

## Report

	scaffolds
# contigs ( $\geq 1000$ bp)	20
# contigs ( $\geq 5000$ bp)	19
# contigs ( $\geq 10000$ bp)	19
# contigs ( $\geq 25000$ bp)	17
# contigs ( $\geq 50000$ bp)	16
Total length ( $\geq 1000$ bp)	4771002
Total length ( $\geq 5000$ bp)	4769479
Total length ( $\geq 10000$ bp)	4769479
Total length ( $\geq 25000$ bp)	4743578
Total length ( $\geq 50000$ bp)	4715727
# contigs	21
Largest contig	663492
Total length	4771828
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 + 1 part
Unaligned length	162886
Genome fraction (%)	99.219
Duplication ratio	1.001
# N's per 100 kbp	0.98
# mismatches per 100 kbp	207.10
# indels per 100 kbp	0.61
Largest alignment	663492
NA50	362589
NGA50	378035
NA75	227737
NGA75	227737
LA50	6
LGA50	5
LA75	9
LGA75	9

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

## Misassemblies report

	scaffolds
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	1
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	9538
# indels	28
# short indels	26
# long indels	2
Indels length	92

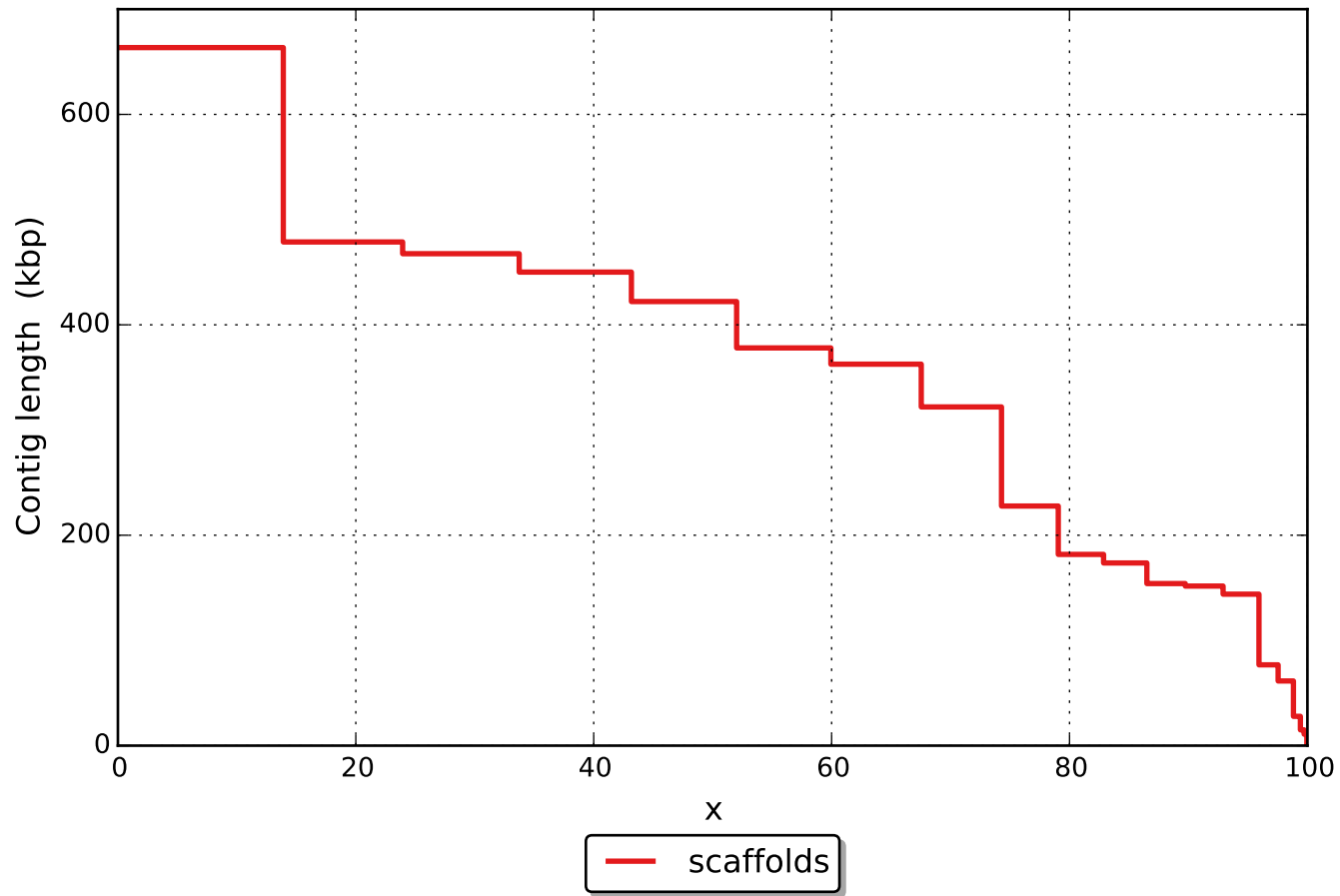
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

