

## Report

	scaffolds
# contigs ( $\geq 1000$ bp)	220
# contigs ( $\geq 5000$ bp)	156
# contigs ( $\geq 10000$ bp)	127
# contigs ( $\geq 25000$ bp)	84
# contigs ( $\geq 50000$ bp)	52
Total length ( $\geq 1000$ bp)	7814423
Total length ( $\geq 5000$ bp)	7652012
Total length ( $\geq 10000$ bp)	7445873
Total length ( $\geq 25000$ bp)	6706003
Total length ( $\geq 50000$ bp)	5605771
# contigs	253
Largest contig	347033
Total length	7835760
Reference length	4641652
GC (%)	50.79
Reference GC (%)	50.78
N50	85464
NG50	160093
N75	42882
NG75	96059
L50	25
LG50	11
L75	58
LG75	20
# misassemblies	156
# misassembled contigs	39
Misassembled contigs length	3025443
# local misassemblies	4
# unaligned contigs	0 + 1 part
Unaligned length	76
Genome fraction (%)	98.423
Duplication ratio	1.715
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1301.27
# indels per 100 kbp	1.12
Largest alignment	347033
NA50	50928
NGA50	80338
NA75	21487
NGA75	54973
LA50	43
LGA50	16
LA75	106
LGA75	34

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).

## Misassemblies report

	scaffolds
# misassemblies	156
# relocations	135
# translocations	0
# inversions	21
# possibly misassembled contigs	1
# misassembled contigs	39
Misassembled contigs length	3025443
# local misassemblies	4
# mismatches	59448
# indels	51
# short indels	51
# long indels	0
Indels length	59

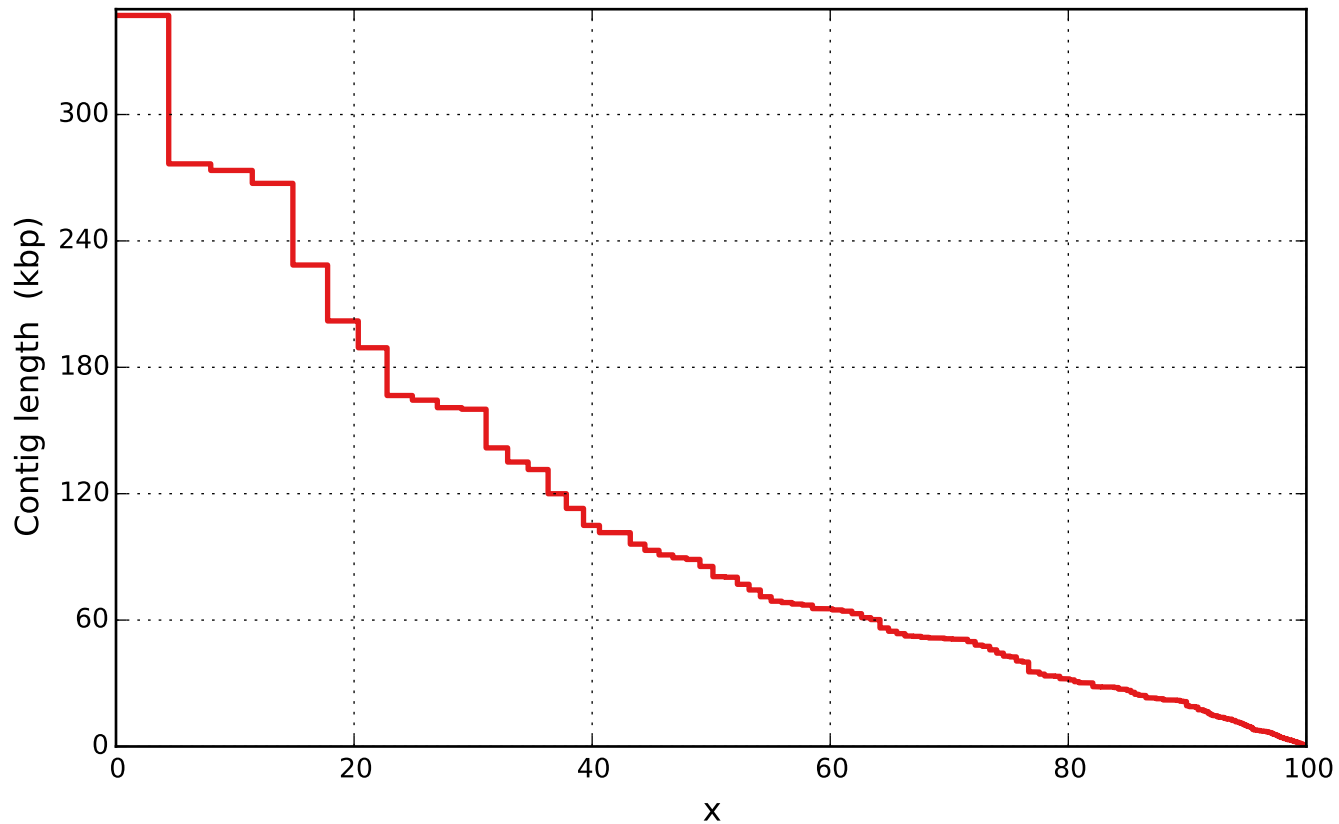
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

