

## Report

	scaffolds
# contigs ( $\geq 1000$ bp)	31
# contigs ( $\geq 5000$ bp)	29
# contigs ( $\geq 10000$ bp)	29
# contigs ( $\geq 25000$ bp)	28
# contigs ( $\geq 50000$ bp)	24
Total length ( $\geq 1000$ bp)	5888108
Total length ( $\geq 5000$ bp)	5882473
Total length ( $\geq 10000$ bp)	5882473
Total length ( $\geq 25000$ bp)	5866071
Total length ( $\geq 50000$ bp)	5734661
# contigs	33
Largest contig	768359
Total length	5889637
Reference length	4641652
GC (%)	50.72
Reference GC (%)	50.79
N50	376748
NG50	404504
N75	197282
NG75	302312
L50	6
LG50	5
L75	12
LG75	8
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	768359
# local misassemblies	1
# unaligned contigs	0 + 11 part
Unaligned length	1096425
Genome fraction (%)	99.487
Duplication ratio	1.038
# N's per 100 kbp	1.63
# mismatches per 100 kbp	299.32
# indels per 100 kbp	1.04
Largest alignment	607862
NA50	368567
NGA50	404504
NA75	70043
NGA75	302312
LA50	7
LGA50	5
LA75	15
LGA75	8

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	6
# misassembled contigs	1
Misassembled contigs length	768359
# local misassemblies	1
# mismatches	13822
# indels	48
# short indels	48
# long indels	0
Indels length	55

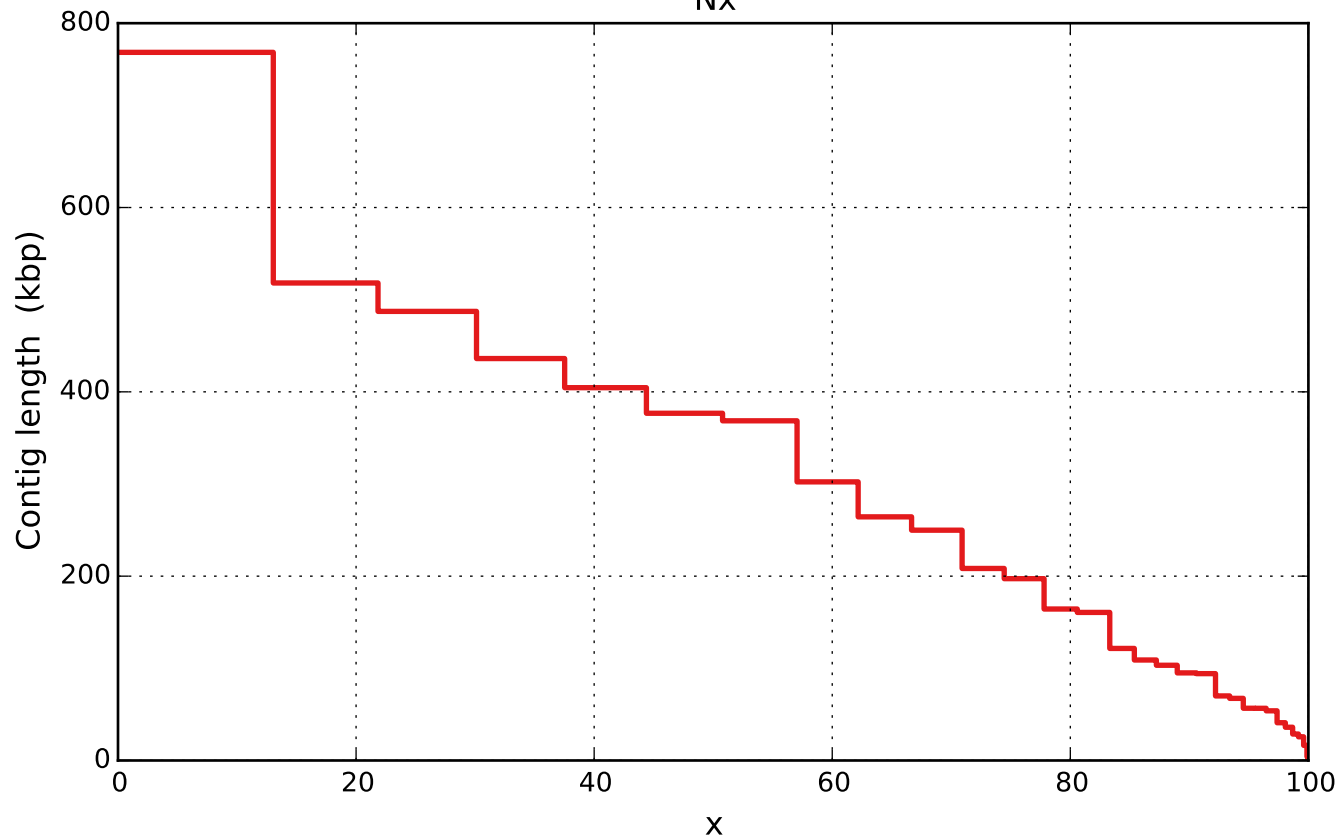
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	11
# with misassembly	2
# both parts are significant	5
Partially unaligned length	1096425
# N's	96

