

Report

	scaffolds
# contigs (>= 1000 bp)	191
# contigs (>= 5000 bp)	139
# contigs (>= 10000 bp)	117
# contigs (>= 25000 bp)	71
# contigs (>= 50000 bp)	27
Total length (>= 1000 bp)	4517569
Total length (>= 5000 bp)	4374580
Total length (>= 10000 bp)	4219421
Total length (>= 25000 bp)	3512915
Total length (>= 50000 bp)	2084849
# contigs	204
Largest contig	138275
Total length	4527463
Reference length	4641652
GC (▼)	50.76
Reference GC (▼)	50.79
N50	44576
NG50	39635
N75	26493
NG75	25734
L50	31
LG50	33
L75	67
LG75	70
# misassemblies	15
# misassembled contigs	14
Misassembled contigs length	568607
# local misassemblies	10
# unaligned contigs	0 + 2 part
Unaligned length	3972
Genome fraction (▼)	97.366
Duplication ratio	1.001
# N's per 100 kbp	147.79
# mismatches per 100 kbp	105.35
# indels per 100 kbp	18.30
Largest alignment	138275
NA50	39635
NGA50	38731
NA75	23916
NGA75	22482
LA50	33
LGA50	35
LA75	70
LGA75	74

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	15
# relocations	15
# translocations	0
# inversions	0
# possibly misassembled contigs	1
# misassembled contigs	14
Misassembled contigs length	568607
# local misassemblies	10
# mismatches	4761
# indels	827
# short indels	604
# long indels	223
Indels length	4119

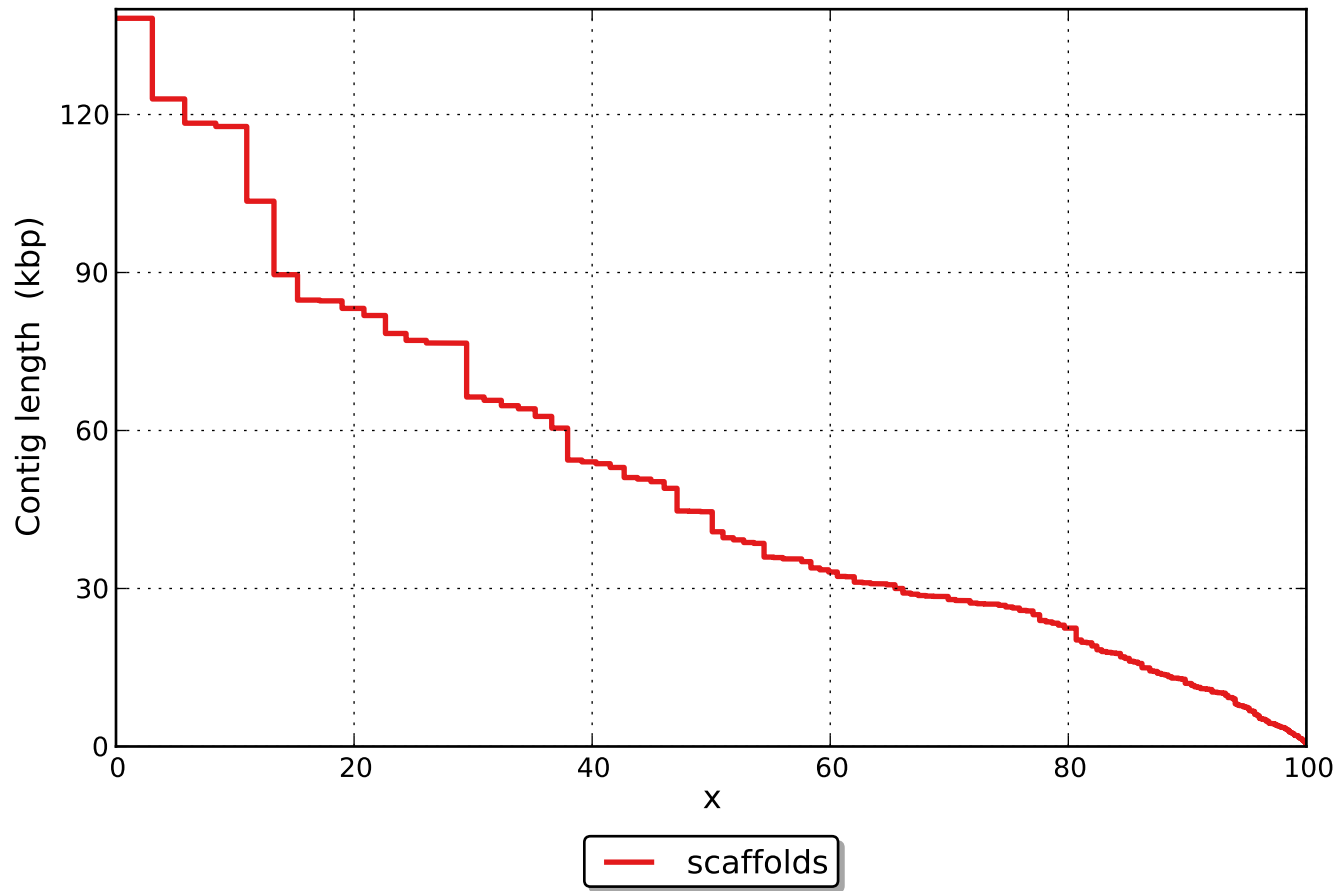
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

