

# Report

	scaffolds
# contigs (>= 1000 bp)	65
# contigs (>= 5000 bp)	50
# contigs (>= 10000 bp)	47
# contigs (>= 25000 bp)	41
# contigs (>= 50000 bp)	27
Total length (>= 1000 bp)	4562692
Total length (>= 5000 bp)	4528217
Total length (>= 10000 bp)	4504264
Total length (>= 25000 bp)	4413070
Total length (>= 50000 bp)	3919931
# contigs	70
Largest contig	327050
Total length	4566115
Reference length	4641652
GC (▼)	50.74
Reference GC (▼)	50.79
N50	173984
NG50	173984
N75	87061
NG75	78609
L50	10
LG50	10
L75	20
LG75	21
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	45684
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (▼)	98.313
Duplication ratio	1.001
# N's per 100 kbp	2.96
# mismatches per 100 kbp	62.83
# indels per 100 kbp	8.88
Largest alignment	327050
NA50	173069
NGA50	173069
NA75	87061
NGA75	78609
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	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	45684
# local misassemblies	1
# mismatches	2867
# indels	405
# short indels	404
# long indels	1
Indels length	595

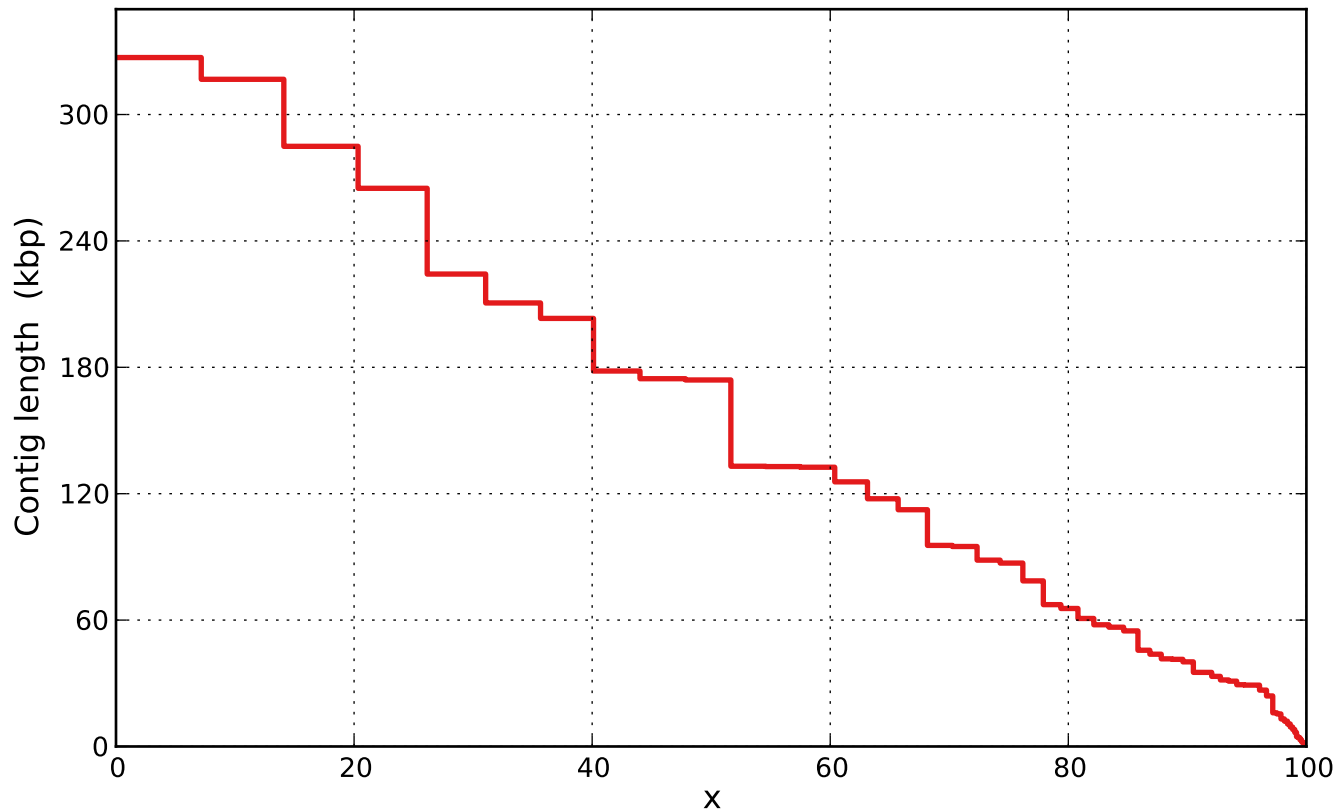
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## 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	135

