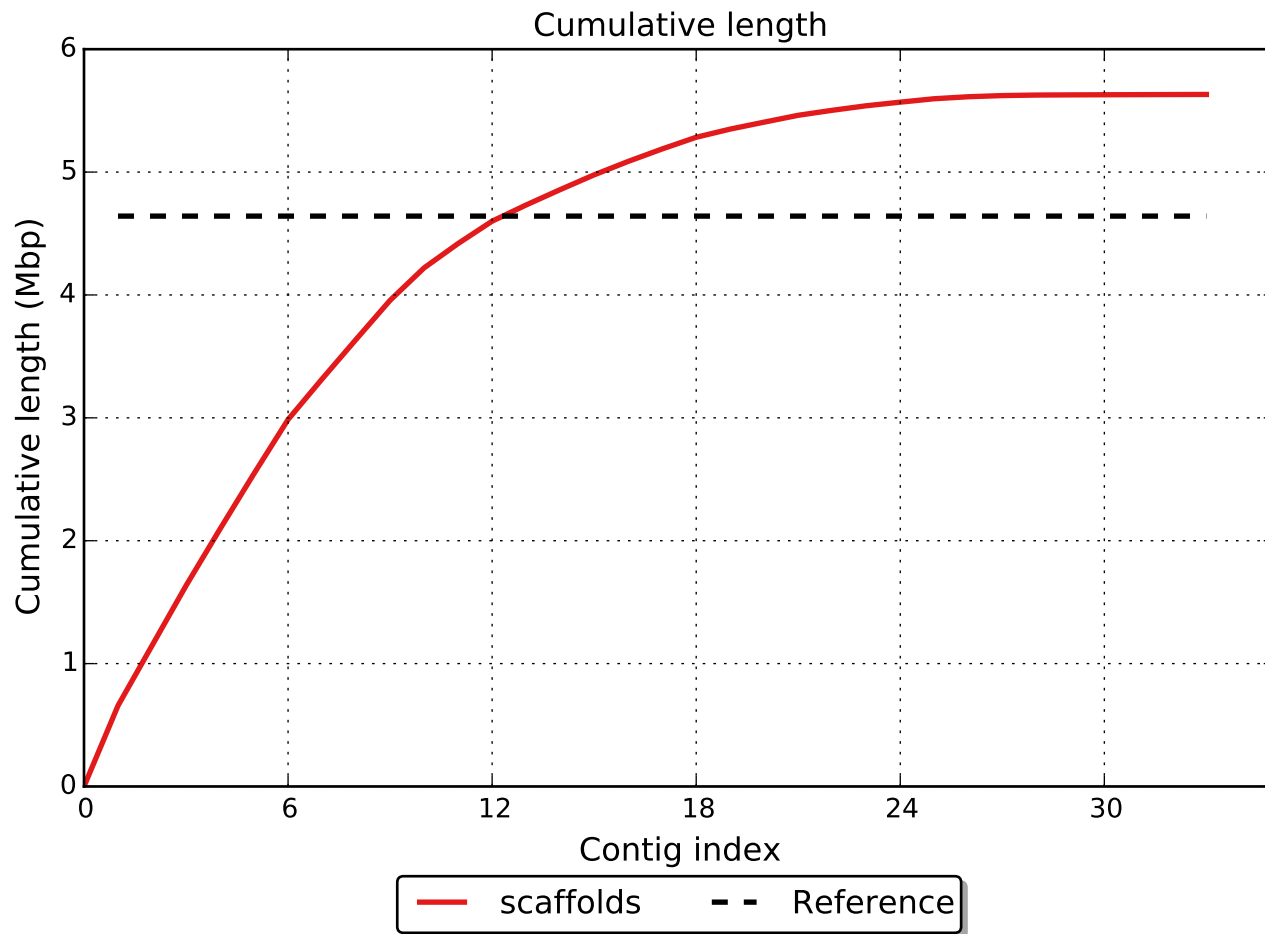
Unaligned report

	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	11
# with misassembly	1
# both parts are significant	3
Partially unaligned length	1008530
# N's	77

