

# Report

	scaffolds
# contigs (>= 1000 bp)	258
# contigs (>= 5000 bp)	197
# contigs (>= 10000 bp)	139
# contigs (>= 25000 bp)	66
# contigs (>= 50000 bp)	12
Total length (>= 1000 bp)	4501264
Total length (>= 5000 bp)	4338910
Total length (>= 10000 bp)	3900987
Total length (>= 25000 bp)	2663145
Total length (>= 50000 bp)	804429
# contigs	266
Largest contig	121503
Total length	4506802
Reference length	4641652
GC (▼)	50.75
Reference GC (▼)	50.79
N50	29078
NG50	28426
N75	16437
NG75	15692
L50	51
LG50	53
L75	101
LG75	107
# misassemblies	14
# misassembled contigs	12
Misassembled contigs length	343554
# local misassemblies	11
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (▼)	96.953
Duplication ratio	1.001
# N's per 100 kbp	149.77
# mismatches per 100 kbp	9.40
# indels per 100 kbp	8.93
Largest alignment	82326
NA50	28464
NGA50	27344
NA75	15692
NGA75	14702
LA50	52
LGA50	55
LA75	104
LGA75	111

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	14
# relocations	13
# translocations	0
# inversions	1
# possibly misassembled contigs	0
# misassembled contigs	12
Misassembled contigs length	343554
# local misassemblies	11
# mismatches	423
# indels	402
# short indels	173
# long indels	229
Indels length	3821

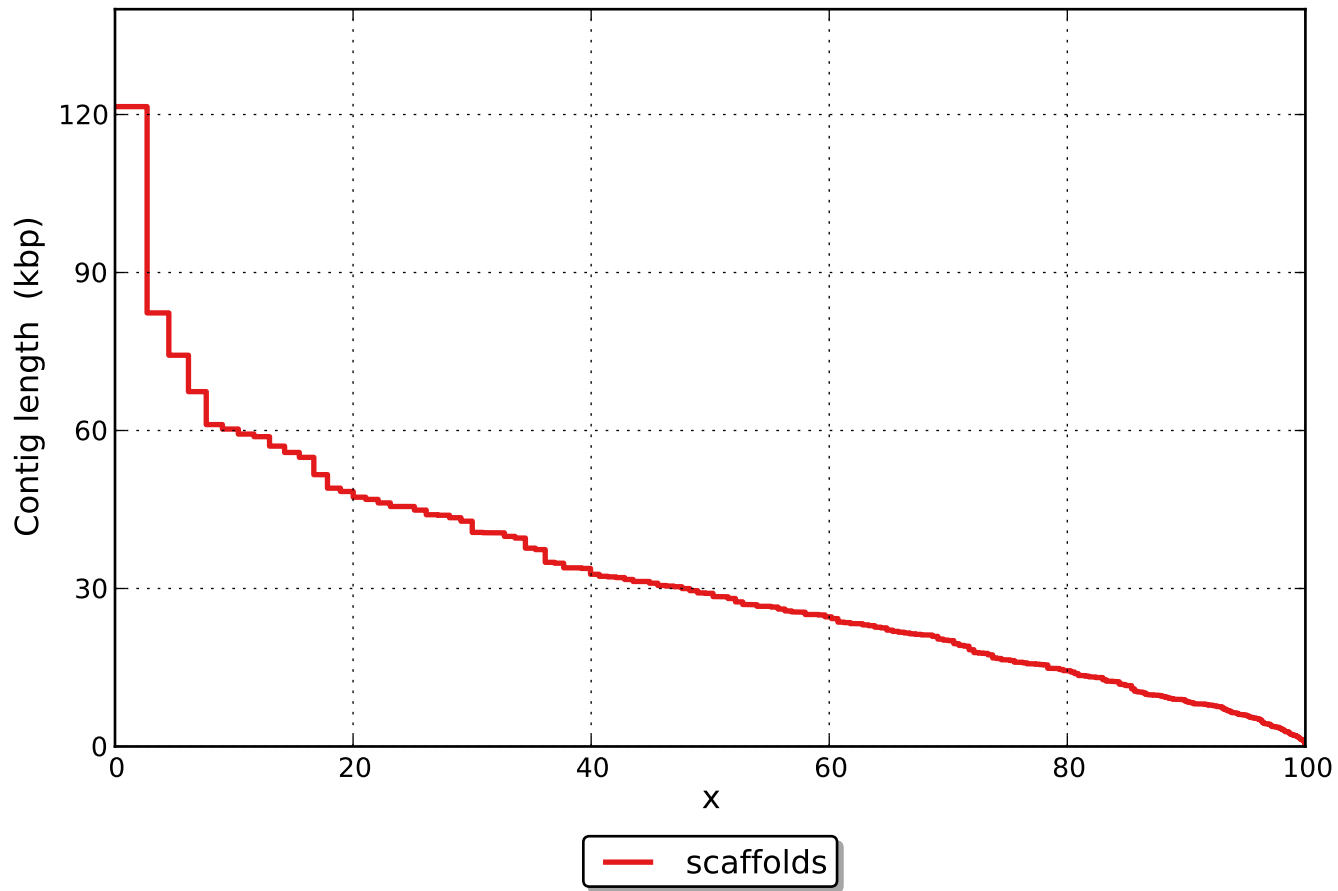
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

