

## Report

	scaffolds
# contigs ( $\geq 1000$ bp)	68
# contigs ( $\geq 5000$ bp)	51
# contigs ( $\geq 10000$ bp)	47
# contigs ( $\geq 25000$ bp)	41
# contigs ( $\geq 50000$ bp)	29
Total length ( $\geq 1000$ bp)	4498931
Total length ( $\geq 5000$ bp)	4468204
Total length ( $\geq 10000$ bp)	4435353
Total length ( $\geq 25000$ bp)	4327692
Total length ( $\geq 50000$ bp)	3927946
# contigs	90
Largest contig	332248
Total length	4514743
Reference length	4641652
GC (%)	50.77
Reference GC (%)	50.79
N50	131793
NG50	124889
N75	82061
NG75	80259
L50	11
LG50	12
L75	22
LG75	23
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	82061
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	96.796
Duplication ratio	1.005
# N's per 100 kbp	0.00
# mismatches per 100 kbp	617.86
# indels per 100 kbp	0.76
Largest alignment	332248
NA50	131793
NGA50	124889
NA75	80259
NGA75	79547
LA50	11
LGA50	12
LA75	22
LGA75	23

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	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	82061
# local misassemblies	1
# mismatches	27760
# indels	34
# short indels	34
# long indels	0
Indels length	41

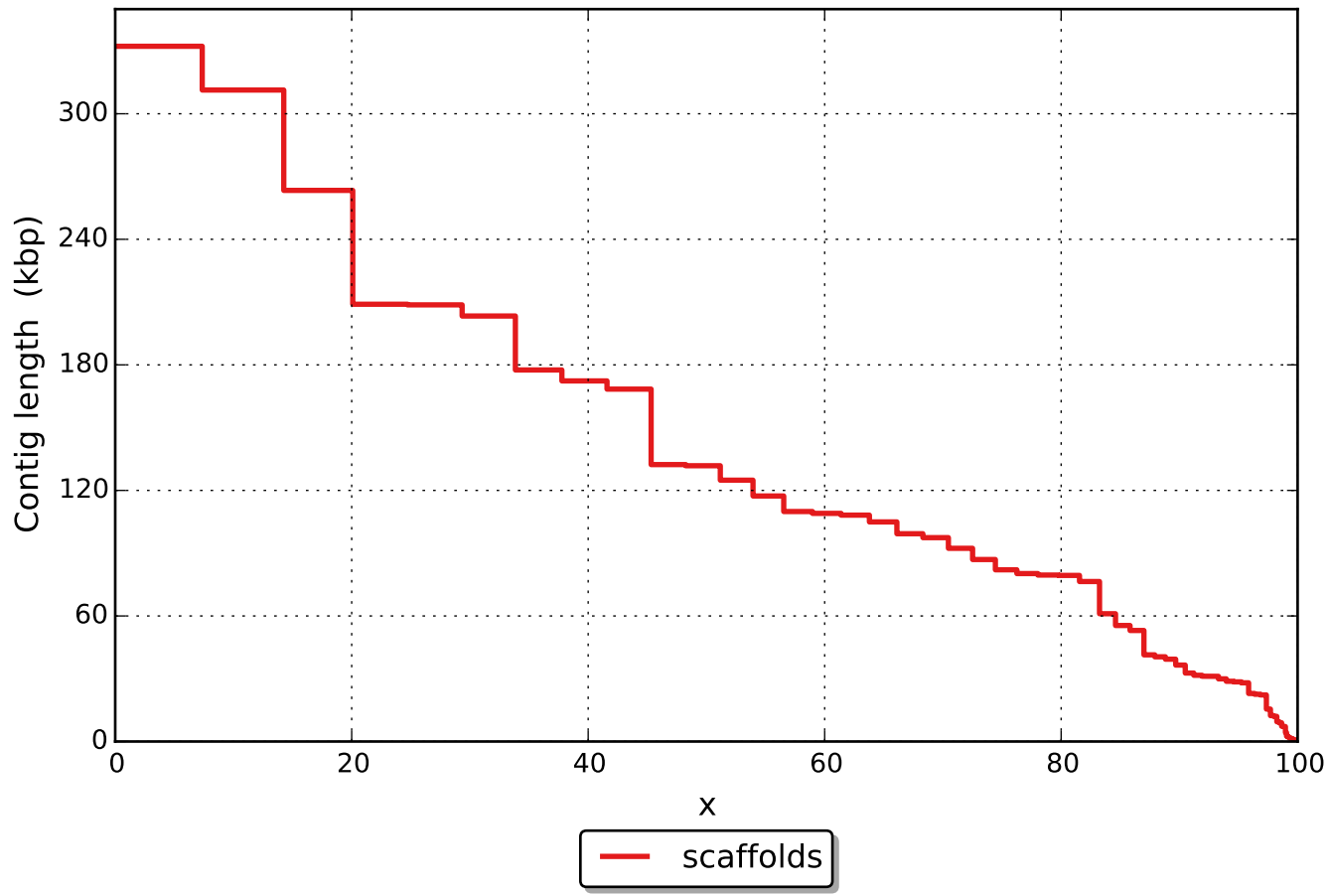
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

