

Report

	scaffolds
# contigs (>= 1000 bp)	77
# contigs (>= 5000 bp)	53
# contigs (>= 10000 bp)	49
# contigs (>= 25000 bp)	44
# contigs (>= 50000 bp)	28
Total length (>= 1000 bp)	4556812
Total length (>= 5000 bp)	4502351
Total length (>= 10000 bp)	4472445
Total length (>= 25000 bp)	4399198
Total length (>= 50000 bp)	3843225
# contigs	83
Largest contig	327064
Total length	4561322
Reference length	4641652
GC (▼)	50.75
Reference GC (▼)	50.79
N50	132876
NG50	132876
N75	78609
NG75	67394
L50	11
LG50	11
L75	22
LG75	23
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	45411
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (▼)	98.205
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3.66
# indels per 100 kbp	0.37
Largest alignment	327064
NA50	132876
NGA50	132876
NA75	78609
NGA75	67394
LA50	11
LGA50	11
LA75	22
LGA75	23

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	45411
# local misassemblies	3
# mismatches	167
# indels	17
# short indels	17
# long indels	0
Indels length	23

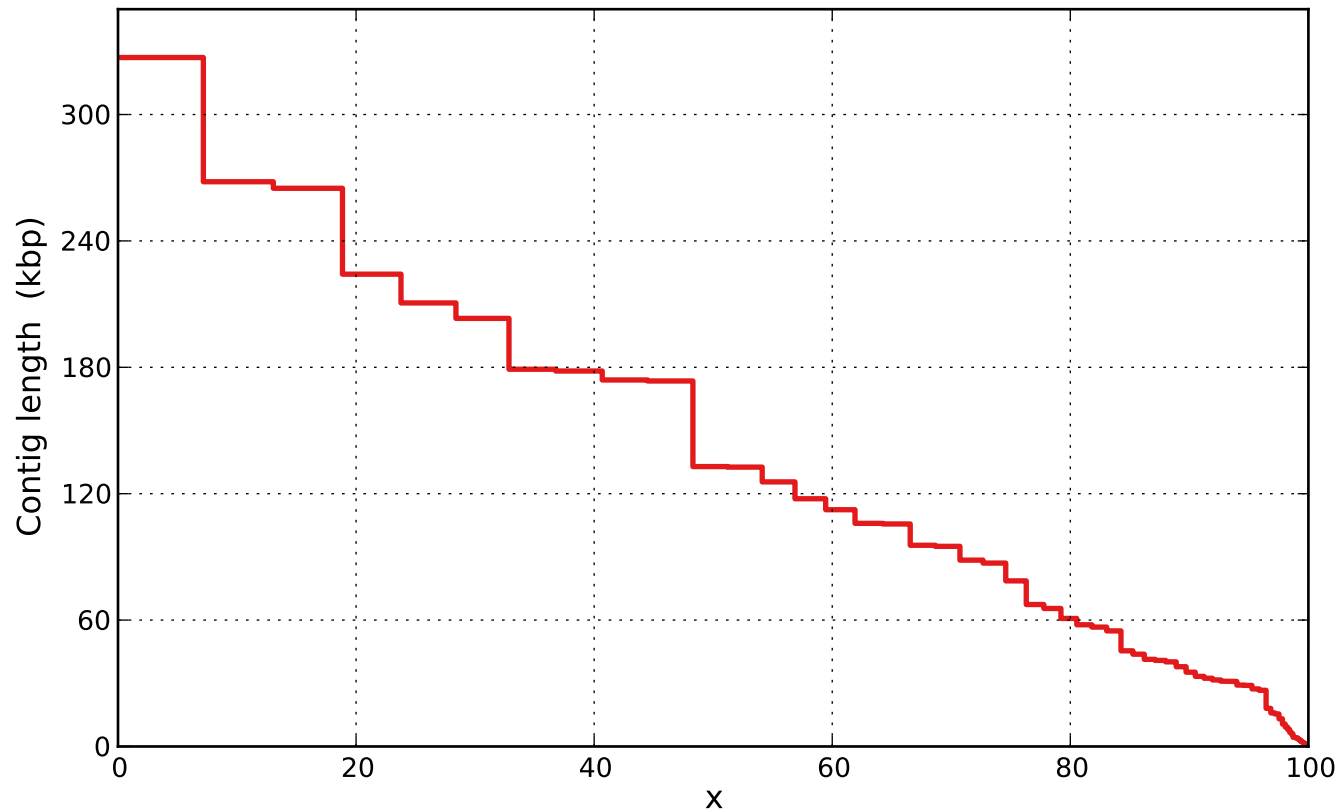
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

