

## Report

	scaffolds
# contigs ( $\geq 1000$ bp)	127
# contigs ( $\geq 5000$ bp)	102
# contigs ( $\geq 10000$ bp)	82
# contigs ( $\geq 25000$ bp)	40
# contigs ( $\geq 50000$ bp)	8
Total length ( $\geq 1000$ bp)	2590370
Total length ( $\geq 5000$ bp)	2531915
Total length ( $\geq 10000$ bp)	2381880
Total length ( $\geq 25000$ bp)	1667521
Total length ( $\geq 50000$ bp)	590787
# contigs	140
Largest contig	125463
Total length	2597753
Reference length	4641652
GC (%)	50.72
Reference GC (%)	50.79
N50	30805
NG50	11986
N75	20647
L50	27
LG50	77
L75	53
# misassemblies	4
# misassembled contigs	4
Misassembled contigs length	152553
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	54.848
Duplication ratio	1.020
# N's per 100 kbp	46.85
# mismatches per 100 kbp	851.35
# indels per 100 kbp	0.63
Largest alignment	125463
NA50	29578
NGA50	11170
NA75	19843
LA50	28
LGA50	80
LA75	55

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	4
# relocations	4
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	4
Misassembled contigs length	152553
# local misassemblies	2
# mismatches	21674
# indels	16
# short indels	12
# long indels	4
Indels length	238

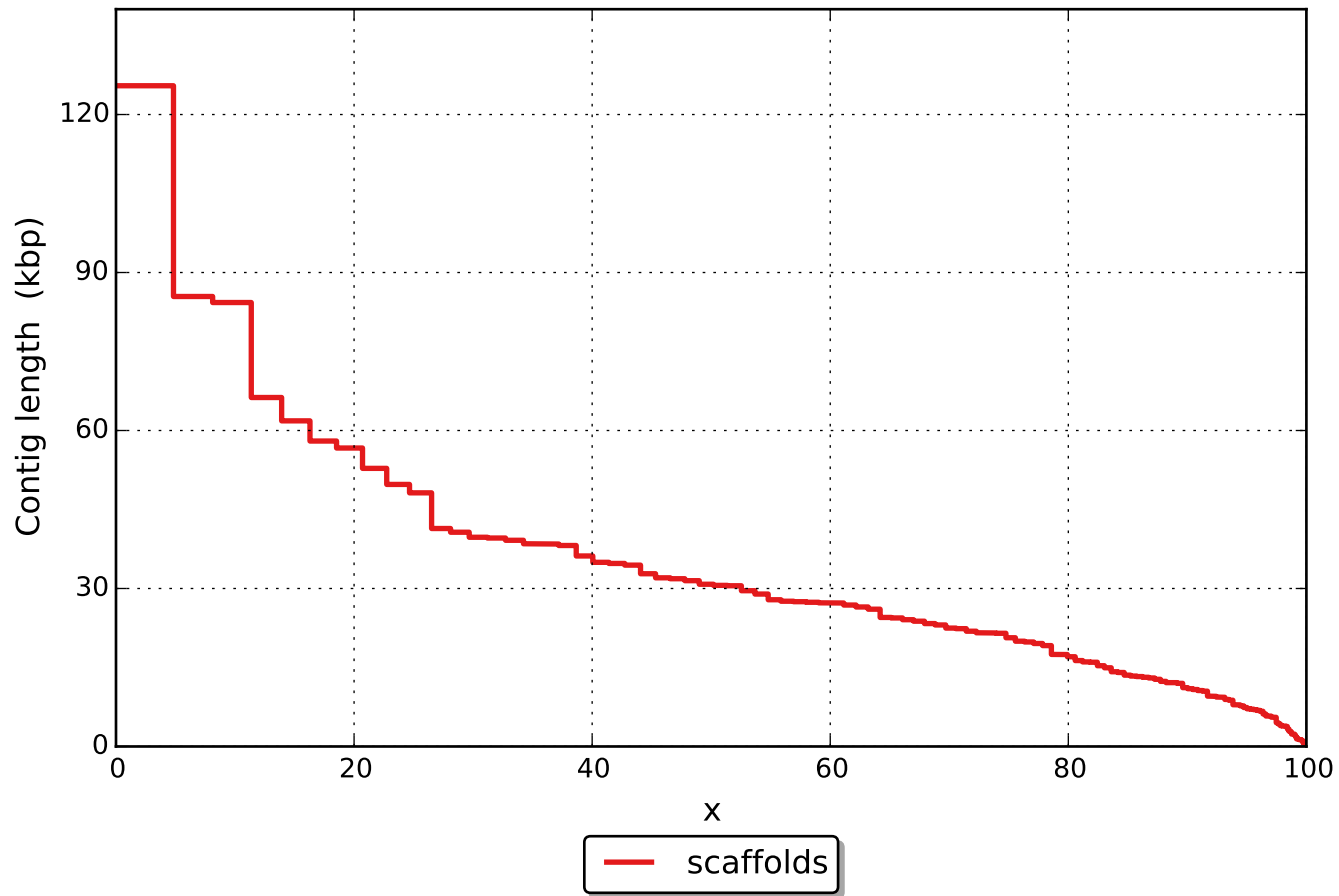
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

