

# Report

	scaffolds
# contigs (>= 1000 bp)	80
# contigs (>= 5000 bp)	58
# contigs (>= 10000 bp)	53
# contigs (>= 25000 bp)	42
# contigs (>= 50000 bp)	30
Total length (>= 1000 bp)	4555230
Total length (>= 5000 bp)	4504638
Total length (>= 10000 bp)	4466805
Total length (>= 25000 bp)	4292037
Total length (>= 50000 bp)	3847017
# contigs	85
Largest contig	327076
Total length	4559095
Reference length	4641652
GC (▼)	50.75
Reference GC (▼)	50.79
N50	133024
NG50	133024
N75	71774
NG75	71774
L50	12
LG50	12
L75	24
LG75	24
# misassemblies	7
# misassembled contigs	6
Misassembled contigs length	806527
# local misassemblies	7
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (▼)	98.174
Duplication ratio	1.000
# N's per 100 kbp	1.43
# mismatches per 100 kbp	67.44
# indels per 100 kbp	9.48
Largest alignment	327076
NA50	117600
NGA50	117600
NA75	62838
NGA75	60705
LA50	13
LGA50	13
LA75	26
LGA75	27

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	6
Misassembled contigs length	806527
# local misassemblies	7
# mismatches	3073
# indels	432
# short indels	429
# long indels	3
Indels length	715

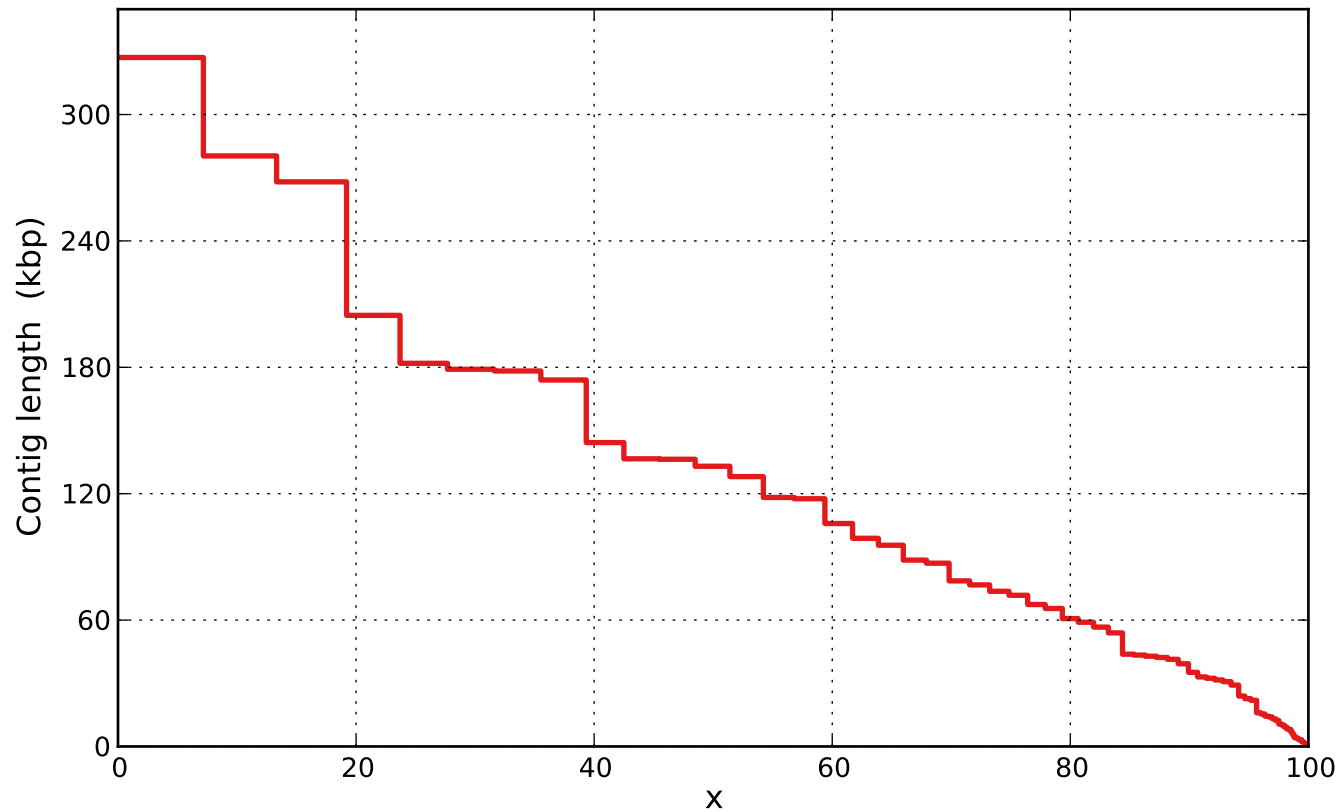
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

