

## Report

	scaffolds
# contigs (>= 1000 bp)	62
# contigs (>= 5000 bp)	51
# contigs (>= 10000 bp)	48
# contigs (>= 25000 bp)	43
# contigs (>= 50000 bp)	28
Total length (>= 1000 bp)	4648192
Total length (>= 5000 bp)	4627894
Total length (>= 10000 bp)	4606207
Total length (>= 25000 bp)	4529453
Total length (>= 50000 bp)	4015407
# contigs	74
Largest contig	332104
Total length	4656975
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	167862
NG50	167862
N75	85064
NG75	85064
L50	10
LG50	10
L75	21
LG75	21
# misassemblies	3
# misassembled contigs	1
Misassembled contigs length	308025
# local misassemblies	2
# unaligned contigs	0 + 3 part
Unaligned length	23832
Genome fraction (%)	97.504
Duplication ratio	1.024
# N's per 100 kbp	0.00
# mismatches per 100 kbp	475.36
# indels per 100 kbp	0.91
Largest alignment	332104
NA50	132188
NGA50	132188
NA75	79547
NGA75	79547
LA50	11
LGA50	11
LA75	22
LGA75	22

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	3
# relocations	3
# translocations	0
# inversions	0
# possibly misassembled contigs	3
# misassembled contigs	1
Misassembled contigs length	308025
# local misassemblies	2
# mismatches	21514
# indels	41
# short indels	36
# long indels	5
Indels length	117

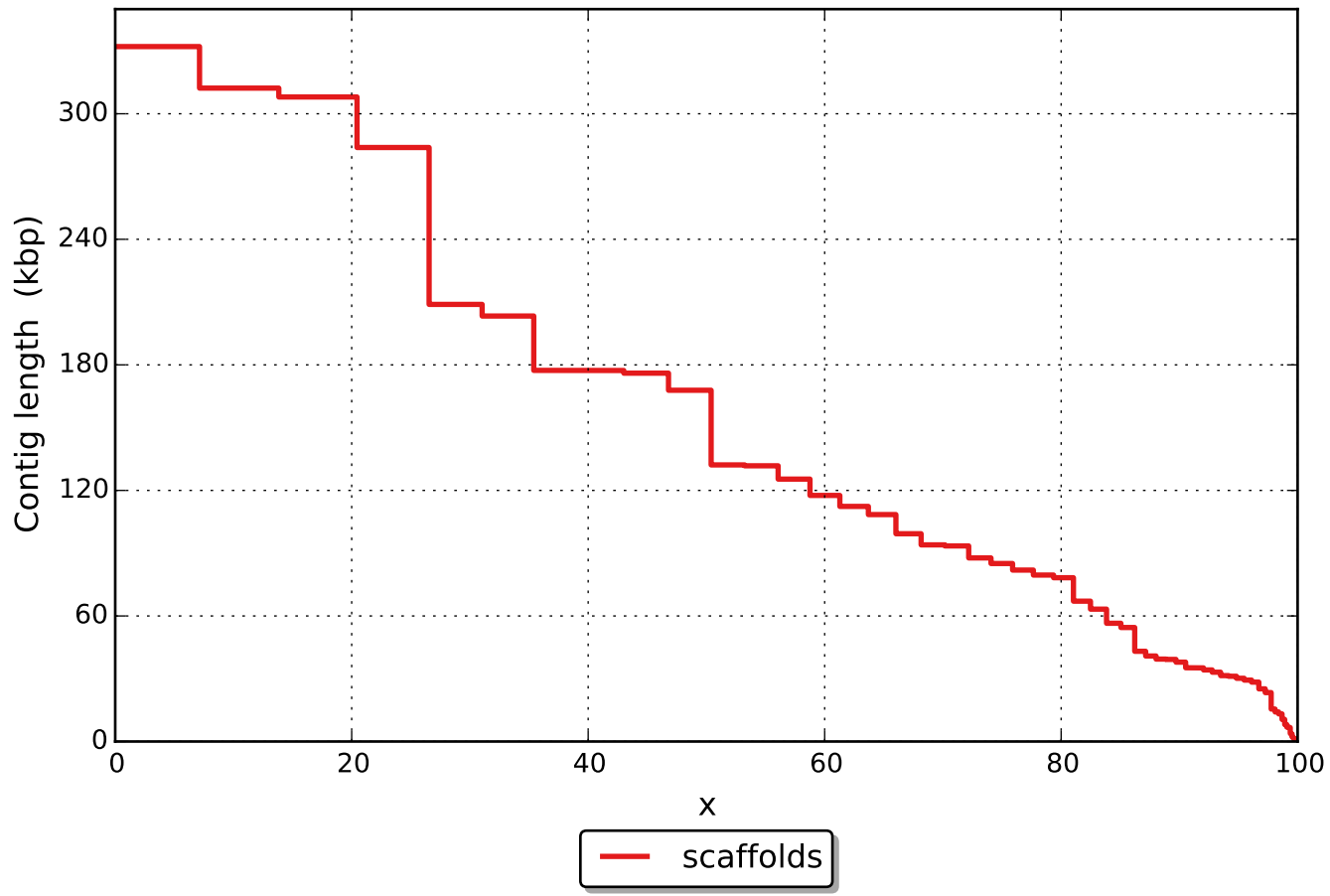
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