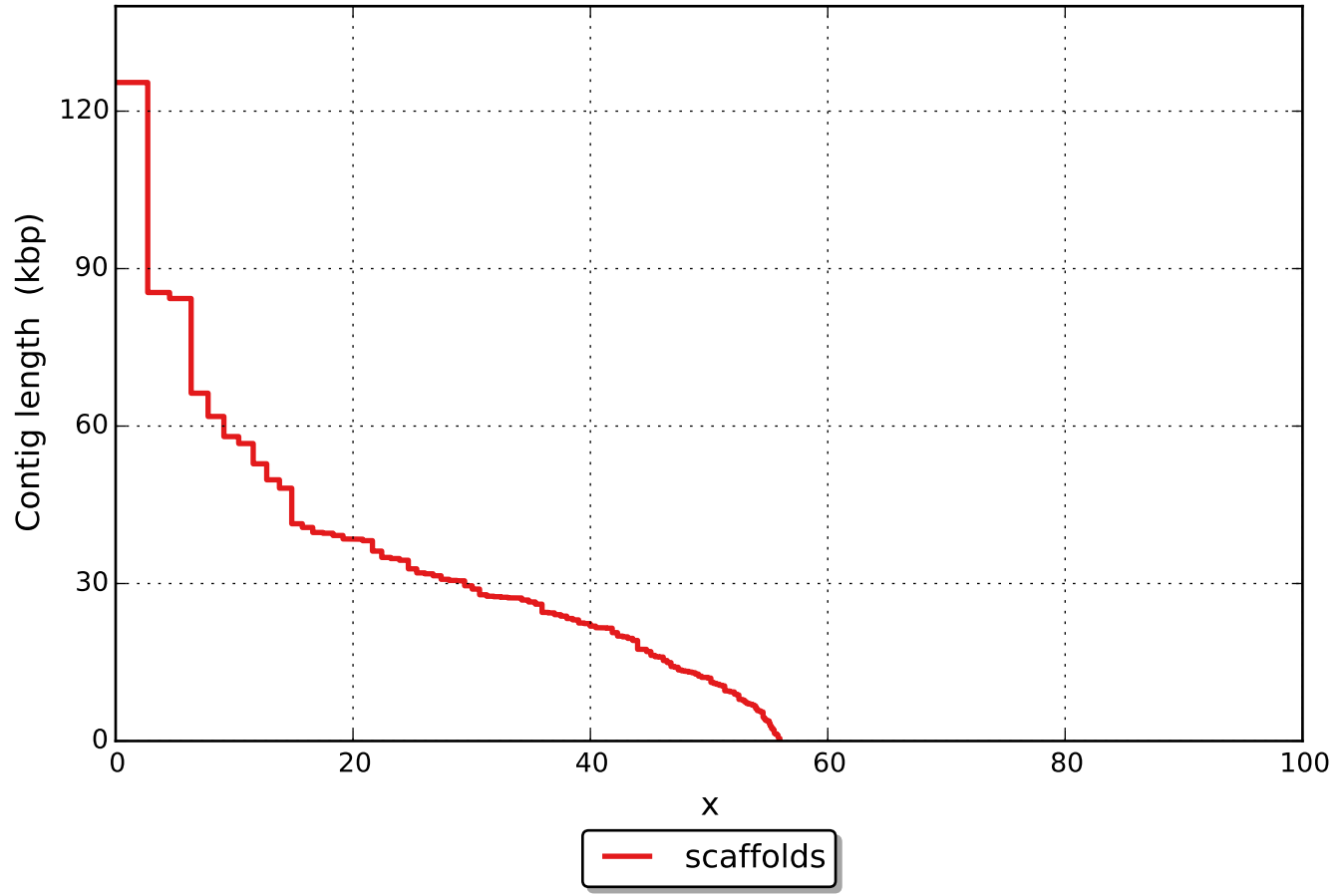
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	1217