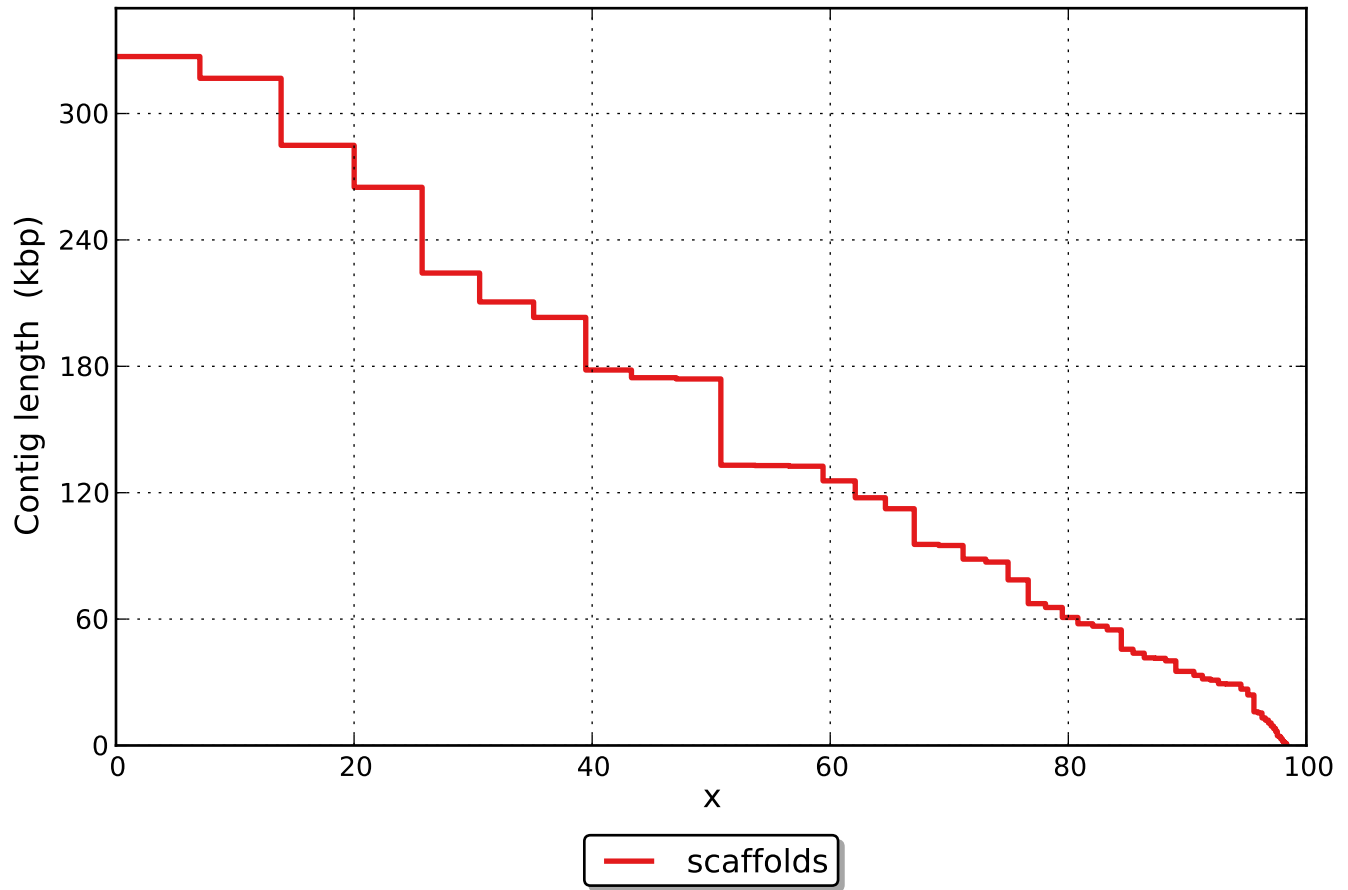
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