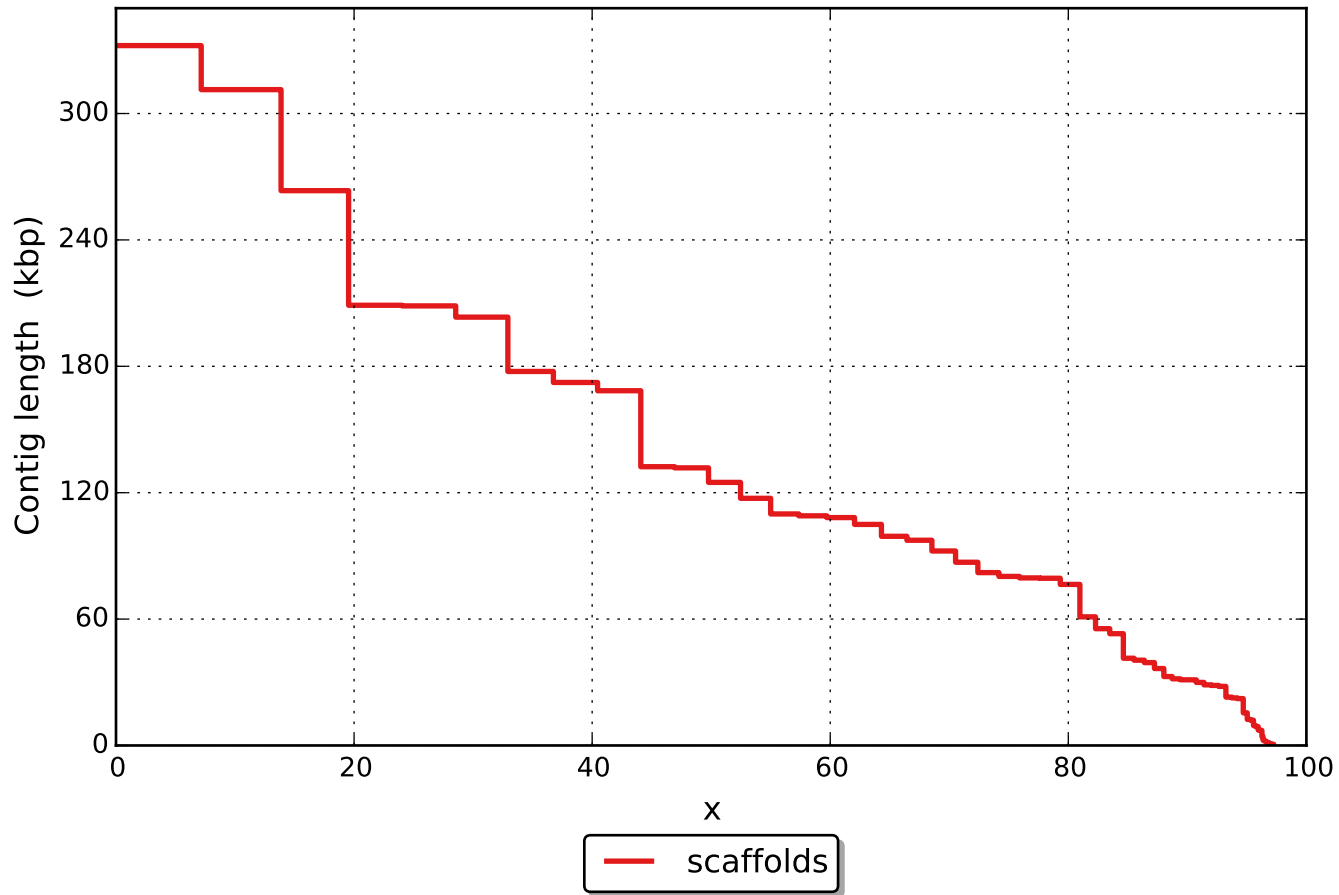
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