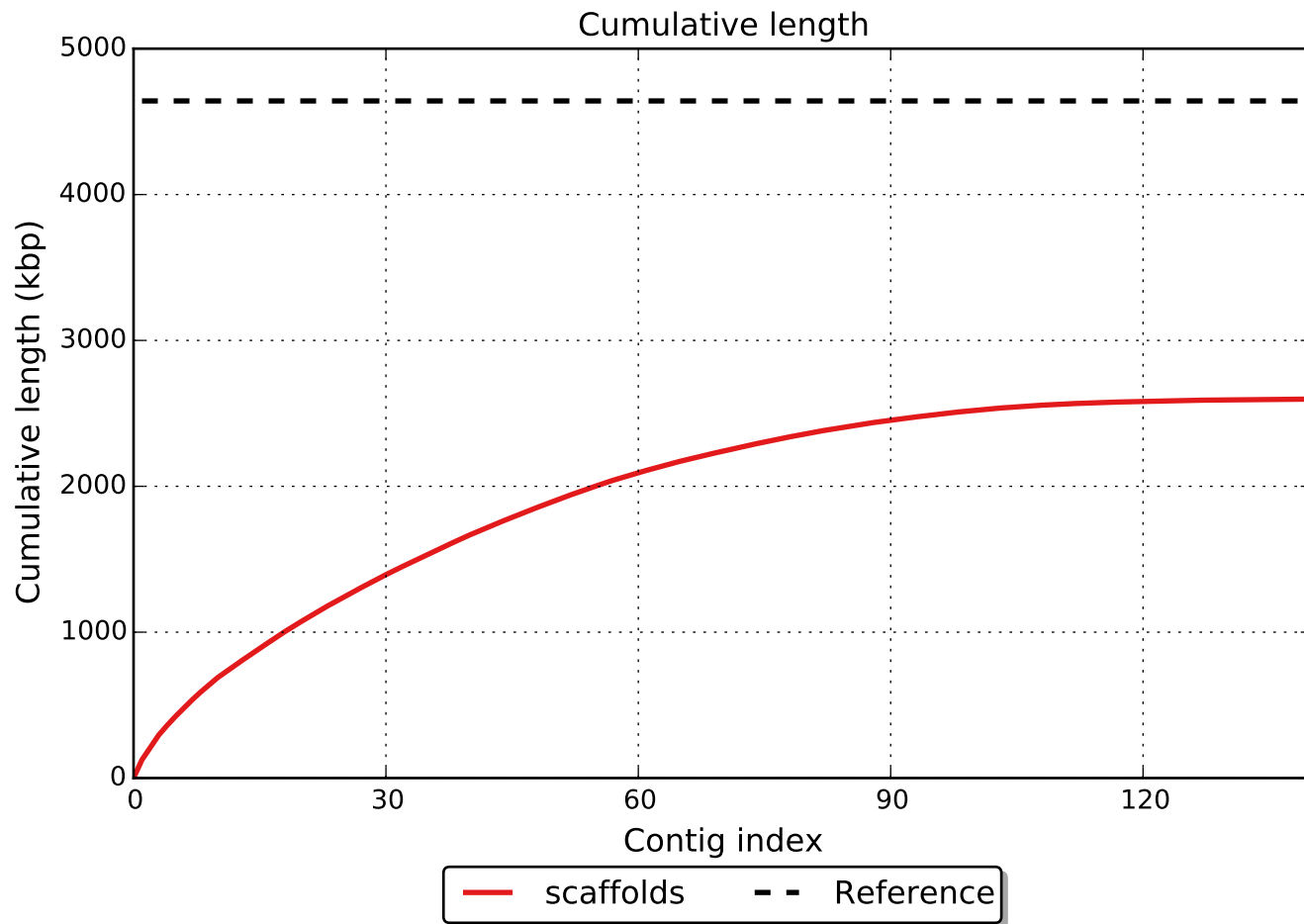
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