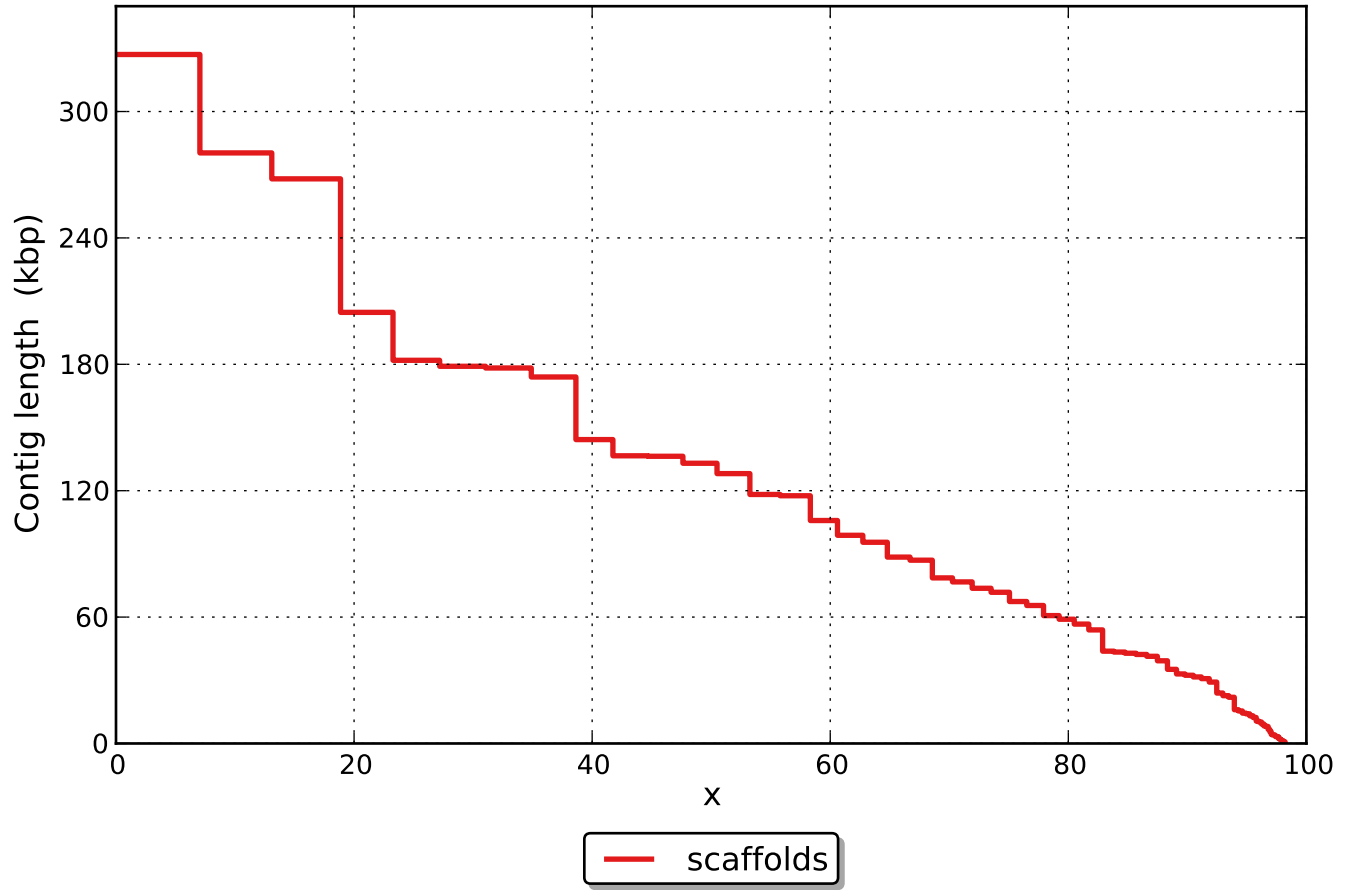
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	65