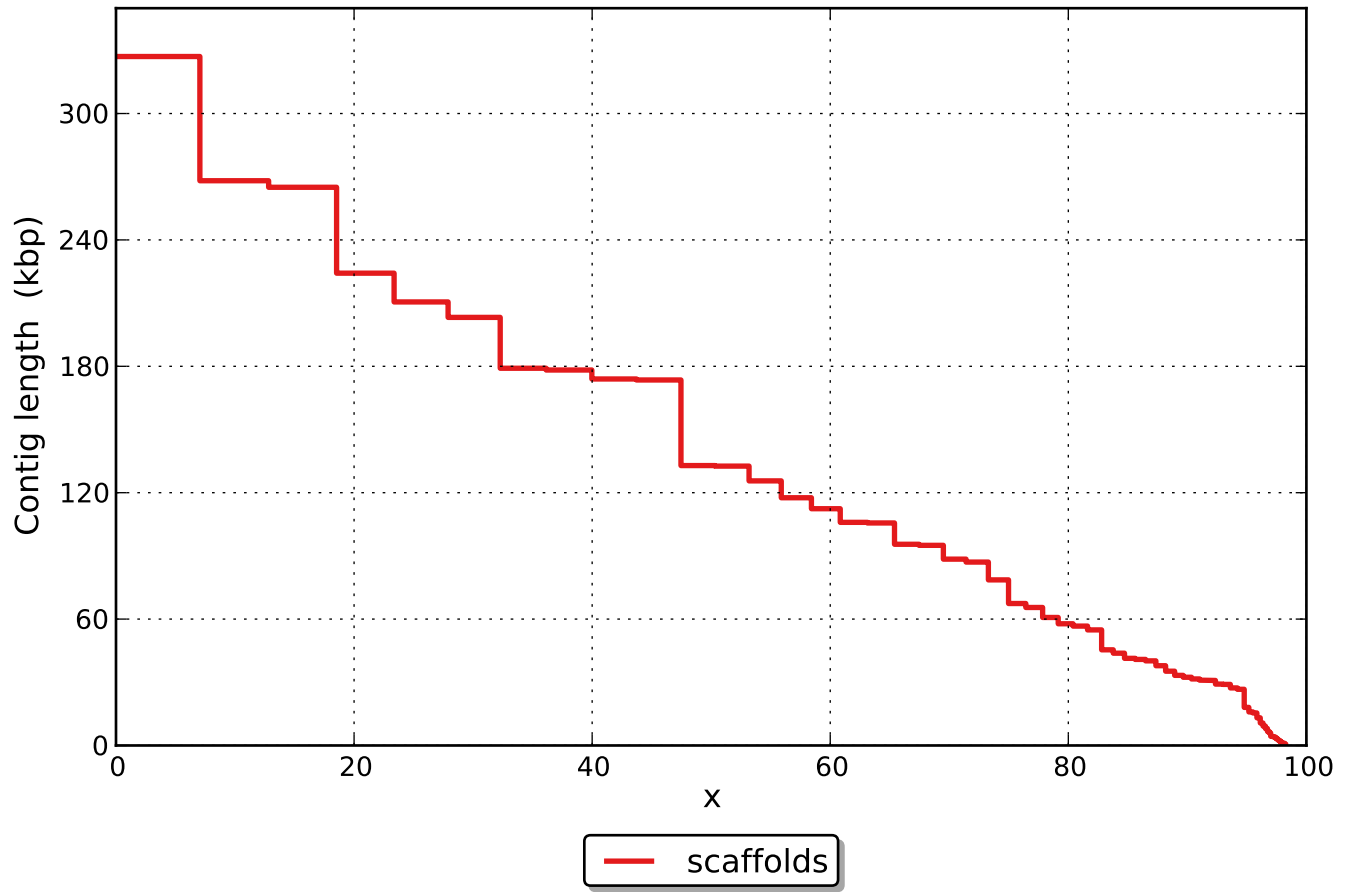
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