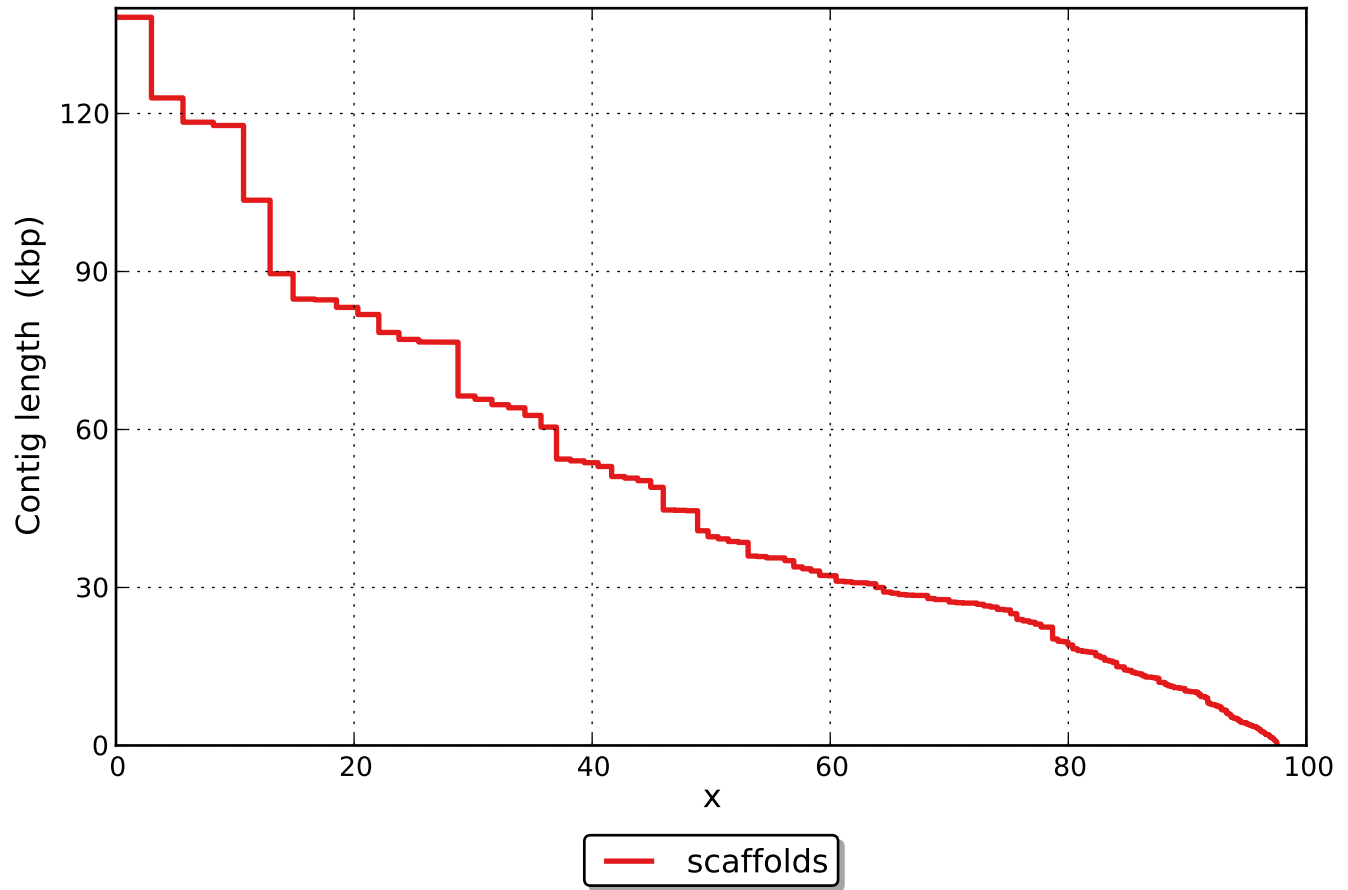
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	1
Partially unaligned length	3972
# N's	6691

