

Report

	scaffolds
# contigs (≥ 1000 bp)	53
# contigs (≥ 5000 bp)	48
# contigs (≥ 10000 bp)	45
# contigs (≥ 25000 bp)	40
# contigs (≥ 50000 bp)	27
Total length (≥ 1000 bp)	5119888
Total length (≥ 5000 bp)	5108486
Total length (≥ 10000 bp)	5085853
Total length (≥ 25000 bp)	5011374
Total length (≥ 50000 bp)	4569212
# contigs	62
Largest contig	768359
Total length	5126269
Reference length	4641652
GC (%)	50.65
Reference GC (%)	50.79
N50	176518
NG50	197282
N75	98460
NG75	122555
L50	9
LG50	8
L75	18
LG75	15
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	36059
# local misassemblies	2
# unaligned contigs	0 + 1 part
Unaligned length	585677
Genome fraction (%)	97.557
Duplication ratio	1.003
# N's per 100 kbp	0.33
# mismatches per 100 kbp	197.76
# indels per 100 kbp	0.57
Largest alignment	333124
NA50	153712
NGA50	164567
NA75	67394
NGA75	88487
LA50	12
LGA50	11
LA75	25
LGA75	20

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	1
# misassembled contigs	1
Misassembled contigs length	36059
# local misassemblies	2
# mismatches	8955
# indels	26
# short indels	26
# long indels	0
Indels length	30

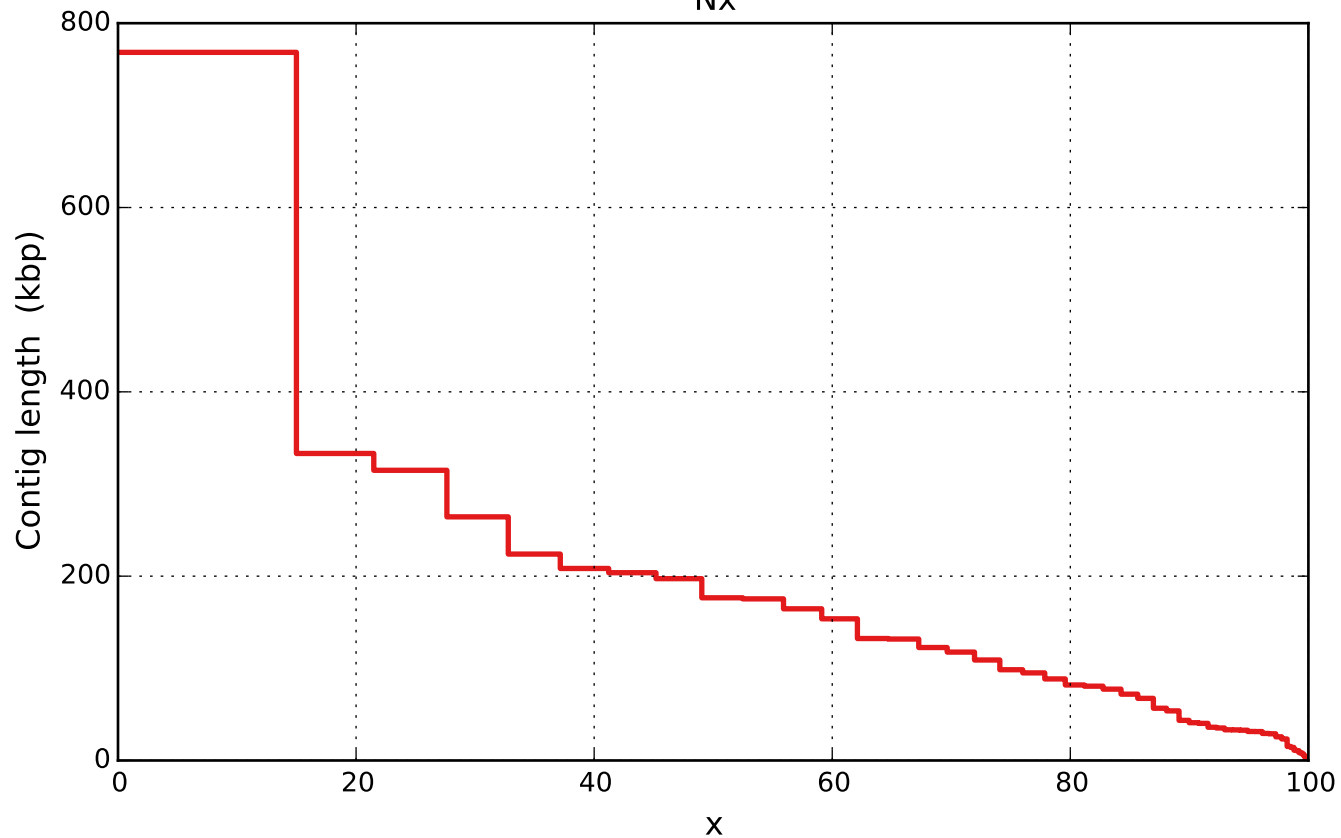
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	1
# both parts are significant	1
Partially unaligned length	585677
# N's	17

