Report

|	scaffolds
# contigs (>= 1000 bp)	23
# contigs (>= 5000 bp)	21
# contigs (>= 10000 bp)	21
# contigs (>= 25000 bp)	19
# contigs (>= 50000 bp)	17
Total length (>= 1000 bp)	4931323
Total length (>= 5000 bp)	4928207
Total length (>= 10000 bp)	4928207
Total length (>= 25000 bp)	4902306
Total length (>= 50000 bp)	4848401
# contigs	24
Largest contig	663492
Total length	4932149
Reference length	4641652
GC (%)	50.71
Reference GC (%)	50.79
N50	422118
NG50	422118
N75	227737
NG75	321943
L50	5
LG50	5
L75	9
LG75	8
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 3 part
Unaligned length	320156
Genome fraction (%)	99.252
Duplication ratio	1.001
# N's per 100 kbp	0.95
# mismatches per 100 kbp	208.36
# indels per 100 kbp	0.61
Largest alignment	663492
NA50	362589
NGA50	378035
NA75	181774
NGA75	227737
LA50	6
LGA50	5
LA75	10
LGA75	9

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	2
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	9599
# indels	28
# short indels	26
# long indels	2
Indels length	92

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).
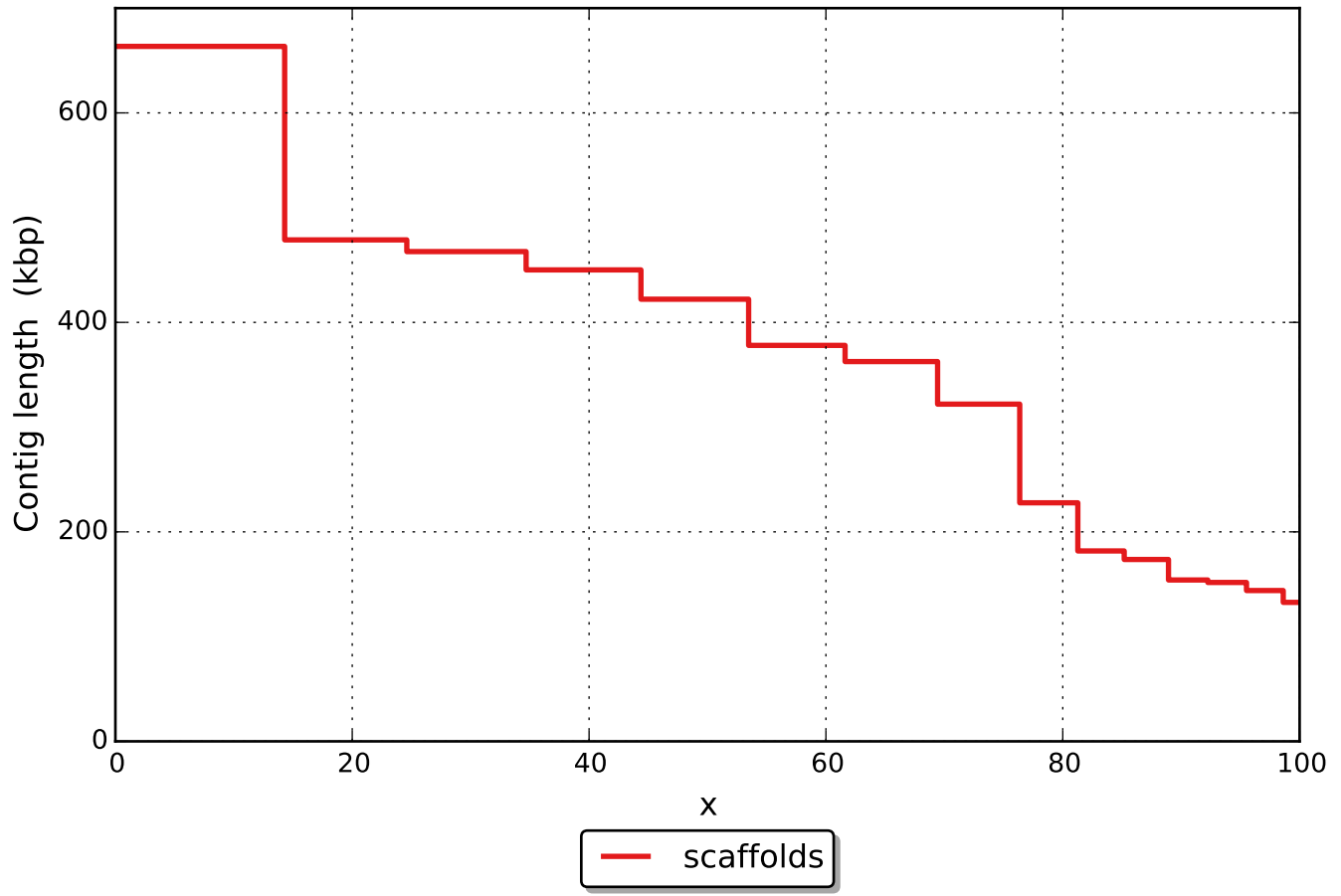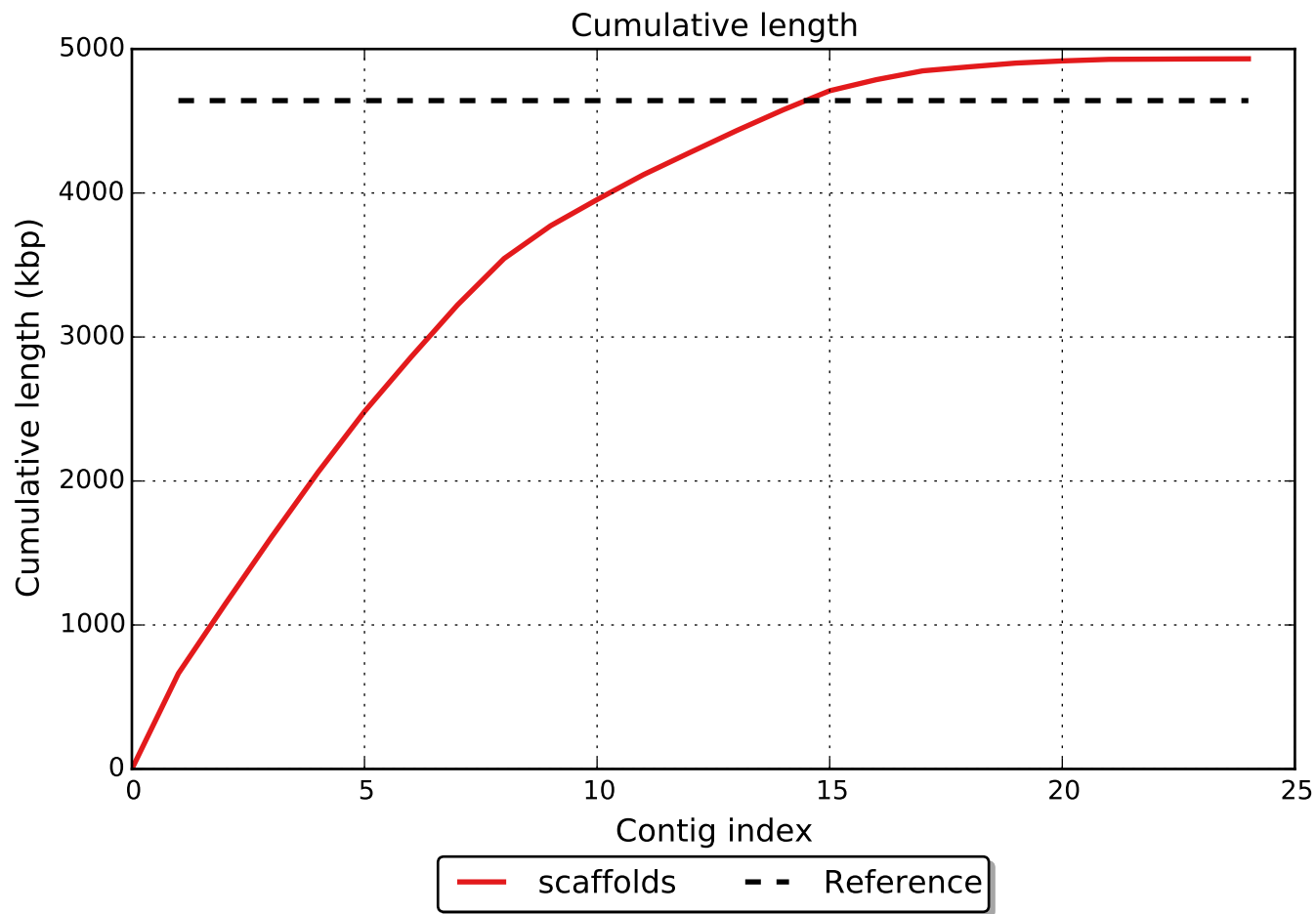
Unaligned report

	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	3
# with misassembly	0
# both parts are significant	2
Partially unaligned length	320156
# N's	47

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).
