

Report

	scaffolds
# contigs (>= 1000 bp)	96
# contigs (>= 5000 bp)	71
# contigs (>= 10000 bp)	61
# contigs (>= 25000 bp)	48
# contigs (>= 50000 bp)	28
Total length (>= 1000 bp)	4547722
Total length (>= 5000 bp)	4483250
Total length (>= 10000 bp)	4405320
Total length (>= 25000 bp)	4186378
Total length (>= 50000 bp)	3493098
# contigs	100
Largest contig	327041
Total length	4551090
Reference length	4641652
GC (▼)	50.75
Reference GC (▼)	50.79
N50	111983
NG50	105850
N75	54869
NG75	53562
L50	13
LG50	14
L75	27
LG75	28
# misassemblies	7
# misassembled contigs	5
Misassembled contigs length	472041
# local misassemblies	12
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (▼)	97.938
Duplication ratio	1.001
# N's per 100 kbp	13.54
# mismatches per 100 kbp	69.29
# indels per 100 kbp	10.62
Largest alignment	327041
NA50	97502
NGA50	97502
NA75	46259
NGA75	43785
LA50	14
LGA50	14
LA75	30
LGA75	31

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	7
# relocations	7
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	5
Misassembled contigs length	472041
# local misassemblies	12
# mismatches	3150
# indels	483
# short indels	474
# long indels	9
Indels length	898

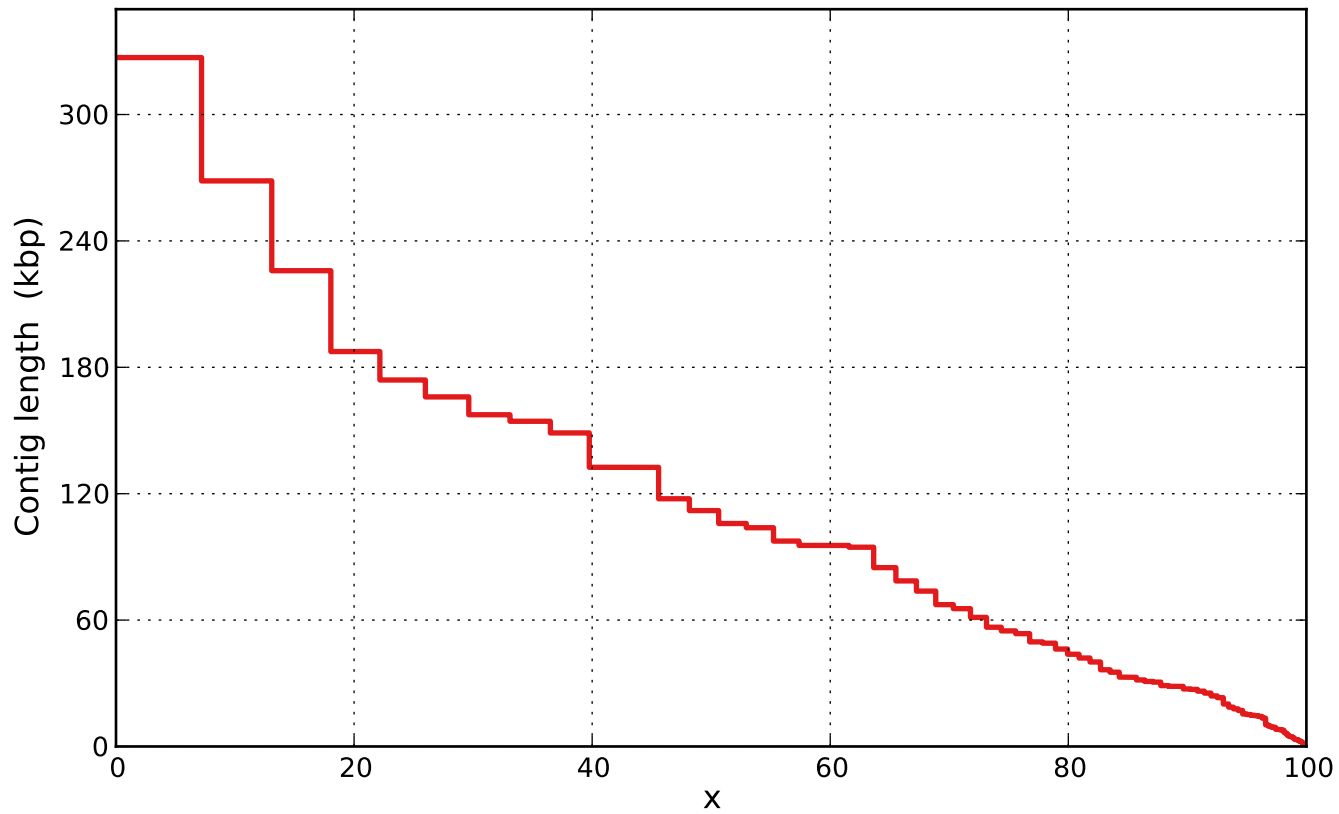
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## 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	616

