

## Report

	scaffolds
# contigs ( $\geq 1000$ bp)	20
# contigs ( $\geq 5000$ bp)	19
# contigs ( $\geq 10000$ bp)	19
# contigs ( $\geq 25000$ bp)	18
# contigs ( $\geq 50000$ bp)	17
Total length ( $\geq 1000$ bp)	4783047
Total length ( $\geq 5000$ bp)	4781640
Total length ( $\geq 10000$ bp)	4781640
Total length ( $\geq 25000$ bp)	4765238
Total length ( $\geq 50000$ bp)	4736548
# contigs	22
Largest contig	768359
Total length	4784576
Reference length	4641652
GC (%)	50.71
Reference GC (%)	50.79
N50	404504
NG50	404504
N75	302312
NG75	302312
L50	5
LG50	5
L75	8
LG75	8
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	768359
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.487
Duplication ratio	1.036
# N's per 100 kbp	2.01
# mismatches per 100 kbp	299.32
# indels per 100 kbp	1.04
Largest alignment	607862
NA50	404504
NGA50	404504
NA75	248289
NGA75	302312
LA50	5
LGA50	5
LA75	9
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	1
# misassembled contigs	1
Misassembled contigs length	768359
# local misassemblies	1
# mismatches	13822
# indels	48
# short indels	48
# long indels	0
Indels length	55

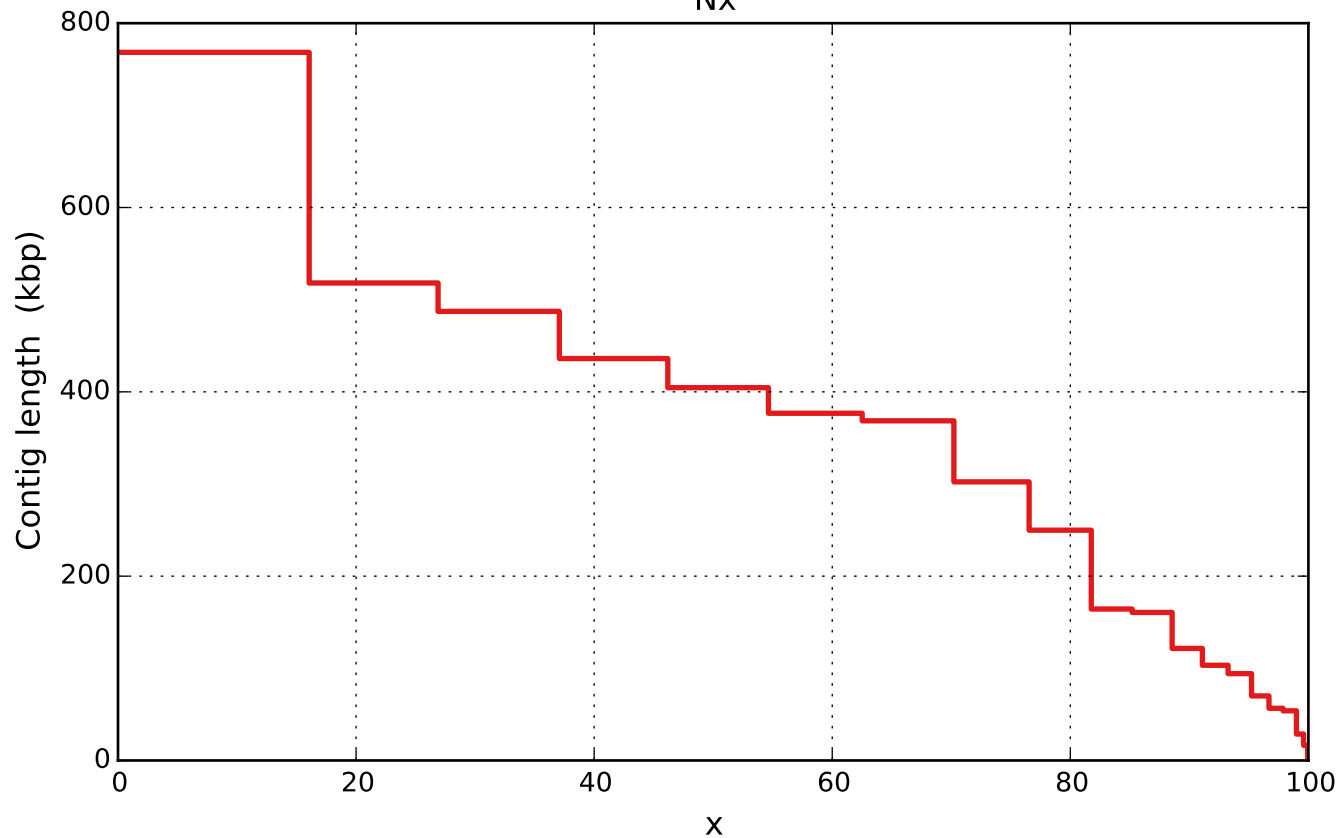
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