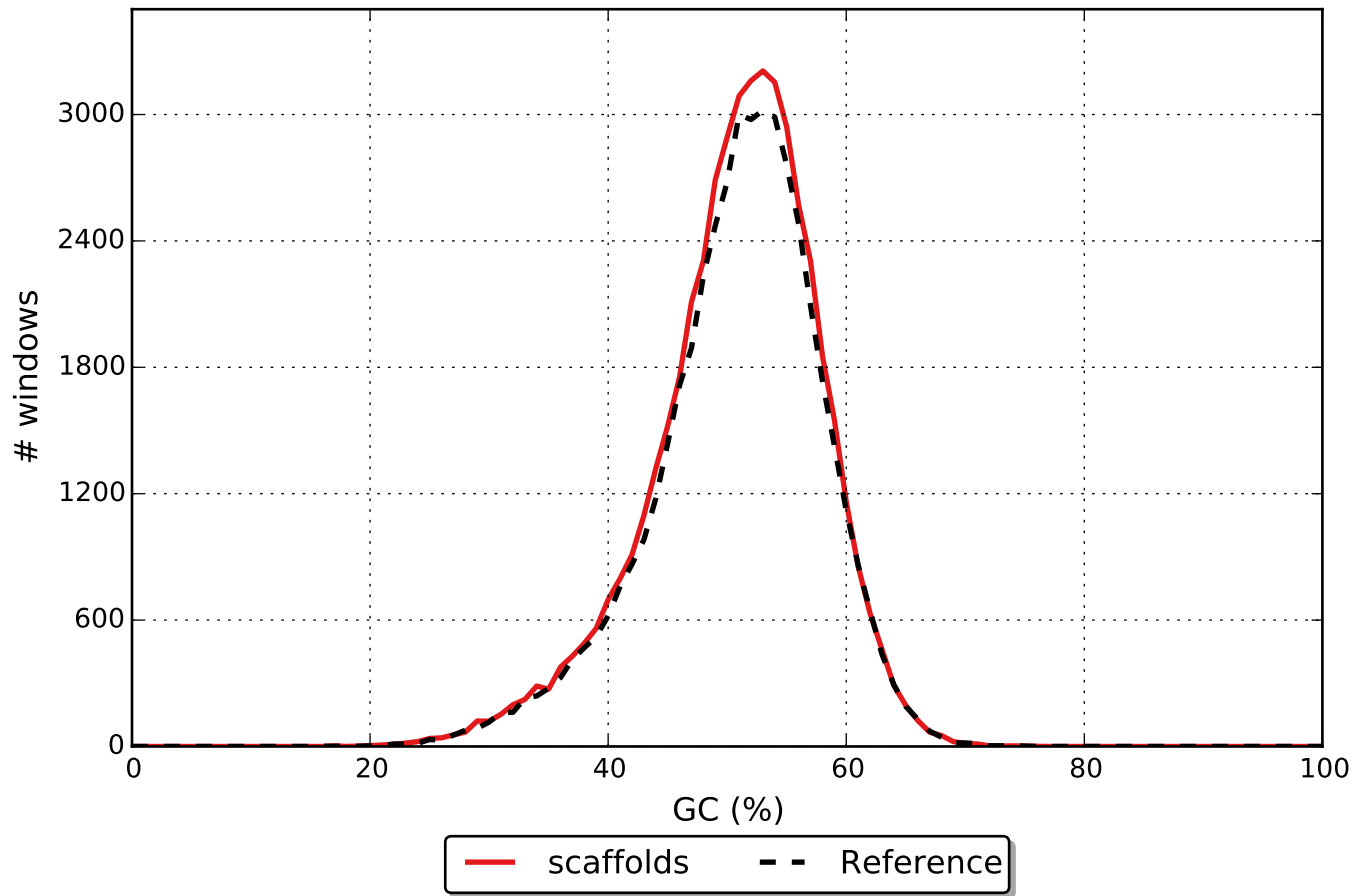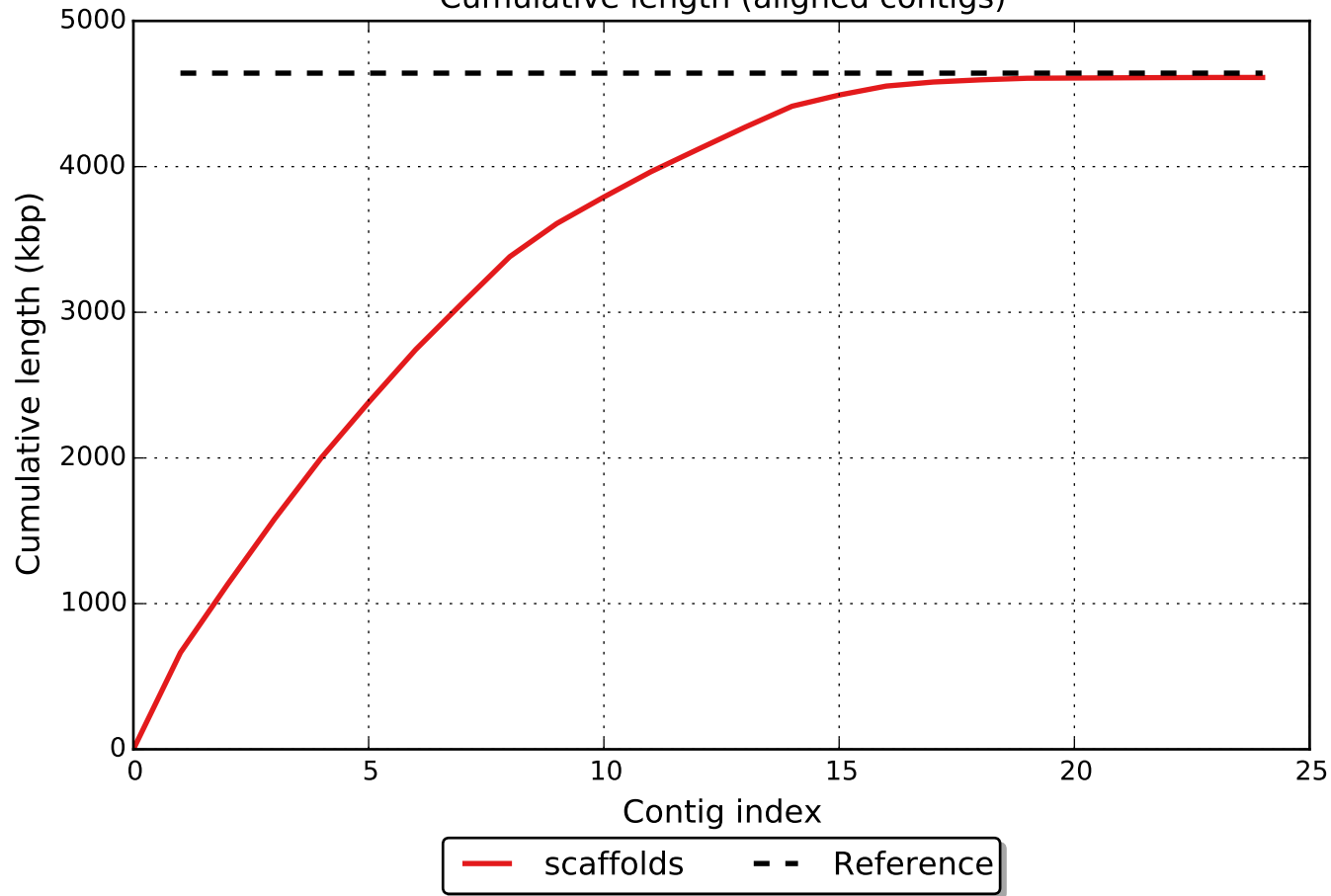