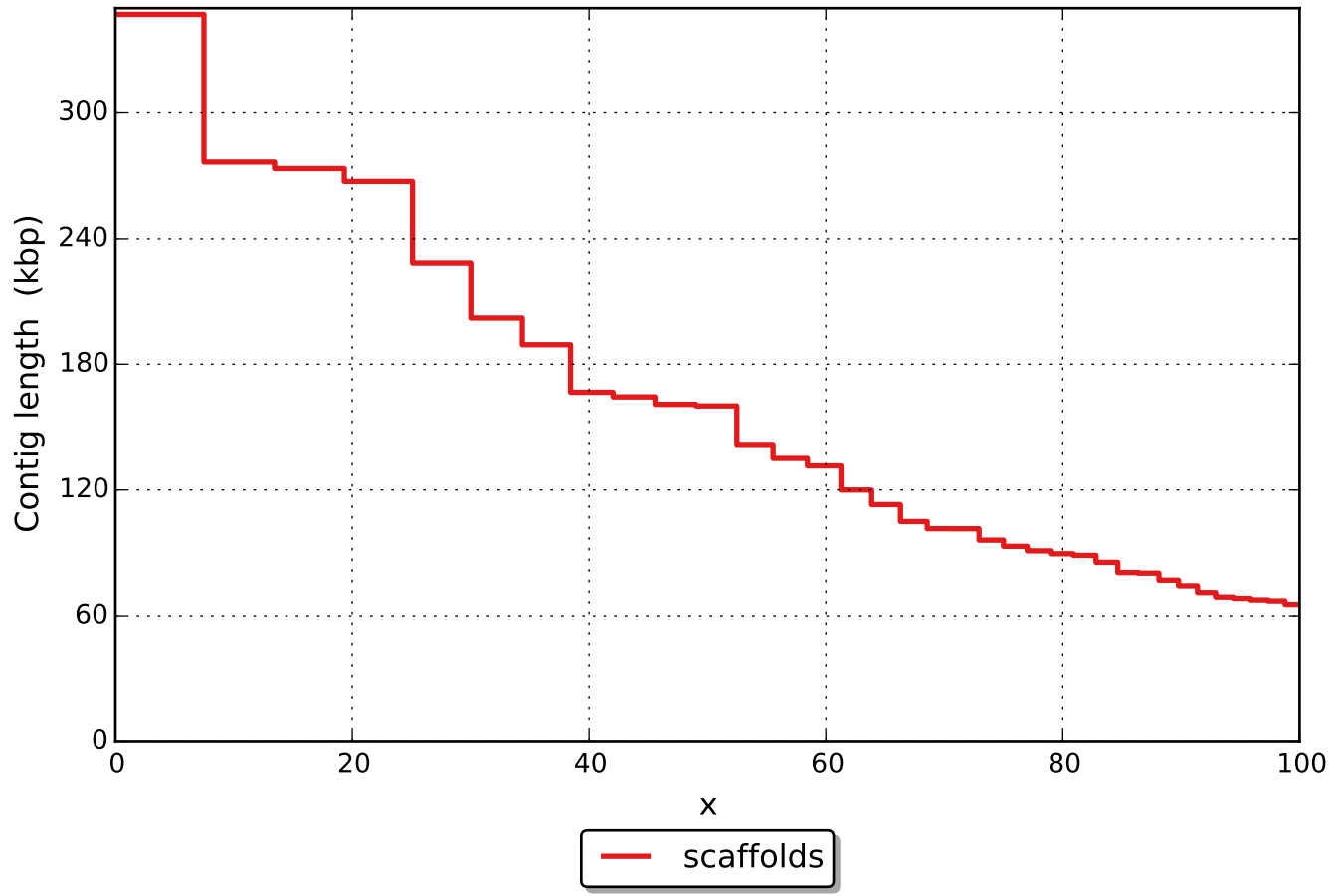
	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	76
# N's	0