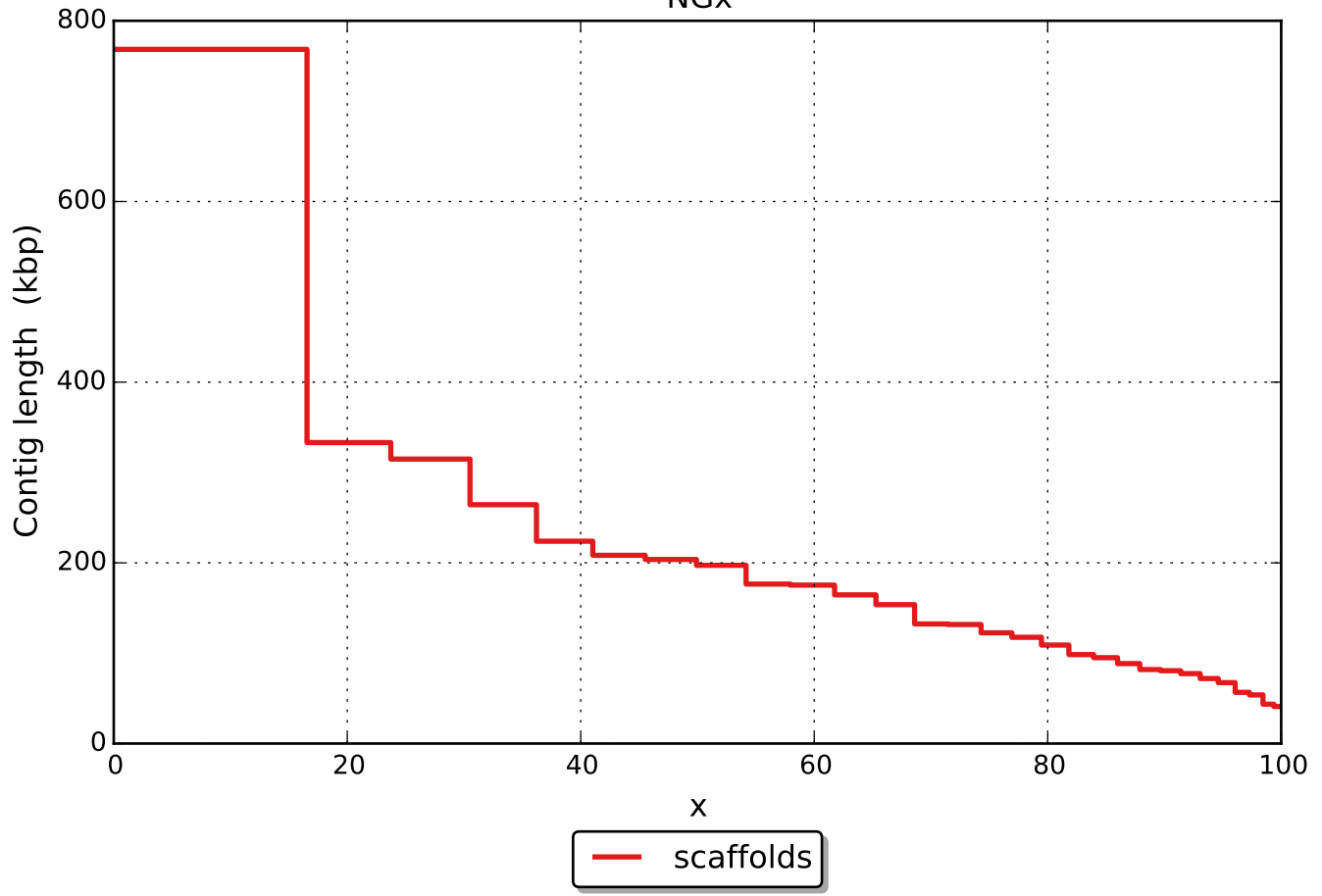
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

