

Report

	scaffolds
# contigs (>= 1000 bp)	72
# contigs (>= 5000 bp)	50
# contigs (>= 10000 bp)	47
# contigs (>= 25000 bp)	41
# contigs (>= 50000 bp)	27
Total length (>= 1000 bp)	4556760
Total length (>= 5000 bp)	4506360
Total length (>= 10000 bp)	4482290
Total length (>= 25000 bp)	4392918
Total length (>= 50000 bp)	3900785
# contigs	79
Largest contig	327053
Total length	4562036
Reference length	4641652
GC (▼)	50.75
Reference GC (▼)	50.79
N50	173981
NG50	173981
N75	87064
NG75	78619
L50	10
LG50	10
L75	20
LG75	21
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (▼)	98.228
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	59.26
# indels per 100 kbp	8.27
Largest alignment	327053
NA50	173981
NGA50	173981
NA75	87064
NGA75	78619
LA50	10
LGA50	10
LA75	20
LGA75	21

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	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# mismatches	2702
# indels	377
# short indels	377
# long indels	0
Indels length	544

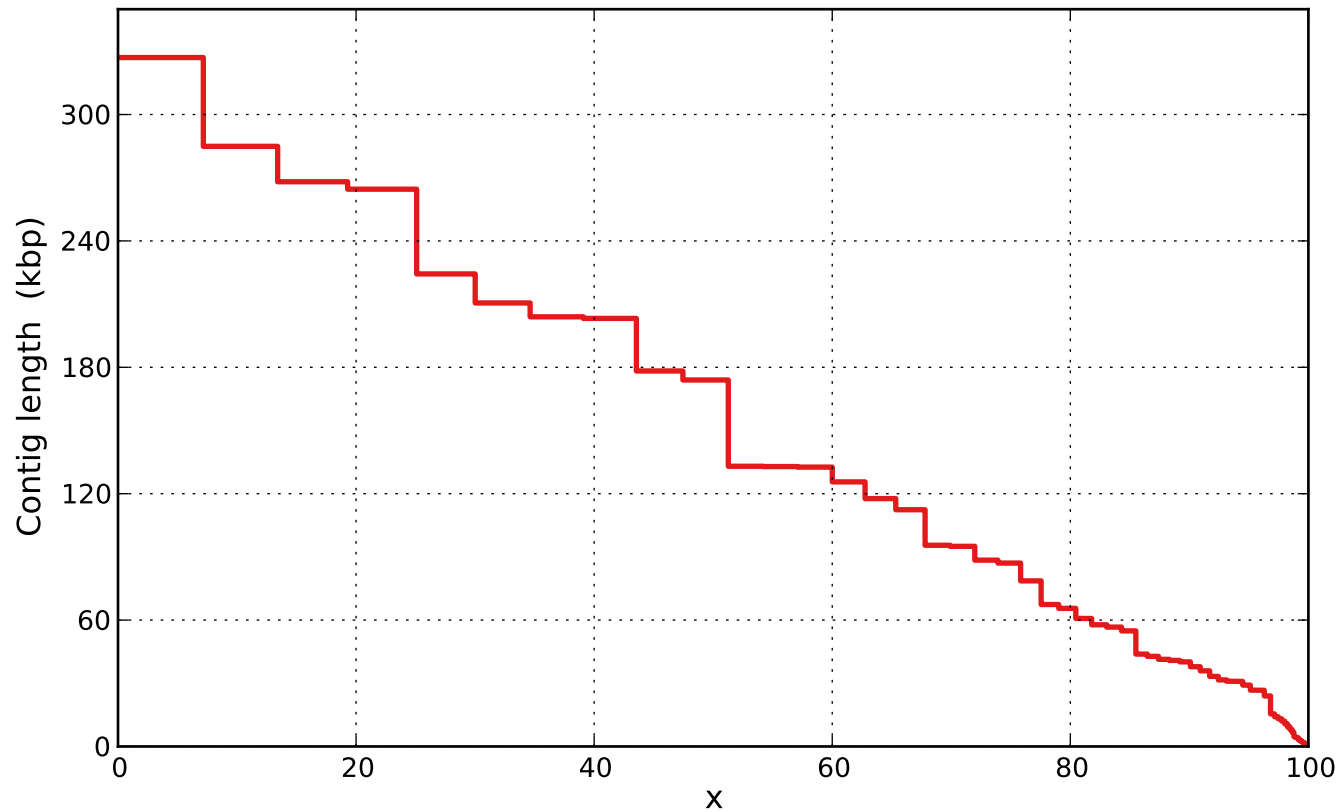
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