Nx

NGx
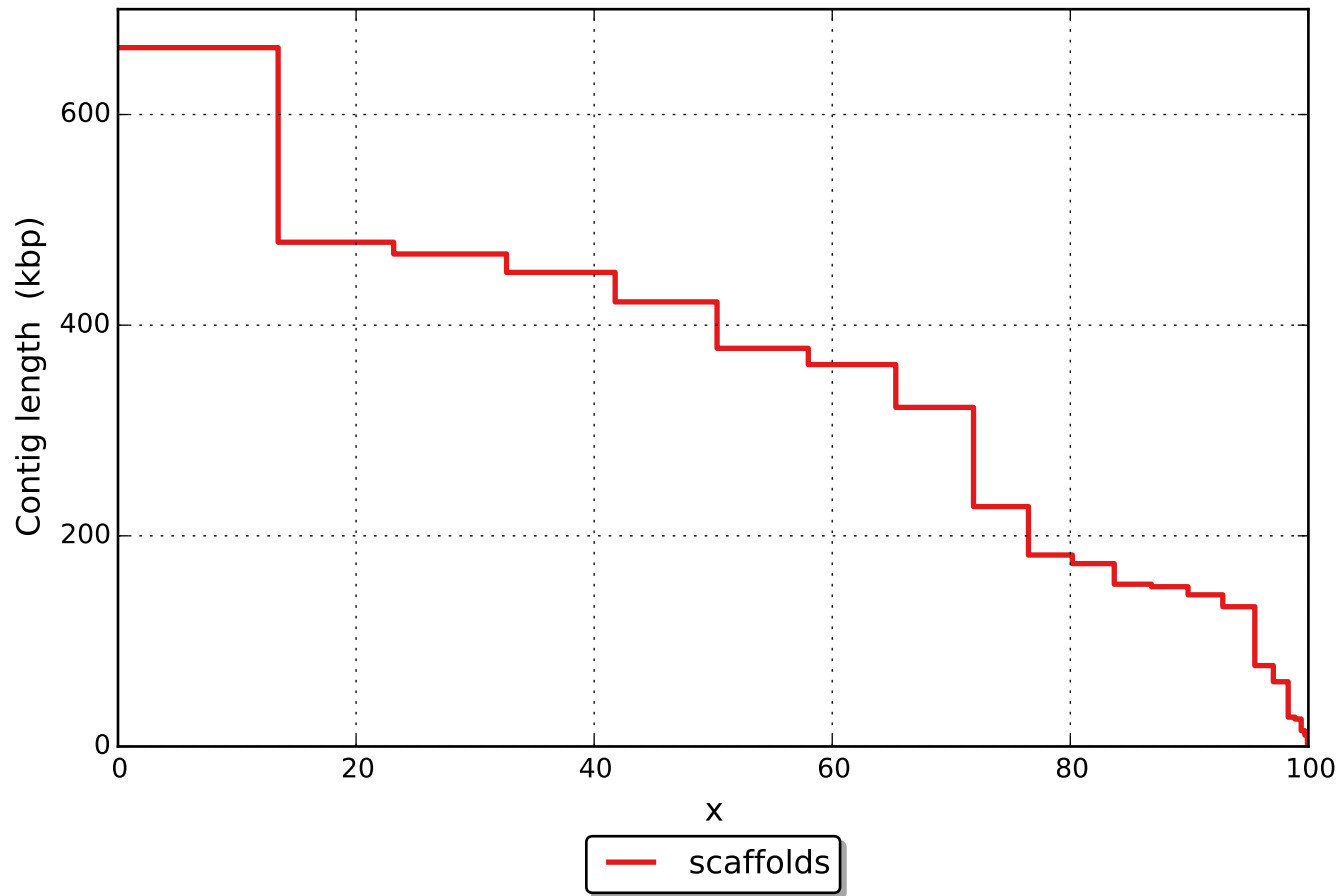