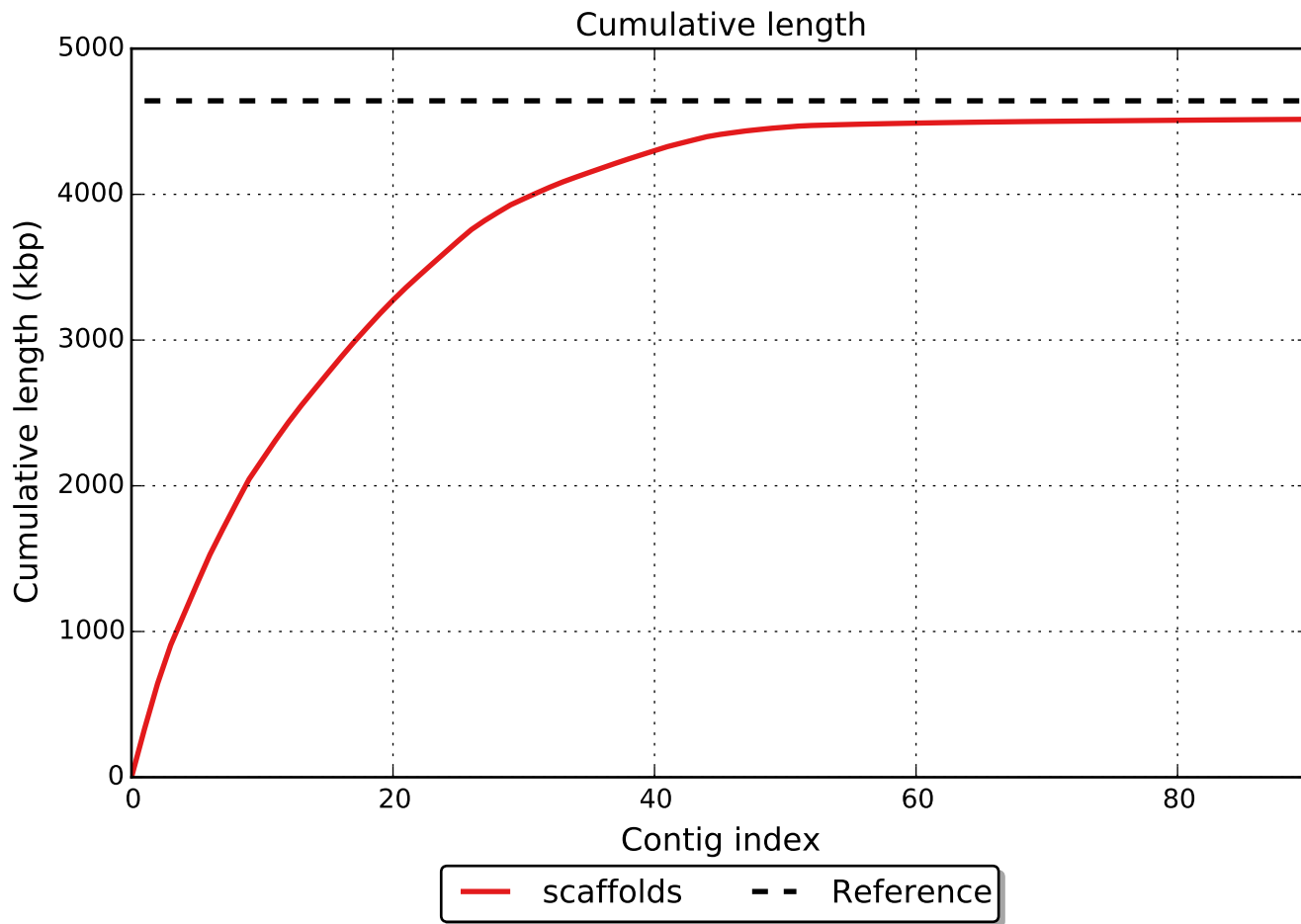
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