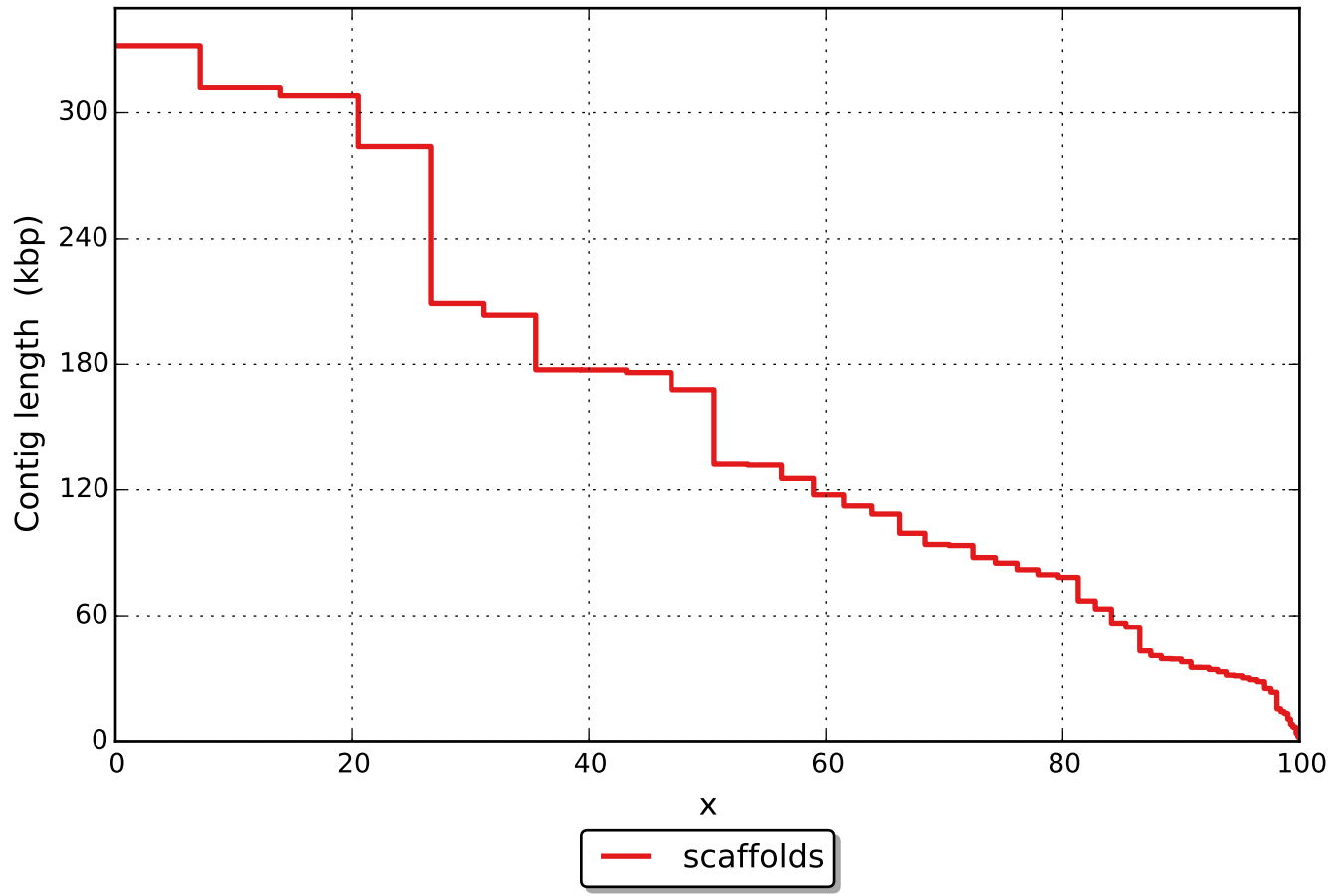
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	3
# with misassembly	0
# both parts are significant	2
Partially unaligned length	23832
# N's	0