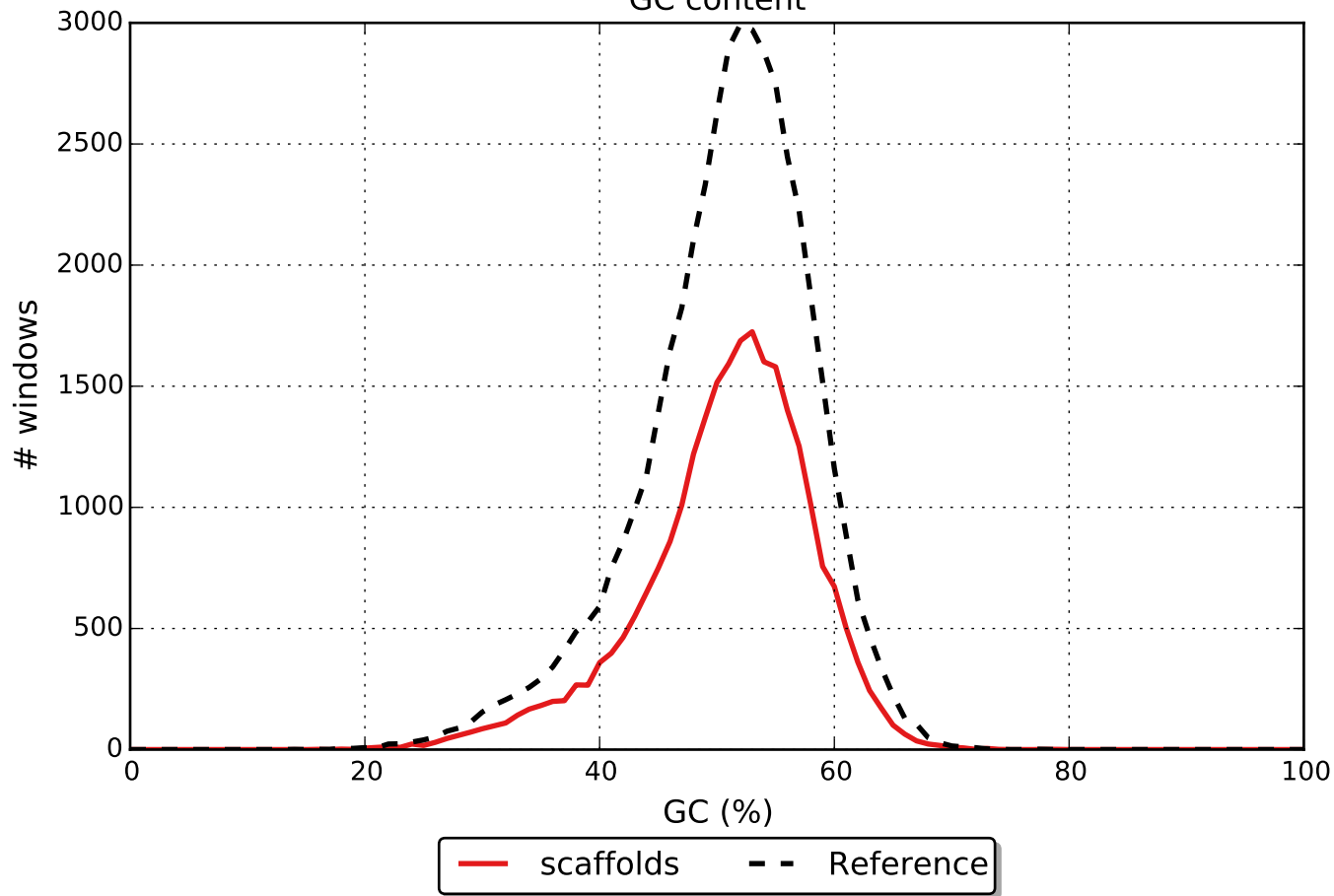