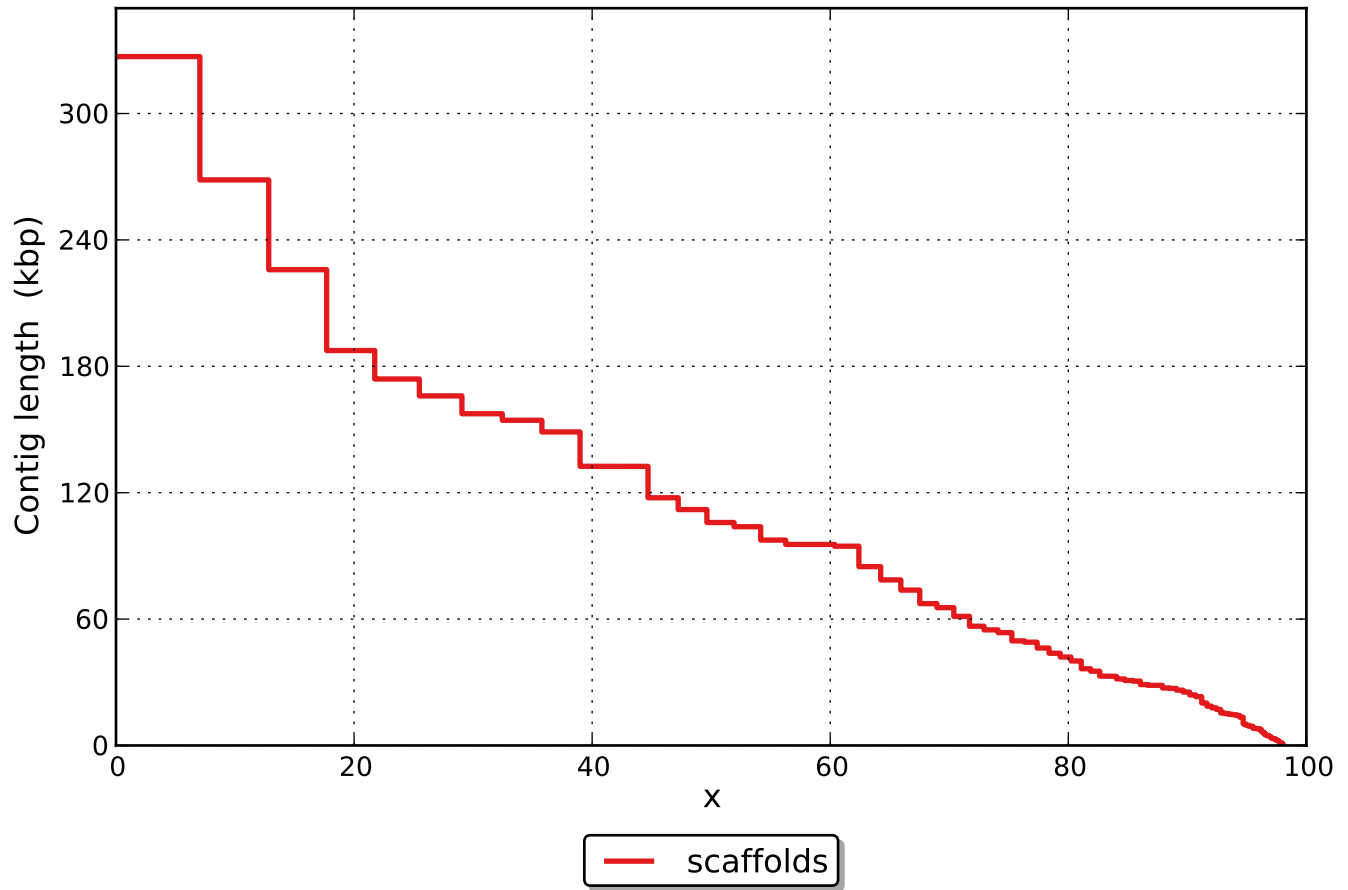
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