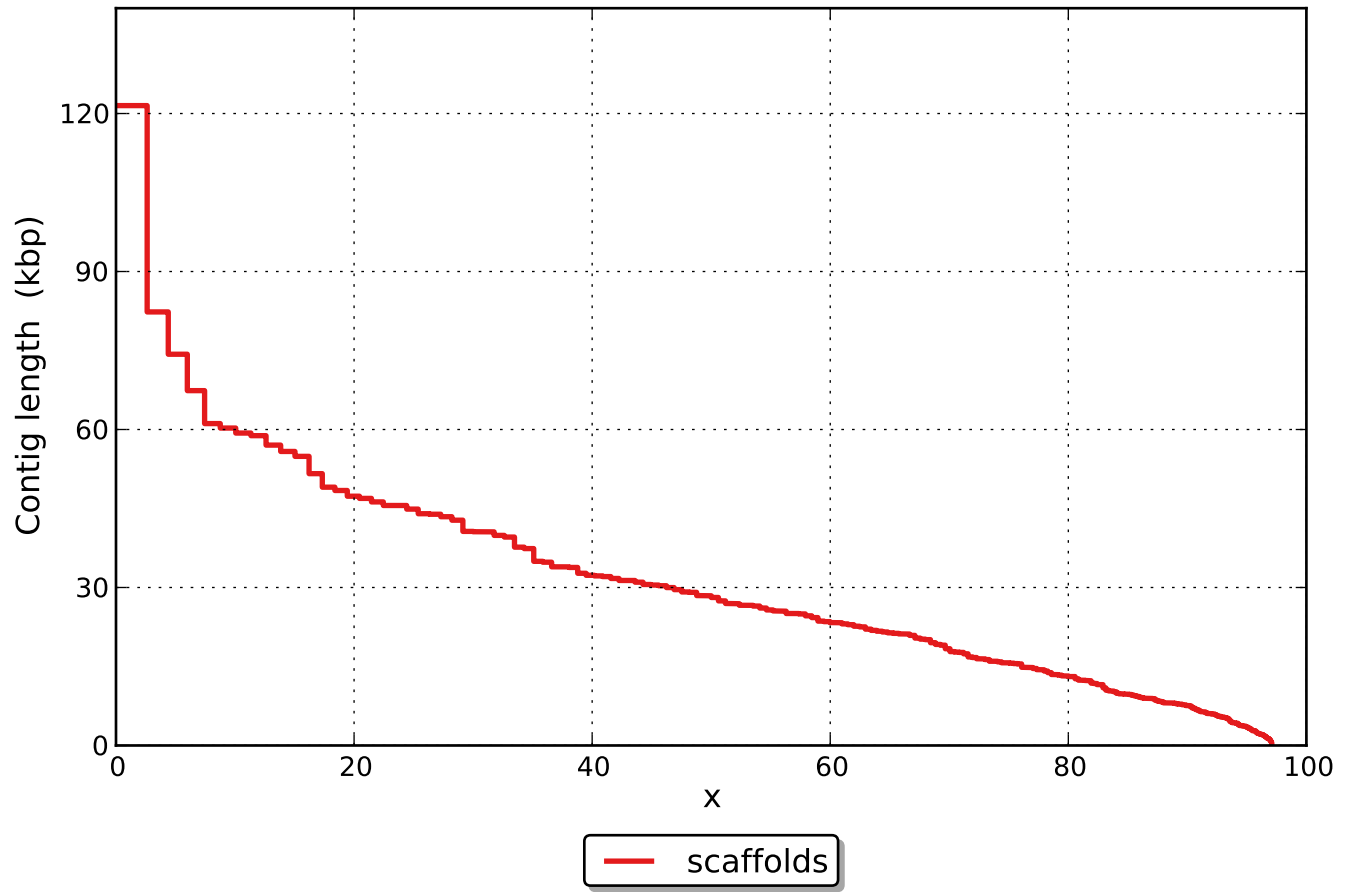
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	6750