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).

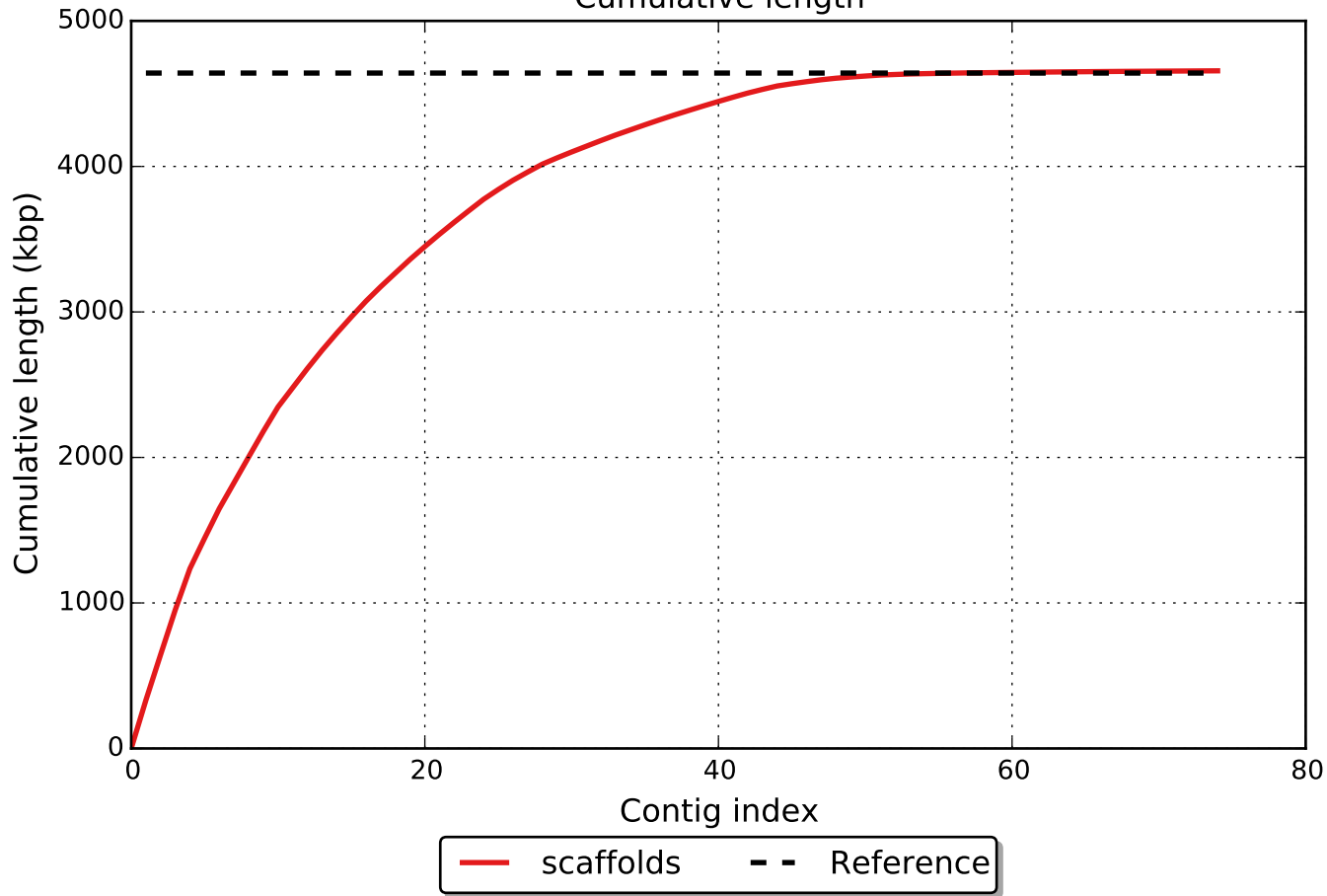
Nx



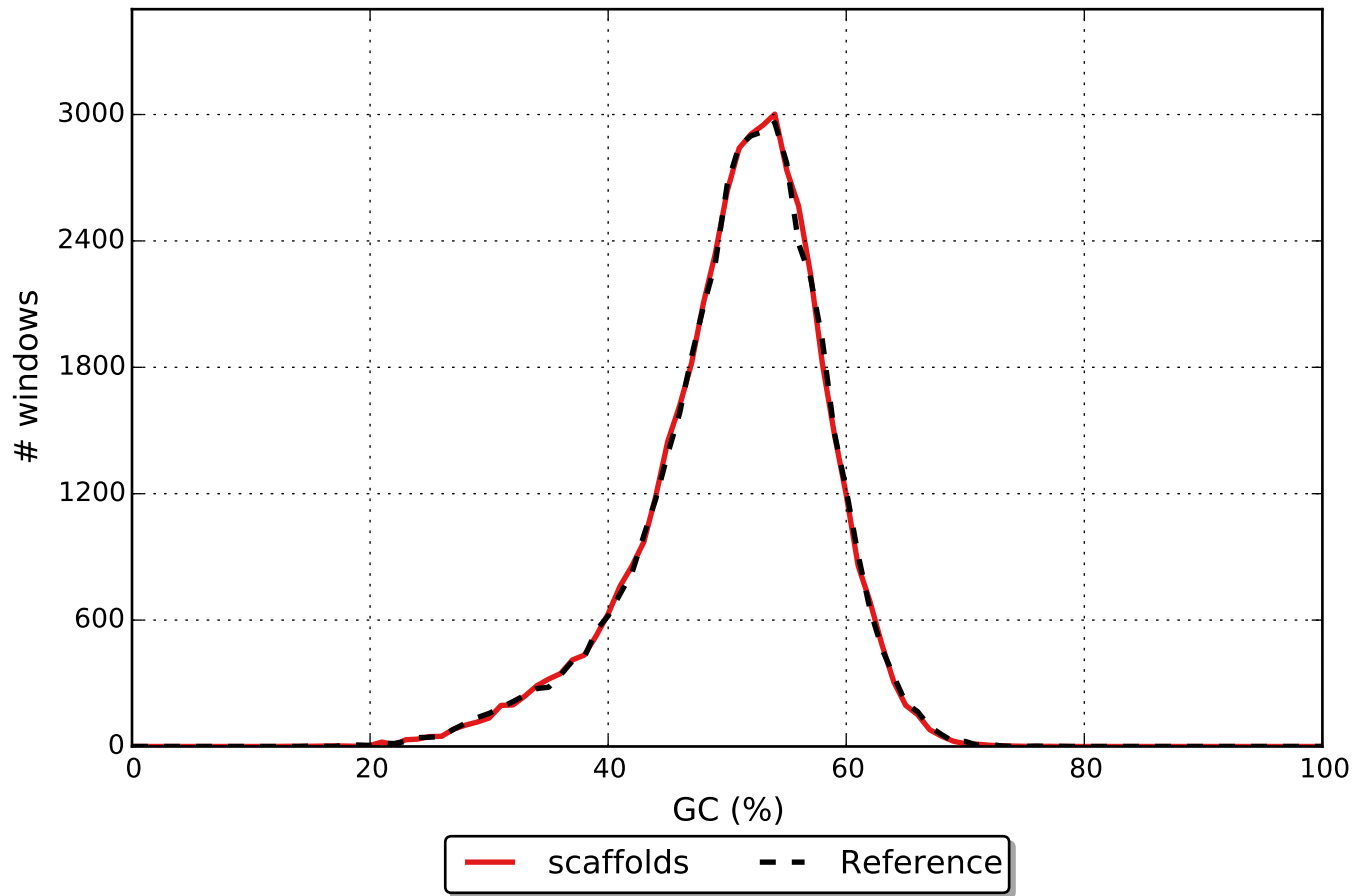