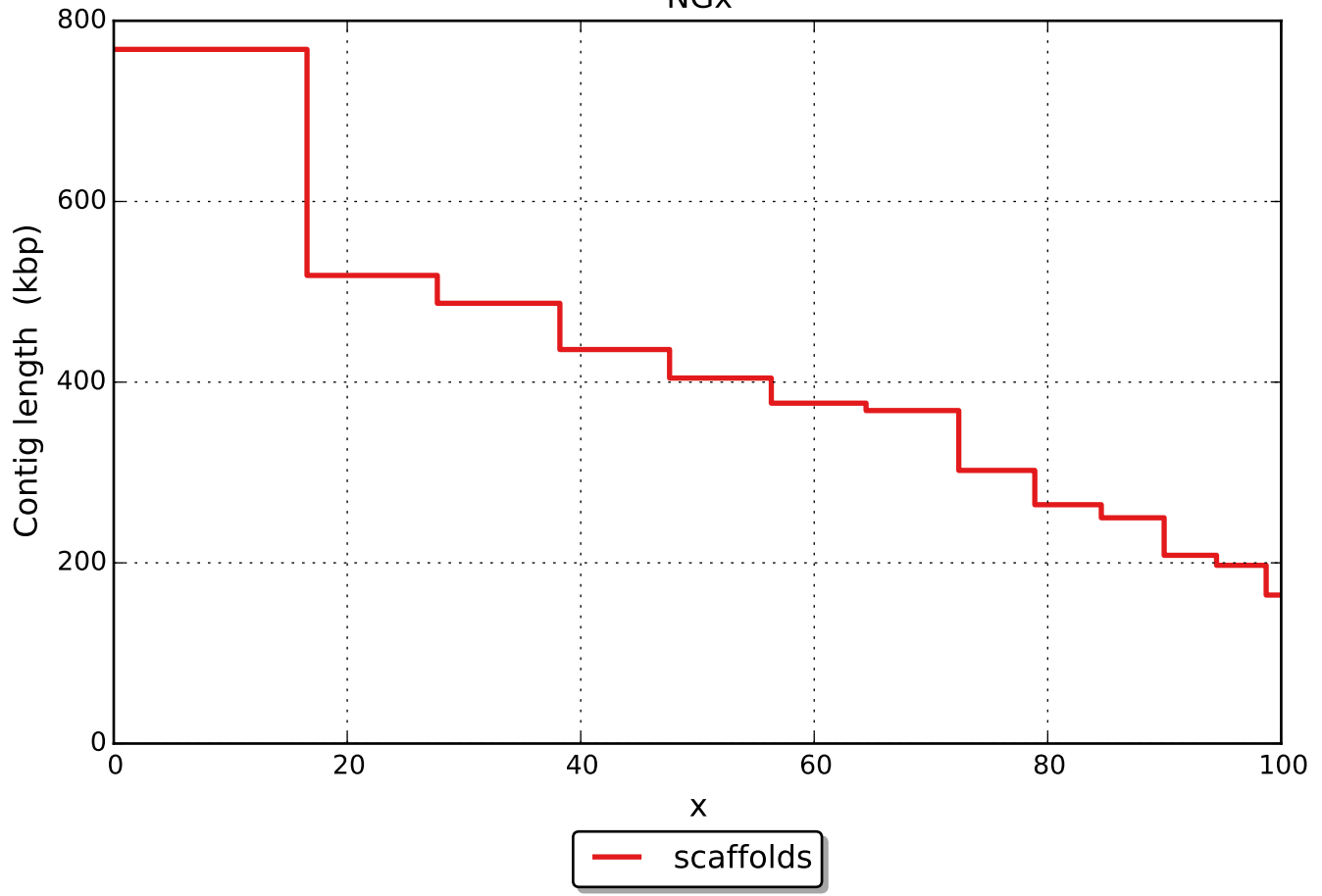
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