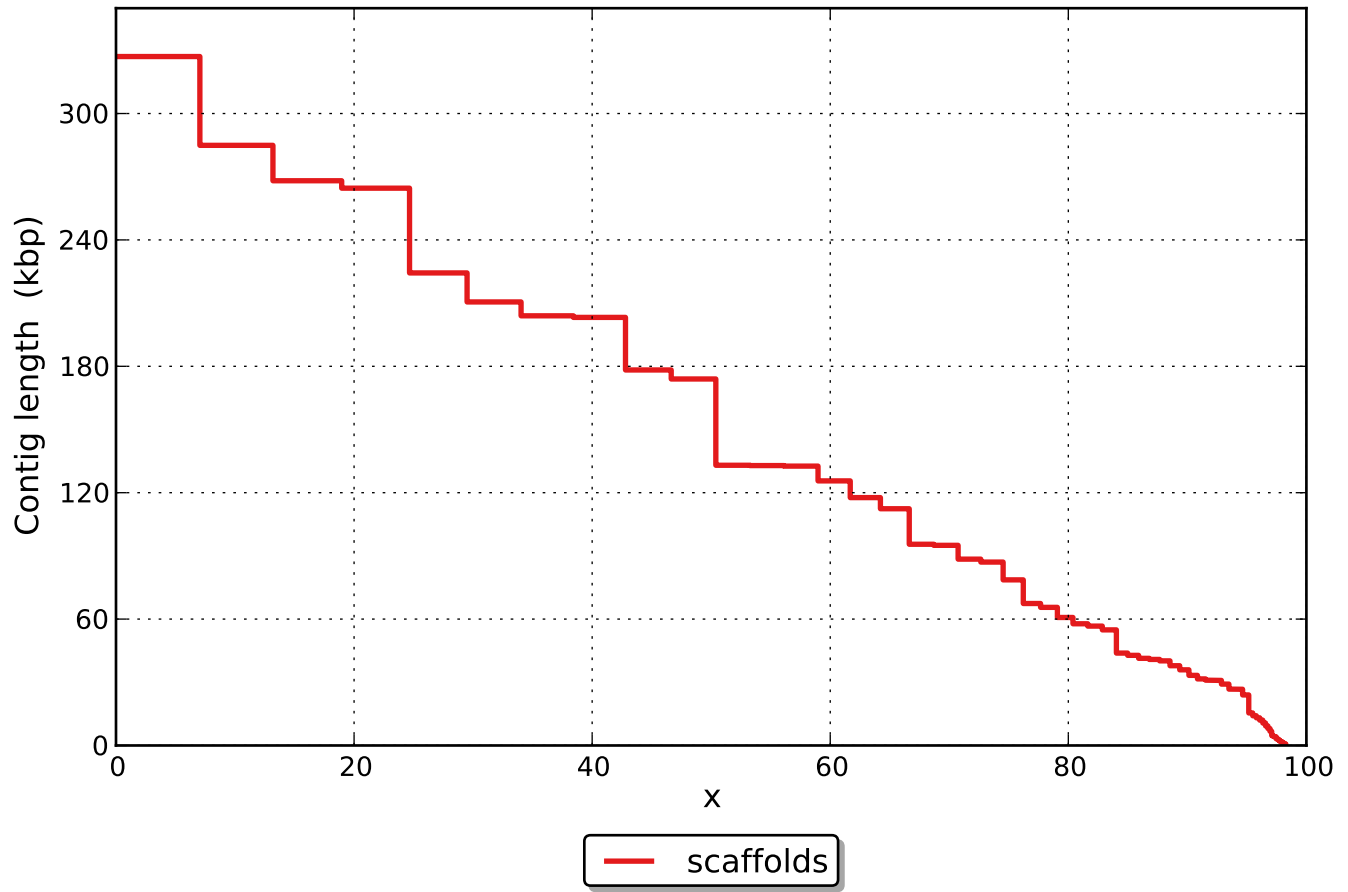
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