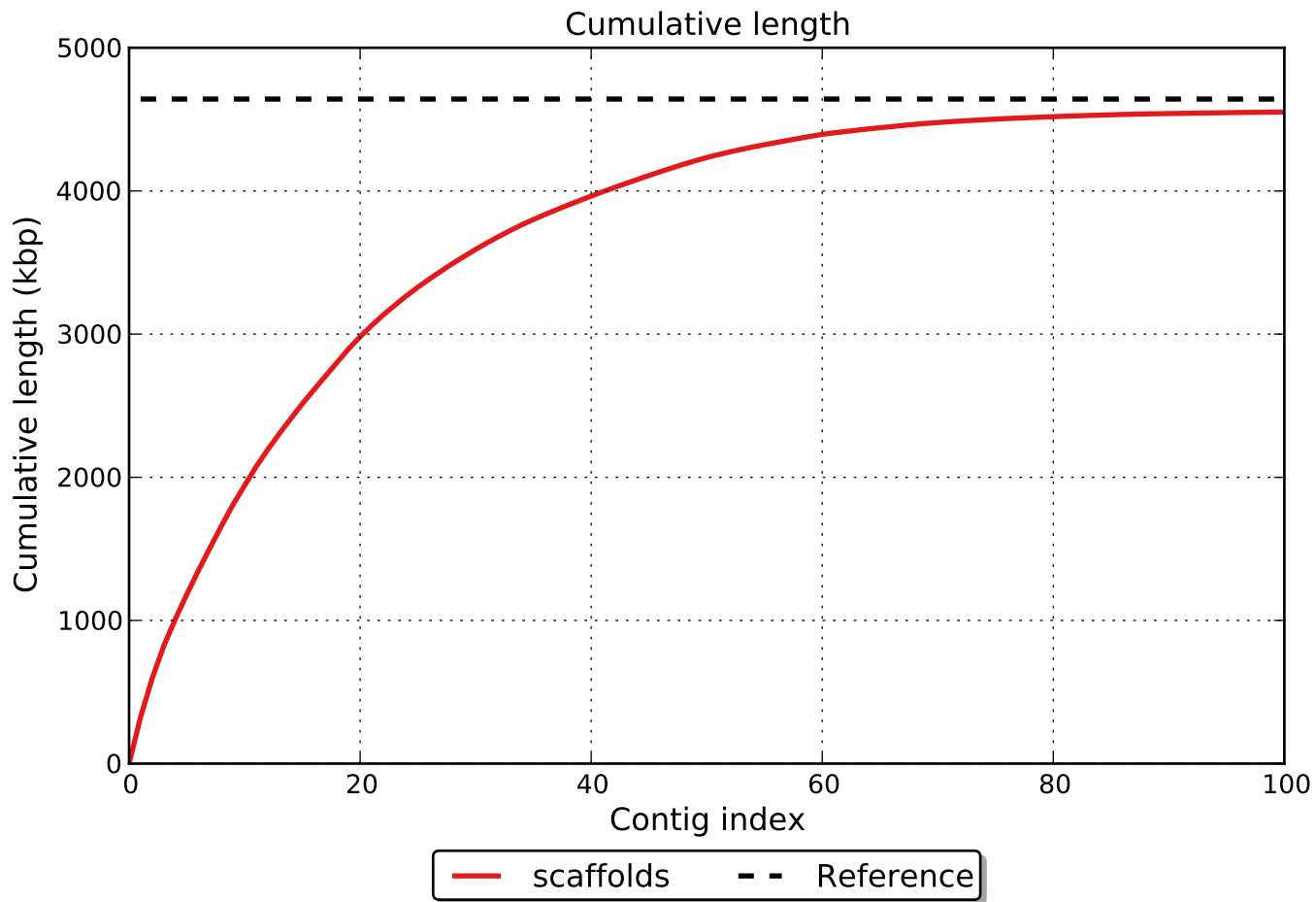
Nx