NGx

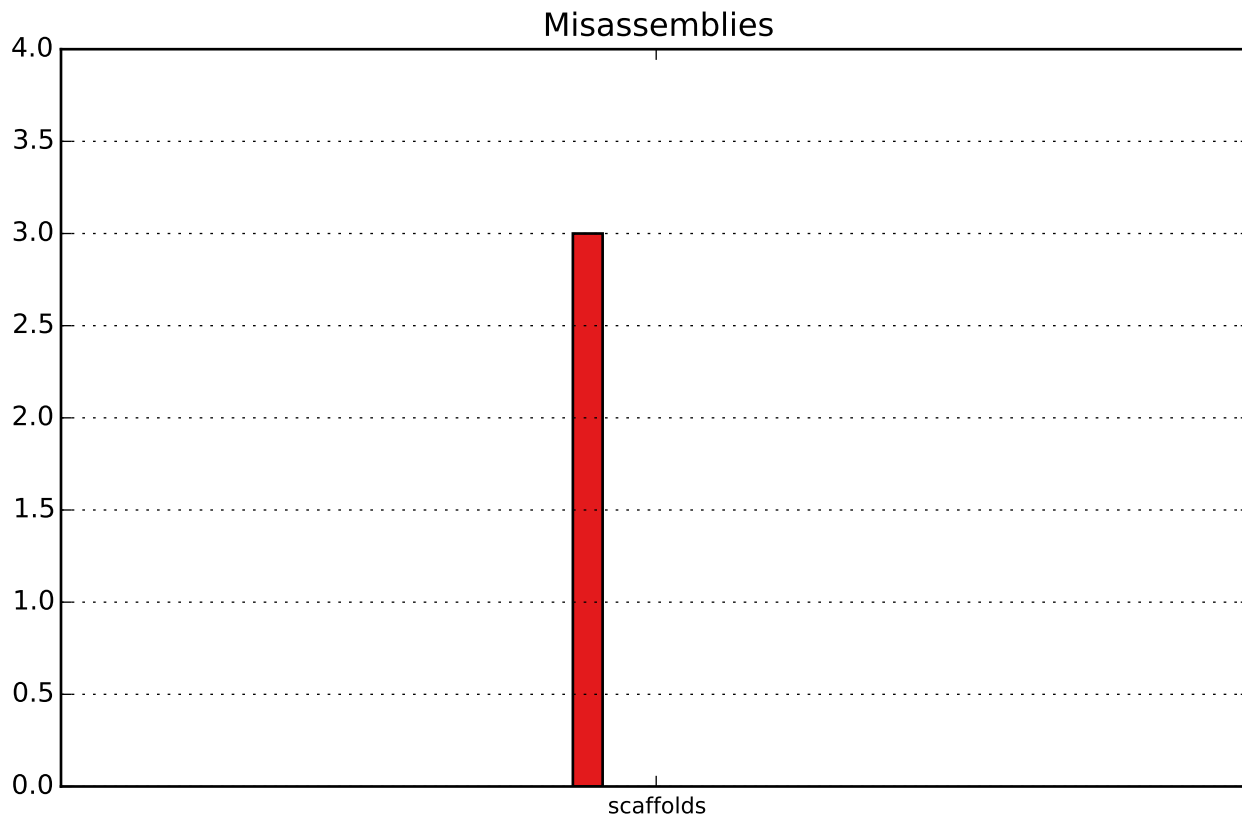


Cumulative length



