

Report

	scaffolds
# contigs (≥ 1000 bp)	54
# contigs (≥ 5000 bp)	44
# contigs (≥ 10000 bp)	44
# contigs (≥ 25000 bp)	38
# contigs (≥ 50000 bp)	33
Total length (≥ 1000 bp)	4744744
Total length (≥ 5000 bp)	4722723
Total length (≥ 10000 bp)	4722723
Total length (≥ 25000 bp)	4634350
Total length (≥ 50000 bp)	4474495
# contigs	71
Largest contig	300358
Total length	4755788
Reference length	4641652
GC (%)	50.85
Reference GC (%)	50.79
N50	167276
NG50	167276
N75	92493
NG75	104699
L50	11
LG50	11
L75	20
LG75	19
# misassemblies	20
# misassembled contigs	1
Misassembled contigs length	210680
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.908
Duplication ratio	1.046
# N's per 100 kbp	0.00
# mismatches per 100 kbp	783.29
# indels per 100 kbp	1.10
Largest alignment	300358
NA50	159904
NGA50	159904
NA75	79751
NGA75	87060
LA50	11
LGA50	11
LA75	22
LGA75	21

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	20
# relocations	18
# translocations	0
# inversions	2
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	210680
# local misassemblies	2
# mismatches	35597
# indels	50
# short indels	49
# long indels	1
Indels length	58

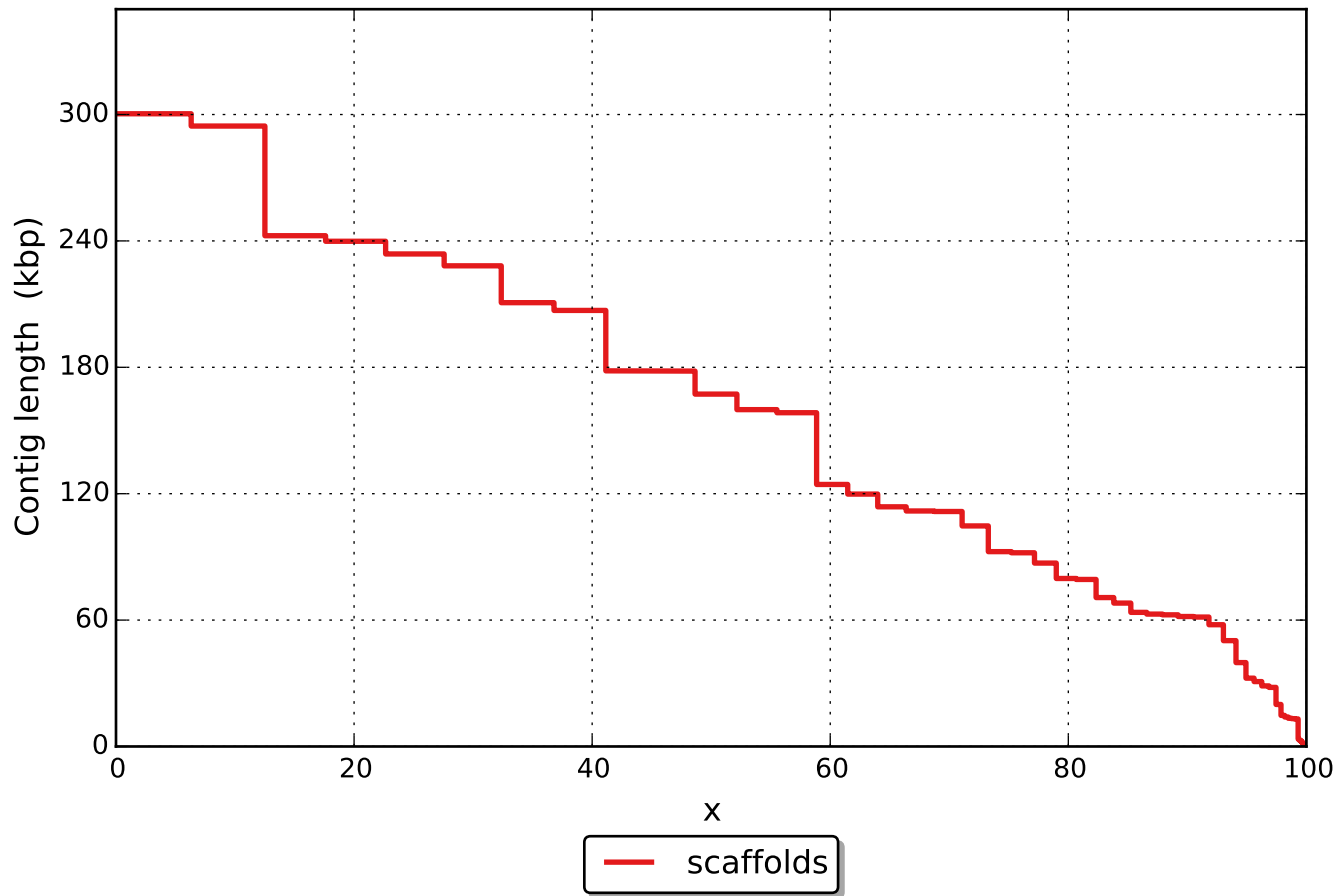
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