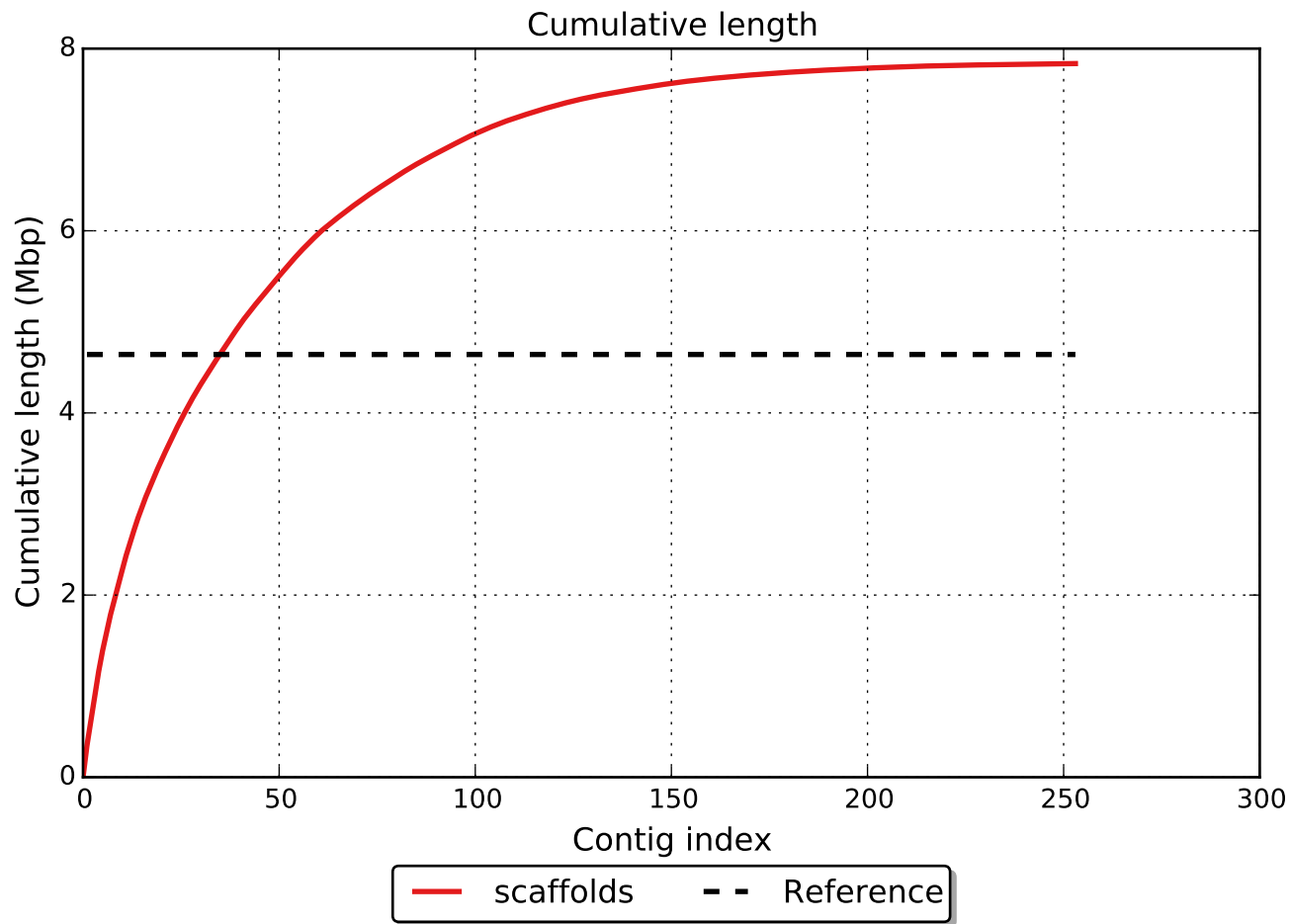
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