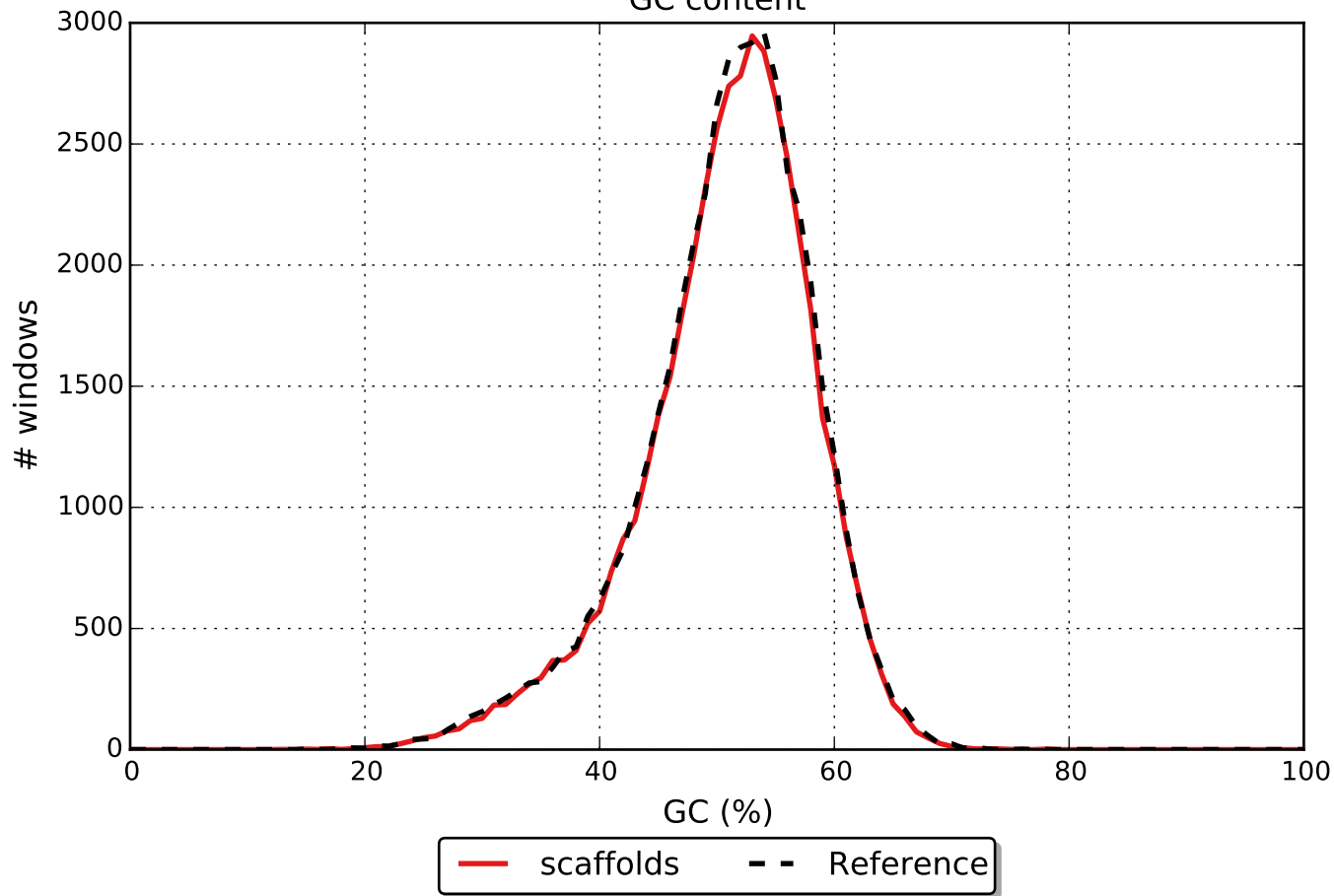


NGx