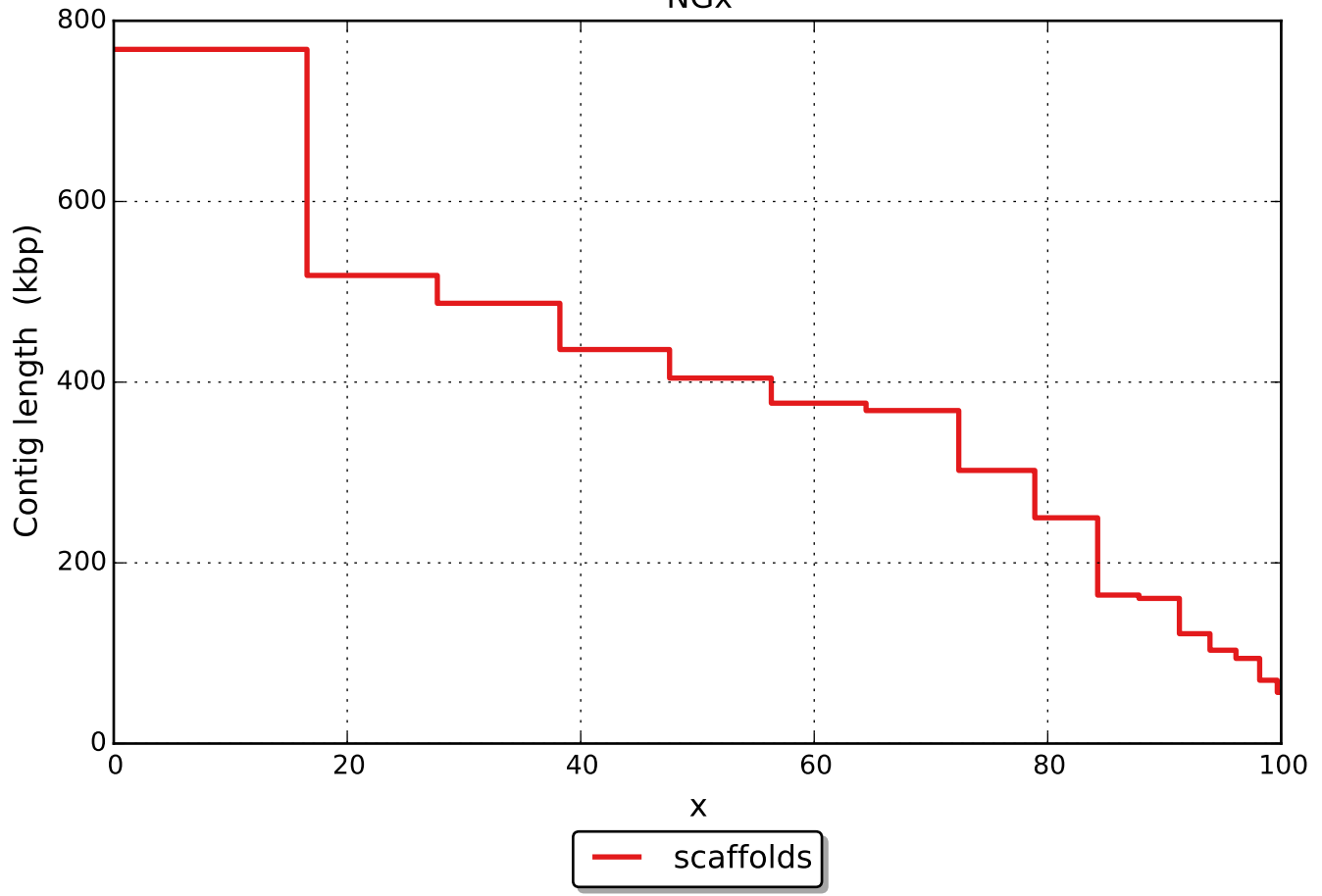
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	96