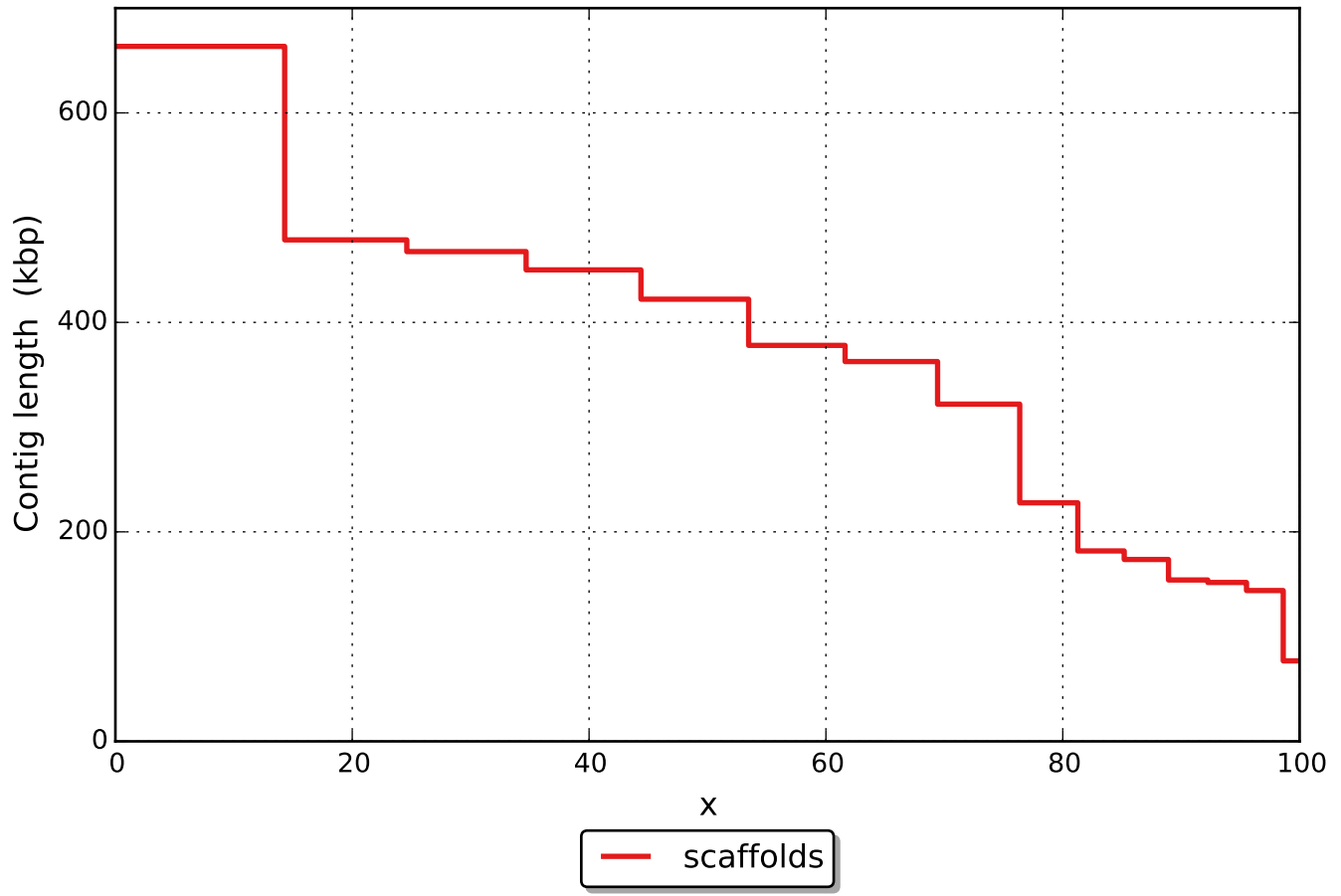
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	1
Partially unaligned length	162886
# N's	47