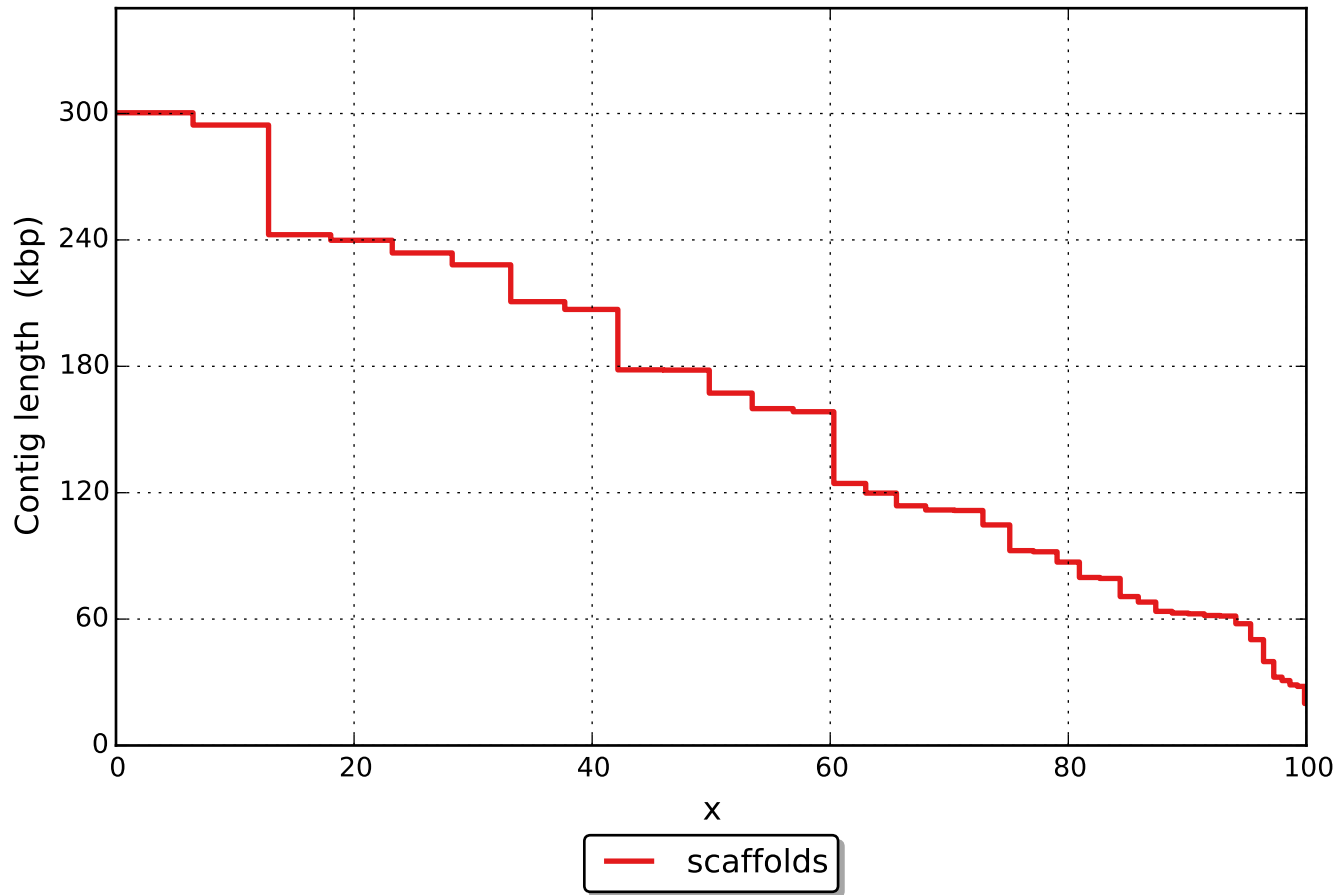
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