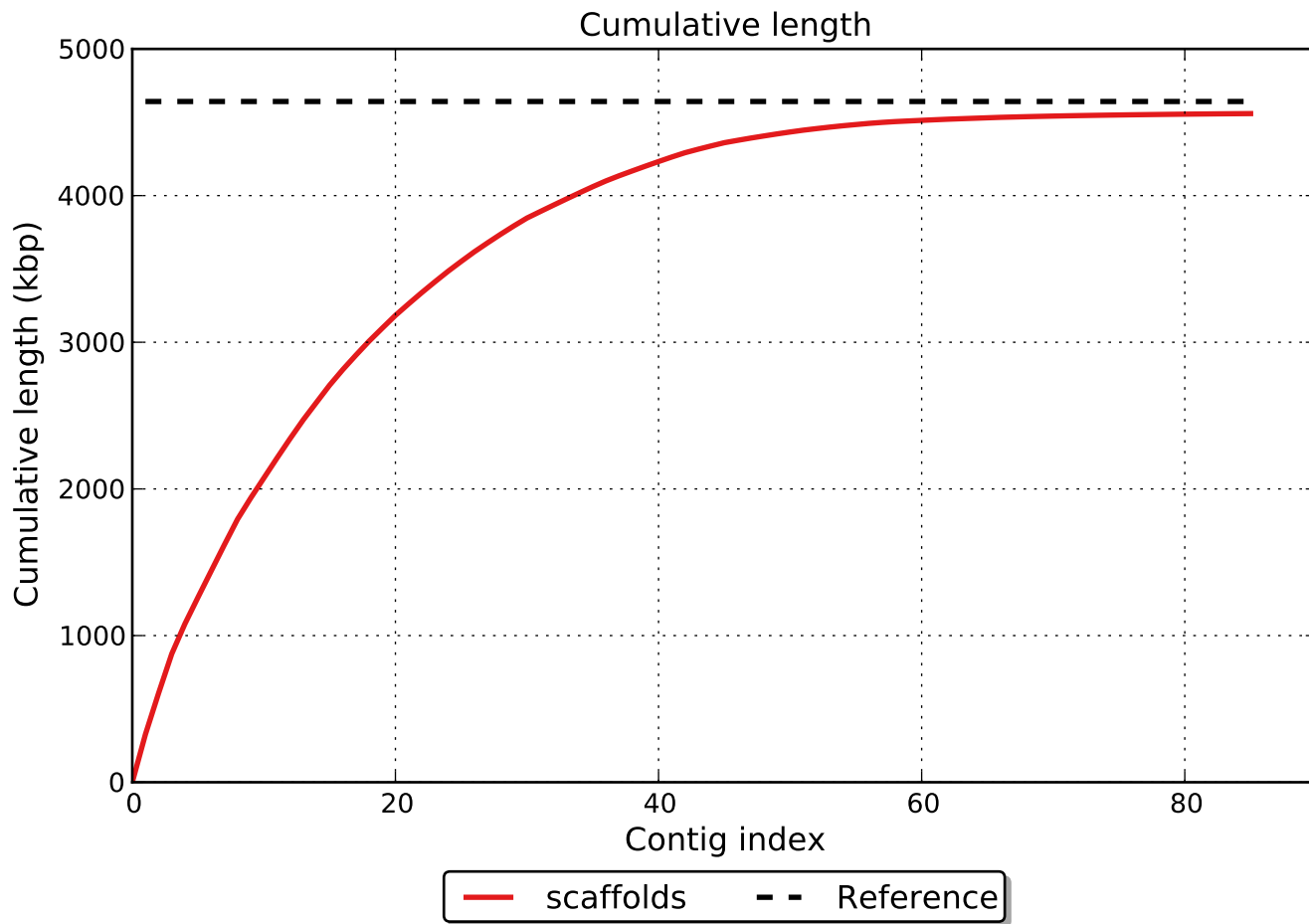
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