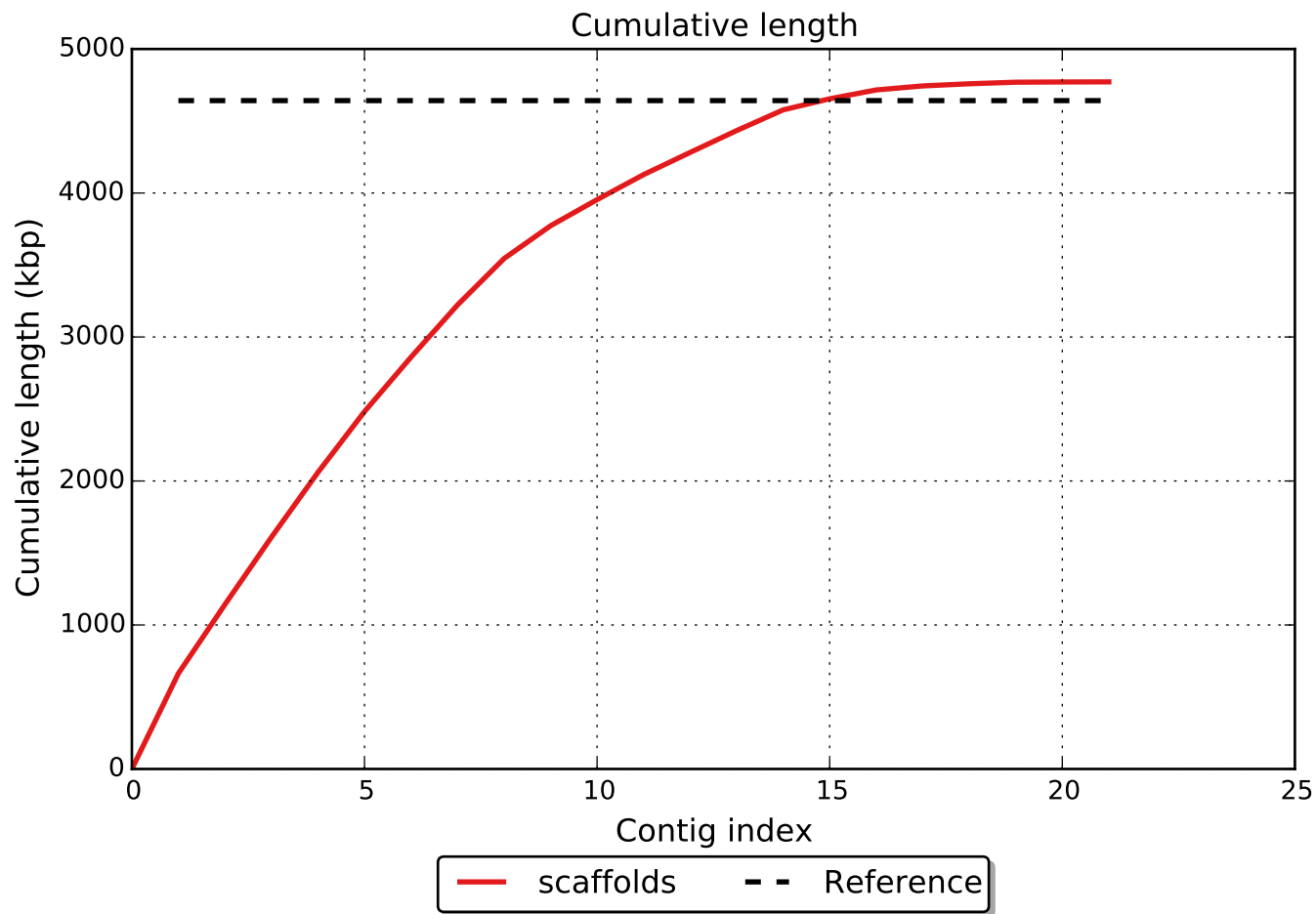
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