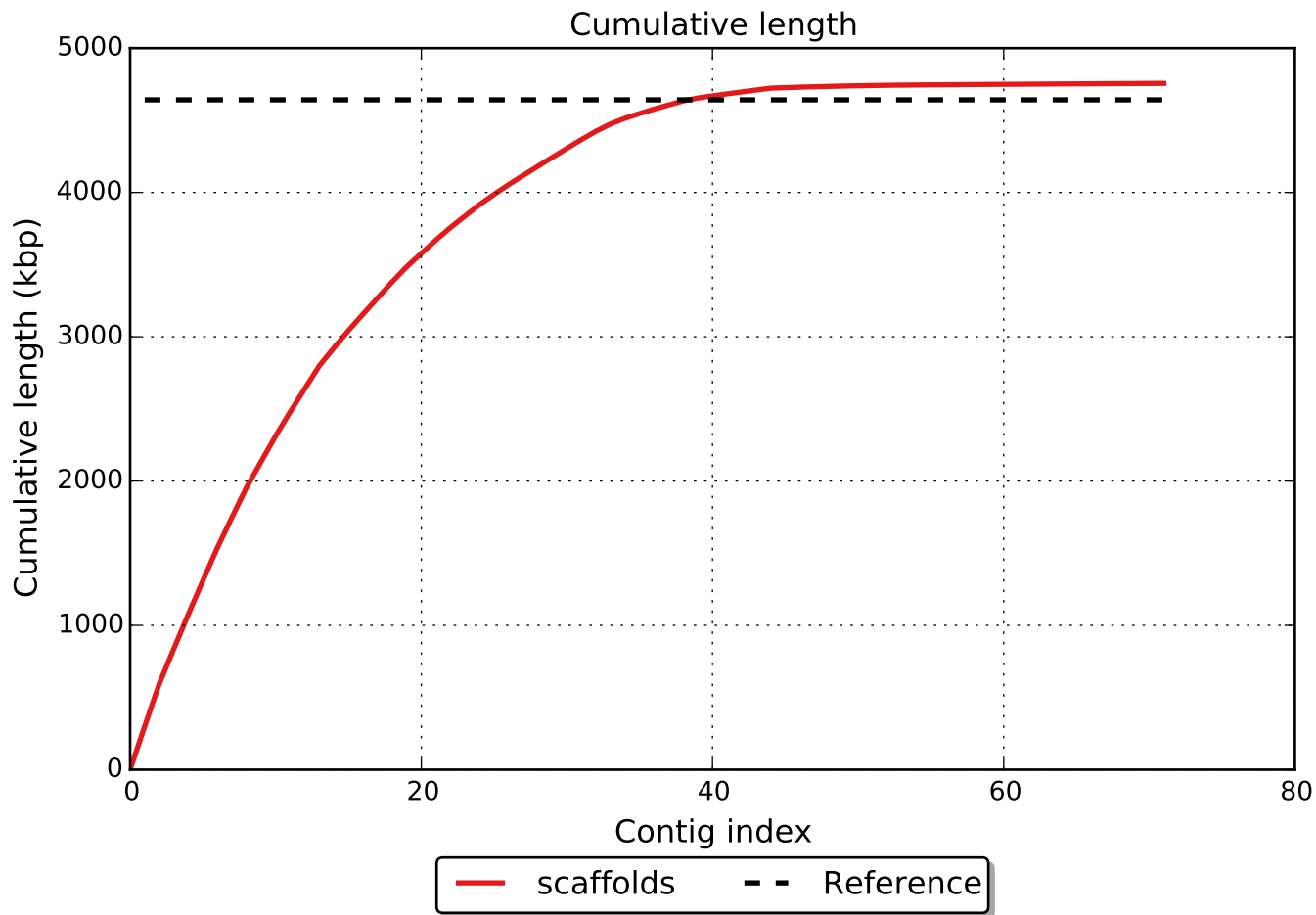
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