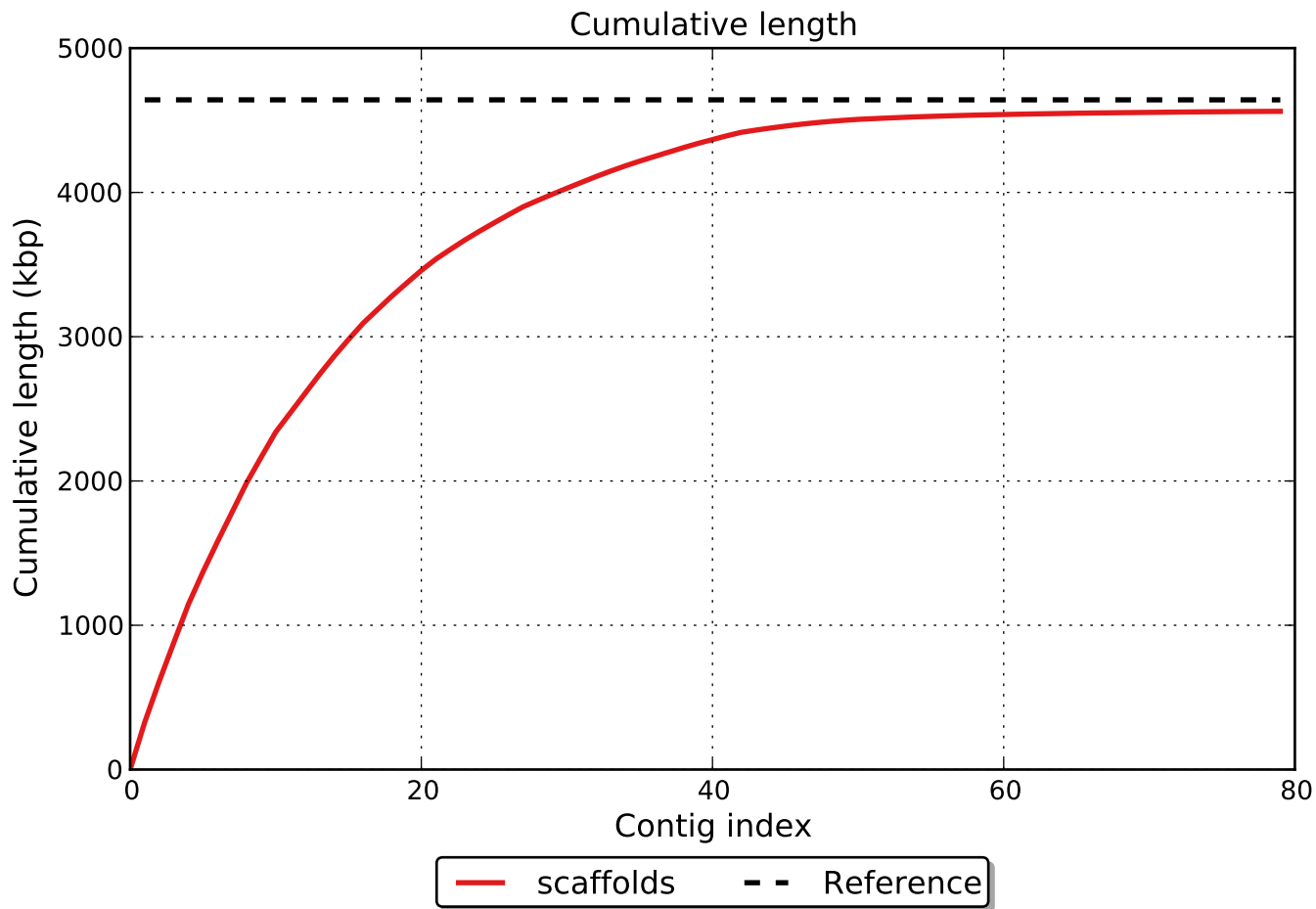
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