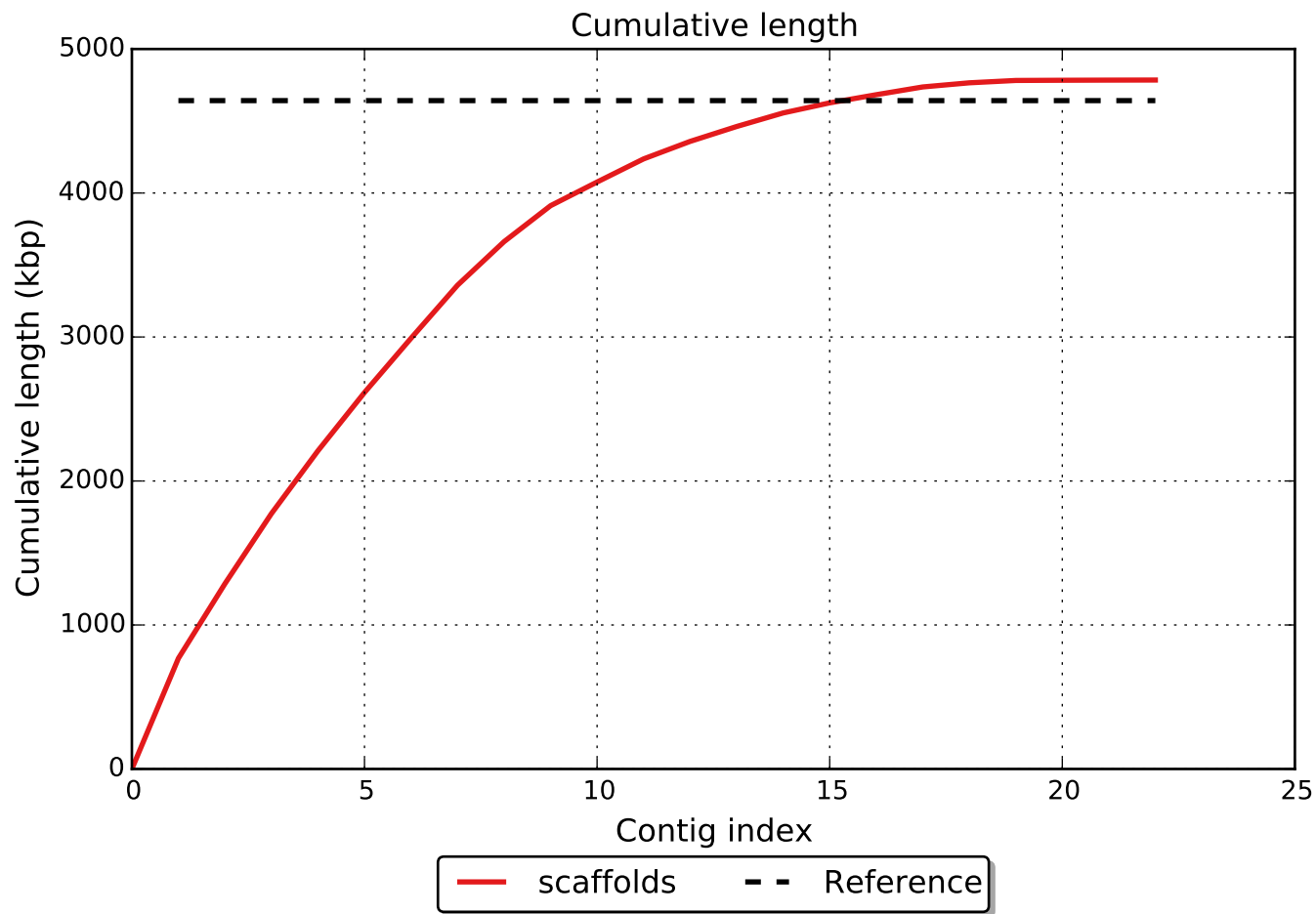
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