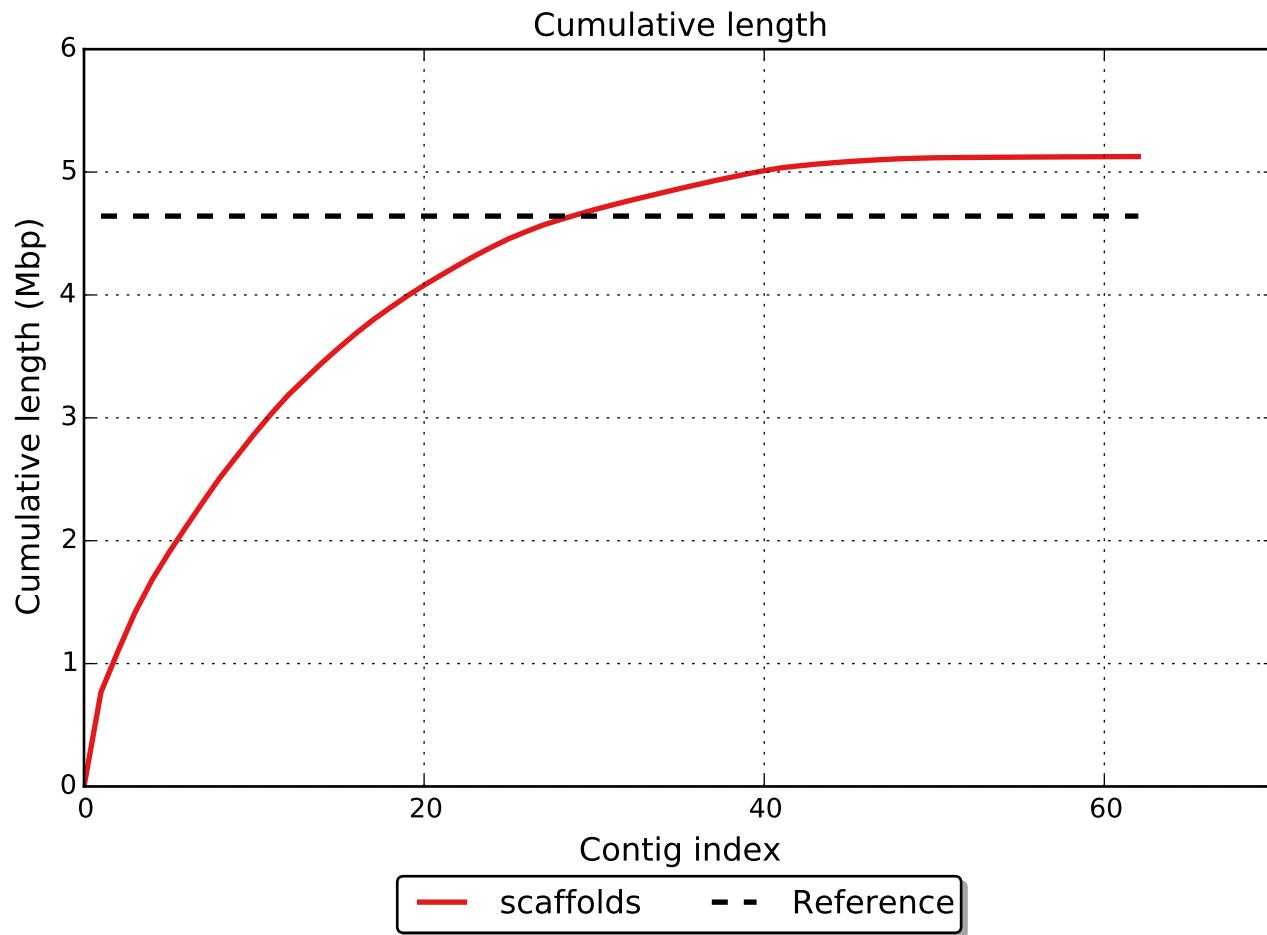
Nx



