

## Report

	scaffolds
# contigs ( $\geq 1000$ bp)	90
# contigs ( $\geq 5000$ bp)	57
# contigs ( $\geq 10000$ bp)	51
# contigs ( $\geq 25000$ bp)	47
# contigs ( $\geq 50000$ bp)	34
Total length ( $\geq 1000$ bp)	4584320
Total length ( $\geq 5000$ bp)	4517868
Total length ( $\geq 10000$ bp)	4475498
Total length ( $\geq 25000$ bp)	4400200
Total length ( $\geq 50000$ bp)	3988767
# contigs	123
Largest contig	330092
Total length	4606871
Reference length	4641652
GC (%)	50.82
Reference GC (%)	50.79
N50	105688
NG50	105688
N75	78911
NG75	78911
L50	13
LG50	13
L75	26
LG75	26
# misassemblies	3
# misassembled contigs	2
Misassembled contigs length	196859
# local misassemblies	5
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	96.361
Duplication ratio	1.030
# N's per 100 kbp	0.00
# mismatches per 100 kbp	931.87
# indels per 100 kbp	0.98
Largest alignment	330092
NA50	102895
NGA50	102895
NA75	65960
NGA75	65960
LA50	13
LGA50	13
LA75	27
LGA75	27

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	3
# relocations	3
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	196859
# local misassemblies	5
# mismatches	41680
# indels	44
# short indels	44
# long indels	0
Indels length	53

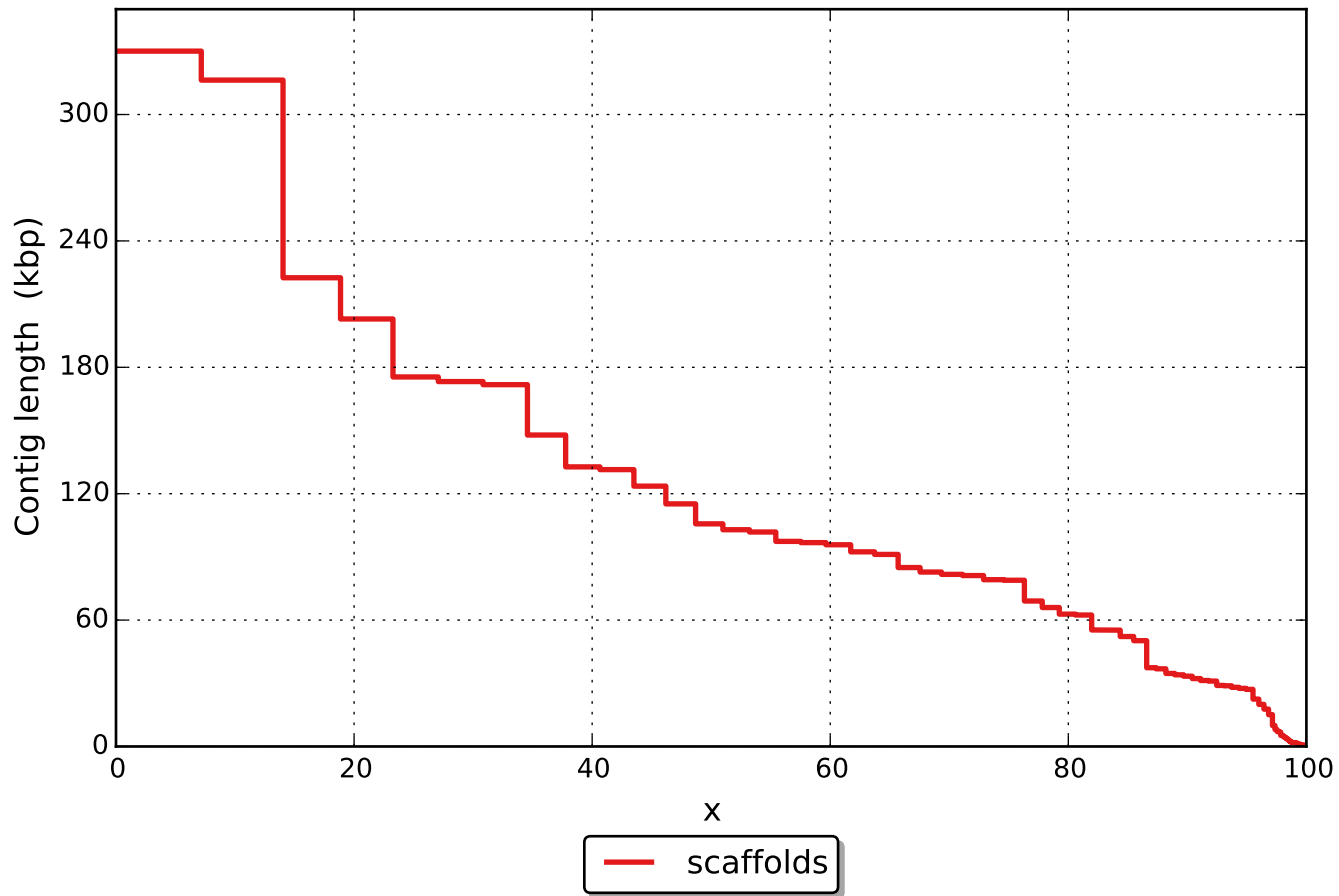
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