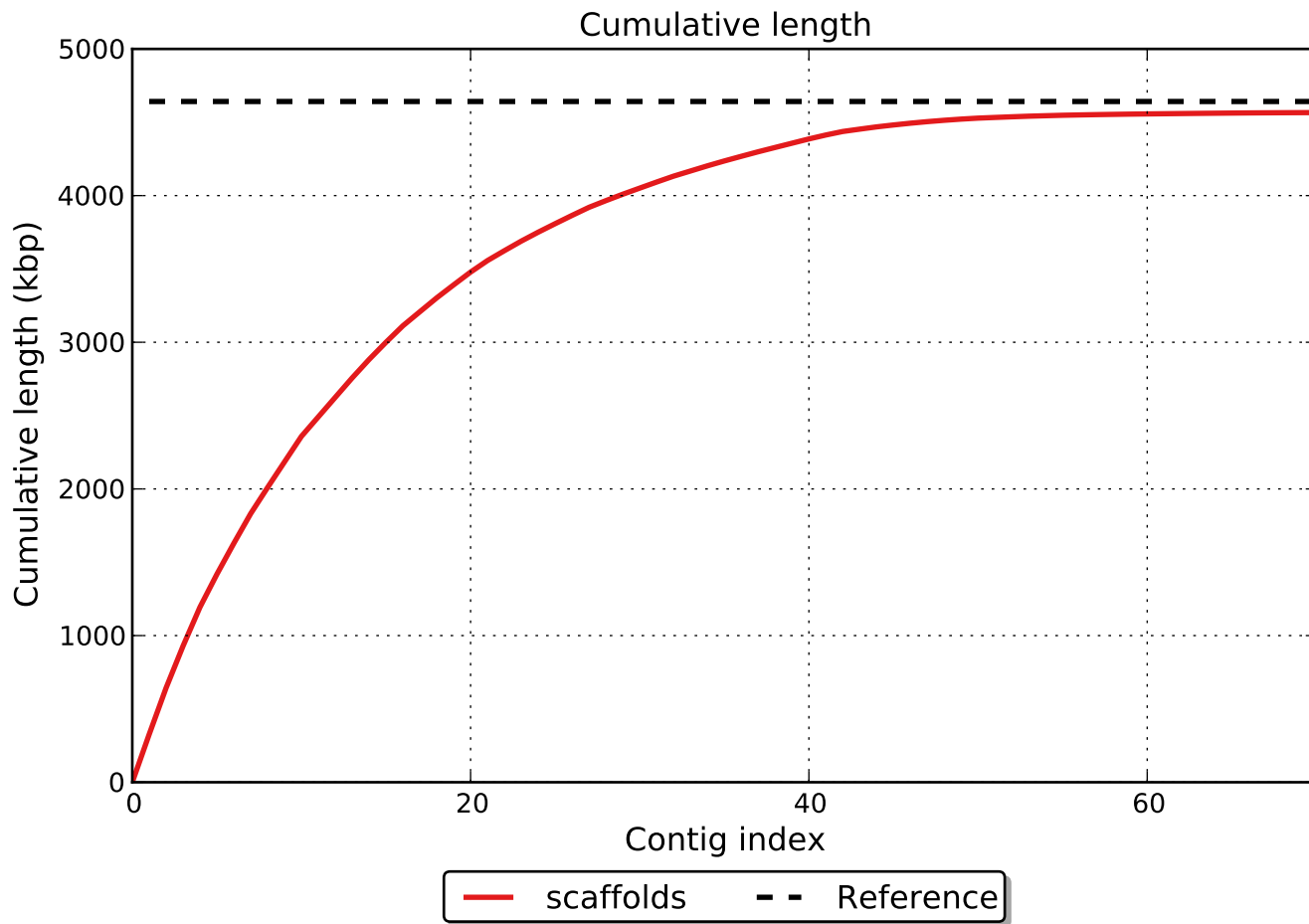
Nx