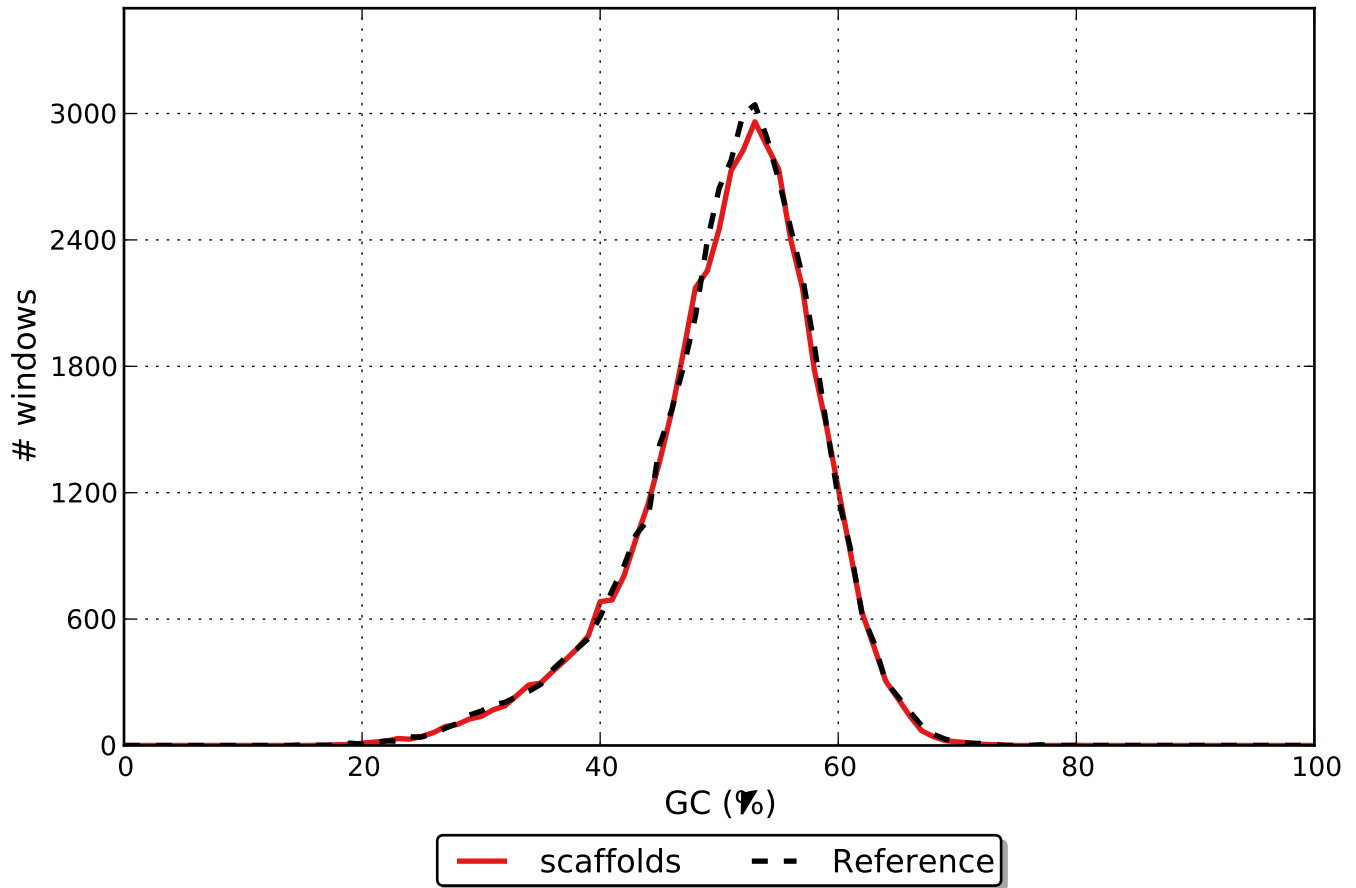


NGx

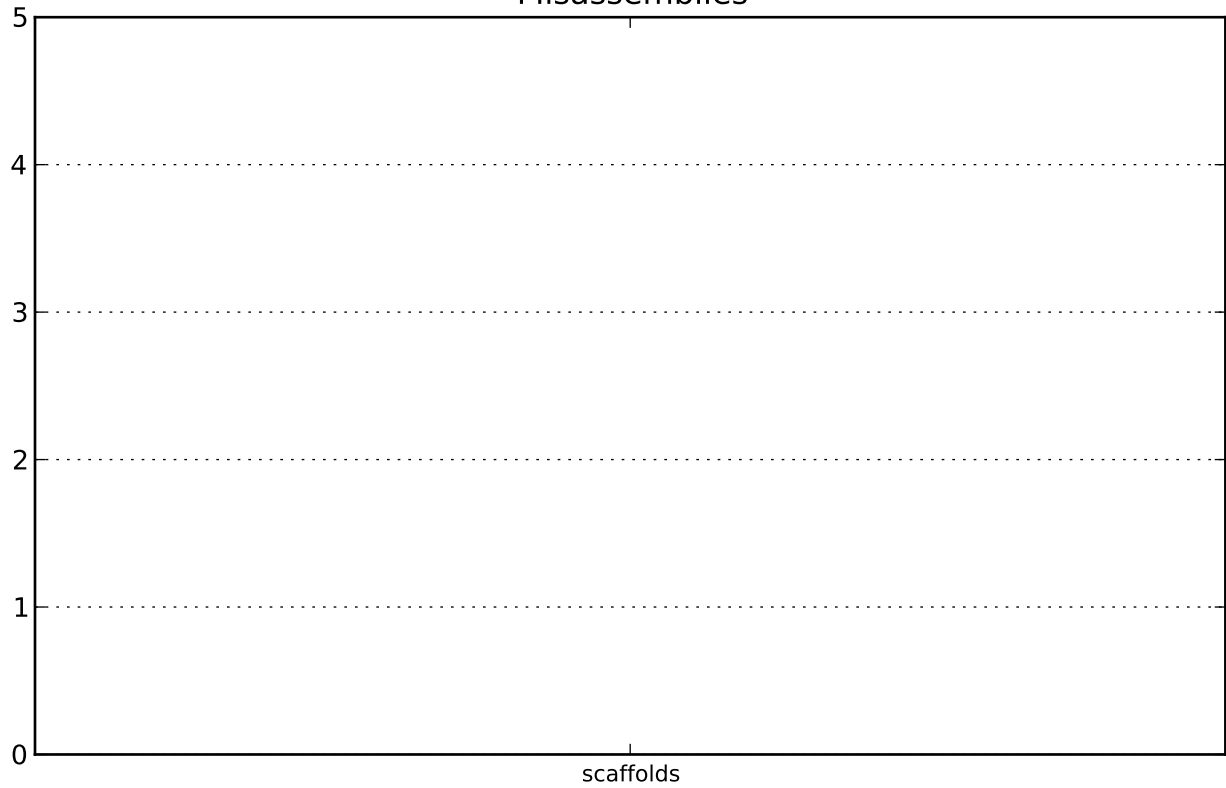