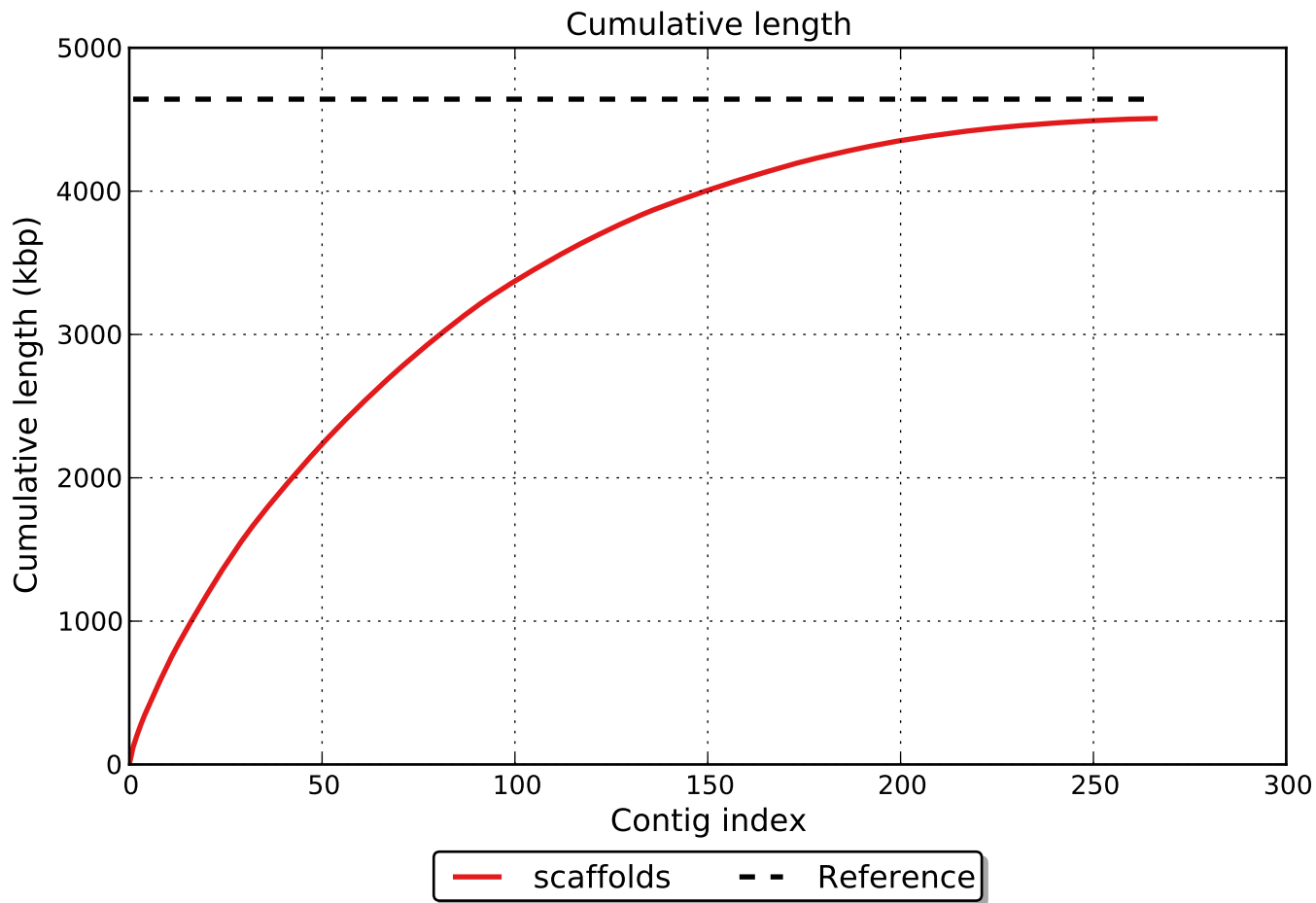
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