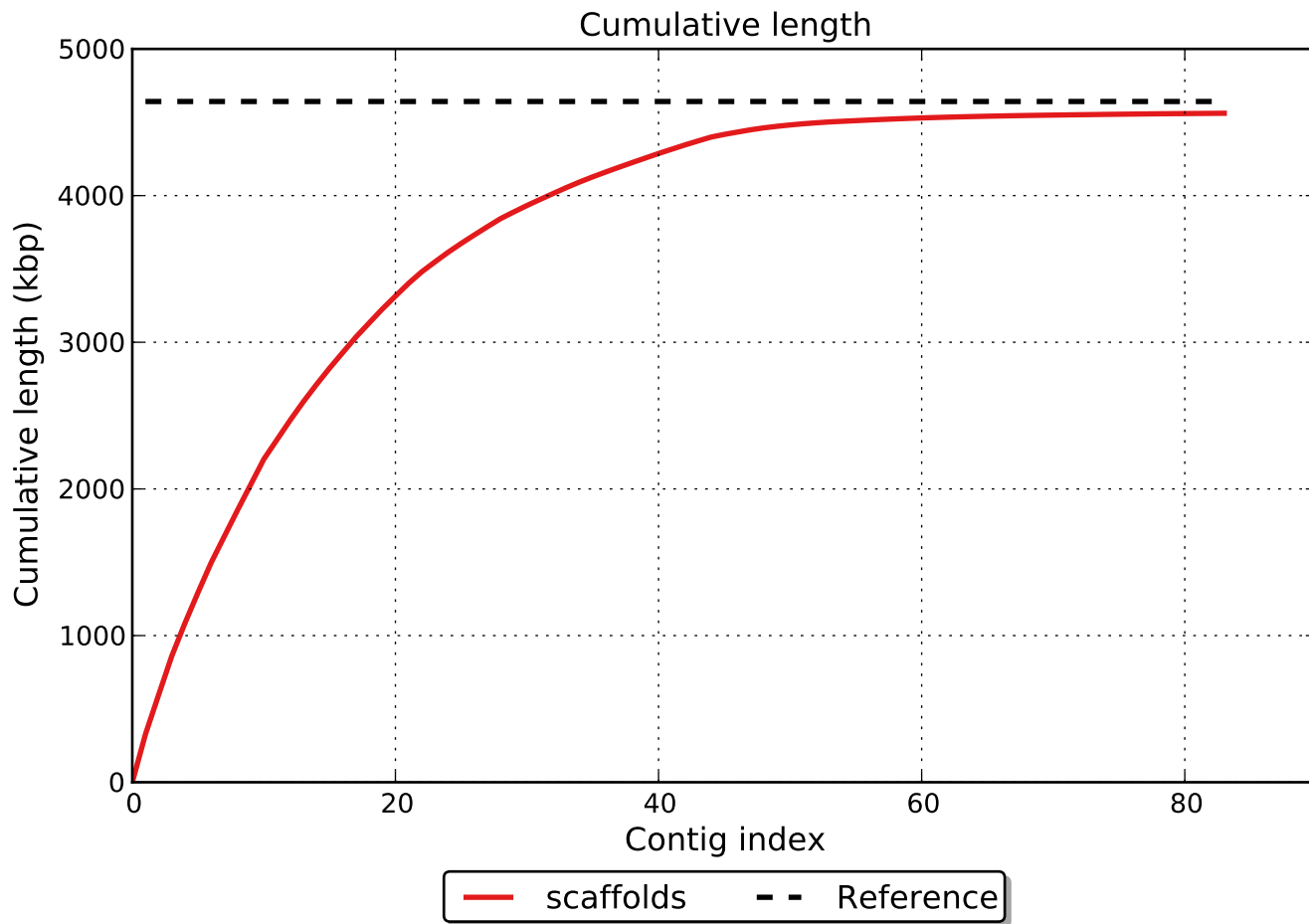
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