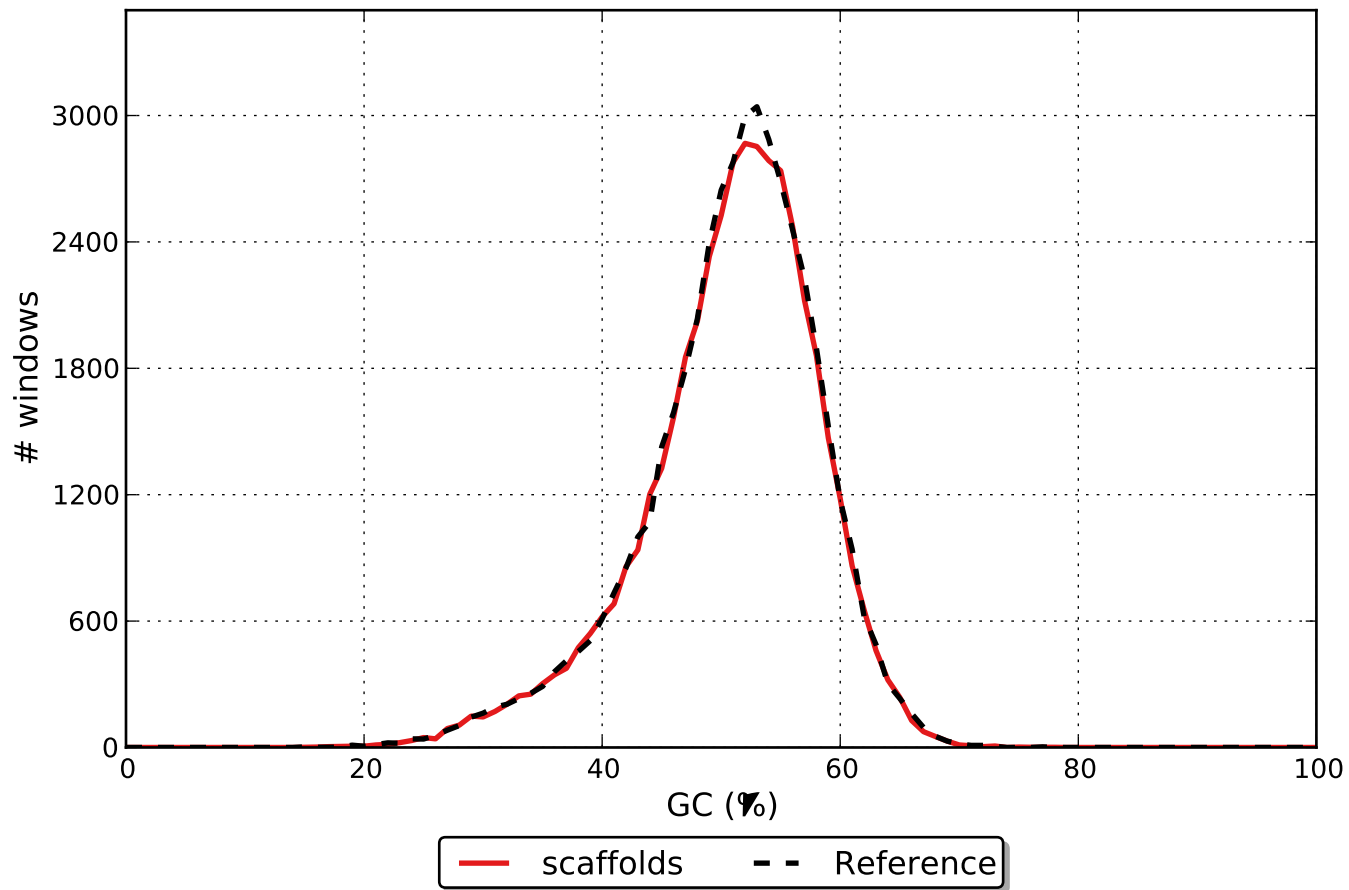
scaffolds

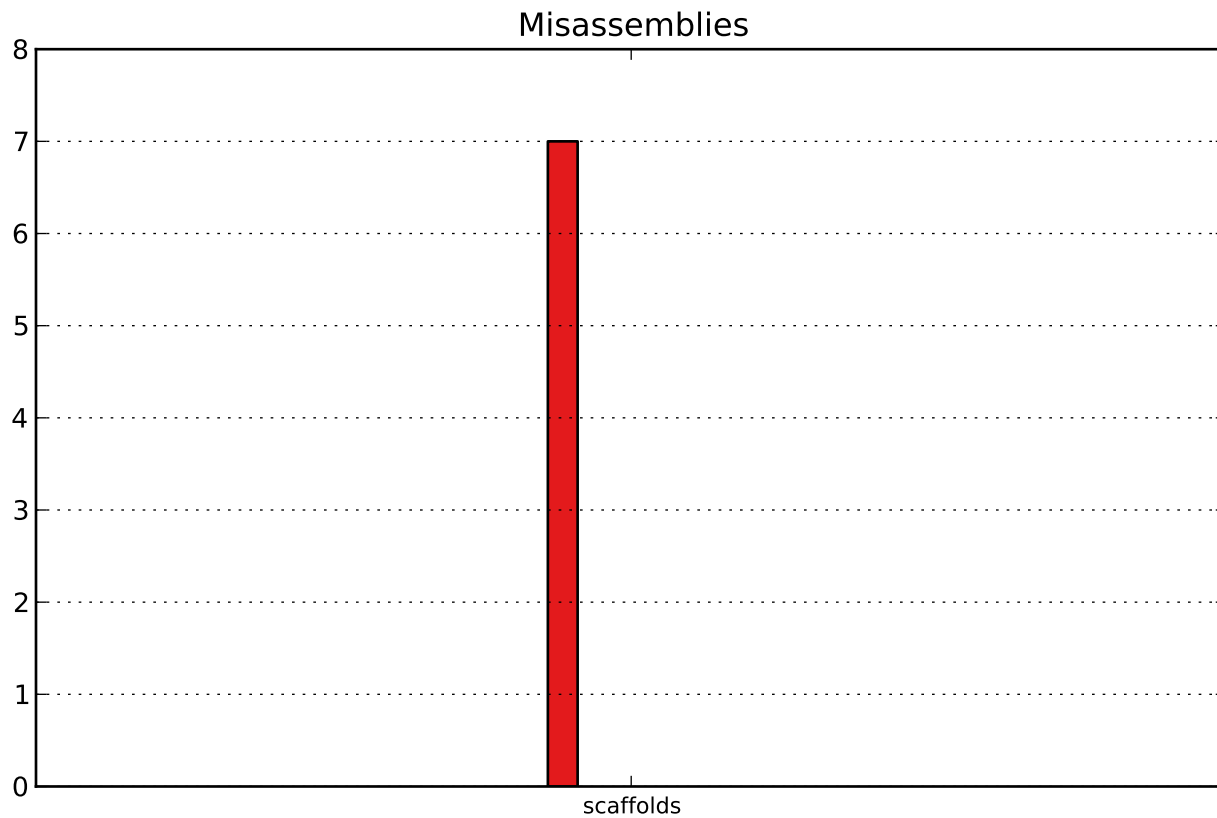