All statistics are based on contigs of size >= 500 bp, unless otherwise noted
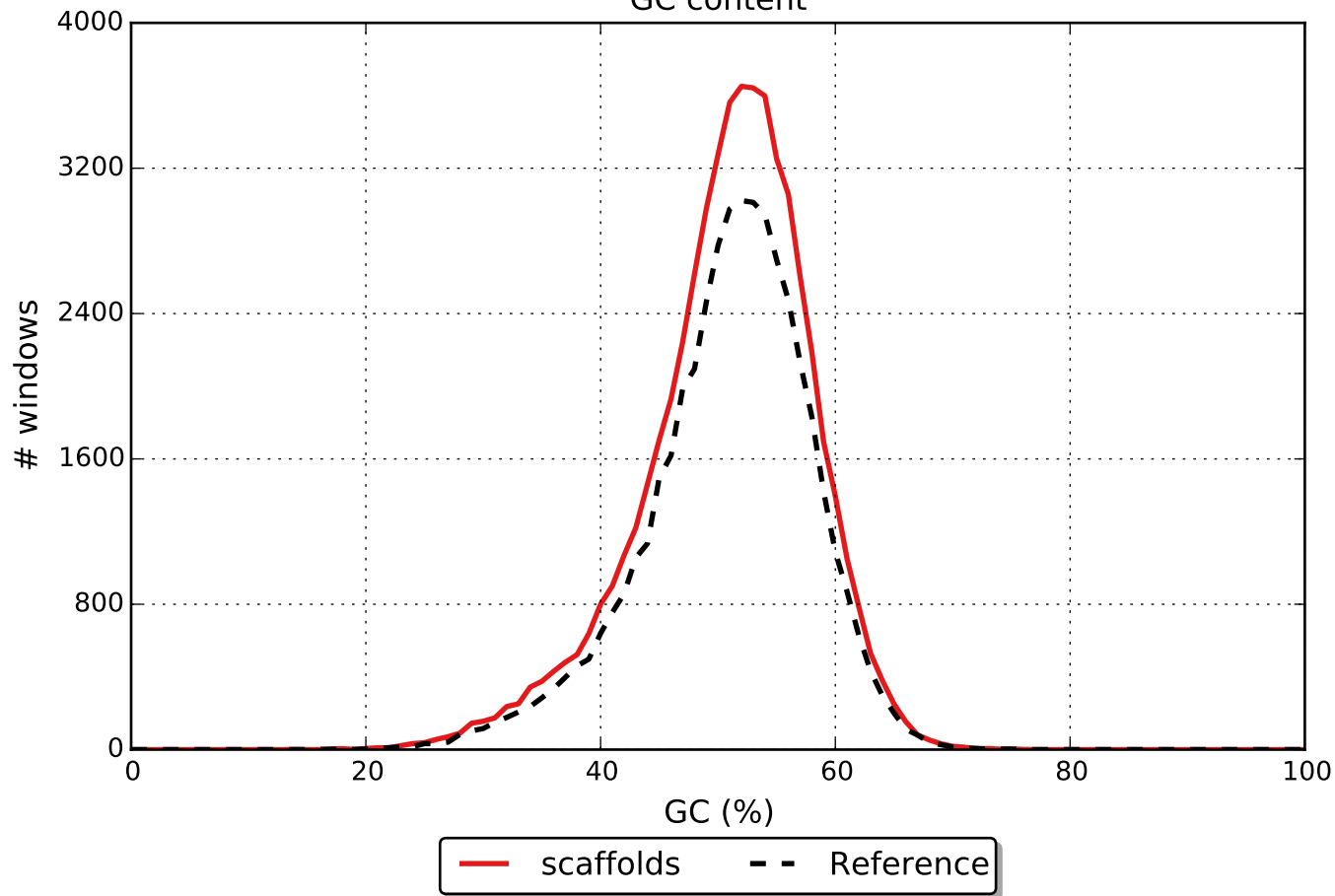