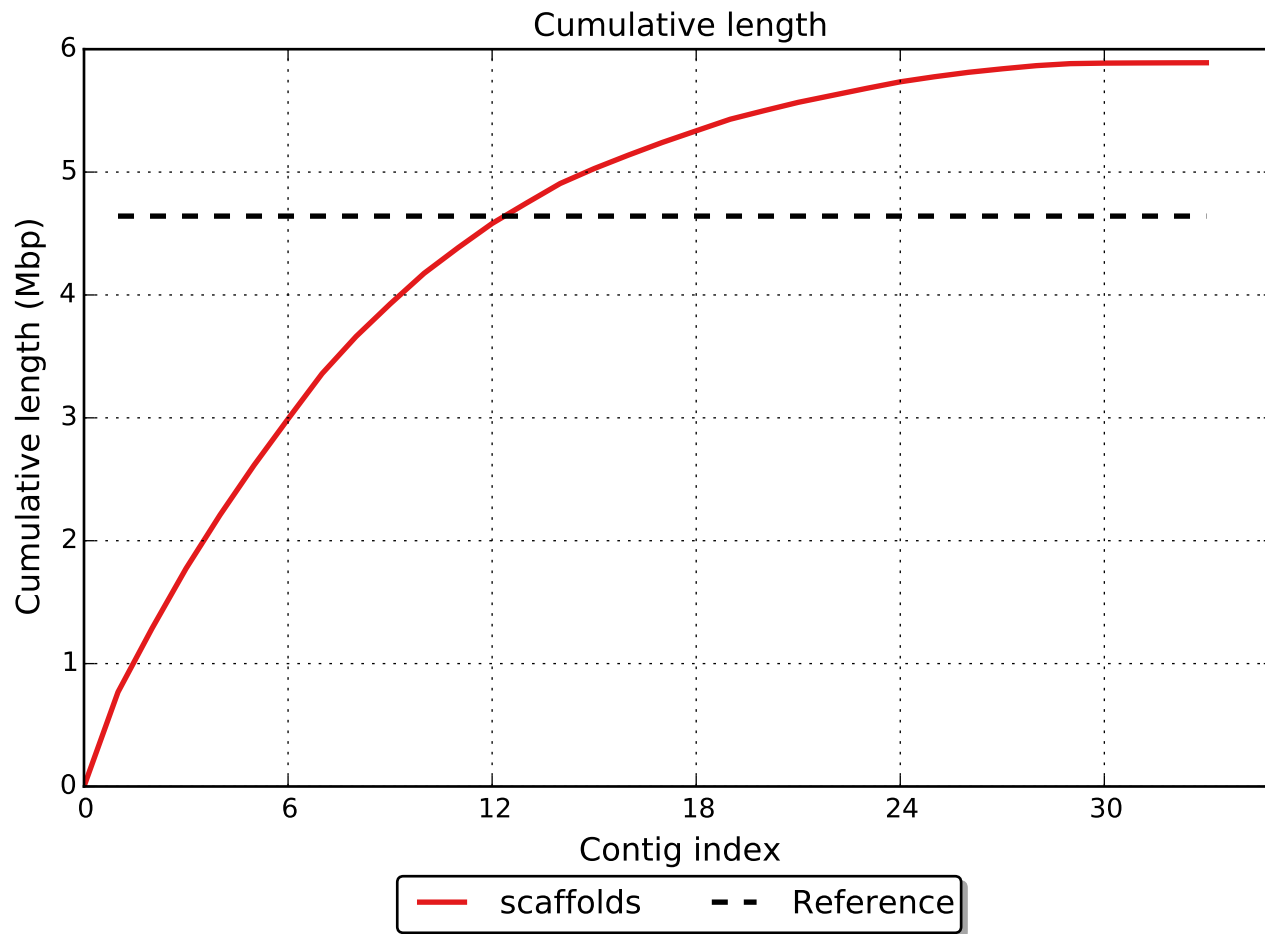
Nx