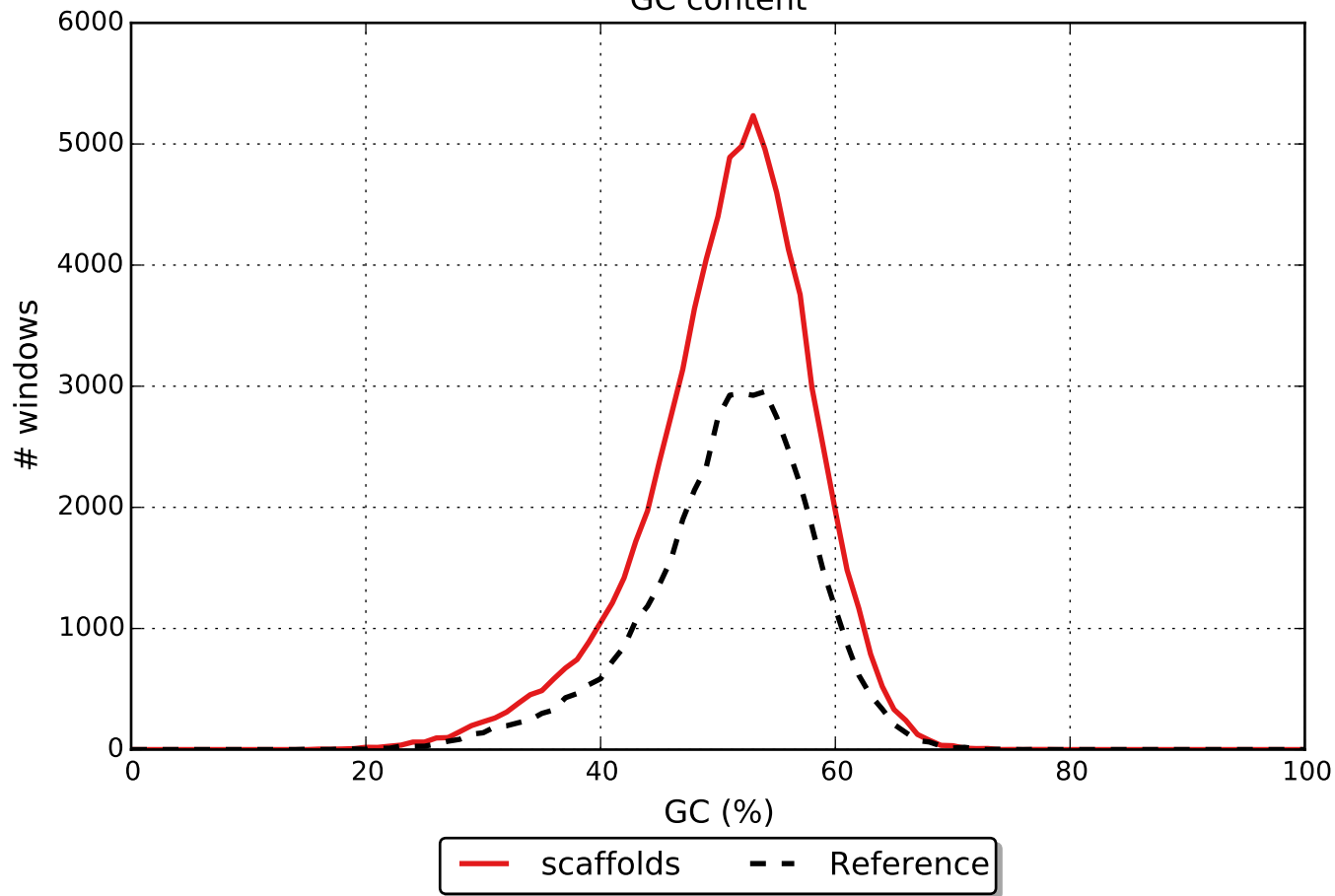


NGx