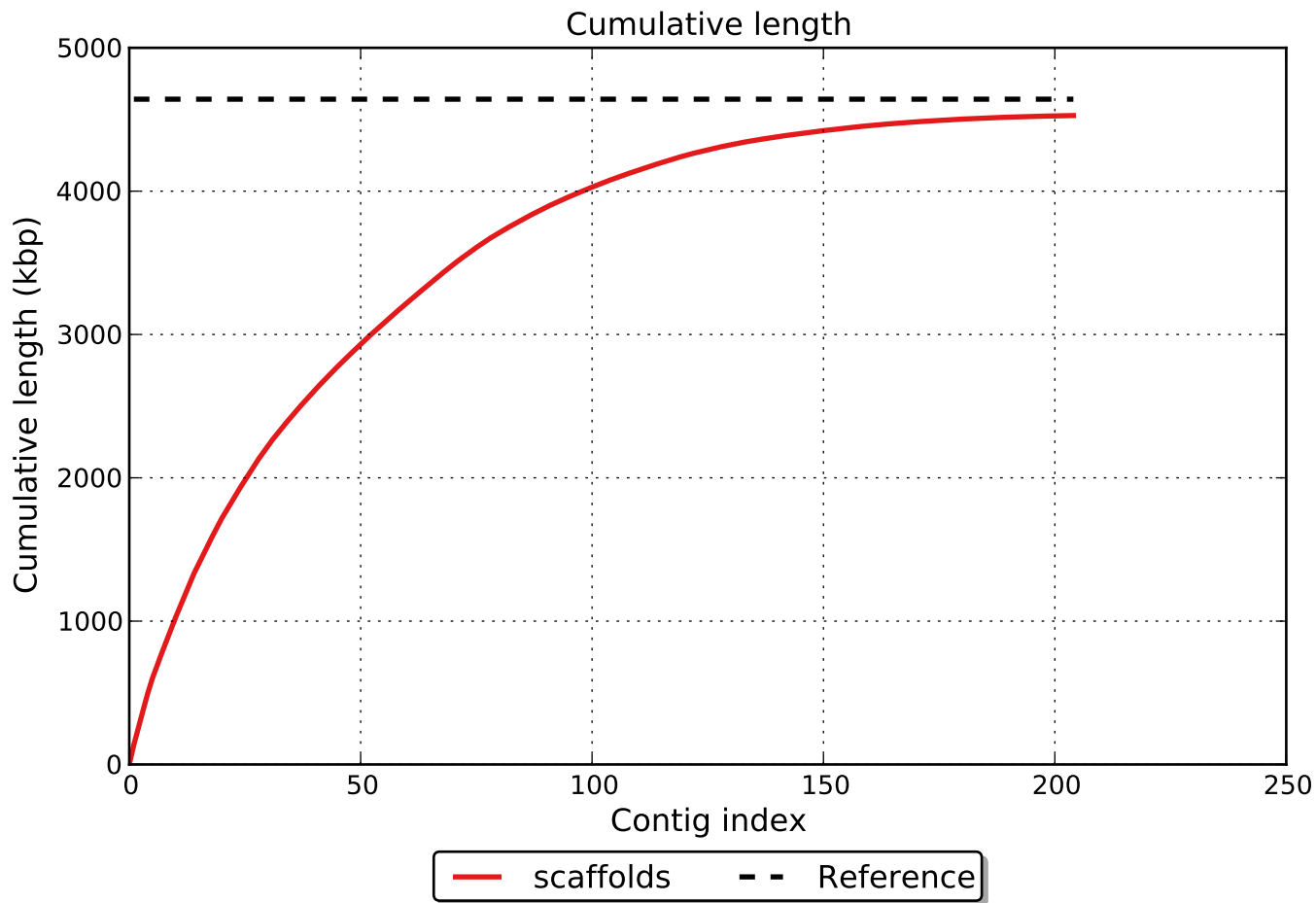
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