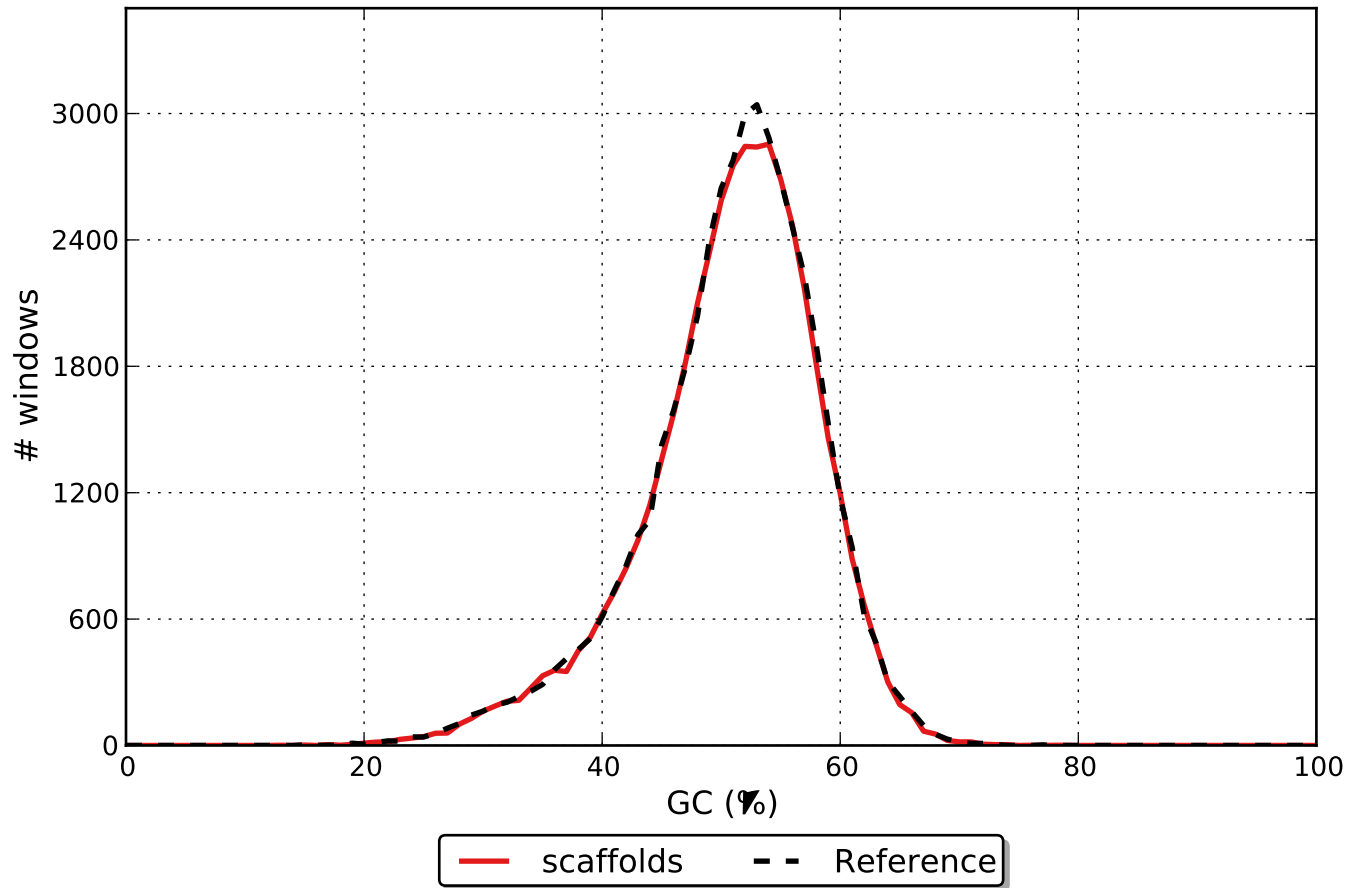


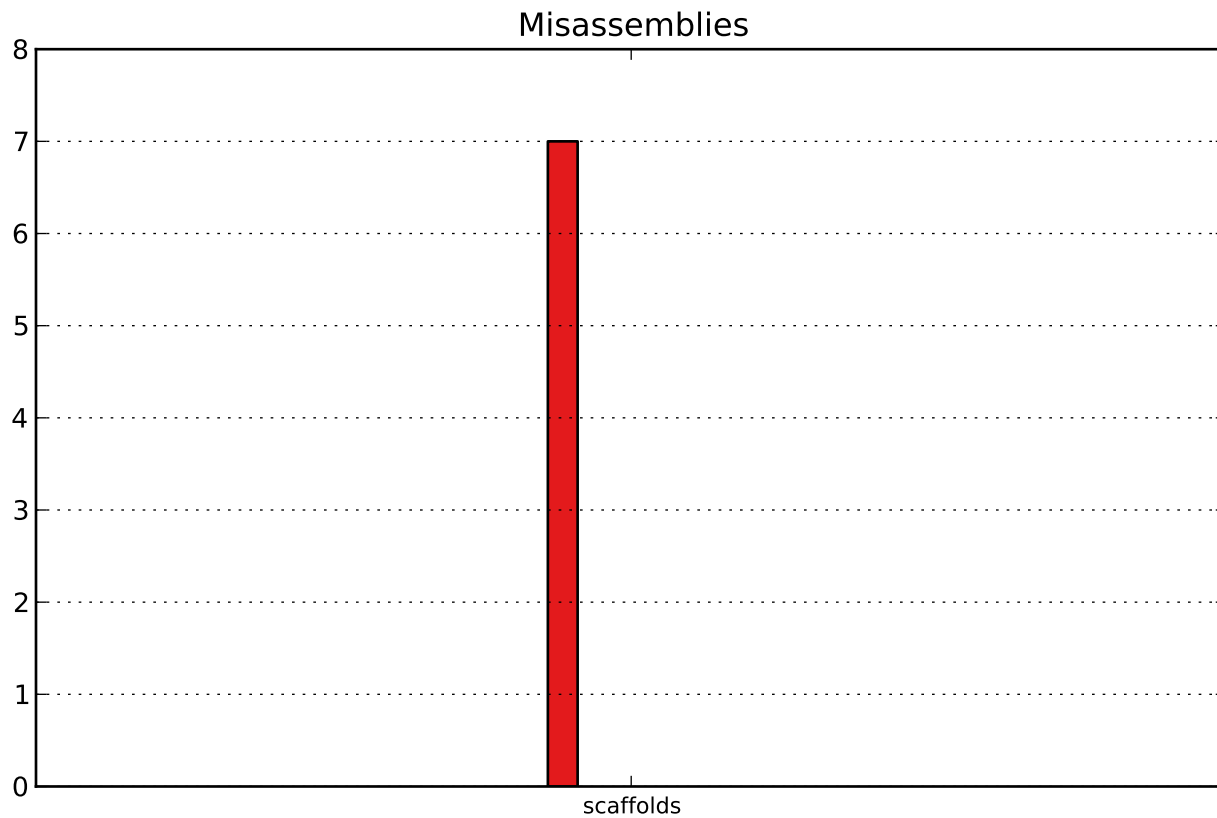