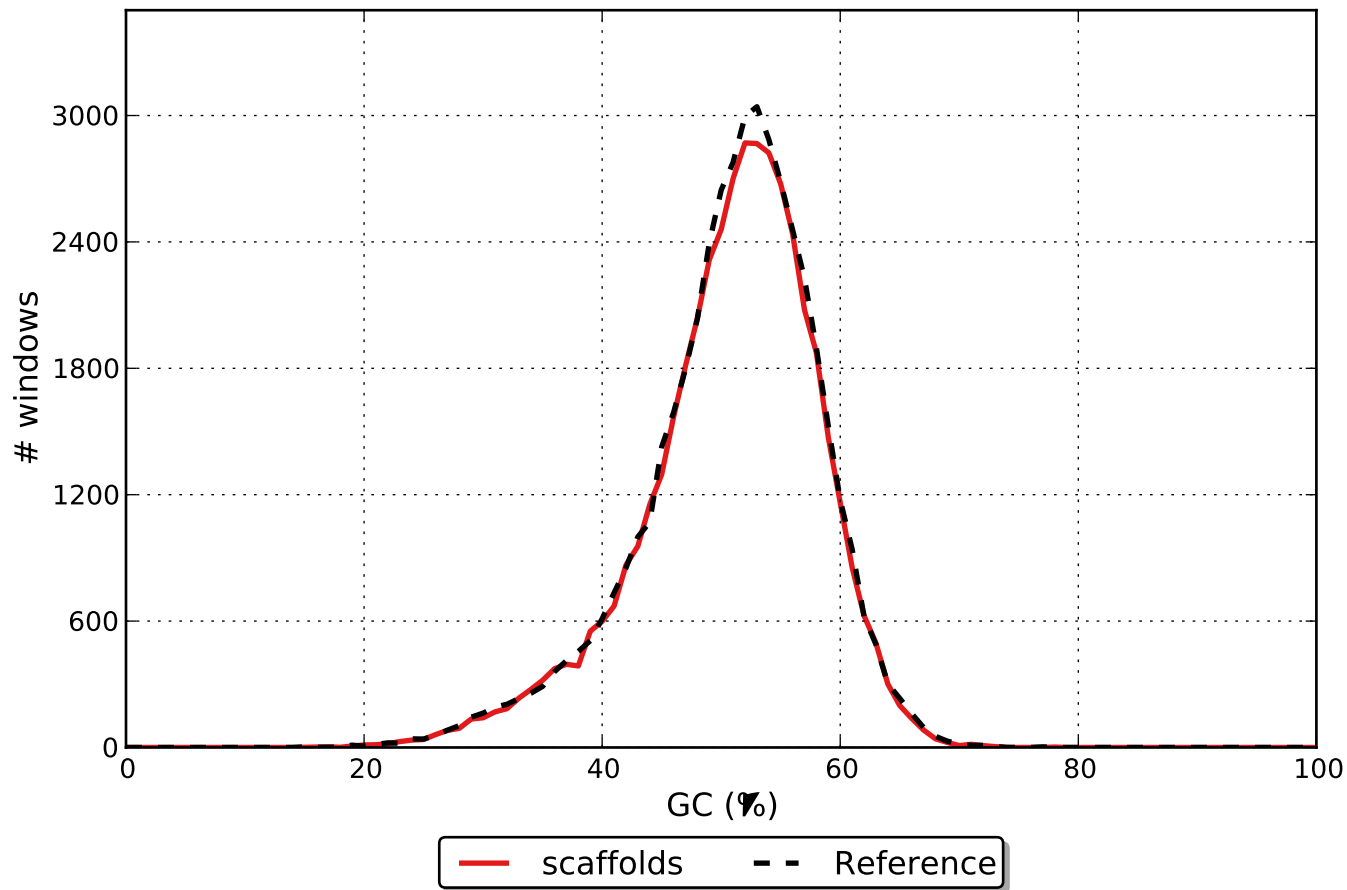


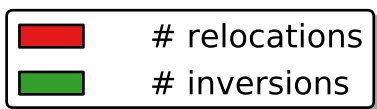