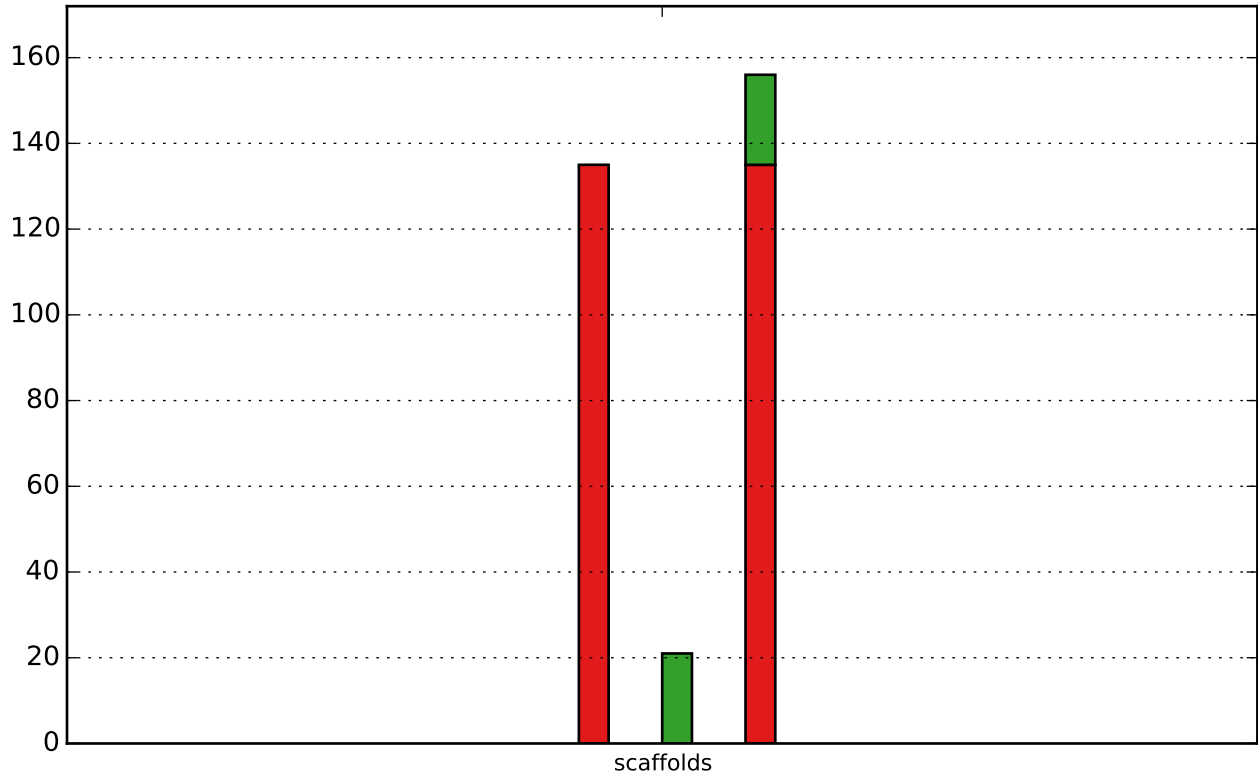




# GC content



# Misassemblies