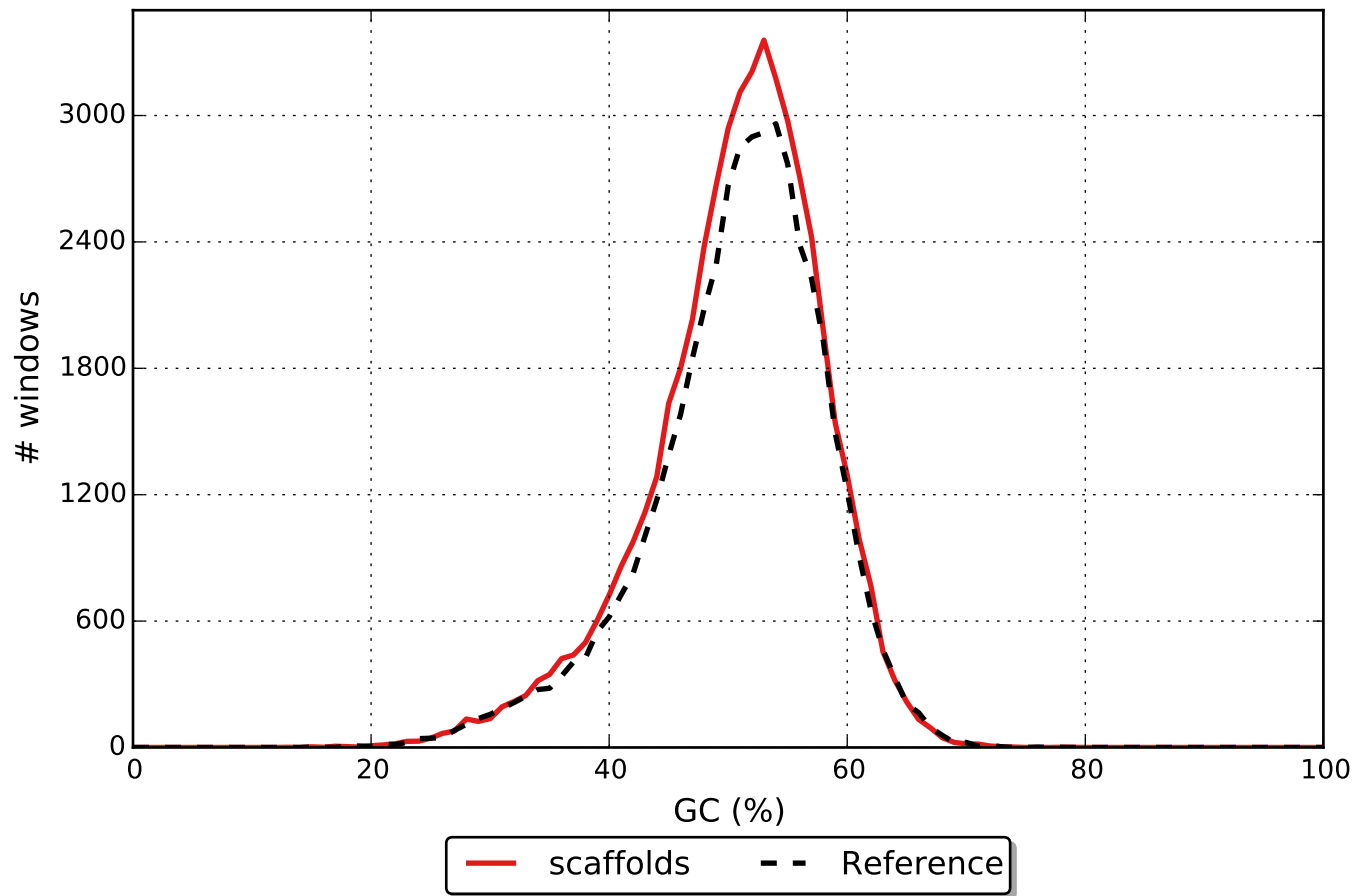
scaffolds

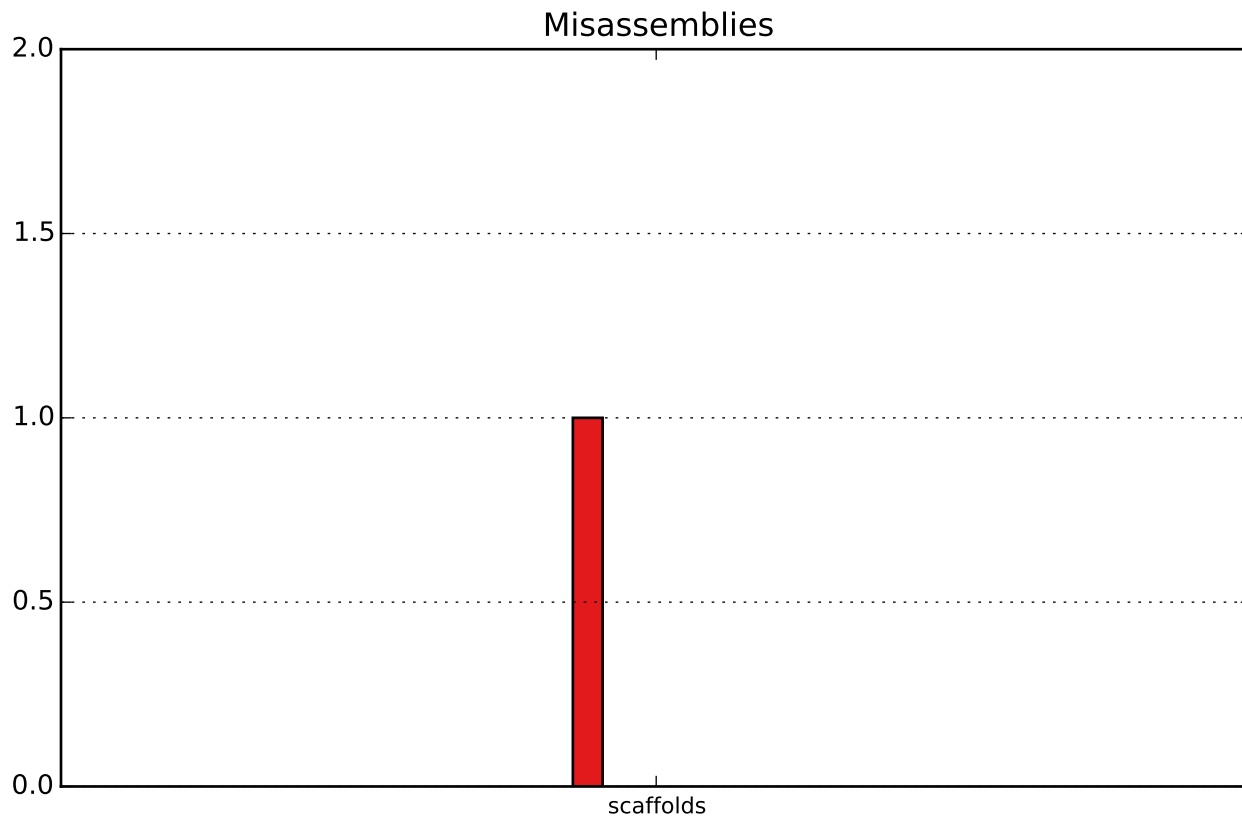