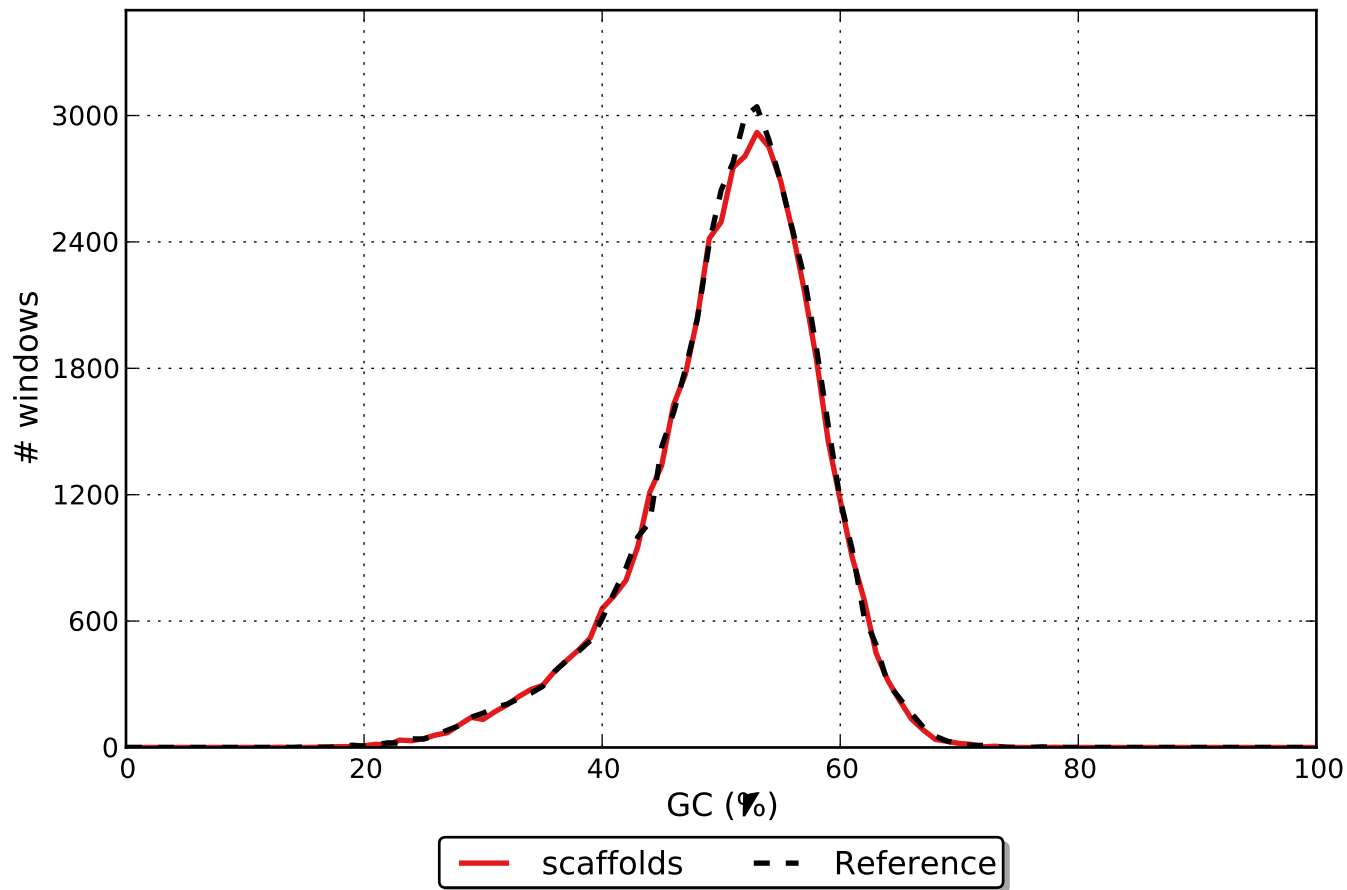
— scaffolds

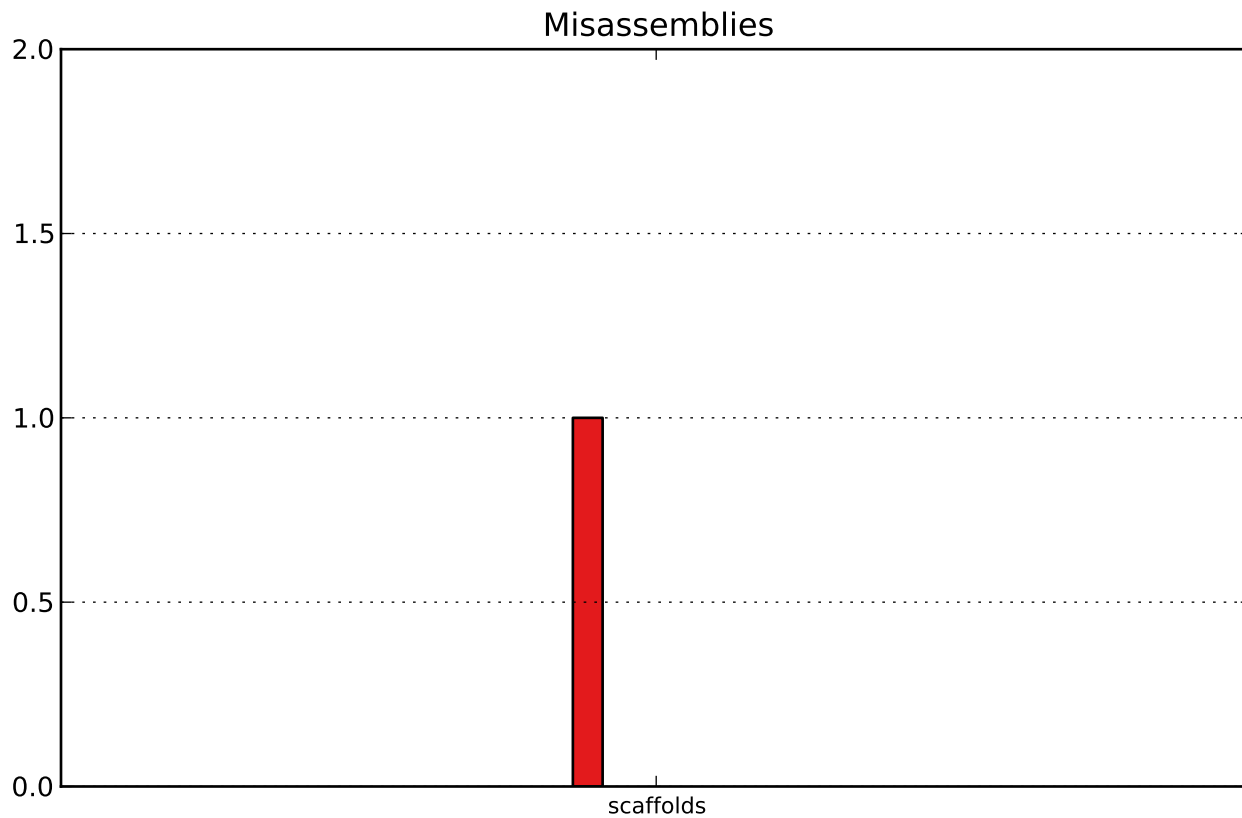