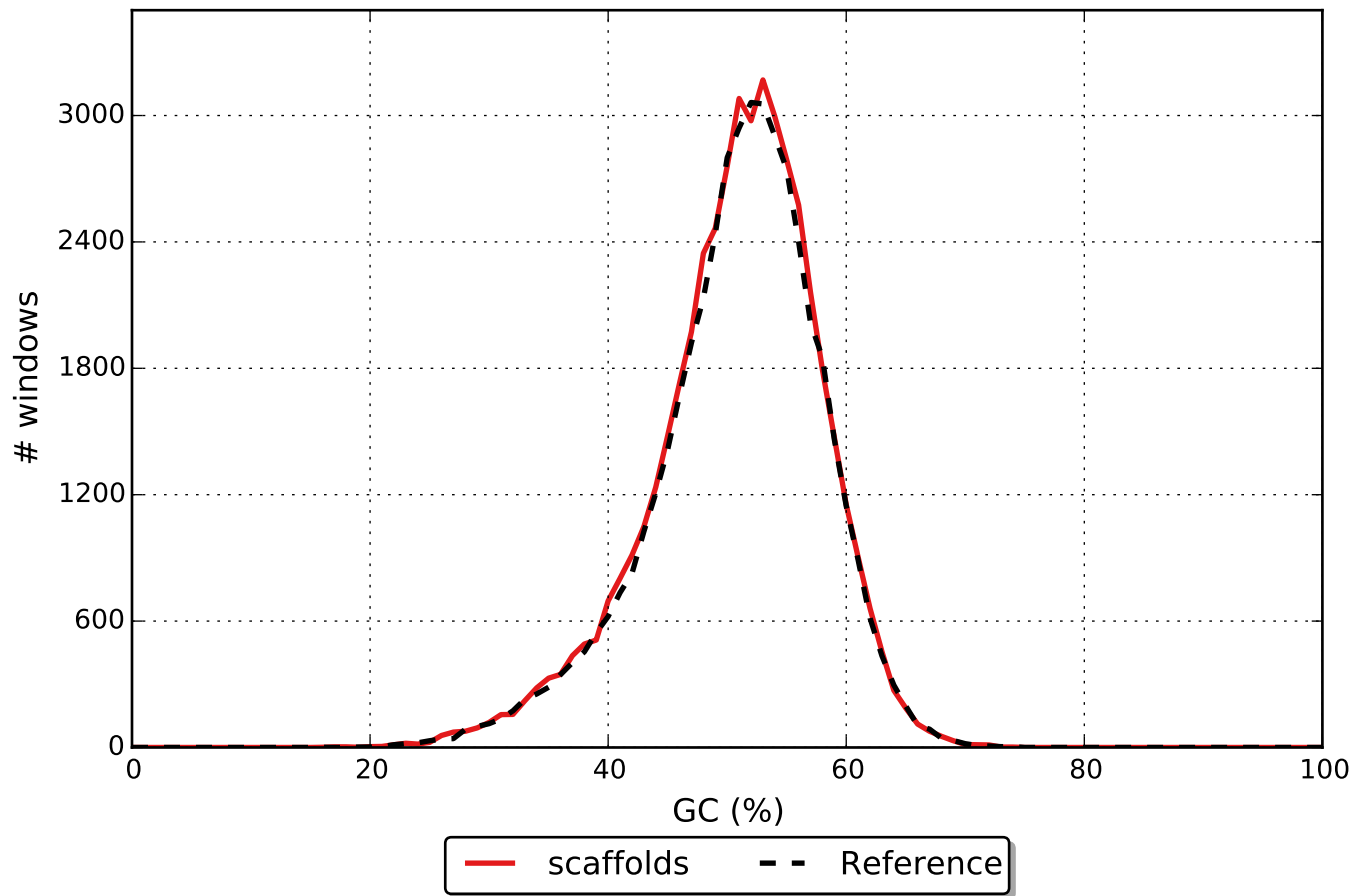


NGx