NGx



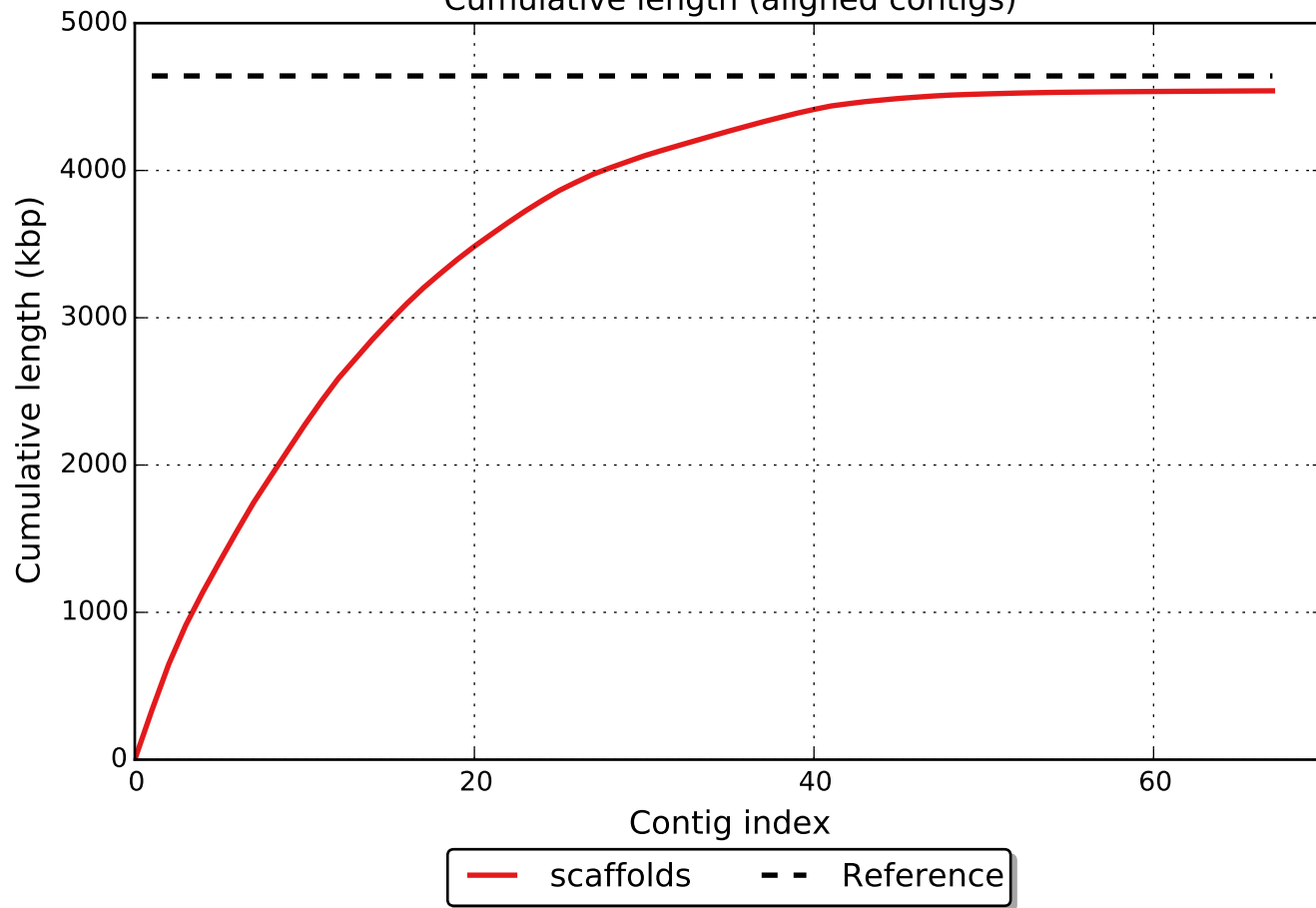