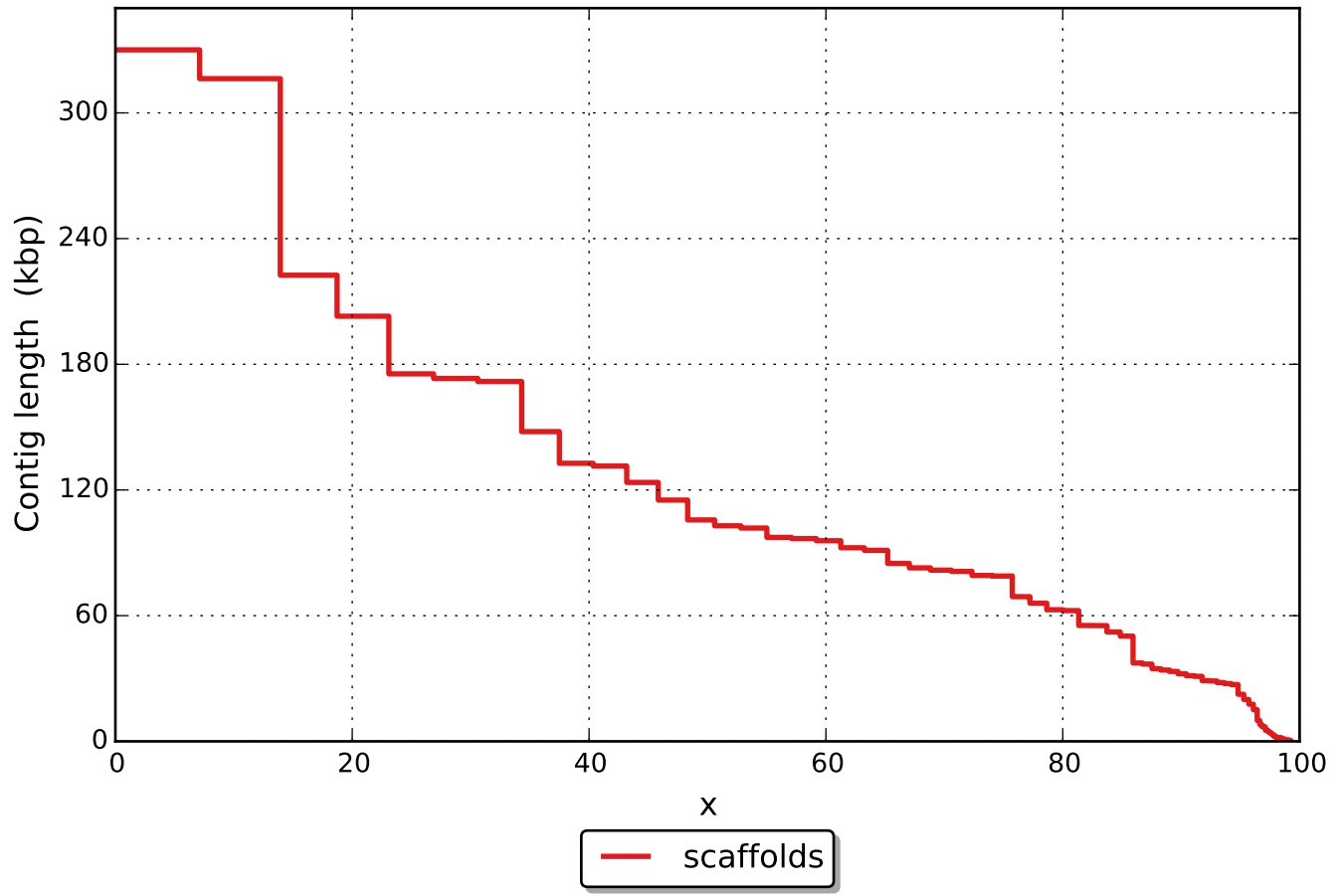
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