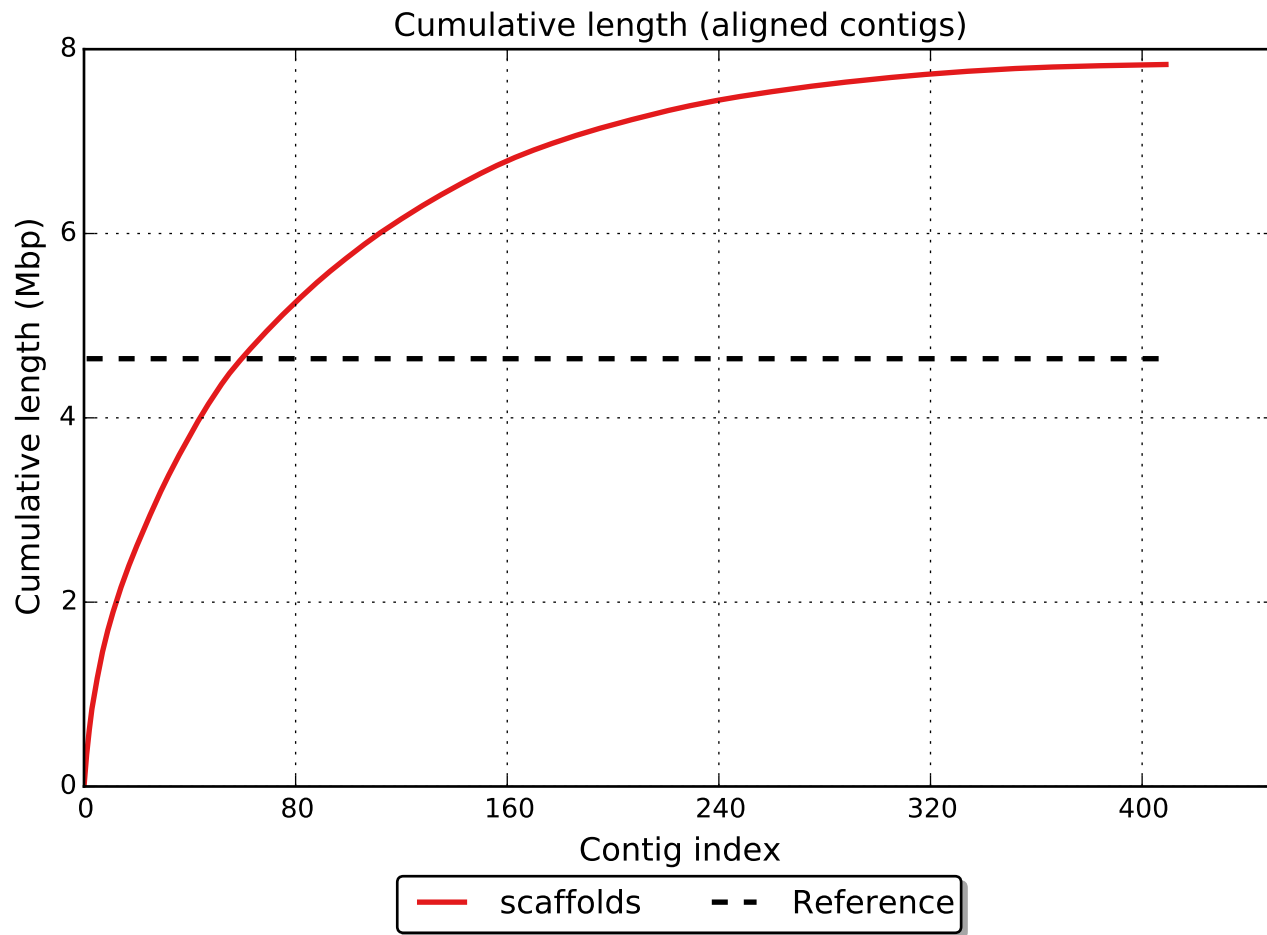


# relocations