NGx





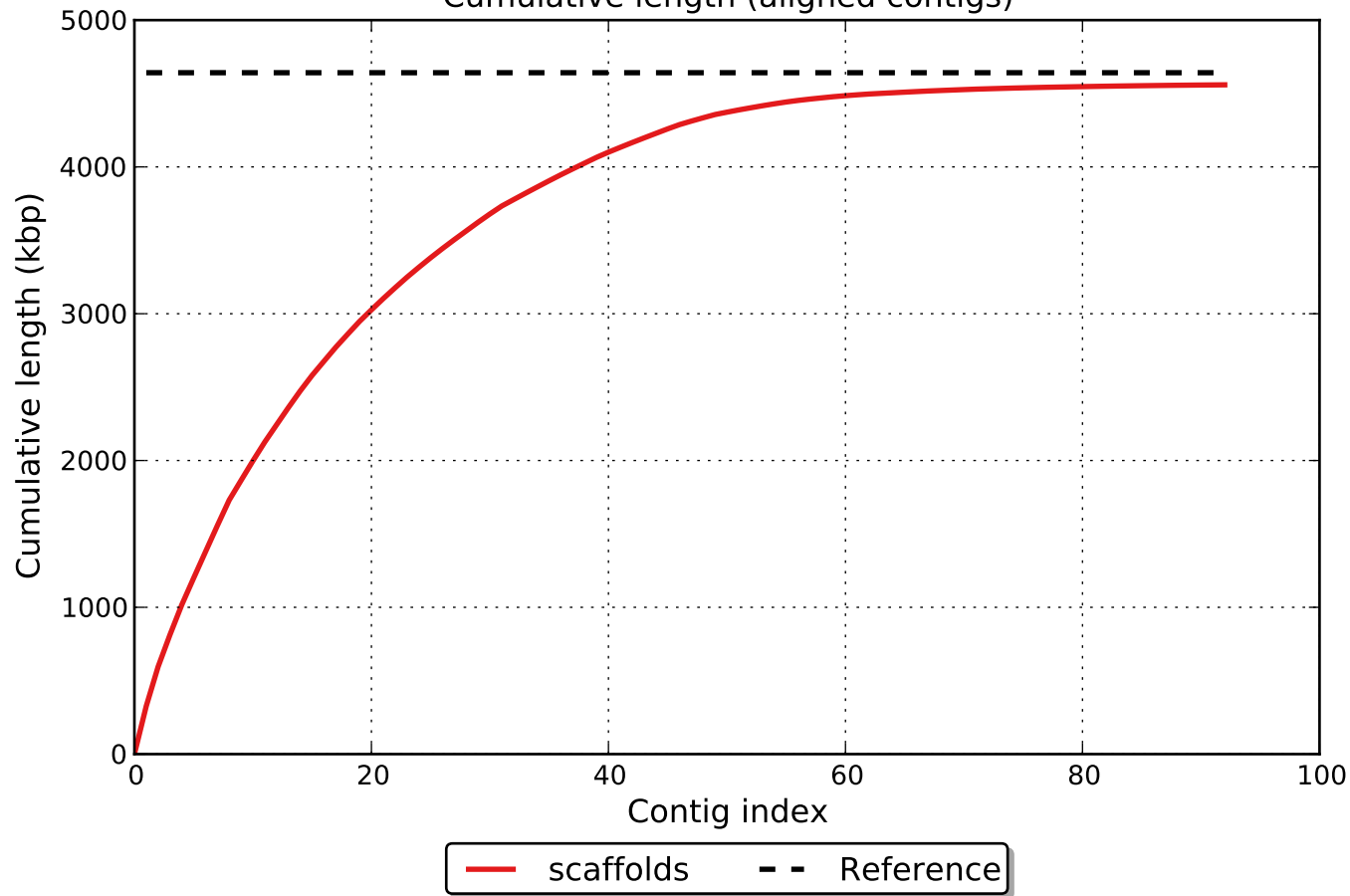