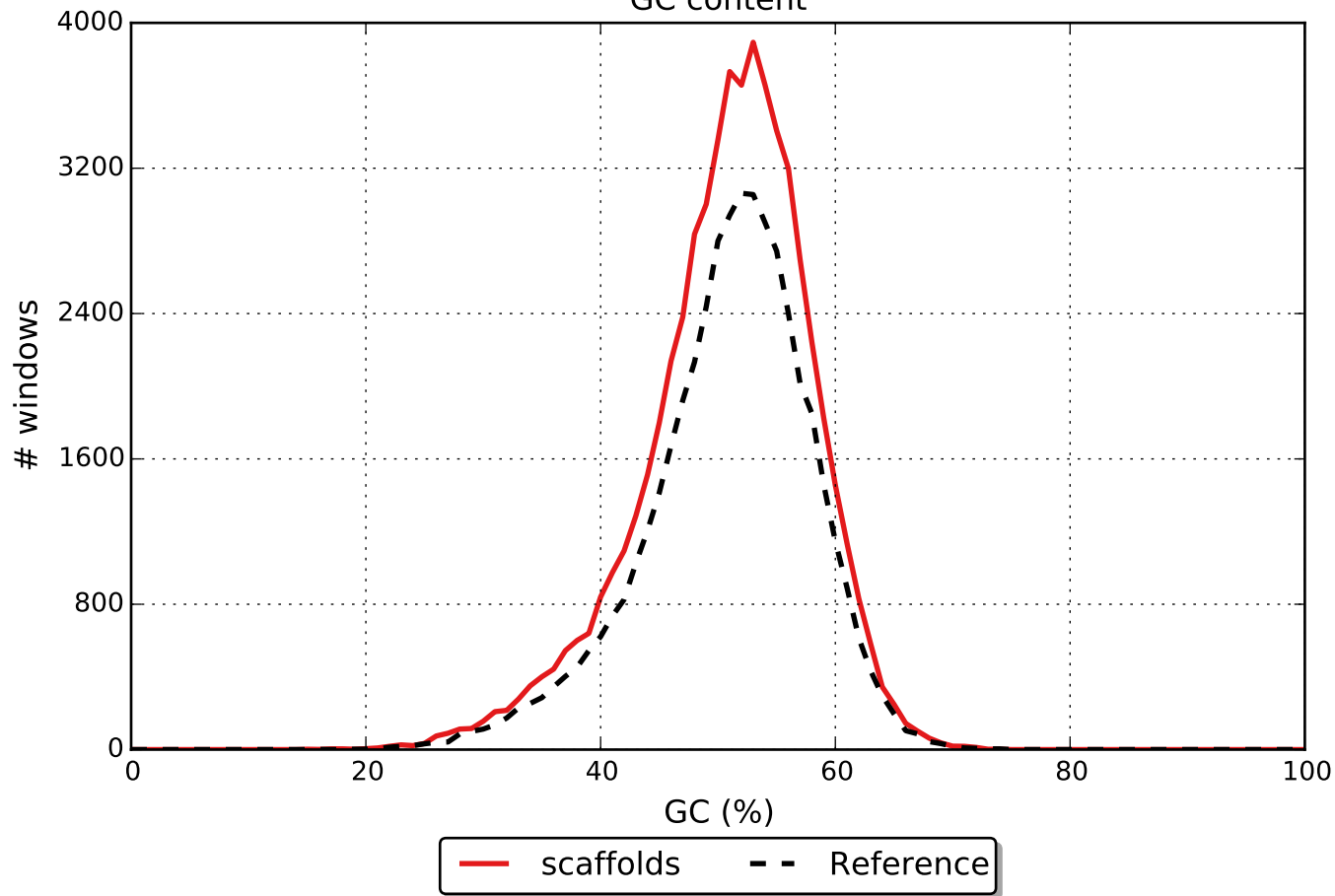
scaffolds

NGx





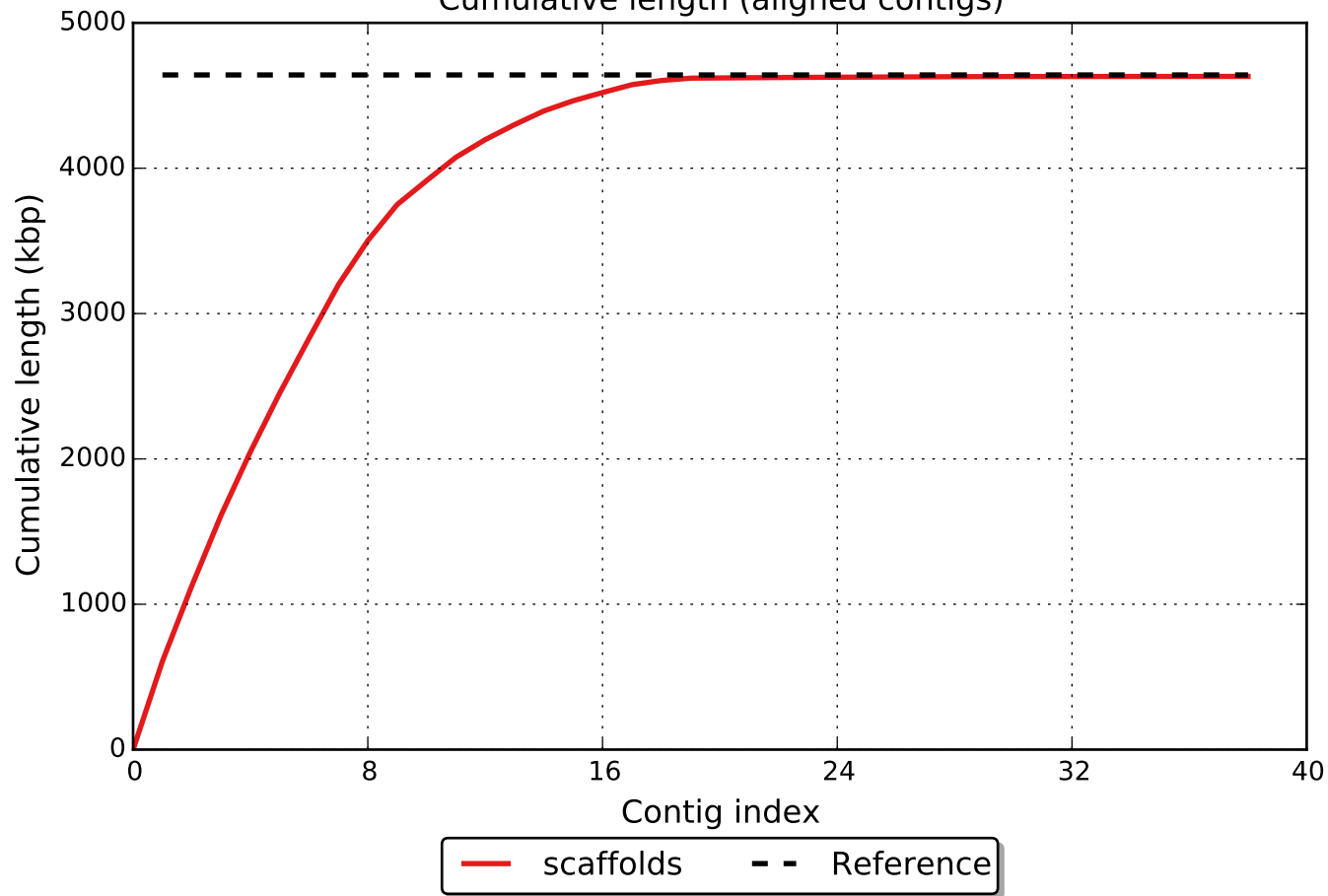