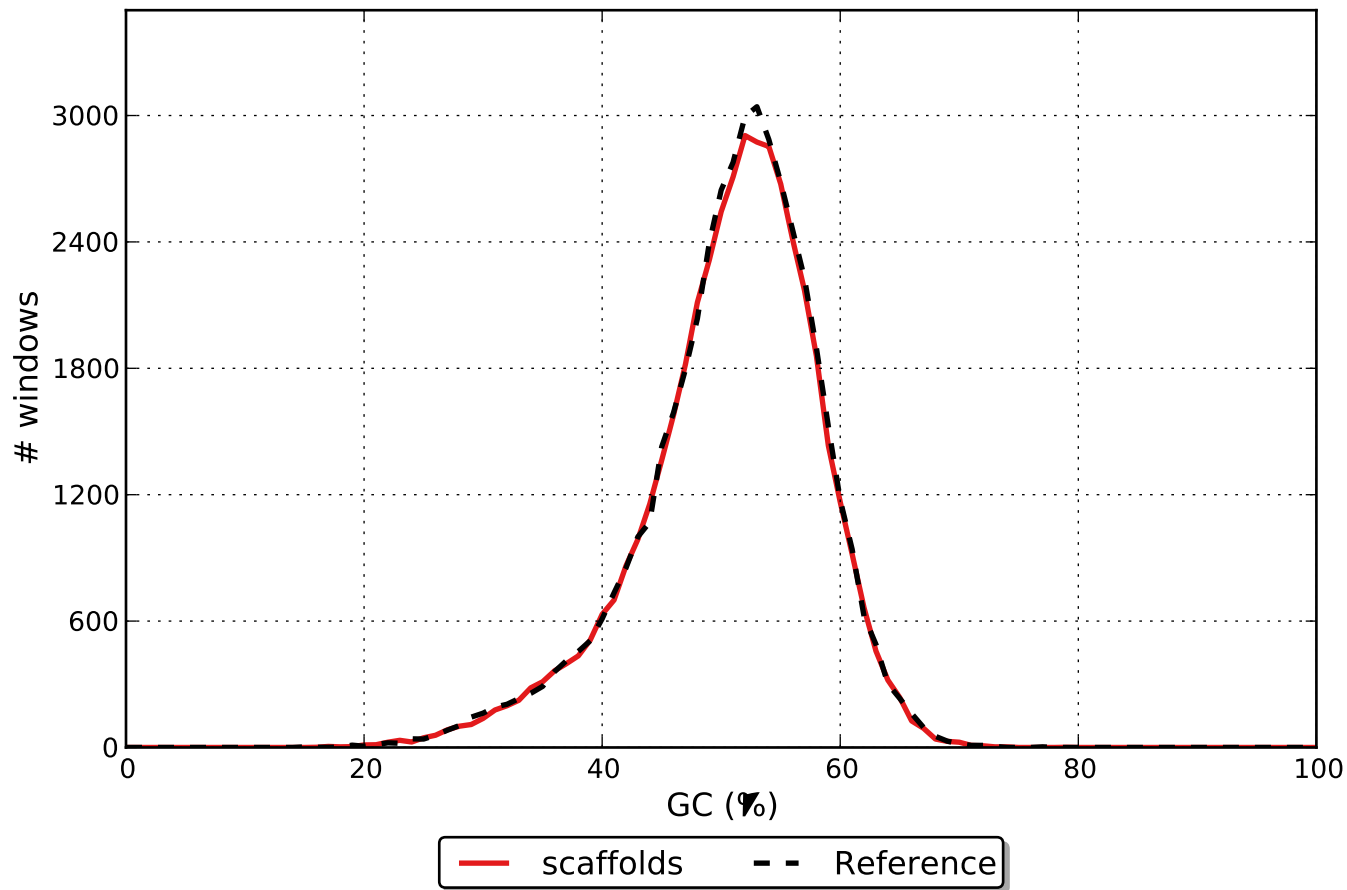


NGx