GC content

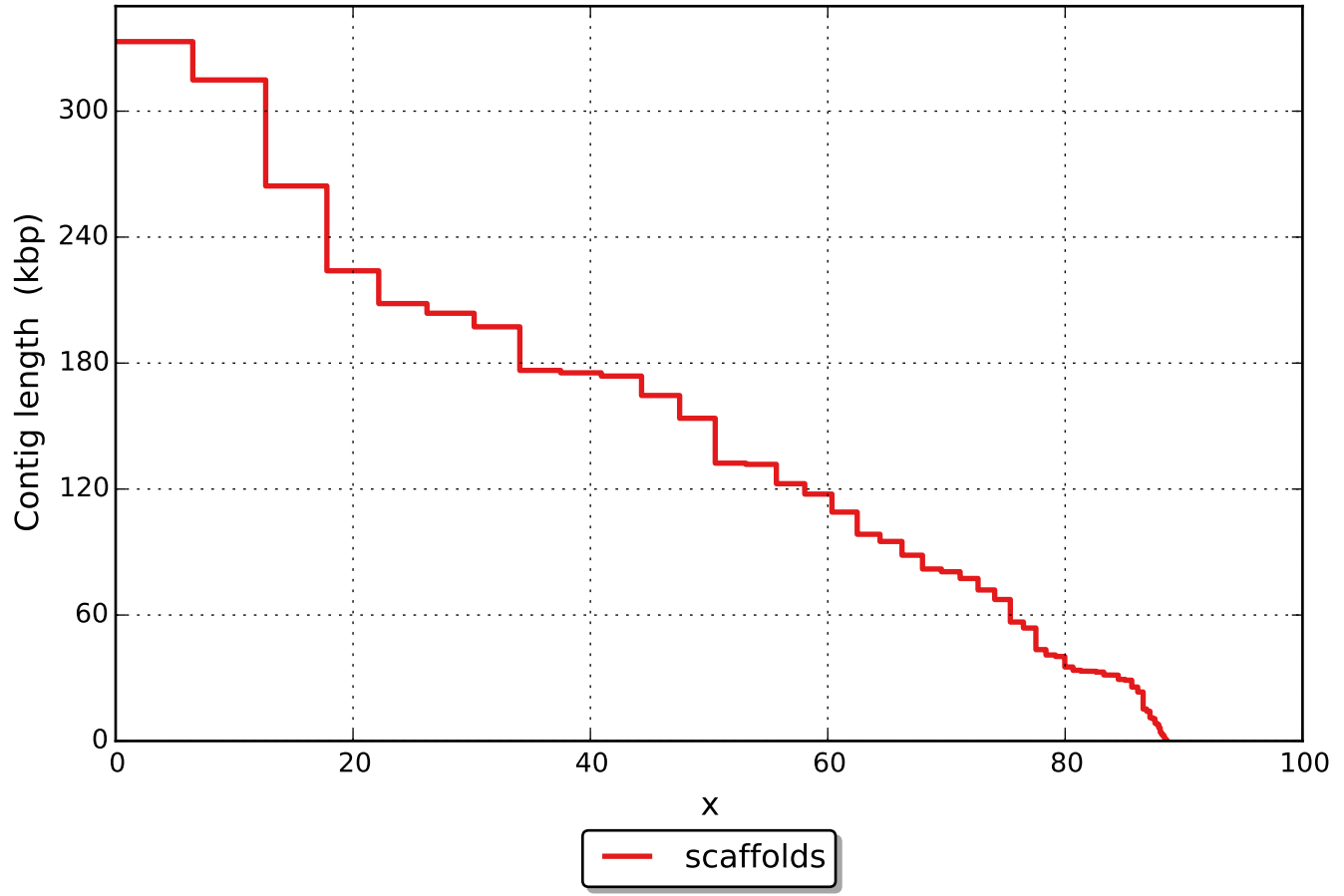




Cumulative length (aligned contigs)



NAx



NGAx