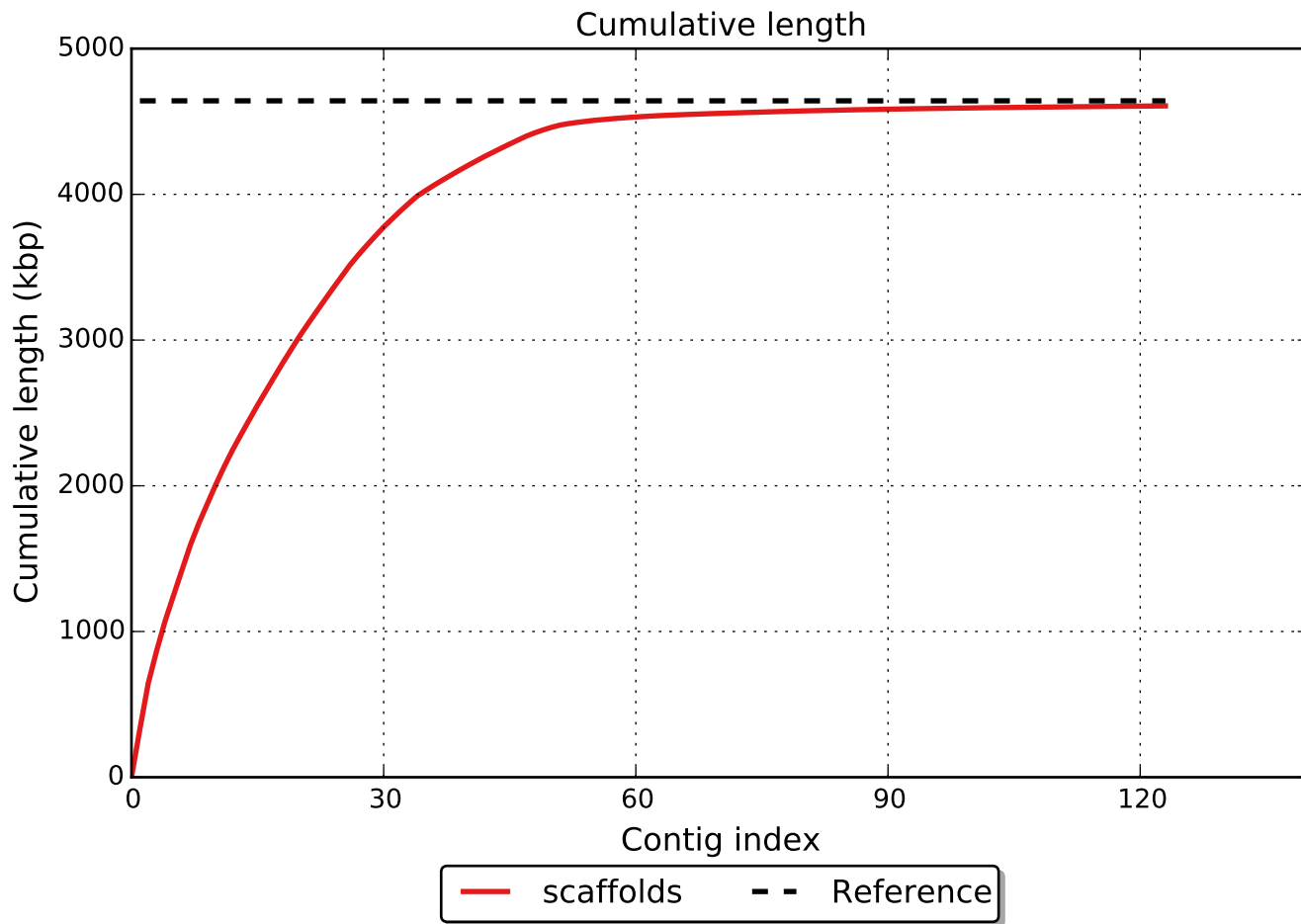
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