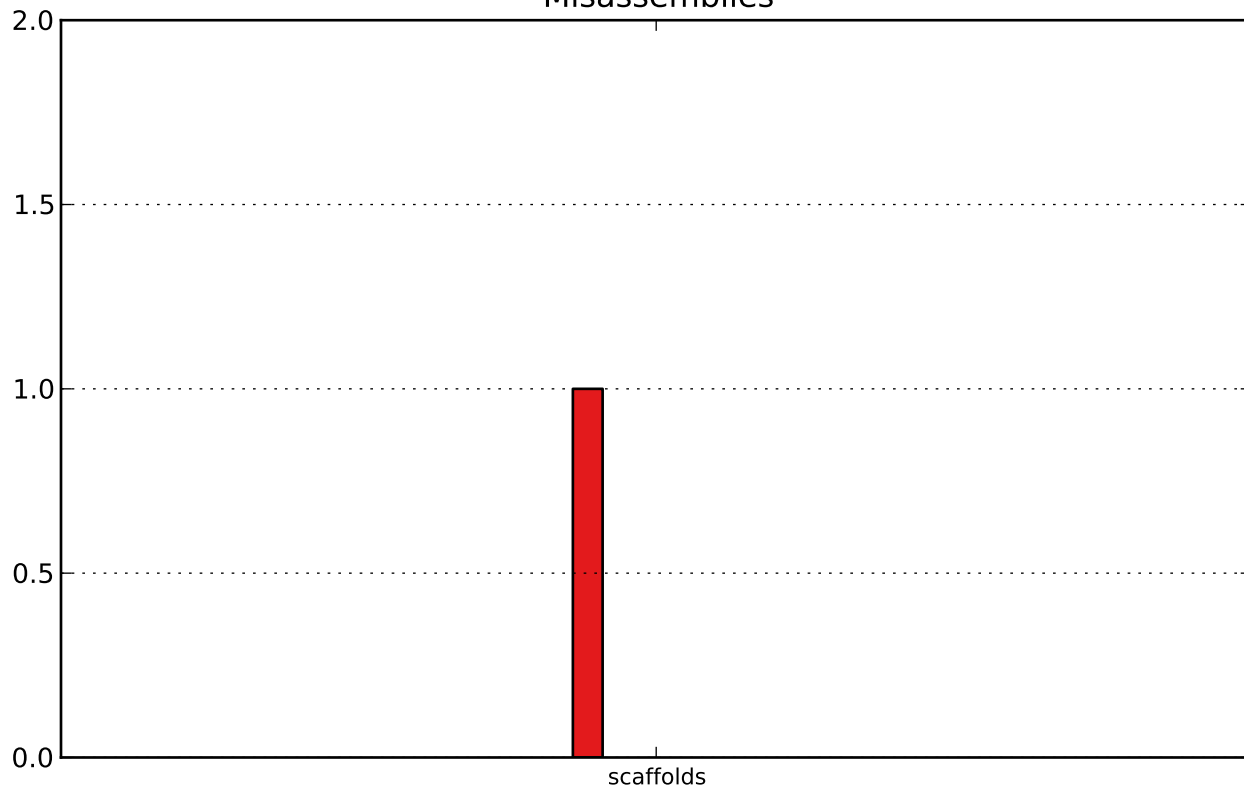




GC content

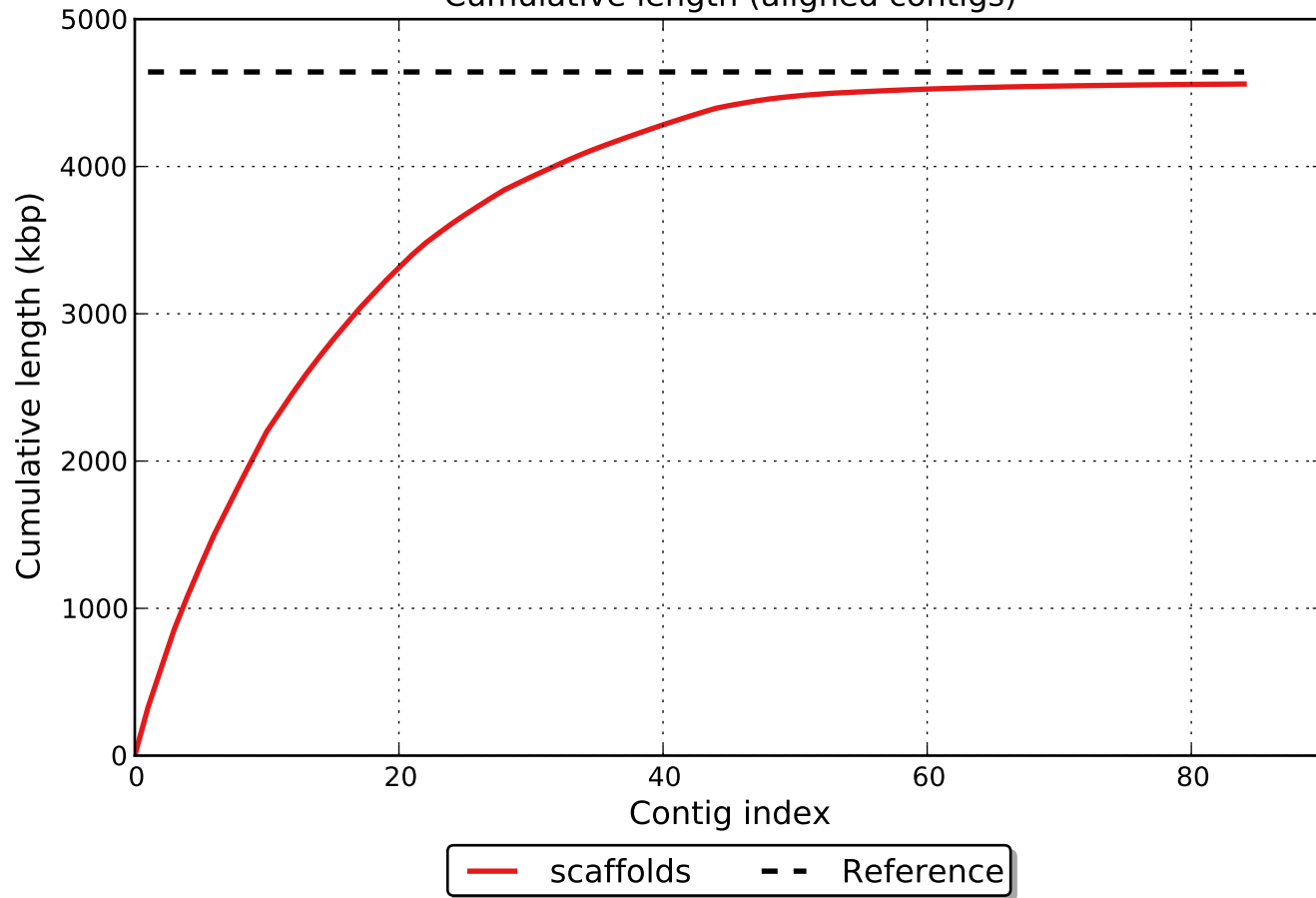