GC content



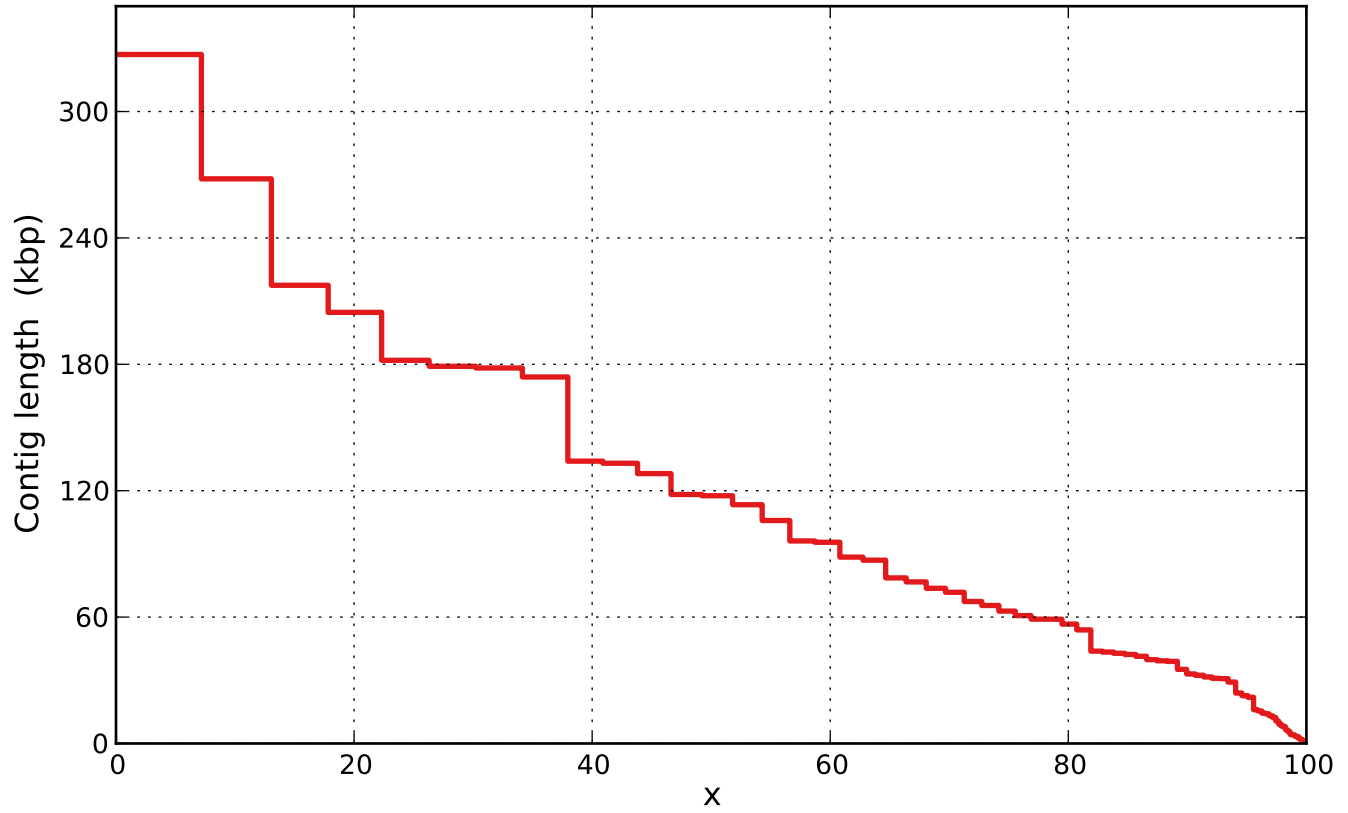




Cumulative length (aligned contigs)



NAx



scaffolds

# NGAx