NGx





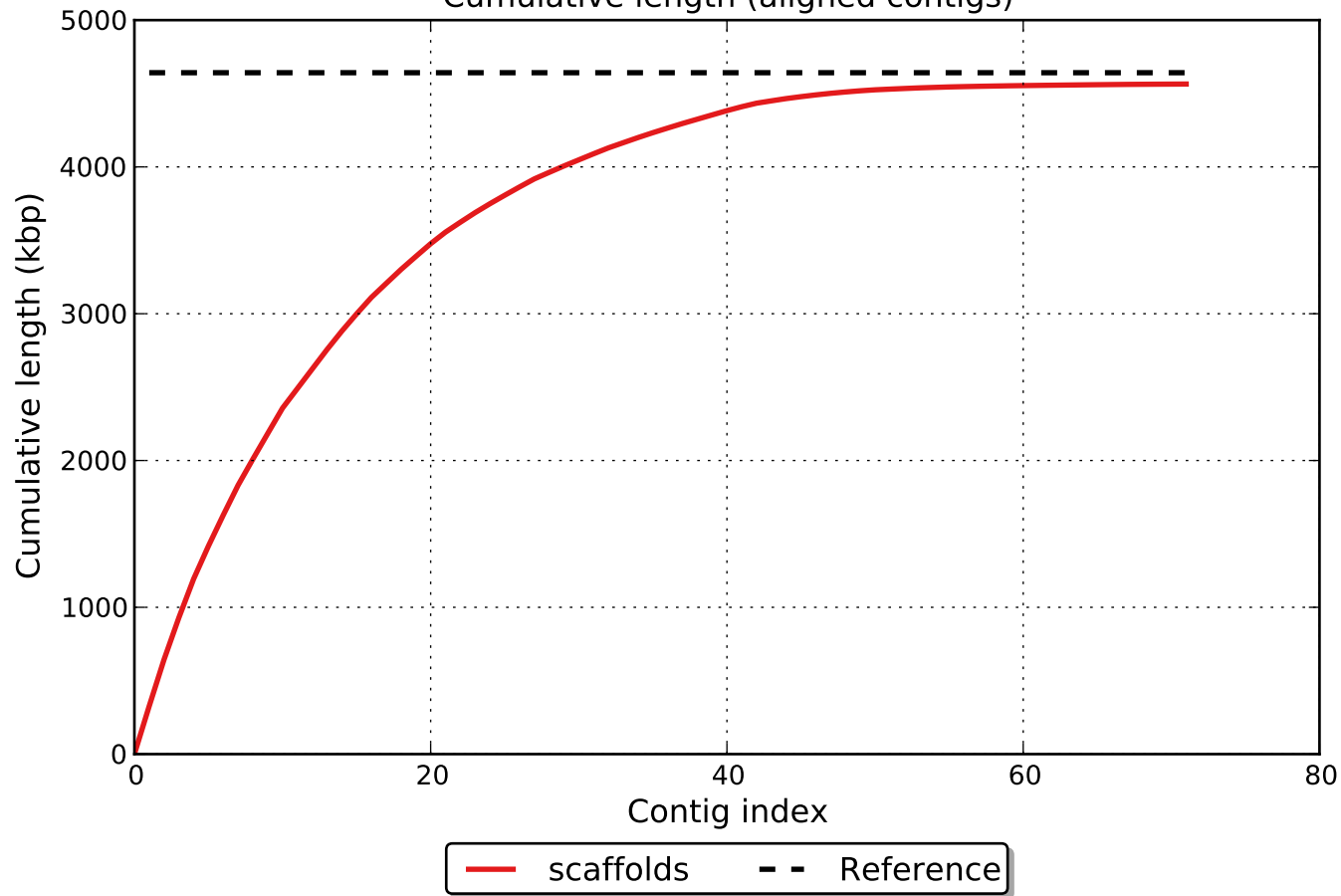