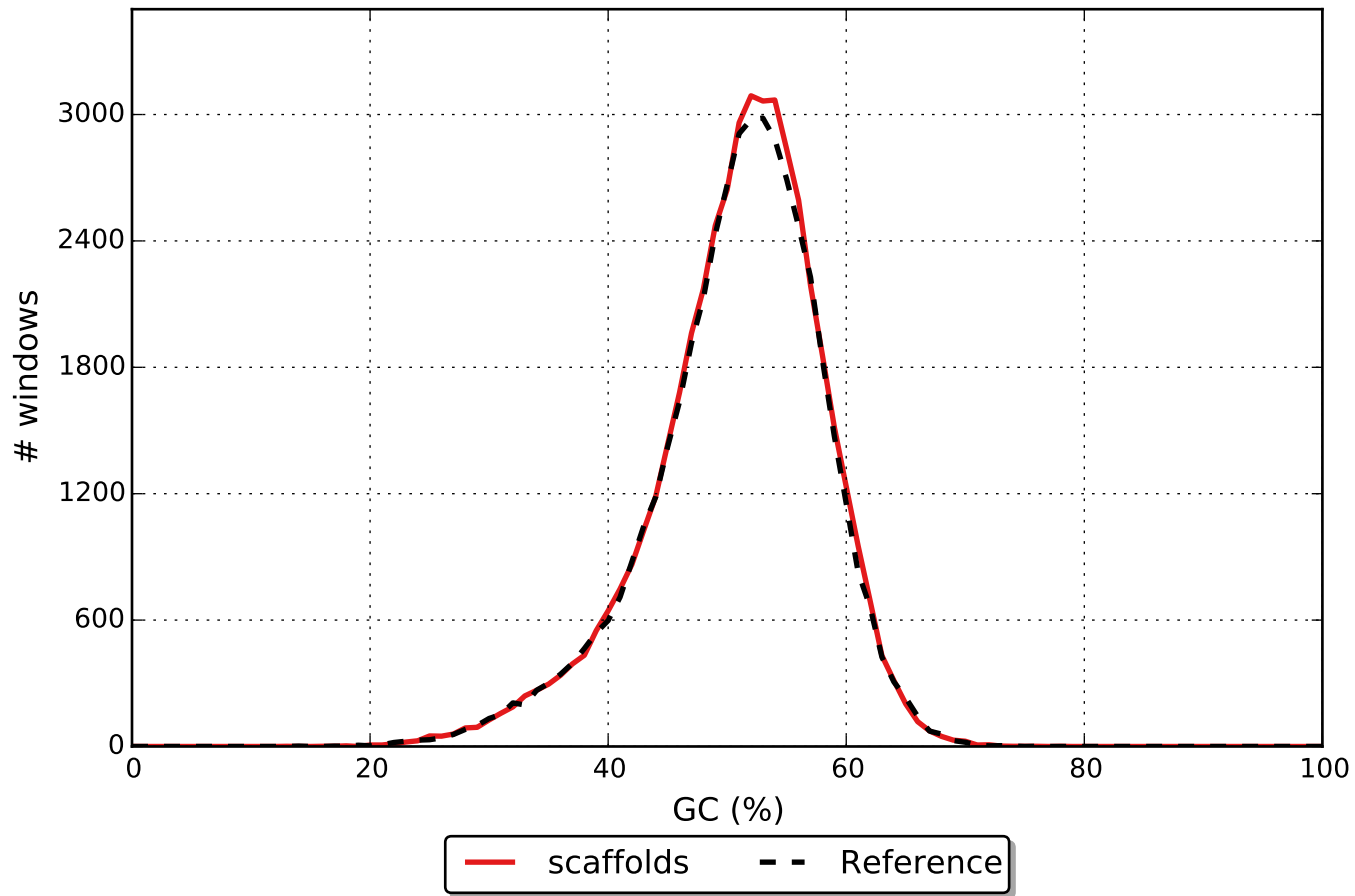


NGx

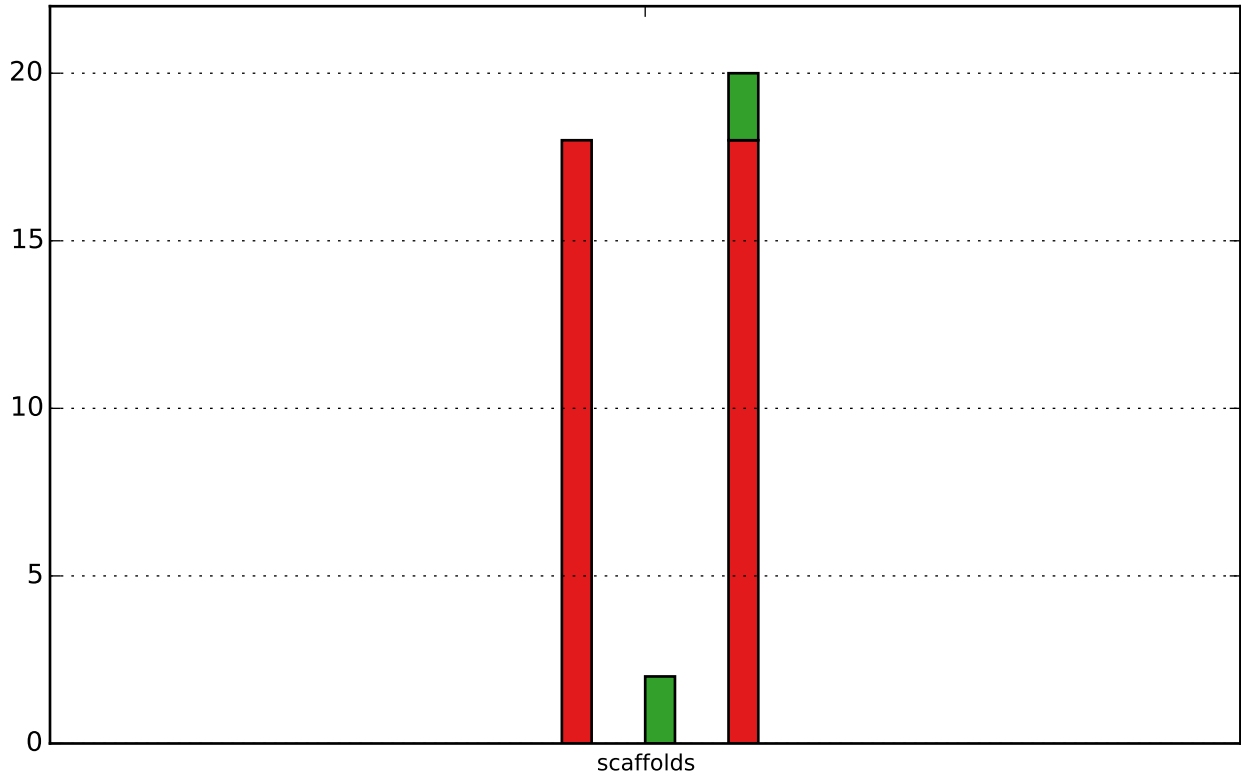