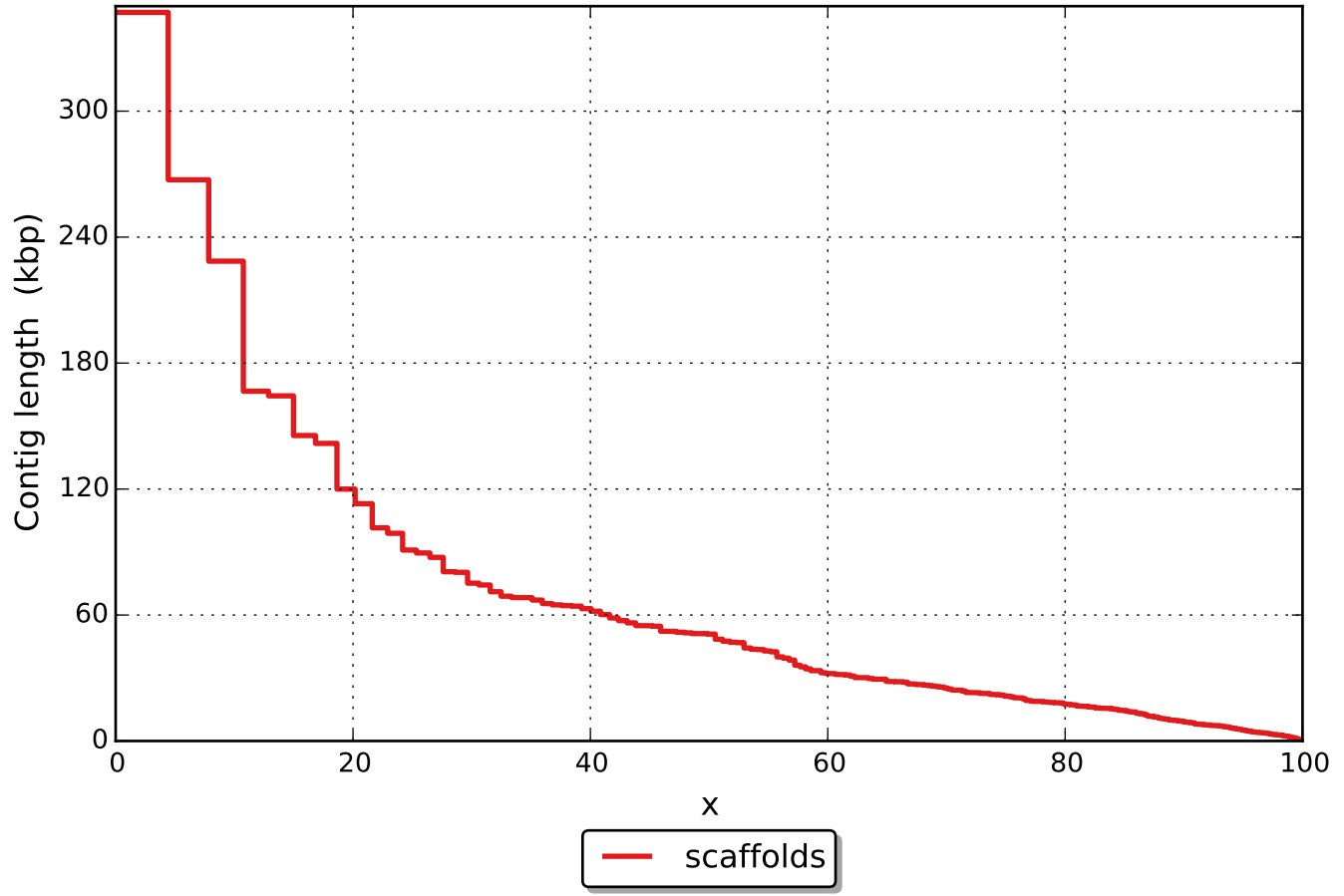


# inversions





NAx



# NGAx