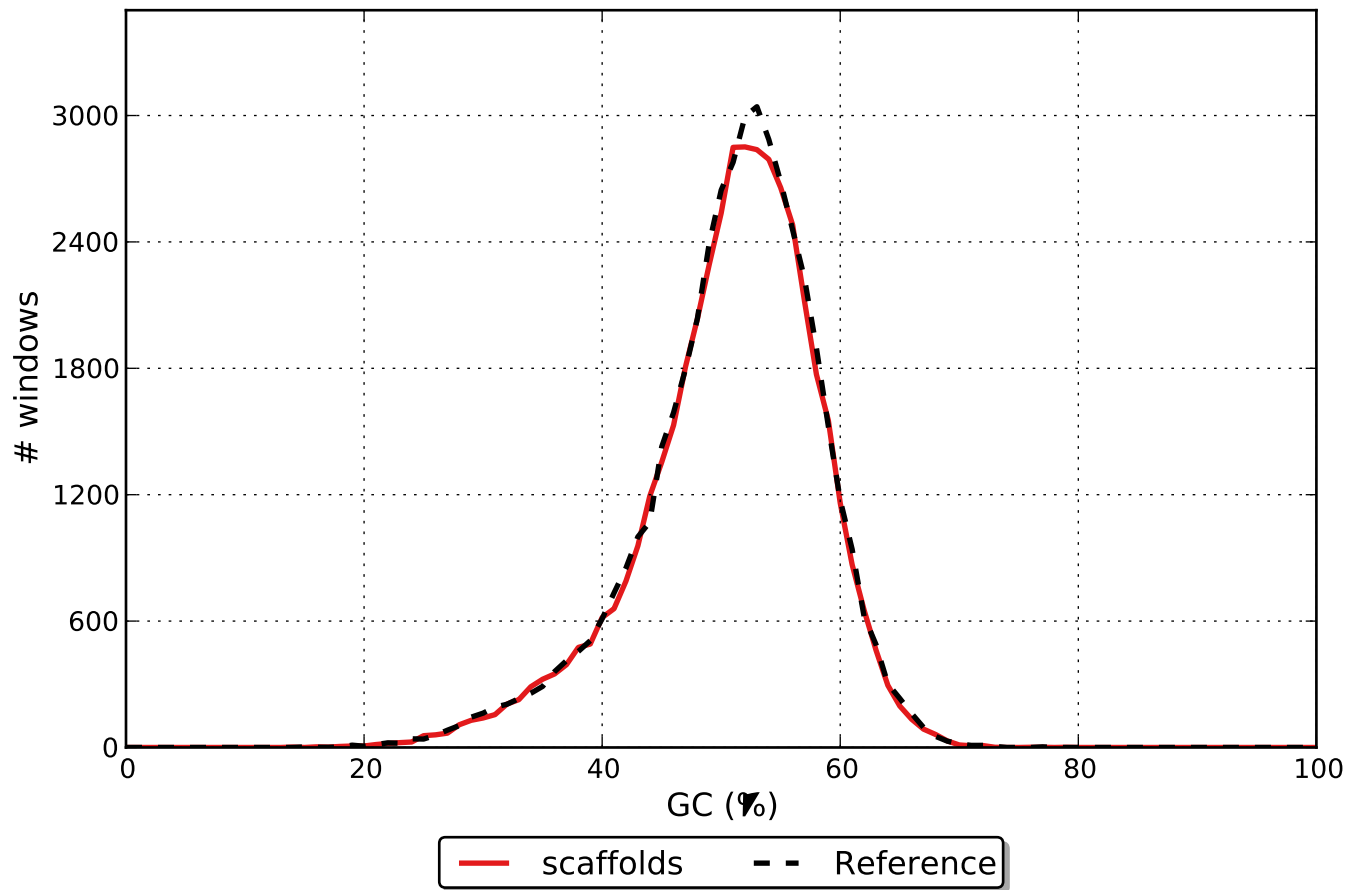


NGx