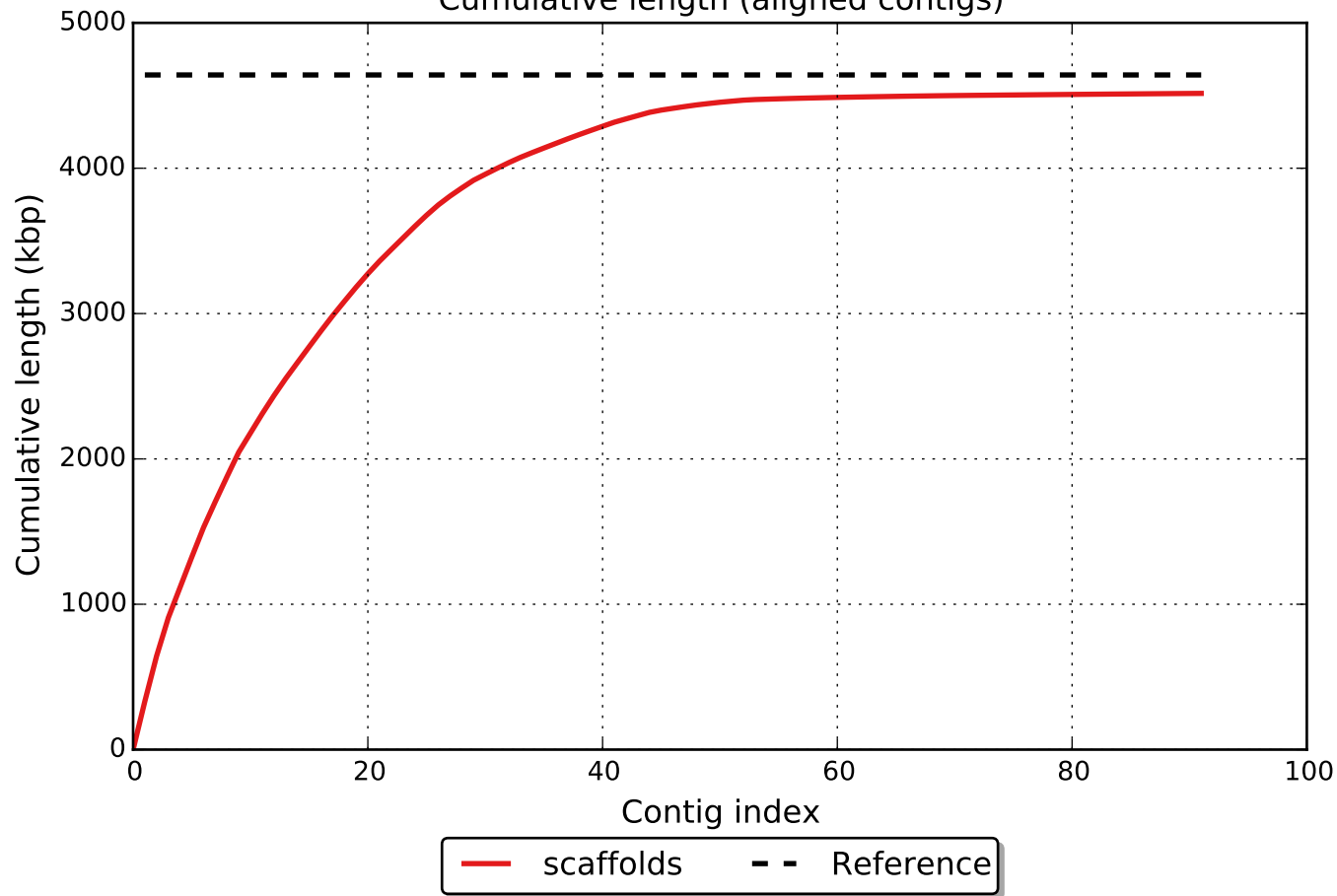
GC content



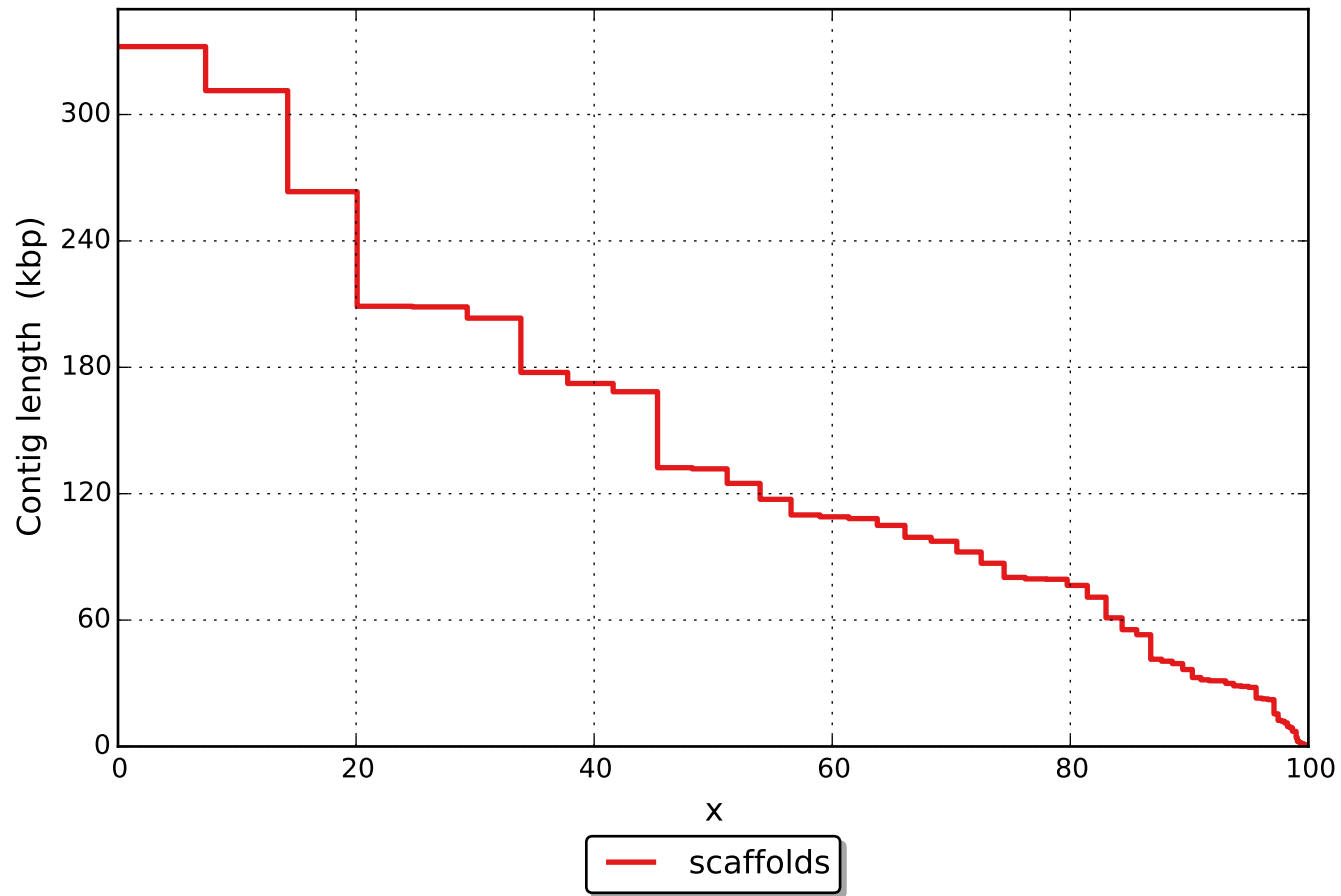




Cumulative length (aligned contigs)



NAx



# NGAx