NGx





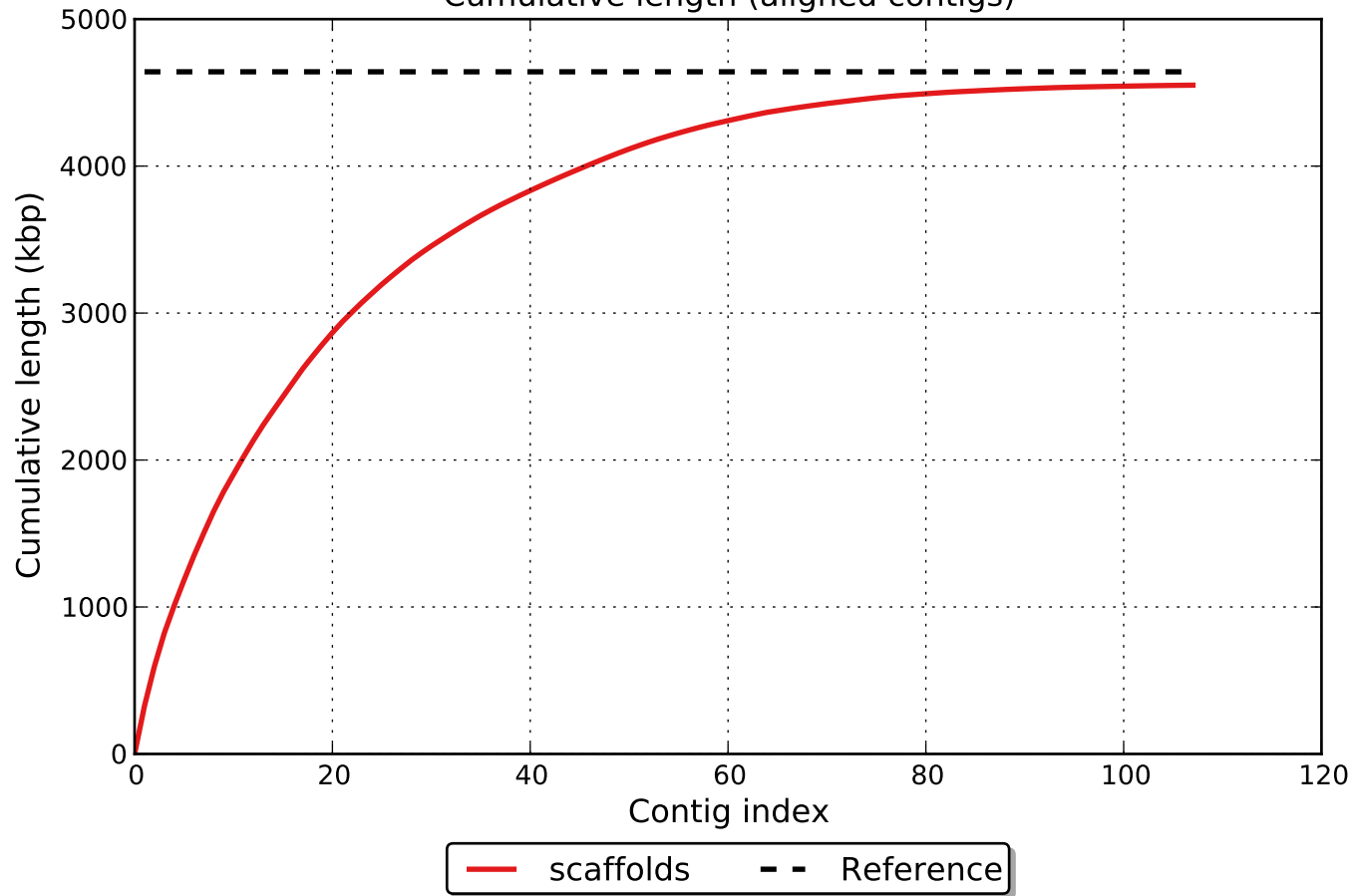