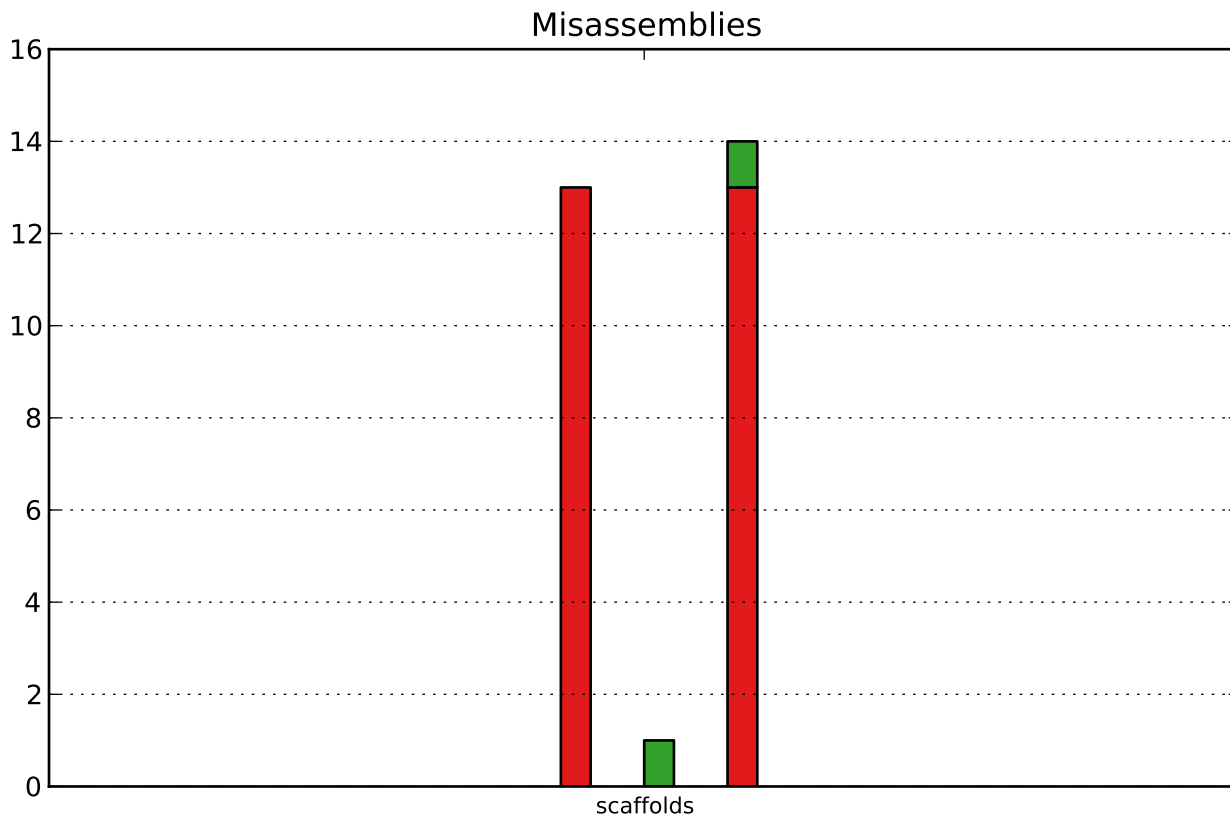
NGx