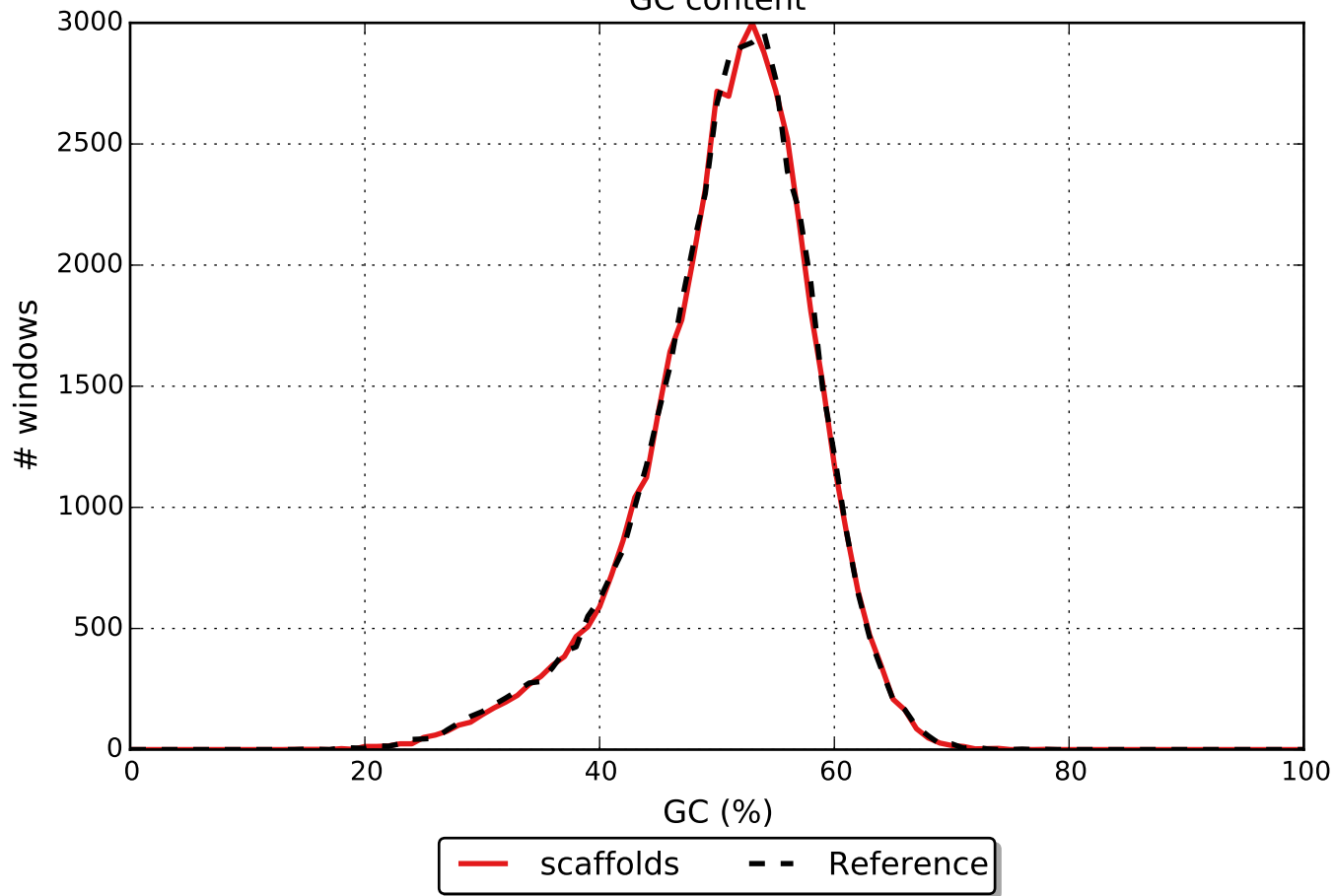