# GC content



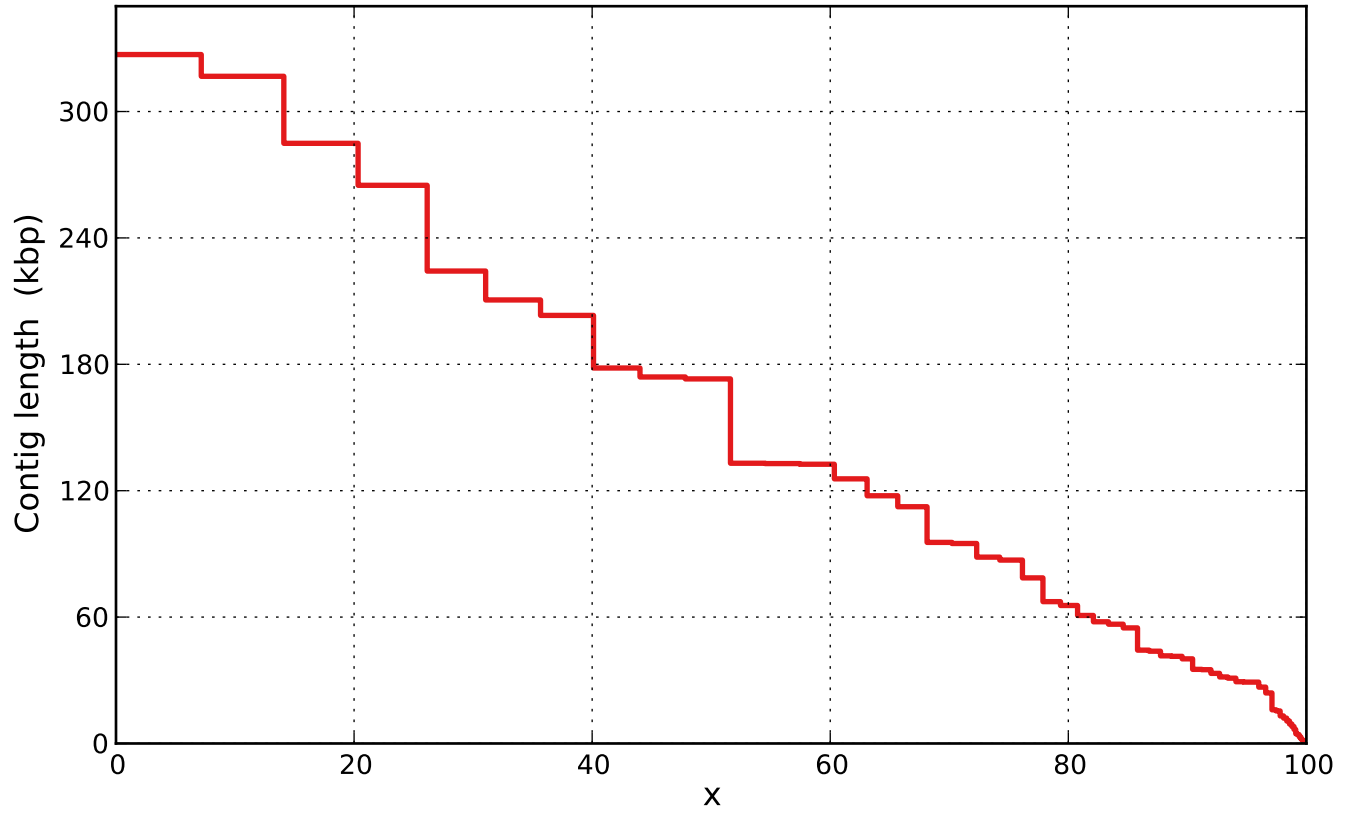




Cumulative length (aligned contigs)



NAx



— scaffolds

# NGAx