# GC content

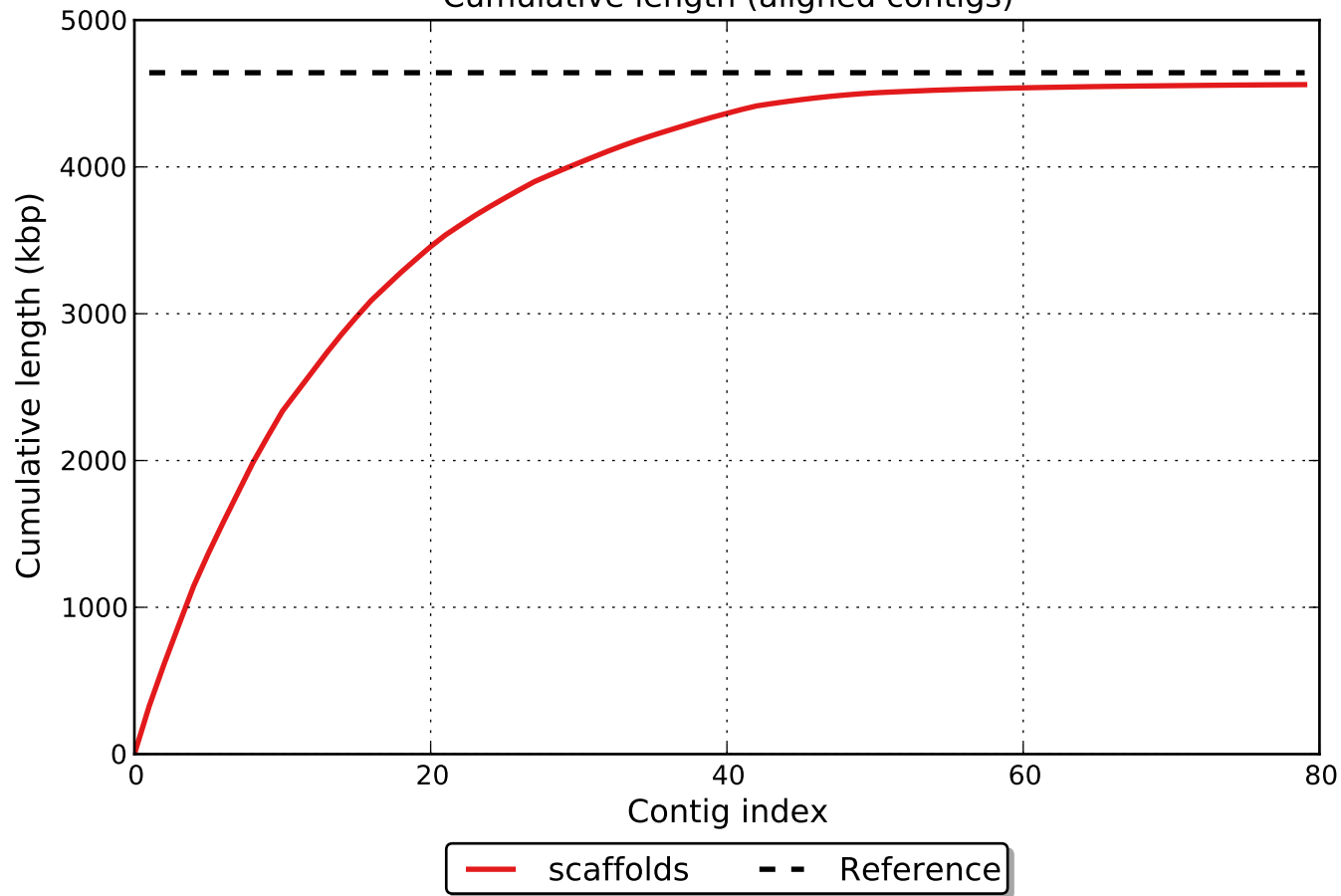