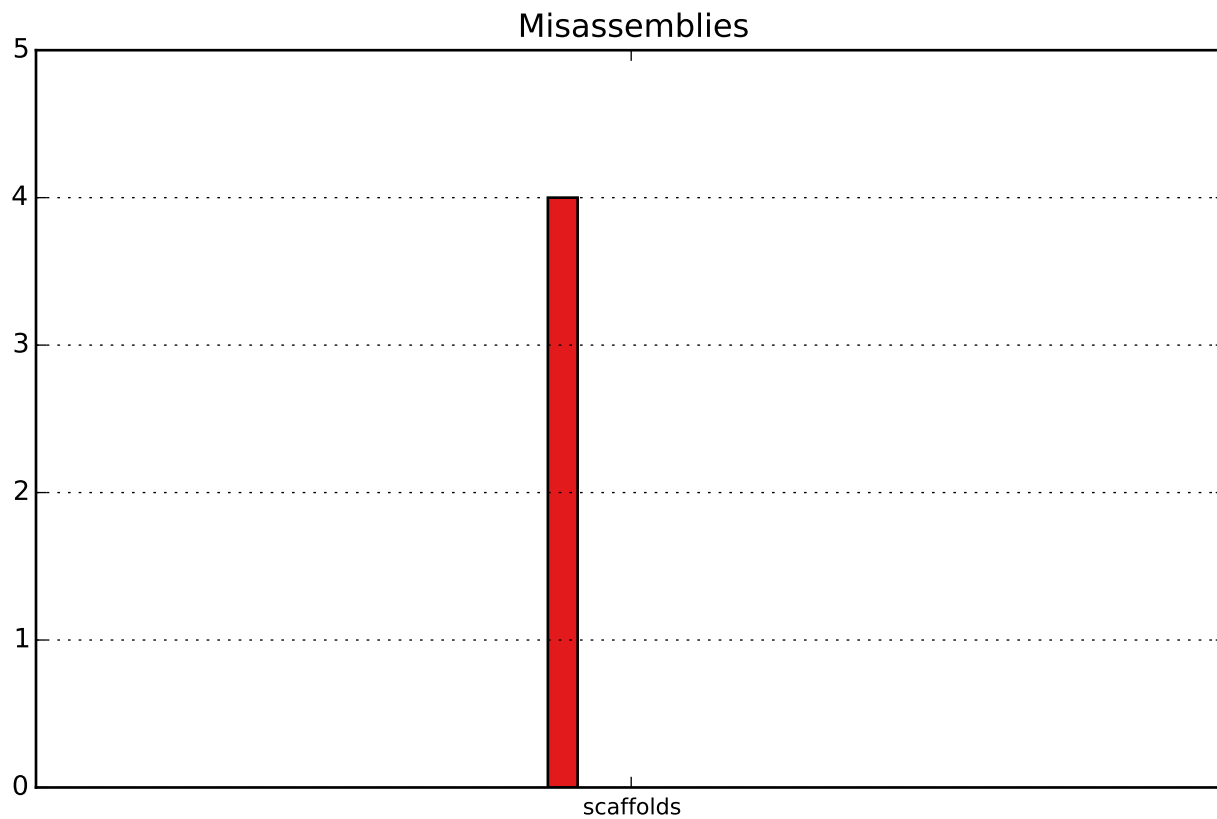
NGx





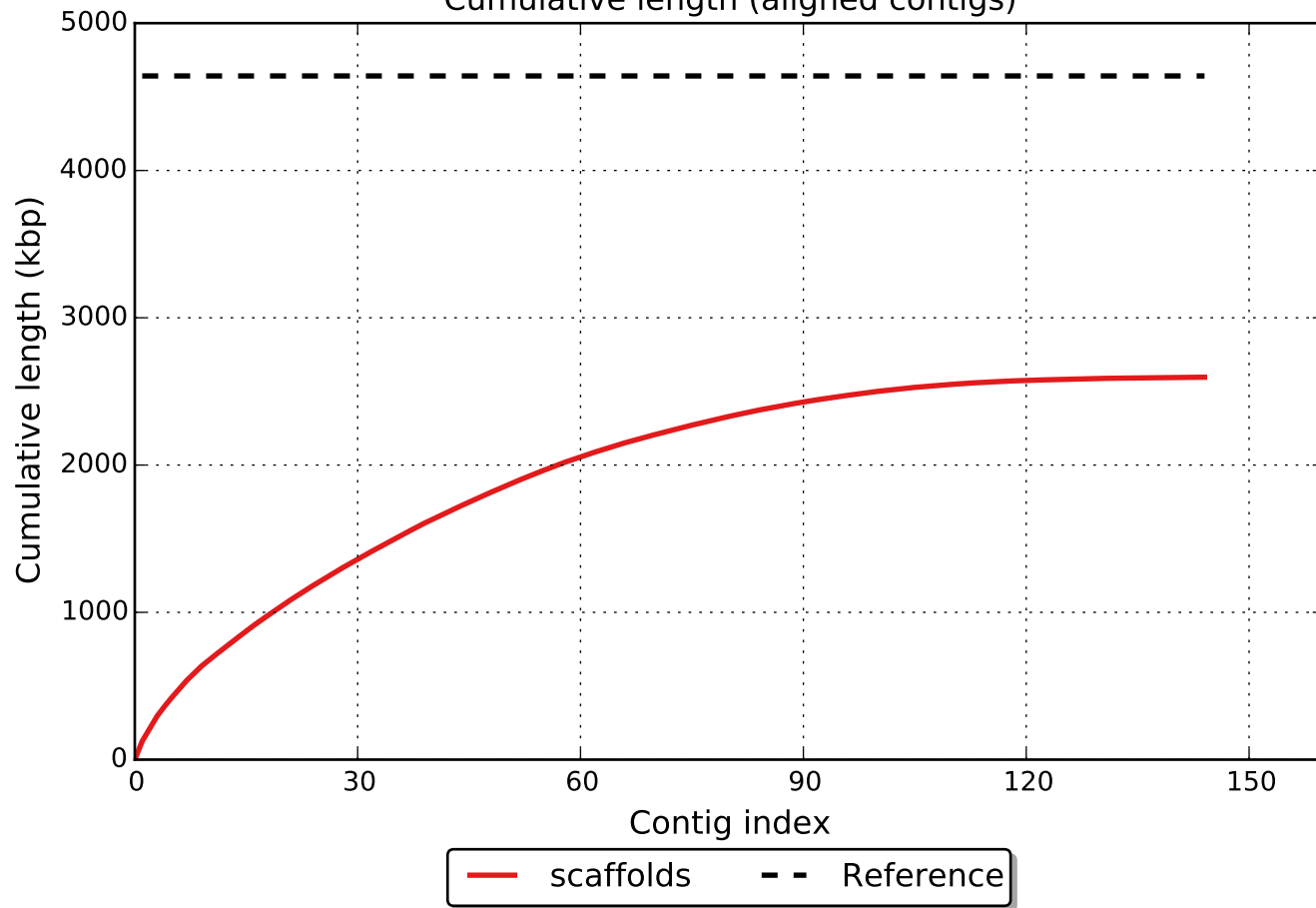