# GC content



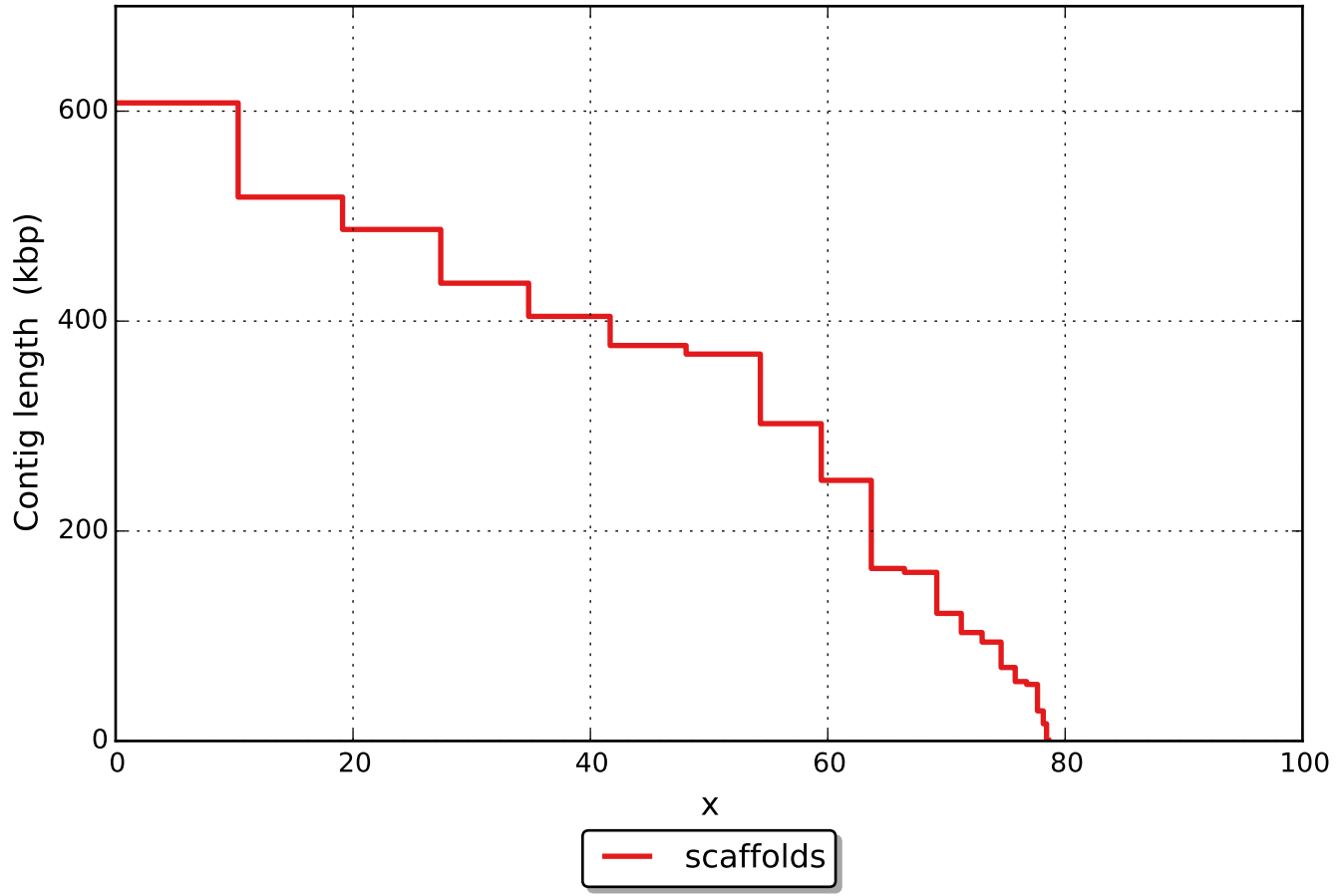




Cumulative length (aligned contigs)



NAx



# NGAx