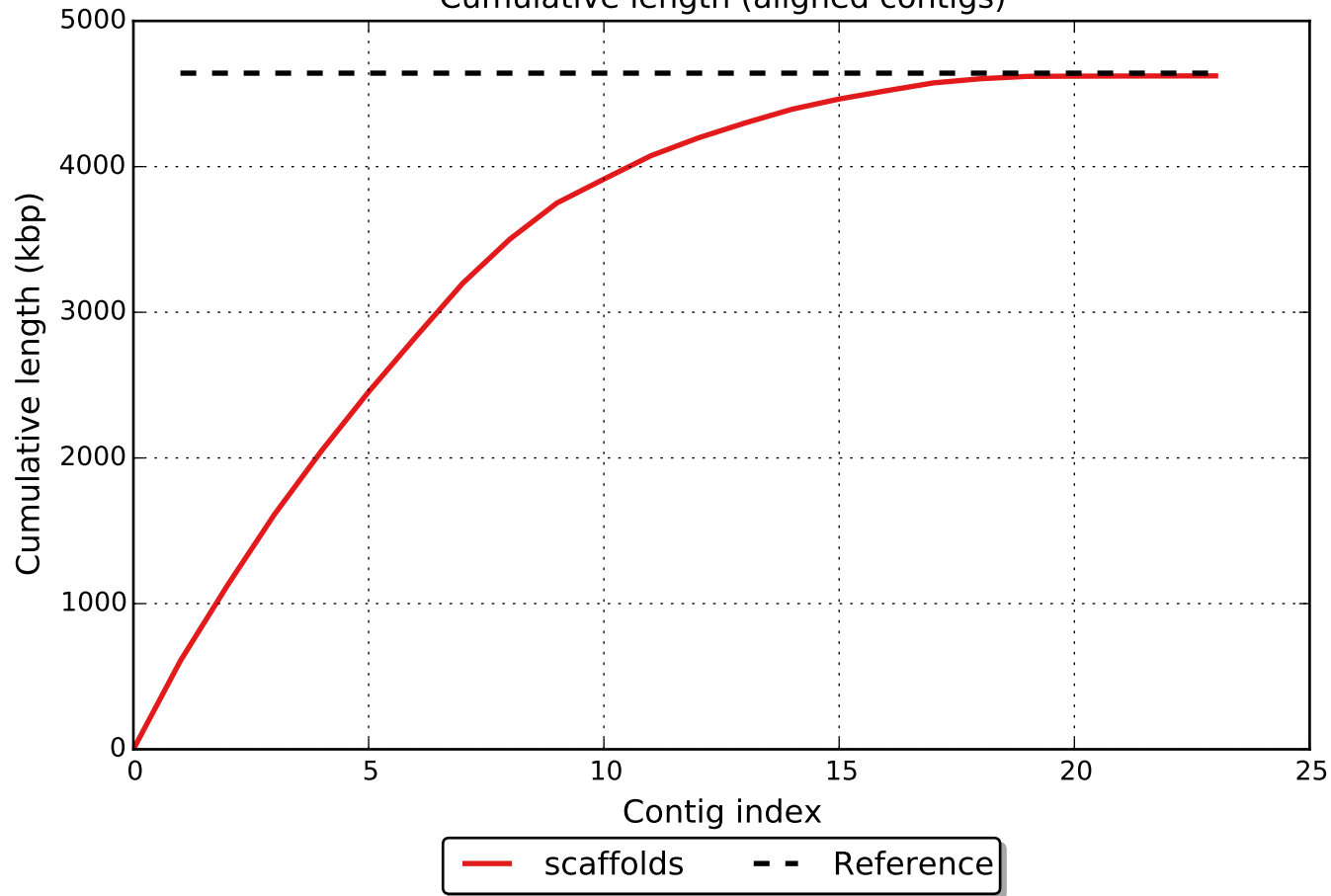
GC content



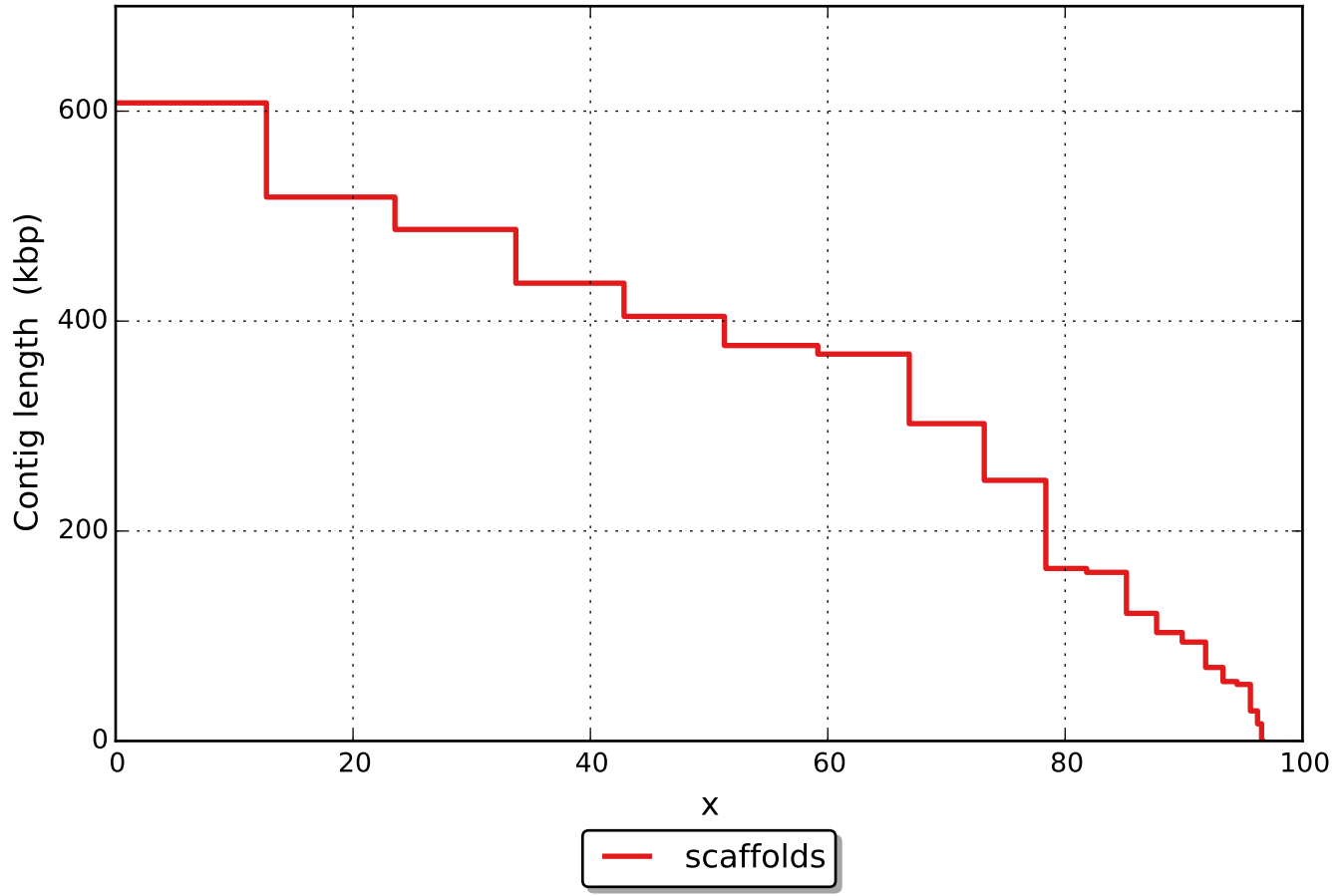




Cumulative length (aligned contigs)



NAx



# NGAx