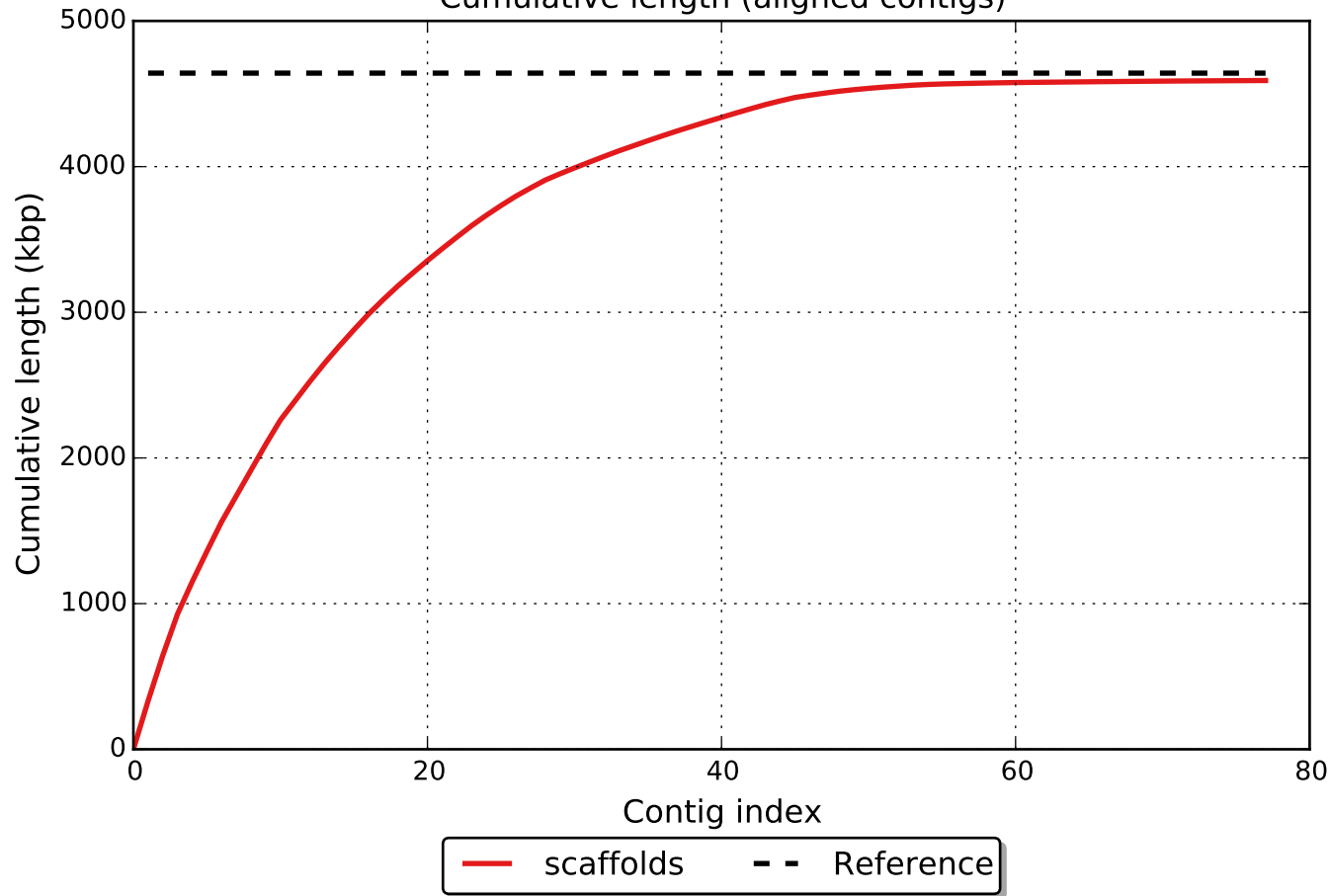
GC content



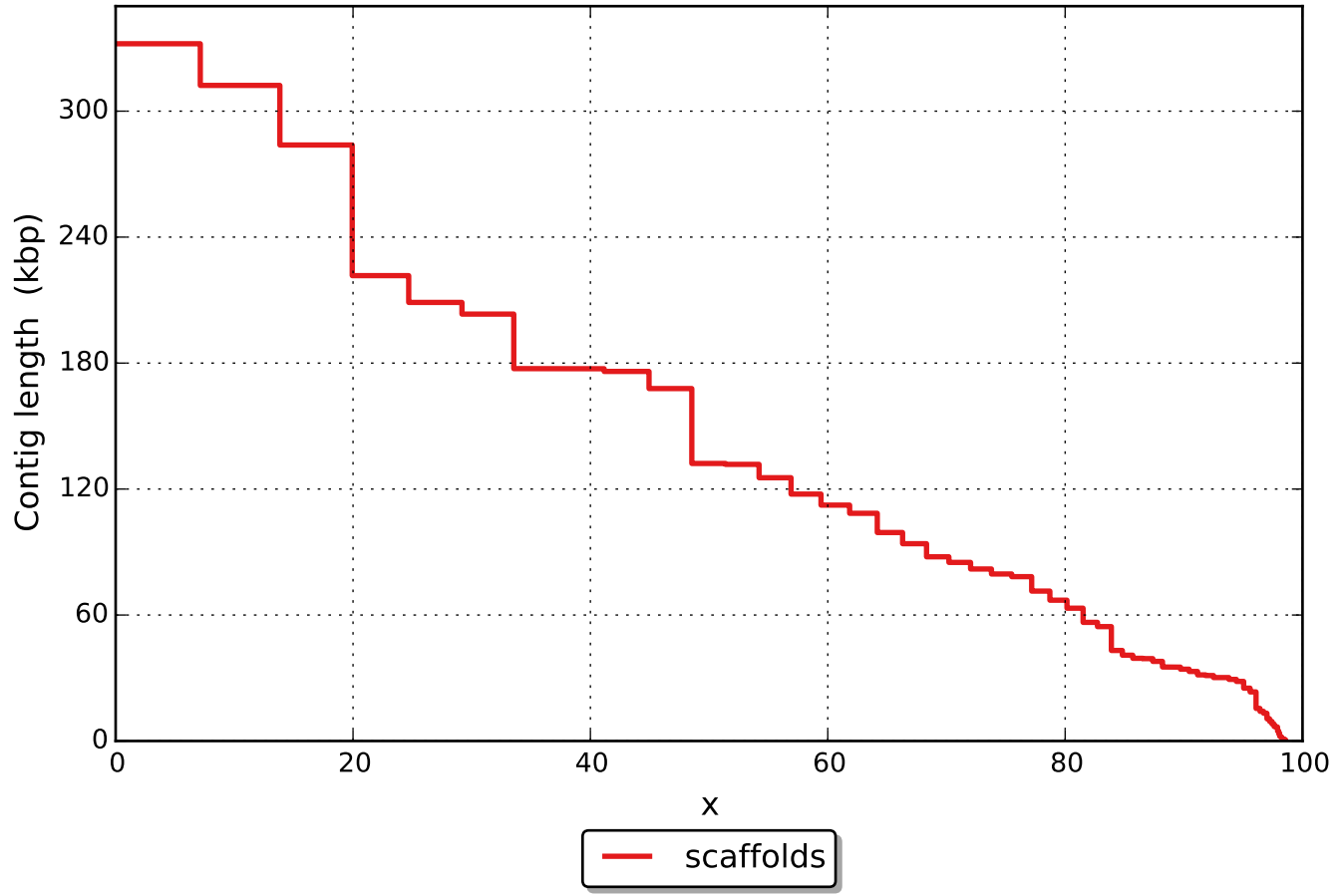




Cumulative length (aligned contigs)



NAx



# NGAx