GC content



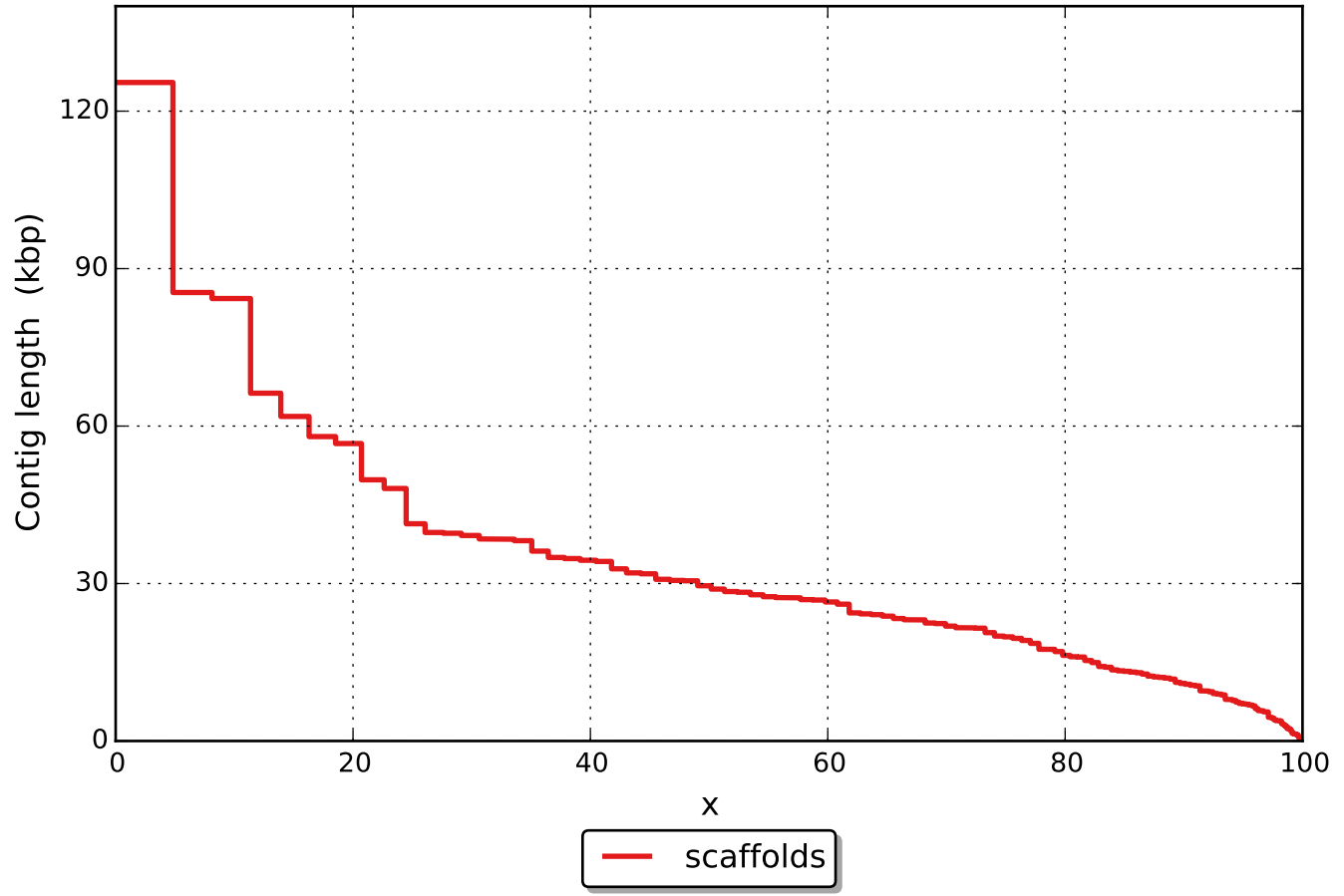




Cumulative length (aligned contigs)



NAx



# NGAx