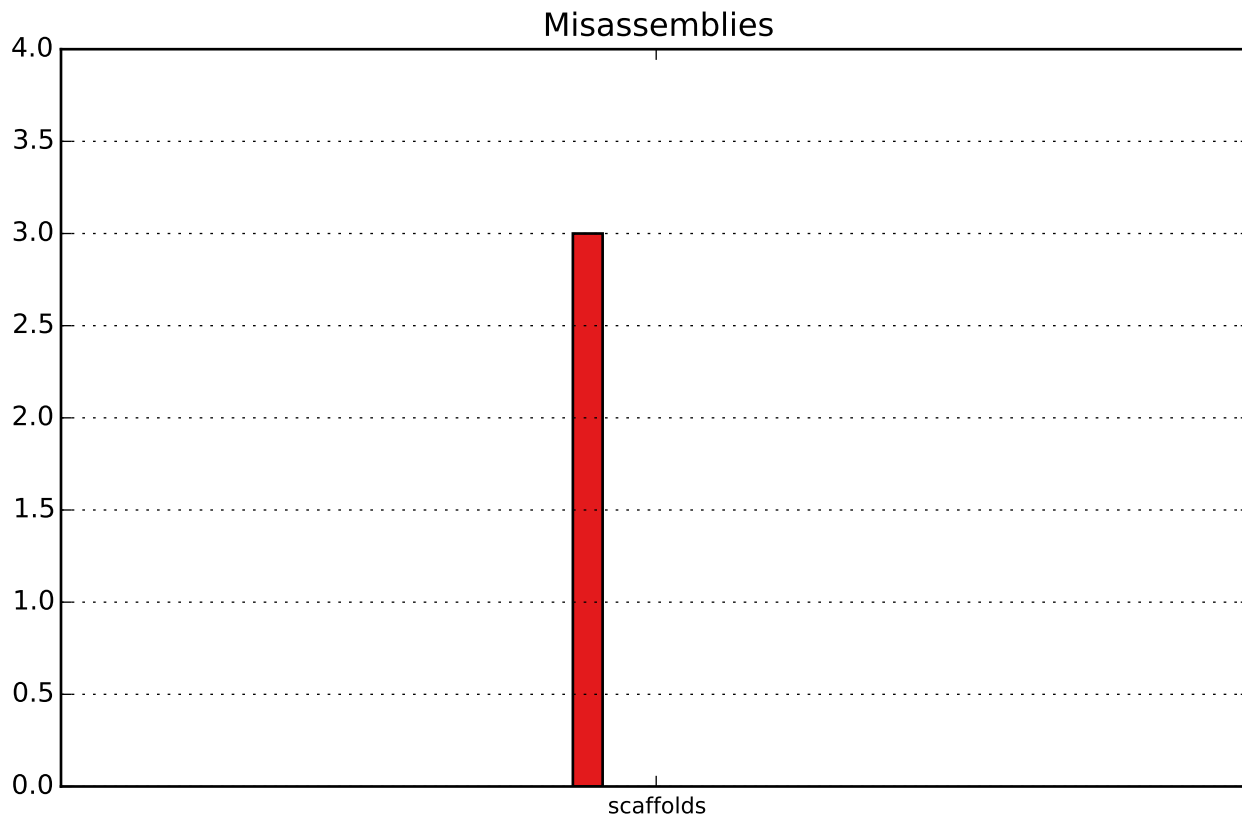
NGx





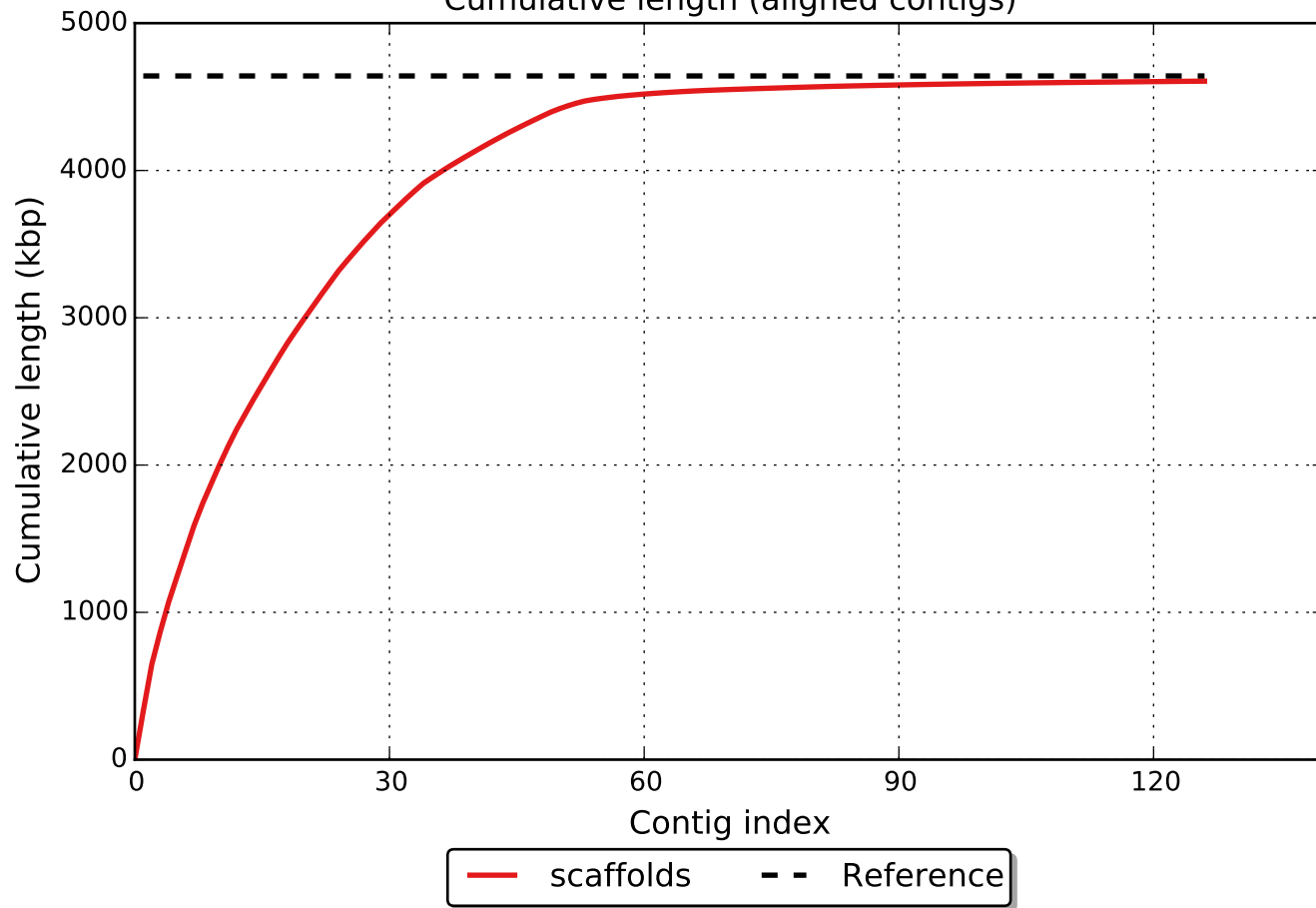