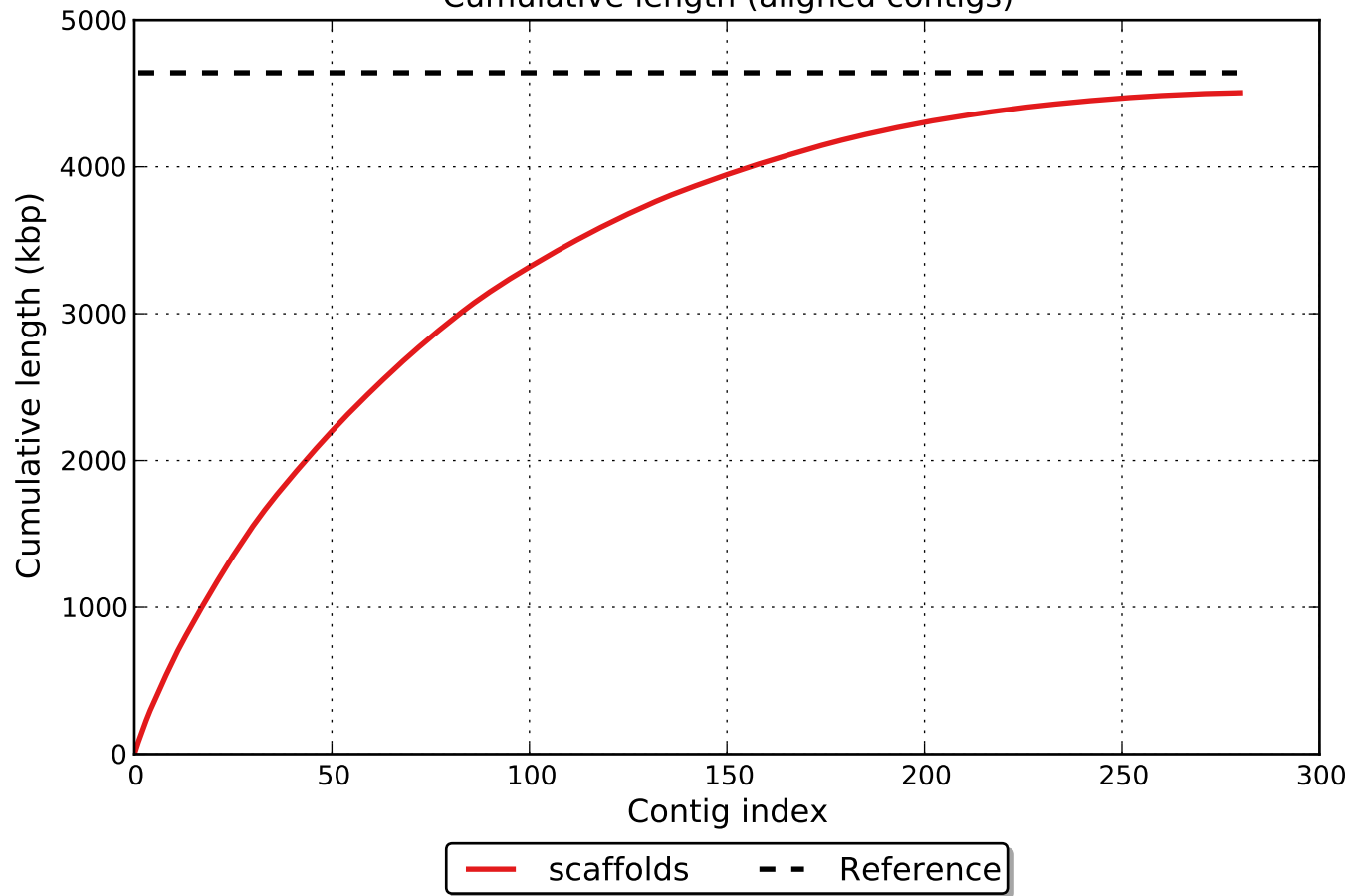
# GC content



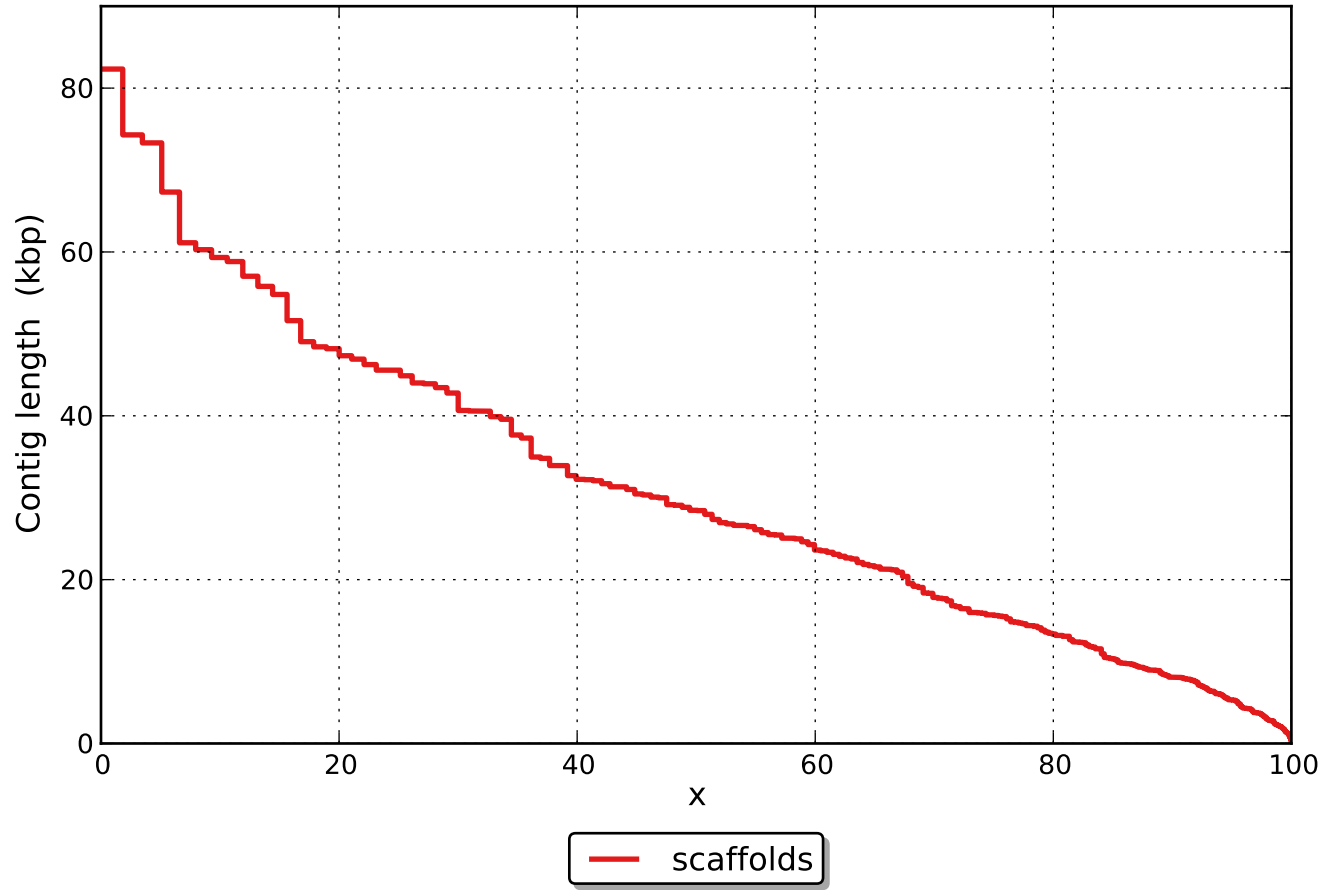




Cumulative length (aligned contigs)



NAx



# NGAx