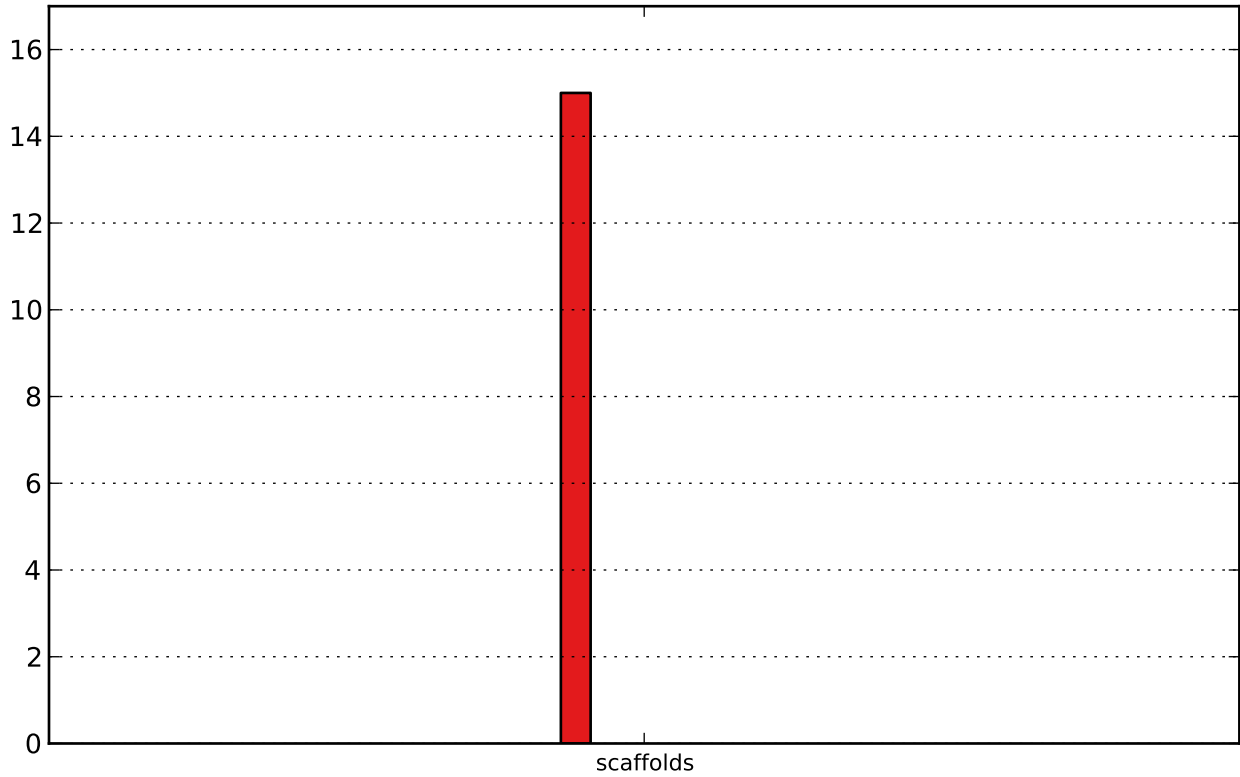




GC content

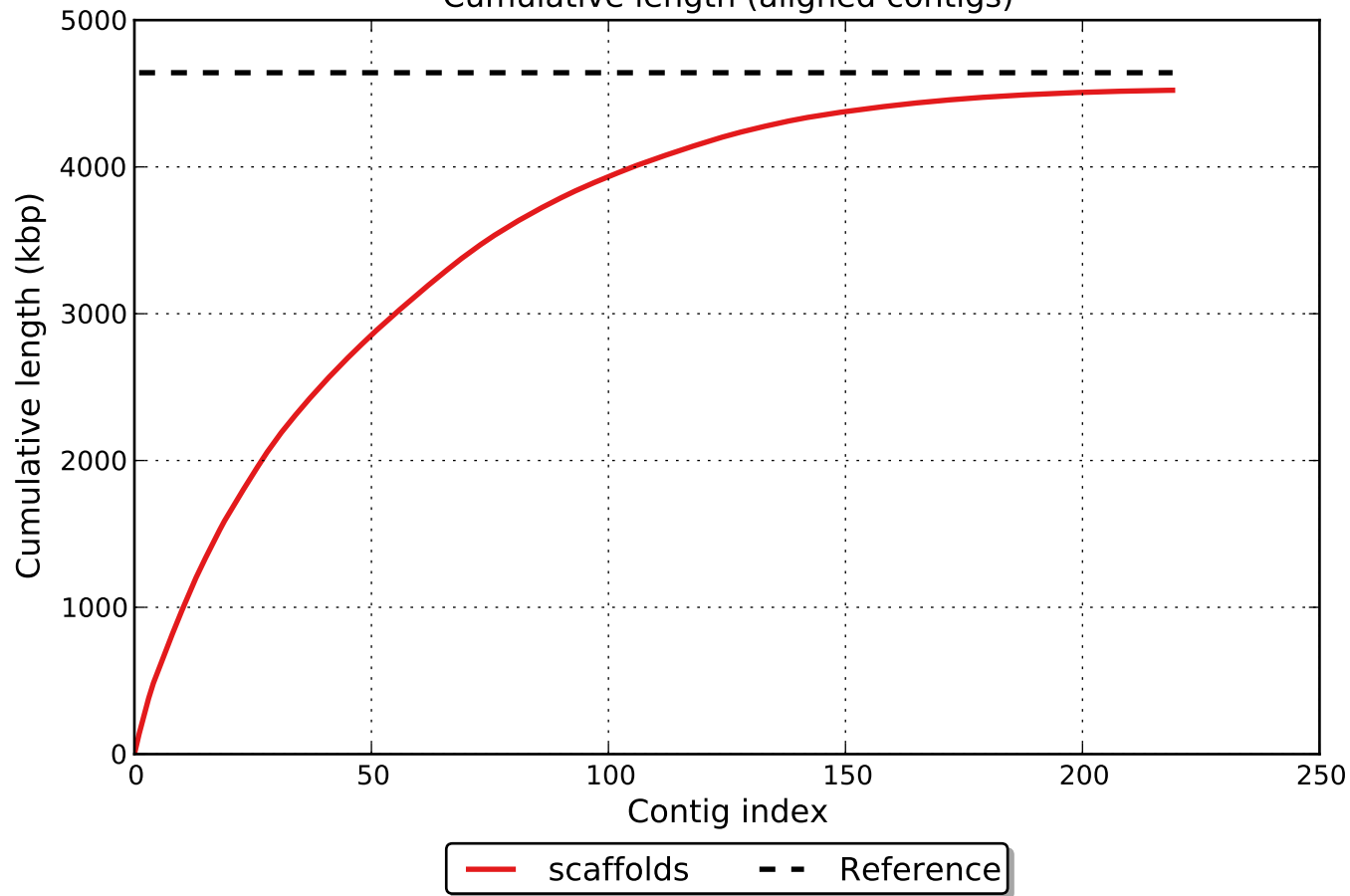