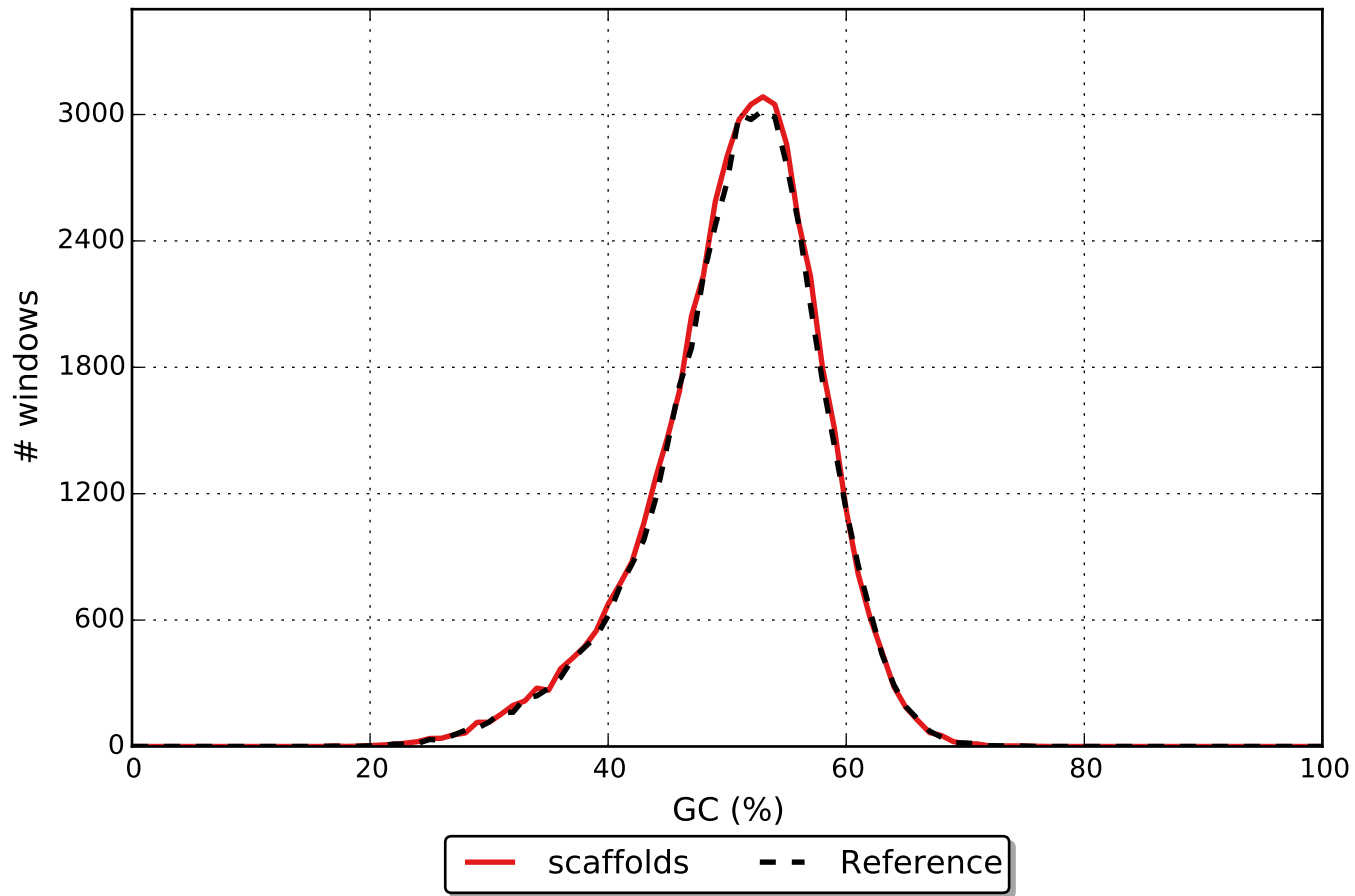


NGx





# GC content