GC content



Misassemblies

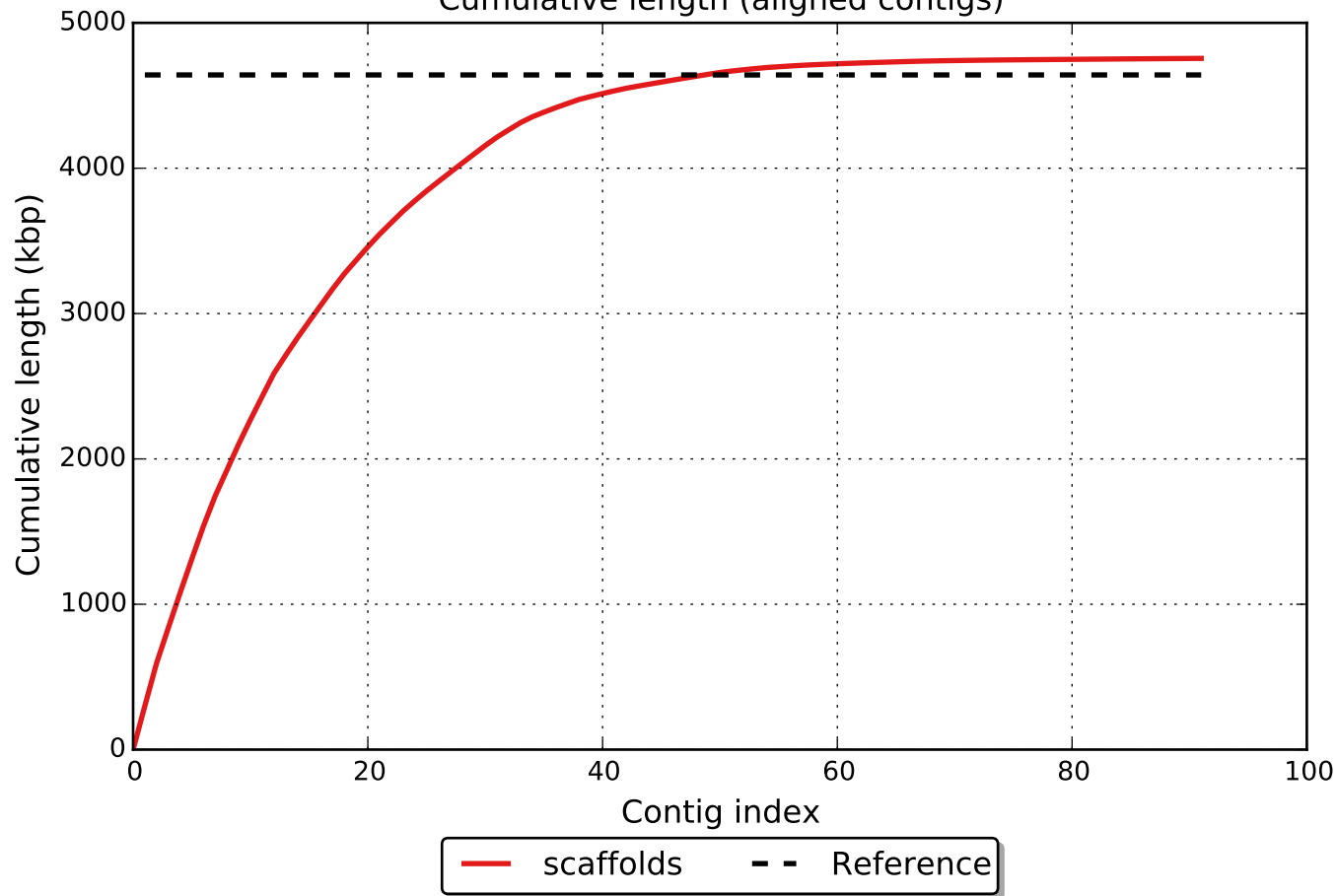


relocations

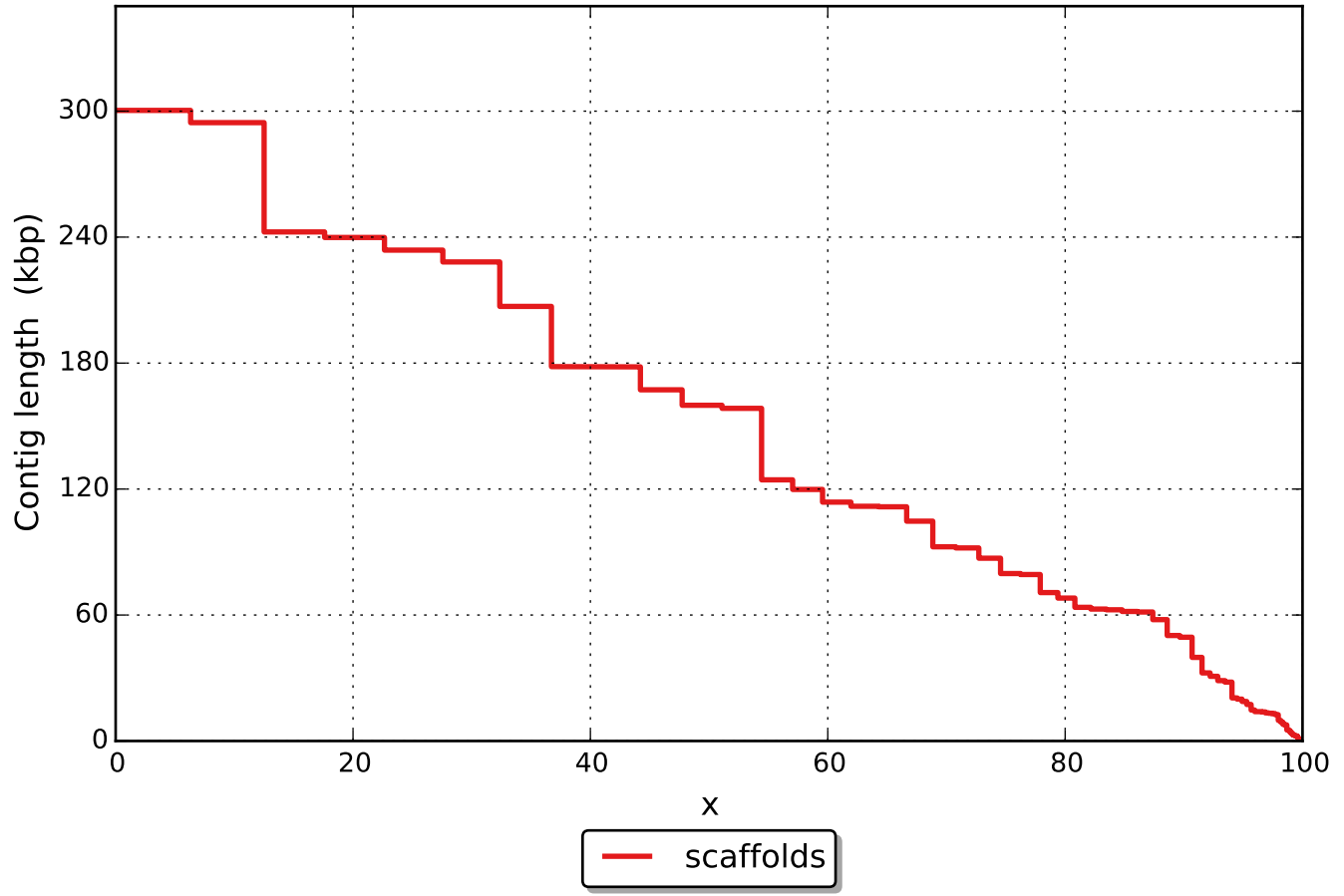


inversions

Cumulative length (aligned contigs)



NAx



NGAx