# GC content



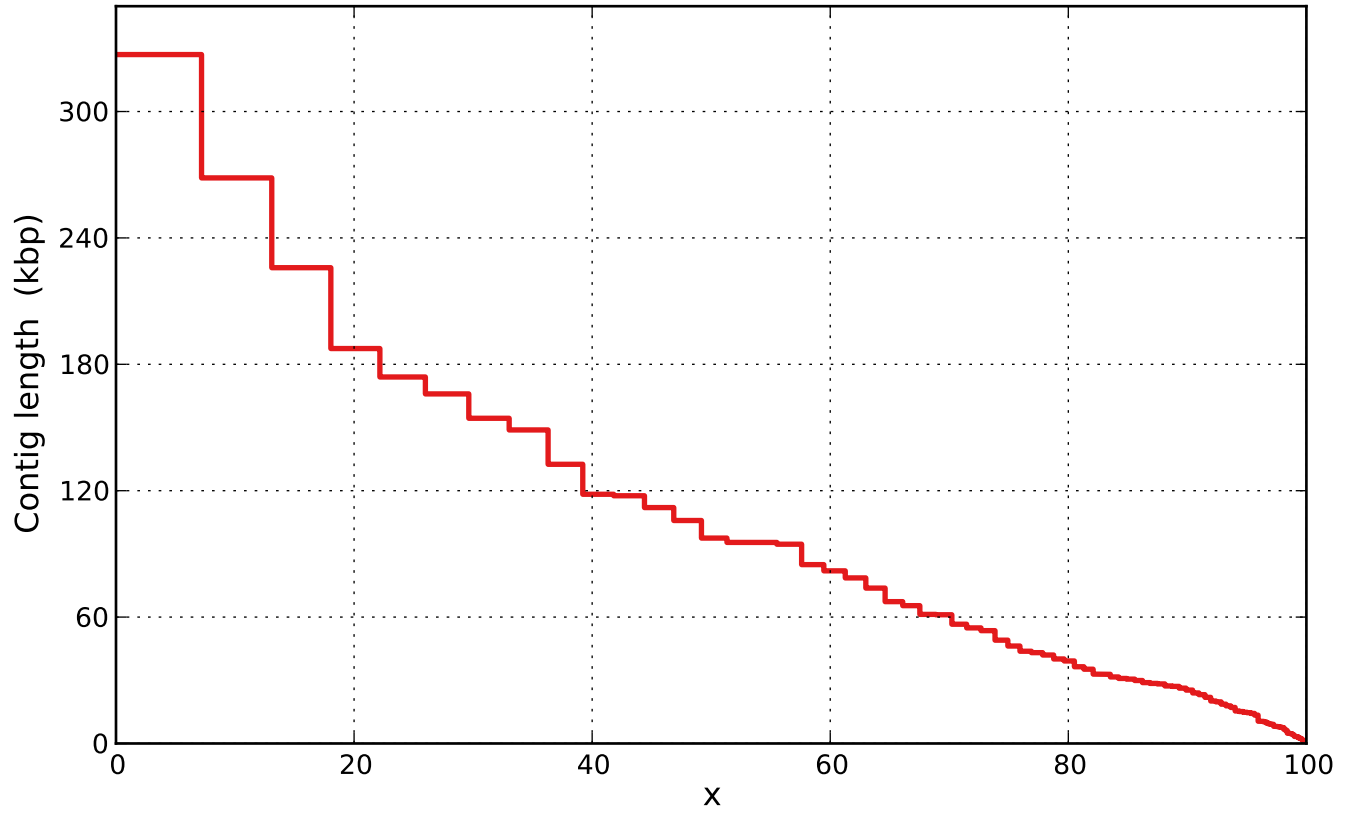




Cumulative length (aligned contigs)



NAx



— scaffolds

# NGAx