Misassemblies

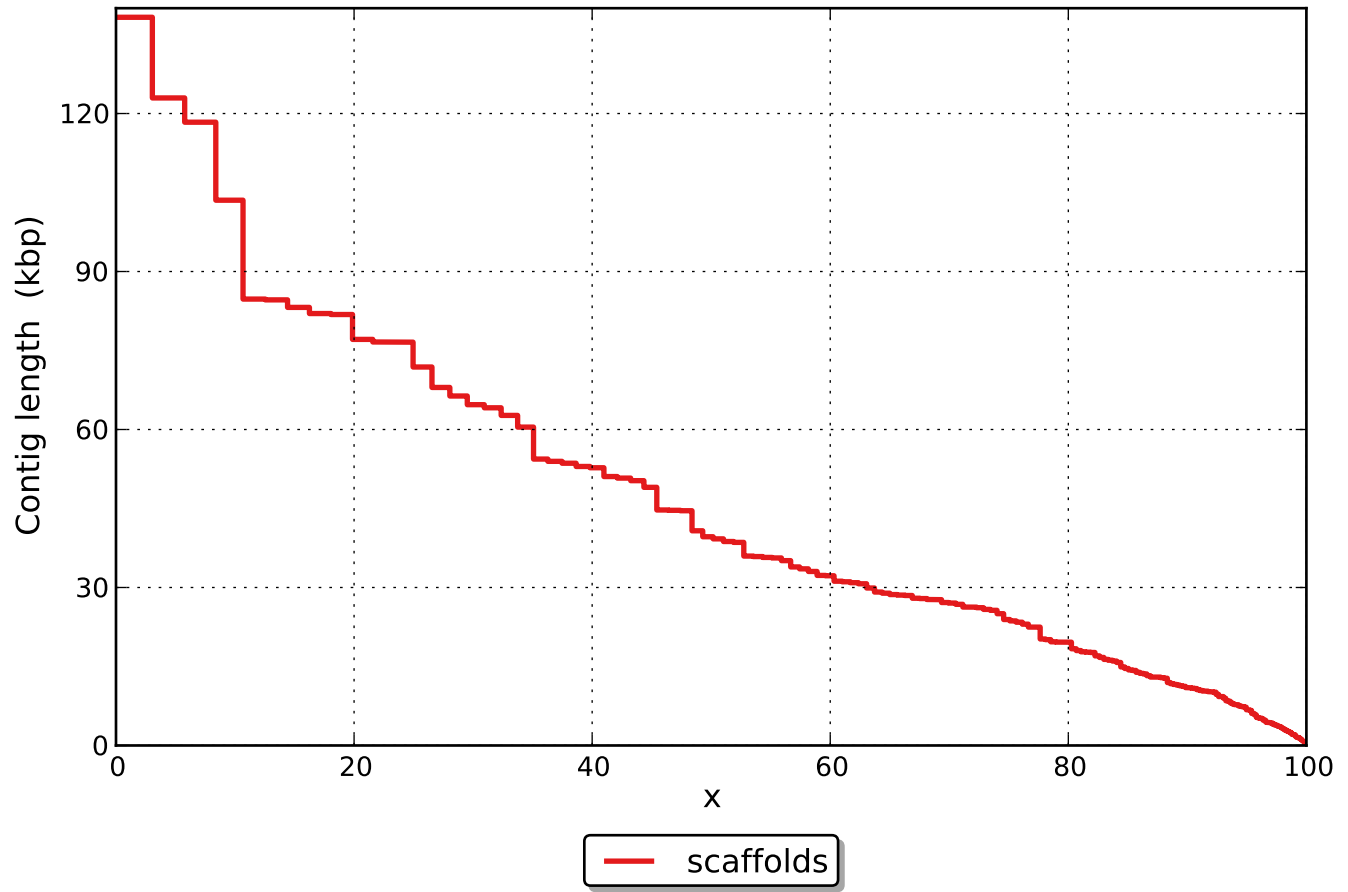


 # relocations

Cumulative length (aligned contigs)



NAx



NGAx