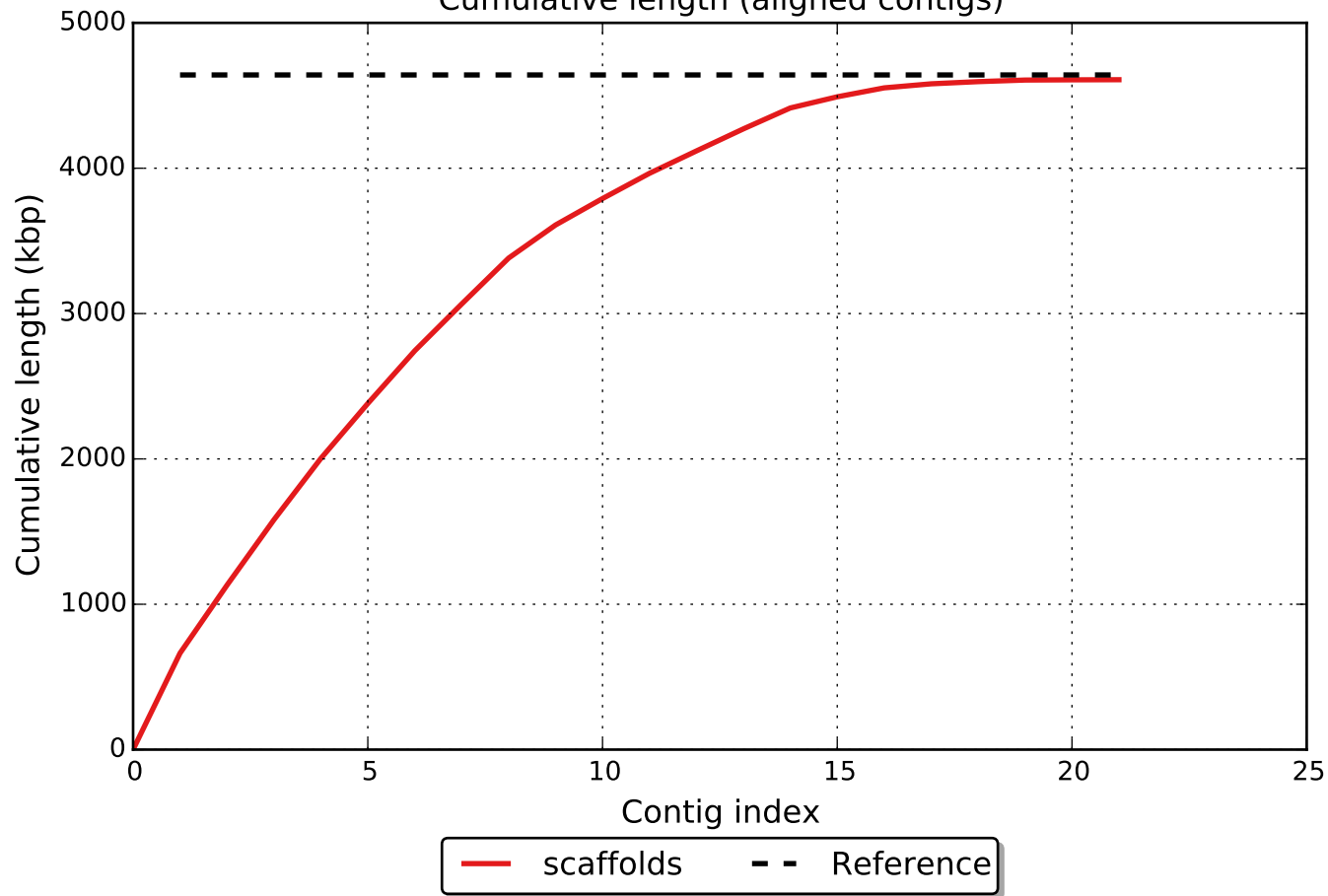


# Misassemblies

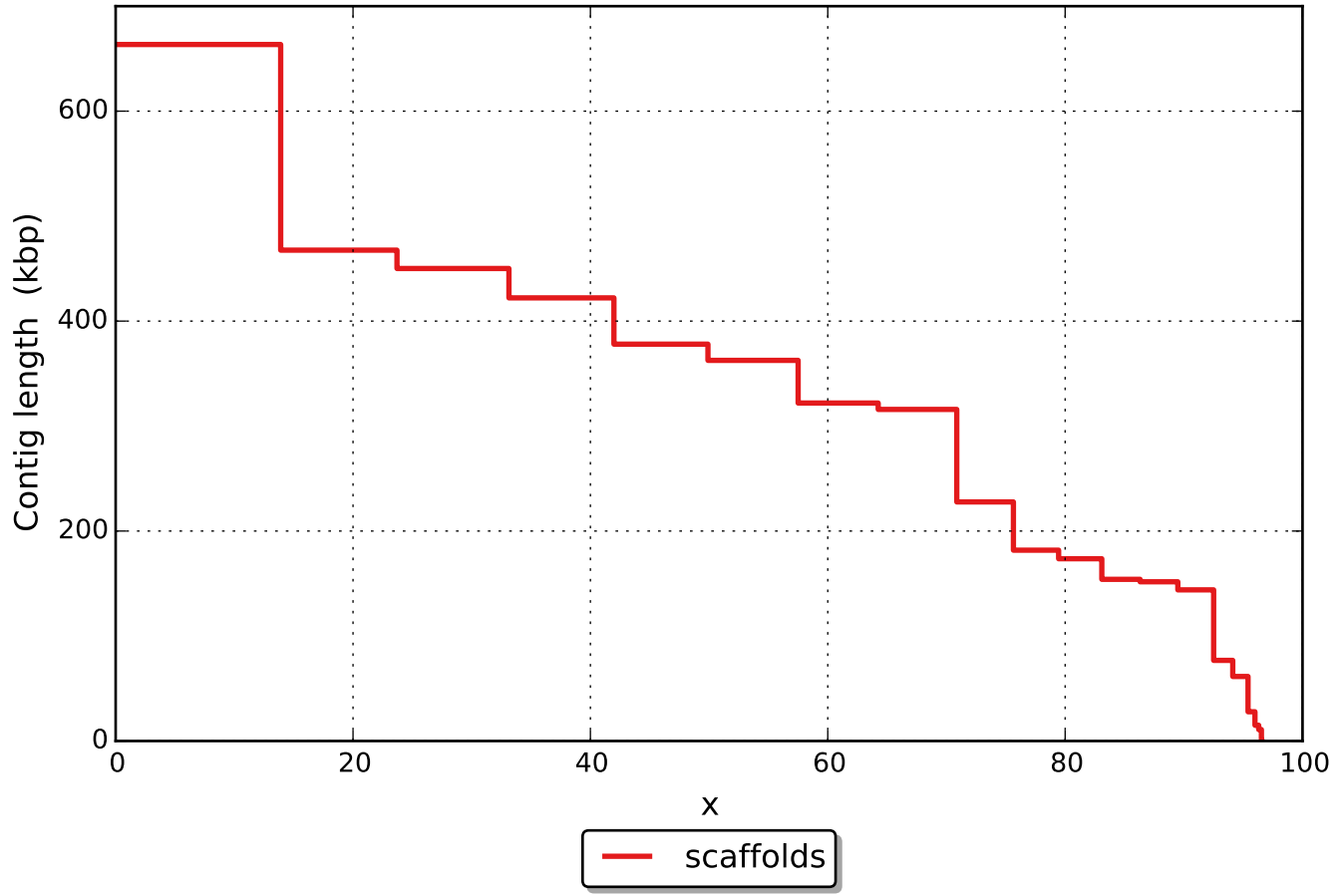




Cumulative length (aligned contigs)



NAx



# NGAx