Misassemblies

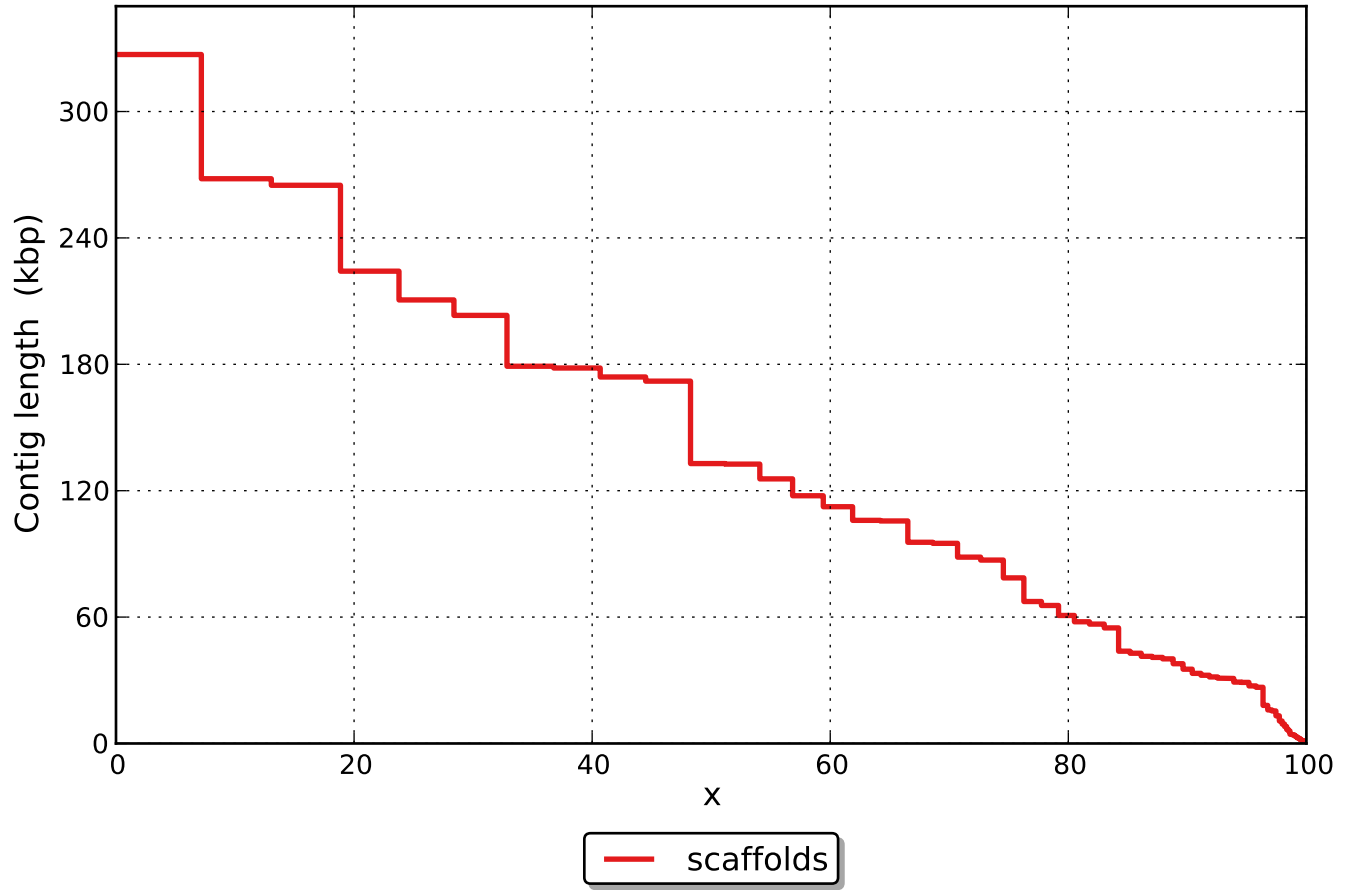


relocations

Cumulative length (aligned contigs)



NAx



NGAx