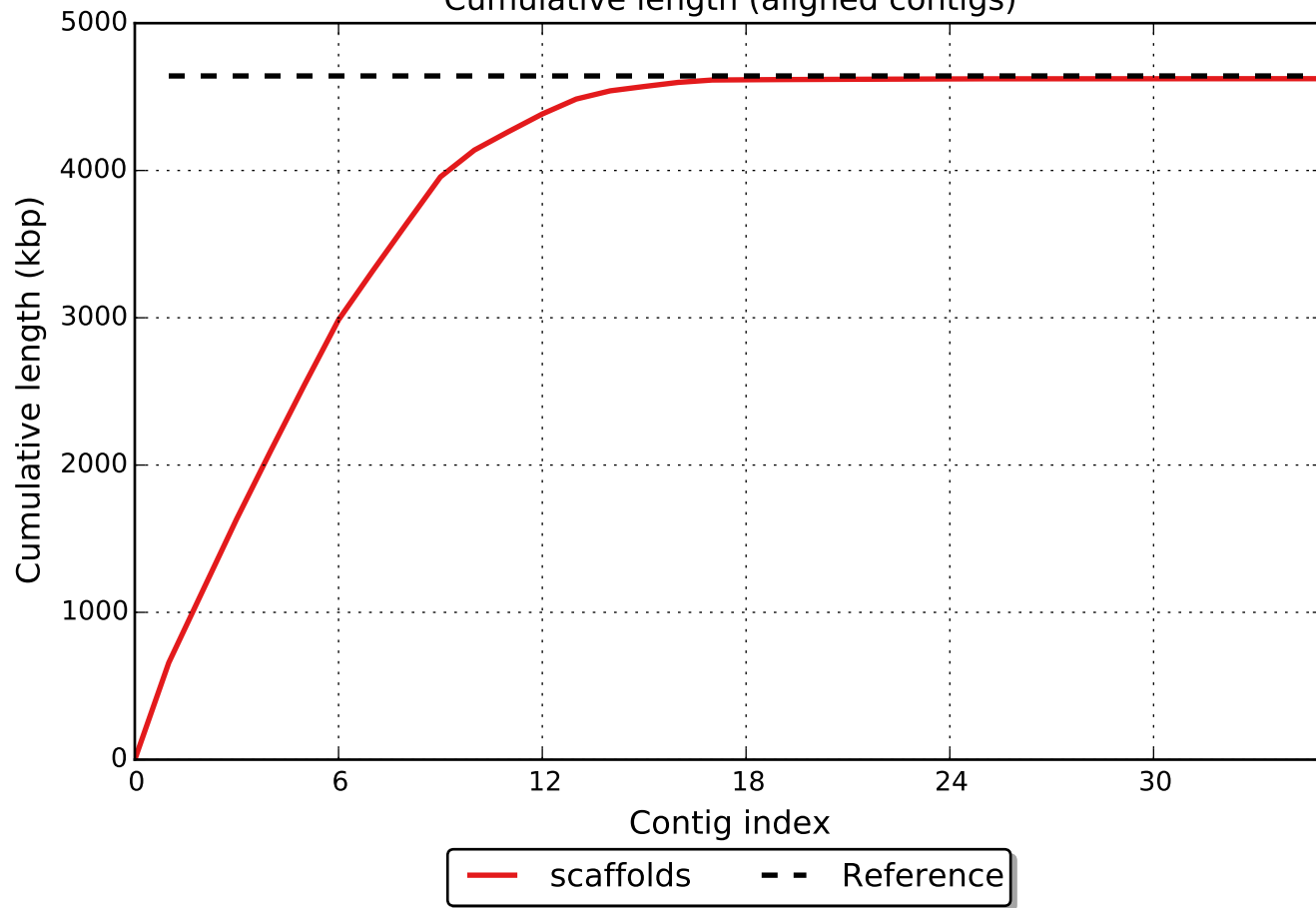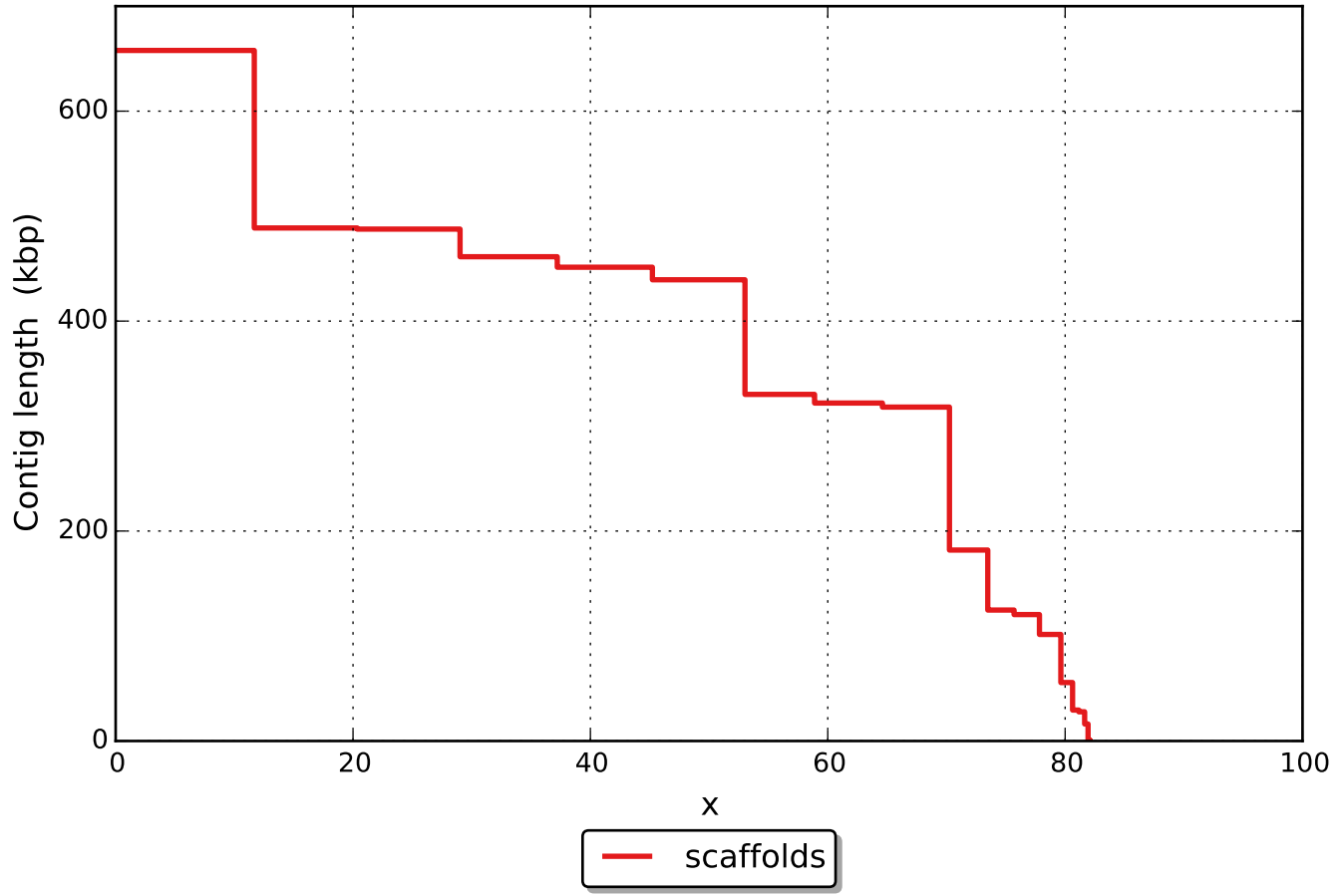(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Cumulative length

GC content

windows

GC (%)

scaffolds — — Reference

Misassemblies

scaffolds

Cumulative length (aligned contigs)