GC content



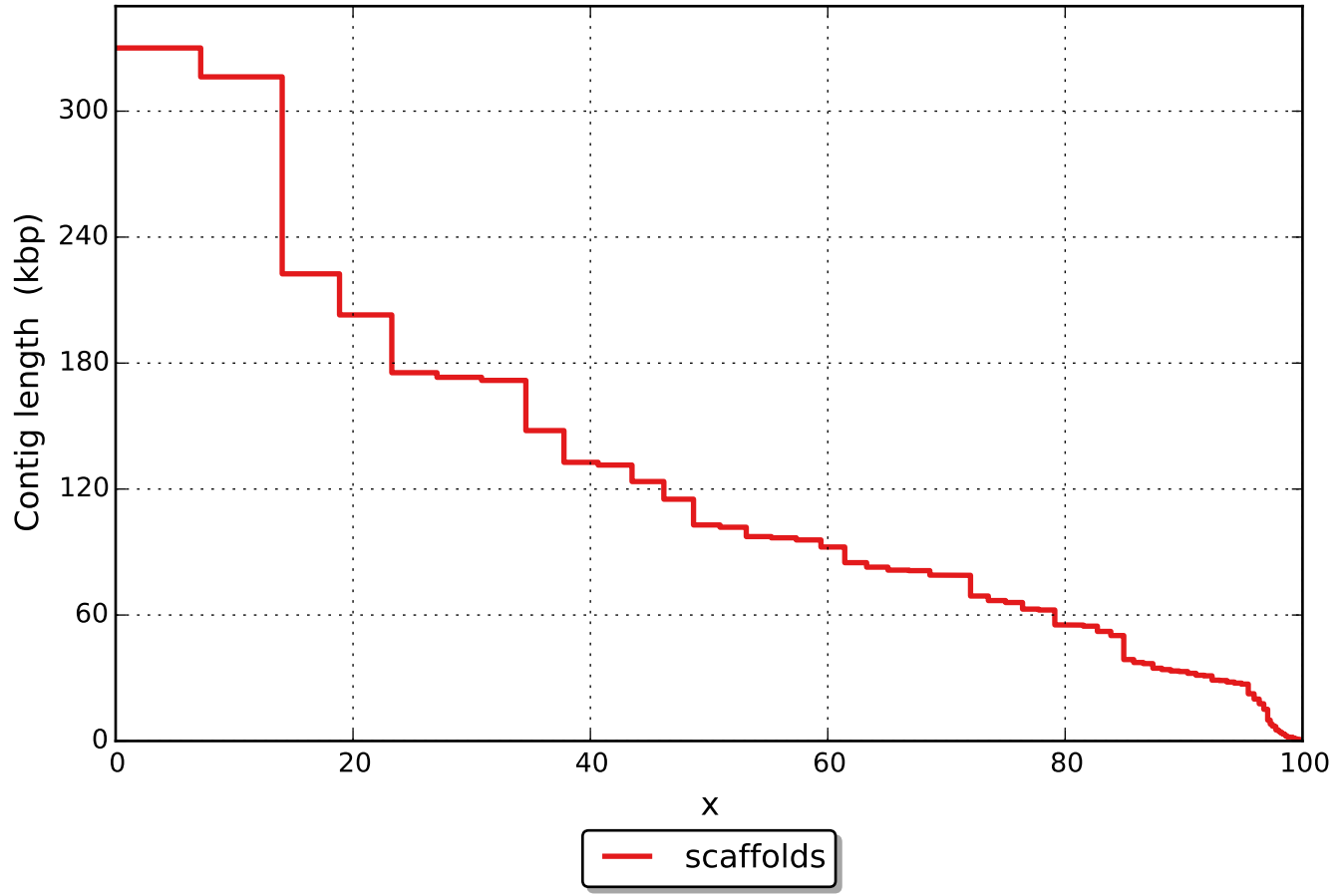




Cumulative length (aligned contigs)



NAx



# NGAx