# Misassemblies

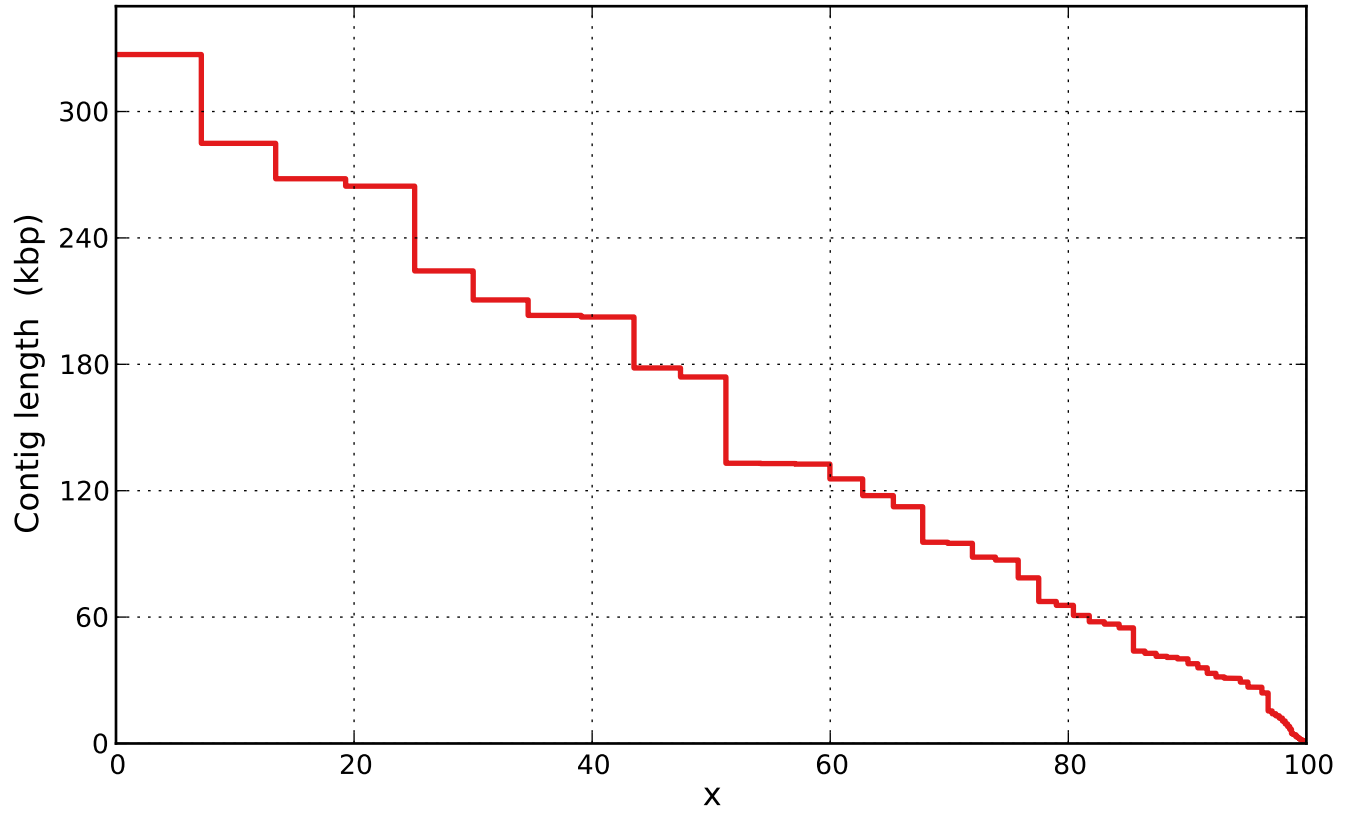




Cumulative length (aligned contigs)



NAx



— scaffolds

# NGAx