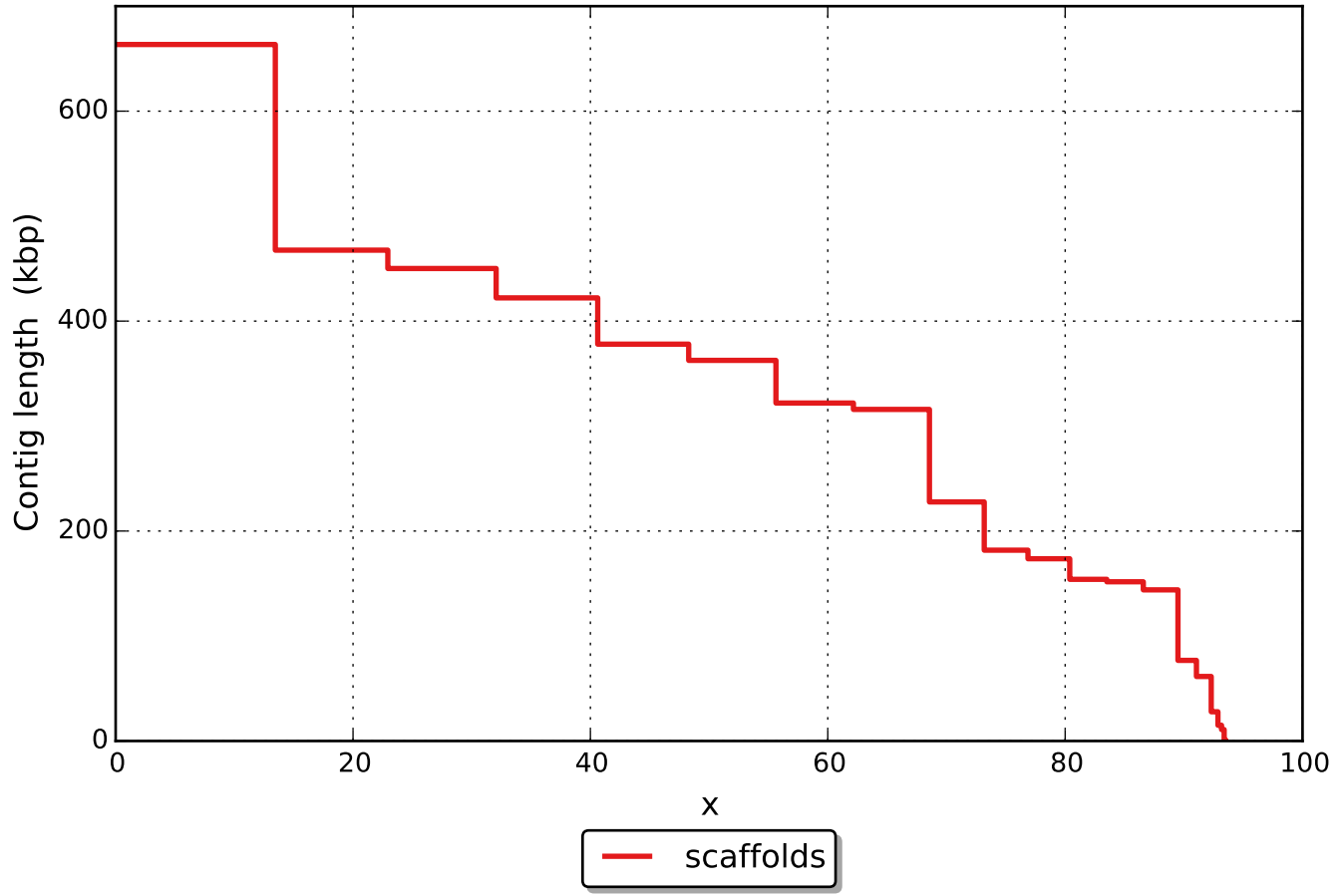Cumulative length

Misassemblies

scaffolds

Cumulative length (aligned contigs)